	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
1	**hypoxia 14-03-03**														
2		thresholds: alignment. 0.25bp. assignment: 0.6bp. variation: 0.45. two ends: 0.25bp													**/**: increased
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
5	Hha1	49	aaa	120.76	121	120.94	120.51	120.83	29 100 000	24 500 000	7 000 000	=-	\ (-)		\(3) -(2) /(2)
6	Hha1	49	aaa	121.435	121	0	121.62	121.25	0	3 300 000	5 800 000	+=	/		\(3) -(2) /(2)
7	Hha1	54	ttt	121.03	121	121.1	121.03	120.96	10 700 000	12 400 000	3 000 000	=-	\ (-)		\(3) -(2) /(2)
8	Taq1	61	tct	143.72	144	143.51	0	143.93	3 100 000	0	11 900 000	=+(+)	/		\(3) -(2) /(2)
9	Taq1	61	tct	144.21	144	144.21	0	0	3 900 000	0	0	-=	\		\(3) -(2) /(2)
10	Taq1	31	gac	131.425	132	131.49	131.36	0	4 800 000	12 200 000	0	+-	A		A(2) \(2)
11	Taq1	31	gac	132.45	132	132.57	132.33	0	14 200 000	8 500 000	0	=-	\		A(2) \(2)
12	Taq1	36	ggt	131.78	132	131.74	131.82	0	12 300 000	28 700 000	0	+-	A		A(2) \(2)
13	Taq1	36	ggt	132.707	132	132.69	132.69	132.74	26 200 000	38 000 000	7 200 000	=-	\ (-)		A(2) \(2)
14	Hha1	59	ttc	100.097	100	99.97	100.31	100.01	171.6	494.42	952.06	=+	/ (-)	(-)	-1
15	Hha1	60	ttg	100.313	100	100.23	100.48	100.23	6 800 000	10 000 000	5 700 000	==	-	(-)	-1
16	Hha1	60	ttg	123.78	124	123.63	123.93	0	9 700 000	4 500 000	0	--	\		-1
17	Hha1	60	ttg	124.64	124	0	124.88	124.4	0	4 200 000	3 300 000	+=	/		-1
18	Taq1	62	tgt	156.85	157	156.83	156.89	156.83	5 200 000	8 800 000	5 100 000	==	-	(-)	
19	Taq1	64	gtt	156.947	157	156.99	156.98	156.87	6 700 000	9 500 000	4 000 000	=-	\ (-)	(-)	
20	Hha1	40	tgg	225.115	226	225.12	225.11	0	4 000 000	3 800 000	0	=-	\		\(2)
21	Hha1	40	tgg	225.76	226	0	225.76	0	0	6 500 000	0	+-	A		\(2)
22	Hha1	59	ttc	225.69	226	225.69	0	0	291.21	0	0	-=	\		\(2)
23	Hha1	59	ttc	226.85	226	226.85	0	0	265.21	0	0	-=	\		\(2)
24	Taq1	55	tca	75.61	76	0	75.61	0	0	6 000 000	0	+-	A		/(2)
25	Taq1	55	tca	76.24	76	76.15	76.33	0	3 300 000	35 400 000	0	+-	A		/(2)
26	Hha1	28	tcg	186.66	187	0	0	186.66	0	0	3 500 000	=+	/		/(2)
27	Hha1	59	ttc	185.925	187	0	185.91	185.94	0	201.21	129.35	+=	/		/(2)
28	Hha1	59	ttc	187.103	187	187.21	187.11	186.99	566.82	413.93	108.65	=-	\ (-)		/(2)
29	Hha1	59	ttc	188.09	187	188.19	188.04	188.04	1 180.44	741.63	388.06	==	-		/(2)
30	Hha1	20	ctc	85.077	85	85.03	85.13	85.07	15 998.62	18 476.26	18 594.939	==	-		-2
31	Hha1	26	ctg	147.13	147	147.09	147.06	147.24	7 700 000	4 900 000	4 100 000	==	-		-2
32	Hha1	39	agg	97.095	97	97.23	0	96.96	329.91	0	309.24	-+(=)	V		\(3)
33	Taq1	39	agg	100.417	100	100.17	100.54	100.54	6 100 000	29 200 000	11 700 000	+-	A		\(3)
34	Taq1	39	agg	100.523	100	100.49	100.54	100.54	4 700 000	293.47	344.62	-=	\ (-)	\	\(3)
35	Taq1	39	agg	100.17	100	100.17	0	0	226.53	0	0	-=	\		\(3)
36	Taq1	39	agg	100.49	100	100.49	0	0	174.53	0	0	-=	\	\	\(3)
37	Taq1	56	tga	100.495	100	100.4	100.59	0	5 100 000	9 000 000	0	=-	\	\	\(3)
38	Taq1	56	tga	99.73	100	0	99.73	0	0	4 600 000	0	+-	A		\(3)
39	Hha1	49	aaa	125.425	126	0	125.52	125.33	0	3 900 000	4 000 000	+=	/		\(3)
40	Hha1	49	aaa	126.207	126	126.38	126.03	126.21	23 600 000	8 000 000	3 600 000	-=	\ (-)		\(3)
41	Taq1	8	gaa	85.95	86	85.95	0	0	48 300 000	0	0	-=	\	\	\(2)
42	Taq1	10	atg	85.8	86	85.8	85.8	0	9 900 000	16 200 000	0	=-	\	\	\(2)
43	Hha1	39	agg	97.095	97	97.23	0	96.96	329.91	0	309.24	-+(=)	V		\(3)
44	Taq1	39	agg	100.417	100	100.17	100.54	100.54	6 100 000	29 200 000	11 700 000	+-	A		\(3)
45	Taq1	39	agg	100.523	100	100.49	100.54	100.54	4 700 000	293.47	344.62	-=	\ (-)	\	\(3)

	P	Q	R	S	T	U	V
1							
2	, **=**: no change, ****: decreased, **A**: increased by mild, **V**: decreased by mild						
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
5	RN100KDP.PE1	nc	100 kDa protein		aaa	ttt	increased
6	RN100KDP.PE1	nc	100 kDa protein		aaa	ttt	increased
7	RN100KDP.PE1	nc	100 kDa protein		aaa	ttt	increased
8	RN100KDP.PE1	nc	100 kDa protein		tct	tca	increased
9	RN100KDP.PE1	nc	100 kDa protein		tct	tca	increased
10	RNLGP107.LGP-107	LGP 107	107 kDa sialoglycoprotein		ggt	gac	increased by mild
11	RNLGP107.LGP-107	LGP 107	107 kDa sialoglycoprotein		ggt	gac	increased by mild
12	RNLGP107.LGP-107	LGP 107	107 kDa sialoglycoprotein		ggt	gac	increased by mild
13	RNLGP107.LGP-107	LGP 107	107 kDa sialoglycoprotein		ggt	gac	increased by mild
14	AF133731.CTCF	CTCF	11-zinc finger protein		ttc	ttg	No change
15	AF133731.CTCF	CTCF	11-zinc finger protein		ttc	ttg	No change
16	AF133731.CTCF	CTCF	11-zinc finger protein		act	ttg	No change
17	AF133731.CTCF	CTCF	11-zinc finger protein		act	ttg	No change
18	U45479.PE1	nc	145 kDa synaptojanin isoform		gtt	tgt	No change
19	U45479.PE1	nc	145 kDa synaptojanin isoform		gtt	tgt	No change
20	AF390544.PE1	nc	15 kDa cytosolic selenoprotein		tgg	ttc	increased
21	AF390544.PE1	nc	15 kDa cytosolic selenoprotein		tgg	ttc	increased
22	AF390544.PE1	nc	15 kDa cytosolic selenoprotein		tgg	ttc	increased
23	AF390544.PE1	nc	15 kDa cytosolic selenoprotein		tgg	ttc	increased
24	RNU41853.ORP150	ORP150	150 kDa oxygen regulated protein		gtg	tca	decreased
25	RNU41853.ORP150	ORP150	150 kDa oxygen regulated protein		gtg	tca	decreased
26	RNU41853.ORP150	ORP150	150 kDa oxygen regulated protein		ttc	tcg	decreased
27	RNU41853.ORP150	ORP150	150 kDa oxygen regulated protein		ttc	tcg	decreased
28	RNU41853.ORP150	ORP150	150 kDa oxygen regulated protein		ttc	tcg	decreased
29	RNU41853.ORP150	ORP150	150 kDa oxygen regulated protein		ttc	tcg	decreased
30	RNDP150.DP-150	nc	150K dynein-associated polypeptide		ctc	tcc	No change
31	RNDP150.DP-150	nc	150K dynein-associated polypeptide		act	ctg	No change
32	RN17BHD.PE1	nc	17 beta hydroxysteroid dehydrogenase type I	*	agg	agg	increased
33	RN17BHD.PE1	nc	17 beta hydroxysteroid dehydrogenase type I	*	agg	tga	increased
34	RN17BHD.PE1	nc	17 beta hydroxysteroid dehydrogenase type I	*	agg	tga	increased
35	RN17BHD.PE1	nc	17 beta hydroxysteroid dehydrogenase type I	*	agg	tga	increased
36	RN17BHD.PE1	nc	17 beta hydroxysteroid dehydrogenase type I	*	agg	tga	increased
37	RN17BHD.PE1	nc	17 beta hydroxysteroid dehydrogenase type I	*	agg	tga	increased
38	RN17BHD.PE1	nc	17 beta hydroxysteroid dehydrogenase type I	*	agg	tga	increased
39	RN17BHD.PE1	nc	17 beta hydroxysteroid dehydrogenase type I	*	cac	aaa	increased
40	RN17BHD.PE1	nc	17 beta hydroxysteroid dehydrogenase type I	*	cac	aaa	increased
41	AF069770.PE1	Hsd17b10/Scl	17beta-hydroxysteroid dehydrogenase type		gaa	atg	increased
42	AF069770.PE1	Hsd17b10/Scl	17beta-hydroxysteroid dehydrogenase type		gaa	atg	increased
43	RNBOHSTDH.PE1	nc	17-beta-hydroxysteroid dehydrogenase type I	*	agg	agg	increased
44	RNBOHSTDH.PE1	nc	17-beta-hydroxysteroid dehydrogenase type I	*	agg	tga	increased
45	RNBOHSTDH.PE1	nc	17-beta-hydroxysteroid dehydrogenase type I	*	agg	tga	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
46	Taq1	39	agg	100.17	100	100.17	0	0	226.53	0	0	-=	\		\(3)
47	Taq1	39	agg	100.49	100	100.49	0	0	174.53	0	0	-=	\	\	\(3)
48	Taq1	56	tga	100.495	100	100.4	100.59	0	5 100 000	9 000 000	0	=-	\	\	\(3)
49	Taq1	56	tga	99.73	100	0	99.73	0	0	4 600 000	0	+-	A		\(3)
50	Hha1	49	aaa	125.425	126	0	125.52	125.33	0	3 900 000	4 000 000	+=	/		\(3)
51	Hha1	49	aaa	126.207	126	126.38	126.03	126.21	23 600 000	8 000 000	3 600 000	-=	\ (-)		\(3)
52	Hha1	2	tta	98.43	99	98.47	98.39	0	89 800 000	47 600 000	0	--	\		\(3)
53	Hha1	2	tta	99.13	99	99.13	0	0	82 100 000	0	0	-=	\		\(3)
54	Hha1	44	cgg	122.3	122	122.42	122.18	0	10 500 000	5 700 000	0	--	\		\(3)
55	Hha1	4	aag	141.14	141	0	141.14	141.14	0	9 100 000	26 600 000	=+	/		\(3)
56	Taq1	8	gaa	283.44	285	0	0	283.44	0	0	8 400 000	=+	/		\(3)
57	Hha1	8	gaa	284.86	285	0	284.86	0	0	3 400 000	0	+-	A		\(3)
58	Hha1	8	gaa	286.61	285	286.61	0	0	3 100 000	0	0	-=	\		\(3)
59	Taq1	54	ttt	120.39	121	120.39	0	0	1 179.89	0	0	-=	\		\(4)
60	Taq1	54	ttt	121.155	121	121.08	0	121.23	386.01	0	7 280.51	=+(+)	/		\(4)
61	Hha1	10	atg	139.21	140	139.22	139.2	0	14 300 000	6 700 000	0	--	\		\(4)
62	Taq1	10	atg	139.3	140	139.3	0	0	8 600 000	0	0	-=	\		\(4)
63	Taq1	10	atg	139.85	140	139.85	0	0	14 600 000	0	0	-=	\	\	\(4)
64	Hha1	10	atg	140.08	140	139.99	140.17	0	6 200 000	4 600 000	0	=-	\	\	\(4)
65	Taq1	41	ccc	132.21	132	0	0	132.21	0	0	3 500 000	=+	/		/(2)
66	Taq1	41	ccc	132.75	132	0	0	132.75	0	0	3 100 000	=+	/		/(2)
67	Hha1	56	tga	176.33	177	176.33	0	0	187.96	0	0	-=	\		/(2)
68	Hha1	56	tga	177.44	177	177.69	177.19	0	670.12	275.2	0	-=	\		/(2)
69	Taq1	20	ctc	192.96	194	0	192.96	0	0	4 300 000	0	+-	A		/(2)
70	Taq1	20	ctc	194.07	194	0	193.99	194.15	0	3 600 000	3 300 000	+=	/		/(2)
71	Hha1	49	aaa	92.243	92	92.45	92.24	92.04	38 300 000	19 200 000	5 900 000	-=	\ (-)		\(6)
72	Hha1	8	gaa	192.223	193	192.17	192.27	192.23	6 900 000	8 500 000	3 300 000	=-	\ (-)		\(6)
73	Taq1	8	gaa	192.62	193	0	192.62	0	0	8 500 000	0	+-	A		\(6)
74	Taq1	8	gaa	193.35	193	0	0	193.35	0	0	4 100 000	=+	/		\(6)
75	Hha1	8	gaa	193.115	193	193.11	193.12	0	4 600 000	11 300 000	0	+-	A		\(6)
76	Hha1	8	gaa	193.97	193	193.91	194.03	0	5 400 000	3 500 000	0	=-	\		\(6)
77	Hha1	7	caa	203.583	204	203.81	203.52	203.42	5 600 000	3 900 000	5 200 000	==	-		\(6)
78	Taq1	7	caa	203.64	204	203.64	0	0	3 400 000	0	0	-=	\		\(6)
79	Hha1	7	caa	204.39	204	204.38	204.4	204.39	11 600 000	6 000 000	6 300 000	-=	\ (-)		\(6)
80	Taq1	61	tct	204.505	204	204.73	204.28	0	3 400 000	6 100 000	0	=-	\		\(6)
81	Hha1	44	cgg	94.56	94	94.61	94.51	0	4 200 000	3 400 000	0	=-	\		/(2)
82	Taq1	40	tgg	131.82	132	0	0	131.82	0	0	4 300 000	=+	/		/(2)
83	Hha1	61	tct	147.073	147	147.05	147.04	147.13	8 600 000	27 600 000	17 800 000	+=	/ (-)		/(2)
84	Hha1	3	aac	191.21	192	191.09	191.33	0	6 500 000	5 200 000	0	=-	\	\	
85	Taq1	39	agg	191.385	192	191.6	191.17	0	308.22	280.4	0	=-	\	\	
86	Hha1	60	ttg	103.547	104	103.35	103.78	103.51	6 900 000	5 400 000	17 000 000	=+	/ (-)		/(2)
87	Hha1	60	ttg	104.277	104	104.21	104.3	104.32	11 400 000	4 300 000	22 100 000	=+	/ (-)		/(2)
88	Taq1	27	acg	151.105	152	151.01	151.2	0	13 600 000	8 800 000	0	=-	\		/(2)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
46	RNBOHSTDH.PE1	nc	17-beta-hydroxysteroid dehydrogenase type I	*	agg	tga	increased
47	RNBOHSTDH.PE1	nc	17-beta-hydroxysteroid dehydrogenase type I	*	agg	tga	increased
48	RNBOHSTDH.PE1	nc	17-beta-hydroxysteroid dehydrogenase type I	*	agg	tga	increased
49	RNBOHSTDH.PE1	nc	17-beta-hydroxysteroid dehydrogenase type I	*	agg	tga	increased
50	RNBOHSTDH.PE1	nc	17-beta-hydroxysteroid dehydrogenase type I	*	cac	aaa	increased
51	RNBOHSTDH.PE1	nc	17-beta-hydroxysteroid dehydrogenase type I	*	cac	aaa	increased
52	AF069525.PE1	nc	190 kDa ankyrin isoform		ata	tta	increased
53	AF069525.PE1	nc	190 kDa ankyrin isoform		ata	tta	increased
54	AF069525.PE1	nc	190 kDa ankyrin isoform		cgt	cgg	increased
55	AF069525.PE1	nc	190 kDa ankyrin isoform		cgc	aag	increased
56	AF069525.PE1	nc	190 kDa ankyrin isoform		gaa	ggc	increased
57	AF069525.PE1	nc	190 kDa ankyrin isoform		gaa	ggc	increased
58	AF069525.PE1	nc	190 kDa ankyrin isoform		gaa	ggc	increased
59	RATDCR.PE1	nc	2,4-dienoyl-CoA reductase precursor		ttt	tta	increased
60	RATDCR.PE1	nc	2,4-dienoyl-CoA reductase precursor		ttt	tta	increased
61	RATDCR.PE1	nc	2,4-dienoyl-CoA reductase precursor		gag	atg	increased
62	RATDCR.PE1	nc	2,4-dienoyl-CoA reductase precursor		gag	atg	increased
63	RATDCR.PE1	nc	2,4-dienoyl-CoA reductase precursor		gag	atg	increased
64	RATDCR.PE1	nc	2,4-dienoyl-CoA reductase precursor		gag	atg	increased
65	AY262823.RNASEL	Rnasel	2',5'-oligoisoadenylate synthetase-dependent		ccc	ttg	decreased
66	AY262823.RNASEL	Rnasel	2',5'-oligoisoadenylate synthetase-dependent		ccc	ttg	decreased
67	AY262823.RNASEL	Rnasel	2',5'-oligoisoadenylate synthetase-dependent		tga	cgt	decreased
68	AY262823.RNASEL	Rnasel	2',5'-oligoisoadenylate synthetase-dependent		tga	cgt	decreased
69	AY262823.RNASEL	Rnasel	2',5'-oligoisoadenylate synthetase-dependent		gag	ctc	decreased
70	AY262823.RNASEL	Rnasel	2',5'-oligoisoadenylate synthetase-dependent		gag	ctc	decreased
71	RAT230P4K.PE1	nc	230kDa phosphatidylinositol 4-kinase		ccg	aaa	increased
72	RAT230P4K.PE1	nc	230kDa phosphatidylinositol 4-kinase		gaa	agc	increased
73	RAT230P4K.PE1	nc	230kDa phosphatidylinositol 4-kinase		gaa	agc	increased
74	RAT230P4K.PE1	nc	230kDa phosphatidylinositol 4-kinase		gaa	agc	increased
75	RAT230P4K.PE1	nc	230kDa phosphatidylinositol 4-kinase		gaa	agc	increased
76	RAT230P4K.PE1	nc	230kDa phosphatidylinositol 4-kinase		gaa	agc	increased
77	RAT230P4K.PE1	nc	230kDa phosphatidylinositol 4-kinase		caa	tct	increased
78	RAT230P4K.PE1	nc	230kDa phosphatidylinositol 4-kinase		caa	tct	increased
79	RAT230P4K.PE1	nc	230kDa phosphatidylinositol 4-kinase		caa	tct	increased
80	RAT230P4K.PE1	nc	230kDa phosphatidylinositol 4-kinase		caa	tct	increased
81	RNAF000139.CYP1	CYP1	25-hydroxyvitamin D 1-hydroxylase		cgg	ctt	decreased
82	RNAF000139.CYP1	CYP1	25-hydroxyvitamin D 1-hydroxylase		tgg	gct	decreased
83	RNAF000139.CYP1	CYP1	25-hydroxyvitamin D 1-hydroxylase		ggt	tct	decreased
84	RATVITD11.CYP24	CYP24	25-hydroxyvitamin D3 24-hydroxylase		aac	agg	increased
85	RATVITD11.CYP24	CYP24	25-hydroxyvitamin D3 24-hydroxylase		aac	agg	increased
86	RN2ARYLCO.PE1	nc	2-arylpropionyl-CoA epimerase		cga	ttg	decreased
87	RN2ARYLCO.PE1	nc	2-arylpropionyl-CoA epimerase		cga	ttg	decreased
88	RN2ARYLCO.PE1	nc	2-arylpropionyl-CoA epimerase		acg	ggc	decreased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
89	Taq1	27	acg	151.65	152	0	0	151.65	0	0	10 600 000	=+	/		/(2)
90	Hha1	12	agt	139.47	140	139.43	139.48	139.5	4 239.91	3 292.58	3 231.76	==	-		A(2) \(2)
91	Hha1	12	agt	140.473	140	140.43	140.51	140.48	2 275.07	1 711.49	3 047.09	==	-		A(2) \(2)
92	Hha1	26	ctg	186.76	187	0	186.76	0	0	3 000 000	0	+-	A	A	A(2) \(2)
93	Hha1	26	ctg	188.1	187	188.1	0	0	3 500 000	0	0	-=	\		A(2) \(2)
94	Hha1	40	tgg	186.515	187	186.31	186.72	0	3 900 000	4 100 000	0	=-	\		A(2) \(2)
95	Hha1	40	tgg	186.89	187	0	186.89	0	0	3 800 000	0	+-	A	A	A(2) \(2)
96	Hha1	40	tgg	187.92	187	0	187.92	0	0	3 100 000	0	+-	A		A(2) \(2)
97	Hha1	59	ttc	124.75	125	124.75	124.75	0	223.6	370.81	0	=-	\		\(2)
98	Hha1	59	ttc	125.685	125	125.59	125.78	0	213.2	218.46	0	=-	\		\(2)
99	Taq1	51	ata	322.68	323	322.68	0	0	4 100 000	0	0	-=	\		\(2)
100	Taq1	55	tca	88.57	89	0	88.35	88.79	0	17 100 000	5 200 000	+-	A		A(2)
101	Taq1	39	agg	104.49	105	104.49	0	0	623.88	0	0	-=	\		A(2)
102	Taq1	39	agg	104.44	105	0	104.44	0	0	880.41	0	+-	A		A(2)
103	Taq1	62	tgt	157.8	158	0	0	157.8	0	0	4 300 000	=+	/		A(2)
104	Taq1	62	tgt	158.943	158	159.05	158.96	158.82	3 300 000	5 400 000	10 500 000	=+	/ (-)		A(2)
105	Taq1	45	gcc	64.753	65	64.91	64.6	64.75	13 900 000	6 600 000	3 300 000	-=	\ (-)		-(4) \(4)
106	Hha1	40	tgg	109.003	109	109.05	109.17	108.79	4 200 000	7 400 000	27 300 000	=+	/ (-)		-(4) \(4)
107	Hha1	40	tgg	109.35	109	0	0	109.35	0	0	21 600 000	=+	/		-(4) \(4)
108	Taq1	31	gac	134.527	135	134.67	134.44	134.47	10 200 000	16 000 000	3 200 000	=-	\ (-)	\	-(4) \(4)
109	Taq1	31	gac	135.577	135	135.72	135.49	135.52	11 900 000	8 500 000	6 100 000	==	-		-(4) \(4)
110	Taq1	39	agg	134.245	135	134.44	0	134.05	22 800 000	0	4 800 000	-=(-)	\		-(4) \(4)
111	Taq1	39	agg	135.003	135	135.27	134.79	134.95	14 500 000	90 500 000	3 300 000	+-	A		-(4) \(4)
112	Taq1	39	agg	134.44	135	134.44	0	0	846.7	0	0	-=	\	\	-(4) \(4)
113	Taq1	39	agg	135.48	135	135.27	135.69	0	538.47	13 500 000	0	+-	A		-(4) \(4)
114	Taq1	39	agg	134.79	135	0	134.79	0	0	909.55	0	+-	A		-(4) \(4)
115	Taq1	39	agg	134.95	135	0	0	134.95	0	0	97.2	=+	/		-(4) \(4)
116	Hha1	39	agg	137.947	138	137.96	138.03	137.85	1 407.62	901.54	406.9	==	-		-(4) \(4)
117	Hha1	25	cag	172.75	173	0	172.77	172.73	0	3 800 000	5 000 000	+=	/		-(4) \(4)
118	Hha1	25	cag	173.84	173	0	174.01	173.67	0	5 500 000	4 100 000	+=	/		-(4) \(4)
119	Taq1	31	gac	172.93	173	0	172.93	0	0	3 100 000	0	+-	A		-(4) \(4)
120	Taq1	31	gac	173.89	173	173.85	173.93	0	5 000 000	3 100 000	0	=-	\		-(4) \(4)
121	Hha1	15	tac	105.483	106	105.64	105.6	105.21	448.9	3 000 000	5 300 000	+=	/ (-)		-1
122	Hha1	15	tac	105.405	106	0	105.6	105.21	0	772.59	1 152.67	+=	/		-1
123	Hha1	39	agg	106.243	106	106.2	106.36	106.17	1 217	12 305.21	14 347.33	+=	/ (-)		-1
124	Hha1	39	agg	64.247	64	64.4	64.03	64.31	3 643.69	1 003.04	1 786.29	-=	\ (-)		-(2) \(2)
125	Hha1	41	ccc	131.893	132	131.81	131.72	132.15	26 500 000	8 600 000	5 100 000	-=	\ (-)		-(2) \(2)
126	Hha1	28	tcg	186.66	186	0	0	186.66	0	0	3 500 000	=+	/		-(2) \(2)
127	Hha1	59	ttc	77.11	77	77.38	77.04	76.91	3 374.93	270.2	760.61	-=	\ (-)		\(6)
128	Hha1	44	cgg	156.1	157	0	156.1	0	0	3 500 000	0	+-	A		\(6)
129	Hha1	44	cgg	157.135	157	157.06	157.21	0	3 600 000	8 100 000	0	+-	A		\(6)
130	Hha1	44	cgg	157.73	157	0	157.73	0	0	4 700 000	0	+-	A		\(6)
131	Hha1	40	tgg	157.975	158	157.8	158.15	0	7 600 000	10 900 000	0	=-	\		\(6)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
89	RN2ARYLCO.PE1	nc	2-arylpropionyl-CoA epimerase		acg	ggc	decreased
90	RNU84727.PE1	nc	2-oxoglutarate carrier		taa	agt	increased by mild
91	RNU84727.PE1	nc	2-oxoglutarate carrier		taa	agt	increased by mild
92	RNU84727.PE1	nc	2-oxoglutarate carrier		ctg	tgg	increased by mild
93	RNU84727.PE1	nc	2-oxoglutarate carrier		ctg	tgg	increased by mild
94	RNU84727.PE1	nc	2-oxoglutarate carrier		ctg	tgg	increased by mild
95	RNU84727.PE1	nc	2-oxoglutarate carrier		ctg	tgg	increased by mild
96	RNU84727.PE1	nc	2-oxoglutarate carrier		ctg	tgg	increased by mild
97	RAT35CA.PE1	nc	3',5'-cyclic AMP phosphodiesterase		cgc	ttc	increased
98	RAT35CA.PE1	nc	3',5'-cyclic AMP phosphodiesterase		cgc	ttc	increased
99	RAT35CA.PE1	nc	3',5'-cyclic AMP phosphodiesterase		ata	acg	increased
100	RNU09457.PDE3	PDE3/IVd gen	3',5'-cyclic AMP phosphodiesterase		tca	gga	increased by mild
101	RNU09457.PDE3	PDE3/IVd gen	3',5'-cyclic AMP phosphodiesterase		ttg	agg	increased by mild
102	RNU09457.PDE3	PDE3/IVd gen	3',5'-cyclic AMP phosphodiesterase		ttg	agg	increased by mild
103	RNU09457.PDE3	PDE3/IVd gen	3',5'-cyclic AMP phosphodiesterase		tgt	tac	increased by mild
104	RNU09457.PDE3	PDE3/IVd gen	3',5'-cyclic AMP phosphodiesterase		tgt	tac	increased by mild
105	AY240873.HS3ST2	HS3ST2	3-O-sulphotransferase 2		gcc	aga	No change
106	AY240873.HS3ST2	HS3ST2	3-O-sulphotransferase 2		aag	tgg	No change
107	AY240873.HS3ST2	HS3ST2	3-O-sulphotransferase 2		aag	tgg	No change
108	AY240873.HS3ST2	HS3ST2	3-O-sulphotransferase 2		gac	agg	increased
109	AY240873.HS3ST2	HS3ST2	3-O-sulphotransferase 2		gac	agg	No change
110	AY240873.HS3ST2	HS3ST2	3-O-sulphotransferase 2		gac	agg	No change
111	AY240873.HS3ST2	HS3ST2	3-O-sulphotransferase 2		gac	agg	No change
112	AY240873.HS3ST2	HS3ST2	3-O-sulphotransferase 2		gac	agg	increased
113	AY240873.HS3ST2	HS3ST2	3-O-sulphotransferase 2		gac	agg	No change
114	AY240873.HS3ST2	HS3ST2	3-O-sulphotransferase 2		gac	agg	No change
115	AY240873.HS3ST2	HS3ST2	3-O-sulphotransferase 2		gac	agg	No change
116	AY240873.HS3ST2	HS3ST2	3-O-sulphotransferase 2		agg	cga	No change
117	AY240873.HS3ST2	HS3ST2	3-O-sulphotransferase 2		cag	gac	No change
118	AY240873.HS3ST2	HS3ST2	3-O-sulphotransferase 2		cag	gac	No change
119	AY240873.HS3ST2	HS3ST2	3-O-sulphotransferase 2		cag	gac	No change
120	AY240873.HS3ST2	HS3ST2	3-O-sulphotransferase 2		cag	gac	No change
121	RNO132352.PE1	rsec 45	45 kDa secretory protein		tac	agg	No change
122	RNO132352.PE1	rsec 45	45 kDa secretory protein		tac	agg	No change
123	RNO132352.PE1	rsec 45	45 kDa secretory protein		tac	agg	No change
124	AY029199.PE1	nc	55 kDa type II phosphatidylinositol 4-kinase		agg	cgc	No change
125	AY029199.PE1	nc	55 kDa type II phosphatidylinositol 4-kinase		ggt	ccc	No change
126	AY029199.PE1	nc	55 kDa type II phosphatidylinositol 4-kinase		agg	tcg	No change
127	RAT5E5ANTE.PE1	nc	5E5 antigen		ggc	ttc	increased
128	RAT5E5ANTE.PE1	nc	5E5 antigen		cgg	tgc	increased
129	RAT5E5ANTE.PE1	nc	5E5 antigen		cgg	tgc	increased
130	RAT5E5ANTE.PE1	nc	5E5 antigen		cgg	tgc	increased
131	RAT5E5ANTE.PE1	nc	5E5 antigen		aag	tgg	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
132	Hha1	40	tgg	158.805	158	159.02	0	158.59	4 200 000	0	4 000 000	-+(=)	V		\(6)
133	Taq1	22	tcc	178.07	179	0	0	178.07	0	0	7 400 000	=+	/		\(6)
134	Taq1	22	tcc	178.945	179	178.9	0	178.99	7 100 000	0	3 500 000	-+(-)	V (\)		\(6)
135	Taq1	22	tcc	179.52	179	179.61	179.43	0	3 900 000	6 900 000	0	=-	\		\(6)
136	Taq1	22	tcc	180.03	179	0	0	180.03	0	0	6 700 000	=+	/		\(6)
137	Hha1	41	ccc	189.29	189	189.29	0	0	3 100 000	0	0	-=	\		\(6)
138	Hha1	3	aac	189.12	190	189.13	189.21	189.02	6 300 000	4 500 000	5 200 000	==	-		\(6)
139	Hha1	3	aac	190.345	190	190.34	190.35	0	4 500 000	4 900 000	0	=-	\		\(6)
140	Taq1	17	cca	189.27	190	0	189.27	0	0	279.21	0	+-	A		\(6)
141	Taq1	17	cca	190.26	190	0	190.26	0	0	425.47	0	+-	A		\(6)
142	Hha1	39	agg	188.97	190	0	0	188.97	0	0	166.82	=+	/		\(6)
143	Hha1	39	agg	189.565	190	0	189.7	189.43	0	238.82	195.31	+=	/		\(6)
144	Hha1	39	agg	190.03	190	0	0	190.03	0	0	146.48	=+	/		\(6)
145	Hha1	39	agg	190.715	190	0	190.77	190.66	0	197.02	146.48	+=	/		\(6)
146	Hha1	41	ccc	218.96	220	0	0	218.96	0	0	3 000 000	=+	/		\(6)
147	Taq1	45	gcc	297.88	298	297.88	0	0	3 200 000	0	0	-=	\		\(6)
148	Hha1	7	caa	228.38	229	228.38	0	0	5 400 000	0	0	-=	\		\(2)
149	Taq1	7	caa	228.91	229	228.91	0	0	3 200 000	0	0	-=	\		\(2)
150	Taq1	25	cat	114.983	115	115	114.86	115.09	716.52	432.84	2 590.24	=+	/ (-)		/(3)
151	Taq1	25	cat	115.55	115	115.55	0	0	627.81	0	0	-=	\		/(3)
152	Hha1	40	tgg	255.845	256	0	255.61	256.08	0	4 500 000	6 100 000	+=	/		/(3)
153	Hha1	59	ttc	256.33	256	0	256.31	256.35	0	129.35	294.93	=+	/		/(3)
154	Hha1	59	ttc	257.53	256	0	257.53	0	0	86.23	0	+-	A		/(3)
155	Hha1	40	tgg	255.845	256	0	255.61	256.08	0	4 500 000	6 100 000	+=	/		/(2)
156	Hha1	59	ttc	256.33	256	0	256.31	256.35	0	129.35	294.93	=+	/		/(2)
157	Hha1	59	ttc	257.53	256	0	257.53	0	0	86.23	0	+-	A		/(2)
158	Hha1	7	caa	222.98	224	0	223.04	222.92	0	3 800 000	3 800 000	+=	/		/(2) A(2)
159	Taq1	7	caa	223.22	224	0	223.22	0	0	3 300 000	0	+-	A		/(2) A(2)
160	Hha1	7	caa	222.92	224	0	0	222.92	0	0	3 800 000	=+	/		/(2) A(2)
161	Hha1	7	caa	224.21	224	224.34	224.08	0	3 800 000	3 300 000	0	=-	\		/(2) A(2)
162	Hha1	7	caa	225.005	224	225.08	224.93	0	4 200 000	4 500 000	0	=-	\		/(2) A(2)
163	Hha1	7	caa	223.04	224	0	223.04	0	0	3 800 000	0	+-	A		/(2) A(2)
164	Hha1	27	acg	80.793	81	80.8	80.87	80.71	27 600 000	3 900 000	13 400 000	-=	\ (-)		\(2)
165	Hha1	61	tct	109.345	110	109.11	0	109.58	7 200 000	0	6 100 000	-+(=)	V		\(2)
166	Hha1	61	tct	109.65	110	109.66	109.64	0	10 200 000	7 100 000	0	=-	\		\(2)
167	Hha1	33	agc	91.3	91	91.16	91.44	0	3 500 000	4 000 000	0	=-	\		\(4)
168	Taq1	41	ccc	111.77	112	0	111.99	111.55	0	13 600 000	3 000 000	+-	A		\(4)
169	Taq1	41	ccc	112.08	112	112.08	0	0	6 400 000	0	0	-=	\		\(4)
170	Taq1	29	gca	131.467	132	131.53	131.44	131.43	20 100 000	14 300 000	7 100 000	==	-		\(4)
171	Taq1	29	gca	132.537	132	132.61	132.56	132.44	20 200 000	18 300 000	8 200 000	=-	\ (-)	\	\(4)
172	Taq1	31	gac	131.425	132	131.49	131.36	0	4 800 000	12 200 000	0	+-	A		\(4)
173	Taq1	31	gac	132.45	132	132.57	132.33	0	14 200 000	8 500 000	0	=-	\	\	\(4)
174	Hha1	57	cta	168.55	169	0	168.58	168.52	0	861.6	838.63	+=	/		\(4)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
132	RAT5E5ANTE.PE1	nc	5E5 antigen		aag	tgg	increased
133	RAT5E5ANTE.PE1	nc	5E5 antigen		gga	tcc	increased
134	RAT5E5ANTE.PE1	nc	5E5 antigen		gga	tcc	increased
135	RAT5E5ANTE.PE1	nc	5E5 antigen		gga	tcc	increased
136	RAT5E5ANTE.PE1	nc	5E5 antigen		gga	tcc	increased
137	RAT5E5ANTE.PE1	nc	5E5 antigen		ccc	agg	increased
138	RAT5E5ANTE.PE1	nc	5E5 antigen		cca	aac	increased
139	RAT5E5ANTE.PE1	nc	5E5 antigen		cca	aac	increased
140	RAT5E5ANTE.PE1	nc	5E5 antigen		cca	aac	increased
141	RAT5E5ANTE.PE1	nc	5E5 antigen		cca	aac	increased
142	RAT5E5ANTE.PE1	nc	5E5 antigen		ccc	agg	increased
143	RAT5E5ANTE.PE1	nc	5E5 antigen		ccc	agg	increased
144	RAT5E5ANTE.PE1	nc	5E5 antigen		ccc	agg	increased
145	RAT5E5ANTE.PE1	nc	5E5 antigen		ccc	agg	increased
146	RAT5E5ANTE.PE1	nc	5E5 antigen		cct	ccc	increased
147	RAT5E5ANTE.PE1	nc	5E5 antigen		gcc	gtt	increased
148	RNU59672.PE1	nc	5HT3 receptor		caa	acg	increased
149	RNU59672.PE1	nc	5HT3 receptor		caa	acg	increased
150	AF155044.PE1	nc	5-hydroxytryptamine 3 receptor B subunit		tga	cat	decreased
151	AF155044.PE1	nc	5-hydroxytryptamine 3 receptor B subunit		tga	cat	decreased
152	AF155044.PE1	nc	5-hydroxytryptamine 3 receptor B subunit		tgg	ttc	decreased
153	AF155044.PE1	nc	5-hydroxytryptamine 3 receptor B subunit		tgg	ttc	decreased
154	AF155044.PE1	nc	5-hydroxytryptamine 3 receptor B subunit		tgg	ttc	decreased
155	AF303447.PE1	nc	5-hydroxytryptamine 3 receptor B subunit splice		tgg	ttc	decreased
156	AF303447.PE1	nc	5-hydroxytryptamine 3 receptor B subunit splice		tgg	ttc	decreased
157	AF303447.PE1	nc	5-hydroxytryptamine 3 receptor B subunit splice		tgg	ttc	decreased
158	D42116.PE1	nc	5I2 antigen		tgg	caa	decreased
159	D42116.PE1	nc	5I2 antigen		tgg	caa	decreased
160	D42116.PE1	nc	5I2 antigen		tgg	caa	decreased
161	D42116.PE1	nc	5I2 antigen		tgg	caa	decreased
162	D42116.PE1	nc	5I2 antigen		tgg	caa	decreased
163	D42116.PE1	nc	5I2 antigen		tgg	caa	decreased
164	RNO131196.PE1	nc	5'OT-EST protein		ggc	acg	increased
165	RNO131196.PE1	nc	5'OT-EST protein		tct	tca	increased
166	RNO131196.PE1	nc	5'OT-EST protein		tct	tca	increased
167	AF063939.5T4	5T4	5T4 oncofetal antigen homolog		agc	cgc	increased
168	AF063939.5T4	5T4	5T4 oncofetal antigen homolog		ccc	agc	increased
169	AF063939.5T4	5T4	5T4 oncofetal antigen homolog		ccc	agc	increased
170	AF063939.5T4	5T4	5T4 oncofetal antigen homolog		gca	gac	increased
171	AF063939.5T4	5T4	5T4 oncofetal antigen homolog		gca	gac	increased
172	AF063939.5T4	5T4	5T4 oncofetal antigen homolog		gca	gac	increased
173	AF063939.5T4	5T4	5T4 oncofetal antigen homolog		gca	gac	increased
174	AF063939.5T4	5T4	5T4 oncofetal antigen homolog		att	cta	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
175	Hha1	57	cta	169.483	169	169.47	169.53	169.45	539.14	2 248.24	1 115.1	+-	A		\(4)
176	Hha1	56	tga	183.085	184	0	183.14	183.03	0	335.75	741.25	++	/		\(4)
177	Hha1	56	tga	184.103	184	183.99	184.19	184.13	388.18	187.14	1 310.11	=+	/ (-)		\(4)
178	Hha1	39	agg	190.03	191	0	0	190.03	0	0	146.48	=+	/		\(4)
179	Hha1	39	agg	190.715	191	0	190.77	190.66	0	197.02	146.48	+=	/		\(4)
180	Hha1	39	agg	191.23	191	0	0	191.23	0	0	183.1	=+	/		\(4)
181	Taq1	9	atc	159.56	159	159.54	159.52	159.62	5 700 000	9 300 000	3 500 000	=-	\ (-)	\	
182	Hha1	9	atc	159.515	159	159.34	159.69	0	9 800 000	15 600 000	0	=-	\	\	
183	Taq1	48	ggg	210.15	210	210.15	0	0	1 137.8	0	0	-=	\	\	
184	Hha1	6	aga	210.285	211	210.13	210.44	0	5 000 000	3 200 000	0	=-	\	\	
185	Hha1	43	cgc	122.23	122	122.19	122.27	0	20 400 000	5 700 000	0	-=	\		\(4)
186	Hha1	26	ctg	123.06	123	123.17	122.89	123.12	6 100 000	8 400 000	3 000 000	=-	\ (-)		\(4)
187	Hha1	49	aaa	145.135	146	145.2	145.07	0	42 900 000	24 500 000	0	=-	\		\(4)
188	Hha1	49	aaa	146.115	146	146.12	146.11	0	16 800 000	11 500 000	0	=-	\		\(4)
189	Hha1	6	aga	167.615	168	167.59	0	167.64	10 500 000	0	3 200 000	-=(-)	\		\(4)
190	Hha1	6	aga	168.64	168	168.64	0	0	6 700 000	0	0	-=	\		\(4)
191	Hha1	15	tac	179.05	178	0	0	179.05	0	0	3 900 000	=+	/		/(2)
192	Hha1	39	agg	176.94	178	0	177.1	176.78	0	310.46	236	+=	/		/(2)
193	Hha1	39	agg	178.22	178	0	178.4	178.04	0	220.9	183.1	+=	/		/(2)
194	Hha1	33	agc	69.835	70	69.78	69.89	0	36 000 000	32 900 000	0	=-	\		\(4)
195	Hha1	60	ttg	138.24	138	138.26	0	138.22	6 100 000	0	10 800 000	-+(=)	V		\(4)
196	Hha1	26	ctg	138.603	139	138.45	138.77	138.59	8 200 000	3 300 000	3 900 000	-=	\ (-)		\(4)
197	Hha1	26	ctg	139.08	139	139.08	0	0	3 600 000	0	0	-=	\		\(4)
198	Taq1	18	cct	153.185	153	153.18	153.19	0	8 300 000	8 900 000	0	=-	\		\(4)
199	Hha1	28	tcg	171.57	172	0	171.57	0	0	3 700 000	0	+-	A		\(4)
200	Hha1	60	ttg	209.15	210	0	209.15	0	0	4 000 000	0	+-	A		\(4)
201	Hha1	60	ttg	210.06	210	210.05	210.07	0	3 100 000	3 800 000	0	=-	\		\(4)
202	Taq1	63	ctt	134.903	135	134.9	134.76	135.05	3 800 000	3 200 000	4 300 000	==	-		\(2) A(2)
203	Taq1	63	ctt	134.99	135	0	134.99	0	0	3 700 000	0	+-	A		\(2) A(2)
204	Taq1	54	ttt	135.905	136	135.89	135.92	0	662.78	893.8	0	=-	\		\(2) A(2)
205	Taq1	54	ttt	136.7	136	0	136.7	0	0	388.09	0	+-	A		\(2) A(2)
206	Taq1	39	agg	141.93	142	141.93	0	0	10 900 000	0	0	-=	\		\(2) A(2)
207	Taq1	39	agg	141.93	142	141.93	0	0	404.78	0	0	-=	\		\(2) A(2)
208	Hha1	33	agc	69.835	70	69.78	69.89	0	36 000 000	32 900 000	0	=-	\		\(4)
209	Hha1	60	ttg	138.24	138	138.26	0	138.22	6 100 000	0	10 800 000	-+(=)	V		\(4)
210	Hha1	26	ctg	138.603	139	138.45	138.77	138.59	8 200 000	3 300 000	3 900 000	-=	\ (-)		\(4)
211	Hha1	26	ctg	139.08	139	139.08	0	0	3 600 000	0	0	-=	\		\(4)
212	Taq1	18	cct	153.185	153	153.18	153.19	0	8 300 000	8 900 000	0	=-	\		\(4)
213	Hha1	28	tcg	171.57	172	0	171.57	0	0	3 700 000	0	+-	A		\(4)
214	Hha1	60	ttg	209.15	210	0	209.15	0	0	4 000 000	0	+-	A		\(4)
215	Hha1	60	ttg	210.06	210	210.05	210.07	0	3 100 000	3 800 000	0	=-	\		\(4)
216	Hha1	60	ttg	213.13	214	0	213.13	0	0	3 000 000	0	+-	A		\(4) A(3)
217	Hha1	61	tct	214.34	214	214.34	0	0	4 900 000	0	0	-=	\		\(4) A(3)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
175	AF063939.5T4	5T4	5T4 oncofetal antigen homolog		att	cta	increased
176	AF063939.5T4	5T4	5T4 oncofetal antigen homolog		ctt	tga	increased
177	AF063939.5T4	5T4	5T4 oncofetal antigen homolog		ctt	tga	increased
178	AF063939.5T4	5T4	5T4 oncofetal antigen homolog		ctt	agg	increased
179	AF063939.5T4	5T4	5T4 oncofetal antigen homolog		ctt	agg	increased
180	AF063939.5T4	5T4	5T4 oncofetal antigen homolog		ctt	agg	increased
181	RATPMP70.PMP70	PMP70	70-kDa peroxisomal membrane protein		atc	gtt	increased
182	RATPMP70.PMP70	PMP70	70-kDa peroxisomal membrane protein		atc	gtt	increased
183	RNU36476.PE1	nc	92-kDa type IV collagenase		ggg	aga	increased
184	RNU36476.PE1	nc	92-kDa type IV collagenase		ggg	aga	increased
185	AF149118.PE1	ADAMTS-1	a disintegrin and metalloproteinase with		ctg	cgc	increased
186	AF149118.PE1	ADAMTS-1	a disintegrin and metalloproteinase with		ctg	cgc	increased
187	AF149118.PE1	ADAMTS-1	a disintegrin and metalloproteinase with		aaa	cct	increased
188	AF149118.PE1	ADAMTS-1	a disintegrin and metalloproteinase with		aaa	cct	increased
189	AF149118.PE1	ADAMTS-1	a disintegrin and metalloproteinase with		aga	ggc	increased
190	AF149118.PE1	ADAMTS-1	a disintegrin and metalloproteinase with		aga	ggc	increased
191	RNO249700.PE1	RT1-A1q	A1q		tac	agg	decreased
192	RNO249700.PE1	RT1-A1q	A1q		tac	agg	decreased
193	RNO249700.PE1	RT1-A1q	A1q		tac	agg	decreased
194	AY318956.PE1	nc	Aa1011	*	agc	ggg	increased
195	AY318956.PE1	nc	Aa1011	*	ttg	aga	increased
196	AY318956.PE1	nc	Aa1011	*	ctg	ggg	increased
197	AY318956.PE1	nc	Aa1011	*	ctg	ggg	increased
198	AY318956.PE1	nc	Aa1011	*	cct	gag	increased
199	AY318956.PE1	nc	Aa1011	*	ctc	tcg	increased
200	AY318956.PE1	nc	Aa1011	*	ttg	cag	increased
201	AY318956.PE1	nc	Aa1011	*	ttg	cag	increased
202	AY318958.PE1	nc	Aa1064	*	ctt	ttt	increased
203	AY318958.PE1	nc	Aa1064	*	ctt	ttt	increased
204	AY318958.PE1	nc	Aa1064	*	ctt	ttt	increased
205	AY318958.PE1	nc	Aa1064	*	ctt	ttt	increased
206	AY318958.PE1	nc	Aa1064	*	agg	cgc	increased
207	AY318958.PE1	nc	Aa1064	*	agg	cgc	increased
208	AY318962.PE1	nc	Aa1262	*	agc	ggg	increased
209	AY318962.PE1	nc	Aa1262	*	ttg	aga	increased
210	AY318962.PE1	nc	Aa1262	*	ctg	ggg	increased
211	AY318962.PE1	nc	Aa1262	*	ctg	ggg	increased
212	AY318962.PE1	nc	Aa1262	*	cct	gag	increased
213	AY318962.PE1	nc	Aa1262	*	ctc	tcg	increased
214	AY318962.PE1	nc	Aa1262	*	ttg	cag	increased
215	AY318962.PE1	nc	Aa1262	*	ttg	cag	increased
216	RNO238717.AATF	aatf	AATF protein		tct	ttg	increased
217	RNO238717.AATF	aatf	AATF protein		tct	ttg	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
218	Taq1	39	agg	219.085	220	218.98	219.19	0	23 800 000	61 600 000	0	+-	A		\(4) A(3)
219	Taq1	39	agg	219.965	220	219.91	220.02	0	6 900 000	66 700 000	0	+-	A		\(4) A(3)
220	Taq1	39	agg	220.56	220	220.56	0	0	6 900 000	0	0	-=	\		\(4) A(3)
221	Taq1	39	agg	218.98	220	218.98	0	0	883.83	0	0	-=	\		\(4) A(3)
222	Taq1	39	agg	219.91	220	219.91	0	0	256.23	0	0	-=	\		\(4) A(3)
223	Taq1	39	agg	220.56	220	220.56	0	0	256.23	0	0	-=	\		\(4) A(3)
224	Taq1	39	agg	221.2	220	0	221.2	0	0	228 600 000	0	+-	A		\(4) A(3)
225	Taq1	39	agg	219.19	220	0	219.19	0	0	619.1	0	+-	A		\(4) A(3)
226	Taq1	39	agg	220.02	220	0	220.02	0	0	670.35	0	+-	A		\(4) A(3)
227	Taq1	39	agg	221.2	220	0	221.2	0	0	2 297.51	0	+-	A		\(4) A(3)
228	Hha1	8	gaa	263.67	265	263.67	0	0	7 000 000	0	0	-=	\		\(4) A(3)
229	Hha1	8	gaa	264.4	265	0	264.4	0	0	3 700 000	0	+-	A		\(4) A(3)
230	Taq1	8	gaa	264.34	265	0	0	264.34	0	0	3 500 000	=+	/		\(4) A(3)
231	Taq1	8	gaa	264.92	265	264.92	264.92	0	11 000 000	10 100 000	0	=-	\		\(4) A(3)
232	Taq1	16	tag	111.43	112	0	111.47	111.39	0	4 600 000	7 100 000	+=	/		\(4)
233	Hha1	16	tag	111.825	112	111.76	0	111.89	11 200 000	0	3 200 000	-=(-)	\		\(4)
234	Taq1	16	tag	112.325	112	112.39	0	112.26	3 100 000	0	6 600 000	-+(+)	V (/)		\(4)
235	Hha1	16	tag	112.64	112	112.64	0	0	3 400 000	0	0	-=	\		\(4)
236	Taq1	18	cct	111.553	112	111.49	111.59	111.58	25 800 000	21 800 000	5 300 000	=-	\ (-)		\(4)
237	Taq1	18	cct	112.613	112	112.59	112.64	112.61	32 900 000	30 500 000	3 000 000	=-	\ (-)		\(4)
238	Taq1	63	ctt	192.08	193	192.08	0	0	3 000 000	0	0	-=	\		\(4)
239	Taq1	63	ctt	193.04	193	193.04	0	193.04	3 100 000	0	3 400 000	-+(=)	V		\(4)
240	Taq1	16	tag	111.43	112	0	111.47	111.39	0	4 600 000	7 100 000	+=	/		\(4)
241	Hha1	16	tag	111.825	112	111.76	0	111.89	11 200 000	0	3 200 000	-=(-)	\		\(4)
242	Taq1	16	tag	112.325	112	112.39	0	112.26	3 100 000	0	6 600 000	-+(+)	V (/)		\(4)
243	Hha1	16	tag	112.64	112	112.64	0	0	3 400 000	0	0	-=	\		\(4)
244	Taq1	18	cct	111.553	112	111.49	111.59	111.58	25 800 000	21 800 000	5 300 000	=-	\ (-)		\(4)
245	Taq1	18	cct	112.613	112	112.59	112.64	112.61	32 900 000	30 500 000	3 000 000	=-	\ (-)		\(4)
246	Taq1	63	ctt	192.08	193	192.08	0	0	3 000 000	0	0	-=	\		\(4)
247	Taq1	63	ctt	193.04	193	193.04	0	193.04	3 100 000	0	3 400 000	-+(=)	V		\(4)
248	Hha1	3	aac	103.785	104	103.81	103.76	0	3 900 000	4 300 000	0	=-	\		\(2)
249	Taq1	34	tgc	104.45	104	104.45	0	0	3 500 000	0	0	-=	\		\(2)
250	Hha1	41	ccc	153.07	153	153.07	0	0	3 700 000	0	0	-=	\	\	
251	Hha1	40	tgg	153.08	154	153.08	0	0	3 500 000	0	0	-=	\	\	
252	Hha1	4	aag	202.535	202	0	202.6	202.47	0	3 700 000	3 500 000	+=	/	/	
253	Taq1	19	cac	202.327	202	202.27	202.28	202.43	3 600 000	3 100 000	9 800 000	=+	/ (-)	/	
254	Hha1	33	agc	69.835	70	69.78	69.89	0	36 000 000	32 900 000	0	=-	\		\(4)
255	Hha1	60	ttg	138.24	138	138.26	0	138.22	6 100 000	0	10 800 000	-+(=)	V		\(4)
256	Hha1	26	ctg	138.603	139	138.45	138.77	138.59	8 200 000	3 300 000	3 900 000	-=	\ (-)		\(4)
257	Hha1	26	ctg	139.08	139	139.08	0	0	3 600 000	0	0	-=	\		\(4)
258	Taq1	18	cct	153.185	153	153.18	153.19	0	8 300 000	8 900 000	0	=-	\		\(4)
259	Hha1	28	tcg	171.57	172	0	171.57	0	0	3 700 000	0	+-	A		\(4)
260	Hha1	60	ttg	209.15	210	0	209.15	0	0	4 000 000	0	+-	A		\(4)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
218	RNO238717.AATF	aatf	AATF protein		agg	agg	increased
219	RNO238717.AATF	aatf	AATF protein		agg	agg	increased
220	RNO238717.AATF	aatf	AATF protein		agg	agg	increased
221	RNO238717.AATF	aatf	AATF protein		agg	agg	increased
222	RNO238717.AATF	aatf	AATF protein		agg	agg	increased
223	RNO238717.AATF	aatf	AATF protein		agg	agg	increased
224	RNO238717.AATF	aatf	AATF protein		agg	agg	increased
225	RNO238717.AATF	aatf	AATF protein		agg	agg	increased
226	RNO238717.AATF	aatf	AATF protein		agg	agg	increased
227	RNO238717.AATF	aatf	AATF protein		agg	agg	increased
228	RNO238717.AATF	aatf	AATF protein		gaa	tac	increased
229	RNO238717.AATF	aatf	AATF protein		gaa	tac	increased
230	RNO238717.AATF	aatf	AATF protein		gaa	tac	increased
231	RNO238717.AATF	aatf	AATF protein		gaa	tac	increased
232	AY325147.PE1	nc	Ab1-181	*	cct	tag	increased
233	AY325147.PE1	nc	Ab1-181	*	cct	tag	increased
234	AY325147.PE1	nc	Ab1-181	*	cct	tag	increased
235	AY325147.PE1	nc	Ab1-181	*	cct	tag	increased
236	AY325147.PE1	nc	Ab1-181	*	cct	tag	increased
237	AY325147.PE1	nc	Ab1-181	*	cct	tag	increased
238	AY325147.PE1	nc	Ab1-181	*	ctt	tta	increased
239	AY325147.PE1	nc	Ab1-181	*	ctt	tta	increased
240	AY325153.PE1	nc	Ab1-216	*	cct	tag	increased
241	AY325153.PE1	nc	Ab1-216	*	cct	tag	increased
242	AY325153.PE1	nc	Ab1-216	*	cct	tag	increased
243	AY325153.PE1	nc	Ab1-216	*	cct	tag	increased
244	AY325153.PE1	nc	Ab1-216	*	cct	tag	increased
245	AY325153.PE1	nc	Ab1-216	*	cct	tag	increased
246	AY325153.PE1	nc	Ab1-216	*	ctt	tta	increased
247	AY325153.PE1	nc	Ab1-216	*	ctt	tta	increased
248	AY325154.PE1	nc	Ab1-219		aac	tgc	increased
249	AY325154.PE1	nc	Ab1-219		aac	tgc	increased
250	AY325180.PE1	nc	Ab2-008		ccc	tgg	increased
251	AY325180.PE1	nc	Ab2-008		ccc	tgg	increased
252	AY325180.PE1	nc	Ab2-008		aag	cac	decreased
253	AY325180.PE1	nc	Ab2-008		aag	cac	decreased
254	AY325183.PE1	nc	Ab2-057	*	agc	ggg	increased
255	AY325183.PE1	nc	Ab2-057	*	ttg	aga	increased
256	AY325183.PE1	nc	Ab2-057	*	ctg	ggg	increased
257	AY325183.PE1	nc	Ab2-057	*	ctg	ggg	increased
258	AY325183.PE1	nc	Ab2-057	*	cct	gag	increased
259	AY325183.PE1	nc	Ab2-057	*	ctc	tcg	increased
260	AY325183.PE1	nc	Ab2-057	*	ttg	cag	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
261	Hha1	60	ttg	210.06	210	210.05	210.07	0	3 100 000	3 800 000	0	=-	\		\(4)
262	Taq1	8	gaa	132.82	133	132.71	132.93	0	4 400 000	6 100 000	0	=-	\	\	
263	Hha1	8	gaa	133.017	133	133.08	133.07	132.9	34 400 000	25 100 000	9 200 000	=-	\ (-)	\	
264	Hha1	41	ccc	148.19	149	147.96	148.26	148.35	6 200 000	12 000 000	22 900 000	=+	/ (-)		A(2) \(2)
265	Hha1	41	ccc	148.78	149	148.78	0	0	4 400 000	0	0	-=	\		A(2) \(2)
266	Taq1	10	atg	246.48	247	0	246.48	0	0	5 500 000	0	+-	A	A	A(2) \(2)
267	Taq1	50	aat	246.545	248	246.34	246.75	0	3 200 000	8 300 000	0	+-	A	A	A(2) \(2)
268	Taq1	50	aat	247.46	248	247.45	247.47	0	6 900 000	7 700 000	0	=-	\		A(2) \(2)
269	Taq1	50	aat	248.04	248	248.04	0	0	13 800 000	0	0	-=	\		A(2) \(2)
270	Taq1	50	aat	249.1	248	249.1	0	0	7 800 000	0	0	-=	\		A(2) \(2)
271	Taq1	50	aat	249.26	248	249.26	0	0	7 400 000	0	0	-=	\		A(2) \(2)
272	Hha1	61	tct	114.59	114	114.59	0	0	3 400 000	0	0	-=	\		\(4)
273	Taq1	17	cca	121.493	122	121.29	121.59	121.6	306.5	219.38	631.48	=+	/ (-)		\(4)
274	Taq1	17	cca	122.58	122	0	122.57	122.59	0	392.23	1 278	=+	/		\(4)
275	Hha1	26	ctg	153.167	154	153.14	153.14	153.22	17 400 000	5 700 000	7 400 000	-=	\ (-)		\(4)
276	Hha1	26	ctg	154.083	154	154.07	154.1	154.08	55 500 000	17 300 000	45 300 000	-+	V		\(4)
277	Taq1	45	gcc	211.55	211	211.55	0	0	5 000 000	0	0	-=	\		\(4)
278	Taq1	51	ata	212.77	213	0	0	212.77	0	0	16 100 000	=+	/		\(4)
279	Hha1	40	tgg	233.26	232	0	0	233.26	0	0	4 900 000	=+	/		\(4)
280	Hha1	7	caa	264.24	263	264.24	0	0	6 200 000	0	0	-=	\		\(4)
281	Taq1	31	gac	98.43	99	98.41	98.36	98.52	10 400 000	15 700 000	18 300 000	==	-		/(2)
282	Taq1	31	gac	99.487	99	99.54	99.43	99.49	5 700 000	3 000 000	31 500 000	=+	/ (-)		/(2)
283	Hha1	59	ttc	161.135	162	161.27	161	0	202.8	301.82	0	=-	\		/(2)
284	Hha1	59	ttc	161.55	162	0	0	161.55	0	0	426.87	=+	/		/(2)
285	Hha1	54	ttt	69.045	69	69.17	0	68.92	5 300 000	0	5 700 000	-+(=)	V		\(6)
286	Hha1	59	ttc	76.257	76	76.46	76.23	76.08	8 107.12	278.83	478.61	-=	\ (-)		\(6)
287	Taq1	56	tga	82.9	83	0	0	82.9	0	0	33 000 000	=+	/		\(6)
288	Taq1	56	tga	83.44	83	0	0	83.44	0	0	11 300 000	=+	/		\(6)
289	Hha1	33	agc	162.513	163	162.57	162.48	162.49	4 300 000	4 100 000	3 700 000	==	-		\(6)
290	Hha1	33	agc	163.62	163	163.55	163.69	0	3 600 000	3 100 000	0	=-	\		\(6)
291	Taq1	29	gca	187.023	188	187.11	186.96	187	3 500 000	3 000 000	3 800 000	==	-		\(6)
292	Taq1	29	gca	188.03	188	187.99	0	188.07	3 800 000	0	3 500 000	-+(=)	V		\(6)
293	Taq1	29	gca	188.997	188	188.98	189.02	188.99	4 800 000	4 700 000	4 100 000	==	-		\(6)
294	Taq1	61	tct	201.24	202	201.03	0	201.45	5 500 000	0	3 400 000	-+(=)	V		\(6)
295	Taq1	61	tct	201.92	202	201.68	202.16	0	3 900 000	3 900 000	0	=-	\		\(6)
296	Taq1	61	tct	202.49	202	0	0	202.49	0	0	6 100 000	=+	/		\(6)
297	Hha1	44	cgg	211.18	212	0	211.18	0	0	4 300 000	0	+-	A		\(6)
298	Hha1	44	cgg	211.37	212	0	211.37	0	0	4 400 000	0	+-	A		\(6)
299	Hha1	44	cgg	212.4	212	212.4	0	0	3 000 000	0	0	-=	\		\(6)
300	Hha1	39	agg	213.6	213	213.6	0	0	219.94	0	0	-=	\		\(6)
301	Hha1	8	gaa	284.86	286	0	284.86	0	0	3 400 000	0	+-	A		\(6)
302	Hha1	8	gaa	286.61	286	286.61	0	0	3 100 000	0	0	-=	\		\(6)
303	Taq1	34	tgc	239.59	240	239.59	0	0	6 300 000	0	0	-=	\		\(2)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
261	AY325183.PE1	nc	Ab2-057	*	ttg	cag	increased
262	AY325188.PE1	nc	Ab2-086		gaa	ggc	increased
263	AY325188.PE1	nc	Ab2-086		gaa	ggc	increased
264	AY325214.PE1	nc	Ab2-417	*	ccc	ccc	increased by mild
265	AY325214.PE1	nc	Ab2-417	*	ccc	ccc	increased by mild
266	AY325214.PE1	nc	Ab2-417	*	aat	atg	increased by mild
267	AY325214.PE1	nc	Ab2-417	*	aat	atg	increased by mild
268	AY325214.PE1	nc	Ab2-417	*	aat	atg	increased by mild
269	AY325214.PE1	nc	Ab2-417	*	aat	atg	increased by mild
270	AY325214.PE1	nc	Ab2-417	*	aat	atg	increased by mild
271	AY325214.PE1	nc	Ab2-417	*	aat	atg	increased by mild
272	AY325216.PE1	nc	Ab2-450		aac	tct	increased
273	AY325216.PE1	nc	Ab2-450		cca	tac	increased
274	AY325216.PE1	nc	Ab2-450		cca	tac	increased
275	AY325216.PE1	nc	Ab2-450		ctg	tgc	increased
276	AY325216.PE1	nc	Ab2-450		ctg	tgc	increased
277	AY325216.PE1	nc	Ab2-450		gcc	ata	increased
278	AY325216.PE1	nc	Ab2-450		gcc	ata	increased
279	AY325216.PE1	nc	Ab2-450		tgg	tgc	increased
280	AY325216.PE1	nc	Ab2-450		caa	aca	increased
281	RNO303374.ABC8	abc8	ABC transporter, white homologue		gct	gac	decreased
282	RNO303374.ABC8	abc8	ABC transporter, white homologue		gct	gac	decreased
283	RNO303374.ABC8	abc8	ABC transporter, white homologue		atc	ttc	decreased
284	RNO303374.ABC8	abc8	ABC transporter, white homologue		atc	ttc	decreased
285	AB037937.ABC2	abc2	ABC2		ttc	ttt	increased
286	AB037937.ABC2	abc2	ABC2		cac	ttc	increased
287	AB037937.ABC2	abc2	ABC2		tga	agc	increased
288	AB037937.ABC2	abc2	ABC2		tga	agc	increased
289	AB037937.ABC2	abc2	ABC2		ttc	agc	increased
290	AB037937.ABC2	abc2	ABC2		ttc	agc	increased
291	AB037937.ABC2	abc2	ABC2		gga	gca	increased
292	AB037937.ABC2	abc2	ABC2		gga	gca	increased
293	AB037937.ABC2	abc2	ABC2		gga	gca	increased
294	AB037937.ABC2	abc2	ABC2		ggg	tct	increased
295	AB037937.ABC2	abc2	ABC2		ggg	tct	increased
296	AB037937.ABC2	abc2	ABC2		ggg	tct	increased
297	AB037937.ABC2	abc2	ABC2		agg	cgg	increased
298	AB037937.ABC2	abc2	ABC2		agg	cgg	increased
299	AB037937.ABC2	abc2	ABC2		agg	cgg	increased
300	AB037937.ABC2	abc2	ABC2		agg	cgg	increased
301	AB037937.ABC2	abc2	ABC2		gaa	act	increased
302	AB037937.ABC2	abc2	ABC2		gaa	act	increased
303	AF293383.PE1	nc	ABC50		aaa	tgc	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
304	Taq1	49	aaa	240.21	241	0	240.21	0	0	19 600 000	0	+-	A		\(2)
305	Taq1	49	aaa	241.02	241	241.08	240.96	0	51 800 000	15 300 000	0	-=	\		\(2)
306	Taq1	49	aaa	242	241	242	0	0	41 000 000	0	0	-=	\		\(2)
307	Taq1	11	act	160.463	161	160.56	160.49	160.34	3 400 000	3 200 000	8 200 000	=+	/ (-)	/	
308	Hha1	11	act	160.6	161	0	0	160.6	0	0	5 000 000	=+	/	/	
309	Taq1	11	act	161.457	161	161.65	161.51	161.21	5 200 000	3 800 000	23 700 000	=+	/ (-)	/	
310	Hha1	11	act	161.543	161	161.48	161.5	161.65	3 600 000	4 100 000	14 400 000	=+	/ (-)	/	
311	Taq1	9	atc	180.007	181	179.95	180.01	180.06	5 900 000	8 600 000	3 200 000	=-	\ (-)		\(6)
312	Hha1	9	atc	180.32	181	0	180.32	0	0	5 200 000	0	+-	A		\(6)
313	Hha1	9	atc	180.92	181	180.92	0	0	11 700 000	0	0	-=	\		\(6)
314	Taq1	23	cga	179.985	181	179.98	179.99	0	9 000 000	6 800 000	0	=-	\		\(6)
315	Taq1	23	cga	181.025	181	181.06	180.99	0	6 000 000	11 400 000	0	+-	A		\(6)
316	Taq1	23	cga	181.985	181	182.02	181.95	0	7 000 000	24 000 000	0	+-	A		\(6)
317	Hha1	4	aag	209.87	211	0	0	209.87	0	0	4 900 000	=+	/		\(6)
318	Hha1	4	aag	210.91	211	210.93	0	210.89	7 200 000	0	3 900 000	-+(-)	V (\)	(\)	\(6)
319	Hha1	4	aag	211.885	211	211.96	0	211.81	4 600 000	0	3 000 000	-+(=)	V		\(6)
320	Hha1	9	atc	210.94	211	210.93	210.95	0	7 800 000	3 500 000	0	-=	\	(\)	\(6)
321	Hha1	9	atc	211.4	211	211.4	0	0	4 500 000	0	0	-=	\		\(6)
322	Hha1	7	caa	219.853	221	219.78	219.86	219.92	3 700 000	3 600 000	3 900 000	==	-		\(6)
323	Hha1	7	caa	220.663	221	220.73	220.66	220.6	41 200 000	6 500 000	7 800 000	-=	\ (-)		\(6)
324	Hha1	7	caa	220.96	221	0	220.96	0	0	5 300 000	0	+-	A		\(6)
325	Hha1	7	caa	221.76	221	0	0	221.76	0	0	3 400 000	=+	/		\(6)
326	Taq1	63	ctt	134.903	135	134.9	134.76	135.05	3 800 000	3 200 000	4 300 000	==	-		\(2) A(2)
327	Taq1	63	ctt	134.99	135	0	134.99	0	0	3 700 000	0	+-	A		\(2) A(2)
328	Taq1	54	ttt	135.905	136	135.89	135.92	0	662.78	893.8	0	=-	\		\(2) A(2)
329	Taq1	54	ttt	136.7	136	0	136.7	0	0	388.09	0	+-	A		\(2) A(2)
330	Taq1	39	agg	141.93	142	141.93	0	0	10 900 000	0	0	-=	\		\(2) A(2)
331	Taq1	39	agg	141.93	142	141.93	0	0	404.78	0	0	-=	\		\(2) A(2)
332	Hha1	33	agc	69.835	70	69.78	69.89	0	36 000 000	32 900 000	0	=-	\		\(4)
333	Hha1	60	ttg	138.24	138	138.26	0	138.22	6 100 000	0	10 800 000	-+(=)	V		\(4)
334	Hha1	26	ctg	138.603	139	138.45	138.77	138.59	8 200 000	3 300 000	3 900 000	-=	\ (-)		\(4)
335	Hha1	26	ctg	139.08	139	139.08	0	0	3 600 000	0	0	-=	\		\(4)
336	Taq1	18	cct	153.185	153	153.18	153.19	0	8 300 000	8 900 000	0	=-	\		\(4)
337	Hha1	28	tcg	171.57	172	0	171.57	0	0	3 700 000	0	+-	A		\(4)
338	Hha1	60	ttg	209.15	210	0	209.15	0	0	4 000 000	0	+-	A		\(4)
339	Hha1	60	ttg	210.06	210	210.05	210.07	0	3 100 000	3 800 000	0	=-	\		\(4)
340	Taq1	45	gcc	81.08	81	0	81.17	80.99	0	11 000 000	23 200 000	++	/		\(4)
341	Taq1	9	atc	180.007	181	179.95	180.01	180.06	5 900 000	8 600 000	3 200 000	=-	\ (-)		\(4)
342	Hha1	9	atc	180.32	181	0	180.32	0	0	5 200 000	0	+-	A		\(4)
343	Hha1	9	atc	180.92	181	180.92	0	0	11 700 000	0	0	-=	\		\(4)
344	Taq1	18	cct	191.205	192	191.16	191.25	0	3 300 000	5 000 000	0	=-	\		\(4)
345	Taq1	18	cct	192.21	192	192.19	192.23	0	8 400 000	11 000 000	0	=-	\	\	\(4)
346	Taq1	51	ata	192.29	193	192.29	0	0	4 000 000	0	0	-=	\	\	\(4)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
304	AF293383.PE1	nc	ABC50		aaa	tgc	increased
305	AF293383.PE1	nc	ABC50		aaa	tgc	increased
306	AF293383.PE1	nc	ABC50		aaa	tgc	increased
307	AY310136.PE1	nc	Ac1002		tcc	act	decreased
308	AY310136.PE1	nc	Ac1002		tcc	act	decreased
309	AY310136.PE1	nc	Ac1002		tcc	act	decreased
310	AY310136.PE1	nc	Ac1002		tcc	act	decreased
311	AY310138.PE1	nc	Ac1055		atc	cga	increased
312	AY310138.PE1	nc	Ac1055		atc	cga	increased
313	AY310138.PE1	nc	Ac1055		atc	cga	increased
314	AY310138.PE1	nc	Ac1055		atc	cga	increased
315	AY310138.PE1	nc	Ac1055		atc	cga	increased
316	AY310138.PE1	nc	Ac1055		atc	cga	increased
317	AY310138.PE1	nc	Ac1055		aag	atc	increased
318	AY310138.PE1	nc	Ac1055		aag	atc	increased
319	AY310138.PE1	nc	Ac1055		aag	atc	increased
320	AY310138.PE1	nc	Ac1055		aag	atc	increased
321	AY310138.PE1	nc	Ac1055		aag	atc	increased
322	AY310138.PE1	nc	Ac1055		gca	caa	increased
323	AY310138.PE1	nc	Ac1055		gca	caa	increased
324	AY310138.PE1	nc	Ac1055		gca	caa	increased
325	AY310138.PE1	nc	Ac1055		gca	caa	increased
326	AY321317.PE1	nc	Ac1-060	*	ctt	ttt	increased
327	AY321317.PE1	nc	Ac1-060	*	ctt	ttt	increased
328	AY321317.PE1	nc	Ac1-060	*	ctt	ttt	increased
329	AY321317.PE1	nc	Ac1-060	*	ctt	ttt	increased
330	AY321317.PE1	nc	Ac1-060	*	agg	cgc	increased
331	AY321317.PE1	nc	Ac1-060	*	agg	cgc	increased
332	AY310143.PE1	nc	Ac1147	*	agc	ggg	increased
333	AY310143.PE1	nc	Ac1147	*	ttg	aga	increased
334	AY310143.PE1	nc	Ac1147	*	ctg	ggg	increased
335	AY310143.PE1	nc	Ac1147	*	ctg	ggg	increased
336	AY310143.PE1	nc	Ac1147	*	cct	gag	increased
337	AY310143.PE1	nc	Ac1147	*	ctc	tcg	increased
338	AY310143.PE1	nc	Ac1147	*	ttg	cag	increased
339	AY310143.PE1	nc	Ac1147	*	ttg	cag	increased
340	AY310154.PE1	nc	Ac1288		aac	gcc	increased
341	AY310154.PE1	nc	Ac1288		atc	gct	increased
342	AY310154.PE1	nc	Ac1288		atc	gct	increased
343	AY310154.PE1	nc	Ac1288		atc	gct	increased
344	AY310154.PE1	nc	Ac1288		ata	cct	increased
345	AY310154.PE1	nc	Ac1288		ata	cct	increased
346	AY310154.PE1	nc	Ac1288		ata	cct	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
347	Taq1	51	ata	193.21	193	193.21	0	0	14 900 000	0	0	-=	\		\(4)
348	Taq1	16	tag	111.43	112	0	111.47	111.39	0	4 600 000	7 100 000	+=	/		\(4)
349	Hha1	16	tag	111.825	112	111.76	0	111.89	11 200 000	0	3 200 000	-=(-)	\		\(4)
350	Taq1	16	tag	112.325	112	112.39	0	112.26	3 100 000	0	6 600 000	-+(+)	V (/)		\(4)
351	Hha1	16	tag	112.64	112	112.64	0	0	3 400 000	0	0	-=	\		\(4)
352	Taq1	18	cct	111.553	112	111.49	111.59	111.58	25 800 000	21 800 000	5 300 000	=-	\ (-)		\(4)
353	Taq1	18	cct	112.613	112	112.59	112.64	112.61	32 900 000	30 500 000	3 000 000	=-	\ (-)		\(4)
354	Taq1	63	ctt	192.08	193	192.08	0	0	3 000 000	0	0	-=	\		\(4)
355	Taq1	63	ctt	193.04	193	193.04	0	193.04	3 100 000	0	3 400 000	-+(=)	V		\(4)
356	Hha1	8	gaa	166.71	167	166.79	166.67	166.67	5 900 000	11 600 000	8 600 000	+=	/ (-)	/	
357	Taq1	8	gaa	166.82	167	0	0	166.82	0	0	3 900 000	=+	/	/	
358	Taq1	45	gcc	86.003	86	85.99	85.93	86.09	14 600 000	21 500 000	4 600 000	=-	\ (-)		\(4)
359	Taq1	45	gcc	86.44	86	86.44	0	0	12 700 000	0	0	-=	\		\(4)
360	Hha1	7	caa	139.295	140	0	139.3	139.29	0	7 800 000	6 200 000	+=	/		\(4)
361	Taq1	7	caa	139.34	140	139.4	0	139.28	3 000 000	0	3 000 000	-+(=)	V		\(4)
362	Taq1	7	caa	140.3	140	140.3	0	0	4 000 000	0	0	-=	\		\(4)
363	Hha1	7	caa	140.363	140	140.45	140.34	140.3	7 400 000	5 100 000	5 300 000	==	-		\(4)
364	Taq1	34	tgc	139.62	140	139.62	0	0	3 000 000	0	0	-=	\		\(4)
365	Hha1	6	aga	242.38	241	242.38	0	0	5 800 000	0	0	-=	\		\(4)
366	Hha1	32	gtc	105.85	106	0	0	105.85	0	0	685.92	=+	/		/(2)
367	Hha1	4	aag	137.21	138	0	137.21	0	0	10 000 000	0	+-	A		/(2)
368	Hha1	4	aag	137.94	138	137.78	0	138.1	44 500 000	0	9 400 000	-=(-)	\		/(2)
369	Taq1	17	cca	137.747	138	137.72	137.69	137.83	283.28	478.65	932.19	=+	/ (-)		/(2)
370	Taq1	17	cca	138.79	138	138.65	138.81	138.91	283.28	265.92	2 044.8	=+	/ (-)		/(2)
371	Hha1	33	agc	77.803	78	77.78	77.86	77.77	56 700 000	20 100 000	9 400 000	-=	\ (-)		/(4)
372	Hha1	49	aaa	78.905	79	78.66	0	79.15	27 100 000	0	20 800 000	-+(=)	V		/(4)
373	Taq1	62	tgt	180.51	181	0	0	180.51	0	0	7 000 000	=+	/		/(4)
374	Taq1	62	tgt	181.645	181	0	181.79	181.5	0	3 400 000	14 700 000	=+	/		/(4)
375	Taq1	11	act	237.38	238	0	0	237.38	0	0	3 200 000	=+	/		/(4)
376	Hha1	11	act	238.51	238	0	0	238.51	0	0	3 200 000	=+	/		/(4)
377	Taq1	11	act	239.28	238	0	0	239.28	0	0	3 000 000	=+	/		/(4)
378	Taq1	1	tat	104.287	104	104.23	104.23	104.4	7 700 000	11 900 000	4 900 000	=-	\ (-)		\(3)
379	Taq1	57	ctg	165.61	166	0	0	165.61	0	0	13 000 000	=+	/		\(3)
380	Taq1	57	ctg	166.6	166	0	0	166.6	0	0	7 900 000	=+	/		\(3)
381	Hha1	25	cag	303.98	305	0	303.87	304.09	0	3 000 000	3 600 000	+=	/		\(3)
382	Hha1	25	cag	305.22	305	305.22	0	0	3 100 000	0	0	-=	\		\(3)
383	Hha1	25	cag	305.89	305	305.89	0	0	3 400 000	0	0	-=	\		\(3)
384	Taq1	56	tga	322.42	323	322.45	322.39	0	5 300 000	6 900 000	0	=-	\		\(3)
385	Hha1	56	tga	131.46	132	131.46	0	0	1 066.48	0	0	-=	\		/(2) \(2)
386	Hha1	56	tga	131.98	132	0	0	131.98	0	0	2 689.19	=+	/		/(2) \(2)
387	Hha1	39	agg	172.59	173	0	0	172.59	0	0	231.93	=+	/		/(2) \(2)
388	Hha1	39	agg	173.35	173	0	173.12	173.58	0	250.76	162.76	+=	/		/(2) \(2)
389	Hha1	49	aaa	173.91	174	173.8	174.21	173.72	35 400 000	10 400 000	3 800 000	-=	\ (-)		/(2) \(2)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
347	AY310154.PE1	nc	Ac1288		ata	cct	increased
348	AY321323.PE1	nc	Ac1-581	*	cct	tag	increased
349	AY321323.PE1	nc	Ac1-581	*	cct	tag	increased
350	AY321323.PE1	nc	Ac1-581	*	cct	tag	increased
351	AY321323.PE1	nc	Ac1-581	*	cct	tag	increased
352	AY321323.PE1	nc	Ac1-581	*	cct	tag	increased
353	AY321323.PE1	nc	Ac1-581	*	cct	tag	increased
354	AY321323.PE1	nc	Ac1-581	*	ctt	tta	increased
355	AY321323.PE1	nc	Ac1-581	*	ctt	tta	increased
356	AY310161.PE1	nc	Ac1873		gaa	gtg	decreased
357	AY310161.PE1	nc	Ac1873		gaa	gtg	decreased
358	AY325220.PE1	nc	Ac2-154		ctc	gcc	increased
359	AY325220.PE1	nc	Ac2-154		ctc	gcc	increased
360	AY325220.PE1	nc	Ac2-154		caa	tgc	increased
361	AY325220.PE1	nc	Ac2-154		caa	tgc	increased
362	AY325220.PE1	nc	Ac2-154		caa	tgc	increased
363	AY325220.PE1	nc	Ac2-154		caa	tgc	increased
364	AY325220.PE1	nc	Ac2-154		caa	tgc	increased
365	AY325220.PE1	nc	Ac2-154		aga	gga	increased
366	AY321340.PE1	nc	Ac2-190		ggc	gtc	decreased
367	AY321340.PE1	nc	Ac2-190		aag	cca	decreased
368	AY321340.PE1	nc	Ac2-190		aag	cca	decreased
369	AY321340.PE1	nc	Ac2-190		aag	cca	decreased
370	AY321340.PE1	nc	Ac2-190		aag	cca	decreased
371	AY321338.PE1	nc	Ac2-210		aaa	agc	decreased
372	AY321338.PE1	nc	Ac2-210		aaa	agc	decreased
373	AY321338.PE1	nc	Ac2-210		gag	tgt	decreased
374	AY321338.PE1	nc	Ac2-210		gag	tgt	decreased
375	AY321338.PE1	nc	Ac2-210		gat	act	decreased
376	AY321338.PE1	nc	Ac2-210		gat	act	decreased
377	AY321338.PE1	nc	Ac2-210		gat	act	decreased
378	AY321342.PE1	nc	Ac2-223		ctt	tat	increased
379	AY321342.PE1	nc	Ac2-223		ctg	tga	increased
380	AY321342.PE1	nc	Ac2-223		ctg	tga	increased
381	AY321342.PE1	nc	Ac2-223		cag	gag	increased
382	AY321342.PE1	nc	Ac2-223		cag	gag	increased
383	AY321342.PE1	nc	Ac2-223		cag	gag	increased
384	AY321342.PE1	nc	Ac2-223		tga	atc	increased
385	AY321345.PE1	nc	Ac2-238		aag	tga	decreased
386	AY321345.PE1	nc	Ac2-238		aag	tga	decreased
387	AY321345.PE1	nc	Ac2-238		agg	aaa	decreased
388	AY321345.PE1	nc	Ac2-238		agg	aaa	decreased
389	AY321345.PE1	nc	Ac2-238		agg	aaa	decreased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
390	Hha1	49	aaa	174.99	174	174.88	175.1	0	6 300 000	14 700 000	0	+-	A		/(2) \(2)
391	Hha1	39	agg	117.867	118	118	117.99	117.61	373.9	352.25	410.97	==	-		-2
392	Hha1	56	tga	179.93	181	179.93	0	0	236.99	0	0	-=	\		-2
393	Hha1	56	tga	180.19	181	180.19	0	0	196.13	0	0	-=	\		-2
394	Hha1	56	tga	181.72	181	181.52	181.73	181.91	780.45	220.16	551.62	-=	\ (-)		-2
395	Taq1	44	cgg	165.55	166	0	165.69	165.41	0	373.26	829.41	++	/		/(2)
396	Taq1	19	cac	166.633	167	166.6	166.68	166.62	6 300 000	5 800 000	9 000 000	==	-		/(2)
397	Taq1	19	cac	167.587	167	167.56	167.63	167.57	4 700 000	6 600 000	20 300 000	=+	/ (-)		/(2)
398	Taq1	44	cgg	165.55	166	0	165.69	165.41	0	373.26	829.41	++	/		/(2)
399	Taq1	19	cac	166.633	167	166.6	166.68	166.62	6 300 000	5 800 000	9 000 000	==	-		/(2)
400	Taq1	19	cac	167.587	167	167.56	167.63	167.57	4 700 000	6 600 000	20 300 000	=+	/ (-)		/(2)
401	Hha1	61	tct	114.59	115	114.59	0	0	3 400 000	0	0	-=	\		/(2)
402	Hha1	20	ctc	123.01	123	0	0	123.01	0	0	989.98	=+	/		/(2)
403	Hha1	41	ccc	147.425	147	0	147.36	147.49	0	6 700 000	7 000 000	+=	/		/(2)
404	Taq1	12	agt	210.343	211	210.43	210.24	210.36	4 000 000	4 500 000	3 000 000	==	-	-	
405	Hha1	16	tag	210.477	211	210.5	210.48	210.45	7 300 000	5 000 000	3 100 000	==	-	-	
406	Hha1	10	atg	188.085	189	188.04	188.13	0	8 000 000	3 900 000	0	--	\		\(4)
407	Taq1	10	atg	188.83	189	188.73	188.93	0	4 900 000	9 900 000	0	+-	A		\(4)
408	Hha1	10	atg	189.1	189	189.1	0	0	4 400 000	0	0	-=	\		\(4)
409	Hha1	10	atg	189.96	189	189.96	0	0	4 900 000	0	0	-=	\		\(4)
410	Taq1	63	ctt	189.01	189	0	188.95	189.07	0	3 100 000	4 100 000	+=	/		\(4)
411	Taq1	17	cca	257.6	259	257.6	0	0	199.69	0	0	-=	\		\(4)
412	Taq1	17	cca	260.08	259	260.08	0	0	190.4	0	0	-=	\		\(4)
413	Taq1	17	cca	349.53	350	0	349.53	0	0	850.95	0	+-	A		\(4)
414	Taq1	17	cca	350.56	350	0	350.56	0	0	8 250.23	0	+-	A		\(4)
415	Taq1	17	cca	351.535	350	0	351.6	351.47	0	651.5	631.48	+=	/		\(4)
416	Taq1	17	cca	352	350	352	0	0	1 657.92	0	0	-=	\		\(4)
417	Taq1	45	gcc	150.34	151	0	150.34	0	0	4 800 000	0	+-	A		A(2)
418	Taq1	39	agg	151.215	152	151.33	151.1	0	14 900 000	38 500 000	0	+-	A		A(2)
419	Taq1	39	agg	152.155	152	152.37	151.94	0	20 800 000	30 900 000	0	=-	\		A(2)
420	Taq1	39	agg	151.33	152	151.33	0	0	553.32	0	0	-=	\		A(2)
421	Taq1	39	agg	152.52	152	152.37	152.63	152.56	772.43	25 800 000	20 700 000	+=	/ (-)		A(2)
422	Taq1	39	agg	151.1	152	0	151.1	0	0	386.93	0	+-	A		A(2)
423	Taq1	39	agg	151.94	152	0	151.94	0	0	310.55	0	+-	A		A(2)
424	Taq1	39	agg	152.595	152	0	152.63	152.56	0	259.29	609.72	=+	/		A(2)
425	Hha1	33	agc	69.835	70	69.78	69.89	0	36 000 000	32 900 000	0	=-	\		\(3)
426	Hha1	27	acg	110.98	111	111.02	110.89	111.03	26 500 000	9 300 000	29 400 000	-+	V		\(3)
427	Hha1	40	tgg	110.9	111	0	110.9	0	0	11 200 000	0	+-	A		\(3)
428	Hha1	40	tgg	111.665	111	111.74	111.59	0	15 700 000	4 400 000	0	-=	\		\(3)
429	Hha1	43	cgc	156.85	156	0	156.85	0	0	6 300 000	0	+-	A		\(3)
430	Hha1	31	gac	156.29	157	156.26	156.32	0	8 400 000	3 800 000	0	--	\		\(3)
431	Hha1	31	gac	157.27	157	157.27	0	0	6 600 000	0	0	-=	\		\(3)
432	Taq1	23	cga	126.45	127	0	0	126.45	0	0	9 800 000	=+	/	/	

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
390	AY321345.PE1	nc	Ac2-238		agg	aaa	decreased
391	AB026291.PE1	nc	acetoacetyl-CoA synthetase		agg	tcc	No change
392	AB026291.PE1	nc	acetoacetyl-CoA synthetase		cca	tga	No change
393	AB026291.PE1	nc	acetoacetyl-CoA synthetase		cca	tga	No change
394	AB026291.PE1	nc	acetoacetyl-CoA synthetase		cca	tga	No change
395	RNACRE.PE1	nc	acetylcholine receptor epsilon subunit		cac	cgg	decreased
396	RNACRE.PE1	nc	acetylcholine receptor epsilon subunit		cac	cgg	decreased
397	RNACRE.PE1	nc	acetylcholine receptor epsilon subunit		cac	cgg	decreased
398	RNACRE1.PE1	nc	acetylcholine receptor epsilon-subunit		cac	cgg	decreased
399	RNACRE1.PE1	nc	acetylcholine receptor epsilon-subunit		cac	cgg	decreased
400	RNACRE1.PE1	nc	acetylcholine receptor epsilon-subunit		cac	cgg	decreased
401	RATNAP22.NAP-22	NAP-22	acidic membrane protein of rat brain		ggg	tct	decreased
402	RATNAP22.NAP-22	NAP-22	acidic membrane protein of rat brain		gga	ctc	decreased
403	RATNAP22.NAP-22	NAP-22	acidic membrane protein of rat brain		ccc	ggg	decreased
404	AY063759.AFAP	Afap	actin filament associated protein		agt	tag	No change
405	AY063759.AFAP	Afap	actin filament associated protein		agt	tag	No change
406	AF252627.PE1	nc	activating transcription factor ATF-4		atg	ctt	increased
407	AF252627.PE1	nc	activating transcription factor ATF-4		atg	ctt	increased
408	AF252627.PE1	nc	activating transcription factor ATF-4		atg	ctt	increased
409	AF252627.PE1	nc	activating transcription factor ATF-4		atg	ctt	increased
410	AF252627.PE1	nc	activating transcription factor ATF-4		atg	ctt	increased
411	AF252627.PE1	nc	activating transcription factor ATF-4		cca	agt	increased
412	AF252627.PE1	nc	activating transcription factor ATF-4		cca	agt	increased
413	AF252627.PE1	nc	activating transcription factor ATF-4		cca	gaa	increased
414	AF252627.PE1	nc	activating transcription factor ATF-4		cca	gaa	increased
415	AF252627.PE1	nc	activating transcription factor ATF-4		cca	gaa	increased
416	AF252627.PE1	nc	activating transcription factor ATF-4		cca	gaa	increased
417	RATACTIREC.PE1	nc	activin type I receptor		agg	gcc	increased by mild
418	RATACTIREC.PE1	nc	activin type I receptor		agg	gcc	increased by mild
419	RATACTIREC.PE1	nc	activin type I receptor		agg	gcc	increased by mild
420	RATACTIREC.PE1	nc	activin type I receptor		agg	gcc	increased by mild
421	RATACTIREC.PE1	nc	activin type I receptor		agg	gcc	increased by mild
422	RATACTIREC.PE1	nc	activin type I receptor		agg	gcc	increased by mild
423	RATACTIREC.PE1	nc	activin type I receptor		agg	gcc	increased by mild
424	RATACTIREC.PE1	nc	activin type I receptor		agg	gcc	increased by mild
425	AB010429.PE1	nc	acyl-CoA hydrolase-like protein		gga	agc	increased
426	AB010429.PE1	nc	acyl-CoA hydrolase-like protein		gga	acg	increased
427	AB010429.PE1	nc	acyl-CoA hydrolase-like protein		tgg	cag	increased
428	AB010429.PE1	nc	acyl-CoA hydrolase-like protein		tgg	cag	increased
429	AB010429.PE1	nc	acyl-CoA hydrolase-like protein		gac	cgc	increased
430	AB010429.PE1	nc	acyl-CoA hydrolase-like protein		gac	cgc	increased
431	AB010429.PE1	nc	acyl-CoA hydrolase-like protein		gac	cgc	increased
432	AB075946.PE1	nc	AcylCoA:Cholesterol Acyltransferase 2		cga	tgg	decreased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
433	Taq1	40	tgg	126.64	127	0	0	126.64	0	0	25 300 000	=+	/	/	
434	Taq1	23	cga	126.45	127	0	0	126.45	0	0	9 800 000	=+	/	/	
435	Taq1	40	tgg	126.64	127	0	0	126.64	0	0	25 300 000	=+	/	/	
436	Hha1	2	tta	111.663	112	111.53	111.71	111.75	8 700 000	9 100 000	16 600 000	=+	/ (-)		/(4)
437	Hha1	2	tta	112.03	112	111.89	0	112.17	8 000 000	0	16 800 000	-+(+)	V (/)		/(4)
438	Hha1	7	caa	124.747	125	124.55	124.81	124.88	5 600 000	67 400 000	74 900 000	+=	/ (-)	/	/(4)
439	Taq1	7	caa	124.927	125	124.96	124.69	125.13	3 100 000	6 300 000	6 300 000	+=	/ (-)	/	/(4)
440	Taq1	55	tca	125.16	125	0	0	125.16	0	0	3 500 000	=+	/		/(4)
441	Hha1	43	cgc	122.23	122	122.19	122.27	0	20 400 000	5 700 000	0	-=	\		\(5)
442	Hha1	26	ctg	123.06	123	123.17	122.89	123.12	6 100 000	8 400 000	3 000 000	=-	\ (-)		\(5)
443	Hha1	41	ccc	130.903	131	130.87	130.9	130.94	11 900 000	4 700 000	4 300 000	-=	\ (-)		\(5)
444	Hha1	49	aaa	145.135	146	145.2	145.07	0	42 900 000	24 500 000	0	=-	\		\(5)
445	Hha1	49	aaa	146.115	146	146.12	146.11	0	16 800 000	11 500 000	0	=-	\		\(5)
446	Hha1	6	aga	167.615	168	167.59	0	167.64	10 500 000	0	3 200 000	-=(-)	\		\(5)
447	Hha1	6	aga	168.64	168	168.64	0	0	6 700 000	0	0	-=	\		\(5)
448	Hha1	26	ctg	99.44	100	99.53	99.35	0	10 500 000	4 000 000	0	-=	\		A(3)
449	Hha1	39	agg	100.65	101	100.4	0	100.9	461.87	0	687.66	-+(=)	V		A(3)
450	Hha1	39	agg	101.02	101	0	101.02	0	0	770.19	0	+-	A		A(3)
451	Hha1	61	tct	162.43	163	0	162.43	0	0	6 800 000	0	+-	A		A(3)
452	Hha1	61	tct	163.493	163	163.61	163.42	163.45	6 800 000	18 000 000	10 400 000	+=	/ (-)		A(3)
453	Hha1	62	tgt	163.16	163	0	0	163.16	0	0	3 100 000	=+	/		A(3)
454	Hha1	39	agg	202.06	203	0	202.17	201.95	0	280.61	130.2	+-	A		A(3)
455	Taq1	12	agt	121.123	121	121.11	121.1	121.16	4 100 000	4 200 000	4 800 000	==	-		-1
456	Taq1	40	tgg	120.38	121	120.22	120.32	120.6	5 900 000	107 000 000	9 700 000	+-	A		-1
457	Taq1	40	tgg	120.94	121	120.79	121.09	0	22 800 000	13 300 000	0	=-	\		-1
458	Taq1	40	tgg	121.58	121	0	0	121.58	0	0	8 700 000	=+	/		-1
459	Taq1	62	tgt	120.55	121	120.53	120.61	120.51	4 300 000	8 300 000	9 100 000	==	-		-1
460	Taq1	62	tgt	121.485	121	121.49	0	121.48	3 400 000	0	10 100 000	=+(+)	/		-1
461	Taq1	49	aaa	170.027	171	169.83	170.12	170.13	9 600 000	4 900 000	3 400 000	-=	\ (-)		-1
462	Taq1	49	aaa	171.005	171	0	170.94	171.07	0	12 900 000	58 400 000	=+	/		-1
463	Taq1	49	aaa	171.86	171	172	171.76	171.82	64 500 000	9 700 000	4 200 000	-=	\ (-)		-1
464	Taq1	56	tga	78.733	79	78.58	79.04	78.58	23 900 000	5 500 000	3 400 000	-=	\ (-)		-3
465	Taq1	12	agt	121.123	121	121.11	121.1	121.16	4 100 000	4 200 000	4 800 000	==	-		-3
466	Taq1	62	tgt	120.55	121	120.53	120.61	120.51	4 300 000	8 300 000	9 100 000	==	-		-3
467	Taq1	62	tgt	121.485	121	121.49	0	121.48	3 400 000	0	10 100 000	=+(+)	/		-3
468	Taq1	56	tga	78.733	79	78.58	79.04	78.58	23 900 000	5 500 000	3 400 000	-=	\ (-)		-4
469	Taq1	12	agt	121.123	121	121.11	121.1	121.16	4 100 000	4 200 000	4 800 000	==	-		-4
470	Taq1	62	tgt	120.55	121	120.53	120.61	120.51	4 300 000	8 300 000	9 100 000	==	-		-4
471	Taq1	62	tgt	121.485	121	121.49	0	121.48	3 400 000	0	10 100 000	=+(+)	/		-4
472	Taq1	49	aaa	170.027	171	169.83	170.12	170.13	9 600 000	4 900 000	3 400 000	-=	\ (-)		-4
473	Taq1	49	aaa	171.005	171	0	170.94	171.07	0	12 900 000	58 400 000	=+	/		-4
474	Taq1	49	aaa	171.86	171	172	171.76	171.82	64 500 000	9 700 000	4 200 000	-=	\ (-)		-4
475	Taq1	56	tga	78.733	79	78.58	79.04	78.58	23 900 000	5 500 000	3 400 000	-=	\ (-)		\(2)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
433	AB075946.PE1	nc	AcylCoA:Cholesterol Acyltransferase 2		cga	tgg	decreased
434	AB101480.ACAT-2	ACAT-2	acyl-coenzyme A:cholesterol acyltransferase-2		cga	tgg	decreased
435	AB101480.ACAT-2	ACAT-2	acyl-coenzyme A:cholesterol acyltransferase-2		cga	tgg	decreased
436	D42151S6.AD4BP	ad4bp	Ad4BP		aca	tta	decreased
437	D42151S6.AD4BP	ad4bp	Ad4BP		aca	tta	decreased
438	D42151S6.AD4BP	ad4bp	Ad4BP		caa	tca	decreased
439	D42151S6.AD4BP	ad4bp	Ad4BP		caa	tca	decreased
440	D42151S6.AD4BP	ad4bp	Ad4BP		caa	tca	decreased
441	AF304446.PE1	nc	ADAMTS-1		ctg	cgc	increased
442	AF304446.PE1	nc	ADAMTS-1		ctg	cgc	increased
443	AF304446.PE1	nc	ADAMTS-1		ccc	taa	increased
444	AF304446.PE1	nc	ADAMTS-1		aaa	cct	increased
445	AF304446.PE1	nc	ADAMTS-1		aaa	cct	increased
446	AF304446.PE1	nc	ADAMTS-1		aga	ggc	increased
447	AF304446.PE1	nc	ADAMTS-1		aga	ggc	increased
448	AF277899.PE1	nc	adapter protein ATH-55		ctg	aga	increased by mild
449	AF277899.PE1	nc	adapter protein ATH-55		cct	agg	increased by mild
450	AF277899.PE1	nc	adapter protein ATH-55		cct	agg	increased by mild
451	AF277899.PE1	nc	adapter protein ATH-55		tct	tgt	increased by mild
452	AF277899.PE1	nc	adapter protein ATH-55		tct	tgt	increased by mild
453	AF277899.PE1	nc	adapter protein ATH-55		tct	tgt	increased by mild
454	AF277899.PE1	nc	adapter protein ATH-55		agg	ggt	increased by mild
455	AF255888.RUK	Ruk	adapter protein RUK-l		tgt	agt	No change
456	AF255888.RUK	Ruk	adapter protein RUK-l		ttg	tgg	No change
457	AF255888.RUK	Ruk	adapter protein RUK-l		ttg	tgg	No change
458	AF255888.RUK	Ruk	adapter protein RUK-l		ttg	tgg	No change
459	AF255888.RUK	Ruk	adapter protein RUK-l		tgt	agt	No change
460	AF255888.RUK	Ruk	adapter protein RUK-l		tgt	agt	No change
461	AF255888.RUK	Ruk	adapter protein RUK-l		aaa	tgc	No change
462	AF255888.RUK	Ruk	adapter protein RUK-l		aaa	tgc	No change
463	AF255888.RUK	Ruk	adapter protein RUK-l		aaa	tgc	No change
464	AF255886.RUK	Ruk	adapter protein RUK-m1		gga	tga	No change
465	AF255886.RUK	Ruk	adapter protein RUK-m1		tgt	agt	No change
466	AF255886.RUK	Ruk	adapter protein RUK-m1		tgt	agt	No change
467	AF255886.RUK	Ruk	adapter protein RUK-m1		tgt	agt	No change
468	AF255887.RUK	Ruk	adapter protein RUK-m3		gga	tga	No change
469	AF255887.RUK	Ruk	adapter protein RUK-m3		tgt	agt	No change
470	AF255887.RUK	Ruk	adapter protein RUK-m3		tgt	agt	No change
471	AF255887.RUK	Ruk	adapter protein RUK-m3		tgt	agt	No change
472	AF255887.RUK	Ruk	adapter protein RUK-m3		aaa	tgc	No change
473	AF255887.RUK	Ruk	adapter protein RUK-m3		aaa	tgc	No change
474	AF255887.RUK	Ruk	adapter protein RUK-m3		aaa	tgc	No change
475	AF255884.RUK	Ruk	adapter protein RUK-s		gga	tga	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
476	Taq1	10	atg	96.625	97	96.64	96.61	0	57 100 000	16 100 000	0	-=	\		\(2)
477	Hha1	60	ttg	96.59	97	96.81	96.37	0	3 700 000	6 600 000	0	=-	\		\(8)
478	Hha1	60	ttg	97.01	97	0	0	97.01	0	0	5 800 000	=+	/		\(8)
479	Hha1	20	ctc	101.455	101	101.45	0	101.46	523.41	0	381.67	-+(=)	V		\(8)
480	Hha1	41	ccc	101.02	101	101.06	101.22	100.78	40 900 000	5 400 000	4 600 000	-=	\ (-)		\(8)
481	Hha1	41	ccc	101.51	101	0	0	101.51	0	0	5 200 000	=+	/		\(8)
482	Hha1	26	ctg	112.757	113	112.71	112.77	112.79	32 400 000	14 800 000	8 000 000	-=	\ (-)		\(8)
483	Hha1	40	tgg	113.48	113	113.23	113.73	0	46 700 000	9 600 000	0	-=	\		\(8)
484	Hha1	62	tgt	138.98	139	138.98	0	138.98	6 400 000	0	3 500 000	-+(-)	V (\)		\(8)
485	Taq1	47	ggc	146.14	147	146.1	146.24	146.08	2 338.46	1 877.78	1 619.87	==	-		\(8)
486	Taq1	47	ggc	147.205	147	147.17	147.24	0	2 092.3	1 050.28	0	--	\		\(8)
487	Taq1	52	att	148.167	149	148.2	148.23	148.07	4 800 000	5 600 000	4 300 000	==	-		\(8)
488	Hha1	56	tga	194.19	195	194.19	0	0	249.25	0	0	-=	\		\(8)
489	Hha1	56	tga	195.79	195	195.67	195.91	0	2 047.15	264.2	0	-=	\		\(8)
490	Hha1	41	ccc	199.18	200	0	0	199.18	0	0	8 400 000	=+	/		\(8)
491	Hha1	41	ccc	200.5	200	0	0	200.5	0	0	4 700 000	=+	/		\(8)
492	Taq1	39	agg	246.91	247	246.86	246.96	0	3 300 000	36 300 000	0	+-	A		\(8)
493	Taq1	39	agg	247.87	247	247.87	0	0	12 800 000	0	0	-=	\		\(8)
494	Taq1	39	agg	246.86	247	246.86	0	0	122.54	0	0	-=	\		\(8)
495	Taq1	39	agg	247.87	247	247.87	0	0	475.34	0	0	-=	\		\(8)
496	Taq1	39	agg	246.96	247	0	246.96	0	0	364.82	0	+-	A		\(8)
497	Taq1	40	tgg	120.94	121	120.79	121.09	0	22 800 000	13 300 000	0	=-	\	\	
498	Taq1	56	tga	121.053	121	121.1	121.04	121.02	49 400 000	57 000 000	3 000 000	=-	\ (-)	\	
499	Hha1	25	cag	186.103	186	185.97	186.17	186.17	5 300 000	6 300 000	5 400 000	==	-	-	
500	Taq1	62	tgt	185.857	186	185.95	186	185.62	3 900 000	5 100 000	3 300 000	==	-	-	
501	Taq1	40	tgg	120.94	121	120.79	121.09	0	22 800 000	13 300 000	0	=-	\	\	
502	Taq1	56	tga	121.053	121	121.1	121.04	121.02	49 400 000	57 000 000	3 000 000	=-	\ (-)	\	
503	Hha1	25	cag	186.103	186	185.97	186.17	186.17	5 300 000	6 300 000	5 400 000	==	-	-	
504	Taq1	62	tgt	185.857	186	185.95	186	185.62	3 900 000	5 100 000	3 300 000	==	-	-	
505	Hha1	8	gaa	144.2	145	144.05	144.49	144.06	14 700 000	4 700 000	10 300 000	-=	\ (-)		\(3)
506	Hha1	8	gaa	144.4	145	0	0	144.4	0	0	10 400 000	=+	/		\(3)
507	Taq1	8	gaa	145.64	145	145.76	145.52	0	3 700 000	3 600 000	0	=-	\		\(3)
508	Hha1	8	gaa	145.41	145	145.41	0	0	6 400 000	0	0	-=	\		\(3)
509	Taq1	12	agt	238.093	238	238.12	238.04	238.12	3 000 000	4 400 000	3 200 000	==	-		\(3)
510	Taq1	12	agt	239.02	238	238.96	239.08	0	3 300 000	6 700 000	0	+-	A		\(3)
511	Hha1	62	tgt	96.245	96	96.23	0	96.26	3 200 000	0	3 100 000	-+(=)	V		V(2)
512	Hha1	26	ctg	153.167	154	153.14	153.14	153.22	17 400 000	5 700 000	7 400 000	-=	\ (-)		V(2)
513	Hha1	26	ctg	154.083	154	154.07	154.1	154.08	55 500 000	17 300 000	45 300 000	-+	V		V(2)
514	Taq1	41	ccc	157.91	157	157.91	0	0	5 900 000	0	0	-=	\	\	
515	Taq1	21	acc	157.87	158	157.87	0	0	9 900 000	0	0	-=	\	\	
516	Hha1	26	ctg	102.86	103	0	0	102.86	0	0	5 200 000	=+	/		\(7)
517	Hha1	40	tgg	102.66	103	102.77	102.55	0	17 300 000	10 800 000	0	=-	\		\(7)
518	Hha1	6	aga	111.76	112	111.69	111.83	0	9 100 000	4 600 000	0	--	\		\(7)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
476	AF255884.RUK	Ruk	adapter protein RUK-s		atg	tgg	increased
477	RATADCYA.PE1	nc	adenylyl cyclase type V		ttg	cgc	increased
478	RATADCYA.PE1	nc	adenylyl cyclase type V		ttg	cgc	increased
479	RATADCYA.PE1	nc	adenylyl cyclase type V		ctc	aca	increased
480	RATADCYA.PE1	nc	adenylyl cyclase type V		ccc	acc	increased
481	RATADCYA.PE1	nc	adenylyl cyclase type V		ccc	acc	increased
482	RATADCYA.PE1	nc	adenylyl cyclase type V		ctg	tgg	increased
483	RATADCYA.PE1	nc	adenylyl cyclase type V		ctg	tgg	increased
484	RATADCYA.PE1	nc	adenylyl cyclase type V		tgt	tca	increased
485	RATADCYA.PE1	nc	adenylyl cyclase type V		ggc	att	increased
486	RATADCYA.PE1	nc	adenylyl cyclase type V		ggc	att	increased
487	RATADCYA.PE1	nc	adenylyl cyclase type V		ggc	att	increased
488	RATADCYA.PE1	nc	adenylyl cyclase type V		tga	cgg	increased
489	RATADCYA.PE1	nc	adenylyl cyclase type V		tga	cgg	increased
490	RATADCYA.PE1	nc	adenylyl cyclase type V		ccc	cca	increased
491	RATADCYA.PE1	nc	adenylyl cyclase type V		ccc	cca	increased
492	RATADCYA.PE1	nc	adenylyl cyclase type V		agg	tca	increased
493	RATADCYA.PE1	nc	adenylyl cyclase type V		agg	tca	increased
494	RATADCYA.PE1	nc	adenylyl cyclase type V		agg	tca	increased
495	RATADCYA.PE1	nc	adenylyl cyclase type V		agg	tca	increased
496	RATADCYA.PE1	nc	adenylyl cyclase type V		agg	tca	increased
497	RATADC.PE1	nc	adenylyl cyclase type VI		tga	tgg	increased
498	RATADC.PE1	nc	adenylyl cyclase type VI		tga	tgg	increased
499	RATADC.PE1	nc	adenylyl cyclase type VI		cag	tgt	No change
500	RATADC.PE1	nc	adenylyl cyclase type VI		cag	tgt	No change
501	RATADCYB.PE1	nc	adenylyl cyclase type VI		tga	tgg	increased
502	RATADCYB.PE1	nc	adenylyl cyclase type VI		tga	tgg	increased
503	RATADCYB.PE1	nc	adenylyl cyclase type VI		cag	tgt	No change
504	RATADCYB.PE1	nc	adenylyl cyclase type VI		cag	tgt	No change
505	RATADPRHA.PE1	nc	ADP-ribosylarginine hydrolase		gaa	tat	increased
506	RATADPRHA.PE1	nc	ADP-ribosylarginine hydrolase		gaa	tat	increased
507	RATADPRHA.PE1	nc	ADP-ribosylarginine hydrolase		gaa	tat	increased
508	RATADPRHA.PE1	nc	ADP-ribosylarginine hydrolase		gaa	tat	increased
509	RATADPRHA.PE1	nc	ADP-ribosylarginine hydrolase		gag	agt	increased
510	RATADPRHA.PE1	nc	ADP-ribosylarginine hydrolase		gag	agt	increased
511	RNARL184.ARL184	ARL184	ADP-ribosylation factor-like protein		tcc	tgt	decreased by mild
512	RNARL184.ARL184	ARL184	ADP-ribosylation factor-like protein		ctg	cag	decreased by mild
513	RNARL184.ARL184	ARL184	ADP-ribosylation factor-like protein		ctg	cag	decreased by mild
514	RATPGCA.PE1	nc	aggrecan		ccc	acc	increased
515	RATPGCA.PE1	nc	aggrecan		ccc	acc	increased
516	RNU04860.PE1	nc	Ah receptor		ctg	tgg	increased
517	RNU04860.PE1	nc	Ah receptor		ctg	tgg	increased
518	RNU04860.PE1	nc	Ah receptor		aga	tgt	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
519	Taq1	62	tgt	111.367	112	111.29	111.61	111.2	16 100 000	6 200 000	6 700 000	-=	\ (-)		\(7)
520	Taq1	62	tgt	112.4	112	112.49	112.53	112.18	4 000 000	13 500 000	27 100 000	=+	/ (-)		\(7)
521	Hha1	40	tgg	187.92	189	0	187.92	0	0	3 100 000	0	+-	A		\(7)
522	Hha1	40	tgg	189.55	189	189.5	0	189.6	3 200 000	0	3 100 000	-+(=)	V		\(7)
523	Hha1	56	tga	188.215	189	188.23	188.2	0	224.73	776.08	0	+-	A		\(7)
524	Hha1	56	tga	189.18	189	189.18	0	0	257.42	0	0	-=	\		\(7)
525	Taq1	45	gcc	255.265	256	255.2	255.33	0	4 000 000	3 200 000	0	=-	\		\(7)
526	Taq1	45	gcc	256.03	256	256.06	256	0	3 900 000	4 800 000	0	=-	\		\(7)
527	Taq1	45	gcc	257.05	256	257.05	0	0	3 400 000	0	0	-=	\	\	\(7)
528	Hha1	22	tcc	257.06	257	257.06	0	0	34 400 000	0	0	-=	\	\	\(7)
529	Taq1	21	acc	271.83	271	271.83	0	0	6 700 000	0	0	-=	\		\(7)
530	Taq1	26	ctg	272.34	271	0	0	272.34	0	0	5 300 000	=+	/		\(7)
531	Hha1	26	ctg	102.86	103	0	0	102.86	0	0	5 200 000	=+	/		\(7)
532	Hha1	40	tgg	102.66	103	102.77	102.55	0	17 300 000	10 800 000	0	=-	\		\(7)
533	Hha1	6	aga	111.76	112	111.69	111.83	0	9 100 000	4 600 000	0	--	\		\(7)
534	Taq1	62	tgt	111.367	112	111.29	111.61	111.2	16 100 000	6 200 000	6 700 000	-=	\ (-)		\(7)
535	Taq1	62	tgt	112.4	112	112.49	112.53	112.18	4 000 000	13 500 000	27 100 000	=+	/ (-)		\(7)
536	Hha1	40	tgg	187.92	189	0	187.92	0	0	3 100 000	0	+-	A		\(7)
537	Hha1	40	tgg	189.55	189	189.5	0	189.6	3 200 000	0	3 100 000	-+(=)	V		\(7)
538	Hha1	56	tga	188.215	189	188.23	188.2	0	224.73	776.08	0	+-	A		\(7)
539	Hha1	56	tga	189.18	189	189.18	0	0	257.42	0	0	-=	\		\(7)
540	Taq1	45	gcc	255.265	256	255.2	255.33	0	4 000 000	3 200 000	0	=-	\		\(7)
541	Taq1	45	gcc	256.03	256	256.06	256	0	3 900 000	4 800 000	0	=-	\		\(7)
542	Taq1	45	gcc	257.05	256	257.05	0	0	3 400 000	0	0	-=	\	\	\(7)
543	Hha1	22	tcc	257.06	257	257.06	0	0	34 400 000	0	0	-=	\	\	\(7)
544	Taq1	21	acc	271.83	271	271.83	0	0	6 700 000	0	0	-=	\		\(7)
545	Taq1	26	ctg	272.34	271	0	0	272.34	0	0	5 300 000	=+	/		\(7)
546	Taq1	39	agg	90.495	91	90.7	0	90.29	125 800 000	0	23 600 000	-=(-)	\		\(3)
547	Taq1	39	agg	90.957	91	90.7	90.97	91.2	4 671.71	172 200 000	3 800 000	+-	A		\(3)
548	Taq1	39	agg	91.085	91	0	90.97	91.2	0	1 730.67	111.92	+-	A		\(3)
549	Hha1	26	ctg	114.717	115	114.71	114.63	114.81	12 300 000	6 500 000	4 700 000	-=	\ (-)		\(3)
550	Taq1	50	aat	121.82	122	0	122.06	121.58	0	7 900 000	13 100 000	+=	/		\(3)
551	Hha1	32	gtc	206.91	208	206.91	0	0	585.86	0	0	-=	\		\(3)
552	Hha1	32	gtc	208.497	208	208.48	208.53	208.48	567.55	305.18	409.14	-=	\ (-)		\(3)
553	Hha1	32	gtc	208.75	208	0	0	208.75	0	0	385.07	=+	/		\(3)
554	Taq1	8	gaa	132.82	133	132.71	132.93	0	4 400 000	6 100 000	0	=-	\	\	
555	Hha1	8	gaa	133.017	133	133.08	133.07	132.9	34 400 000	25 100 000	9 200 000	=-	\ (-)	\	
556	Hha1	20	ctc	65.19	65	65.1	65.11	65.36	495.86	3 606.08	8 826.33	=+	/ (-)		/(2)
557	Taq1	36	ggt	143.93	144	0	0	143.93	0	0	4 400 000	=+	/		/(2)
558	Hha1	59	ttc	192.56	193	192.56	0	0	306.81	0	0	-=	\		\(2)
559	Hha1	59	ttc	267.955	268	268.09	0	267.82	286.01	0	87.96	-=(-)	\		\(2)
560	Hha1	59	ttc	69.62	70	69.62	0	0	930.83	0	0	-=	\		\(2)
561	Hha1	49	aaa	70.745	71	0	70.56	70.93	0	31 500 000	3 400 000	+-	A		\(2)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
519	RNU04860.PE1	nc	Ah receptor		aga	tgt	increased
520	RNU04860.PE1	nc	Ah receptor		aga	tgt	increased
521	RNU04860.PE1	nc	Ah receptor		tga	tgg	increased
522	RNU04860.PE1	nc	Ah receptor		tga	tgg	increased
523	RNU04860.PE1	nc	Ah receptor		tga	tgg	increased
524	RNU04860.PE1	nc	Ah receptor		tga	tgg	increased
525	RNU04860.PE1	nc	Ah receptor		gcc	tcc	increased
526	RNU04860.PE1	nc	Ah receptor		gcc	tcc	increased
527	RNU04860.PE1	nc	Ah receptor		gcc	tcc	increased
528	RNU04860.PE1	nc	Ah receptor		gcc	tcc	increased
529	RNU04860.PE1	nc	Ah receptor		acc	ctg	increased
530	RNU04860.PE1	nc	Ah receptor		acc	ctg	increased
531	RNU09000.PE1	nc	Ah receptor		ctg	tgg	increased
532	RNU09000.PE1	nc	Ah receptor		ctg	tgg	increased
533	RNU09000.PE1	nc	Ah receptor		aga	tgt	increased
534	RNU09000.PE1	nc	Ah receptor		aga	tgt	increased
535	RNU09000.PE1	nc	Ah receptor		aga	tgt	increased
536	RNU09000.PE1	nc	Ah receptor		tga	tgg	increased
537	RNU09000.PE1	nc	Ah receptor		tga	tgg	increased
538	RNU09000.PE1	nc	Ah receptor		tga	tgg	increased
539	RNU09000.PE1	nc	Ah receptor		tga	tgg	increased
540	RNU09000.PE1	nc	Ah receptor		gcc	tcc	increased
541	RNU09000.PE1	nc	Ah receptor		gcc	tcc	increased
542	RNU09000.PE1	nc	Ah receptor		gcc	tcc	increased
543	RNU09000.PE1	nc	Ah receptor		gcc	tcc	increased
544	RNU09000.PE1	nc	Ah receptor		acc	ctg	increased
545	RNU09000.PE1	nc	Ah receptor		acc	ctg	increased
546	D89731.PE1	nc	AIM-1		ata	agg	increased
547	D89731.PE1	nc	AIM-1		ata	agg	increased
548	D89731.PE1	nc	AIM-1		ata	agg	increased
549	D89731.PE1	nc	AIM-1		taa	ctg	increased
550	D89731.PE1	nc	AIM-1		aat	gta	increased
551	D89731.PE1	nc	AIM-1		acc	gtc	increased
552	D89731.PE1	nc	AIM-1		acc	gtc	increased
553	D89731.PE1	nc	AIM-1		acc	gtc	increased
554	AF453776.PE1	nc	airway trypsin-like protease		gaa	aat	increased
555	AF453776.PE1	nc	airway trypsin-like protease		gaa	aat	increased
556	AF139518.PE1	nc	A-kinase anchor protein		ctc	ttg	decreased
557	AF139518.PE1	nc	A-kinase anchor protein		gga	ggt	decreased
558	RNALDOG2.PE1	aldolase A	aldolase A		tgt	ttc	increased
559	RNALDOG2.PE1	aldolase A	aldolase A		ttc	tca	increased
560	RSXLAS.ALEX	ALEX	ALEX protein		aaa	ttc	increased
561	RSXLAS.ALEX	ALEX	ALEX protein		aaa	ttc	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
562	Hha1	49	aaa	71.09	71	71.09	0	0	54 300 000	0	0	-=	\		\(2)
563	Hha1	33	agc	72.64	73	0	0	72.64	0	0	33 300 000	=+	/		\(2)
564	Taq1	45	gcc	282.48	283	282.48	0	0	3 600 000	0	0	-=	\		\(2)
565	Taq1	17	cca	285.64	284	285.64	0	0	143.96	0	0	-=	\		\(2)
566	Hha1	59	ttc	74.587	75	74.58	74.6	74.58	618.82	2 365.75	1 122.81	+-	A		/(4)
567	Hha1	59	ttc	75.45	75	75.5	75.4	0	2 407.69	991.72	0	-=	\		/(4)
568	Hha1	41	ccc	119.87	120	0	0	119.87	0	0	6 500 000	=+	/		/(4)
569	Taq1	12	agt	130.17	130	130.16	130.14	130.21	21 600 000	15 700 000	50 300 000	=+	/ (-)		/(4)
570	Taq1	23	cga	129.55	130	0	0	129.55	0	0	4 600 000	=+	/		/(4)
571	Taq1	23	cga	130.51	130	0	0	130.51	0	0	3 800 000	=+	/		/(4)
572	Hha1	39	agg	246.39	247	0	0	246.39	0	0	162.76	=+	/		/(4)
573	Hha1	39	agg	247.09	247	247.25	246.93	0	249.26	232.84	0	=-	\		/(4)
574	Hha1	39	agg	248.16	247	248.16	0	0	227.27	0	0	-=	\		/(4)
575	Taq1	26	ctg	171.56	171	0	0	171.56	0	0	3 500 000	=+	/	/	
576	Taq1	57	ctg	171.73	171	0	0	171.73	0	0	3 100 000	=+	/	/	
577	Hha1	39	agg	106.243	106	106.2	106.36	106.17	1 217	12 305.21	14 347.33	+=	/ (-)		/(2)
578	Hha1	41	ccc	218.96	220	0	0	218.96	0	0	3 000 000	=+	/		/(2)
579	Taq1	11	act	131.54	131	0	0	131.54	0	0	17 100 000	=+	/	/	
580	Hha1	11	act	131.72	131	0	0	131.72	0	0	3 300 000	=+	/	/	
581	Taq1	17	cca	224.36	225	224.36	0	0	139.32	0	0	-=	\		\(2)
582	Taq1	17	cca	224.88	225	0	224.88	0	0	206.08	0	+-	A		\(2)
583	Taq1	17	cca	225.71	225	225.71	0	0	236.84	0	0	-=	\		\(2)
584	Taq1	64	gtt	249.16	250	249.16	0	0	4 000 000	0	0	-=	\		\(2)
585	Taq1	64	gtt	250.055	250	250.12	249.99	0	3 000 000	3 600 000	0	=-	\		\(2)
586	Taq1	64	gtt	251.085	250	251.17	251	0	3 300 000	3 000 000	0	=-	\		\(2)
587	Taq1	26	ctg	171.56	171	0	0	171.56	0	0	3 500 000	=+	/	/	
588	Taq1	57	ctg	171.73	171	0	0	171.73	0	0	3 100 000	=+	/	/	
589	Hha1	39	agg	106.243	106	106.2	106.36	106.17	1 217	12 305.21	14 347.33	+=	/ (-)		/(3)
590	Taq1	31	gac	134.527	135	134.67	134.44	134.47	10 200 000	16 000 000	3 200 000	=-	\ (-)		/(3)
591	Taq1	31	gac	135.577	135	135.72	135.49	135.52	11 900 000	8 500 000	6 100 000	==	-		/(3)
592	Taq1	35	gga	134.85	135	0	0	134.85	0	0	7 700 000	=+	/		/(3)
593	Hha1	41	ccc	218.96	220	0	0	218.96	0	0	3 000 000	=+	/		/(3)
594	Hha1	39	agg	106.243	106	106.2	106.36	106.17	1 217	12 305.21	14 347.33	+=	/ (-)		/(3)
595	Taq1	31	gac	134.527	135	134.67	134.44	134.47	10 200 000	16 000 000	3 200 000	=-	\ (-)		/(3)
596	Taq1	31	gac	135.577	135	135.72	135.49	135.52	11 900 000	8 500 000	6 100 000	==	-		/(3)
597	Taq1	35	gga	134.85	135	0	0	134.85	0	0	7 700 000	=+	/		/(3)
598	Hha1	2	tta	212.14	211	0	0	212.14	0	0	3 700 000	=+	/		/(3)
599	Hha1	56	tga	205.307	206	205.08	205.51	205.33	138.92	539.4	758.48	+=	/ (-)		\(2)
600	Hha1	56	tga	205.3	206	205.3	0	0	138.92	0	0	-=	\		\(2)
601	Hha1	56	tga	206.195	206	206.18	0	206.21	171.61	0	844.68	=+(+)	/		\(2)
602	Hha1	56	tga	207.14	206	0	0	207.14	0	0	568.86	=+	/		\(2)
603	Hha1	8	gaa	215.7	217	215.7	0	0	3 300 000	0	0	-=	\		\(2)
604	Hha1	56	tga	205.307	206	205.08	205.51	205.33	138.92	539.4	758.48	+=	/ (-)		\(2)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
562	RSXLAS.ALEX	ALEX	ALEX protein		aaa	ttc	increased
563	RSXLAS.ALEX	ALEX	ALEX protein		agc	ggg	increased
564	AB016536.ALF-C1	alf-c1	AlF-C1		gcc	cca	increased
565	AB016536.ALF-C1	alf-c1	AlF-C1		gcc	cca	increased
566	RNU58860.RFUC-T	rFuc-T	alpha 1,3-fucosyltransferase		ttc	ggt	decreased
567	RNU58860.RFUC-T	rFuc-T	alpha 1,3-fucosyltransferase		ttc	ggt	decreased
568	RNU58860.RFUC-T	rFuc-T	alpha 1,3-fucosyltransferase		ggc	ccc	decreased
569	RNU58860.RFUC-T	rFuc-T	alpha 1,3-fucosyltransferase		cga	agt	decreased
570	RNU58860.RFUC-T	rFuc-T	alpha 1,3-fucosyltransferase		cga	agt	decreased
571	RNU58860.RFUC-T	rFuc-T	alpha 1,3-fucosyltransferase		cga	agt	decreased
572	RNU58860.RFUC-T	rFuc-T	alpha 1,3-fucosyltransferase		gga	agg	decreased
573	RNU58860.RFUC-T	rFuc-T	alpha 1,3-fucosyltransferase		gga	agg	decreased
574	RNU58860.RFUC-T	rFuc-T	alpha 1,3-fucosyltransferase		gga	agg	decreased
575	RATA1DA.PE1	nc	alpha 1a/d adrenergic receptor		ccg	ctg	decreased
576	RATA1DA.PE1	nc	alpha 1a/d adrenergic receptor		ccg	ctg	decreased
577	RATGENOME.PE1	nc	alpha 1B adrenergic receptor		tcc	agg	decreased
578	RATGENOME.PE1	nc	alpha 1B adrenergic receptor		ctt	ccc	decreased
579	RATA26S.PE1	nc	alpha 2,6-sialyltransferase		act	aac	decreased
580	RATA26S.PE1	nc	alpha 2,6-sialyltransferase		act	aac	decreased
581	RNAINF.PE1	nc	alpha initiation factor		cca	gat	increased
582	RNAINF.PE1	nc	alpha initiation factor		cca	gat	increased
583	RNAINF.PE1	nc	alpha initiation factor		cca	gat	increased
584	RNAINF.PE1	nc	alpha initiation factor		gtt	tca	increased
585	RNAINF.PE1	nc	alpha initiation factor		gtt	tca	increased
586	RNAINF.PE1	nc	alpha initiation factor		gtt	tca	increased
587	RATADRA1A.PE1	alpha-1A-adre	alpha-1A-adrenergic receptor		ccg	ctg	decreased
588	RATADRA1A.PE1	alpha-1A-adre	alpha-1A-adrenergic receptor		ccg	ctg	decreased
589	RATAADRE02.PE1	nc	alpha-1B adrenergic receptor		tcc	agg	decreased
590	RATAADRE02.PE1	nc	alpha-1B adrenergic receptor		gga	gac	decreased
591	RATAADRE02.PE1	nc	alpha-1B adrenergic receptor		gga	gac	decreased
592	RATAADRE02.PE1	nc	alpha-1B adrenergic receptor		gga	gac	decreased
593	RATAADRE02.PE1	nc	alpha-1B adrenergic receptor		ctt	ccc	decreased
594	RATADRA1B.PE1	alpha-1B adre	alpha-1B adrenergic receptor		tcc	agg	decreased
595	RATADRA1B.PE1	alpha-1B adre	alpha-1B adrenergic receptor		gga	gac	decreased
596	RATADRA1B.PE1	alpha-1B adre	alpha-1B adrenergic receptor		gga	gac	decreased
597	RATADRA1B.PE1	alpha-1B adre	alpha-1B adrenergic receptor		gga	gac	decreased
598	RATADRA1B.PE1	alpha-1B adre	alpha-1B adrenergic receptor		tta	aca	decreased
599	RRU07126.PE1	nc	alpha1c adrenergic receptor		tat	tga	increased
600	RRU07126.PE1	nc	alpha1c adrenergic receptor		tat	tga	increased
601	RRU07126.PE1	nc	alpha1c adrenergic receptor		tat	tga	increased
602	RRU07126.PE1	nc	alpha1c adrenergic receptor		tat	tga	increased
603	RRU07126.PE1	nc	alpha1c adrenergic receptor		gtc	gaa	increased
604	RNU13368.PE1	nc	alpha1C-adrenergic receptor		tat	tga	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
605	Hha1	56	tga	205.3	206	205.3	0	0	138.92	0	0	-=	\		\(2)
606	Hha1	56	tga	206.195	206	206.18	0	206.21	171.61	0	844.68	=+(+)	/		\(2)
607	Hha1	56	tga	207.14	206	0	0	207.14	0	0	568.86	=+	/		\(2)
608	Hha1	8	gaa	215.7	217	215.7	0	0	3 300 000	0	0	-=	\		\(2)
609	Taq1	52	att	127.025	127	0	126.97	127.08	0	12 600 000	4 700 000	+-	A		/(2)
610	Taq1	52	att	127.365	127	0	127.49	127.24	0	5 500 000	4 200 000	+=	/		/(2)
611	Taq1	52	att	127.39	127	0	0	127.39	0	0	4 200 000	=+	/		/(2)
612	Taq1	25	cat	162.63	163	0	0	162.63	0	0	1 019.56	=+	/		/(2)
613	Taq1	25	cat	163.817	163	163.89	163.88	163.68	1 173.74	1 387.65	1 460.45	==	-		/(2)
614	Taq1	49	aaa	419.37	417	419.45	419.29	0	21 900 000	3 200 000	0	-=	\		/(2)
615	Taq1	52	att	127.025	127	0	126.97	127.08	0	12 600 000	4 700 000	+-	A		/(2)
616	Taq1	52	att	127.365	127	0	127.49	127.24	0	5 500 000	4 200 000	+=	/		/(2)
617	Taq1	52	att	127.39	127	0	0	127.39	0	0	4 200 000	=+	/		/(2)
618	Taq1	25	cat	162.63	163	0	0	162.63	0	0	1 019.56	=+	/		/(2)
619	Taq1	25	cat	163.817	163	163.89	163.88	163.68	1 173.74	1 387.65	1 460.45	==	-		/(2)
620	Taq1	49	aaa	419.37	417	419.45	419.29	0	21 900 000	3 200 000	0	-=	\		/(2)
621	Hha1	54	ttt	75.16	75	75.11	75.21	75.16	46 500 000	45 100 000	46 900 000	==	-		/(4)
622	Hha1	59	ttc	95.125	95	0	95.22	95.03	0	195.46	2 750.1	=+	/		/(4)
623	Hha1	41	ccc	101.02	101	101.06	101.22	100.78	40 900 000	5 400 000	4 600 000	-=	\ (-)		/(4)
624	Hha1	41	ccc	101.51	101	0	0	101.51	0	0	5 200 000	=+	/		/(4)
625	Taq1	30	cgt	118.15	118	118.15	0	0	3 200 000	0	0	-=	\		/(4)
626	Taq1	40	tgg	117.5	118	0	0	117.5	0	0	9 000 000	=+	/		/(4)
627	Taq1	40	tgg	118.44	118	118.44	118.37	118.51	4 200 000	3 900 000	23 900 000	=+	/ (-)		/(4)
628	Hha1	40	tgg	128.37	129	0	128.13	128.61	0	4 400 000	17 700 000	=+	/		/(4)
629	Hha1	40	tgg	128.86	129	128.86	0	0	3 500 000	0	0	-=	\		/(4)
630	Hha1	54	ttt	75.16	75	75.11	75.21	75.16	46 500 000	45 100 000	46 900 000	==	-		-1
631	Hha1	59	ttc	95.125	95	0	95.22	95.03	0	195.46	2 750.1	=+	/		-1
632	Hha1	41	ccc	101.02	101	101.06	101.22	100.78	40 900 000	5 400 000	4 600 000	-=	\ (-)		-1
633	Hha1	41	ccc	101.51	101	0	0	101.51	0	0	5 200 000	=+	/		-1
634	Hha1	40	tgg	104.833	105	104.65	104.74	105.11	7 900 000	13 200 000	18 200 000	==	-		-1
635	Taq1	30	cgt	118.15	118	118.15	0	0	3 200 000	0	0	-=	\		-1
636	Taq1	40	tgg	117.5	118	0	0	117.5	0	0	9 000 000	=+	/		-1
637	Taq1	40	tgg	118.44	118	118.44	118.37	118.51	4 200 000	3 900 000	23 900 000	=+	/ (-)		-1
638	Hha1	40	tgg	128.37	129	0	128.13	128.61	0	4 400 000	17 700 000	=+	/		-1
639	Hha1	40	tgg	128.86	129	128.86	0	0	3 500 000	0	0	-=	\		-1
640	Taq1	17	cca	138.79	139	138.65	138.81	138.91	283.28	265.92	2 044.8	=+	/ (-)		-3
641	Taq1	17	cca	139.775	139	139.67	0	139.88	171.82	0	1 037.43	=+(+)	/		-3
642	Taq1	40	tgg	139.085	139	139.26	0	138.91	8 500 000	0	13 000 000	-+(=)	V		-3
643	Hha1	44	cgg	154.99	155	155.01	155.05	154.91	4 300 000	5 800 000	3 000 000	=-	\ (-)		-3
644	Hha1	6	aga	165.59	166	165.63	165.53	165.61	7 400 000	4 900 000	5 400 000	==	-		-3
645	Hha1	6	aga	166.585	166	166.62	0	166.55	6 200 000	0	4 300 000	-+(=)	V		-3
646	Taq1	12	agt	152.683	153	152.69	152.61	152.75	9 200 000	10 800 000	19 700 000	=+	/ (-)		\(9)
647	Taq1	12	agt	153.727	153	153.72	153.64	153.82	3 700 000	4 400 000	3 000 000	==	-		\(9)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
605	RNU13368.PE1	nc	alpha1C-adrenergic receptor		tat	tga	increased
606	RNU13368.PE1	nc	alpha1C-adrenergic receptor		tat	tga	increased
607	RNU13368.PE1	nc	alpha1C-adrenergic receptor		tat	tga	increased
608	RNU13368.PE1	nc	alpha1C-adrenergic receptor		gtc	gaa	increased
609	RATALPH1M.PE1	alpha1 M	alpha-1-macroglobulin		gtg	att	decreased
610	RATALPH1M.PE1	alpha1 M	alpha-1-macroglobulin		gtg	att	decreased
611	RATALPH1M.PE1	alpha1 M	alpha-1-macroglobulin		gtg	att	decreased
612	RATALPH1M.PE1	alpha1 M	alpha-1-macroglobulin		cat	ccg	decreased
613	RATALPH1M.PE1	alpha1 M	alpha-1-macroglobulin		cat	ccg	decreased
614	RATALPH1M.PE1	alpha1 M	alpha-1-macroglobulin		aaa	tga	decreased
615	RATMGA1A.PE1	alpha-1-macr	alpha-1-macroglobulin		gtg	att	decreased
616	RATMGA1A.PE1	alpha-1-macr	alpha-1-macroglobulin		gtg	att	decreased
617	RATMGA1A.PE1	alpha-1-macr	alpha-1-macroglobulin		gtg	att	decreased
618	RATMGA1A.PE1	alpha-1-macr	alpha-1-macroglobulin		cat	ccg	decreased
619	RATMGA1A.PE1	alpha-1-macr	alpha-1-macroglobulin		cat	ccg	decreased
620	RATMGA1A.PE1	alpha-1-macr	alpha-1-macroglobulin		aaa	tga	decreased
621	RATRG20.RG20	RG20	alpha-2-adrenergic receptor		ctt	ttt	decreased
622	RATRG20.RG20	RG20	alpha-2-adrenergic receptor		cat	ttc	decreased
623	RATRG20.RG20	RG20	alpha-2-adrenergic receptor		ggg	ccc	decreased
624	RATRG20.RG20	RG20	alpha-2-adrenergic receptor		ggg	ccc	decreased
625	RATRG20.RG20	RG20	alpha-2-adrenergic receptor		cgt	tgg	decreased
626	RATRG20.RG20	RG20	alpha-2-adrenergic receptor		cgt	tgg	decreased
627	RATRG20.RG20	RG20	alpha-2-adrenergic receptor		cgt	tgg	decreased
628	RATRG20.RG20	RG20	alpha-2-adrenergic receptor		tgg	gaa	decreased
629	RATRG20.RG20	RG20	alpha-2-adrenergic receptor		tgg	gaa	decreased
630	RRU79031.PE1	nc	alpha2D adrenergic receptor		ctt	ttt	No change
631	RRU79031.PE1	nc	alpha2D adrenergic receptor		cat	ttc	No change
632	RRU79031.PE1	nc	alpha2D adrenergic receptor		ggg	ccc	No change
633	RRU79031.PE1	nc	alpha2D adrenergic receptor		ggg	ccc	No change
634	RRU79031.PE1	nc	alpha2D adrenergic receptor		tgg	tcg	No change
635	RRU79031.PE1	nc	alpha2D adrenergic receptor		cgt	tgg	No change
636	RRU79031.PE1	nc	alpha2D adrenergic receptor		cgt	tgg	No change
637	RRU79031.PE1	nc	alpha2D adrenergic receptor		cgt	tgg	No change
638	RRU79031.PE1	nc	alpha2D adrenergic receptor		tgg	gaa	No change
639	RRU79031.PE1	nc	alpha2D adrenergic receptor		tgg	gaa	No change
640	AF190909.PE1	nc	alpha-actinin 4		cca	tgg	No change
641	AF190909.PE1	nc	alpha-actinin 4		cca	tgg	No change
642	AF190909.PE1	nc	alpha-actinin 4		cca	tgg	No change
643	AF190909.PE1	nc	alpha-actinin 4		aga	cgg	No change
644	AF190909.PE1	nc	alpha-actinin 4		gat	aga	No change
645	AF190909.PE1	nc	alpha-actinin 4		gat	aga	No change
646	AF084186.A2A	A2A	alpha-fodrin		gac	agt	increased
647	AF084186.A2A	A2A	alpha-fodrin		gac	agt	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
648	Taq1	31	gac	152.9	153	153.08	152.72	0	4 300 000	10 900 000	0	+-	A		\(9)
649	Hha1	9	atc	187.41	188	0	0	187.41	0	0	3 400 000	=+	/		\(9)
650	Hha1	9	atc	188.275	188	188.17	188.38	0	5 600 000	3 600 000	0	=-	\		\(9)
651	Taq1	39	agg	188.86	190	0	188.86	0	0	20 800 000	0	+-	A		\(9)
652	Taq1	39	agg	190.35	190	190.45	0	190.25	27 700 000	0	31 700 000	-+(=)	V		\(9)
653	Taq1	39	agg	190.25	190	0	0	190.25	0	0	933.72	=+	/		\(9)
654	Taq1	39	agg	188.86	190	0	188.86	0	0	209.04	0	+-	A		\(9)
655	Taq1	39	agg	190.45	190	190.45	0	0	1 028.66	0	0	-=	\		\(9)
656	Hha1	40	tgg	209.925	211	0	210.06	209.79	0	3 000 000	4 400 000	+=	/		\(9)
657	Hha1	40	tgg	210.2	211	0	0	210.2	0	0	4 100 000	=+	/		\(9)
658	Hha1	40	tgg	210.95	211	210.85	211.05	0	5 400 000	7 700 000	0	=-	\		\(9)
659	Hha1	49	aaa	211.225	212	211.14	211.31	0	16 300 000	18 600 000	0	=-	\		\(9)
660	Hha1	49	aaa	212.11	212	212.16	212.06	0	31 900 000	12 100 000	0	-=	\		\(9)
661	Hha1	49	aaa	213.17	212	0	213.17	0	0	5 600 000	0	+-	A		\(9)
662	Hha1	40	tgg	212.87	214	0	212.87	0	0	3 300 000	0	+-	A		\(9)
663	Hha1	40	tgg	214.3	214	214.3	0	0	5 900 000	0	0	-=	\		\(9)
664	Taq1	29	gca	222.67	224	222.67	0	0	3 200 000	0	0	-=	\		\(9)
665	Hha1	7	caa	259.145	259	259.18	0	259.11	3 300 000	0	3 600 000	-+(=)	V		\(9)
666	Taq1	7	caa	259.46	259	0	259.46	0	0	3 900 000	0	+-	A		\(9)
667	Taq1	7	caa	260.11	259	260.11	0	0	3 600 000	0	0	-=	\		\(9)
668	Hha1	7	caa	267.18	268	267.18	0	0	4 400 000	0	0	-=	\		\(9)
669	Taq1	7	caa	268.66	268	268.66	0	0	4 400 000	0	0	-=	\		\(9)
670	Taq1	26	ctg	285.71	285	0	0	285.71	0	0	7 100 000	=+	/		\(9)
671	Taq1	12	agt	152.683	153	152.69	152.61	152.75	9 200 000	10 800 000	19 700 000	=+	/ (-)		\(9)
672	Taq1	12	agt	153.727	153	153.72	153.64	153.82	3 700 000	4 400 000	3 000 000	==	-		\(9)
673	Taq1	31	gac	152.9	153	153.08	152.72	0	4 300 000	10 900 000	0	+-	A		\(9)
674	Hha1	9	atc	187.41	188	0	0	187.41	0	0	3 400 000	=+	/		\(9)
675	Hha1	9	atc	188.275	188	188.17	188.38	0	5 600 000	3 600 000	0	=-	\		\(9)
676	Taq1	39	agg	188.86	190	0	188.86	0	0	20 800 000	0	+-	A		\(9)
677	Taq1	39	agg	190.35	190	190.45	0	190.25	27 700 000	0	31 700 000	-+(=)	V		\(9)
678	Taq1	39	agg	190.25	190	0	0	190.25	0	0	933.72	=+	/		\(9)
679	Taq1	39	agg	188.86	190	0	188.86	0	0	209.04	0	+-	A		\(9)
680	Taq1	39	agg	190.45	190	190.45	0	0	1 028.66	0	0	-=	\		\(9)
681	Hha1	40	tgg	209.925	211	0	210.06	209.79	0	3 000 000	4 400 000	+=	/		\(9)
682	Hha1	40	tgg	210.2	211	0	0	210.2	0	0	4 100 000	=+	/		\(9)
683	Hha1	40	tgg	210.95	211	210.85	211.05	0	5 400 000	7 700 000	0	=-	\		\(9)
684	Hha1	49	aaa	211.225	212	211.14	211.31	0	16 300 000	18 600 000	0	=-	\		\(9)
685	Hha1	49	aaa	212.11	212	212.16	212.06	0	31 900 000	12 100 000	0	-=	\		\(9)
686	Hha1	49	aaa	213.17	212	0	213.17	0	0	5 600 000	0	+-	A		\(9)
687	Hha1	40	tgg	212.87	214	0	212.87	0	0	3 300 000	0	+-	A		\(9)
688	Hha1	40	tgg	214.3	214	214.3	0	0	5 900 000	0	0	-=	\		\(9)
689	Taq1	29	gca	222.67	224	222.67	0	0	3 200 000	0	0	-=	\		\(9)
690	Hha1	7	caa	259.145	259	259.18	0	259.11	3 300 000	0	3 600 000	-+(=)	V		\(9)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
648	AF084186.A2A	A2A	alpha-fodrin		gac	agt	increased
649	AF084186.A2A	A2A	alpha-fodrin		tgc	atc	increased
650	AF084186.A2A	A2A	alpha-fodrin		tgc	atc	increased
651	AF084186.A2A	A2A	alpha-fodrin		gag	agg	increased
652	AF084186.A2A	A2A	alpha-fodrin		gag	agg	increased
653	AF084186.A2A	A2A	alpha-fodrin		gag	agg	increased
654	AF084186.A2A	A2A	alpha-fodrin		gag	agg	increased
655	AF084186.A2A	A2A	alpha-fodrin		gag	agg	increased
656	AF084186.A2A	A2A	alpha-fodrin		aaa	tgg	increased
657	AF084186.A2A	A2A	alpha-fodrin		aaa	tgg	increased
658	AF084186.A2A	A2A	alpha-fodrin		aaa	tgg	increased
659	AF084186.A2A	A2A	alpha-fodrin		aaa	tgg	increased
660	AF084186.A2A	A2A	alpha-fodrin		aaa	tgg	increased
661	AF084186.A2A	A2A	alpha-fodrin		aaa	tgg	increased
662	AF084186.A2A	A2A	alpha-fodrin		tgg	tgc	increased
663	AF084186.A2A	A2A	alpha-fodrin		tgg	tgc	increased
664	AF084186.A2A	A2A	alpha-fodrin		tga	gca	increased
665	AF084186.A2A	A2A	alpha-fodrin		caa	tct	increased
666	AF084186.A2A	A2A	alpha-fodrin		caa	tct	increased
667	AF084186.A2A	A2A	alpha-fodrin		caa	tct	increased
668	AF084186.A2A	A2A	alpha-fodrin		caa	cct	increased
669	AF084186.A2A	A2A	alpha-fodrin		caa	cct	increased
670	AF084186.A2A	A2A	alpha-fodrin		ctg	agc	increased
671	RNALIISPE.PE1	nc	alphaII spectrin		gac	agt	increased
672	RNALIISPE.PE1	nc	alphaII spectrin		gac	agt	increased
673	RNALIISPE.PE1	nc	alphaII spectrin		gac	agt	increased
674	RNALIISPE.PE1	nc	alphaII spectrin		tgc	atc	increased
675	RNALIISPE.PE1	nc	alphaII spectrin		tgc	atc	increased
676	RNALIISPE.PE1	nc	alphaII spectrin		gag	agg	increased
677	RNALIISPE.PE1	nc	alphaII spectrin		gag	agg	increased
678	RNALIISPE.PE1	nc	alphaII spectrin		gag	agg	increased
679	RNALIISPE.PE1	nc	alphaII spectrin		gag	agg	increased
680	RNALIISPE.PE1	nc	alphaII spectrin		gag	agg	increased
681	RNALIISPE.PE1	nc	alphaII spectrin		aaa	tgg	increased
682	RNALIISPE.PE1	nc	alphaII spectrin		aaa	tgg	increased
683	RNALIISPE.PE1	nc	alphaII spectrin		aaa	tgg	increased
684	RNALIISPE.PE1	nc	alphaII spectrin		aaa	tgg	increased
685	RNALIISPE.PE1	nc	alphaII spectrin		aaa	tgg	increased
686	RNALIISPE.PE1	nc	alphaII spectrin		aaa	tgg	increased
687	RNALIISPE.PE1	nc	alphaII spectrin		tgg	tgc	increased
688	RNALIISPE.PE1	nc	alphaII spectrin		tgg	tgc	increased
689	RNALIISPE.PE1	nc	alphaII spectrin		tga	gca	increased
690	RNALIISPE.PE1	nc	alphaII spectrin		caa	tct	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
691	Taq1	7	caa	259.46	259	0	259.46	0	0	3 900 000	0	+-	A		\(9)
692	Taq1	7	caa	260.11	259	260.11	0	0	3 600 000	0	0	-=	\		\(9)
693	Hha1	7	caa	267.18	268	267.18	0	0	4 400 000	0	0	-=	\		\(9)
694	Taq1	7	caa	268.66	268	268.66	0	0	4 400 000	0	0	-=	\		\(9)
695	Taq1	26	ctg	285.71	285	0	0	285.71	0	0	7 100 000	=+	/		\(9)
696	Hha1	60	ttg	103.547	104	103.35	103.78	103.51	6 900 000	5 400 000	17 000 000	=+	/ (-)		/(2)
697	Hha1	60	ttg	104.277	104	104.21	104.3	104.32	11 400 000	4 300 000	22 100 000	=+	/ (-)		/(2)
698	Taq1	27	acg	151.105	152	151.01	151.2	0	13 600 000	8 800 000	0	=-	\		/(2)
699	Taq1	27	acg	151.65	152	0	0	151.65	0	0	10 600 000	=+	/		/(2)
700	Taq1	25	cat	138.755	139	138.85	138.66	0	777.94	2 062.38	0	+-	A		\(2)
701	Taq1	25	cat	139.41	139	0	139.63	139.19	0	1 234.88	992	+=	/		\(2)
702	Taq1	25	cat	139.7	139	139.7	0	0	1 344.34	0	0	-=	\	\	\(2)
703	Taq1	34	tgc	139.62	139	139.62	0	0	3 000 000	0	0	-=	\	\	\(2)
704	Hha1	26	ctg	99.44	100	99.53	99.35	0	10 500 000	4 000 000	0	-=	\		\(2)
705	Hha1	6	aga	228.935	230	228.92	228.95	0	74 800 000	6 100 000	0	-=	\		\(2)
706	Hha1	6	aga	231.02	230	231.02	0	0	18 200 000	0	0	-=	\		\(2)
707	Taq1	56	tga	269.47	271	0	0	269.47	0	0	5 400 000	=+	/		\(2)
708	Taq1	22	tcc	159.33	160	0	0	159.33	0	0	9 900 000	=+	/		/(4)
709	Hha1	22	tcc	159.96	160	0	159.96	0	0	3 900 000	0	+-	A		/(4)
710	Taq1	22	tcc	160.37	160	0	0	160.37	0	0	4 000 000	=+	/		/(4)
711	Taq1	54	ttt	160.17	161	160.17	0	0	997.81	0	0	-=	\		/(4)
712	Taq1	54	ttt	160.8	161	160.71	160.91	160.78	1 988.34	858.52	3 875.8	=+	/ (-)		/(4)
713	Taq1	54	ttt	161.917	161	161.97	161.87	161.91	2 097.59	1 023.16	3 019.27	=+	/ (-)		/(4)
714	Hha1	9	atc	207.44	208	207.43	207.47	207.42	16 400 000	19 600 000	37 700 000	=+	/ (-)	(-)	/(4)
715	Hha1	9	atc	208.77	208	0	208.93	208.61	0	3 300 000	3 900 000	+=	/		/(4)
716	Taq1	19	cac	207.43	208	207.39	207.47	207.43	6 800 000	4 900 000	3 500 000	==	-	(-)	/(4)
717	Taq1	19	cac	208.407	208	208.43	208.38	208.41	4 500 000	4 800 000	6 400 000	==	-		/(4)
718	Taq1	22	tcc	159.33	160	0	0	159.33	0	0	9 900 000	=+	/		/(4)
719	Hha1	22	tcc	159.96	160	0	159.96	0	0	3 900 000	0	+-	A		/(4)
720	Taq1	22	tcc	160.37	160	0	0	160.37	0	0	4 000 000	=+	/		/(4)
721	Taq1	54	ttt	160.17	161	160.17	0	0	997.81	0	0	-=	\		/(4)
722	Taq1	54	ttt	160.8	161	160.71	160.91	160.78	1 988.34	858.52	3 875.8	=+	/ (-)		/(4)
723	Taq1	54	ttt	161.917	161	161.97	161.87	161.91	2 097.59	1 023.16	3 019.27	=+	/ (-)		/(4)
724	Hha1	9	atc	207.44	208	207.43	207.47	207.42	16 400 000	19 600 000	37 700 000	=+	/ (-)	(-)	/(4)
725	Hha1	9	atc	208.77	208	0	208.93	208.61	0	3 300 000	3 900 000	+=	/		/(4)
726	Taq1	19	cac	207.43	208	207.39	207.47	207.43	6 800 000	4 900 000	3 500 000	==	-	(-)	/(4)
727	Taq1	19	cac	208.407	208	208.43	208.38	208.41	4 500 000	4 800 000	6 400 000	==	-		/(4)
728	Hha1	12	agt	139.47	140	139.43	139.48	139.5	4 239.91	3 292.58	3 231.76	==	-		-2
729	Hha1	12	agt	140.473	140	140.43	140.51	140.48	2 275.07	1 711.49	3 047.09	==	-		-2
730	Taq1	45	gcc	170.59	171	170.59	0	0	4 500 000	0	0	-=	\		-2
731	Taq1	45	gcc	171.75	171	171.59	0	171.91	3 200 000	0	7 100 000	-+(+)	V (/)		-2
732	Taq1	14	gat	171.67	172	171.61	171.61	171.79	4 200 000	4 200 000	5 900 000	==	-		-2
733	Taq1	14	gat	172.67	172	172.64	172.64	172.73	3 600 000	3 600 000	4 300 000	==	-		-2

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
691	RNALIISPE.PE1	nc	alphaII spectrin		caa	tct	increased
692	RNALIISPE.PE1	nc	alphaII spectrin		caa	tct	increased
693	RNALIISPE.PE1	nc	alphaII spectrin		caa	cct	increased
694	RNALIISPE.PE1	nc	alphaII spectrin		caa	cct	increased
695	RNALIISPE.PE1	nc	alphaII spectrin		ctg	agc	increased
696	RNU89905.PE1	nc	alpha-methylacyl-CoA racemase		cga	ttg	decreased
697	RNU89905.PE1	nc	alpha-methylacyl-CoA racemase		cga	ttg	decreased
698	RNU89905.PE1	nc	alpha-methylacyl-CoA racemase		acg	ggc	decreased
699	RNU89905.PE1	nc	alpha-methylacyl-CoA racemase		acg	ggc	decreased
700	RNSNAPGEN.SNAP	snap	alpha-soluble NSF attachment protein		cat	tgc	increased
701	RNSNAPGEN.SNAP	snap	alpha-soluble NSF attachment protein		cat	tgc	increased
702	RNSNAPGEN.SNAP	snap	alpha-soluble NSF attachment protein		cat	tgc	increased
703	RNSNAPGEN.SNAP	snap	alpha-soluble NSF attachment protein		cat	tgc	increased
704	RNNAC.PE1	nc	amiloride sensitive Na+ channel		ctg	aag	increased
705	RNNAC.PE1	nc	amiloride sensitive Na+ channel		aga	aga	increased
706	RNNAC.PE1	nc	amiloride sensitive Na+ channel		aga	aga	increased
707	RNNAC.PE1	nc	amiloride sensitive Na+ channel		tgg	tga	increased
708	AF273024.PE1	nc	amino acid system A transporter	*	ttt	tcc	decreased
709	AF273024.PE1	nc	amino acid system A transporter	*	ttt	tcc	decreased
710	AF273024.PE1	nc	amino acid system A transporter	*	ttt	tcc	decreased
711	AF273024.PE1	nc	amino acid system A transporter	*	ttt	tcc	decreased
712	AF273024.PE1	nc	amino acid system A transporter	*	ttt	tcc	decreased
713	AF273024.PE1	nc	amino acid system A transporter	*	ttt	tcc	decreased
714	AF273024.PE1	nc	amino acid system A transporter	*	atc	cac	No change
715	AF273024.PE1	nc	amino acid system A transporter	*	atc	cac	decreased
716	AF273024.PE1	nc	amino acid system A transporter	*	atc	cac	No change
717	AF273024.PE1	nc	amino acid system A transporter	*	atc	cac	decreased
718	AF249673.ATA2	ATA2	amino acid transporter system A		ttt	tcc	decreased
719	AF249673.ATA2	ATA2	amino acid transporter system A		ttt	tcc	decreased
720	AF249673.ATA2	ATA2	amino acid transporter system A		ttt	tcc	decreased
721	AF249673.ATA2	ATA2	amino acid transporter system A		ttt	tcc	decreased
722	AF249673.ATA2	ATA2	amino acid transporter system A		ttt	tcc	decreased
723	AF249673.ATA2	ATA2	amino acid transporter system A		ttt	tcc	decreased
724	AF249673.ATA2	ATA2	amino acid transporter system A		atc	cac	No change
725	AF249673.ATA2	ATA2	amino acid transporter system A		atc	cac	decreased
726	AF249673.ATA2	ATA2	amino acid transporter system A		atc	cac	No change
727	AF249673.ATA2	ATA2	amino acid transporter system A		atc	cac	decreased
728	RNU61696.PE1	nc	aminopeptidase B		ctt	agt	No change
729	RNU61696.PE1	nc	aminopeptidase B		ctt	agt	No change
730	RNU61696.PE1	nc	aminopeptidase B		gat	gcc	No change
731	RNU61696.PE1	nc	aminopeptidase B		gat	gcc	No change
732	RNU61696.PE1	nc	aminopeptidase B		gat	gcc	No change
733	RNU61696.PE1	nc	aminopeptidase B		gat	gcc	No change

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
734	Hha1	59	ttc	218.29	219	218.29	0	0	187.2	0	0	-=	\		\(2)
735	Taq1	19	cac	238.08	239	238.08	0	0	3 400 000	0	0	-=	\		\(2)
736	Taq1	19	cac	239.115	239	239.08	0	239.15	4 000 000	0	3 100 000	-+(=)	V		\(2)
737	Taq1	19	cac	240.17	239	0	0	240.17	0	0	3 600 000	=+	/		\(2)
738	Hha1	11	act	218.97	220	0	0	218.97	0	0	3 400 000	=+	/		/(5)
739	Taq1	11	act	219.64	220	0	0	219.64	0	0	3 200 000	=+	/		/(5)
740	Hha1	11	act	220.01	220	0	0	220.01	0	0	3 300 000	=+	/		/(5)
741	Hha1	11	act	220.935	220	220.93	220.94	0	3 100 000	5 200 000	0	=-	\		/(5)
742	Taq1	11	act	220.76	220	0	0	220.76	0	0	3 900 000	=+	/	/	/(5)
743	Hha1	11	act	220.9	220	0	0	220.9	0	0	3 800 000	=+	/	/	/(5)
744	Taq1	47	ggc	117.703	118	117.61	117.63	117.87	7 015.38	6 524.5	6 155.5	==	-		-4
745	Taq1	47	ggc	118.66	118	118.52	118.65	118.81	6 092.3	5 060.47	4 751.61	==	-		-4
746	Taq1	12	agt	119.103	119	119.06	119.05	119.2	5 100 000	7 000 000	3 800 000	=-	\ (-)		-4
747	Hha1	39	agg	121.03	121	121.19	121.17	120.73	373.9	268.67	297.03	==	-		-4
748	Hha1	39	agg	121.6	121	0	0	121.6	0	0	337.72	=+	/		-4
749	Hha1	40	tgg	120.58	121	0	120.52	120.64	0	5 500 000	6 800 000	+=	/		-4
750	Hha1	40	tgg	121.487	121	121.74	121.29	121.43	8 400 000	4 900 000	4 000 000	==	-		-4
751	Taq1	21	acc	318.36	320	318.36	0	0	4 000 000	0	0	-=	\		-4
752	Taq1	21	acc	319.49	320	319.49	0	0	3 600 000	0	0	-=	\		-4
753	Taq1	9	atc	172.7	173	0	172.7	0	0	4 100 000	0	+-	A		A(4)
754	Hha1	9	atc	172.98	173	0	172.98	0	0	4 400 000	0	+-	A		A(4)
755	Hha1	9	atc	173.7	173	173.64	0	173.76	4 100 000	0	4 400 000	-+(=)	V		A(4)
756	Taq1	9	atc	173.785	173	173.73	173.84	0	3 500 000	6 400 000	0	+-	A	A	A(4)
757	Hha1	9	atc	174.03	173	0	174.03	0	0	8 000 000	0	+-	A	A	A(4)
758	Taq1	12	agt	172.507	173	172.52	172.44	172.56	4 100 000	3 300 000	3 600 000	==	-		A(4)
759	Taq1	12	agt	173.553	173	173.55	173.48	173.63	7 100 000	7 700 000	8 100 000	==	-		A(4)
760	Taq1	9	atc	172.7	173	0	172.7	0	0	4 100 000	0	+-	A		A(4)
761	Hha1	9	atc	172.98	173	0	172.98	0	0	4 400 000	0	+-	A		A(4)
762	Hha1	9	atc	173.7	173	173.64	0	173.76	4 100 000	0	4 400 000	-+(=)	V		A(4)
763	Taq1	9	atc	173.785	173	173.73	173.84	0	3 500 000	6 400 000	0	+-	A	A	A(4)
764	Hha1	9	atc	174.03	173	0	174.03	0	0	8 000 000	0	+-	A	A	A(4)
765	Taq1	12	agt	172.507	173	172.52	172.44	172.56	4 100 000	3 300 000	3 600 000	==	-		A(4)
766	Taq1	12	agt	173.553	173	173.55	173.48	173.63	7 100 000	7 700 000	8 100 000	==	-		A(4)
767	Hha1	49	aaa	69.087	69	68.93	69.38	68.95	15 400 000	17 900 000	3 500 000	=-	\ (-)		-(4) \(4)
768	Hha1	26	ctg	130.91	131	130.91	0	0	7 800 000	0	0	-=	\		-(4) \(4)
769	Hha1	3	aac	133.207	134	133.21	133.02	133.39	5 800 000	3 800 000	3 700 000	==	-		-(4) \(4)
770	Hha1	3	aac	134.06	134	134.06	0	0	5 500 000	0	0	-=	\		-(4) \(4)
771	Taq1	31	gac	155.917	156	156.15	155.73	155.87	9 200 000	3 700 000	7 000 000	-=	\ (-)		-(4) \(4)
772	Hha1	55	tca	155.483	156	155.56	155.46	155.43	4 400 000	3 100 000	3 000 000	==	-		-(4) \(4)
773	Hha1	49	aaa	69.087	69	68.93	69.38	68.95	15 400 000	17 900 000	3 500 000	=-	\ (-)		-(4) \(4)
774	Hha1	26	ctg	130.91	131	130.91	0	0	7 800 000	0	0	-=	\		-(4) \(4)
775	Hha1	3	aac	133.207	134	133.21	133.02	133.39	5 800 000	3 800 000	3 700 000	==	-		-(4) \(4)
776	Hha1	3	aac	134.06	134	134.06	0	0	5 500 000	0	0	-=	\		-(4) \(4)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
734	RATAPMK.APM	APM	aminopeptidase M		aga	ttc	increased
735	RATAPMK.APM	APM	aminopeptidase M		cac	gca	increased
736	RATAPMK.APM	APM	aminopeptidase M		cac	gca	increased
737	RATAPMK.APM	APM	aminopeptidase M		cac	gca	increased
738	RATCARPA.CARP	Carp	ankyrin-repeat protein		gta	act	decreased
739	RATCARPA.CARP	Carp	ankyrin-repeat protein		gta	act	decreased
740	RATCARPA.CARP	Carp	ankyrin-repeat protein		gta	act	decreased
741	RATCARPA.CARP	Carp	ankyrin-repeat protein		gta	act	decreased
742	RATCARPA.CARP	Carp	ankyrin-repeat protein		gta	act	decreased
743	RATCARPA.CARP	Carp	ankyrin-repeat protein		gta	act	decreased
744	AF199411.PE1	nc	antifreeze-enhancer binding protein AEP		ggc	agt	No change
745	AF199411.PE1	nc	antifreeze-enhancer binding protein AEP		ggc	agt	No change
746	AF199411.PE1	nc	antifreeze-enhancer binding protein AEP		ggc	agt	No change
747	AF199411.PE1	nc	antifreeze-enhancer binding protein AEP		agg	tgg	No change
748	AF199411.PE1	nc	antifreeze-enhancer binding protein AEP		agg	tgg	No change
749	AF199411.PE1	nc	antifreeze-enhancer binding protein AEP		agg	tgg	No change
750	AF199411.PE1	nc	antifreeze-enhancer binding protein AEP		agg	tgg	No change
751	AF199411.PE1	nc	antifreeze-enhancer binding protein AEP		gtc	acc	No change
752	AF199411.PE1	nc	antifreeze-enhancer binding protein AEP		gtc	acc	No change
753	AF442133.ACF	ACF	APOBEC-1 complementation factor 43 kDa variant		agt	atc	increased by mild
754	AF442133.ACF	ACF	APOBEC-1 complementation factor 43 kDa variant		agt	atc	increased by mild
755	AF442133.ACF	ACF	APOBEC-1 complementation factor 43 kDa variant		agt	atc	increased by mild
756	AF442133.ACF	ACF	APOBEC-1 complementation factor 43 kDa variant		agt	atc	increased by mild
757	AF442133.ACF	ACF	APOBEC-1 complementation factor 43 kDa variant		agt	atc	increased by mild
758	AF442133.ACF	ACF	APOBEC-1 complementation factor 43 kDa variant		agt	atc	increased by mild
759	AF442133.ACF	ACF	APOBEC-1 complementation factor 43 kDa variant		agt	atc	increased by mild
760	AF442134.ACF	ACF	APOBEC-1 complementation factor 45 kDa variant		agt	atc	increased by mild
761	AF442134.ACF	ACF	APOBEC-1 complementation factor 45 kDa variant		agt	atc	increased by mild
762	AF442134.ACF	ACF	APOBEC-1 complementation factor 45 kDa variant		agt	atc	increased by mild
763	AF442134.ACF	ACF	APOBEC-1 complementation factor 45 kDa variant		agt	atc	increased by mild
764	AF442134.ACF	ACF	APOBEC-1 complementation factor 45 kDa variant		agt	atc	increased by mild
765	AF442134.ACF	ACF	APOBEC-1 complementation factor 45 kDa variant		agt	atc	increased by mild
766	AF442134.ACF	ACF	APOBEC-1 complementation factor 45 kDa variant		agt	atc	increased by mild
767	RSU79576.PE1	nc	apolipoprotein A-I		aaa	atc	No change
768	RSU79576.PE1	nc	apolipoprotein A-I		ctg	ggg	No change
769	RSU79576.PE1	nc	apolipoprotein A-I		ggc	aac	No change
770	RSU79576.PE1	nc	apolipoprotein A-I		ggc	aac	No change
771	RSU79576.PE1	nc	apolipoprotein A-I		gac	tca	No change
772	RSU79576.PE1	nc	apolipoprotein A-I		gac	tca	No change
773	RSU79577.PE1	nc	apolipoprotein A-I	*	aaa	atc	No change
774	RSU79577.PE1	nc	apolipoprotein A-I	*	ctg	ggg	No change
775	RSU79577.PE1	nc	apolipoprotein A-I	*	ggc	aac	No change
776	RSU79577.PE1	nc	apolipoprotein A-I	*	ggc	aac	No change

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
777	Taq1	31	gac	155.917	156	156.15	155.73	155.87	9 200 000	3 700 000	7 000 000	-=	\ (-)		-(4) \(4)
778	Hha1	55	tca	155.483	156	155.56	155.46	155.43	4 400 000	3 100 000	3 000 000	==	-		-(4) \(4)
779	Hha1	49	aaa	69.087	69	68.93	69.38	68.95	15 400 000	17 900 000	3 500 000	=-	\ (-)		-(4) \(4)
780	Hha1	26	ctg	130.91	131	130.91	0	0	7 800 000	0	0	-=	\		-(4) \(4)
781	Hha1	3	aac	133.207	134	133.21	133.02	133.39	5 800 000	3 800 000	3 700 000	==	-		-(4) \(4)
782	Hha1	3	aac	134.06	134	134.06	0	0	5 500 000	0	0	-=	\		-(4) \(4)
783	Taq1	31	gac	155.917	156	156.15	155.73	155.87	9 200 000	3 700 000	7 000 000	-=	\ (-)		-(4) \(4)
784	Hha1	55	tca	155.483	156	155.56	155.46	155.43	4 400 000	3 100 000	3 000 000	==	-		-(4) \(4)
785	Taq1	39	agg	145.807	146	146.07	145.65	145.7	23 800 000	54 100 000	5 100 000	+-	A		\(2)
786	Taq1	39	agg	145.885	146	146.07	0	145.7	883.83	0	150.22	-=(-)	\		\(2)
787	Taq1	39	agg	146.33	146	0	146.33	0	0	46 200 000	0	+-	A		\(2)
788	Taq1	39	agg	145.65	146	0	145.65	0	0	543.72	0	+-	A		\(2)
789	Taq1	39	agg	146.33	146	0	146.33	0	0	464.32	0	+-	A		\(2)
790	Taq1	50	aat	146.545	147	146.34	0	146.75	6 700 000	0	11 600 000	-+(=)	V		\(2)
791	Taq1	50	aat	147.35	147	147.35	0	0	11 500 000	0	0	-=	\		\(2)
792	Taq1	50	aat	147.805	147	147.7	0	147.91	9 600 000	0	11 300 000	-+(=)	V		\(2)
793	Hha1	28	tcg	108.88	109	108.89	108.86	108.89	24 900 000	32 000 000	44 800 000	==	-		-2
794	Taq1	17	cca	122.58	123	0	122.57	122.59	0	392.23	1 278	=+	/		-2
795	Taq1	17	cca	123.607	123	123.64	123.6	123.58	325.08	226.03	526.23	=+	/ (-)		-2
796	Taq1	40	tgg	110.32	110	0	0	110.32	0	0	5 600 000	=+	/		/(2)
797	Hha1	6	aga	231.02	232	231.02	0	0	18 200 000	0	0	-=	\		/(2)
798	Hha1	6	aga	231.68	232	0	0	231.68	0	0	3 600 000	=+	/		/(2)
799	Hha1	6	aga	232.65	232	232.68	0	232.62	9 400 000	0	3 300 000	-=(-)	\		/(2)
800	Hha1	40	tgg	116.43	117	116.43	0	0	8 900 000	0	0	-=	\		-(4) \(4)
801	Hha1	40	tgg	117.457	117	117.51	117.29	117.57	13 300 000	10 500 000	3 100 000	=-	\ (-)		-(4) \(4)
802	Hha1	12	agt	120.145	120	120.12	120.17	0	3 360.91	1 874.49	0	=-	\		-(4) \(4)
803	Hha1	59	ttc	132.867	133	132.98	132.83	132.79	358.81	592.15	328.56	==	-	-	-(4) \(4)
804	Hha1	59	ttc	133.55	133	0	133.55	0	0	238.58	0	+-	A		-(4) \(4)
805	Hha1	61	tct	132.68	133	132.57	132.69	132.78	17 200 000	40 300 000	55 400 000	==	-	-	-(4) \(4)
806	Hha1	61	tct	133.78	133	133.78	0	0	5 700 000	0	0	-=	\		-(4) \(4)
807	Hha1	40	tgg	169.29	170	169.37	169.22	169.28	180 800 000	17 500 000	9 100 000	-=	\ (-)		-(4) \(4)
808	Hha1	40	tgg	170.36	170	170.46	170.26	0	7 700 000	8 800 000	0	=-	\		-(4) \(4)
809	Hha1	40	tgg	171	170	171	0	0	6 700 000	0	0	-=	\		-(4) \(4)
810	Taq1	11	act	206.53	207	206.5	206.53	206.56	3 400 000	3 400 000	5 700 000	==	-	-	
811	Hha1	11	act	206.6	207	206.63	206.64	206.53	5 400 000	4 100 000	3 100 000	==	-	-	
812	Hha1	26	ctg	102.86	103	0	0	102.86	0	0	5 200 000	=+	/		\(7)
813	Hha1	40	tgg	102.66	103	102.77	102.55	0	17 300 000	10 800 000	0	=-	\		\(7)
814	Hha1	6	aga	111.76	112	111.69	111.83	0	9 100 000	4 600 000	0	--	\		\(7)
815	Taq1	62	tgt	111.367	112	111.29	111.61	111.2	16 100 000	6 200 000	6 700 000	-=	\ (-)		\(7)
816	Taq1	62	tgt	112.4	112	112.49	112.53	112.18	4 000 000	13 500 000	27 100 000	=+	/ (-)		\(7)
817	Hha1	40	tgg	187.92	189	0	187.92	0	0	3 100 000	0	+-	A		\(7)
818	Hha1	40	tgg	189.55	189	189.5	0	189.6	3 200 000	0	3 100 000	-+(=)	V		\(7)
819	Hha1	56	tga	188.215	189	188.23	188.2	0	224.73	776.08	0	+-	A		\(7)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
777	RSU79577.PE1	nc	apolipoprotein A-I	*	gac	tca	No change
778	RSU79577.PE1	nc	apolipoprotein A-I	*	gac	tca	No change
779	RSU79578.PE1	nc	apolipoprotein A-I	*	aaa	atc	No change
780	RSU79578.PE1	nc	apolipoprotein A-I	*	ctg	ggg	No change
781	RSU79578.PE1	nc	apolipoprotein A-I	*	ggc	aac	No change
782	RSU79578.PE1	nc	apolipoprotein A-I	*	ggc	aac	No change
783	RSU79578.PE1	nc	apolipoprotein A-I	*	gac	tca	No change
784	RSU79578.PE1	nc	apolipoprotein A-I	*	gac	tca	No change
785	RATAPOBED.PE1	nc	apolipoprotein B mRNA editing protein		aat	agg	increased
786	RATAPOBED.PE1	nc	apolipoprotein B mRNA editing protein		aat	agg	increased
787	RATAPOBED.PE1	nc	apolipoprotein B mRNA editing protein		aat	agg	increased
788	RATAPOBED.PE1	nc	apolipoprotein B mRNA editing protein		aat	agg	increased
789	RATAPOBED.PE1	nc	apolipoprotein B mRNA editing protein		aat	agg	increased
790	RATAPOBED.PE1	nc	apolipoprotein B mRNA editing protein		aat	agg	increased
791	RATAPOBED.PE1	nc	apolipoprotein B mRNA editing protein		aat	agg	increased
792	RATAPOBED.PE1	nc	apolipoprotein B mRNA editing protein		aat	agg	increased
793	AF513015.PE1	nc	APP770		atg	tcg	No change
794	AF513015.PE1	nc	APP770		cca	agc	No change
795	AF513015.PE1	nc	APP770		cca	agc	No change
796	RNU90829.PE1	nc	APP-binding protein 1		tgg	ttc	decreased
797	RNU90829.PE1	nc	APP-binding protein 1		ggc	aga	decreased
798	RNU90829.PE1	nc	APP-binding protein 1		ggc	aga	decreased
799	RNU90829.PE1	nc	APP-binding protein 1		ggc	aga	decreased
800	AF095576.PE1	nc	APS protein		tgg	act	No change
801	AF095576.PE1	nc	APS protein		tgg	act	No change
802	AF095576.PE1	nc	APS protein		agt	ggc	No change
803	AF095576.PE1	nc	APS protein		ttc	tct	No change
804	AF095576.PE1	nc	APS protein		ttc	tct	No change
805	AF095576.PE1	nc	APS protein		ttc	tct	No change
806	AF095576.PE1	nc	APS protein		ttc	tct	No change
807	AF095576.PE1	nc	APS protein		atc	tgg	No change
808	AF095576.PE1	nc	APS protein		atc	tgg	No change
809	AF095576.PE1	nc	APS protein		atc	tgg	No change
810	RNARP1.PE1	nc	ARF-related protein 1		gtg	act	No change
811	RNARP1.PE1	nc	ARF-related protein 1		gtg	act	No change
812	AF082124.AHR	AHR	aryl hydrocarbon receptor		ctg	tgg	increased
813	AF082124.AHR	AHR	aryl hydrocarbon receptor		ctg	tgg	increased
814	AF082124.AHR	AHR	aryl hydrocarbon receptor		aga	tgt	increased
815	AF082124.AHR	AHR	aryl hydrocarbon receptor		aga	tgt	increased
816	AF082124.AHR	AHR	aryl hydrocarbon receptor		aga	tgt	increased
817	AF082124.AHR	AHR	aryl hydrocarbon receptor		tga	tgg	increased
818	AF082124.AHR	AHR	aryl hydrocarbon receptor		tga	tgg	increased
819	AF082124.AHR	AHR	aryl hydrocarbon receptor		tga	tgg	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
820	Hha1	56	tga	189.18	189	189.18	0	0	257.42	0	0	-=	\		\(7)
821	Taq1	45	gcc	255.265	256	255.2	255.33	0	4 000 000	3 200 000	0	=-	\		\(7)
822	Taq1	45	gcc	256.03	256	256.06	256	0	3 900 000	4 800 000	0	=-	\		\(7)
823	Taq1	45	gcc	257.05	256	257.05	0	0	3 400 000	0	0	-=	\	\	\(7)
824	Hha1	22	tcc	257.06	257	257.06	0	0	34 400 000	0	0	-=	\	\	\(7)
825	Taq1	21	acc	271.83	271	271.83	0	0	6 700 000	0	0	-=	\		\(7)
826	Taq1	26	ctg	272.34	271	0	0	272.34	0	0	5 300 000	=+	/		\(7)
827	Hha1	26	ctg	102.86	103	0	0	102.86	0	0	5 200 000	=+	/		\(7)
828	Hha1	40	tgg	102.66	103	102.77	102.55	0	17 300 000	10 800 000	0	=-	\		\(7)
829	Hha1	6	aga	111.76	112	111.69	111.83	0	9 100 000	4 600 000	0	--	\		\(7)
830	Taq1	62	tgt	111.367	112	111.29	111.61	111.2	16 100 000	6 200 000	6 700 000	-=	\ (-)		\(7)
831	Taq1	62	tgt	112.4	112	112.49	112.53	112.18	4 000 000	13 500 000	27 100 000	=+	/ (-)		\(7)
832	Hha1	40	tgg	187.92	189	0	187.92	0	0	3 100 000	0	+-	A		\(7)
833	Hha1	40	tgg	189.55	189	189.5	0	189.6	3 200 000	0	3 100 000	-+(=)	V		\(7)
834	Hha1	56	tga	188.215	189	188.23	188.2	0	224.73	776.08	0	+-	A		\(7)
835	Hha1	56	tga	189.18	189	189.18	0	0	257.42	0	0	-=	\		\(7)
836	Taq1	45	gcc	255.265	256	255.2	255.33	0	4 000 000	3 200 000	0	=-	\		\(7)
837	Taq1	45	gcc	256.03	256	256.06	256	0	3 900 000	4 800 000	0	=-	\		\(7)
838	Taq1	45	gcc	257.05	256	257.05	0	0	3 400 000	0	0	-=	\	\	\(7)
839	Hha1	22	tcc	257.06	257	257.06	0	0	34 400 000	0	0	-=	\	\	\(7)
840	Taq1	21	acc	271.83	271	271.83	0	0	6 700 000	0	0	-=	\		\(7)
841	Taq1	26	ctg	272.34	271	0	0	272.34	0	0	5 300 000	=+	/		\(7)
842	Hha1	26	ctg	102.86	103	0	0	102.86	0	0	5 200 000	=+	/		\(7)
843	Hha1	40	tgg	102.66	103	102.77	102.55	0	17 300 000	10 800 000	0	=-	\		\(7)
844	Hha1	6	aga	111.76	112	111.69	111.83	0	9 100 000	4 600 000	0	--	\		\(7)
845	Taq1	62	tgt	111.367	112	111.29	111.61	111.2	16 100 000	6 200 000	6 700 000	-=	\ (-)		\(7)
846	Taq1	62	tgt	112.4	112	112.49	112.53	112.18	4 000 000	13 500 000	27 100 000	=+	/ (-)		\(7)
847	Hha1	40	tgg	187.92	189	0	187.92	0	0	3 100 000	0	+-	A		\(7)
848	Hha1	40	tgg	189.55	189	189.5	0	189.6	3 200 000	0	3 100 000	-+(=)	V		\(7)
849	Hha1	56	tga	188.215	189	188.23	188.2	0	224.73	776.08	0	+-	A		\(7)
850	Hha1	56	tga	189.18	189	189.18	0	0	257.42	0	0	-=	\		\(7)
851	Taq1	45	gcc	255.265	256	255.2	255.33	0	4 000 000	3 200 000	0	=-	\		\(7)
852	Taq1	45	gcc	256.03	256	256.06	256	0	3 900 000	4 800 000	0	=-	\		\(7)
853	Taq1	45	gcc	257.05	256	257.05	0	0	3 400 000	0	0	-=	\	\	\(7)
854	Hha1	22	tcc	257.06	257	257.06	0	0	34 400 000	0	0	-=	\	\	\(7)
855	Taq1	21	acc	271.83	271	271.83	0	0	6 700 000	0	0	-=	\		\(7)
856	Taq1	26	ctg	272.34	271	0	0	272.34	0	0	5 300 000	=+	/		\(7)
857	Hha1	44	cgg	76.835	77	76.71	76.96	0	6 200 000	16 600 000	0	+-	A		/(2)
858	Hha1	44	cgg	77.32	77	0	0	77.32	0	0	4 200 000	=+	/		/(2)
859	Hha1	39	agg	194.28	195	0	0	194.28	0	0	195.31	=+	/		/(2)
860	Hha1	39	agg	195.23	195	0	0	195.23	0	0	134.27	=+	/		/(2)
861	Taq1	56	tga	87.863	88	87.7	87.87	88.02	6 500 000	7 900 000	15 400 000	=+	/ (-)		-(3) \(2)
862	Hha1	6	aga	162.405	163	162.45	0	162.36	4 500 000	0	5 900 000	-+(=)	V		-(3) \(2)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
820	AF082124.AHR	AHR	aryl hydrocarbon receptor		tga	tgg	increased
821	AF082124.AHR	AHR	aryl hydrocarbon receptor		gcc	tcc	increased
822	AF082124.AHR	AHR	aryl hydrocarbon receptor		gcc	tcc	increased
823	AF082124.AHR	AHR	aryl hydrocarbon receptor		gcc	tcc	increased
824	AF082124.AHR	AHR	aryl hydrocarbon receptor		gcc	tcc	increased
825	AF082124.AHR	AHR	aryl hydrocarbon receptor		acc	ctg	increased
826	AF082124.AHR	AHR	aryl hydrocarbon receptor		acc	ctg	increased
827	AF082125.AHR	AHR	aryl hydrocarbon receptor	*	ctg	tgg	increased
828	AF082125.AHR	AHR	aryl hydrocarbon receptor	*	ctg	tgg	increased
829	AF082125.AHR	AHR	aryl hydrocarbon receptor	*	aga	tgt	increased
830	AF082125.AHR	AHR	aryl hydrocarbon receptor	*	aga	tgt	increased
831	AF082125.AHR	AHR	aryl hydrocarbon receptor	*	aga	tgt	increased
832	AF082125.AHR	AHR	aryl hydrocarbon receptor	*	tga	tgg	increased
833	AF082125.AHR	AHR	aryl hydrocarbon receptor	*	tga	tgg	increased
834	AF082125.AHR	AHR	aryl hydrocarbon receptor	*	tga	tgg	increased
835	AF082125.AHR	AHR	aryl hydrocarbon receptor	*	tga	tgg	increased
836	AF082125.AHR	AHR	aryl hydrocarbon receptor	*	gcc	tcc	increased
837	AF082125.AHR	AHR	aryl hydrocarbon receptor	*	gcc	tcc	increased
838	AF082125.AHR	AHR	aryl hydrocarbon receptor	*	gcc	tcc	increased
839	AF082125.AHR	AHR	aryl hydrocarbon receptor	*	gcc	tcc	increased
840	AF082125.AHR	AHR	aryl hydrocarbon receptor	*	acc	ctg	increased
841	AF082125.AHR	AHR	aryl hydrocarbon receptor	*	acc	ctg	increased
842	AF082126.AHR	AHR	aryl hydrocarbon receptor	*	ctg	tgg	increased
843	AF082126.AHR	AHR	aryl hydrocarbon receptor	*	ctg	tgg	increased
844	AF082126.AHR	AHR	aryl hydrocarbon receptor	*	aga	tgt	increased
845	AF082126.AHR	AHR	aryl hydrocarbon receptor	*	aga	tgt	increased
846	AF082126.AHR	AHR	aryl hydrocarbon receptor	*	aga	tgt	increased
847	AF082126.AHR	AHR	aryl hydrocarbon receptor	*	tga	tgg	increased
848	AF082126.AHR	AHR	aryl hydrocarbon receptor	*	tga	tgg	increased
849	AF082126.AHR	AHR	aryl hydrocarbon receptor	*	tga	tgg	increased
850	AF082126.AHR	AHR	aryl hydrocarbon receptor	*	tga	tgg	increased
851	AF082126.AHR	AHR	aryl hydrocarbon receptor	*	gcc	tcc	increased
852	AF082126.AHR	AHR	aryl hydrocarbon receptor	*	gcc	tcc	increased
853	AF082126.AHR	AHR	aryl hydrocarbon receptor	*	gcc	tcc	increased
854	AF082126.AHR	AHR	aryl hydrocarbon receptor	*	gcc	tcc	increased
855	AF082126.AHR	AHR	aryl hydrocarbon receptor	*	acc	ctg	increased
856	AF082126.AHR	AHR	aryl hydrocarbon receptor	*	acc	ctg	increased
857	RNU61157.PE1	nc	aryl hydrocarbon receptor nuclear translocator		cgg	cgg	decreased
858	RNU61157.PE1	nc	aryl hydrocarbon receptor nuclear translocator		cgg	cgg	decreased
859	RNU61157.PE1	nc	aryl hydrocarbon receptor nuclear translocator		agg	cgt	decreased
860	RNU61157.PE1	nc	aryl hydrocarbon receptor nuclear translocator		agg	cgt	decreased
861	RNO6519.PE1	nc	ASIC-beta		agc	tga	No change
862	RNO6519.PE1	nc	ASIC-beta		cca	aga	No change

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
863	Hha1	6	aga	163.67	163	163.92	163.51	163.58	15 700 000	3 600 000	3 000 000	-=	\ (-)	(-)	-(3) \(2)
864	Taq1	17	cca	162.45	163	162.45	0	0	218.26	0	0	-=	\		-(3) \(2)
865	Taq1	17	cca	163.46	163	163.15	163.63	163.6	190.4	339.05	586.37	==	-	(-)	-(3) \(2)
866	Taq1	61	tct	132.773	133	132.74	132.72	132.86	4 100 000	3 200 000	7 600 000	=+	/ (-)		\(2)
867	Taq1	61	tct	133.13	133	0	133.13	0	0	4 300 000	0	+-	A		\(2)
868	Taq1	61	tct	133.775	133	133.64	0	133.91	3 400 000	0	7 100 000	-+(+)	V (/)		\(2)
869	Taq1	63	ctt	132.86	133	132.86	132.86	0	3 000 000	3 500 000	0	=-	\		\(2)
870	Hha1	16	tag	268.21	267	268.21	0	0	3 200 000	0	0	-=	\		\(2)
871	Taq1	61	tct	132.773	133	132.74	132.72	132.86	4 100 000	3 200 000	7 600 000	=+	/ (-)		\(2)
872	Taq1	61	tct	133.13	133	0	133.13	0	0	4 300 000	0	+-	A		\(2)
873	Taq1	61	tct	133.775	133	133.64	0	133.91	3 400 000	0	7 100 000	-+(+)	V (/)		\(2)
874	Taq1	63	ctt	132.86	133	132.86	132.86	0	3 000 000	3 500 000	0	=-	\		\(2)
875	Hha1	16	tag	268.21	267	268.21	0	0	3 200 000	0	0	-=	\		\(2)
876	Hha1	22	tcc	135.305	136	0	135.43	135.18	0	8 700 000	5 000 000	+=	/		/(2)
877	Taq1	22	tcc	135.645	136	135.57	0	135.72	6 100 000	0	38 300 000	=+(+)	/		/(2)
878	Taq1	22	tcc	136.1	136	136.1	0	0	5 700 000	0	0	-=	\		/(2)
879	Taq1	22	tcc	136.737	136	136.64	136.88	136.69	4 400 000	7 800 000	35 600 000	=+	/ (-)		/(2)
880	Hha1	6	aga	263.63	263	263.63	0	0	3 900 000	0	0	-=	\	\	
881	Hha1	8	gaa	263.67	263	263.67	0	0	7 000 000	0	0	-=	\	\	
882	Taq1	9	atc	171.675	172	171.66	171.69	0	6 800 000	5 700 000	0	=-	\	\	
883	Hha1	9	atc	171.78	172	171.68	171.88	0	5 600 000	5 500 000	0	=-	\	\	
884	Taq1	11	act	204.33	205	0	0	204.33	0	0	5 600 000	=+	/	/	
885	Hha1	11	act	204.5	205	0	0	204.5	0	0	3 500 000	=+	/	/	
886	Taq1	9	atc	171.675	172	171.66	171.69	0	6 800 000	5 700 000	0	=-	\	\	
887	Hha1	9	atc	171.78	172	171.68	171.88	0	5 600 000	5 500 000	0	=-	\	\	
888	Taq1	11	act	204.33	205	0	0	204.33	0	0	5 600 000	=+	/	/	
889	Hha1	11	act	204.5	205	0	0	204.5	0	0	3 500 000	=+	/	/	
890	Taq1	9	atc	171.675	172	171.66	171.69	0	6 800 000	5 700 000	0	=-	\	\	
891	Hha1	9	atc	171.78	172	171.68	171.88	0	5 600 000	5 500 000	0	=-	\	\	
892	Taq1	11	act	204.33	205	0	0	204.33	0	0	5 600 000	=+	/	/	
893	Hha1	11	act	204.5	205	0	0	204.5	0	0	3 500 000	=+	/	/	
894	Taq1	9	atc	171.675	172	171.66	171.69	0	6 800 000	5 700 000	0	=-	\	\	
895	Hha1	9	atc	171.78	172	171.68	171.88	0	5 600 000	5 500 000	0	=-	\	\	
896	Taq1	11	act	204.33	205	0	0	204.33	0	0	5 600 000	=+	/	/	
897	Hha1	11	act	204.5	205	0	0	204.5	0	0	3 500 000	=+	/	/	
898	Taq1	26	ctg	114.19	114	0	114.23	114.15	0	4 400 000	5 200 000	+=	/	/	\(4)
899	Taq1	57	ctg	114.057	114	114.06	114.06	114.05	4 700 000	3 900 000	13 300 000	=+	/ (-)	/	\(4)
900	Taq1	57	ctg	114.665	114	114.43	114.9	0	5 400 000	11 000 000	0	+-	A		\(4)
901	Taq1	61	tct	113.88	114	0	113.97	113.79	0	7 400 000	135 300 000	=+	/		\(4)
902	Taq1	34	tgc	142.99	143	142.97	143.01	0	14 700 000	7 700 000	0	--	\		\(4)
903	Taq1	52	att	144.15	144	0	144.15	0	0	6 900 000	0	+-	A		\(4)
904	Taq1	52	att	144.85	144	144.84	144.86	0	6 200 000	3 100 000	0	--	\		\(4)
905	Taq1	17	cca	321.96	321	321.96	0	0	218.26	0	0	-=	\		\(4)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
863	RNO6519.PE1	nc	ASIC-beta		cca	aga	No change
864	RNO6519.PE1	nc	ASIC-beta		cca	aga	No change
865	RNO6519.PE1	nc	ASIC-beta		cca	aga	No change
866	RNAP180.PE1	nc	assembly protein 180 (AP180)		ctt	tct	increased
867	RNAP180.PE1	nc	assembly protein 180 (AP180)		ctt	tct	increased
868	RNAP180.PE1	nc	assembly protein 180 (AP180)		ctt	tct	increased
869	RNAP180.PE1	nc	assembly protein 180 (AP180)		ctt	tct	increased
870	RNAP180.PE1	nc	assembly protein 180 (AP180)		gtc	tag	increased
871	RNAP180I.PE1	nc	assembly protein 180 (AP180) + insert		ctt	tct	increased
872	RNAP180I.PE1	nc	assembly protein 180 (AP180) + insert		ctt	tct	increased
873	RNAP180I.PE1	nc	assembly protein 180 (AP180) + insert		ctt	tct	increased
874	RNAP180I.PE1	nc	assembly protein 180 (AP180) + insert		ctt	tct	increased
875	RNAP180I.PE1	nc	assembly protein 180 (AP180) + insert		gtc	tag	increased
876	RATOXIMETA.ATP5C	ATP5c	ATP synthase gamma-subunit		gtg	tcc	decreased
877	RATOXIMETA.ATP5C	ATP5c	ATP synthase gamma-subunit		gtg	tcc	decreased
878	RATOXIMETA.ATP5C	ATP5c	ATP synthase gamma-subunit		gtg	tcc	decreased
879	RATOXIMETA.ATP5C	ATP5c	ATP synthase gamma-subunit		gtg	tcc	decreased
880	RATATPIF2.PMCA	PMCA	ATPase		gaa	aga	increased
881	RATATPIF2.PMCA	PMCA	ATPase		gaa	aga	increased
882	AB017790.ATP7B	Atp7b	ATPase 7B		agg	atc	increased
883	AB017790.ATP7B	Atp7b	ATPase 7B		agg	atc	increased
884	AB017790.ATP7B	Atp7b	ATPase 7B		act	tga	decreased
885	AB017790.ATP7B	Atp7b	ATPase 7B		act	tga	decreased
886	AB017791.ATP7B	Atp7b	ATPase 7B	*	agg	atc	increased
887	AB017791.ATP7B	Atp7b	ATPase 7B	*	agg	atc	increased
888	AB017791.ATP7B	Atp7b	ATPase 7B	*	act	tga	decreased
889	AB017791.ATP7B	Atp7b	ATPase 7B	*	act	tga	decreased
890	AB017792.ATP7B	Atp7b	ATPase 7B	*	agg	atc	increased
891	AB017792.ATP7B	Atp7b	ATPase 7B	*	agg	atc	increased
892	AB017792.ATP7B	Atp7b	ATPase 7B	*	act	tga	decreased
893	AB017792.ATP7B	Atp7b	ATPase 7B	*	act	tga	decreased
894	AB017793.ATP7B	Atp7b	ATPase 7B		agg	atc	increased
895	AB017793.ATP7B	Atp7b	ATPase 7B		agg	atc	increased
896	AB017793.ATP7B	Atp7b	ATPase 7B		act	tga	decreased
897	AB017793.ATP7B	Atp7b	ATPase 7B		act	tga	decreased
898	AY208182.ABCA1	Abca1	ATP-binding cassette 1		tct	ctg	decreased
899	AY208182.ABCA1	Abca1	ATP-binding cassette 1		tct	ctg	decreased
900	AY208182.ABCA1	Abca1	ATP-binding cassette 1		tct	ctg	increased
901	AY208182.ABCA1	Abca1	ATP-binding cassette 1		tct	ctg	increased
902	AY208182.ABCA1	Abca1	ATP-binding cassette 1		tgc	att	increased
903	AY208182.ABCA1	Abca1	ATP-binding cassette 1		tgc	att	increased
904	AY208182.ABCA1	Abca1	ATP-binding cassette 1		tgc	att	increased
905	AY208182.ABCA1	Abca1	ATP-binding cassette 1		cgt	cca	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
906	Taq1	49	aaa	468.17	467	468.28	468.06	0	3 100 000	3 700 000	0	=-	\		\(4)
907	Taq1	10	atg	219.445	220	219.37	219.52	0	47 400 000	8 200 000	0	-=	\		\(2)
908	Hha1	10	atg	219.873	220	219.9	219.82	219.9	6 800 000	8 500 000	8 000 000	==	-		\(2)
909	Hha1	10	atg	220.893	220	220.89	220.92	220.87	65 800 000	124 200 000	163 300 000	==	-		\(2)
910	Taq1	51	ata	219.84	221	219.84	0	0	6 400 000	0	0	-=	\		\(2)
911	Taq1	51	ata	221.86	221	221.86	0	0	8 500 000	0	0	-=	\		\(2)
912	Taq1	29	gca	111.443	112	111.45	111.52	111.36	31 900 000	22 900 000	12 100 000	==	-	-	-5
913	Taq1	29	gca	112.417	112	112.41	112.41	112.43	98 300 000	83 200 000	8 800 000	=-	\ (-)	(-)	-5
914	Taq1	36	ggt	111.507	112	111.35	111.52	111.65	3 000 000	5 000 000	3 500 000	==	-	-	-5
915	Taq1	36	ggt	112.537	112	112.59	112.56	112.46	5 000 000	8 200 000	5 100 000	==	-	(-)	-5
916	Hha1	35	gga	113.63	114	113.52	113.84	113.53	1 381.16	3 016.24	4 382.92	==	-		-5
917	Hha1	35	gga	114.66	114	114.53	114.85	114.6	3 798.19	3 634.95	5 767.01	==	-	(-)	-5
918	Hha1	59	ttc	114.603	114	114.73	114.55	114.53	218.4	526.04	488.96	+=	/ (-)	(-)	-5
919	Hha1	59	ttc	122.57	123	0	122.8	122.34	0	244.33	501.9	++	/		-5
920	Hha1	59	ttc	123.08	123	122.94	0	123.22	187.2	0	5 570.07	=+(+)	/		-5
921	Hha1	59	ttc	123.37	123	123.37	0	0	218.4	0	0	-=	\		-5
922	Hha1	54	ttt	174.085	175	174.11	174.06	0	5 700 000	4 100 000	0	=-	\		-5
923	Hha1	54	ttt	174.963	175	174.95	175.11	174.83	13 300 000	4 800 000	6 700 000	-=	\ (-)		-5
924	Hha1	54	ttt	175.893	175	175.94	175.84	175.9	15 300 000	11 600 000	3 800 000	=-	\ (-)		-5
925	Hha1	39	agg	85.905	86	0	86.1	85.71	0	991.1	895.18	+=	/		-3
926	Hha1	39	agg	86.31	86	86.31	0	0	791.78	0	0	-=	\		-3
927	Hha1	33	agc	88.273	88	88.16	88.2	88.46	57 000 000	40 900 000	16 400 000	==	-		-3
928	Hha1	59	ttc	87.55	88	0	87.55	0	0	649.64	0	+-	A		-3
929	Hha1	59	ttc	88.253	88	88.57	88.11	88.08	249.6	1 954.69	139.7	+-	A		-3
930	Taq1	61	tct	97.33	97	97.22	97.46	97.31	10 400 000	16 700 000	28 600 000	==	-		-3
931	Taq1	62	tgt	96.507	97	96.37	96.38	96.77	6 900 000	9 300 000	15 900 000	==	-		-3
932	Taq1	62	tgt	97.33	97	97.16	97.5	0	5 900 000	12 100 000	0	+-	A		-3
933	Taq1	62	tgt	97.34	97	97.34	0	0	5 600 000	0	0	-=	\		-3
934	Hha1	44	cgg	71.307	71	71.21	71.39	71.32	26 500 000	4 100 000	9 300 000	-=	\ (-)		\(2)
935	Hha1	39	agg	73.733	74	73.74	73.57	73.89	4 428.15	12 096.24	4 785.15	+-	A		\(2)
936	Taq1	50	aat	229.445	230	229.59	229.3	0	6 700 000	5 600 000	0	=-	\		\(2)
937	Taq1	50	aat	230.565	230	230.43	230.7	0	9 600 000	7 600 000	0	=-	\		\(2)
938	Hha1	44	cgg	71.307	71	71.21	71.39	71.32	26 500 000	4 100 000	9 300 000	-=	\ (-)		\(2)
939	Hha1	39	agg	73.733	74	73.74	73.57	73.89	4 428.15	12 096.24	4 785.15	+-	A		\(2)
940	Taq1	50	aat	229.445	230	229.59	229.3	0	6 700 000	5 600 000	0	=-	\		\(2)
941	Taq1	50	aat	230.565	230	230.43	230.7	0	9 600 000	7 600 000	0	=-	\		\(2)
942	Taq1	8	gaa	60.69	61	0	0	60.69	0	0	20 000 000	=+	/		/(4)
943	Taq1	29	gca	112.417	113	112.41	112.41	112.43	98 300 000	83 200 000	8 800 000	=-	\ (-)		/(4)
944	Taq1	29	gca	113.45	113	113.44	113.48	113.43	19 900 000	19 700 000	10 300 000	=-	\ (-)		/(4)
945	Taq1	56	tga	113	113	0	0	113	0	0	6 200 000	=+	/		/(4)
946	Taq1	64	gtt	120.803	121	120.65	120.63	121.13	5 700 000	14 500 000	8 000 000	+=	/ (-)		/(4)
947	Taq1	51	ata	122.36	122	0	122.54	122.18	0	18 300 000	62 200 000	=+	/		/(4)
948	Hha1	6	aga	153.31	154	153.31	0	0	8 700 000	0	0	-=	\		/(4)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
906	AY208182.ABCA1	Abca1	ATP-binding cassette 1		aaa	tgt	increased
907	RNO426052.ABCA5	abca5	ATP-binding cassette protein 5		ata	atg	increased
908	RNO426052.ABCA5	abca5	ATP-binding cassette protein 5		ata	atg	increased
909	RNO426052.ABCA5	abca5	ATP-binding cassette protein 5		ata	atg	increased
910	RNO426052.ABCA5	abca5	ATP-binding cassette protein 5		ata	atg	increased
911	RNO426052.ABCA5	abca5	ATP-binding cassette protein 5		ata	atg	increased
912	AY082609.PE1	nc	ATP-binding cassette protein B1b		ggt	gca	No change
913	AY082609.PE1	nc	ATP-binding cassette protein B1b		ggt	gca	No change
914	AY082609.PE1	nc	ATP-binding cassette protein B1b		ggt	gca	No change
915	AY082609.PE1	nc	ATP-binding cassette protein B1b		ggt	gca	No change
916	AY082609.PE1	nc	ATP-binding cassette protein B1b		ttc	gga	No change
917	AY082609.PE1	nc	ATP-binding cassette protein B1b		ttc	gga	No change
918	AY082609.PE1	nc	ATP-binding cassette protein B1b		ttc	gga	No change
919	AY082609.PE1	nc	ATP-binding cassette protein B1b		cct	ttc	No change
920	AY082609.PE1	nc	ATP-binding cassette protein B1b		cct	ttc	No change
921	AY082609.PE1	nc	ATP-binding cassette protein B1b		cct	ttc	No change
922	AY082609.PE1	nc	ATP-binding cassette protein B1b		acc	ttt	No change
923	AY082609.PE1	nc	ATP-binding cassette protein B1b		acc	ttt	No change
924	AY082609.PE1	nc	ATP-binding cassette protein B1b		acc	ttt	No change
925	RNU31777.DRPLA	DRPLA	atrophin-1		tgt	agg	No change
926	RNU31777.DRPLA	DRPLA	atrophin-1		tgt	agg	No change
927	RNU31777.DRPLA	DRPLA	atrophin-1		agc	ttc	No change
928	RNU31777.DRPLA	DRPLA	atrophin-1		agc	ttc	No change
929	RNU31777.DRPLA	DRPLA	atrophin-1		agc	ttc	No change
930	RNU31777.DRPLA	DRPLA	atrophin-1		tgt	tct	No change
931	RNU31777.DRPLA	DRPLA	atrophin-1		tgt	tct	No change
932	RNU31777.DRPLA	DRPLA	atrophin-1		tgt	tct	No change
933	RNU31777.DRPLA	DRPLA	atrophin-1		tgt	tct	No change
934	AB038387.ATRN	atrn	attractin	*	cgg	ccg	increased
935	AB038387.ATRN	atrn	attractin	*	ccg	agg	increased
936	AB038387.ATRN	atrn	attractin	*	aat	agc	increased
937	AB038387.ATRN	atrn	attractin	*	aat	agc	increased
938	AB038388.ATRN	Atrn	attractin		cgg	ccg	increased
939	AB038388.ATRN	Atrn	attractin		ccg	agg	increased
940	AB038388.ATRN	Atrn	attractin		aat	agc	increased
941	AB038388.ATRN	Atrn	attractin		aat	agc	increased
942	AB005549.ASBP	asbp	atypical PKC specific binding protein		gaa	gct	decreased
943	AB005549.ASBP	asbp	atypical PKC specific binding protein		tga	gca	decreased
944	AB005549.ASBP	asbp	atypical PKC specific binding protein		tga	gca	decreased
945	AB005549.ASBP	asbp	atypical PKC specific binding protein		tga	gca	decreased
946	AB005549.ASBP	asbp	atypical PKC specific binding protein		ata	gtt	decreased
947	AB005549.ASBP	asbp	atypical PKC specific binding protein		ata	gtt	decreased
948	AB005549.ASBP	asbp	atypical PKC specific binding protein		ggc	aga	decreased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
949	Hha1	6	aga	154.4	154	154.27	0	154.53	14 200 000	0	12 300 000	-+(=)	V		/(4)
950	Taq1	47	ggc	118.66	119	118.52	118.65	118.81	6 092.3	5 060.47	4 751.61	==	-		-2
951	Hha1	41	ccc	164.633	165	164.51	164.57	164.82	3 100 000	3 100 000	4 700 000	==	-		-2
952	Hha1	41	ccc	165.76	165	0	0	165.76	0	0	10 700 000	=+	/		-2
953	Hha1	61	tct	99.33	99	0	0	99.33	0	0	6 200 000	=+	/		/(2)
954	Hha1	56	tga	121.79	122	0	0	121.79	0	0	930.87	=+	/		/(2)
955	Hha1	41	ccc	122.71	123	122.62	0	122.8	6 000 000	0	15 000 000	=+(+)	/		\(6)
956	Hha1	33	agc	123.97	124	123.91	124.03	0	3 500 000	4 200 000	0	=-	\		\(6)
957	Taq1	9	atc	157.455	158	157.47	157.44	0	10 600 000	13 700 000	0	=-	\		\(6)
958	Hha1	9	atc	157.54	158	157.35	157.73	0	4 000 000	11 900 000	0	+-	A		\(6)
959	Taq1	9	atc	158.58	158	158.53	158.63	0	6 400 000	6 800 000	0	=-	\		\(6)
960	Hha1	9	atc	158.603	158	158.38	158.75	158.68	7 400 000	6 100 000	3 000 000	==	-		\(6)
961	Taq1	45	gcc	157.285	158	157.45	157.12	0	3 300 000	3 000 000	0	=-	\		\(6)
962	Taq1	45	gcc	158.307	158	158.33	158.06	158.53	7 900 000	7 700 000	3 200 000	=-	\ (-)		\(6)
963	Taq1	39	agg	204.01	205	204.03	203.99	0	8 600 000	59 700 000	0	+-	A		\(6)
964	Taq1	39	agg	204.42	205	0	204.42	0	0	52 400 000	0	+-	A		\(6)
965	Taq1	39	agg	205.345	205	205.13	205.56	0	14 600 000	98 100 000	0	+-	A		\(6)
966	Taq1	39	agg	203.99	205	0	203.99	0	0	600	0	+-	A		\(6)
967	Taq1	39	agg	204.42	205	0	204.42	0	0	526.63	0	+-	A		\(6)
968	Taq1	39	agg	205.56	205	0	205.56	0	0	985.93	0	+-	A		\(6)
969	Taq1	39	agg	204.03	205	204.03	0	0	319.37	0	0	-=	\		\(6)
970	Taq1	39	agg	205.13	205	205.13	0	0	542.18	0	0	-=	\		\(6)
971	Taq1	39	agg	206.22	205	206.22	0	0	393.64	0	0	-=	\		\(6)
972	Taq1	10	atg	280.42	281	280.42	0	0	6 000 000	0	0	-=	\		\(6)
973	Taq1	10	atg	281.11	281	281.19	281.03	0	8 400 000	3 600 000	0	-=	\		\(6)
974	Hha1	61	tct	148.11	149	0	0	148.11	0	0	3 200 000	=+	/		/(2)
975	Hha1	61	tct	149.107	149	149.03	149.07	149.22	8 700 000	14 000 000	14 200 000	==	-		/(2)
976	Hha1	62	tgt	148.85	149	0	0	148.85	0	0	5 100 000	=+	/		/(2)
977	Hha1	15	tac	133.3	134	133.3	133.42	133.18	28 600 000	12 100 000	6 900 000	-=	\ (-)		\(2)
978	Hha1	15	tac	134.565	134	134.58	134.55	0	6 100 000	4 700 000	0	=-	\	\	\(2)
979	Hha1	15	tac	133.44	134	133.46	133.42	0	6 045.18	3 116.14	0	--	\		\(2)
980	Hha1	15	tac	134.545	134	134.54	134.55	0	1 167.14	1 210.4	0	=-	\	\	\(2)
981	Hha1	61	tct	133.78	134	133.78	0	0	5 700 000	0	0	-=	\		\(2)
982	Hha1	61	tct	134.76	134	134.76	0	0	4 000 000	0	0	-=	\	\	\(2)
983	Hha1	40	tgg	100.115	100	100.28	99.95	0	3 400 000	11 500 000	0	+-	A		/(5)
984	Hha1	40	tgg	99.57	100	0	0	99.57	0	0	9 300 000	=+	/		/(5)
985	Hha1	22	tcc	156.27	157	0	156.27	0	0	3 900 000	0	+-	A		/(5)
986	Hha1	22	tcc	156.39	157	0	156.39	0	0	3 500 000	0	+-	A		/(5)
987	Taq1	22	tcc	156.405	157	156.47	0	156.34	3 800 000	0	13 200 000	=+(+)	/		/(5)
988	Hha1	22	tcc	156.64	157	0	156.64	0	0	3 800 000	0	+-	A		/(5)
989	Taq1	22	tcc	157.48	157	157.37	157.73	157.34	3 300 000	4 500 000	14 200 000	=+	/ (-)		/(5)
990	Taq1	27	acg	156.53	157	0	0	156.53	0	0	3 600 000	=+	/		/(5)
991	Taq1	27	acg	157.58	157	0	0	157.58	0	0	5 700 000	=+	/		/(5)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
949	AB005549.ASBP	asbp	atypical PKC specific binding protein		ggc	aga	decreased
950	AF017757.PE1	nc	Axil		ggc	gtg	No change
951	AF017757.PE1	nc	Axil		ccc	caa	No change
952	AF017757.PE1	nc	Axil		ccc	caa	No change
953	AY228143.ABO2	Abo2	B blood group galactosyltransferase	*	tct	tca	decreased
954	AY228143.ABO2	Abo2	B blood group galactosyltransferase	*	ttt	tga	decreased
955	RNU30831.PE1	nc	B/K protein		ccc	agc	increased
956	RNU30831.PE1	nc	B/K protein		ccc	agc	increased
957	RNU30831.PE1	nc	B/K protein		atc	tca	increased
958	RNU30831.PE1	nc	B/K protein		atc	tca	increased
959	RNU30831.PE1	nc	B/K protein		atc	tca	increased
960	RNU30831.PE1	nc	B/K protein		atc	tca	increased
961	RNU30831.PE1	nc	B/K protein		gcc	ttg	increased
962	RNU30831.PE1	nc	B/K protein		gcc	ttg	increased
963	RNU30831.PE1	nc	B/K protein		ggc	agg	increased
964	RNU30831.PE1	nc	B/K protein		ggc	agg	increased
965	RNU30831.PE1	nc	B/K protein		ggc	agg	increased
966	RNU30831.PE1	nc	B/K protein		ggc	agg	increased
967	RNU30831.PE1	nc	B/K protein		ggc	agg	increased
968	RNU30831.PE1	nc	B/K protein		ggc	agg	increased
969	RNU30831.PE1	nc	B/K protein		ggc	agg	increased
970	RNU30831.PE1	nc	B/K protein		ggc	agg	increased
971	RNU30831.PE1	nc	B/K protein		ggc	agg	increased
972	RNU30831.PE1	nc	B/K protein		gat	atg	increased
973	RNU30831.PE1	nc	B/K protein		gat	atg	increased
974	AY190319.B7H3	B7h3	B7-H3		tct	tgt	decreased
975	AY190319.B7H3	B7h3	B7-H3		tct	tgt	decreased
976	AY190319.B7H3	B7h3	B7-H3		tct	tgt	decreased
977	AY325231.PE1	nc	Ba1-647		tct	tac	increased
978	AY325231.PE1	nc	Ba1-647		tct	tac	increased
979	AY325231.PE1	nc	Ba1-647		tct	tac	increased
980	AY325231.PE1	nc	Ba1-647		tct	tac	increased
981	AY325231.PE1	nc	Ba1-647		tct	tac	increased
982	AY325231.PE1	nc	Ba1-647		tct	tac	increased
983	AY325227.PE1	nc	Ba1-651		cat	tgg	decreased
984	AY325227.PE1	nc	Ba1-651		cat	tgg	decreased
985	AY325227.PE1	nc	Ba1-651		acg	tcc	decreased
986	AY325227.PE1	nc	Ba1-651		acg	tcc	decreased
987	AY325227.PE1	nc	Ba1-651		acg	tcc	decreased
988	AY325227.PE1	nc	Ba1-651		acg	tcc	decreased
989	AY325227.PE1	nc	Ba1-651		acg	tcc	decreased
990	AY325227.PE1	nc	Ba1-651		acg	tcc	decreased
991	AY325227.PE1	nc	Ba1-651		acg	tcc	decreased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
992	Hha1	32	gtc	177.525	178	177.56	177.49	0	1 354.81	437.43	0	-=	\		/(5)
993	Hha1	32	gtc	178.37	178	178.37	0	0	622.48	0	0	-=	\		/(5)
994	Hha1	33	agc	176.96	178	0	0	176.96	0	0	8 500 000	=+	/		/(5)
995	Hha1	33	agc	178.01	178	0	0	178.01	0	0	12 200 000	=+	/		/(5)
996	Hha1	33	agc	178.92	178	0	0	178.92	0	0	15 700 000	=+	/		/(5)
997	Hha1	41	ccc	148.19	149	147.96	148.26	148.35	6 200 000	12 000 000	22 900 000	=+	/ (-)		A(2) \(2)
998	Hha1	41	ccc	148.78	149	148.78	0	0	4 400 000	0	0	-=	\		A(2) \(2)
999	Taq1	10	atg	246.48	247	0	246.48	0	0	5 500 000	0	+-	A	A	A(2) \(2)
1000	Taq1	50	aat	246.545	248	246.34	246.75	0	3 200 000	8 300 000	0	+-	A	A	A(2) \(2)
1001	Taq1	50	aat	247.46	248	247.45	247.47	0	6 900 000	7 700 000	0	=-	\		A(2) \(2)
1002	Taq1	50	aat	248.04	248	248.04	0	0	13 800 000	0	0	-=	\		A(2) \(2)
1003	Taq1	50	aat	249.1	248	249.1	0	0	7 800 000	0	0	-=	\		A(2) \(2)
1004	Taq1	50	aat	249.26	248	249.26	0	0	7 400 000	0	0	-=	\		A(2) \(2)
1005	Hha1	4	aag	220.94	222	0	220.94	0	0	11 800 000	0	+-	A		A(2)
1006	Hha1	4	aag	222.92	222	0	0	222.92	0	0	3 200 000	=+	/		A(2)
1007	Hha1	40	tgg	225.115	225	225.12	225.11	0	4 000 000	3 800 000	0	=-	\		A(2)
1008	Hha1	40	tgg	225.76	225	0	225.76	0	0	6 500 000	0	+-	A		A(2)
1009	Hha1	44	cgg	77.89	78	77.89	0	0	3 200 000	0	0	-=	\		\(3)
1010	Hha1	43	cgc	119.45	120	119.47	119.43	0	50 800 000	6 900 000	0	-=	\		\(3)
1011	Hha1	4	aag	220.94	222	0	220.94	0	0	11 800 000	0	+-	A		\(3)
1012	Hha1	4	aag	222.92	222	0	0	222.92	0	0	3 200 000	=+	/		\(3)
1013	Hha1	40	tgg	225.115	225	225.12	225.11	0	4 000 000	3 800 000	0	=-	\		\(3)
1014	Hha1	40	tgg	225.76	225	0	225.76	0	0	6 500 000	0	+-	A		\(3)
1015	Hha1	44	cgg	102.62	103	0	102.62	0	0	5 400 000	0	+-	A		/(4)
1016	Hha1	44	cgg	103.53	103	0	0	103.53	0	0	5 200 000	=+	/		/(4)
1017	Hha1	27	acg	115.727	116	115.75	115.63	115.8	6 500 000	4 600 000	13 100 000	=+	/ (-)	/	/(4)
1018	Hha1	59	ttc	115.51	116	0	115.28	115.74	0	201.21	152.64	+=	/	/	/(4)
1019	Hha1	59	ttc	116.287	116	116.49	116	116.37	447.21	580.65	155.22	=-	\ (-)		/(4)
1020	Hha1	59	ttc	116.49	116	0	116.49	0	0	117.85	0	+-	A		/(4)
1021	Hha1	33	agc	218.86	220	0	0	218.86	0	0	3 500 000	=+	/		/(4)
1022	Hha1	33	agc	219.92	220	0	0	219.92	0	0	3 100 000	=+	/		/(4)
1023	Hha1	39	agg	66.61	67	0	66.57	66.65	0	1 629.94	2 937.82	+=	/		-1,166666667
1024	Hha1	54	ttt	68.19	68	68.18	68.28	68.11	7 500 000	3 900 000	13 100 000	=+	/ (-)		-1,166666667
1025	Hha1	64	gtt	70.367	70	70.31	70.37	70.42	6 400 000	5 200 000	17 000 000	=+	/ (-)		-1,166666667
1026	Hha1	54	ttt	71.17	71	71.25	71.28	70.98	8 900 000	5 000 000	3 200 000	==	-		-1,166666667
1027	Hha1	6	aga	121.083	121	121.14	121.23	120.88	15 100 000	6 600 000	6 200 000	-=	\ (-)		-1,166666667
1028	Taq1	52	att	121.445	122	0	121.5	121.39	0	3 000 000	3 300 000	+=	/		-1,166666667
1029	Taq1	52	att	121.73	122	0	0	121.73	0	0	4 300 000	=+	/		-1,166666667
1030	Taq1	44	cgg	136.91	137	136.77	0	137.05	611.04	0	829.41	-+(=)	V		-1,166666667
1031	Taq1	44	cgg	137.803	137	137.66	137.75	138	545.08	502.47	941.49	=+	/ (-)		-1,166666667
1032	Taq1	31	gac	155.917	156	156.15	155.73	155.87	9 200 000	3 700 000	7 000 000	-=	\ (-)		-1,166666667
1033	Hha1	49	aaa	200.177	201	200.28	200.21	200.04	5 200 000	6 700 000	3 600 000	=-	\ (-)		-1,166666667
1034	Hha1	49	aaa	201.345	201	201.46	201.23	0	11 400 000	15 700 000	0	=-	\		-1,166666667

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
992	AY325227.PE1	nc	Ba1-651		gtc	agc	decreased
993	AY325227.PE1	nc	Ba1-651		gtc	agc	decreased
994	AY325227.PE1	nc	Ba1-651		gtc	agc	decreased
995	AY325227.PE1	nc	Ba1-651		gtc	agc	decreased
996	AY325227.PE1	nc	Ba1-651		gtc	agc	decreased
997	AY325230.PE1	nc	Ba1-667		ccc	ccc	increased by mild
998	AY325230.PE1	nc	Ba1-667		ccc	ccc	increased by mild
999	AY325230.PE1	nc	Ba1-667		aat	atg	increased by mild
1000	AY325230.PE1	nc	Ba1-667		aat	atg	increased by mild
1001	AY325230.PE1	nc	Ba1-667		aat	atg	increased by mild
1002	AY325230.PE1	nc	Ba1-667		aat	atg	increased by mild
1003	AY325230.PE1	nc	Ba1-667		aat	atg	increased by mild
1004	AY325230.PE1	nc	Ba1-667		aat	atg	increased by mild
1005	AB003504.PE1	nc	BAF60b		cct	aag	increased by mild
1006	AB003504.PE1	nc	BAF60b		cct	aag	increased by mild
1007	AB003504.PE1	nc	BAF60b		agt	tgg	increased by mild
1008	AB003504.PE1	nc	BAF60b		agt	tgg	increased by mild
1009	AB003505.PE1	nc	BAF60b		cgc	cgg	increased
1010	AB003505.PE1	nc	BAF60b		tca	cgc	increased
1011	AB003505.PE1	nc	BAF60b		cct	aag	increased
1012	AB003505.PE1	nc	BAF60b		cct	aag	increased
1013	AB003505.PE1	nc	BAF60b		agt	tgg	increased
1014	AB003505.PE1	nc	BAF60b		agt	tgg	increased
1015	AB043981.MBH2	mbh2	Bar-class homeodomain protein MBH2		tcc	cgg	decreased
1016	AB043981.MBH2	mbh2	Bar-class homeodomain protein MBH2		tcc	cgg	decreased
1017	AB043981.MBH2	mbh2	Bar-class homeodomain protein MBH2		ttc	acg	decreased
1018	AB043981.MBH2	mbh2	Bar-class homeodomain protein MBH2		ttc	acg	decreased
1019	AB043981.MBH2	mbh2	Bar-class homeodomain protein MBH2		ttc	acg	decreased
1020	AB043981.MBH2	mbh2	Bar-class homeodomain protein MBH2		ttc	acg	decreased
1021	AB043981.MBH2	mbh2	Bar-class homeodomain protein MBH2		agc	cga	decreased
1022	AB043981.MBH2	mbh2	Bar-class homeodomain protein MBH2		agc	cga	decreased
1023	AB077475.PE1	nc	barmotin		agg	ttt	No change
1024	AB077475.PE1	nc	barmotin		agg	ttt	No change
1025	AB077475.PE1	nc	barmotin		gtt	tag	No change
1026	AB077475.PE1	nc	barmotin		tga	ttt	No change
1027	AB077475.PE1	nc	barmotin		att	aga	No change
1028	AB077475.PE1	nc	barmotin		att	aga	No change
1029	AB077475.PE1	nc	barmotin		att	aga	No change
1030	AB077475.PE1	nc	barmotin		cta	cgg	No change
1031	AB077475.PE1	nc	barmotin		cta	cgg	No change
1032	AB077475.PE1	nc	barmotin		agc	gac	No change
1033	AB077475.PE1	nc	barmotin		aaa	gaa	No change
1034	AB077475.PE1	nc	barmotin		aaa	gaa	No change

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
1035	Taq1	29	gca	227.715	228	227.65	227.78	0	3 000 000	3 100 000	0	=-	\		-1,166666667
1036	Taq1	29	gca	228.87	228	0	0	228.87	0	0	3 100 000	=+	/		-1,166666667
1037	Taq1	17	cca	112.43	113	112.17	112.55	112.57	506.19	1 914.63	2 435.72	+=	/ (-)	(-)	
1038	Taq1	17	cca	113.45	113	113.16	113.62	113.57	701.24	924.07	4 104.64	=+	/ (-)	/	
1039	Taq1	20	ctc	112.503	113	112.57	112.35	112.59	5 600 000	6 300 000	7 700 000	==	-	(-)	
1040	Taq1	20	ctc	113.383	113	113.37	113.27	113.51	5 700 000	4 400 000	37 800 000	=+	/ (-)	/	
1041	Hha1	7	caa	161.567	161	161.64	161.53	161.53	35 200 000	23 800 000	20 900 000	==	-	(-)	
1042	Taq1	7	caa	161.78	161	161.64	161.87	161.83	4 300 000	4 600 000	10 500 000	=+	/ (-)	(-)	
1043	Taq1	48	ggg	133.415	134	133.19	133.64	0	1 011.37	1 795.14	0	=-	\		/(2)
1044	Taq1	48	ggg	134.31	134	134.23	134.39	0	1 390.64	2 479.58	0	=-	\		/(2)
1045	Taq1	26	ctg	134.29	135	0	134.24	134.34	0	9 800 000	6 000 000	+=	/		/(2)
1046	Taq1	26	ctg	135.4	135	0	135.4	0	0	5 300 000	0	+-	A		/(2)
1047	Taq1	57	ctg	135.083	135	135.3	135.02	134.93	4 900 000	3 600 000	8 900 000	=+	/ (-)		/(2)
1048	Hha1	40	tgg	139.54	140	139.54	0	0	5 600 000	0	0	-=	\		\(2)
1049	Hha1	40	tgg	140.665	140	140.67	140.66	0	13 800 000	9 700 000	0	=-	\		\(2)
1050	Hha1	26	ctg	248.75	250	248.75	0	0	3 600 000	0	0	-=	\		\(2)
1051	Hha1	59	ttc	148.135	148	0	148.05	148.22	0	89.11	77.61	+=	/		/(2)
1052	Hha1	54	ttt	148.59	149	0	0	148.59	0	0	3 600 000	=+	/		/(2)
1053	Hha1	31	gac	60.763	61	60.78	60.77	60.74	11 300 000	7 200 000	27 300 000	=+	/ (-)		-1
1054	Hha1	20	ctc	65.19	65	65.1	65.11	65.36	495.86	3 606.08	8 826.33	=+	/ (-)		-1
1055	Hha1	20	ctc	68.973	69	68.95	69.09	68.88	550.96	485.18	1 145.03	=+	/ (-)		-1
1056	Hha1	59	ttc	94.35	94	94.22	94.34	94.49	754.03	845.11	333.73	=-	\ (-)		-1
1057	Hha1	56	tga	113.573	114	113.53	113.49	113.7	429.04	726.55	3 464.91	=+	/ (-)		-1
1058	Hha1	56	tga	114.53	114	114.39	114.45	114.75	2 202.42	308.23	896.39	-=	\ (-)		-1
1059	Hha1	20	ctc	129.17	129	0	129.32	129.02	0	406.5	584.44	+=	/		-1
1060	Hha1	40	tgg	145.52	146	145.53	145.44	145.59	3 100 000	9 400 000	9 100 000	+=	/ (-)		-1
1061	Hha1	40	tgg	146.47	146	0	146.34	146.6	0	9 800 000	16 400 000	+=	/		-1
1062	Hha1	40	tgg	238.06	237	0	238.06	0	0	3 900 000	0	+-	A		-1
1063	Taq1	17	cca	250.98	252	250.98	0	0	213.62	0	0	-=	\		\(2)
1064	Taq1	17	cca	252.41	252	252.41	0	0	208.98	0	0	-=	\	\	\(2)
1065	Taq1	39	agg	250.95	252	0	250.95	0	0	9 100 000	0	+-	A		\(2)
1066	Taq1	39	agg	251.575	252	251.54	251.61	0	5 000 000	8 300 000	0	=-	\		\(2)
1067	Taq1	39	agg	252.59	252	252.58	252.6	0	42 900 000	108 100 000	0	+-	A		\(2)
1068	Taq1	39	agg	253.475	252	253.39	253.56	0	8 100 000	6 100 000	0	=-	\		\(2)
1069	Taq1	39	agg	250.95	252	0	250.95	0	0	91.45	0	+-	A		\(2)
1070	Taq1	39	agg	251.575	252	251.54	251.61	0	185.68	83.41	0	-=	\		\(2)
1071	Taq1	39	agg	252.59	252	252.58	252.6	0	1 593.13	1 086.44	0	=-	\	\	\(2)
1072	Taq1	39	agg	253.475	252	253.39	253.56	0	300.8	61.3	0	-=	\		\(2)
1073	Taq1	45	gcc	111.91	112	0	111.86	111.96	0	12 800 000	9 200 000	+=	/		/(3)
1074	Hha1	25	cag	112.955	113	0	113	112.91	0	5 200 000	13 700 000	=+	/		/(3)
1075	Taq1	52	att	172.305	172	0	172.26	172.35	0	3 600 000	3 100 000	+=	/		/(3)
1076	Hha1	8	gaa	263.67	265	263.67	0	0	7 000 000	0	0	-=	\		\(2)
1077	Hha1	8	gaa	264.4	265	0	264.4	0	0	3 700 000	0	+-	A		\(2)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
1035	AB077475.PE1	nc	barmotin		gca	tgg	No change
1036	AB077475.PE1	nc	barmotin		gca	tgg	No change
1037	RNU82626.PE1	nc	basement membrane-associated chondroitin		cca	ctc	No change
1038	RNU82626.PE1	nc	basement membrane-associated chondroitin		cca	ctc	decreased
1039	RNU82626.PE1	nc	basement membrane-associated chondroitin		cca	ctc	No change
1040	RNU82626.PE1	nc	basement membrane-associated chondroitin		cca	ctc	decreased
1041	RNU82626.PE1	nc	basement membrane-associated chondroitin		caa	tgg	No change
1042	RNU82626.PE1	nc	basement membrane-associated chondroitin		caa	tgg	No change
1043	AB018791.BAT3	BAT3	BAT3		ggg	ctg	decreased
1044	AB018791.BAT3	BAT3	BAT3		ggg	ctg	decreased
1045	AB018791.BAT3	BAT3	BAT3		ggg	ctg	decreased
1046	AB018791.BAT3	BAT3	BAT3		ggg	ctg	decreased
1047	AB018791.BAT3	BAT3	BAT3		ggg	ctg	decreased
1048	AF279911.PE1	Bad-beta	bcl-2 associated death agonist beta		tgg	gag	increased
1049	AF279911.PE1	Bad-beta	bcl-2 associated death agonist beta		tgg	gag	increased
1050	AF279911.PE1	Bad-beta	bcl-2 associated death agonist beta		tat	ctg	increased
1051	RNBEST5.PE1	nc	Best5 protein		ttt	ttc	decreased
1052	RNBEST5.PE1	nc	Best5 protein		ttt	ttc	decreased
1053	RATB1ARA.PE1	nc	beta-1 adrenergic receptor		tcc	gac	No change
1054	RATB1ARA.PE1	nc	beta-1 adrenergic receptor		ctc	ctt	No change
1055	RATB1ARA.PE1	nc	beta-1 adrenergic receptor		ctc	ggc	No change
1056	RATB1ARA.PE1	nc	beta-1 adrenergic receptor		tgg	ttc	No change
1057	RATB1ARA.PE1	nc	beta-1 adrenergic receptor		ggc	tga	No change
1058	RATB1ARA.PE1	nc	beta-1 adrenergic receptor		ggc	tga	No change
1059	RATB1ARA.PE1	nc	beta-1 adrenergic receptor		ctc	ggg	No change
1060	RATB1ARA.PE1	nc	beta-1 adrenergic receptor		tca	tgg	No change
1061	RATB1ARA.PE1	nc	beta-1 adrenergic receptor		tca	tgg	No change
1062	RATB1ARA.PE1	nc	beta-1 adrenergic receptor		tca	tgg	No change
1063	D87839.PE1	nc	beta-alanine oxoglutarate aminotransferase		cca	agg	increased
1064	D87839.PE1	nc	beta-alanine oxoglutarate aminotransferase		cca	agg	increased
1065	D87839.PE1	nc	beta-alanine oxoglutarate aminotransferase		cca	agg	increased
1066	D87839.PE1	nc	beta-alanine oxoglutarate aminotransferase		cca	agg	increased
1067	D87839.PE1	nc	beta-alanine oxoglutarate aminotransferase		cca	agg	increased
1068	D87839.PE1	nc	beta-alanine oxoglutarate aminotransferase		cca	agg	increased
1069	D87839.PE1	nc	beta-alanine oxoglutarate aminotransferase		cca	agg	increased
1070	D87839.PE1	nc	beta-alanine oxoglutarate aminotransferase		cca	agg	increased
1071	D87839.PE1	nc	beta-alanine oxoglutarate aminotransferase		cca	agg	increased
1072	D87839.PE1	nc	beta-alanine oxoglutarate aminotransferase		cca	agg	increased
1073	RATBARRES2.PE1	nc	beta-arrestin2		gcc	cag	decreased
1074	RATBARRES2.PE1	nc	beta-arrestin2		gcc	cag	decreased
1075	RATBARRES2.PE1	nc	beta-arrestin2		ggc	att	decreased
1076	RATBG.BETAGLYCAN	betaglycan	betaglycan		gaa	gag	increased
1077	RATBG.BETAGLYCAN	betaglycan	betaglycan		gaa	gag	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
1078	Taq1	8	gaa	264.34	265	0	0	264.34	0	0	3 500 000	=+	/		\(2)
1079	Taq1	8	gaa	264.92	265	264.92	264.92	0	11 000 000	10 100 000	0	=-	\		\(2)
1080	Taq1	39	agg	68.35	68	68.41	68.28	68.36	10 400 000	26 700 000	8 000 000	+-	A		-(3) \(3)
1081	Taq1	39	agg	68.35	68	68.41	68.28	68.36	386.21	268.34	235.64	==	-		-(3) \(3)
1082	Hha1	6	aga	133.97	134	133.97	0	0	12 700 000	0	0	-=	\		-(3) \(3)
1083	Taq1	62	tgt	133.643	134	133.7	133.7	133.53	4 300 000	8 400 000	3 600 000	+-	A		-(3) \(3)
1084	Taq1	62	tgt	134.583	134	134.59	134.55	134.61	8 000 000	12 100 000	4 500 000	=-	\ (-)		-(3) \(3)
1085	Taq1	12	agt	180.85	181	180.85	0	0	4 100 000	0	0	-=	\		-(3) \(3)
1086	Taq1	12	agt	181.807	181	181.77	181.84	181.81	6 100 000	5 300 000	5 200 000	==	-		-(3) \(3)
1087	Taq1	39	agg	68.35	68	68.41	68.28	68.36	10 400 000	26 700 000	8 000 000	+-	A		-(3) \(3)
1088	Taq1	39	agg	68.35	68	68.41	68.28	68.36	386.21	268.34	235.64	==	-		-(3) \(3)
1089	Hha1	6	aga	133.97	134	133.97	0	0	12 700 000	0	0	-=	\		-(3) \(3)
1090	Taq1	62	tgt	133.643	134	133.7	133.7	133.53	4 300 000	8 400 000	3 600 000	+-	A		-(3) \(3)
1091	Taq1	62	tgt	134.583	134	134.59	134.55	134.61	8 000 000	12 100 000	4 500 000	=-	\ (-)		-(3) \(3)
1092	Taq1	12	agt	180.85	181	180.85	0	0	4 100 000	0	0	-=	\		-(3) \(3)
1093	Taq1	12	agt	181.807	181	181.77	181.84	181.81	6 100 000	5 300 000	5 200 000	==	-		-(3) \(3)
1094	Hha1	27	acg	132.99	133	132.98	132.95	133.04	22 200 000	6 000 000	10 000 000	-=	\ (-)	(-)	
1095	Hha1	40	tgg	133.193	133	133.22	133.26	133.1	3 800 000	8 000 000	6 900 000	+=	/ (-)	(-)	
1096	Taq1	51	ata	97.483	98	97.54	97.42	97.49	92 500 000	35 900 000	44 800 000	-=	\ (-)	(-)	-(3) \(2)
1097	Taq1	51	ata	98.365	98	0	98.41	98.32	0	3 700 000	3 700 000	+=	/		-(3) \(2)
1098	Taq1	54	ttt	97.627	98	97.63	97.38	97.87	2 723.96	1 705.28	2 655.24	==	-	(-)	-(3) \(2)
1099	Taq1	54	ttt	98.3	98	98.21	98.39	0	1 638.74	1 340.7	0	=-	\		-(3) \(2)
1100	Hha1	44	cgg	116.863	117	116.81	116.78	117	5 300 000	3 900 000	3 300 000	==	-		-(3) \(2)
1101	Hha1	64	gtt	68.403	68	68.48	68.31	68.42	72 300 000	13 000 000	31 700 000	-=	\ (-)		\(3)
1102	Hha1	20	ctc	82.09	82	0	82.09	0	0	472.06	0	+-	A		\(3)
1103	Hha1	27	acg	93.515	93	93.45	0	93.58	5 600 000	0	3 700 000	-+(=)	V		\(3)
1104	Hha1	33	agc	94.285	94	94.26	94.31	0	4 500 000	3 800 000	0	=-	\		\(3)
1105	Hha1	59	ttc	240.84	240	240.84	0	0	166.4	0	0	-=	\		\(3)
1106	Taq1	9	atc	159.56	160	159.54	159.52	159.62	5 700 000	9 300 000	3 500 000	=-	\ (-)	\	
1107	Hha1	9	atc	159.515	160	159.34	159.69	0	9 800 000	15 600 000	0	=-	\	\	
1108	Taq1	10	atg	160.47	160	160.29	160.65	0	5 700 000	3 500 000	0	=-	\	\	
1109	Hha1	10	atg	160.56	160	160.56	0	0	3 600 000	0	0	-=	\	\	
1110	Hha1	10	atg	106.79	107	106.79	0	0	4 800 000	0	0	-=	\	\	
1111	Taq1	10	atg	106.69	107	106.69	0	0	8 900 000	0	0	-=	\	\	
1112	Hha1	43	cgc	183.3	183	0	183.25	183.35	0	3 600 000	7 200 000	++	/	/	/(2)
1113	Hha1	39	agg	183.51	184	0	183.67	183.35	0	220.9	142.41	+=	/	/	/(2)
1114	Hha1	20	ctc	68.973	69	68.95	69.09	68.88	550.96	485.18	1 145.03	=+	/ (-)		-3
1115	Hha1	28	tcg	165.28	166	0	0	165.28	0	0	9 100 000	=+	/		-3
1116	Hha1	64	gtt	165.277	166	165.26	165.35	165.22	12 100 000	3 200 000	4 900 000	-=	\ (-)		-3
1117	Hha1	64	gtt	166.45	166	166.45	0	0	3 300 000	0	0	-=	\		-3
1118	Hha1	25	cag	223.873	225	223.9	223.86	223.86	293 900 000	127 000 000	238 000 000	-=	\ (-)		-3
1119	Hha1	25	cag	224.68	225	0	224.68	0	0	20 400 000	0	+-	A		-3
1120	Hha1	25	cag	225.99	225	225.91	225.86	226.2	3 300 000	3 700 000	6 000 000	==	-		-3

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
1078	RATBG.BETAGLYCAN	betaglycan	betaglycan		gaa	gag	increased
1079	RATBG.BETAGLYCAN	betaglycan	betaglycan		gaa	gag	increased
1080	AF038870.BHMT	BHMT	betaine homocysteine methyltransferase		ata	agg	No change
1081	AF038870.BHMT	BHMT	betaine homocysteine methyltransferase		ata	agg	No change
1082	AF038870.BHMT	BHMT	betaine homocysteine methyltransferase		tgt	aga	No change
1083	AF038870.BHMT	BHMT	betaine homocysteine methyltransferase		tgt	aga	No change
1084	AF038870.BHMT	BHMT	betaine homocysteine methyltransferase		tgt	aga	No change
1085	AF038870.BHMT	BHMT	betaine homocysteine methyltransferase		ggc	agt	No change
1086	AF038870.BHMT	BHMT	betaine homocysteine methyltransferase		ggc	agt	No change
1087	RNU96133.BHMT	BHMT	betaine-homocysteine methyltransferase		ata	agg	No change
1088	RNU96133.BHMT	BHMT	betaine-homocysteine methyltransferase		ata	agg	No change
1089	RNU96133.BHMT	BHMT	betaine-homocysteine methyltransferase		tgt	aga	No change
1090	RNU96133.BHMT	BHMT	betaine-homocysteine methyltransferase		tgt	aga	No change
1091	RNU96133.BHMT	BHMT	betaine-homocysteine methyltransferase		tgt	aga	No change
1092	RNU96133.BHMT	BHMT	betaine-homocysteine methyltransferase		ggc	agt	No change
1093	RNU96133.BHMT	BHMT	betaine-homocysteine methyltransferase		ggc	agt	No change
1094	AB008551.PE1	nc	beta-spectrin III		acg	tgg	No change
1095	AB008551.PE1	nc	beta-spectrin III		acg	tgg	No change
1096	AB050103.NXF	nxf	bHLH PAS type transcription factor NXF		ttt	ata	No change
1097	AB050103.NXF	nxf	bHLH PAS type transcription factor NXF		ttt	ata	No change
1098	AB050103.NXF	nxf	bHLH PAS type transcription factor NXF		ttt	ata	No change
1099	AB050103.NXF	nxf	bHLH PAS type transcription factor NXF		ttt	ata	No change
1100	AB050103.NXF	nxf	bHLH PAS type transcription factor NXF		cag	cgg	No change
1101	RAT4.PE1	nc	bHLH protein		tcc	gtt	increased
1102	RAT4.PE1	nc	bHLH protein		cta	ctc	increased
1103	RAT4.PE1	nc	bHLH protein		tgc	acg	increased
1104	RAT4.PE1	nc	bHLH protein		aag	agc	increased
1105	RAT4.PE1	nc	bHLH protein		cgc	ttc	increased
1106	AF242189.PE1	nc	bile acid CoA ligase		atg	atc	increased
1107	AF242189.PE1	nc	bile acid CoA ligase		atg	atc	increased
1108	AF242189.PE1	nc	bile acid CoA ligase		atg	atc	increased
1109	AF242189.PE1	nc	bile acid CoA ligase		atg	atc	increased
1110	RNU69487.SPGP	spgp	bile salt export pump		atc	atg	increased
1111	RNU69487.SPGP	spgp	bile salt export pump		atc	atg	increased
1112	RNO243974.BM1	BM1	BM1av1		cgc	agg	decreased
1113	RNO243974.BM1	BM1	BM1av1		cgc	agg	decreased
1114	AY325260.PE1	nc	Bm403207		cac	ctc	No change
1115	AY325260.PE1	nc	Bm403207		tcg	gtt	No change
1116	AY325260.PE1	nc	Bm403207		tcg	gtt	No change
1117	AY325260.PE1	nc	Bm403207		tcg	gtt	No change
1118	AY325260.PE1	nc	Bm403207		cag	ggg	No change
1119	AY325260.PE1	nc	Bm403207		cag	ggg	No change
1120	AY325260.PE1	nc	Bm403207		cag	ggg	No change

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
1121	Hha1	25	cag	226.15	225	226.15	0	0	3 300 000	0	0	-=	\		-3
1122	Taq1	56	tga	118.02	118	0	0	118.02	0	0	3 700 000	=+	/		/(2)
1123	Taq1	61	tct	202.325	203	0	202.16	202.49	0	3 900 000	6 100 000	+=	/		/(2)
1124	Hha1	7	caa	106.513	106	106.47	106.53	106.54	6 100 000	7 600 000	3 700 000	=-	\ (-)		\(2)
1125	Hha1	40	tgg	201.08	202	0	201.08	0	0	6 200 000	0	+-	A		\(2)
1126	Hha1	40	tgg	202.96	202	202.96	0	0	4 200 000	0	0	-=	\		\(2)
1127	Taq1	18	cct	151.165	151	151.13	151.2	0	16 300 000	24 700 000	0	=-	\		A(2) \(2)
1128	Taq1	40	tgg	150.207	151	150.09	150.41	150.12	5 300 000	10 100 000	3 600 000	+-	A		A(2) \(2)
1129	Taq1	40	tgg	151.16	151	0	0	151.16	0	0	10 100 000	=+	/		A(2) \(2)
1130	Hha1	41	ccc	193.06	193	193.06	0	0	4 200 000	0	0	-=	\		A(2) \(2)
1131	Hha1	41	ccc	193.64	193	0	193.64	0	0	3 000 000	0	+-	A		A(2) \(2)
1132	Hha1	31	gac	178.83	179	0	178.8	178.86	0	3 300 000	8 100 000	=+	/	/	/(2)
1133	Hha1	33	agc	178.01	179	0	0	178.01	0	0	12 200 000	=+	/		/(2)
1134	Hha1	33	agc	178.92	179	0	0	178.92	0	0	15 700 000	=+	/	/	/(2)
1135	Taq1	9	atc	96.553	97	96.55	96.57	96.54	13 600 000	19 600 000	3 500 000	=-	\ (-)		\(8)
1136	Hha1	9	atc	97.07	97	97.07	0	0	6 600 000	0	0	-=	\		\(8)
1137	Taq1	9	atc	97.555	97	97.48	97.63	0	8 400 000	22 500 000	0	+-	A		\(8)
1138	Taq1	39	agg	96.895	97	96.66	97.13	0	4 200 000	104 500 000	0	+-	A		\(8)
1139	Taq1	39	agg	97.27	97	97.16	0	97.38	9 400 000	0	6 600 000	-+(=)	V		\(8)
1140	Taq1	39	agg	96.66	97	96.66	0	0	155.97	0	0	-=	\		\(8)
1141	Taq1	39	agg	97.16	97	97.16	0	0	349.07	0	0	-=	\		\(8)
1142	Taq1	39	agg	97.13	97	0	97.13	0	0	1 050.26	0	+-	A		\(8)
1143	Taq1	48	ggg	104.49	105	104.33	104.65	0	2 212.38	1 476.94	0	=-	\		\(8)
1144	Taq1	48	ggg	105.5	105	0	105.53	105.47	0	2 929.87	1 430.7	+-	A		\(8)
1145	Taq1	54	ttt	106.78	107	106.7	106.86	0	480.69	1 070.21	0	+-	A		\(8)
1146	Taq1	54	ttt	107.32	107	107.43	107.21	0	473.41	1 011.4	0	+-	A		\(8)
1147	Hha1	60	ttg	120.855	121	0	120.83	120.88	0	4 900 000	4 700 000	+=	/		\(8)
1148	Hha1	60	ttg	121.49	121	121.38	121.52	121.57	10 100 000	10 000 000	5 400 000	=-	\ (-)		\(8)
1149	Taq1	41	ccc	144.41	145	0	144.41	0	0	8 600 000	0	+-	A		\(8)
1150	Taq1	41	ccc	145.325	145	145.25	145.4	0	22 900 000	22 800 000	0	=-	\		\(8)
1151	Taq1	8	gaa	145.64	146	145.76	145.52	0	3 700 000	3 600 000	0	=-	\		\(8)
1152	Hha1	8	gaa	145.41	146	145.41	0	0	6 400 000	0	0	-=	\		\(8)
1153	Hha1	8	gaa	146.07	146	0	0	146.07	0	0	5 700 000	=+	/		\(8)
1154	Taq1	8	gaa	146.76	146	0	146.76	0	0	4 200 000	0	+-	A		\(8)
1155	Hha1	27	acg	132.99	133	132.98	132.95	133.04	22 200 000	6 000 000	10 000 000	-=	\ (-)	(-)	
1156	Hha1	40	tgg	133.193	133	133.22	133.26	133.1	3 800 000	8 000 000	6 900 000	+=	/ (-)	(-)	
1157	Taq1	12	agt	127.13	127	127.13	127.07	127.19	14 000 000	11 600 000	3 600 000	=-	\ (-)		\(4)
1158	Taq1	35	gga	126.785	127	0	126.87	126.7	0	6 700 000	3 200 000	+-	A		\(4)
1159	Taq1	47	ggc	144.03	144	144	144.06	0	2 092.3	1 432.2	0	=-	\		\(4)
1160	Taq1	29	gca	144.72	145	144.71	0	144.73	3 200 000	0	8 300 000	=+(+)	/		\(4)
1161	Taq1	29	gca	145.72	145	0	0	145.72	0	0	5 900 000	=+	/		\(4)
1162	Hha1	39	agg	166.445	167	0	166.44	166.45	0	244.79	227.86	+=	/		\(4)
1163	Hha1	39	agg	167.917	167	167.73	168.16	167.86	799.12	232.84	199.38	-=	\ (-)		\(4)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
1121	AY325260.PE1	nc	Bm403207		cag	ggg	No change
1122	AB012600.BMAL1B	BMAL1b	BMAL1b		cta	tga	decreased
1123	AB012600.BMAL1B	BMAL1b	BMAL1b		tgc	tct	decreased
1124	AB051356.BRINP	BRINP	BMP/retinoic acid-inducible neural-specific		ccg	caa	increased
1125	AB051356.BRINP	BRINP	BMP/retinoic acid-inducible neural-specific		tgc	tgg	increased
1126	AB051356.BRINP	BRINP	BMP/retinoic acid-inducible neural-specific		tgc	tgg	increased
1127	RNBMP2.PE1	nc	bone morphogenetic protein 2		cct	tgg	increased by mild
1128	RNBMP2.PE1	nc	bone morphogenetic protein 2		cct	tgg	increased by mild
1129	RNBMP2.PE1	nc	bone morphogenetic protein 2		cct	tgg	increased by mild
1130	RNBMP2.PE1	nc	bone morphogenetic protein 2		ccc	tcc	increased by mild
1131	RNBMP2.PE1	nc	bone morphogenetic protein 2		ccc	tcc	increased by mild
1132	RNBOMPR4A.PE1	nc	bone morphogenetic protein 4		gac	agc	decreased
1133	RNBOMPR4A.PE1	nc	bone morphogenetic protein 4		gac	agc	decreased
1134	RNBOMPR4A.PE1	nc	bone morphogenetic protein 4		gac	agc	decreased
1135	RNO504723.BRG-1	brg-1	brahma-related protein 1		atc	agg	increased
1136	RNO504723.BRG-1	brg-1	brahma-related protein 1		atc	agg	increased
1137	RNO504723.BRG-1	brg-1	brahma-related protein 1		atc	agg	increased
1138	RNO504723.BRG-1	brg-1	brahma-related protein 1		atc	agg	increased
1139	RNO504723.BRG-1	brg-1	brahma-related protein 1		atc	agg	increased
1140	RNO504723.BRG-1	brg-1	brahma-related protein 1		atc	agg	increased
1141	RNO504723.BRG-1	brg-1	brahma-related protein 1		atc	agg	increased
1142	RNO504723.BRG-1	brg-1	brahma-related protein 1		atc	agg	increased
1143	RNO504723.BRG-1	brg-1	brahma-related protein 1		ggg	ttt	increased
1144	RNO504723.BRG-1	brg-1	brahma-related protein 1		ggg	ttt	increased
1145	RNO504723.BRG-1	brg-1	brahma-related protein 1		ggg	ttt	increased
1146	RNO504723.BRG-1	brg-1	brahma-related protein 1		ggg	ttt	increased
1147	RNO504723.BRG-1	brg-1	brahma-related protein 1		atc	ttg	increased
1148	RNO504723.BRG-1	brg-1	brahma-related protein 1		atc	ttg	increased
1149	RNO504723.BRG-1	brg-1	brahma-related protein 1		gaa	ccc	increased
1150	RNO504723.BRG-1	brg-1	brahma-related protein 1		gaa	ccc	increased
1151	RNO504723.BRG-1	brg-1	brahma-related protein 1		gaa	ccc	increased
1152	RNO504723.BRG-1	brg-1	brahma-related protein 1		gaa	ccc	increased
1153	RNO504723.BRG-1	brg-1	brahma-related protein 1		gaa	ccc	increased
1154	RNO504723.BRG-1	brg-1	brahma-related protein 1		gaa	ccc	increased
1155	AB001347.SPNB-3	Spnb-3	brain beta 3 spectrin		acg	tgg	No change
1156	AB001347.SPNB-3	Spnb-3	brain beta 3 spectrin		acg	tgg	No change
1157	AB049056.BRAL1	bral1	brain link protein-1		gga	agt	increased
1158	AB049056.BRAL1	bral1	brain link protein-1		gga	agt	increased
1159	AB049056.BRAL1	bral1	brain link protein-1		ggc	gca	increased
1160	AB049056.BRAL1	bral1	brain link protein-1		ggc	gca	increased
1161	AB049056.BRAL1	bral1	brain link protein-1		ggc	gca	increased
1162	AB049056.BRAL1	bral1	brain link protein-1		cag	agg	increased
1163	AB049056.BRAL1	bral1	brain link protein-1		cag	agg	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
1164	Hha1	26	ctg	220.85	220	220.85	0	0	5 000 000	0	0	-=	\		\(4)
1165	Taq1	10	atg	165.297	166	165.31	165.14	165.44	5 400 000	3 000 000	6 600 000	=+	/ (-)		\(4)
1166	Hha1	10	atg	165.48	166	165.43	165.53	0	6 700 000	3 800 000	0	=-	\		\(4)
1167	Taq1	10	atg	165.86	166	165.86	0	0	4 000 000	0	0	-=	\		\(4)
1168	Taq1	10	atg	166.48	166	166.48	0	0	5 600 000	0	0	-=	\		\(4)
1169	Hha1	10	atg	166.54	166	166.54	0	0	4 000 000	0	0	-=	\		\(4)
1170	Taq1	10	atg	317.55	319	317.55	0	0	3 900 000	0	0	-=	\		\(4)
1171	Taq1	10	atg	165.297	166	165.31	165.14	165.44	5 400 000	3 000 000	6 600 000	=+	/ (-)		\(4)
1172	Hha1	10	atg	165.48	166	165.43	165.53	0	6 700 000	3 800 000	0	=-	\		\(4)
1173	Taq1	10	atg	165.86	166	165.86	0	0	4 000 000	0	0	-=	\		\(4)
1174	Taq1	10	atg	166.48	166	166.48	0	0	5 600 000	0	0	-=	\		\(4)
1175	Hha1	10	atg	166.54	166	166.54	0	0	4 000 000	0	0	-=	\		\(4)
1176	Taq1	10	atg	317.55	319	317.55	0	0	3 900 000	0	0	-=	\		\(4)
1177	Hha1	44	cgg	69.333	69	69.35	69.13	69.52	6 600 000	6 300 000	4 600 000	==	-		-3
1178	Hha1	27	acg	87.243	87	87.23	87.26	87.24	71 300 000	19 700 000	10 100 000	-=	\ (-)		-3
1179	Hha1	64	gtt	91.893	92	91.92	91.8	91.96	4 500 000	3 500 000	4 600 000	==	-		-3
1180	Hha1	61	tct	143.213	144	143.25	143.1	143.29	4 500 000	21 600 000	5 100 000	+-	A		-3
1181	Hha1	61	tct	144.17	144	0	144.17	0	0	3 500 000	0	+-	A		-3
1182	Taq1	12	agt	153.727	154	153.72	153.64	153.82	3 700 000	4 400 000	3 000 000	==	-		-2
1183	Taq1	12	agt	154.81	154	154.79	154.75	154.89	8 600 000	12 600 000	9 000 000	==	-		-2
1184	Hha1	25	cag	153.403	154	153.64	153.25	153.32	5 900 000	4 700 000	4 500 000	==	-		-2
1185	Hha1	25	cag	154.14	154	0	154.14	0	0	6 500 000	0	+-	A		-2
1186	Taq1	19	cac	220.645	221	220.6	0	220.69	3 400 000	0	5 000 000	-+(=)	V		-2
1187	Taq1	19	cac	221.68	221	0	0	221.68	0	0	3 800 000	=+	/		-2
1188	Taq1	56	tga	129.21	129	0	0	129.21	0	0	4 300 000	=+	/		/(3)
1189	Taq1	49	aaa	130.593	130	130.46	130.66	130.66	33 200 000	16 700 000	112 100 000	=+	/ (-)		/(3)
1190	Hha1	40	tgg	155.06	155	0	0	155.06	0	0	5 700 000	=+	/		/(3)
1191	Hha1	4	aag	147.105	147	0	147.12	147.09	0	19 900 000	11 500 000	+=	/		\(2)
1192	Taq1	34	tgc	146.13	147	146.25	146.01	0	3 200 000	3 600 000	0	=-	\		\(2)
1193	Taq1	56	tga	196.315	197	196.32	196.31	0	3 700 000	4 300 000	0	=-	\		\(2)
1194	Taq1	56	tga	197.28	197	197.28	0	0	3 900 000	0	0	-=	\		\(2)
1195	Hha1	10	atg	201.445	202	201.33	201.56	0	9 200 000	3 400 000	0	-=	\		\(4)
1196	Taq1	10	atg	201.73	202	201.73	0	0	3 700 000	0	0	-=	\		\(4)
1197	Hha1	10	atg	202.34	202	202.34	0	0	3 200 000	0	0	-=	\		\(4)
1198	Taq1	39	agg	201.075	202	201.22	200.93	0	11 500 000	11 100 000	0	=-	\		\(4)
1199	Taq1	39	agg	201.935	202	201.96	201.91	0	8 700 000	38 600 000	0	+-	A		\(4)
1200	Taq1	39	agg	202.85	202	202.85	0	0	8 800 000	0	0	-=	\		\(4)
1201	Taq1	39	agg	201.075	202	201.22	200.93	0	427.06	111.55	0	-=	\		\(4)
1202	Taq1	39	agg	201.935	202	201.96	201.91	0	323.08	387.94	0	=-	\		\(4)
1203	Taq1	39	agg	202.85	202	202.85	0	0	326.79	0	0	-=	\		\(4)
1204	Taq1	34	tgc	177.75	178	177.75	0	0	6 300 000	0	0	-=	\		\(2)
1205	Taq1	51	ata	178.11	179	178.11	0	0	5 300 000	0	0	-=	\		\(2)
1206	Taq1	51	ata	179.12	179	179.12	0	0	40 900 000	0	0	-=	\		\(2)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
1164	AB049056.BRAL1	bral1	brain link protein-1		ctg	acg	increased
1165	RNO300165.BMCP1	Bmcp1	brain mitochondrial carrier protein BMCP1	*	atg	agc	increased
1166	RNO300165.BMCP1	Bmcp1	brain mitochondrial carrier protein BMCP1	*	atg	agc	increased
1167	RNO300165.BMCP1	Bmcp1	brain mitochondrial carrier protein BMCP1	*	atg	agc	increased
1168	RNO300165.BMCP1	Bmcp1	brain mitochondrial carrier protein BMCP1	*	atg	agc	increased
1169	RNO300165.BMCP1	Bmcp1	brain mitochondrial carrier protein BMCP1	*	atg	agc	increased
1170	RNO300165.BMCP1	Bmcp1	brain mitochondrial carrier protein BMCP1	*	atg	gtt	increased
1171	AF300424.BMCP1	BMCP1	brain mitochondrial carrier protein-1	*	atg	agc	increased
1172	AF300424.BMCP1	BMCP1	brain mitochondrial carrier protein-1	*	atg	agc	increased
1173	AF300424.BMCP1	BMCP1	brain mitochondrial carrier protein-1	*	atg	agc	increased
1174	AF300424.BMCP1	BMCP1	brain mitochondrial carrier protein-1	*	atg	agc	increased
1175	AF300424.BMCP1	BMCP1	brain mitochondrial carrier protein-1	*	atg	agc	increased
1176	AF300424.BMCP1	BMCP1	brain mitochondrial carrier protein-1	*	atg	gtt	increased
1177	AB028891.PE1	nc	brain specific binding protein		tac	cgg	No change
1178	AB028891.PE1	nc	brain specific binding protein		cct	acg	No change
1179	AB028891.PE1	nc	brain specific binding protein		tgg	gtt	No change
1180	AB028891.PE1	nc	brain specific binding protein		ccg	tct	No change
1181	AB028891.PE1	nc	brain specific binding protein		ccg	tct	No change
1182	RNU89653.BRCA2	BRCA2	breast cancer susceptibility		agt	cag	No change
1183	RNU89653.BRCA2	BRCA2	breast cancer susceptibility		agt	cag	No change
1184	RNU89653.BRCA2	BRCA2	breast cancer susceptibility		agt	cag	No change
1185	RNU89653.BRCA2	BRCA2	breast cancer susceptibility		agt	cag	No change
1186	RNU89653.BRCA2	BRCA2	breast cancer susceptibility		cac	taa	No change
1187	RNU89653.BRCA2	BRCA2	breast cancer susceptibility		cac	taa	No change
1188	RATCA2ATPA.PE1	nc	Ca2+/Mg2+ ATPase		aaa	tga	decreased
1189	RATCA2ATPA.PE1	nc	Ca2+/Mg2+ ATPase		aaa	tga	decreased
1190	RATCA2ATPA.PE1	nc	Ca2+/Mg2+ ATPase		tgg	caa	decreased
1191	AF061947.PE1	nc	cain		aag	tgc	increased
1192	AF061947.PE1	nc	cain		aag	tgc	increased
1193	AF061947.PE1	nc	cain		gtg	tga	increased
1194	AF061947.PE1	nc	cain		gtg	tga	increased
1195	RATCNRAA.PE1	nc	calcineurin A alpha	*	atg	agg	increased
1196	RATCNRAA.PE1	nc	calcineurin A alpha	*	atg	agg	increased
1197	RATCNRAA.PE1	nc	calcineurin A alpha	*	atg	agg	increased
1198	RATCNRAA.PE1	nc	calcineurin A alpha	*	atg	agg	increased
1199	RATCNRAA.PE1	nc	calcineurin A alpha	*	atg	agg	increased
1200	RATCNRAA.PE1	nc	calcineurin A alpha	*	atg	agg	increased
1201	RATCNRAA.PE1	nc	calcineurin A alpha	*	atg	agg	increased
1202	RATCNRAA.PE1	nc	calcineurin A alpha	*	atg	agg	increased
1203	RATCNRAA.PE1	nc	calcineurin A alpha	*	atg	agg	increased
1204	RATRSCDPP.PE1	nc	calcineurin B		tgc	ata	increased
1205	RATRSCDPP.PE1	nc	calcineurin B		tgc	ata	increased
1206	RATRSCDPP.PE1	nc	calcineurin B		tgc	ata	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
1207	Taq1	34	tgc	177.75	178	177.75	0	0	6 300 000	0	0	-=	\		\(2)
1208	Taq1	51	ata	178.11	179	178.11	0	0	5 300 000	0	0	-=	\		\(2)
1209	Taq1	51	ata	179.12	179	179.12	0	0	40 900 000	0	0	-=	\		\(2)
1210	Hha1	20	ctc	67.16	67	67.27	0	67.05	282.36	0	536.73	-+(+)	V (/)		V(2)
1211	Hha1	61	tct	128.763	129	128.69	128.75	128.85	13 000 000	21 700 000	16 000 000	==	-		V(2)
1212	Hha1	40	tgg	252.785	253	252.6	0	252.97	6 600 000	0	5 200 000	-+(=)	V		V(2)
1213	Hha1	40	tgg	253.49	253	253.49	0	0	7 300 000	0	0	-=	\		V(2)
1214	Hha1	40	tgg	254.44	253	254.41	254.47	0	3 900 000	6 300 000	0	=-	\		V(2)
1215	Taq1	39	agg	90.495	91	90.7	0	90.29	125 800 000	0	23 600 000	-=(-)	\		\(5)
1216	Taq1	39	agg	90.957	91	90.7	90.97	91.2	4 671.71	172 200 000	3 800 000	+-	A		\(5)
1217	Taq1	39	agg	91.085	91	0	90.97	91.2	0	1 730.67	111.92	+-	A		\(5)
1218	Hha1	59	ttc	165.58	165	165.44	165.5	165.8	166.4	135.1	85.37	==	-		\(5)
1219	Taq1	7	caa	250.34	251	250.34	0	0	5 000 000	0	0	-=	\		\(5)
1220	Hha1	7	caa	251.52	251	251.52	0	0	4 500 000	0	0	-=	\	\	\(5)
1221	Taq1	7	caa	251.62	251	251.62	0	0	3 900 000	0	0	-=	\	\	\(5)
1222	Hha1	7	caa	252.07	251	252.07	0	0	5 900 000	0	0	-=	\		\(5)
1223	Taq1	39	agg	90.495	91	90.7	0	90.29	125 800 000	0	23 600 000	-=(-)	\		\(5)
1224	Taq1	39	agg	90.957	91	90.7	90.97	91.2	4 671.71	172 200 000	3 800 000	+-	A		\(5)
1225	Taq1	39	agg	91.085	91	0	90.97	91.2	0	1 730.67	111.92	+-	A		\(5)
1226	Hha1	59	ttc	165.58	165	165.44	165.5	165.8	166.4	135.1	85.37	==	-		\(5)
1227	Taq1	7	caa	250.34	251	250.34	0	0	5 000 000	0	0	-=	\		\(5)
1228	Hha1	7	caa	251.52	251	251.52	0	0	4 500 000	0	0	-=	\	\	\(5)
1229	Taq1	7	caa	251.62	251	251.62	0	0	3 900 000	0	0	-=	\	\	\(5)
1230	Hha1	7	caa	252.07	251	252.07	0	0	5 900 000	0	0	-=	\		\(5)
1231	Hha1	41	ccc	181.43	182	0	0	181.43	0	0	3 400 000	=+	/		\(2)
1232	Hha1	41	ccc	182.45	182	182.45	0	0	4 300 000	0	0	-=	\		\(2)
1233	Hha1	44	cgg	207.37	207	207.37	0	0	4 700 000	0	0	-=	\		\(2)
1234	Hha1	44	cgg	71.307	71	71.21	71.39	71.32	26 500 000	4 100 000	9 300 000	-=	\ (-)		\(6)
1235	Hha1	39	agg	144.21	145	0	144.41	144.01	0	191.05	211.58	+=	/		\(6)
1236	Hha1	39	agg	144.63	145	0	0	144.63	0	0	215.65	=+	/		\(6)
1237	Hha1	39	agg	145.82	145	0	146	145.64	0	770.19	797.52	+=	/		\(6)
1238	Taq1	39	agg	147.14	148	0	147.14	0	0	45 500 000	0	+-	A		\(6)
1239	Taq1	39	agg	148.14	148	148.24	148.04	0	11 300 000	15 600 000	0	=-	\		\(6)
1240	Taq1	39	agg	147.14	148	0	147.14	0	0	457.29	0	+-	A		\(6)
1241	Taq1	39	agg	148.14	148	148.24	148.04	0	419.63	156.78	0	-=	\		\(6)
1242	Taq1	44	cgg	177.595	178	177.37	177.82	0	1 024.19	602.97	0	=-	\		\(6)
1243	Taq1	44	cgg	178.5	178	0	178.5	0	0	861.38	0	+-	A		\(6)
1244	Taq1	21	acc	178.015	179	177.93	0	178.1	4 900 000	0	4 000 000	-+(=)	V		\(6)
1245	Taq1	21	acc	179.055	179	178.84	179.27	0	8 600 000	3 200 000	0	-=	\		\(6)
1246	Hha1	21	acc	179.96	179	0	0	179.96	0	0	6 200 000	=+	/		\(6)
1247	Hha1	40	tgg	209.925	210	0	210.06	209.79	0	3 000 000	4 400 000	+=	/		\(6)
1248	Hha1	40	tgg	210.2	210	0	0	210.2	0	0	4 100 000	=+	/		\(6)
1249	Hha1	40	tgg	210.95	210	210.85	211.05	0	5 400 000	7 700 000	0	=-	\		\(6)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
1207	RATCALCB.PE1	nc	calcineurin B subunit		tgc	ata	increased
1208	RATCALCB.PE1	nc	calcineurin B subunit		tgc	ata	increased
1209	RATCALCB.PE1	nc	calcineurin B subunit		tgc	ata	increased
1210	RNCALCBP.PE1	nc	Calcium binding protein	*	ctc	ccc	decreased by mild
1211	RNCALCBP.PE1	nc	Calcium binding protein	*	tcc	tct	decreased by mild
1212	RNCALCBP.PE1	nc	Calcium binding protein	*	atg	tgg	decreased by mild
1213	RNCALCBP.PE1	nc	Calcium binding protein	*	atg	tgg	decreased by mild
1214	RNCALCBP.PE1	nc	Calcium binding protein	*	atg	tgg	decreased by mild
1215	RATRBCI.RBC-I	rbC-I	calcium channel alpha-1 subunit		ctt	agg	increased
1216	RATRBCI.RBC-I	rbC-I	calcium channel alpha-1 subunit		ctt	agg	increased
1217	RATRBCI.RBC-I	rbC-I	calcium channel alpha-1 subunit		ctt	agg	increased
1218	RATRBCI.RBC-I	rbC-I	calcium channel alpha-1 subunit		cca	ttc	increased
1219	RATRBCI.RBC-I	rbC-I	calcium channel alpha-1 subunit		caa	gct	increased
1220	RATRBCI.RBC-I	rbC-I	calcium channel alpha-1 subunit		caa	gct	increased
1221	RATRBCI.RBC-I	rbC-I	calcium channel alpha-1 subunit		caa	gct	increased
1222	RATRBCI.RBC-I	rbC-I	calcium channel alpha-1 subunit		caa	gct	increased
1223	RATRBCII.RBC-II	rbC-II	calcium channel alpha-1 subunit		ctt	agg	increased
1224	RATRBCII.RBC-II	rbC-II	calcium channel alpha-1 subunit		ctt	agg	increased
1225	RATRBCII.RBC-II	rbC-II	calcium channel alpha-1 subunit		ctt	agg	increased
1226	RATRBCII.RBC-II	rbC-II	calcium channel alpha-1 subunit		cca	ttc	increased
1227	RATRBCII.RBC-II	rbC-II	calcium channel alpha-1 subunit		caa	gct	increased
1228	RATRBCII.RBC-II	rbC-II	calcium channel alpha-1 subunit		caa	gct	increased
1229	RATRBCII.RBC-II	rbC-II	calcium channel alpha-1 subunit		caa	gct	increased
1230	RATRBCII.RBC-II	rbC-II	calcium channel alpha-1 subunit		caa	gct	increased
1231	AF346817.CACNA1I	Cacna1i	calcium channel alpha13.3 subunit delta 36B		cgc	ccc	increased
1232	AF346817.CACNA1I	Cacna1i	calcium channel alpha13.3 subunit delta 36B		cgc	ccc	increased
1233	AF346817.CACNA1I	Cacna1i	calcium channel alpha13.3 subunit delta 36B		cag	cgg	increased
1234	AF290212.PE1	nc	calcium channel alpha-1-G subunit	*	gga	cgg	increased
1235	AF290212.PE1	nc	calcium channel alpha-1-G subunit	*	atc	agg	increased
1236	AF290212.PE1	nc	calcium channel alpha-1-G subunit	*	atc	agg	increased
1237	AF290212.PE1	nc	calcium channel alpha-1-G subunit	*	atc	agg	increased
1238	AF290212.PE1	nc	calcium channel alpha-1-G subunit	*	gcg	agg	increased
1239	AF290212.PE1	nc	calcium channel alpha-1-G subunit	*	gcg	agg	increased
1240	AF290212.PE1	nc	calcium channel alpha-1-G subunit	*	gcg	agg	increased
1241	AF290212.PE1	nc	calcium channel alpha-1-G subunit	*	gcg	agg	increased
1242	AF290212.PE1	nc	calcium channel alpha-1-G subunit	*	cgg	acc	increased
1243	AF290212.PE1	nc	calcium channel alpha-1-G subunit	*	cgg	acc	increased
1244	AF290212.PE1	nc	calcium channel alpha-1-G subunit	*	cgg	acc	increased
1245	AF290212.PE1	nc	calcium channel alpha-1-G subunit	*	cgg	acc	increased
1246	AF290212.PE1	nc	calcium channel alpha-1-G subunit	*	cgg	acc	increased
1247	AF290212.PE1	nc	calcium channel alpha-1-G subunit	*	tag	tgg	increased
1248	AF290212.PE1	nc	calcium channel alpha-1-G subunit	*	tag	tgg	increased
1249	AF290212.PE1	nc	calcium channel alpha-1-G subunit	*	tag	tgg	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
1250	Taq1	50	aat	472.41	470	472.41	0	0	3 200 000	0	0	-=	\		\(6)
1251	Hha1	6	aga	150.743	151	150.74	150.79	150.7	63 700 000	38 400 000	13 400 000	==	-	-	
1252	Taq1	29	gca	150.953	151	150.99	151	150.87	9 600 000	8 600 000	6 900 000	==	-	-	
1253	Taq1	39	agg	86.555	87	86.62	86.49	0	17 400 000	39 900 000	0	+-	A		\(3)
1254	Taq1	39	agg	86.49	87	0	86.49	0	0	401	0	+-	A		\(3)
1255	Taq1	39	agg	87.285	87	87.28	0	87.29	10 100 000	0	86 600 000	=+(+)	/		\(3)
1256	Taq1	39	agg	86.62	87	86.62	0	0	646.16	0	0	-=	\		\(3)
1257	Taq1	39	agg	87.285	87	87.28	0	87.29	375.07	0	2 550.81	=+(+)	/		\(3)
1258	Taq1	17	cca	201.29	202	201.29	0	0	283.28	0	0	-=	\		\(3)
1259	Taq1	17	cca	228.665	230	228.47	228.86	0	408.67	272.57	0	=-	\		\(3)
1260	Taq1	17	cca	229.95	230	0	229.95	0	0	285.86	0	+-	A		\(3)
1261	Taq1	17	cca	230.823	230	230.71	230.85	230.91	413.31	1 515.75	706.66	+-	A		\(3)
1262	Hha1	49	aaa	231.417	232	231.49	231.36	231.4	17 200 000	34 300 000	25 000 000	+=	/ (-)		\(3)
1263	Hha1	49	aaa	232.39	232	232.41	232.38	232.38	4 100 000	41 000 000	22 900 000	+=	/ (-)		\(3)
1264	Taq1	39	agg	86.555	87	86.62	86.49	0	17 400 000	39 900 000	0	+-	A		\(3)
1265	Taq1	39	agg	86.49	87	0	86.49	0	0	401	0	+-	A		\(3)
1266	Taq1	39	agg	87.285	87	87.28	0	87.29	10 100 000	0	86 600 000	=+(+)	/		\(3)
1267	Taq1	39	agg	86.62	87	86.62	0	0	646.16	0	0	-=	\		\(3)
1268	Taq1	39	agg	87.285	87	87.28	0	87.29	375.07	0	2 550.81	=+(+)	/		\(3)
1269	Taq1	17	cca	201.29	202	201.29	0	0	283.28	0	0	-=	\		\(3)
1270	Taq1	17	cca	228.665	230	228.47	228.86	0	408.67	272.57	0	=-	\		\(3)
1271	Taq1	17	cca	229.95	230	0	229.95	0	0	285.86	0	+-	A		\(3)
1272	Taq1	17	cca	230.823	230	230.71	230.85	230.91	413.31	1 515.75	706.66	+-	A		\(3)
1273	Hha1	49	aaa	231.417	232	231.49	231.36	231.4	17 200 000	34 300 000	25 000 000	+=	/ (-)		\(3)
1274	Hha1	49	aaa	232.39	232	232.41	232.38	232.38	4 100 000	41 000 000	22 900 000	+=	/ (-)		\(3)
1275	Taq1	41	ccc	213.36	213	0	213.36	0	0	4 200 000	0	+-	A		A(2)
1276	Hha1	6	aga	212.985	214	213.04	0	212.93	13 800 000	0	3 900 000	-=(-)	\		A(2)
1277	Hha1	6	aga	213.49	214	0	213.49	0	0	3 100 000	0	+-	A		A(2)
1278	Taq1	47	ggc	128.817	129	128.78	128.88	128.79	2 092.3	1 686.82	1 781.85	==	-		A(3)
1279	Taq1	17	cca	129.817	130	129.76	129.96	129.73	9 213.76	20 216.721	1 232.89	+-	A		A(3)
1280	Taq1	17	cca	130.707	130	130.74	130.57	130.81	31 337.939	2 526.25	796.87	-=	\ (-)		A(3)
1281	Taq1	39	agg	183.253	184	182.95	183.38	183.43	13 800 000	55 500 000	5 800 000	+-	A		A(3)
1282	Taq1	39	agg	183.535	184	183.64	0	183.43	5 400 000	0	170.83	-=(-)	\		A(3)
1283	Taq1	39	agg	184.48	184	184.38	184.58	0	7 100 000	8 600 000	0	=-	\		A(3)
1284	Taq1	39	agg	183.165	184	182.95	183.38	0	512.47	557.79	0	=-	\		A(3)
1285	Taq1	39	agg	183.64	184	183.64	0	0	200.53	0	0	-=	\		A(3)
1286	Taq1	39	agg	184.48	184	184.38	184.58	0	263.66	86.43	0	-=	\		A(3)
1287	Taq1	62	tgt	183.84	184	0	184.04	183.64	0	3 800 000	9 000 000	=+	/		A(3)
1288	Taq1	18	cct	252.35	253	0	252.35	0	0	3 300 000	0	+-	A		A(3)
1289	Hha1	58	gta	143.29	144	143.3	143.26	143.31	34 900 000	80 400 000	17 000 000	+-	A	A	
1290	Hha1	61	tct	143.213	144	143.25	143.1	143.29	4 500 000	21 600 000	5 100 000	+-	A	A	
1291	Hha1	6	aga	125.095	125	125.23	0	124.96	7 500 000	0	3 700 000	-+(-)	V (\)		\(4)
1292	Taq1	49	aaa	126.08	126	126.06	126.1	0	17 000 000	8 200 000	0	--	\		\(4)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
1250	AF290212.PE1	nc	calcium channel alpha-1-G subunit	*	gta	aat	increased
1251	AF290214.PE1	nc	calcium channel alpha-1-I subunit		gca	aga	No change
1252	AF290214.PE1	nc	calcium channel alpha-1-I subunit		gca	aga	No change
1253	AY214122.PE1	nc	calcium sensing receptor		ttc	agg	increased
1254	AY214122.PE1	nc	calcium sensing receptor		ttc	agg	increased
1255	AY214122.PE1	nc	calcium sensing receptor		ttc	agg	increased
1256	AY214122.PE1	nc	calcium sensing receptor		ttc	agg	increased
1257	AY214122.PE1	nc	calcium sensing receptor		ttc	agg	increased
1258	AY214122.PE1	nc	calcium sensing receptor		gta	cca	increased
1259	AY214122.PE1	nc	calcium sensing receptor		cca	tga	increased
1260	AY214122.PE1	nc	calcium sensing receptor		cca	tga	increased
1261	AY214122.PE1	nc	calcium sensing receptor		cca	tga	increased
1262	AY214122.PE1	nc	calcium sensing receptor		aaa	aat	increased
1263	AY214122.PE1	nc	calcium sensing receptor		aaa	aat	increased
1264	RNU20289.PE1	nc	calcium sensing receptor		ttc	agg	increased
1265	RNU20289.PE1	nc	calcium sensing receptor		ttc	agg	increased
1266	RNU20289.PE1	nc	calcium sensing receptor		ttc	agg	increased
1267	RNU20289.PE1	nc	calcium sensing receptor		ttc	agg	increased
1268	RNU20289.PE1	nc	calcium sensing receptor		ttc	agg	increased
1269	RNU20289.PE1	nc	calcium sensing receptor		gta	cca	increased
1270	RNU20289.PE1	nc	calcium sensing receptor		cca	tga	increased
1271	RNU20289.PE1	nc	calcium sensing receptor		cca	tga	increased
1272	RNU20289.PE1	nc	calcium sensing receptor		cca	tga	increased
1273	RNU20289.PE1	nc	calcium sensing receptor		aaa	aat	increased
1274	RNU20289.PE1	nc	calcium sensing receptor		aaa	aat	increased
1275	RATCTA.SERCA1A	SERCA1a	calcium transporting ATPase		ggc	ccc	increased by mild
1276	RATCTA.SERCA1A	SERCA1a	calcium transporting ATPase		aga	tgg	increased by mild
1277	RATCTA.SERCA1A	SERCA1a	calcium transporting ATPase		aga	tgg	increased by mild
1278	RNCCDPPK2.PE1	nc	calcium/calmodulin-dependent protein kinase II,		ggc	cca	increased by mild
1279	RNCCDPPK2.PE1	nc	calcium/calmodulin-dependent protein kinase II,		ggc	cca	increased by mild
1280	RNCCDPPK2.PE1	nc	calcium/calmodulin-dependent protein kinase II,		ggc	cca	increased by mild
1281	RNCCDPPK2.PE1	nc	calcium/calmodulin-dependent protein kinase II,		agg	tgt	increased by mild
1282	RNCCDPPK2.PE1	nc	calcium/calmodulin-dependent protein kinase II,		agg	tgt	increased by mild
1283	RNCCDPPK2.PE1	nc	calcium/calmodulin-dependent protein kinase II,		agg	tgt	increased by mild
1284	RNCCDPPK2.PE1	nc	calcium/calmodulin-dependent protein kinase II,		agg	tgt	increased by mild
1285	RNCCDPPK2.PE1	nc	calcium/calmodulin-dependent protein kinase II,		agg	tgt	increased by mild
1286	RNCCDPPK2.PE1	nc	calcium/calmodulin-dependent protein kinase II,		agg	tgt	increased by mild
1287	RNCCDPPK2.PE1	nc	calcium/calmodulin-dependent protein kinase II,		agg	tgt	increased by mild
1288	RNCCDPPK2.PE1	nc	calcium/calmodulin-dependent protein kinase II,		cct	tgg	increased by mild
1289	AF063103.CIRL-3	CIRL-3	calcium-independent alpha-latrotoxin receptor		tct	gta	increased by mild
1290	AF063103.CIRL-3	CIRL-3	calcium-independent alpha-latrotoxin receptor		tct	gta	increased by mild
1291	AF302085.PE1	nc	calcium-modulating cyclophilin ligand		aga	aaa	increased
1292	AF302085.PE1	nc	calcium-modulating cyclophilin ligand		aga	aaa	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
1293	Hha1	49	aaa	129.23	130	129.19	129.38	129.12	48 400 000	55 900 000	6 200 000	=-	\ (-)		\(4)
1294	Hha1	49	aaa	129.907	130	129.8	129.97	129.95	10 300 000	30 100 000	9 800 000	+-	A		\(4)
1295	Hha1	49	aaa	130.74	130	130.88	0	130.6	8 200 000	0	5 600 000	-+(=)	V		\(4)
1296	Hha1	43	cgc	151.167	151	151.19	151.16	151.15	21 000 000	27 100 000	9 100 000	=-	\ (-)		\(4)
1297	Hha1	44	cgg	133.813	134	133.85	133.56	134.03	3 900 000	6 100 000	4 200 000	==	-		/(4)
1298	Hha1	44	cgg	134.697	134	134.72	134.74	134.63	10 900 000	10 200 000	4 800 000	=-	\ (-)		/(4)
1299	Hha1	33	agc	134.21	135	134.21	0	0	3 800 000	0	0	-=	\		/(4)
1300	Hha1	33	agc	135.22	135	0	135.32	135.12	0	3 000 000	3 600 000	+=	/		/(4)
1301	Hha1	6	aga	156.663	157	156.64	156.75	156.6	17 700 000	5 500 000	15 400 000	-+	V		/(4)
1302	Hha1	6	aga	157.54	157	0	0	157.54	0	0	22 000 000	=+	/		/(4)
1303	Taq1	56	tga	157.19	157	157.19	0	0	3 300 000	0	0	-=	\		/(4)
1304	Hha1	41	ccc	174.61	174	0	0	174.61	0	0	3 400 000	=+	/		/(4)
1305	Taq1	56	tga	269.47	271	0	0	269.47	0	0	5 400 000	=+	/		/(4)
1306	Hha1	6	aga	257.24	258	257.24	0	0	6 000 000	0	0	-=	\		\(2)
1307	Hha1	6	aga	258.19	258	258.19	0	0	5 300 000	0	0	-=	\	\	\(2)
1308	Taq1	39	agg	256.83	258	0	256.83	0	0	11 900 000	0	+-	A		\(2)
1309	Taq1	39	agg	257.89	258	258.11	257.67	0	7 900 000	3 400 000	0	-=	\		\(2)
1310	Taq1	39	agg	258.69	258	258.77	258.61	0	8 200 000	29 000 000	0	+-	A		\(2)
1311	Taq1	39	agg	256.83	258	0	256.83	0	0	119.59	0	+-	A		\(2)
1312	Taq1	39	agg	257.67	258	0	257.67	0	0	34.17	0	+-	A		\(2)
1313	Taq1	39	agg	258.61	258	0	258.61	0	0	291.46	0	+-	A		\(2)
1314	Taq1	39	agg	258.11	258	258.11	0	0	293.37	0	0	-=	\	\	\(2)
1315	Taq1	39	agg	258.77	258	258.77	0	0	304.51	0	0	-=	\		\(2)
1316	Hha1	6	aga	257.24	258	257.24	0	0	6 000 000	0	0	-=	\		\(2)
1317	Hha1	6	aga	258.19	258	258.19	0	0	5 300 000	0	0	-=	\	\	\(2)
1318	Taq1	39	agg	256.83	258	0	256.83	0	0	11 900 000	0	+-	A		\(2)
1319	Taq1	39	agg	257.89	258	258.11	257.67	0	7 900 000	3 400 000	0	-=	\		\(2)
1320	Taq1	39	agg	258.69	258	258.77	258.61	0	8 200 000	29 000 000	0	+-	A		\(2)
1321	Taq1	39	agg	256.83	258	0	256.83	0	0	119.59	0	+-	A		\(2)
1322	Taq1	39	agg	257.67	258	0	257.67	0	0	34.17	0	+-	A		\(2)
1323	Taq1	39	agg	258.61	258	0	258.61	0	0	291.46	0	+-	A		\(2)
1324	Taq1	39	agg	258.11	258	258.11	0	0	293.37	0	0	-=	\	\	\(2)
1325	Taq1	39	agg	258.77	258	258.77	0	0	304.51	0	0	-=	\		\(2)
1326	Taq1	10	atg	185.96	185	185.96	0	0	4 700 000	0	0	-=	\	\	
1327	Hha1	10	atg	185.97	185	185.97	0	0	3 200 000	0	0	-=	\	\	
1328	Taq1	11	act	206.53	207	206.5	206.53	206.56	3 400 000	3 400 000	5 700 000	==	-	-	
1329	Hha1	11	act	206.6	207	206.63	206.64	206.53	5 400 000	4 100 000	3 100 000	==	-	-	
1330	Hha1	21	acc	102.6	103	102.73	102.62	102.45	23 900 000	3 100 000	10 100 000	-=	\ (-)	\	
1331	Taq1	21	acc	102.665	103	102.55	102.78	0	21 100 000	3 000 000	0	-=	\	\	
1332	Hha1	21	acc	103.33	103	0	103.33	103.33	0	3 900 000	16 800 000	=+	/	/	
1333	Taq1	21	acc	103.5	103	0	0	103.5	0	0	3 500 000	=+	/	/	
1334	Hha1	21	acc	102.6	103	102.73	102.62	102.45	23 900 000	3 100 000	10 100 000	-=	\ (-)	\	
1335	Taq1	21	acc	102.665	103	102.55	102.78	0	21 100 000	3 000 000	0	-=	\	\	

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
1293	AF302085.PE1	nc	calcium-modulating cyclophilin ligand		aaa	acc	increased
1294	AF302085.PE1	nc	calcium-modulating cyclophilin ligand		aaa	acc	increased
1295	AF302085.PE1	nc	calcium-modulating cyclophilin ligand		aaa	acc	increased
1296	AF302085.PE1	nc	calcium-modulating cyclophilin ligand		cct	cgc	increased
1297	RNCALDE.PE1	nc	caldendrin		cgg	agc	decreased
1298	RNCALDE.PE1	nc	caldendrin		cgg	agc	decreased
1299	RNCALDE.PE1	nc	caldendrin		cgg	agc	decreased
1300	RNCALDE.PE1	nc	caldendrin		cgg	agc	decreased
1301	RNCALDE.PE1	nc	caldendrin		aga	tga	decreased
1302	RNCALDE.PE1	nc	caldendrin		aga	tga	decreased
1303	RNCALDE.PE1	nc	caldendrin		aga	tga	decreased
1304	RNCALDE.PE1	nc	caldendrin		ccc	atg	decreased
1305	RNCALDE.PE1	nc	caldendrin		tga	agt	decreased
1306	RATCLS4A.CLS4	cls4	calpain		aga	agg	increased
1307	RATCLS4A.CLS4	cls4	calpain		aga	agg	increased
1308	RATCLS4A.CLS4	cls4	calpain		aga	agg	increased
1309	RATCLS4A.CLS4	cls4	calpain		aga	agg	increased
1310	RATCLS4A.CLS4	cls4	calpain		aga	agg	increased
1311	RATCLS4A.CLS4	cls4	calpain		aga	agg	increased
1312	RATCLS4A.CLS4	cls4	calpain		aga	agg	increased
1313	RATCLS4A.CLS4	cls4	calpain		aga	agg	increased
1314	RATCLS4A.CLS4	cls4	calpain		aga	agg	increased
1315	RATCLS4A.CLS4	cls4	calpain		aga	agg	increased
1316	RATCLS4B.CLS4	cls4	calpain		aga	agg	increased
1317	RATCLS4B.CLS4	cls4	calpain		aga	agg	increased
1318	RATCLS4B.CLS4	cls4	calpain		aga	agg	increased
1319	RATCLS4B.CLS4	cls4	calpain		aga	agg	increased
1320	RATCLS4B.CLS4	cls4	calpain		aga	agg	increased
1321	RATCLS4B.CLS4	cls4	calpain		aga	agg	increased
1322	RATCLS4B.CLS4	cls4	calpain		aga	agg	increased
1323	RATCLS4B.CLS4	cls4	calpain		aga	agg	increased
1324	RATCLS4B.CLS4	cls4	calpain		aga	agg	increased
1325	RATCLS4B.CLS4	cls4	calpain		aga	agg	increased
1326	RATCALPIIA.PE1	nc	calpain II 80 kDa subunit		atg	gcc	increased
1327	RATCALPIIA.PE1	nc	calpain II 80 kDa subunit		atg	gcc	increased
1328	RNU89514.NCL-4	nCL-4	calpain large subunit		att	act	No change
1329	RNU89514.NCL-4	nCL-4	calpain large subunit		att	act	No change
1330	RATRC3.PE1	nc	calreticulin	*	acc	tat	increased
1331	RATRC3.PE1	nc	calreticulin	*	acc	tat	increased
1332	RATRC3.PE1	nc	calreticulin	*	acc	tat	decreased
1333	RATRC3.PE1	nc	calreticulin	*	acc	tat	decreased
1334	RNSPCALR.PE1	calreticulin	calreticulin		acc	tat	increased
1335	RNSPCALR.PE1	calreticulin	calreticulin		acc	tat	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
1336	Hha1	21	acc	103.33	103	0	103.33	103.33	0	3 900 000	16 800 000	=+	/	/	
1337	Taq1	21	acc	103.5	103	0	0	103.5	0	0	3 500 000	=+	/	/	
1338	Hha1	4	aag	94.56	95	94.6	94.51	94.57	10 200 000	19 200 000	4 400 000	+-	A		A(2)
1339	Taq1	29	gca	95.34	95	95.38	95.36	95.28	13 000 000	11 700 000	8 100 000	==	-		A(2)
1340	Taq1	20	ctc	110.395	111	0	110.29	110.5	0	5 100 000	3 500 000	+=	/		A(2)
1341	Taq1	20	ctc	111.32	111	0	111.32	0	0	8 000 000	0	+-	A		A(2)
1342	Taq1	55	tca	88.57	89	0	88.35	88.79	0	17 100 000	5 200 000	+-	A		A(2)
1343	Taq1	39	agg	104.49	105	104.49	0	0	623.88	0	0	-=	\		A(2)
1344	Taq1	39	agg	104.44	105	0	104.44	0	0	880.41	0	+-	A		A(2)
1345	Taq1	62	tgt	157.8	158	0	0	157.8	0	0	4 300 000	=+	/		A(2)
1346	Taq1	62	tgt	158.943	158	159.05	158.96	158.82	3 300 000	5 400 000	10 500 000	=+	/ (-)		A(2)
1347	Taq1	55	tca	88.57	89	0	88.35	88.79	0	17 100 000	5 200 000	+-	A		A(2)
1348	Taq1	39	agg	104.49	105	104.49	0	0	623.88	0	0	-=	\		A(2)
1349	Taq1	39	agg	104.44	105	0	104.44	0	0	880.41	0	+-	A		A(2)
1350	Taq1	62	tgt	157.8	158	0	0	157.8	0	0	4 300 000	=+	/		A(2)
1351	Taq1	62	tgt	158.943	158	159.05	158.96	158.82	3 300 000	5 400 000	10 500 000	=+	/ (-)		A(2)
1352	Hha1	20	ctc	165.705	166	0	165.87	165.54	0	511.4	405.53	+=	/	/	
1353	Hha1	31	gac	165.69	166	0	0	165.69	0	0	3 600 000	=+	/	/	
1354	Taq1	25	cat	111.765	112	111.7	111.83	0	648.28	1 133.03	0	=-	\		\(3) A(3)
1355	Taq1	25	cat	112.595	112	112.55	112.64	0	620.99	1 502.22	0	+-	A		\(3) A(3)
1356	Taq1	56	tga	201.22	202	0	201.22	0	0	3 200 000	0	+-	A		\(3) A(3)
1357	Taq1	56	tga	202.23	202	0	202.23	0	0	5 700 000	0	+-	A		\(3) A(3)
1358	Hha1	40	tgg	225.115	226	225.12	225.11	0	4 000 000	3 800 000	0	=-	\		\(3) A(3)
1359	Hha1	40	tgg	225.76	226	0	225.76	0	0	6 500 000	0	+-	A		\(3) A(3)
1360	Hha1	26	ctg	228.08	229	228.08	0	0	7 500 000	0	0	-=	\		\(3) A(3)
1361	Hha1	26	ctg	229.185	229	229.14	0	229.23	14 300 000	0	3 300 000	-=(-)	\		\(3) A(3)
1362	Hha1	26	ctg	230.06	229	230.11	230.01	0	8 300 000	3 300 000	0	-=	\		\(3) A(3)
1363	Taq1	25	cat	111.765	112	111.7	111.83	0	648.28	1 133.03	0	=-	\		\(3) A(3)
1364	Taq1	25	cat	112.595	112	112.55	112.64	0	620.99	1 502.22	0	+-	A		\(3) A(3)
1365	Taq1	56	tga	201.22	202	0	201.22	0	0	3 200 000	0	+-	A		\(3) A(3)
1366	Taq1	56	tga	202.23	202	0	202.23	0	0	5 700 000	0	+-	A		\(3) A(3)
1367	Hha1	40	tgg	225.115	226	225.12	225.11	0	4 000 000	3 800 000	0	=-	\		\(3) A(3)
1368	Hha1	40	tgg	225.76	226	0	225.76	0	0	6 500 000	0	+-	A		\(3) A(3)
1369	Hha1	26	ctg	228.08	229	228.08	0	0	7 500 000	0	0	-=	\		\(3) A(3)
1370	Hha1	26	ctg	229.185	229	229.14	0	229.23	14 300 000	0	3 300 000	-=(-)	\		\(3) A(3)
1371	Hha1	26	ctg	230.06	229	230.11	230.01	0	8 300 000	3 300 000	0	-=	\		\(3) A(3)
1372	Hha1	11	act	218.97	220	0	0	218.97	0	0	3 400 000	=+	/		/(5)
1373	Taq1	11	act	219.64	220	0	0	219.64	0	0	3 200 000	=+	/		/(5)
1374	Hha1	11	act	220.01	220	0	0	220.01	0	0	3 300 000	=+	/		/(5)
1375	Hha1	11	act	220.935	220	220.93	220.94	0	3 100 000	5 200 000	0	=-	\		/(5)
1376	Taq1	11	act	220.76	220	0	0	220.76	0	0	3 900 000	=+	/	/	/(5)
1377	Hha1	11	act	220.9	220	0	0	220.9	0	0	3 800 000	=+	/	/	/(5)
1378	Hha1	7	caa	234.51	234	234.51	0	0	7 500 000	0	0	-=	\		\(2)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
1336	RNSPCALR.PE1	calreticulin	calreticulin		acc	tat	decreased
1337	RNSPCALR.PE1	calreticulin	calreticulin		acc	tat	decreased
1338	RNU78517.PE1	cAMP-GEFII	cAMP-regulated guanine nucleotide exchange		aag	gca	increased by mild
1339	RNU78517.PE1	cAMP-GEFII	cAMP-regulated guanine nucleotide exchange		aag	gca	increased by mild
1340	RNU78517.PE1	cAMP-GEFII	cAMP-regulated guanine nucleotide exchange		ctc	gct	increased by mild
1341	RNU78517.PE1	cAMP-GEFII	cAMP-regulated guanine nucleotide exchange		ctc	gct	increased by mild
1342	RNPDE4D.PDE4D	PDE4D	cAMP-specific phosphodiesterase		tca	gga	increased by mild
1343	RNPDE4D.PDE4D	PDE4D	cAMP-specific phosphodiesterase		ttg	agg	increased by mild
1344	RNPDE4D.PDE4D	PDE4D	cAMP-specific phosphodiesterase		ttg	agg	increased by mild
1345	RNPDE4D.PDE4D	PDE4D	cAMP-specific phosphodiesterase		tgt	tac	increased by mild
1346	RNPDE4D.PDE4D	PDE4D	cAMP-specific phosphodiesterase		tgt	tac	increased by mild
1347	AF536979.PDE4D	Pde4d	cAMP-specific phosphodiesterase PDE4D7		tca	gga	increased by mild
1348	AF536979.PDE4D	Pde4d	cAMP-specific phosphodiesterase PDE4D7		ttg	agg	increased by mild
1349	AF536979.PDE4D	Pde4d	cAMP-specific phosphodiesterase PDE4D7		ttg	agg	increased by mild
1350	AF536979.PDE4D	Pde4d	cAMP-specific phosphodiesterase PDE4D7		tgt	tac	increased by mild
1351	AF536979.PDE4D	Pde4d	cAMP-specific phosphodiesterase PDE4D7		tgt	tac	increased by mild
1352	RNU62897.CPD	Cpd	carboxypeptidase D precursor		ctc	gac	decreased
1353	RNU62897.CPD	Cpd	carboxypeptidase D precursor		ctc	gac	decreased
1354	AF017637.PE1	nc	carboxypeptidase Z		cat	gag	increased
1355	AF017637.PE1	nc	carboxypeptidase Z		cat	gag	increased
1356	AF017637.PE1	nc	carboxypeptidase Z		gga	tga	increased
1357	AF017637.PE1	nc	carboxypeptidase Z		gga	tga	increased
1358	AF017637.PE1	nc	carboxypeptidase Z		agc	tgg	increased
1359	AF017637.PE1	nc	carboxypeptidase Z		agc	tgg	increased
1360	AF017637.PE1	nc	carboxypeptidase Z		ctg	aca	increased
1361	AF017637.PE1	nc	carboxypeptidase Z		ctg	aca	increased
1362	AF017637.PE1	nc	carboxypeptidase Z		ctg	aca	increased
1363	AF017638.PE1	nc	carboxypeptidase Z		cat	gag	increased
1364	AF017638.PE1	nc	carboxypeptidase Z		cat	gag	increased
1365	AF017638.PE1	nc	carboxypeptidase Z		gga	tga	increased
1366	AF017638.PE1	nc	carboxypeptidase Z		gga	tga	increased
1367	AF017638.PE1	nc	carboxypeptidase Z		agc	tgg	increased
1368	AF017638.PE1	nc	carboxypeptidase Z		agc	tgg	increased
1369	AF017638.PE1	nc	carboxypeptidase Z		ctg	aca	increased
1370	AF017638.PE1	nc	carboxypeptidase Z		ctg	aca	increased
1371	AF017638.PE1	nc	carboxypeptidase Z		ctg	aca	increased
1372	RNU50736.PE1	nc	CARP		gta	act	decreased
1373	RNU50736.PE1	nc	CARP		gta	act	decreased
1374	RNU50736.PE1	nc	CARP		gta	act	decreased
1375	RNU50736.PE1	nc	CARP		gta	act	decreased
1376	RNU50736.PE1	nc	CARP		gta	act	decreased
1377	RNU50736.PE1	nc	CARP		gta	act	decreased
1378	RRU03628.PE1	nc	C-arrestin		cct	caa	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
1379	Taq1	18	cct	233.12	234	0	233.12	0	0	3 400 000	0	+-	A		\(2)
1380	Taq1	18	cct	234.07	234	234.11	234.03	0	3 400 000	3 900 000	0	=-	\		\(2)
1381	Taq1	18	cct	235.13	234	235.17	235.09	0	3 300 000	3 300 000	0	=-	\		\(2)
1382	Hha1	44	cgg	86.575	87	86.59	0	86.56	3 100 000	0	4 600 000	-+(=)	V		-5
1383	Taq1	61	tct	126.947	127	127.08	126.92	126.84	6 000 000	15 100 000	10 400 000	+=	/ (-)		-5
1384	Taq1	61	tct	127.683	127	127.72	127.44	127.89	5 600 000	11 700 000	11 800 000	+=	/ (-)	/	-5
1385	Taq1	62	tgt	126.573	127	126.54	126.64	126.54	5 600 000	10 400 000	6 400 000	+=	/ (-)		-5
1386	Taq1	62	tgt	127.55	127	0	127.74	127.36	0	5 000 000	8 700 000	+=	/	/	-5
1387	Hha1	31	gac	151.147	151	151.28	151.06	151.1	5 400 000	6 100 000	20 700 000	=+	/ (-)	(-)	-5
1388	Hha1	61	tct	150.977	151	150.89	150.96	151.08	12 300 000	21 300 000	34 900 000	==	-	(-)	-5
1389	Hha1	31	gac	168.56	169	0	0	168.56	0	0	4 800 000	=+	/		-5
1390	Hha1	31	gac	169.545	169	169.47	0	169.62	4 600 000	0	4 300 000	-+(=)	V		-5
1391	Hha1	3	aac	178.02	178	177.94	177.87	178.25	3 500 000	6 100 000	4 400 000	==	-		-5
1392	Hha1	40	tgg	191.925	193	191.73	192.12	0	3 900 000	4 200 000	0	=-	\		-5
1393	Hha1	40	tgg	193.56	193	0	193.56	0	0	5 600 000	0	+-	A		-5
1394	Hha1	40	tgg	193.88	193	0	193.88	0	0	3 900 000	0	+-	A		-5
1395	Taq1	56	tga	68.65	69	68.65	0	0	9 700 000	0	0	-=	\		\(5)
1396	Taq1	56	tga	69.41	69	69.48	0	69.34	3 000 000	0	5 500 000	-+(+)	V (/)		\(5)
1397	Taq1	10	atg	72.67	73	72.66	72.68	72.67	9 000 000	34 500 000	4 300 000	+-	A		\(5)
1398	Taq1	21	acc	105.44	106	105.35	105.44	105.53	108 600 000	93 300 000	16 000 000	=-	\ (-)		\(5)
1399	Hha1	21	acc	106.475	106	0	106.29	106.66	0	5 200 000	9 700 000	++	/		\(5)
1400	Hha1	21	acc	106.58	106	0	106.58	0	0	3 900 000	0	+-	A		\(5)
1401	Taq1	21	acc	106.53	106	106.49	0	106.57	18 200 000	0	37 000 000	-+(+)	V (/)		\(5)
1402	Hha1	6	aga	121.083	121	121.14	121.23	120.88	15 100 000	6 600 000	6 200 000	-=	\ (-)	\	\(5)
1403	Taq1	56	tga	121.053	121	121.1	121.04	121.02	49 400 000	57 000 000	3 000 000	=-	\ (-)	\	\(5)
1404	Taq1	14	gat	170.57	171	170.57	170.57	0	3 500 000	3 500 000	0	=-	\		\(5)
1405	Taq1	14	gat	171.67	171	171.61	171.61	171.79	4 200 000	4 200 000	5 900 000	==	-		\(5)
1406	Taq1	8	gaa	60.69	61	0	0	60.69	0	0	20 000 000	=+	/		/(3)
1407	Taq1	39	agg	82.73	83	82.8	82.63	82.76	3 100 000	101 700 000	4 700 000	+-	A		/(3)
1408	Taq1	39	agg	82.76	83	0	0	82.76	0	0	138.43	=+	/		/(3)
1409	Taq1	39	agg	82.715	83	82.8	82.63	0	115.12	1 022.12	0	+-	A		/(3)
1410	Taq1	40	tgg	125.63	126	0	0	125.63	0	0	13 400 000	=+	/		/(3)
1411	Taq1	40	tgg	126.64	126	0	0	126.64	0	0	25 300 000	=+	/		/(3)
1412	Taq1	64	gtt	216.533	217	216.5	216.51	216.59	4 200 000	4 000 000	3 500 000	==	-		/(3)
1413	Taq1	64	gtt	217.51	217	217.56	217.46	0	4 900 000	4 600 000	0	=-	\		/(3)
1414	Taq1	10	atg	117.84	118	117.89	117.79	0	8 800 000	8 300 000	0	=-	\		\(4)
1415	Taq1	21	acc	117.717	118	117.73	117.76	117.66	27 600 000	7 800 000	12 300 000	-=	\ (-)		\(4)
1416	Taq1	21	acc	118.435	118	118.34	0	118.53	11 200 000	0	6 700 000	-+(=)	V		\(4)
1417	Hha1	21	acc	118.35	118	118.35	0	0	12 200 000	0	0	-=	\		\(4)
1418	Taq1	49	aaa	229.73	230	229.73	0	0	17 900 000	0	0	-=	\		\(4)
1419	Hha1	7	caa	228.38	229	228.38	0	0	5 400 000	0	0	-=	\		\(2)
1420	Taq1	7	caa	228.91	229	228.91	0	0	3 200 000	0	0	-=	\		\(2)
1421	Taq1	10	atg	72.67	73	72.66	72.68	72.67	9 000 000	34 500 000	4 300 000	+-	A		-(4) \(4)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
1379	RRU03628.PE1	nc	C-arrestin		cct	caa	increased
1380	RRU03628.PE1	nc	C-arrestin		cct	caa	increased
1381	RRU03628.PE1	nc	C-arrestin		cct	caa	increased
1382	RNCOMP.PE1	nc	cartilage oligomeric matrix protein (comp)		acc	cgg	No change
1383	RNCOMP.PE1	nc	cartilage oligomeric matrix protein (comp)		tgt	tct	No change
1384	RNCOMP.PE1	nc	cartilage oligomeric matrix protein (comp)		tgt	tct	decreased
1385	RNCOMP.PE1	nc	cartilage oligomeric matrix protein (comp)		tgt	tct	No change
1386	RNCOMP.PE1	nc	cartilage oligomeric matrix protein (comp)		tgt	tct	decreased
1387	RNCOMP.PE1	nc	cartilage oligomeric matrix protein (comp)		gac	tct	No change
1388	RNCOMP.PE1	nc	cartilage oligomeric matrix protein (comp)		gac	tct	No change
1389	RNCOMP.PE1	nc	cartilage oligomeric matrix protein (comp)		tgc	gac	No change
1390	RNCOMP.PE1	nc	cartilage oligomeric matrix protein (comp)		tgc	gac	No change
1391	RNCOMP.PE1	nc	cartilage oligomeric matrix protein (comp)		aac	tcg	No change
1392	RNCOMP.PE1	nc	cartilage oligomeric matrix protein (comp)		cag	tgg	No change
1393	RNCOMP.PE1	nc	cartilage oligomeric matrix protein (comp)		cag	tgg	No change
1394	RNCOMP.PE1	nc	cartilage oligomeric matrix protein (comp)		cag	tgg	No change
1395	AB042192.RCK1E-3	rCK1e-3	casein kinase 1 epsilon-3		ctg	tga	increased
1396	AB042192.RCK1E-3	rCK1e-3	casein kinase 1 epsilon-3		ctg	tga	increased
1397	AB042192.RCK1E-3	rCK1e-3	casein kinase 1 epsilon-3		atg	tgt	increased
1398	AB042192.RCK1E-3	rCK1e-3	casein kinase 1 epsilon-3		ggt	acc	increased
1399	AB042192.RCK1E-3	rCK1e-3	casein kinase 1 epsilon-3		ggt	acc	increased
1400	AB042192.RCK1E-3	rCK1e-3	casein kinase 1 epsilon-3		ggt	acc	increased
1401	AB042192.RCK1E-3	rCK1e-3	casein kinase 1 epsilon-3		ggt	acc	increased
1402	AB042192.RCK1E-3	rCK1e-3	casein kinase 1 epsilon-3		tga	aga	increased
1403	AB042192.RCK1E-3	rCK1e-3	casein kinase 1 epsilon-3		tga	aga	increased
1404	AB042192.RCK1E-3	rCK1e-3	casein kinase 1 epsilon-3		gat	tcg	increased
1405	AB042192.RCK1E-3	rCK1e-3	casein kinase 1 epsilon-3		gat	tcg	increased
1406	RNU22296.PE1	nc	casein kinase 1 gamma 1 isoform		gaa	tcc	decreased
1407	RNU22296.PE1	nc	casein kinase 1 gamma 1 isoform		agc	agg	decreased
1408	RNU22296.PE1	nc	casein kinase 1 gamma 1 isoform		agc	agg	decreased
1409	RNU22296.PE1	nc	casein kinase 1 gamma 1 isoform		agc	agg	decreased
1410	RNU22296.PE1	nc	casein kinase 1 gamma 1 isoform		ggc	tgg	decreased
1411	RNU22296.PE1	nc	casein kinase 1 gamma 1 isoform		ggc	tgg	decreased
1412	RNU22296.PE1	nc	casein kinase 1 gamma 1 isoform		tat	gtt	decreased
1413	RNU22296.PE1	nc	casein kinase 1 gamma 1 isoform		tat	gtt	decreased
1414	RATCK2ALPH.CK2	CK2	casein kinase II alpha subunit		acc	atg	increased
1415	RATCK2ALPH.CK2	CK2	casein kinase II alpha subunit		acc	atg	increased
1416	RATCK2ALPH.CK2	CK2	casein kinase II alpha subunit		acc	atg	increased
1417	RATCK2ALPH.CK2	CK2	casein kinase II alpha subunit		acc	atg	increased
1418	RATCK2ALPH.CK2	CK2	casein kinase II alpha subunit		aaa	gac	increased
1419	RATCK2BETA.CK2	CK2	casein kinase II beta subunit		caa	gga	increased
1420	RATCK2BETA.CK2	CK2	casein kinase II beta subunit		caa	gga	increased
1421	AB056113.CK1E-2	Ck1e-2	casein kinase1 epsilon-2		atg	tgt	No change

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
1422	Taq1	21	acc	105.44	106	105.35	105.44	105.53	108 600 000	93 300 000	16 000 000	=-	\ (-)		-(4) \(4)
1423	Hha1	21	acc	106.475	106	0	106.29	106.66	0	5 200 000	9 700 000	++	/		-(4) \(4)
1424	Hha1	21	acc	106.58	106	0	106.58	0	0	3 900 000	0	+-	A		-(4) \(4)
1425	Taq1	21	acc	106.53	106	106.49	0	106.57	18 200 000	0	37 000 000	-+(+)	V (/)		-(4) \(4)
1426	Hha1	6	aga	121.083	121	121.14	121.23	120.88	15 100 000	6 600 000	6 200 000	-=	\ (-)	\	-(4) \(4)
1427	Taq1	56	tga	121.053	121	121.1	121.04	121.02	49 400 000	57 000 000	3 000 000	=-	\ (-)	\	-(4) \(4)
1428	Taq1	14	gat	170.57	171	170.57	170.57	0	3 500 000	3 500 000	0	=-	\		-(4) \(4)
1429	Taq1	14	gat	171.67	171	171.61	171.61	171.79	4 200 000	4 200 000	5 900 000	==	-		-(4) \(4)
1430	Taq1	19	cac	121.59	122	121.56	0	121.62	3 100 000	0	3 500 000	-+(=)	V		V(2)
1431	Taq1	19	cac	122.44	122	122.32	0	122.56	4 500 000	0	12 700 000	=+(+)	/		V(2)
1432	Taq1	39	agg	121.93	122	121.71	122.15	0	12 000 000	5 500 000	0	--	\		V(2)
1433	Taq1	39	agg	122.61	122	122.68	0	122.54	5 100 000	0	4 600 000	-+(=)	V		V(2)
1434	Taq1	39	agg	121.71	122	121.71	0	0	445.63	0	0	-=	\		V(2)
1435	Taq1	39	agg	122.61	122	122.68	0	122.54	189.39	0	135.49	-+(=)	V		V(2)
1436	Taq1	39	agg	122.15	122	0	122.15	0	0	55.27	0	+-	A		V(2)
1437	Taq1	8	gaa	79.33	79	79.63	79.22	79.14	8 400 000	10 000 000	10 900 000	==	-		-(2) \(2)
1438	Taq1	44	cgg	177.595	178	177.37	177.82	0	1 024.19	602.97	0	=-	\		-(2) \(2)
1439	Taq1	44	cgg	178.5	178	0	178.5	0	0	861.38	0	+-	A		-(2) \(2)
1440	Taq1	12	agt	178.63	179	178.69	178.63	178.57	4 400 000	7 600 000	3 800 000	=-	\ (-)		-(2) \(2)
1441	Taq1	12	agt	179.777	179	179.85	179.71	179.77	7 400 000	13 300 000	6 400 000	=-	\ (-)		-(2) \(2)
1442	Taq1	45	gcc	150.34	151	0	150.34	0	0	4 800 000	0	+-	A		A(2)
1443	Taq1	22	tcc	152.11	152	152.09	152.06	152.18	7 400 000	4 700 000	6 400 000	==	-		A(2)
1444	Taq1	22	tcc	152.57	152	0	152.57	0	0	3 000 000	0	+-	A		A(2)
1445	Taq1	45	gcc	150.34	151	0	150.34	0	0	4 800 000	0	+-	A		A(2)
1446	Taq1	22	tcc	152.11	152	152.09	152.06	152.18	7 400 000	4 700 000	6 400 000	==	-		A(2)
1447	Taq1	22	tcc	152.57	152	0	152.57	0	0	3 000 000	0	+-	A		A(2)
1448	Hha1	59	ttc	103.43	104	0	103.43	0	0	937.1	0	+-	A		A(3) \(2)
1449	Hha1	59	ttc	104.52	104	104.61	104.43	0	312.01	1 046.33	0	+-	A		A(3) \(2)
1450	Taq1	39	agg	180.27	181	0	180.27	0	0	17 400 000	0	+-	A		A(3) \(2)
1451	Taq1	39	agg	181.01	181	180.86	181.16	0	25 700 000	63 700 000	0	+-	A		A(3) \(2)
1452	Taq1	39	agg	180.27	181	0	180.27	0	0	174.87	0	+-	A		A(3) \(2)
1453	Taq1	39	agg	181.16	181	0	181.16	0	0	640.2	0	+-	A		A(3) \(2)
1454	Taq1	39	agg	180.86	181	180.86	0	0	954.39	0	0	-=	\		A(3) \(2)
1455	Hha1	25	cag	204.635	205	204.64	0	204.63	4 600 000	0	4 800 000	-+(=)	V		A(3) \(2)
1456	Hha1	25	cag	205.345	205	205.2	205.49	0	3 300 000	8 100 000	0	+-	A		A(3) \(2)
1457	Hha1	25	cag	205.43	205	205.43	0	0	3 600 000	0	0	-=	\		A(3) \(2)
1458	Hha1	59	ttc	103.43	104	0	103.43	0	0	937.1	0	+-	A		A(3) \(2)
1459	Hha1	59	ttc	104.52	104	104.61	104.43	0	312.01	1 046.33	0	+-	A		A(3) \(2)
1460	Taq1	39	agg	180.27	181	0	180.27	0	0	17 400 000	0	+-	A		A(3) \(2)
1461	Taq1	39	agg	181.01	181	180.86	181.16	0	25 700 000	63 700 000	0	+-	A		A(3) \(2)
1462	Taq1	39	agg	180.27	181	0	180.27	0	0	174.87	0	+-	A		A(3) \(2)
1463	Taq1	39	agg	181.16	181	0	181.16	0	0	640.2	0	+-	A		A(3) \(2)
1464	Taq1	39	agg	180.86	181	180.86	0	0	954.39	0	0	-=	\		A(3) \(2)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
1422	AB056113.CK1E-2	Ck1e-2	casein kinase1 epsilon-2		ggt	acc	No change
1423	AB056113.CK1E-2	Ck1e-2	casein kinase1 epsilon-2		ggt	acc	No change
1424	AB056113.CK1E-2	Ck1e-2	casein kinase1 epsilon-2		ggt	acc	No change
1425	AB056113.CK1E-2	Ck1e-2	casein kinase1 epsilon-2		ggt	acc	No change
1426	AB056113.CK1E-2	Ck1e-2	casein kinase1 epsilon-2		tga	aga	increased
1427	AB056113.CK1E-2	Ck1e-2	casein kinase1 epsilon-2		tga	aga	increased
1428	AB056113.CK1E-2	Ck1e-2	casein kinase1 epsilon-2		gat	tcg	No change
1429	AB056113.CK1E-2	Ck1e-2	casein kinase1 epsilon-2		gat	tcg	No change
1430	AF025670.MCH2	Mch2	caspase 6		agg	cac	decreased by mild
1431	AF025670.MCH2	Mch2	caspase 6		agg	cac	decreased by mild
1432	AF025670.MCH2	Mch2	caspase 6		agg	cac	decreased by mild
1433	AF025670.MCH2	Mch2	caspase 6		agg	cac	decreased by mild
1434	AF025670.MCH2	Mch2	caspase 6		agg	cac	decreased by mild
1435	AF025670.MCH2	Mch2	caspase 6		agg	cac	decreased by mild
1436	AF025670.MCH2	Mch2	caspase 6		agg	cac	decreased by mild
1437	AF072124.PE1	nc	caspase-7		gaa	agt	No change
1438	AF072124.PE1	nc	caspase-7		cgg	agt	No change
1439	AF072124.PE1	nc	caspase-7		cgg	agt	No change
1440	AF072124.PE1	nc	caspase-7		cgg	agt	No change
1441	AF072124.PE1	nc	caspase-7		cgg	agt	No change
1442	AF279308.CASP8	CASP8	caspase-8		gcc	tcc	increased by mild
1443	AF279308.CASP8	CASP8	caspase-8		gcc	tcc	increased by mild
1444	AF279308.CASP8	CASP8	caspase-8		gcc	tcc	increased by mild
1445	AF288372.PE1	nc	caspase-8		gcc	tcc	increased by mild
1446	AF288372.PE1	nc	caspase-8		gcc	tcc	increased by mild
1447	AF288372.PE1	nc	caspase-8		gcc	tcc	increased by mild
1448	AF262319.PE1	nc	caspase-9	*	ttc	cat	increased by mild
1449	AF262319.PE1	nc	caspase-9	*	ttc	cat	increased by mild
1450	AF262319.PE1	nc	caspase-9	*	gag	agg	increased by mild
1451	AF262319.PE1	nc	caspase-9	*	gag	agg	increased by mild
1452	AF262319.PE1	nc	caspase-9	*	gag	agg	increased by mild
1453	AF262319.PE1	nc	caspase-9	*	gag	agg	increased by mild
1454	AF262319.PE1	nc	caspase-9	*	gag	agg	increased by mild
1455	AF262319.PE1	nc	caspase-9	*	cag	tgt	increased by mild
1456	AF262319.PE1	nc	caspase-9	*	cag	tgt	increased by mild
1457	AF262319.PE1	nc	caspase-9	*	cag	tgt	increased by mild
1458	AF271996.RNCASP9	RNCASP9	caspase-9	*	ttc	cat	increased by mild
1459	AF271996.RNCASP9	RNCASP9	caspase-9	*	ttc	cat	increased by mild
1460	AF271996.RNCASP9	RNCASP9	caspase-9	*	gag	agg	increased by mild
1461	AF271996.RNCASP9	RNCASP9	caspase-9	*	gag	agg	increased by mild
1462	AF271996.RNCASP9	RNCASP9	caspase-9	*	gag	agg	increased by mild
1463	AF271996.RNCASP9	RNCASP9	caspase-9	*	gag	agg	increased by mild
1464	AF271996.RNCASP9	RNCASP9	caspase-9	*	gag	agg	increased by mild

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
1465	Hha1	25	cag	204.635	205	204.64	0	204.63	4 600 000	0	4 800 000	-+(=)	V		A(3) \(2)
1466	Hha1	25	cag	205.345	205	205.2	205.49	0	3 300 000	8 100 000	0	+-	A		A(3) \(2)
1467	Hha1	25	cag	205.43	205	205.43	0	0	3 600 000	0	0	-=	\		A(3) \(2)
1468	Hha1	59	ttc	103.43	104	0	103.43	0	0	937.1	0	+-	A		A(3) \(2)
1469	Hha1	59	ttc	104.52	104	104.61	104.43	0	312.01	1 046.33	0	+-	A		A(3) \(2)
1470	Taq1	39	agg	180.27	181	0	180.27	0	0	17 400 000	0	+-	A		A(3) \(2)
1471	Taq1	39	agg	181.01	181	180.86	181.16	0	25 700 000	63 700 000	0	+-	A		A(3) \(2)
1472	Taq1	39	agg	180.27	181	0	180.27	0	0	174.87	0	+-	A		A(3) \(2)
1473	Taq1	39	agg	181.16	181	0	181.16	0	0	640.2	0	+-	A		A(3) \(2)
1474	Taq1	39	agg	180.86	181	180.86	0	0	954.39	0	0	-=	\		A(3) \(2)
1475	Hha1	25	cag	204.635	205	204.64	0	204.63	4 600 000	0	4 800 000	-+(=)	V		A(3) \(2)
1476	Hha1	25	cag	205.345	205	205.2	205.49	0	3 300 000	8 100 000	0	+-	A		A(3) \(2)
1477	Hha1	25	cag	205.43	205	205.43	0	0	3 600 000	0	0	-=	\		A(3) \(2)
1478	Hha1	59	ttc	103.43	104	0	103.43	0	0	937.1	0	+-	A		A(3) \(2)
1479	Hha1	59	ttc	104.52	104	104.61	104.43	0	312.01	1 046.33	0	+-	A		A(3) \(2)
1480	Taq1	39	agg	180.27	181	0	180.27	0	0	17 400 000	0	+-	A		A(3) \(2)
1481	Taq1	39	agg	181.01	181	180.86	181.16	0	25 700 000	63 700 000	0	+-	A		A(3) \(2)
1482	Taq1	39	agg	180.27	181	0	180.27	0	0	174.87	0	+-	A		A(3) \(2)
1483	Taq1	39	agg	181.16	181	0	181.16	0	0	640.2	0	+-	A		A(3) \(2)
1484	Taq1	39	agg	180.86	181	180.86	0	0	954.39	0	0	-=	\		A(3) \(2)
1485	Hha1	25	cag	204.635	205	204.64	0	204.63	4 600 000	0	4 800 000	-+(=)	V		A(3) \(2)
1486	Hha1	25	cag	205.345	205	205.2	205.49	0	3 300 000	8 100 000	0	+-	A		A(3) \(2)
1487	Hha1	25	cag	205.43	205	205.43	0	0	3 600 000	0	0	-=	\		A(3) \(2)
1488	Taq1	39	agg	180.27	181	0	180.27	0	0	17 400 000	0	+-	A		A(2) \(2)
1489	Taq1	39	agg	181.01	181	180.86	181.16	0	25 700 000	63 700 000	0	+-	A		A(2) \(2)
1490	Taq1	39	agg	180.27	181	0	180.27	0	0	174.87	0	+-	A		A(2) \(2)
1491	Taq1	39	agg	181.16	181	0	181.16	0	0	640.2	0	+-	A		A(2) \(2)
1492	Taq1	39	agg	180.86	181	180.86	0	0	954.39	0	0	-=	\		A(2) \(2)
1493	Hha1	25	cag	204.635	205	204.64	0	204.63	4 600 000	0	4 800 000	-+(=)	V		A(2) \(2)
1494	Hha1	25	cag	205.345	205	205.2	205.49	0	3 300 000	8 100 000	0	+-	A		A(2) \(2)
1495	Hha1	25	cag	205.43	205	205.43	0	0	3 600 000	0	0	-=	\		A(2) \(2)
1496	Hha1	33	agc	131.333	131	131.13	131.45	131.42	12 100 000	69 700 000	46 800 000	+=	/ (-)		-2
1497	Taq1	50	aat	216.46	217	216.53	216.39	0	4 700 000	6 400 000	0	=-	\		-2
1498	Taq1	50	aat	217.5	217	217.42	217.59	217.49	34 800 000	8 000 000	7 500 000	-=	\ (-)		-2
1499	Hha1	59	ttc	257.53	259	0	257.53	0	0	86.23	0	+-	A		-2
1500	Taq1	20	ctc	100.397	101	100.41	100.42	100.36	61 700 000	45 600 000	12 400 000	=-	\ (-)		-(2) \(2)
1501	Taq1	20	ctc	101.325	101	101.23	101.42	0	16 400 000	16 900 000	0	=-	\		-(2) \(2)
1502	Taq1	54	ttt	101.897	102	102.01	101.91	101.77	2 687.54	1 034.92	749.46	-=	\ (-)		-(2) \(2)
1503	Taq1	54	ttt	102.36	102	0	0	102.36	0	0	1 477.51	=+	/		-(2) \(2)
1504	Taq1	17	cca	107.653	108	107.65	107.71	107.6	775.55	472.01	1 774.16	=+	/ (-)		-2
1505	Taq1	26	ctg	108.245	108	108.19	108.3	0	4 000 000	4 700 000	0	=-	\		-2
1506	Taq1	57	ctg	107.97	108	107.97	107.94	108	6 600 000	5 500 000	6 100 000	==	-		-2
1507	Taq1	25	cat	144.58	145	144.72	144.69	144.33	627.81	1 273.07	1 488.01	==	-	-	\(3)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
1465	AF271996.RNCASP9	RNCASP9	caspase-9	*	cag	tgt	increased by mild
1466	AF271996.RNCASP9	RNCASP9	caspase-9	*	cag	tgt	increased by mild
1467	AF271996.RNCASP9	RNCASP9	caspase-9	*	cag	tgt	increased by mild
1468	AF308469.PE1	nc	caspase-9		ttc	cat	increased by mild
1469	AF308469.PE1	nc	caspase-9		ttc	cat	increased by mild
1470	AF308469.PE1	nc	caspase-9		gag	agg	increased by mild
1471	AF308469.PE1	nc	caspase-9		gag	agg	increased by mild
1472	AF308469.PE1	nc	caspase-9		gag	agg	increased by mild
1473	AF308469.PE1	nc	caspase-9		gag	agg	increased by mild
1474	AF308469.PE1	nc	caspase-9		gag	agg	increased by mild
1475	AF308469.PE1	nc	caspase-9		cag	tgt	increased by mild
1476	AF308469.PE1	nc	caspase-9		cag	tgt	increased by mild
1477	AF308469.PE1	nc	caspase-9		cag	tgt	increased by mild
1478	AY027667.PE1	nc	caspase-9	*	ttc	cat	increased by mild
1479	AY027667.PE1	nc	caspase-9	*	ttc	cat	increased by mild
1480	AY027667.PE1	nc	caspase-9	*	gag	agg	increased by mild
1481	AY027667.PE1	nc	caspase-9	*	gag	agg	increased by mild
1482	AY027667.PE1	nc	caspase-9	*	gag	agg	increased by mild
1483	AY027667.PE1	nc	caspase-9	*	gag	agg	increased by mild
1484	AY027667.PE1	nc	caspase-9	*	gag	agg	increased by mild
1485	AY027667.PE1	nc	caspase-9	*	cag	tgt	increased by mild
1486	AY027667.PE1	nc	caspase-9	*	cag	tgt	increased by mild
1487	AY027667.PE1	nc	caspase-9	*	cag	tgt	increased by mild
1488	AF286006.PE1	nc	caspase-9 long isoform	*	gag	agg	increased by mild
1489	AF286006.PE1	nc	caspase-9 long isoform	*	gag	agg	increased by mild
1490	AF286006.PE1	nc	caspase-9 long isoform	*	gag	agg	increased by mild
1491	AF286006.PE1	nc	caspase-9 long isoform	*	gag	agg	increased by mild
1492	AF286006.PE1	nc	caspase-9 long isoform	*	gag	agg	increased by mild
1493	AF286006.PE1	nc	caspase-9 long isoform	*	cag	tgt	increased by mild
1494	AF286006.PE1	nc	caspase-9 long isoform	*	cag	tgt	increased by mild
1495	AF286006.PE1	nc	caspase-9 long isoform	*	cag	tgt	increased by mild
1496	AF136598.CAD	CAD	caspase-activated deoxyribonuclease		ggt	agc	No change
1497	AF136598.CAD	CAD	caspase-activated deoxyribonuclease		ttc	aat	No change
1498	AF136598.CAD	CAD	caspase-activated deoxyribonuclease		ttc	aat	No change
1499	AF136598.CAD	CAD	caspase-activated deoxyribonuclease		acc	ttc	No change
1500	RATCTHS.PE1	nc	cathepsin S precursor		ctc	ttt	No change
1501	RATCTHS.PE1	nc	cathepsin S precursor		ctc	ttt	No change
1502	RATCTHS.PE1	nc	cathepsin S precursor		ctc	ttt	No change
1503	RATCTHS.PE1	nc	cathepsin S precursor		ctc	ttt	No change
1504	AY325234.PE1	nc	Cb1-727		ctg	cca	No change
1505	AY325234.PE1	nc	Cb1-727		ctg	cca	No change
1506	AY325234.PE1	nc	Cb1-727		ctg	cca	No change
1507	AB071283.CBLB	Cblb	Cbl-b		cat	tgt	No change

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
1508	Taq1	25	cat	145.555	145	0	145.71	145.4	0	1 374.92	2 590.24	++	/		\(3)
1509	Taq1	62	tgt	144.817	145	144.88	144.87	144.7	5 900 000	12 100 000	20 800 000	==	-	-	\(3)
1510	Taq1	62	tgt	145.75	145	145.72	145.78	0	3 500 000	5 900 000	0	=-	\		\(3)
1511	Taq1	45	gcc	197.18	198	0	197.18	0	0	4 700 000	0	+-	A		\(3)
1512	Taq1	56	tga	198.49	199	198.49	0	0	3 800 000	0	0	-=	\		\(3)
1513	Taq1	52	att	201.375	202	201.32	201.43	0	3 200 000	4 500 000	0	=-	\		\(3)
1514	Hha1	41	ccc	148.19	149	147.96	148.26	148.35	6 200 000	12 000 000	22 900 000	=+	/ (-)		A(2) \(2)
1515	Hha1	41	ccc	148.78	149	148.78	0	0	4 400 000	0	0	-=	\		A(2) \(2)
1516	Taq1	10	atg	246.48	247	0	246.48	0	0	5 500 000	0	+-	A	A	A(2) \(2)
1517	Taq1	50	aat	246.545	248	246.34	246.75	0	3 200 000	8 300 000	0	+-	A	A	A(2) \(2)
1518	Taq1	50	aat	247.46	248	247.45	247.47	0	6 900 000	7 700 000	0	=-	\		A(2) \(2)
1519	Taq1	50	aat	248.04	248	248.04	0	0	13 800 000	0	0	-=	\		A(2) \(2)
1520	Taq1	50	aat	249.1	248	249.1	0	0	7 800 000	0	0	-=	\		A(2) \(2)
1521	Taq1	50	aat	249.26	248	249.26	0	0	7 400 000	0	0	-=	\		A(2) \(2)
1522	Hha1	4	aag	153.23	153	153.47	153.13	153.09	3 800 000	5 300 000	7 000 000	==	-	(-)	-2
1523	Taq1	25	cat	152.47	153	152.47	0	0	354.85	0	0	-=	\		-2
1524	Taq1	25	cat	153.38	153	153.49	153.38	153.27	10 065.51	7 918.52	3 279.14	=-	\ (-)	(-)	-2
1525	Hha1	33	agc	122.127	122	122.29	122.07	122.02	3 600 000	5 300 000	7 000 000	==	-		-3
1526	Taq1	12	agt	147.573	148	147.56	147.56	147.6	11 300 000	13 700 000	4 400 000	=-	\ (-)		-3
1527	Taq1	12	agt	148.6	148	148.59	148.55	148.66	23 300 000	36 400 000	18 100 000	=-	\ (-)	\	-3
1528	Taq1	17	cca	147.97	148	147.76	147.99	148.16	185.76	737.93	1 112.61	+=	/ (-)		-3
1529	Taq1	17	cca	148.42	148	148.42	0	0	362.23	0	0	-=	\	\	-3
1530	Taq1	34	tgc	384.57	386	0	0	384.57	0	0	6 100 000	=+	/		-3
1531	Taq1	40	tgg	118.44	119	118.44	118.37	118.51	4 200 000	3 900 000	23 900 000	=+	/ (-)		\(4)
1532	Taq1	40	tgg	119.665	119	119.69	119.64	0	8 000 000	13 700 000	0	=-	\		\(4)
1533	Hha1	43	cgc	119.45	120	119.47	119.43	0	50 800 000	6 900 000	0	-=	\		\(4)
1534	Hha1	27	acg	121.525	121	121.53	0	121.52	3 800 000	0	11 500 000	=+(+)	/		\(4)
1535	Taq1	45	gcc	138.683	139	138.69	138.86	138.5	4 900 000	4 800 000	13 500 000	=+	/ (-)		\(4)
1536	Taq1	45	gcc	139.21	139	0	139.21	0	0	4 500 000	0	+-	A		\(4)
1537	Taq1	56	tga	139.383	140	139.51	139.44	139.2	37 300 000	35 400 000	4 700 000	=-	\ (-)		\(4)
1538	Hha1	20	ctc	157.125	157	157.24	0	157.01	289.25	0	441.31	-+(=)	V		\(4)
1539	Hha1	43	cgc	157.54	158	157.54	0	0	4 400 000	0	0	-=	\		\(4)
1540	Hha1	43	cgc	158.18	158	0	158.18	0	0	5 500 000	0	+-	A		\(4)
1541	Taq1	45	gcc	134.23	134	0	0	134.23	0	0	5 800 000	=+	/	/	/(2)
1542	Taq1	56	tga	134.19	135	0	0	134.19	0	0	3 400 000	=+	/	/	/(2)
1543	Taq1	56	tga	135.23	135	0	0	135.23	0	0	31 300 000	=+	/		/(2)
1544	Taq1	40	tgg	123.5	124	0	0	123.5	0	0	18 400 000	=+	/	/	/(2)
1545	Taq1	40	tgg	124.435	124	0	124.28	124.59	0	5 600 000	39 000 000	=+	/	/	/(2)
1546	Taq1	62	tgt	123.497	124	123.62	123.49	123.38	3 000 000	4 200 000	29 100 000	=+	/ (-)	/	/(2)
1547	Taq1	62	tgt	124.54	124	124.59	124.62	124.41	5 100 000	7 400 000	69 100 000	=+	/ (-)	/	/(2)
1548	Taq1	40	tgg	123.5	124	0	0	123.5	0	0	18 400 000	=+	/	/	/(3)
1549	Taq1	40	tgg	124.435	124	0	124.28	124.59	0	5 600 000	39 000 000	=+	/	/	/(3)
1550	Taq1	62	tgt	123.497	124	123.62	123.49	123.38	3 000 000	4 200 000	29 100 000	=+	/ (-)	/	/(3)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
1508	AB071283.CBLB	Cblb	Cbl-b		cat	tgt	increased
1509	AB071283.CBLB	Cblb	Cbl-b		cat	tgt	No change
1510	AB071283.CBLB	Cblb	Cbl-b		cat	tgt	increased
1511	AB071283.CBLB	Cblb	Cbl-b		gcc	tga	increased
1512	AB071283.CBLB	Cblb	Cbl-b		gcc	tga	increased
1513	AB071283.CBLB	Cblb	Cbl-b		att	gga	increased
1514	AY325241.PE1	nc	Cc1-8	*	ccc	ccc	increased by mild
1515	AY325241.PE1	nc	Cc1-8	*	ccc	ccc	increased by mild
1516	AY325241.PE1	nc	Cc1-8	*	aat	atg	increased by mild
1517	AY325241.PE1	nc	Cc1-8	*	aat	atg	increased by mild
1518	AY325241.PE1	nc	Cc1-8	*	aat	atg	increased by mild
1519	AY325241.PE1	nc	Cc1-8	*	aat	atg	increased by mild
1520	AY325241.PE1	nc	Cc1-8	*	aat	atg	increased by mild
1521	AY325241.PE1	nc	Cc1-8	*	aat	atg	increased by mild
1522	AY325245.PE1	nc	Cc2-5		aag	cat	No change
1523	AY325245.PE1	nc	Cc2-5		aag	cat	No change
1524	AY325245.PE1	nc	Cc2-5		aag	cat	No change
1525	AB000215.CCA1	cca1	CCA1 protein		cag	agc	No change
1526	AB000215.CCA1	cca1	CCA1 protein		cca	agt	No change
1527	AB000215.CCA1	cca1	CCA1 protein		cca	agt	increased
1528	AB000215.CCA1	cca1	CCA1 protein		cca	agt	No change
1529	AB000215.CCA1	cca1	CCA1 protein		cca	agt	increased
1530	AB000215.CCA1	cca1	CCA1 protein		cca	tgc	No change
1531	AB000216.CCA3	cca3	CCA3		gct	tgg	increased
1532	AB000216.CCA3	cca3	CCA3		gct	tgg	increased
1533	AB000216.CCA3	cca3	CCA3		cgc	acg	increased
1534	AB000216.CCA3	cca3	CCA3		cgc	acg	increased
1535	AB000216.CCA3	cca3	CCA3		gcc	tga	increased
1536	AB000216.CCA3	cca3	CCA3		gcc	tga	increased
1537	AB000216.CCA3	cca3	CCA3		gcc	tga	increased
1538	AB000216.CCA3	cca3	CCA3		tgc	ctc	increased
1539	AB000216.CCA3	cca3	CCA3		cgc	gag	increased
1540	AB000216.CCA3	cca3	CCA3		cgc	gag	increased
1541	RNU17607.PE1	nc	CCAAT binding transcription factor CBF subunit		gcc	tga	decreased
1542	RNU17607.PE1	nc	CCAAT binding transcription factor CBF subunit		gcc	tga	decreased
1543	RNU17607.PE1	nc	CCAAT binding transcription factor CBF subunit		gcc	tga	decreased
1544	A30543.PE1	nc	CD44 p-Meta-1		tgg	tgt	decreased
1545	A30543.PE1	nc	CD44 p-Meta-1		tgg	tgt	decreased
1546	A30543.PE1	nc	CD44 p-Meta-1		tgg	tgt	decreased
1547	A30543.PE1	nc	CD44 p-Meta-1		tgg	tgt	decreased
1548	RNU96138.CD44	CD44	CD44 protein		tgg	tgt	decreased
1549	RNU96138.CD44	CD44	CD44 protein		tgg	tgt	decreased
1550	RNU96138.CD44	CD44	CD44 protein		tgg	tgt	decreased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
1551	Taq1	62	tgt	124.54	124	124.59	124.62	124.41	5 100 000	7 400 000	69 100 000	=+	/ (-)	/	/(3)
1552	Hha1	6	aga	260	261	260	0	0	29 900 000	0	0	-=	\		/(3)
1553	Hha1	6	aga	261.68	261	261.68	0	0	7 800 000	0	0	-=	\		/(3)
1554	Hha1	6	aga	262.38	261	262.38	0	0	3 500 000	0	0	-=	\		/(3)
1555	Taq1	17	cca	290.28	290	0	0	290.28	0	0	451.05	=+	/		/(3)
1556	Taq1	17	cca	291.03	290	291.03	0	0	185.76	0	0	-=	\		/(3)
1557	Hha1	6	aga	102.225	102	102.47	0	101.98	17 500 000	0	6 500 000	-=(-)	\		\(2)
1558	Taq1	25	cat	101.59	102	101.59	0	0	464.03	0	0	-=	\		\(2)
1559	Taq1	25	cat	102.27	102	102.33	0	102.21	211.54	0	1 763.57	=+(+)	/		\(2)
1560	Taq1	35	gga	135.88	136	0	0	135.88	0	0	5 700 000	=+	/	/	/(2)
1561	Taq1	62	tgt	135.63	136	135.74	135.61	135.54	3 100 000	3 200 000	8 200 000	=+	/ (-)	/	/(2)
1562	Taq1	62	tgt	136.76	136	0	0	136.76	0	0	5 100 000	=+	/		/(2)
1563	Hha1	4	aag	137.1	137	137.22	136.84	137.24	92 600 000	9 800 000	35 200 000	-=	\ (-)		-(2) \(2)
1564	Hha1	4	aag	137.21	137	0	137.21	0	0	10 000 000	0	+-	A		-(2) \(2)
1565	Taq1	25	cat	136.403	137	136.49	136.52	136.2	1 658.25	878.42	1 322.67	-=	\ (-)		-(2) \(2)
1566	Taq1	25	cat	137.373	137	137.34	137.57	137.21	1 931.21	1 489.49	1 873.79	==	-		-(2) \(2)
1567	Hha1	64	gtt	70.367	70	70.31	70.37	70.42	6 400 000	5 200 000	17 000 000	=+	/ (-)		\(10)
1568	Taq1	47	ggc	108.45	108	108.45	0	0	1 969.23	0	0	-=	\		\(10)
1569	Taq1	39	agg	108.75	109	108.92	108.58	0	13 900 000	56 000 000	0	+-	A		\(10)
1570	Taq1	39	agg	109.455	109	109.31	109.6	0	12 800 000	59 600 000	0	+-	A		\(10)
1571	Taq1	39	agg	108.75	109	108.92	108.58	0	516.19	562.81	0	=-	\		\(10)
1572	Taq1	39	agg	109.455	109	109.31	109.6	0	475.34	599	0	=-	\		\(10)
1573	Taq1	39	agg	117.575	118	0	117.49	117.66	0	53 300 000	4 600 000	+-	A		\(10)
1574	Taq1	39	agg	117.875	118	118.09	0	117.66	17 600 000	0	135.49	-=(-)	\		\(10)
1575	Taq1	39	agg	117.49	118	0	117.49	0	0	535.68	0	+-	A		\(10)
1576	Taq1	39	agg	118.09	118	118.09	0	0	653.59	0	0	-=	\		\(10)
1577	Hha1	33	agc	209.64	209	0	209.64	0	0	3 300 000	0	+-	A		\(10)
1578	Hha1	59	ttc	208.45	209	0	208.45	0	0	169.59	0	+-	A		\(10)
1579	Hha1	59	ttc	208.945	209	209.09	208.8	0	306.81	250.08	0	=-	\		\(10)
1580	Hha1	59	ttc	209.33	209	0	209.33	0	0	333.44	0	+-	A		\(10)
1581	Taq1	61	tct	215.85	217	0	0	215.85	0	0	3 300 000	=+	/		\(10)
1582	Taq1	61	tct	216.9	217	0	0	216.9	0	0	6 300 000	=+	/		\(10)
1583	Taq1	61	tct	217.88	217	217.88	0	0	3 900 000	0	0	-=	\		\(10)
1584	Taq1	50	aat	217.5	218	217.42	217.59	217.49	34 800 000	8 000 000	7 500 000	-=	\ (-)		\(10)
1585	Taq1	50	aat	218.655	218	218.44	218.87	0	6 000 000	4 400 000	0	=-	\		\(10)
1586	Hha1	6	aga	225.19	226	225.19	0	0	7 000 000	0	0	-=	\		\(10)
1587	Taq1	8	gaa	235.63	237	235.63	0	0	3 800 000	0	0	-=	\		\(10)
1588	Hha1	8	gaa	236.3	237	236.33	236.27	0	3 900 000	3 100 000	0	=-	\		\(10)
1589	Taq1	45	gcc	237.79	237	237.79	0	0	3 100 000	0	0	-=	\		\(10)
1590	Taq1	45	gcc	143.37	144	143.53	0	143.21	5 200 000	0	3 000 000	-+(=)	V		/(2)
1591	Taq1	45	gcc	144.28	144	0	0	144.28	0	0	3 600 000	=+	/	/	/(2)
1592	Taq1	12	agt	144.48	145	144.5	144.51	144.43	9 500 000	6 800 000	19 000 000	=+	/ (-)	/	/(2)
1593	Taq1	12	agt	145.487	145	145.52	145.45	145.49	10 500 000	10 000 000	3 800 000	=-	\ (-)		/(2)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
1551	RNU96138.CD44	CD44	CD44 protein		tgg	tgt	decreased
1552	RNU96138.CD44	CD44	CD44 protein		aga	aac	decreased
1553	RNU96138.CD44	CD44	CD44 protein		aga	aac	decreased
1554	RNU96138.CD44	CD44	CD44 protein		aga	aac	decreased
1555	RNU96138.CD44	CD44	CD44 protein		ccc	cca	decreased
1556	RNU96138.CD44	CD44	CD44 protein		ccc	cca	decreased
1557	RRCDC2MR.PE1	nc	cdc2(+)		cat	aga	increased
1558	RRCDC2MR.PE1	nc	cdc2(+)		cat	aga	increased
1559	RRCDC2MR.PE1	nc	cdc2(+)		cat	aga	increased
1560	RATCDC25A.PE1	nc	cdc25A		tgt	gga	decreased
1561	RATCDC25A.PE1	nc	cdc25A		tgt	gga	decreased
1562	RATCDC25A.PE1	nc	cdc25A		tgt	gga	decreased
1563	RATCDC2LK.PE1	nc	cdc2-related protein kinase		cat	aag	No change
1564	RATCDC2LK.PE1	nc	cdc2-related protein kinase		cat	aag	No change
1565	RATCDC2LK.PE1	nc	cdc2-related protein kinase		cat	aag	No change
1566	RATCDC2LK.PE1	nc	cdc2-related protein kinase		cat	aag	No change
1567	AY277590.PE1	Cdc42bpb	CDC42-binding protein kinase beta		gtt	tgt	increased
1568	AY277590.PE1	Cdc42bpb	CDC42-binding protein kinase beta		ggc	agg	increased
1569	AY277590.PE1	Cdc42bpb	CDC42-binding protein kinase beta		ggc	agg	increased
1570	AY277590.PE1	Cdc42bpb	CDC42-binding protein kinase beta		ggc	agg	increased
1571	AY277590.PE1	Cdc42bpb	CDC42-binding protein kinase beta		ggc	agg	increased
1572	AY277590.PE1	Cdc42bpb	CDC42-binding protein kinase beta		ggc	agg	increased
1573	AY277590.PE1	Cdc42bpb	CDC42-binding protein kinase beta		gct	agg	increased
1574	AY277590.PE1	Cdc42bpb	CDC42-binding protein kinase beta		gct	agg	increased
1575	AY277590.PE1	Cdc42bpb	CDC42-binding protein kinase beta		gct	agg	increased
1576	AY277590.PE1	Cdc42bpb	CDC42-binding protein kinase beta		gct	agg	increased
1577	AY277590.PE1	Cdc42bpb	CDC42-binding protein kinase beta		ttc	agc	increased
1578	AY277590.PE1	Cdc42bpb	CDC42-binding protein kinase beta		ttc	agc	increased
1579	AY277590.PE1	Cdc42bpb	CDC42-binding protein kinase beta		ttc	agc	increased
1580	AY277590.PE1	Cdc42bpb	CDC42-binding protein kinase beta		ttc	agc	increased
1581	AY277590.PE1	Cdc42bpb	CDC42-binding protein kinase beta		aat	tct	increased
1582	AY277590.PE1	Cdc42bpb	CDC42-binding protein kinase beta		aat	tct	increased
1583	AY277590.PE1	Cdc42bpb	CDC42-binding protein kinase beta		aat	tct	increased
1584	AY277590.PE1	Cdc42bpb	CDC42-binding protein kinase beta		aat	tct	increased
1585	AY277590.PE1	Cdc42bpb	CDC42-binding protein kinase beta		aat	tct	increased
1586	AY277590.PE1	Cdc42bpb	CDC42-binding protein kinase beta		tgc	aga	increased
1587	AY277590.PE1	Cdc42bpb	CDC42-binding protein kinase beta		gaa	tgg	increased
1588	AY277590.PE1	Cdc42bpb	CDC42-binding protein kinase beta		gaa	tgg	increased
1589	AY277590.PE1	Cdc42bpb	CDC42-binding protein kinase beta		agc	gcc	increased
1590	AF000578.PE1	nc	Cdc5-like protein		gcc	agt	decreased
1591	AF000578.PE1	nc	Cdc5-like protein		gcc	agt	decreased
1592	AF000578.PE1	nc	Cdc5-like protein		gcc	agt	decreased
1593	AF000578.PE1	nc	Cdc5-like protein		gcc	agt	decreased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
1594	Taq1	45	gcc	108.68	109	108.65	108.71	0	4 600 000	7 200 000	0	=-	\		\(4)
1595	Taq1	45	gcc	109.61	109	0	0	109.61	0	0	4 400 000	=+	/	/	\(4)
1596	Hha1	4	aag	109.845	110	0	109.78	109.91	0	6 800 000	5 600 000	+=	/	/	\(4)
1597	Hha1	21	acc	213.37	214	213.37	0	0	24 000 000	0	0	-=	\		\(4)
1598	Taq1	21	acc	214.61	214	214.61	0	0	7 500 000	0	0	-=	\		\(4)
1599	Hha1	21	acc	214.53	214	214.53	0	0	4 100 000	0	0	-=	\		\(4)
1600	Hha1	21	acc	215.23	214	0	215.23	0	0	3 200 000	0	+-	A		\(4)
1601	Taq1	10	atg	132.3	133	132.3	0	0	6 800 000	0	0	-=	\		\(5)
1602	Taq1	10	atg	132.83	133	0	132.83	0	0	4 300 000	0	+-	A		\(5)
1603	Hha1	10	atg	132.85	133	132.85	0	0	10 200 000	0	0	-=	\		\(5)
1604	Taq1	10	atg	133.225	133	133.35	0	133.1	20 400 000	0	4 800 000	-=(-)	\		\(5)
1605	Taq1	49	aaa	319.7	321	0	319.7	0	0	9 300 000	0	+-	A		\(5)
1606	Taq1	49	aaa	320.505	321	320.36	320.65	0	8 600 000	13 500 000	0	=-	\		\(5)
1607	Taq1	49	aaa	468.17	466	468.28	468.06	0	3 100 000	3 700 000	0	=-	\		\(5)
1608	Hha1	8	gaa	192.223	193	192.17	192.27	192.23	6 900 000	8 500 000	3 300 000	=-	\ (-)		\(3)
1609	Taq1	8	gaa	192.62	193	0	192.62	0	0	8 500 000	0	+-	A		\(3)
1610	Taq1	8	gaa	193.35	193	0	0	193.35	0	0	4 100 000	=+	/		\(3)
1611	Hha1	8	gaa	193.115	193	193.11	193.12	0	4 600 000	11 300 000	0	+-	A		\(3)
1612	Hha1	8	gaa	193.97	193	193.91	194.03	0	5 400 000	3 500 000	0	=-	\		\(3)
1613	Taq1	63	ctt	192.08	193	192.08	0	0	3 000 000	0	0	-=	\		\(3)
1614	Taq1	63	ctt	193.04	193	193.04	0	193.04	3 100 000	0	3 400 000	-+(=)	V		\(3)
1615	Hha1	4	aag	175.01	175	174.98	0	175.04	11 200 000	0	3 200 000	-=(-)	\		\(2)
1616	Hha1	4	aag	176.01	175	176.06	0	175.96	18 400 000	0	8 200 000	-=(-)	\		\(2)
1617	Taq1	49	aaa	311.91	313	0	311.91	0	0	3 100 000	0	+-	A		\(2)
1618	Taq1	49	aaa	312.61	313	312.61	0	0	6 500 000	0	0	-=	\		\(2)
1619	Taq1	36	ggt	149.03	149	0	0	149.03	0	0	4 400 000	=+	/		/(3)
1620	Taq1	49	aaa	149.53	150	0	149.51	149.55	0	16 700 000	5 000 000	+-	A		/(3)
1621	Taq1	49	aaa	150.427	150	150.37	150.5	150.41	51 400 000	26 100 000	112 600 000	=+	/ (-)		/(3)
1622	Taq1	40	tgg	175.59	175	0	0	175.59	0	0	7 000 000	=+	/		/(3)
1623	Taq1	45	gcc	66.68	67	66.86	66.68	66.5	33 500 000	13 000 000	7 900 000	-=	\ (-)		\(2)
1624	Taq1	8	gaa	67.66	68	67.66	0	0	5 400 000	0	0	-=	\		\(2)
1625	Taq1	8	gaa	68.05	68	68.05	0	0	7 200 000	0	0	-=	\		\(2)
1626	Taq1	45	gcc	66.68	67	66.86	66.68	66.5	33 500 000	13 000 000	7 900 000	-=	\ (-)		\(2)
1627	Taq1	8	gaa	67.66	68	67.66	0	0	5 400 000	0	0	-=	\		\(2)
1628	Taq1	8	gaa	68.05	68	68.05	0	0	7 200 000	0	0	-=	\		\(2)
1629	Taq1	23	cga	148.69	149	0	148.69	0	0	3 200 000	0	+-	A		A(2)
1630	Taq1	54	ttt	149.73	150	149.91	149.55	0	619.08	1 669.99	0	+-	A		A(2)
1631	Taq1	54	ttt	150.645	150	150.51	150.78	0	2 039.32	540.98	0	-=	\		A(2)
1632	Taq1	47	ggc	114.615	114	114.6	114.63	0	4 246.15	1 718.65	0	-=	\	\	\(2)
1633	Taq1	18	cct	114.52	115	114.5	114.54	114.52	21 700 000	29 300 000	7 500 000	=-	\ (-)	\	\(2)
1634	Taq1	18	cct	115.39	115	115.34	115.38	115.45	58 000 000	74 100 000	4 000 000	=-	\ (-)		\(2)
1635	Hha1	20	ctc	93.51	94	93.44	93.58	0	1 494.49	576.97	0	-=	\		\(3)
1636	Hha1	20	ctc	94.37	94	94.37	0	0	530.3	0	0	-=	\	\	\(3)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
1594	AF004840.CDO	cdo	CDO		aag	gcc	increased
1595	AF004840.CDO	cdo	CDO		aag	gcc	decreased
1596	AF004840.CDO	cdo	CDO		aag	gcc	decreased
1597	AF004840.CDO	cdo	CDO		tgg	acc	increased
1598	AF004840.CDO	cdo	CDO		tgg	acc	increased
1599	AF004840.CDO	cdo	CDO		tgg	acc	increased
1600	AF004840.CDO	cdo	CDO		tgg	acc	increased
1601	AB057433.PAPKCD	pAPkCD	ceramidase		atg	tac	increased
1602	AB057433.PAPKCD	pAPkCD	ceramidase		atg	tac	increased
1603	AB057433.PAPKCD	pAPkCD	ceramidase		atg	tac	increased
1604	AB057433.PAPKCD	pAPkCD	ceramidase		atg	tac	increased
1605	AB057433.PAPKCD	pAPkCD	ceramidase		aaa	ttt	increased
1606	AB057433.PAPKCD	pAPkCD	ceramidase		aaa	ttt	increased
1607	AB057433.PAPKCD	pAPkCD	ceramidase		aga	aaa	increased
1608	RNCERBATR.PE1	nc	c-erb-A thyroid hormone receptor		gaa	ctt	increased
1609	RNCERBATR.PE1	nc	c-erb-A thyroid hormone receptor		gaa	ctt	increased
1610	RNCERBATR.PE1	nc	c-erb-A thyroid hormone receptor		gaa	ctt	increased
1611	RNCERBATR.PE1	nc	c-erb-A thyroid hormone receptor		gaa	ctt	increased
1612	RNCERBATR.PE1	nc	c-erb-A thyroid hormone receptor		gaa	ctt	increased
1613	RNCERBATR.PE1	nc	c-erb-A thyroid hormone receptor		gaa	ctt	increased
1614	RNCERBATR.PE1	nc	c-erb-A thyroid hormone receptor		gaa	ctt	increased
1615	AF350421.PE1	nc	CGI-94		aag	cta	increased
1616	AF350421.PE1	nc	CGI-94		aag	cta	increased
1617	AF350421.PE1	nc	CGI-94		aaa	ttt	increased
1618	AF350421.PE1	nc	CGI-94		aaa	ttt	increased
1619	AF372654.PDE9A	PDE9A	cGMP phosphodiesterase		aaa	ggt	decreased
1620	AF372654.PDE9A	PDE9A	cGMP phosphodiesterase		aaa	ggt	decreased
1621	AF372654.PDE9A	PDE9A	cGMP phosphodiesterase		aaa	ggt	decreased
1622	AF372654.PDE9A	PDE9A	cGMP phosphodiesterase		tgg	tgg	decreased
1623	RNCHIP28.PE1	nc	channel integral membrane protein 28		gaa	gcc	increased
1624	RNCHIP28.PE1	nc	channel integral membrane protein 28		gaa	gcc	increased
1625	RNCHIP28.PE1	nc	channel integral membrane protein 28		gaa	gcc	increased
1626	RNCHIPA.PE1	nc	CHIP28		gaa	gcc	increased
1627	RNCHIPA.PE1	nc	CHIP28		gaa	gcc	increased
1628	RNCHIPA.PE1	nc	CHIP28		gaa	gcc	increased
1629	AF005720.PE2	ClC-2	chloride channel 2		cga	ttt	increased by mild
1630	AF005720.PE2	ClC-2	chloride channel 2		cga	ttt	increased by mild
1631	AF005720.PE2	ClC-2	chloride channel 2		cga	ttt	increased by mild
1632	AB055423.CHM1L	ChM1L	ChM1L	*	ggc	cct	increased
1633	AB055423.CHM1L	ChM1L	ChM1L	*	ggc	cct	increased
1634	AB055423.CHM1L	ChM1L	ChM1L	*	ggc	cct	increased
1635	RATCCK3.CCK	CCK	cholecystokinin	*	agc	ctc	increased
1636	RATCCK3.CCK	CCK	cholecystokinin	*	agc	ctc	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
1637	Hha1	33	agc	94.285	94	94.26	94.31	0	4 500 000	3 800 000	0	=-	\	\	\(3)
1638	Hha1	44	cgg	174.45	175	0	174.45	0	0	3 800 000	0	+-	A		\(3)
1639	Hha1	44	cgg	175.29	175	175.29	0	0	12 200 000	0	0	-=	\		\(3)
1640	Hha1	9	atc	227.17	227	227.17	0	0	4 800 000	0	0	-=	\		\(2)
1641	Hha1	25	cag	225.99	227	225.91	225.86	226.2	3 300 000	3 700 000	6 000 000	==	-		\(2)
1642	Hha1	25	cag	226.15	227	226.15	0	0	3 300 000	0	0	-=	\		\(2)
1643	Hha1	25	cag	226.88	227	226.88	0	0	3 700 000	0	0	-=	\		\(2)
1644	Hha1	25	cag	228.24	227	228.24	0	0	3 300 000	0	0	-=	\		\(2)
1645	Hha1	9	atc	227.17	227	227.17	0	0	4 800 000	0	0	-=	\		\(2)
1646	Hha1	25	cag	225.99	227	225.91	225.86	226.2	3 300 000	3 700 000	6 000 000	==	-		\(2)
1647	Hha1	25	cag	226.15	227	226.15	0	0	3 300 000	0	0	-=	\		\(2)
1648	Hha1	25	cag	226.88	227	226.88	0	0	3 700 000	0	0	-=	\		\(2)
1649	Hha1	25	cag	228.24	227	228.24	0	0	3 300 000	0	0	-=	\		\(2)
1650	Taq1	8	gaa	65.95	66	0	65.92	65.98	0	3 200 000	7 600 000	=+	/		A(2)
1651	Hha1	58	gta	143.29	144	143.3	143.26	143.31	34 900 000	80 400 000	17 000 000	+-	A	A	A(2)
1652	Hha1	58	gta	144.283	144	144.36	144.19	144.3	14 500 000	12 100 000	4 800 000	=-	\ (-)		A(2)
1653	Hha1	61	tct	143.213	144	143.25	143.1	143.29	4 500 000	21 600 000	5 100 000	+-	A	A	A(2)
1654	Hha1	61	tct	144.17	144	0	144.17	0	0	3 500 000	0	+-	A		A(2)
1655	Taq1	8	gaa	65.95	66	0	65.92	65.98	0	3 200 000	7 600 000	=+	/		A(2)
1656	Hha1	58	gta	143.29	144	143.3	143.26	143.31	34 900 000	80 400 000	17 000 000	+-	A	A	A(2)
1657	Hha1	58	gta	144.283	144	144.36	144.19	144.3	14 500 000	12 100 000	4 800 000	=-	\ (-)		A(2)
1658	Hha1	61	tct	143.213	144	143.25	143.1	143.29	4 500 000	21 600 000	5 100 000	+-	A	A	A(2)
1659	Hha1	61	tct	144.17	144	0	144.17	0	0	3 500 000	0	+-	A		A(2)
1660	Taq1	8	gaa	65.95	66	0	65.92	65.98	0	3 200 000	7 600 000	=+	/		A(2)
1661	Hha1	58	gta	143.29	144	143.3	143.26	143.31	34 900 000	80 400 000	17 000 000	+-	A	A	A(2)
1662	Hha1	58	gta	144.283	144	144.36	144.19	144.3	14 500 000	12 100 000	4 800 000	=-	\ (-)		A(2)
1663	Hha1	61	tct	143.213	144	143.25	143.1	143.29	4 500 000	21 600 000	5 100 000	+-	A	A	A(2)
1664	Hha1	61	tct	144.17	144	0	144.17	0	0	3 500 000	0	+-	A		A(2)
1665	Hha1	58	gta	143.29	144	143.3	143.26	143.31	34 900 000	80 400 000	17 000 000	+-	A	A	
1666	Hha1	61	tct	143.213	144	143.25	143.1	143.29	4 500 000	21 600 000	5 100 000	+-	A	A	
1667	Hha1	58	gta	143.29	144	143.3	143.26	143.31	34 900 000	80 400 000	17 000 000	+-	A	A	
1668	Hha1	61	tct	143.213	144	143.25	143.1	143.29	4 500 000	21 600 000	5 100 000	+-	A	A	
1669	Hha1	58	gta	143.29	144	143.3	143.26	143.31	34 900 000	80 400 000	17 000 000	+-	A	A	
1670	Hha1	61	tct	143.213	144	143.25	143.1	143.29	4 500 000	21 600 000	5 100 000	+-	A	A	
1671	Hha1	27	acg	73.113	73	73.01	73.21	73.12	16 100 000	8 700 000	14 200 000	-=	\ (-)		\(3) -(2)
1672	Hha1	40	tgg	147.74	148	147.74	0	0	7 500 000	0	0	-=	\		\(3) -(2)
1673	Hha1	40	tgg	148.755	148	148.88	148.63	0	6 300 000	3 900 000	0	=-	\		\(3) -(2)
1674	Hha1	61	tct	221.88	223	221.88	221.88	221.88	10 000 000	8 200 000	6 100 000	==	-		\(3) -(2)
1675	Hha1	61	tct	222.903	223	222.89	222.92	222.9	145 900 000	74 900 000	90 600 000	-=	\ (-)		\(3) -(2)
1676	Hha1	61	tct	223.88	223	223.85	223.91	0	10 500 000	7 000 000	0	=-	\		\(3) -(2)
1677	Hha1	59	ttc	79.593	80	79.5	79.64	79.64	4 362.97	2 230.65	2 129.2	-=	\ (-)		\(2)
1678	Hha1	59	ttc	80.225	80	80.31	0	80.14	2 028.08	0	1 836.85	-+(=)	V		\(2)
1679	Taq1	25	cat	120.315	121	120.32	120.31	0	832.53	980.26	0	=-	\		\(2)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
1637	RATCCK3.CCK	CCK	cholecystokinin	*	agc	ctc	increased
1638	RATCCK3.CCK	CCK	cholecystokinin	*	act	cgg	increased
1639	RATCCK3.CCK	CCK	cholecystokinin	*	act	cgg	increased
1640	RATCCKAR.CCKAR	CCKAR	cholecystokinin receptor		cag	atc	increased
1641	RATCCKAR.CCKAR	CCKAR	cholecystokinin receptor		cag	atc	increased
1642	RATCCKAR.CCKAR	CCKAR	cholecystokinin receptor		cag	atc	increased
1643	RATCCKAR.CCKAR	CCKAR	cholecystokinin receptor		cag	atc	increased
1644	RATCCKAR.CCKAR	CCKAR	cholecystokinin receptor		cag	atc	increased
1645	RATCCKARA.CCKAR	CCKAR	cholecystokinin type-A receptor		cag	atc	increased
1646	RATCCKARA.CCKAR	CCKAR	cholecystokinin type-A receptor		cag	atc	increased
1647	RATCCKARA.CCKAR	CCKAR	cholecystokinin type-A receptor		cag	atc	increased
1648	RATCCKARA.CCKAR	CCKAR	cholecystokinin type-A receptor		cag	atc	increased
1649	RATCCKARA.CCKAR	CCKAR	cholecystokinin type-A receptor		cag	atc	increased
1650	AF081154.PE1	nc	CL3AA		ttg	gaa	increased by mild
1651	AF081154.PE1	nc	CL3AA		tct	gta	increased by mild
1652	AF081154.PE1	nc	CL3AA		tct	gta	increased by mild
1653	AF081154.PE1	nc	CL3AA		tct	gta	increased by mild
1654	AF081154.PE1	nc	CL3AA		tct	gta	increased by mild
1655	AF081155.PE1	nc	CL3AB		ttg	gaa	increased by mild
1656	AF081155.PE1	nc	CL3AB		tct	gta	increased by mild
1657	AF081155.PE1	nc	CL3AB		tct	gta	increased by mild
1658	AF081155.PE1	nc	CL3AB		tct	gta	increased by mild
1659	AF081155.PE1	nc	CL3AB		tct	gta	increased by mild
1660	AF081156.PE1	nc	CL3AC		ttg	gaa	increased by mild
1661	AF081156.PE1	nc	CL3AC		tct	gta	increased by mild
1662	AF081156.PE1	nc	CL3AC		tct	gta	increased by mild
1663	AF081156.PE1	nc	CL3AC		tct	gta	increased by mild
1664	AF081156.PE1	nc	CL3AC		tct	gta	increased by mild
1665	AF081157.PE1	nc	CL3BA		tct	gta	increased by mild
1666	AF081157.PE1	nc	CL3BA		tct	gta	increased by mild
1667	AF081158.PE1	nc	CL3BB		tct	gta	increased by mild
1668	AF081158.PE1	nc	CL3BB		tct	gta	increased by mild
1669	AF081159.PE1	nc	CL3BC		tct	gta	increased by mild
1670	AF081159.PE1	nc	CL3BC		tct	gta	increased by mild
1671	AF051526.BCCA1	BCCA1	class A calcium channel variant riA-I		ccc	acg	increased
1672	AF051526.BCCA1	BCCA1	class A calcium channel variant riA-I		tgg	cgc	increased
1673	AF051526.BCCA1	BCCA1	class A calcium channel variant riA-I		tgg	cgc	increased
1674	AF051526.BCCA1	BCCA1	class A calcium channel variant riA-I		tct	tcc	increased
1675	AF051526.BCCA1	BCCA1	class A calcium channel variant riA-I		tct	tcc	increased
1676	AF051526.BCCA1	BCCA1	class A calcium channel variant riA-I		tct	tcc	increased
1677	RNU50448.PE1	RT1.A(n)	class I MHC heavy chain RT1.A(n) antigen		ttc	ccg	increased
1678	RNU50448.PE1	RT1.A(n)	class I MHC heavy chain RT1.A(n) antigen		ttc	ccg	increased
1679	RNU50448.PE1	RT1.A(n)	class I MHC heavy chain RT1.A(n) antigen		cat	agc	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
1680	Taq1	25	cat	121.21	121	121.19	121.23	0	1 044.08	954.8	0	=-	\		\(2)
1681	Taq1	9	atc	124.52	125	124.52	0	0	8 800 000	0	0	-=	\		\(8)
1682	Hha1	9	atc	124.995	125	124.94	125.05	0	13 600 000	6 200 000	0	--	\		\(8)
1683	Taq1	9	atc	125.075	125	125.09	0	125.06	5 500 000	0	19 600 000	=+(+)	/		\(8)
1684	Taq1	18	cct	124.58	125	124.51	124.78	124.45	10 700 000	7 400 000	17 100 000	=+	/ (-)		\(8)
1685	Taq1	18	cct	125.427	125	125.38	125.43	125.47	5 200 000	4 700 000	5 200 000	==	-		\(8)
1686	Taq1	9	atc	135.247	136	135.22	135.19	135.33	16 100 000	12 500 000	3 200 000	=-	\ (-)		\(8)
1687	Hha1	9	atc	136.12	136	135.96	136.28	0	4 400 000	3 000 000	0	=-	\	\	\(8)
1688	Taq1	9	atc	136.215	136	136.26	136.17	0	5 300 000	6 900 000	0	=-	\	\	\(8)
1689	Taq1	31	gac	135.577	136	135.72	135.49	135.52	11 900 000	8 500 000	6 100 000	==	-		\(8)
1690	Taq1	31	gac	136.6	136	136.69	136.54	136.57	9 200 000	8 100 000	6 800 000	==	-		\(8)
1691	Hha1	3	aac	154.31	155	154.28	154.34	0	38 200 000	6 800 000	0	-=	\		\(8)
1692	Hha1	3	aac	155.577	155	155.46	155.53	155.74	5 600 000	7 500 000	4 800 000	==	-		\(8)
1693	Taq1	20	ctc	154.583	155	154.65	154.75	154.35	44 500 000	59 500 000	11 100 000	=-	\ (-)		\(8)
1694	Taq1	20	ctc	155.33	155	0	0	155.33	0	0	10 900 000	=+	/		\(8)
1695	Taq1	50	aat	241.79	242	241.57	242.01	0	4 200 000	3 400 000	0	=-	\		\(8)
1696	Hha1	60	ttg	272.37	274	0	272.37	0	0	4 900 000	0	+-	A		\(8)
1697	Hha1	26	ctg	174.13	175	174.13	0	0	3 400 000	0	0	-=	\		\(2)
1698	Hha1	56	tga	174.61	175	174.43	174.79	0	298.28	231.17	0	=-	\		\(2)
1699	Hha1	56	tga	175.17	175	175.17	0	0	228.82	0	0	-=	\		\(2)
1700	Hha1	6	aga	126.475	127	126.51	0	126.44	89 200 000	0	7 100 000	-=(-)	\		\(4)
1701	Hha1	6	aga	127.097	127	127.18	127.06	127.05	30 600 000	3 500 000	5 400 000	-=	\ (-)		\(4)
1702	Hha1	6	aga	127.6	127	0	127.54	127.66	0	3 100 000	6 300 000	++	/		\(4)
1703	Hha1	4	aag	162.55	163	0	0	162.55	0	0	3 100 000	=+	/		\(4)
1704	Hha1	4	aag	163.56	163	0	163.55	163.57	0	5 000 000	13 900 000	=+	/		\(4)
1705	Taq1	39	agg	162.23	163	162.23	0	0	6 900 000	0	0	-=	\		\(4)
1706	Taq1	39	agg	162.87	163	0	162.87	0	0	19 600 000	0	+-	A		\(4)
1707	Taq1	39	agg	163.42	163	163.42	0	0	14 800 000	0	0	-=	\		\(4)
1708	Taq1	39	agg	162.23	163	162.23	0	0	256.23	0	0	-=	\		\(4)
1709	Taq1	39	agg	163.42	163	163.42	0	0	549.61	0	0	-=	\		\(4)
1710	Taq1	39	agg	162.87	163	0	162.87	0	0	196.98	0	+-	A		\(4)
1711	Taq1	63	ctt	180.76	181	0	0	180.76	0	0	3 000 000	=+	/		\(4)
1712	Taq1	63	ctt	181.76	181	0	0	181.76	0	0	3 000 000	=+	/		\(4)
1713	Taq1	50	aat	181.155	182	181.28	181.03	0	3 600 000	3 700 000	0	=-	\		\(4)
1714	Taq1	50	aat	181.2	182	181.2	0	0	3 800 000	0	0	-=	\		\(4)
1715	Taq1	50	aat	182.075	182	182.32	0	181.83	9 500 000	0	3 600 000	-=(-)	\		\(4)
1716	Taq1	50	aat	182.755	182	182.6	0	182.91	9 600 000	0	5 400 000	-+(=)	V		\(4)
1717	Taq1	45	gcc	251.93	253	251.75	252.11	0	158 600 000	3 100 000	0	-=	\		\(4)
1718	Taq1	45	gcc	252.22	253	252.22	0	0	5 200 000	0	0	-=	\		\(4)
1719	Taq1	45	gcc	254.26	253	0	254.26	0	0	3 700 000	0	+-	A		\(4)
1720	Hha1	20	ctc	68	68	68	0	0	426.99	0	0	-=	\		\(3)
1721	Taq1	25	cat	136.403	137	136.49	136.52	136.2	1 658.25	878.42	1 322.67	-=	\ (-)		\(3)
1722	Taq1	25	cat	137.373	137	137.34	137.57	137.21	1 931.21	1 489.49	1 873.79	==	-		\(3)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
1680	RNU50448.PE1	RT1.A(n)	class I MHC heavy chain RT1.A(n) antigen		cat	agc	increased
1681	RNCLC7MR.PE1	nc	CLC-7 chloride channel protein	*	cct	atc	increased
1682	RNCLC7MR.PE1	nc	CLC-7 chloride channel protein	*	cct	atc	increased
1683	RNCLC7MR.PE1	nc	CLC-7 chloride channel protein	*	cct	atc	increased
1684	RNCLC7MR.PE1	nc	CLC-7 chloride channel protein	*	cct	atc	increased
1685	RNCLC7MR.PE1	nc	CLC-7 chloride channel protein	*	cct	atc	increased
1686	RNCLC7MR.PE1	nc	CLC-7 chloride channel protein	*	atc	gac	increased
1687	RNCLC7MR.PE1	nc	CLC-7 chloride channel protein	*	atc	gac	increased
1688	RNCLC7MR.PE1	nc	CLC-7 chloride channel protein	*	atc	gac	increased
1689	RNCLC7MR.PE1	nc	CLC-7 chloride channel protein	*	atc	gac	increased
1690	RNCLC7MR.PE1	nc	CLC-7 chloride channel protein	*	atc	gac	increased
1691	RNCLC7MR.PE1	nc	CLC-7 chloride channel protein	*	ctc	aac	increased
1692	RNCLC7MR.PE1	nc	CLC-7 chloride channel protein	*	ctc	aac	increased
1693	RNCLC7MR.PE1	nc	CLC-7 chloride channel protein	*	ctc	aac	increased
1694	RNCLC7MR.PE1	nc	CLC-7 chloride channel protein	*	ctc	aac	increased
1695	RNCLC7MR.PE1	nc	CLC-7 chloride channel protein	*	cgt	aat	increased
1696	RNCLC7MR.PE1	nc	CLC-7 chloride channel protein	*	cag	ttg	increased
1697	RNO237670.CYLN1	cyln1	CLIP-170		tga	ctg	increased
1698	RNO237670.CYLN1	cyln1	CLIP-170		tga	ctg	increased
1699	RNO237670.CYLN1	cyln1	CLIP-170		tga	ctg	increased
1700	RNO288060.PE1	nc	CLIP-associating protein CLASP2		aga	gag	increased
1701	RNO288060.PE1	nc	CLIP-associating protein CLASP2		aga	gag	increased
1702	RNO288060.PE1	nc	CLIP-associating protein CLASP2		aga	gag	increased
1703	RNO288060.PE1	nc	CLIP-associating protein CLASP2		aag	agg	increased
1704	RNO288060.PE1	nc	CLIP-associating protein CLASP2		aag	agg	increased
1705	RNO288060.PE1	nc	CLIP-associating protein CLASP2		aag	agg	increased
1706	RNO288060.PE1	nc	CLIP-associating protein CLASP2		aag	agg	increased
1707	RNO288060.PE1	nc	CLIP-associating protein CLASP2		aag	agg	increased
1708	RNO288060.PE1	nc	CLIP-associating protein CLASP2		aag	agg	increased
1709	RNO288060.PE1	nc	CLIP-associating protein CLASP2		aag	agg	increased
1710	RNO288060.PE1	nc	CLIP-associating protein CLASP2		aag	agg	increased
1711	RNO288060.PE1	nc	CLIP-associating protein CLASP2		aat	ctt	increased
1712	RNO288060.PE1	nc	CLIP-associating protein CLASP2		aat	ctt	increased
1713	RNO288060.PE1	nc	CLIP-associating protein CLASP2		aat	ctt	increased
1714	RNO288060.PE1	nc	CLIP-associating protein CLASP2		aat	ctt	increased
1715	RNO288060.PE1	nc	CLIP-associating protein CLASP2		aat	ctt	increased
1716	RNO288060.PE1	nc	CLIP-associating protein CLASP2		aat	ctt	increased
1717	RNO288060.PE1	nc	CLIP-associating protein CLASP2		gcc	gag	increased
1718	RNO288060.PE1	nc	CLIP-associating protein CLASP2		gcc	gag	increased
1719	RNO288060.PE1	nc	CLIP-associating protein CLASP2		gcc	gag	increased
1720	RNCLK3PRT.CLK3	clk3	CLK3 protein		ctc	tta	increased
1721	RNCLK3PRT.CLK3	clk3	CLK3 protein		cat	gga	increased
1722	RNCLK3PRT.CLK3	clk3	CLK3 protein		cat	gga	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
1723	Taq1	35	gga	136.97	137	0	0	136.97	0	0	4 800 000	=+	/		\(3)
1724	Hha1	8	gaa	207.473	208	207.57	207.41	207.44	5 800 000	3 700 000	3 200 000	==	-		\(3)
1725	Hha1	8	gaa	208.62	208	208.58	208.66	0	10 000 000	6 400 000	0	=-	\		\(3)
1726	Hha1	59	ttc	91.13	91	91.33	90.98	91.08	447.21	1 644.24	447.57	+-	A		-4
1727	Taq1	24	cgt	141.467	142	141.42	141.39	141.59	15 900 000	18 300 000	6 900 000	=-	\ (-)	(-)	-4
1728	Taq1	24	cgt	142.49	142	142.48	142.44	142.55	11 700 000	15 800 000	10 100 000	==	-	-	-4
1729	Taq1	25	cat	141.587	142	141.72	141.65	141.39	232.01	903.88	1 543.12	==	-	(-)	-4
1730	Taq1	25	cat	142.583	142	142.77	142.7	142.28	750.64	980.26	1 267.56	==	-	-	-4
1731	Taq1	30	cgt	141.5	142	141.57	141.53	141.4	5 700 000	3 500 000	5 700 000	==	-		-4
1732	Taq1	30	cgt	142.58	142	142.58	0	0	3 300 000	0	0	-=	\		-4
1733	Taq1	29	gca	181.89	182	0	0	181.89	0	0	4 100 000	=+	/		-4
1734	Taq1	29	gca	182.9	182	0	0	182.9	0	0	3 900 000	=+	/		-4
1735	Taq1	40	tgg	181.71	182	181.63	0	181.79	3 800 000	0	3 500 000	-+(=)	V		-4
1736	Hha1	41	ccc	229.483	230	229.5	229.47	229.48	8 100 000	38 800 000	140 800 000	=+	/ (-)		-4
1737	Hha1	41	ccc	230.377	230	230.35	230.4	230.38	10 900 000	145 700 000	699 400 000	=+	/ (-)		-4
1738	Hha1	44	cgg	60.04	60	0	0	60.04	0	0	92 100 000	=+	/		/(2)
1739	Taq1	12	agt	112.097	112	112.11	112.08	112.1	11 900 000	6 200 000	73 600 000	=+	/ (-)		/(2)
1740	Taq1	25	cat	111.765	112	111.7	111.83	0	648.28	1 133.03	0	=-	\		/(2)
1741	Taq1	25	cat	112.595	112	112.55	112.64	0	620.99	1 502.22	0	+-	A		/(2)
1742	Hha1	20	ctc	68.973	69	68.95	69.09	68.88	550.96	485.18	1 145.03	=+	/ (-)		-1
1743	Hha1	54	ttt	70.13	70	70.27	70.09	70.03	4 900 000	22 200 000	16 600 000	+=	/ (-)		-1
1744	Hha1	7	caa	118.12	118	0	118.09	118.15	0	3 100 000	3 500 000	+=	/	/	
1745	Hha1	7	caa	118.3	118	0	0	118.3	0	0	3 800 000	=+	/	/	
1746	Taq1	7	caa	118.215	118	0	118.31	118.12	0	4 000 000	5 700 000	+=	/	/	
1747	Hha1	4	aag	122.89	123	0	122.91	122.87	0	13 100 000	36 900 000	=+	/	/	
1748	Taq1	12	agt	123.133	123	123.16	123.15	123.09	4 800 000	3 000 000	7 900 000	=+	/ (-)	/	
1749	Hha1	10	atg	170.45	171	170.45	0	0	3 500 000	0	0	-=	\	\	\(5)
1750	Taq1	10	atg	170.505	171	170.38	170.63	0	3 400 000	3 100 000	0	=-	\	\	\(5)
1751	Hha1	10	atg	171.51	171	171.51	0	0	4 200 000	0	0	-=	\		\(5)
1752	Taq1	10	atg	171.21	171	171.21	0	0	3 200 000	0	0	-=	\		\(5)
1753	Taq1	10	atg	171.93	171	0	171.93	0	0	8 400 000	0	+-	A		\(5)
1754	Taq1	40	tgg	171.46	171	0	0	171.46	0	0	6 800 000	=+	/		\(5)
1755	Taq1	56	tga	322.42	321	322.45	322.39	0	5 300 000	6 900 000	0	=-	\		\(5)
1756	Hha1	27	acg	127.297	127	127.21	127.29	127.39	15 900 000	5 600 000	6 400 000	-=	\ (-)		\(2)
1757	Taq1	49	aaa	323.89	323	323.89	0	0	15 300 000	0	0	-=	\		\(2)
1758	Hha1	20	ctc	189.2	190	189.2	0	0	337.46	0	0	-=	\		\(3)
1759	Hha1	20	ctc	190.18	190	0	0	190.18	0	0	405.53	=+	/		\(3)
1760	Hha1	9	atc	214.92	215	214.79	215.05	0	4 300 000	4 000 000	0	=-	\		\(3)
1761	Hha1	9	atc	215.71	215	215.71	0	0	5 200 000	0	0	-=	\		\(3)
1762	Hha1	6	aga	232.65	234	232.68	0	232.62	9 400 000	0	3 300 000	-=(-)	\		\(3)
1763	Hha1	58	gta	128.243	129	128.27	128.25	128.21	15 800 000	12 100 000	17 300 000	==	-		\(6) A(5)
1764	Hha1	58	gta	129.233	129	129.24	129.25	129.21	6 600 000	40 500 000	10 200 000	+-	A		\(6) A(5)
1765	Taq1	48	ggg	132.387	133	132.18	132.66	132.32	2 212.38	408.26	2 071.32	-+	V		\(6) A(5)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
1723	RNCLK3PRT.CLK3	clk3	CLK3 protein		cat	gga	increased
1724	RNCLK3PRT.CLK3	clk3	CLK3 protein		cta	gaa	increased
1725	RNCLK3PRT.CLK3	clk3	CLK3 protein		cta	gaa	increased
1726	RATCOLLII.PE1	nc	collagen alpha 1 type II		ttc	cag	No change
1727	RATCOLLII.PE1	nc	collagen alpha 1 type II		cat	cgt	No change
1728	RATCOLLII.PE1	nc	collagen alpha 1 type II		cat	cgt	No change
1729	RATCOLLII.PE1	nc	collagen alpha 1 type II		cat	cgt	No change
1730	RATCOLLII.PE1	nc	collagen alpha 1 type II		cat	cgt	No change
1731	RATCOLLII.PE1	nc	collagen alpha 1 type II		cat	cgt	No change
1732	RATCOLLII.PE1	nc	collagen alpha 1 type II		cat	cgt	No change
1733	RATCOLLII.PE1	nc	collagen alpha 1 type II		tgg	gca	No change
1734	RATCOLLII.PE1	nc	collagen alpha 1 type II		tgg	gca	No change
1735	RATCOLLII.PE1	nc	collagen alpha 1 type II		tgg	gca	No change
1736	RATCOLLII.PE1	nc	collagen alpha 1 type II		gga	ccc	No change
1737	RATCOLLII.PE1	nc	collagen alpha 1 type II		gga	ccc	No change
1738	AY313450.P4HA3	P4ha3	collagen prolyl 4-hydroxylase alpha III subunit		cgg	ctc	decreased
1739	AY313450.P4HA3	P4ha3	collagen prolyl 4-hydroxylase alpha III subunit		cat	agt	decreased
1740	AY313450.P4HA3	P4ha3	collagen prolyl 4-hydroxylase alpha III subunit		cat	agt	decreased
1741	AY313450.P4HA3	P4ha3	collagen prolyl 4-hydroxylase alpha III subunit		cat	agt	decreased
1742	AY136824.CTHRC1	Cthrc1	collagen triple helix repeat-containing protein		ctc	ttt	No change
1743	AY136824.CTHRC1	Cthrc1	collagen triple helix repeat-containing protein		ctc	ttt	No change
1744	RATGP46CBP.GP46	gp46	collagen-binding protein		caa	agg	decreased
1745	RATGP46CBP.GP46	gp46	collagen-binding protein		caa	agg	decreased
1746	RATGP46CBP.GP46	gp46	collagen-binding protein		caa	agg	decreased
1747	AY149995.PE1	nc	complement component C4		aag	agt	decreased
1748	AY149995.PE1	nc	complement component C4		aag	agt	decreased
1749	AY230250.PE1	nc	complement factor 6		atg	tgg	increased
1750	AY230250.PE1	nc	complement factor 6		atg	tgg	increased
1751	AY230250.PE1	nc	complement factor 6		atg	tgg	increased
1752	AY230250.PE1	nc	complement factor 6		atg	tgg	increased
1753	AY230250.PE1	nc	complement factor 6		atg	tgg	increased
1754	AY230250.PE1	nc	complement factor 6		atg	tgg	increased
1755	AY230250.PE1	nc	complement factor 6		aac	tga	increased
1756	RNC1QB.PE1	nc	complement protein C1q beta chain precursor		agt	acg	increased
1757	RNC1QB.PE1	nc	complement protein C1q beta chain precursor		aaa	cgc	increased
1758	RATCXN33A.CXN-33	CXN-33	connexin		ctc	ctt	increased
1759	RATCXN33A.CXN-33	CXN-33	connexin		ctc	ctt	increased
1760	RATCXN33A.CXN-33	CXN-33	connexin		gtc	atc	increased
1761	RATCXN33A.CXN-33	CXN-33	connexin		gtc	atc	increased
1762	RATCXN33A.CXN-33	CXN-33	connexin		cag	aga	increased
1763	RNU87224.CASPR	Caspr	contactin associated protein		gta	tgc	increased
1764	RNU87224.CASPR	Caspr	contactin associated protein		gta	tgc	increased
1765	RNU87224.CASPR	Caspr	contactin associated protein		ggg	cgt	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
1766	Taq1	48	ggg	133.415	133	133.19	133.64	0	1 011.37	1 795.14	0	=-	\	\	\(6) A(5)
1767	Taq1	30	cgt	133.28	134	133.24	133.32	0	4 400 000	4 400 000	0	=-	\	\	\(6) A(5)
1768	Taq1	22	tcc	152.11	153	152.09	152.06	152.18	7 400 000	4 700 000	6 400 000	==	-		\(6) A(5)
1769	Taq1	22	tcc	152.57	153	0	152.57	0	0	3 000 000	0	+-	A		\(6) A(5)
1770	Taq1	22	tcc	153.17	153	0	0	153.17	0	0	9 900 000	=+	/		\(6) A(5)
1771	Hha1	22	tcc	153.445	153	0	153.65	153.24	0	6 200 000	3 100 000	+-	A		\(6) A(5)
1772	Taq1	22	tcc	153.625	153	153.61	153.64	0	22 200 000	18 200 000	0	=-	\		\(6) A(5)
1773	Taq1	39	agg	186.487	187	186.76	186.39	186.31	11 500 000	7 700 000	3 900 000	==	-		\(6) A(5)
1774	Taq1	39	agg	186.31	187	0	0	186.31	0	0	114.87	=+	/		\(6) A(5)
1775	Taq1	39	agg	187.38	187	187.52	187.24	0	6 200 000	40 100 000	0	+-	A		\(6) A(5)
1776	Taq1	39	agg	186.76	187	186.76	0	0	427.06	0	0	-=	\		\(6) A(5)
1777	Taq1	39	agg	187.52	187	187.52	0	0	230.24	0	0	-=	\	\	\(6) A(5)
1778	Taq1	39	agg	186.39	187	0	186.39	0	0	77.38	0	+-	A		\(6) A(5)
1779	Taq1	39	agg	187.24	187	0	187.24	0	0	403.01	0	+-	A		\(6) A(5)
1780	Taq1	49	aaa	187.55	188	187.55	0	0	14 100 000	0	0	-=	\	\	\(6) A(5)
1781	Taq1	49	aaa	188.285	188	188.37	188.2	0	41 600 000	18 100 000	0	-=	\		\(6) A(5)
1782	Hha1	40	tgg	201.08	202	0	201.08	0	0	6 200 000	0	+-	A		\(6) A(5)
1783	Hha1	40	tgg	202.96	202	202.96	0	0	4 200 000	0	0	-=	\		\(6) A(5)
1784	Taq1	9	atc	171.675	172	171.66	171.69	0	6 800 000	5 700 000	0	=-	\	\	
1785	Hha1	9	atc	171.78	172	171.68	171.88	0	5 600 000	5 500 000	0	=-	\	\	
1786	Taq1	11	act	204.33	205	0	0	204.33	0	0	5 600 000	=+	/	/	
1787	Hha1	11	act	204.5	205	0	0	204.5	0	0	3 500 000	=+	/	/	
1788	Taq1	64	gtt	97.34	97	97.3	97.26	97.46	14 000 000	12 900 000	14 000 000	==	-		\(4)
1789	Taq1	18	cct	174.815	175	174.79	174.84	0	12 100 000	15 700 000	0	=-	\		\(4)
1790	Taq1	18	cct	175.8	175	175.78	175.82	0	4 700 000	4 600 000	0	=-	\		\(4)
1791	Taq1	20	ctc	174.807	175	174.77	174.61	175.04	5 600 000	3 700 000	3 900 000	==	-		\(4)
1792	Taq1	20	ctc	175.59	175	0	175.59	0	0	6 600 000	0	+-	A		\(4)
1793	Hha1	6	aga	250.32	251	250.32	0	0	3 700 000	0	0	-=	\		\(4)
1794	Taq1	39	agg	249.96	251	0	249.96	0	0	9 400 000	0	+-	A		\(4)
1795	Taq1	39	agg	250.95	251	0	250.95	0	0	9 100 000	0	+-	A		\(4)
1796	Taq1	39	agg	251.575	251	251.54	251.61	0	5 000 000	8 300 000	0	=-	\		\(4)
1797	Taq1	39	agg	249.96	251	0	249.96	0	0	94.47	0	+-	A		\(4)
1798	Taq1	39	agg	250.95	251	0	250.95	0	0	91.45	0	+-	A		\(4)
1799	Taq1	39	agg	251.61	251	0	251.61	0	0	83.41	0	+-	A		\(4)
1800	Taq1	39	agg	251.54	251	251.54	0	0	185.68	0	0	-=	\		\(4)
1801	Taq1	45	gcc	273.6	275	273.6	0	0	7 500 000	0	0	-=	\		\(4)
1802	Taq1	45	gcc	274.97	275	274.97	0	0	6 300 000	0	0	-=	\		\(4)
1803	Hha1	33	agc	76.7	77	76.7	0	0	3 200 000	0	0	-=	\		\(3)
1804	Taq1	18	cct	126.43	127	0	0	126.43	0	0	7 900 000	=+	/		\(3)
1805	Taq1	18	cct	127.63	127	127.59	127.67	0	4 100 000	4 100 000	0	=-	\		\(3)
1806	Hha1	40	tgg	151.76	152	151.76	0	0	7 700 000	0	0	-=	\		\(3)
1807	Hha1	40	tgg	152.725	152	152.8	152.65	0	4 000 000	10 100 000	0	+-	A		\(3)
1808	Taq1	23	cga	104.377	105	104.3	104.35	104.48	16 900 000	9 300 000	9 300 000	==	-		-3

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
1766	RNU87224.CASPR	Caspr	contactin associated protein		ggg	cgt	increased
1767	RNU87224.CASPR	Caspr	contactin associated protein		ggg	cgt	increased
1768	RNU87224.CASPR	Caspr	contactin associated protein		gtg	tcc	increased
1769	RNU87224.CASPR	Caspr	contactin associated protein		gtg	tcc	increased
1770	RNU87224.CASPR	Caspr	contactin associated protein		gtg	tcc	increased
1771	RNU87224.CASPR	Caspr	contactin associated protein		gtg	tcc	increased
1772	RNU87224.CASPR	Caspr	contactin associated protein		gtg	tcc	increased
1773	RNU87224.CASPR	Caspr	contactin associated protein		aaa	agg	increased
1774	RNU87224.CASPR	Caspr	contactin associated protein		aaa	agg	increased
1775	RNU87224.CASPR	Caspr	contactin associated protein		aaa	agg	increased
1776	RNU87224.CASPR	Caspr	contactin associated protein		aaa	agg	increased
1777	RNU87224.CASPR	Caspr	contactin associated protein		aaa	agg	increased
1778	RNU87224.CASPR	Caspr	contactin associated protein		aaa	agg	increased
1779	RNU87224.CASPR	Caspr	contactin associated protein		aaa	agg	increased
1780	RNU87224.CASPR	Caspr	contactin associated protein		aaa	agg	increased
1781	RNU87224.CASPR	Caspr	contactin associated protein		aaa	agg	increased
1782	RNU87224.CASPR	Caspr	contactin associated protein		tgg	cca	increased
1783	RNU87224.CASPR	Caspr	contactin associated protein		tgg	cca	increased
1784	RNU08344.PE1	nc	copper-transporting ATPase		agg	atc	increased
1785	RNU08344.PE1	nc	copper-transporting ATPase		agg	atc	increased
1786	RNU08344.PE1	nc	copper-transporting ATPase		act	tga	decreased
1787	RNU08344.PE1	nc	copper-transporting ATPase		act	tga	decreased
1788	AF272892.PE1	nc	corneal wound healing related protein		gtt	gta	increased
1789	AF272892.PE1	nc	corneal wound healing related protein		ctc	cct	increased
1790	AF272892.PE1	nc	corneal wound healing related protein		ctc	cct	increased
1791	AF272892.PE1	nc	corneal wound healing related protein		ctc	cct	increased
1792	AF272892.PE1	nc	corneal wound healing related protein		ctc	cct	increased
1793	AF272892.PE1	nc	corneal wound healing related protein		agg	aga	increased
1794	AF272892.PE1	nc	corneal wound healing related protein		agg	aga	increased
1795	AF272892.PE1	nc	corneal wound healing related protein		agg	aga	increased
1796	AF272892.PE1	nc	corneal wound healing related protein		agg	aga	increased
1797	AF272892.PE1	nc	corneal wound healing related protein		agg	aga	increased
1798	AF272892.PE1	nc	corneal wound healing related protein		agg	aga	increased
1799	AF272892.PE1	nc	corneal wound healing related protein		agg	aga	increased
1800	AF272892.PE1	nc	corneal wound healing related protein		agg	aga	increased
1801	AF272892.PE1	nc	corneal wound healing related protein		gag	gcc	increased
1802	AF272892.PE1	nc	corneal wound healing related protein		gag	gcc	increased
1803	RNU33935.PE1	nc	corticotensin	*	tac	agc	increased
1804	RNU33935.PE1	nc	corticotensin	*	cct	ata	increased
1805	RNU33935.PE1	nc	corticotensin	*	cct	ata	increased
1806	RNU33935.PE1	nc	corticotensin	*	ggg	tgg	increased
1807	RNU33935.PE1	nc	corticotensin	*	ggg	tgg	increased
1808	AF092091.PE1	nc	cp431		cga	cgc	No change

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
1809	Taq1	23	cga	105.52	105	0	0	105.52	0	0	10 500 000	=+	/		-3
1810	Hha1	61	tct	127.86	128	127.89	127.74	127.95	11 100 000	5 600 000	3 700 000	-=	\ (-)		-3
1811	Hha1	61	tct	128.763	128	128.69	128.75	128.85	13 000 000	21 700 000	16 000 000	==	-		-3
1812	Hha1	44	cgg	156.1	157	0	156.1	0	0	3 500 000	0	+-	A		-3
1813	Hha1	44	cgg	157.135	157	157.06	157.21	0	3 600 000	8 100 000	0	+-	A		-3
1814	Hha1	44	cgg	157.73	157	0	157.73	0	0	4 700 000	0	+-	A		-3
1815	Hha1	26	ctg	158.155	158	0	158.2	158.11	0	3 200 000	3 100 000	+=	/		-3
1816	Hha1	26	ctg	158.87	158	158.87	0	0	3 500 000	0	0	-=	\		-3
1817	Taq1	64	gtt	213.44	214	213.43	213.41	213.48	3 200 000	5 100 000	3 600 000	==	-		-3
1818	Taq1	64	gtt	214.513	214	214.51	214.5	214.53	4 100 000	3 200 000	3 100 000	==	-		-3
1819	Taq1	44	cgg	98.92	99	98.69	0	99.15	249.97	0	1 300.15	=+(+)	/		/(2)
1820	Taq1	44	cgg	99.495	99	99.59	99.4	0	1 086.69	3 007.68	0	+-	A		/(2)
1821	Taq1	62	tgt	99.61	100	0	0	99.61	0	0	22 600 000	=+	/		/(2)
1822	Hha1	8	gaa	157.313	157	157.36	157.31	157.27	22 700 000	11 900 000	5 600 000	-=	\ (-)	\	
1823	Taq1	8	gaa	157.43	157	157.43	0	0	3 200 000	0	0	-=	\	\	
1824	Taq1	49	aaa	122.42	123	0	122.42	0	0	9 000 000	0	+-	A		A(2)
1825	Taq1	49	aaa	123.49	123	123.71	123.27	0	39 000 000	6 500 000	0	-=	\		A(2)
1826	Taq1	51	ata	122.36	123	0	122.54	122.18	0	18 300 000	62 200 000	=+	/		A(2)
1827	Taq1	51	ata	123.34	123	0	123.34	0	0	22 900 000	0	+-	A		A(2)
1828	Taq1	8	gaa	212.1	213	212.1	0	0	3 100 000	0	0	-=	\		\(3) A(3)
1829	Taq1	8	gaa	212.67	213	0	212.67	0	0	3 000 000	0	+-	A		\(3) A(3)
1830	Hha1	8	gaa	212.66	213	212.66	212.66	0	4 200 000	3 400 000	0	=-	\		\(3) A(3)
1831	Hha1	8	gaa	213.55	213	213.55	213.55	0	4 100 000	6 800 000	0	=-	\		\(3) A(3)
1832	Taq1	8	gaa	213.79	213	0	213.79	0	0	4 400 000	0	+-	A		\(3) A(3)
1833	Taq1	12	agt	212.365	213	212.38	212.35	0	3 900 000	5 700 000	0	=-	\		\(3) A(3)
1834	Taq1	12	agt	213.31	213	0	213.31	0	0	3 700 000	0	+-	A		\(3) A(3)
1835	Taq1	26	ctg	179.47	180	0	179.47	0	0	5 700 000	0	+-	A		/(2)
1836	Taq1	57	ctg	178.95	180	0	0	178.95	0	0	3 900 000	=+	/		/(2)
1837	Taq1	57	ctg	180.18	180	0	0	180.18	0	0	5 700 000	=+	/		/(2)
1838	Taq1	51	ata	180.573	181	180.25	180.74	180.73	29 300 000	8 200 000	4 200 000	-=	\ (-)		/(2)
1839	Taq1	51	ata	182.07	181	182	0	182.14	7 300 000	0	15 400 000	-+(+)	V (/)		/(2)
1840	Taq1	47	ggc	115.707	116	115.59	115.65	115.88	7 753.84	4 646.72	3 833.69	==	-		-3
1841	Hha1	25	cag	168.86	169	168.92	0	168.8	3 900 000	0	5 400 000	-+(=)	V		-3
1842	Hha1	25	cag	169.7	169	169.61	169.85	169.64	8 500 000	3 500 000	6 300 000	-=	\ (-)		-3
1843	Taq1	52	att	170.607	170	170.8	170.63	170.39	3 200 000	3 300 000	4 500 000	==	-		-3
1844	Taq1	7	caa	208.05	209	0	208.05	0	0	6 500 000	0	+-	A		\(3)
1845	Taq1	7	caa	209	209	209	0	0	5 500 000	0	0	-=	\		\(3)
1846	Hha1	7	caa	208.67	209	208.67	0	0	6 600 000	0	0	-=	\		\(3)
1847	Taq1	7	caa	209.04	209	0	209.04	0	0	10 100 000	0	+-	A		\(3)
1848	Hha1	7	caa	209.73	209	209.73	0	0	3 100 000	0	0	-=	\		\(3)
1849	Taq1	7	caa	208.05	209	0	208.05	0	0	6 500 000	0	+-	A		\(3)
1850	Taq1	7	caa	209	209	209	0	0	5 500 000	0	0	-=	\		\(3)
1851	Hha1	7	caa	208.67	209	208.67	0	0	6 600 000	0	0	-=	\		\(3)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
1809	AF092091.PE1	nc	cp431		cga	cgc	No change
1810	AF092091.PE1	nc	cp431		tct	aga	No change
1811	AF092091.PE1	nc	cp431		tct	aga	No change
1812	AF092091.PE1	nc	cp431		cgg	ctg	No change
1813	AF092091.PE1	nc	cp431		cgg	ctg	No change
1814	AF092091.PE1	nc	cp431		cgg	ctg	No change
1815	AF092091.PE1	nc	cp431		cgg	ctg	No change
1816	AF092091.PE1	nc	cp431		cgg	ctg	No change
1817	AF092091.PE1	nc	cp431		tgc	gtt	No change
1818	AF092091.PE1	nc	cp431		tgc	gtt	No change
1819	AF352572.CPI17	Cpi17	CPI17	*	cgg	tgt	decreased
1820	AF352572.CPI17	Cpi17	CPI17	*	cgg	tgt	decreased
1821	AF352572.CPI17	Cpi17	CPI17	*	cgg	tgt	decreased
1822	RATCKBU.CKB	CKB	creatine kinase-B		gaa	aga	increased
1823	RATCKBU.CKB	CKB	creatine kinase-B		gaa	aga	increased
1824	RNO238278.CRM1	crm1	CRM1 protein		ata	aaa	increased by mild
1825	RNO238278.CRM1	crm1	CRM1 protein		ata	aaa	increased by mild
1826	RNO238278.CRM1	crm1	CRM1 protein		ata	aaa	increased by mild
1827	RNO238278.CRM1	crm1	CRM1 protein		ata	aaa	increased by mild
1828	AB038038.CBP	cbp	Csk binding protein Cbp		gaa	agt	increased
1829	AB038038.CBP	cbp	Csk binding protein Cbp		gaa	agt	increased
1830	AB038038.CBP	cbp	Csk binding protein Cbp		gaa	agt	increased
1831	AB038038.CBP	cbp	Csk binding protein Cbp		gaa	agt	increased
1832	AB038038.CBP	cbp	Csk binding protein Cbp		gaa	agt	increased
1833	AB038038.CBP	cbp	Csk binding protein Cbp		gaa	agt	increased
1834	AB038038.CBP	cbp	Csk binding protein Cbp		gaa	agt	increased
1835	AF190256.PE1	nc	CTP:phosphocholine cytidylyltransferase		ctg	ata	decreased
1836	AF190256.PE1	nc	CTP:phosphocholine cytidylyltransferase		ctg	ata	decreased
1837	AF190256.PE1	nc	CTP:phosphocholine cytidylyltransferase		ctg	ata	decreased
1838	AF190256.PE1	nc	CTP:phosphocholine cytidylyltransferase		ctg	ata	decreased
1839	AF190256.PE1	nc	CTP:phosphocholine cytidylyltransferase		ctg	ata	decreased
1840	RNU21101.PDE2A2	PDE2A2	cyclic GMP stimulated phosphodiesterase		gat	ggc	No change
1841	RNU21101.PDE2A2	PDE2A2	cyclic GMP stimulated phosphodiesterase		cag	att	No change
1842	RNU21101.PDE2A2	PDE2A2	cyclic GMP stimulated phosphodiesterase		cag	att	No change
1843	RNU21101.PDE2A2	PDE2A2	cyclic GMP stimulated phosphodiesterase		cag	att	No change
1844	AB057409.RNPDE7B	RNPDE7B	cyclic nucleotide phosphodiesterase 7B1		aca	caa	increased
1845	AB057409.RNPDE7B	RNPDE7B	cyclic nucleotide phosphodiesterase 7B1		aca	caa	increased
1846	AB057409.RNPDE7B	RNPDE7B	cyclic nucleotide phosphodiesterase 7B1		aca	caa	increased
1847	AB057409.RNPDE7B	RNPDE7B	cyclic nucleotide phosphodiesterase 7B1		aca	caa	increased
1848	AB057409.RNPDE7B	RNPDE7B	cyclic nucleotide phosphodiesterase 7B1		aca	caa	increased
1849	AB057410.RNPDE7B	RNPDE7B	cyclic nucleotide phosphodiesterase 7B3		aca	caa	increased
1850	AB057410.RNPDE7B	RNPDE7B	cyclic nucleotide phosphodiesterase 7B3		aca	caa	increased
1851	AB057410.RNPDE7B	RNPDE7B	cyclic nucleotide phosphodiesterase 7B3		aca	caa	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
1852	Taq1	7	caa	209.04	209	0	209.04	0	0	10 100 000	0	+-	A		\(3)
1853	Hha1	7	caa	209.73	209	209.73	0	0	3 100 000	0	0	-=	\		\(3)
1854	Taq1	7	caa	208.05	209	0	208.05	0	0	6 500 000	0	+-	A		\(3)
1855	Taq1	7	caa	209	209	209	0	0	5 500 000	0	0	-=	\		\(3)
1856	Hha1	7	caa	208.67	209	208.67	0	0	6 600 000	0	0	-=	\		\(3)
1857	Taq1	7	caa	209.04	209	0	209.04	0	0	10 100 000	0	+-	A		\(3)
1858	Hha1	7	caa	209.73	209	209.73	0	0	3 100 000	0	0	-=	\		\(3)
1859	Hha1	3	aac	190.345	190	190.34	190.35	0	4 500 000	4 900 000	0	=-	\	\	
1860	Taq1	18	cct	190.3	190	190.41	190.19	0	3 000 000	4 900 000	0	=-	\	\	
1861	Hha1	39	agg	106.243	106	106.2	106.36	106.17	1 217	12 305.21	14 347.33	+=	/ (-)		-2
1862	Hha1	58	gta	105.933	106	105.87	106.03	105.9	4 300 000	7 500 000	6 500 000	==	-		-2
1863	Hha1	39	agg	106.243	106	106.2	106.36	106.17	1 217	12 305.21	14 347.33	+=	/ (-)		-2
1864	Hha1	58	gta	105.933	106	105.87	106.03	105.9	4 300 000	7 500 000	6 500 000	==	-		-2
1865	Hha1	33	agc	87.413	87	87.37	87.58	87.29	8 100 000	13 600 000	18 100 000	==	-		-2
1866	Hha1	41	ccc	109.51	110	109.75	109.29	109.49	11 900 000	3 000 000	5 900 000	-=	\ (-)		-2
1867	Hha1	41	ccc	110.295	110	0	110.09	110.5	0	4 800 000	16 400 000	=+	/		-2
1868	Hha1	41	ccc	109.51	110	109.75	109.29	109.49	11 900 000	3 000 000	5 900 000	-=	\ (-)		-2
1869	Hha1	41	ccc	110.295	110	0	110.09	110.5	0	4 800 000	16 400 000	=+	/		-2
1870	Taq1	19	cac	155.123	156	155.12	155.07	155.18	8 900 000	6 100 000	16 500 000	=+	/ (-)		\(3) /(2)
1871	Taq1	19	cac	156.16	156	156.11	156.17	156.2	11 800 000	5 900 000	3 500 000	-=	\ (-)		\(3) /(2)
1872	Taq1	54	ttt	156.845	157	156.84	156.85	0	1 602.33	1 599.43	0	=-	\		\(3) /(2)
1873	Taq1	54	ttt	157.72	157	0	0	157.72	0	0	1 006.42	=+	/		\(3) /(2)
1874	Hha1	40	tgg	238.845	240	238.71	238.98	0	3 900 000	3 200 000	0	=-	\		\(3) /(2)
1875	Hha1	40	tgg	239.97	240	239.97	0	0	4 500 000	0	0	-=	\		\(3) /(2)
1876	Hha1	40	tgg	241.28	240	0	241.28	0	0	3 300 000	0	+-	A		\(3) /(2)
1877	Hha1	11	act	173.71	173	173.62	173.62	173.89	10 000 000	8 900 000	5 100 000	==	-	-	
1878	Taq1	11	act	173.763	173	173.78	173.76	173.75	8 400 000	13 500 000	16 100 000	==	-	-	
1879	Hha1	11	act	173.71	173	173.62	173.62	173.89	10 000 000	8 900 000	5 100 000	==	-	-	
1880	Taq1	11	act	173.763	173	173.78	173.76	173.75	8 400 000	13 500 000	16 100 000	==	-	-	
1881	Hha1	20	ctc	70.987	71	70.8	71.18	70.98	977.96	786.78	918.41	==	-		-2
1882	Hha1	44	cgg	79.327	79	79.34	79.27	79.37	37 600 000	23 400 000	20 600 000	==	-		-2
1883	Hha1	20	ctc	70.987	71	70.8	71.18	70.98	977.96	786.78	918.41	==	-		-2
1884	Hha1	44	cgg	79.327	79	79.34	79.27	79.37	37 600 000	23 400 000	20 600 000	==	-		-2
1885	Hha1	26	ctg	97.47	98	0	97.47	0	0	4 100 000	0	+-	A		\(5)
1886	Hha1	26	ctg	98.155	98	98.13	98.18	0	5 200 000	3 900 000	0	=-	\		\(5)
1887	Hha1	39	agg	107.28	107	0	107.46	107.1	0	656.75	1 257.32	++	/		\(5)
1888	Hha1	20	ctc	139.71	140	139.73	0	139.69	550.96	0	477.09	-+(=)	V		\(5)
1889	Hha1	62	tgt	140.06	140	140.06	0	0	3 000 000	0	0	-=	\		\(5)
1890	Hha1	26	ctg	186.76	187	0	186.76	0	0	3 000 000	0	+-	A		\(5)
1891	Hha1	26	ctg	188.1	187	188.1	0	0	3 500 000	0	0	-=	\		\(5)
1892	Hha1	60	ttg	206.48	206	206.48	0	0	3 000 000	0	0	-=	\		\(5)
1893	Hha1	60	ttg	207.21	206	207.19	207.23	0	4 400 000	3 000 000	0	=-	\		\(5)
1894	Taq1	20	ctc	208.35	209	208.35	0	0	3 200 000	0	0	-=	\		\(5)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
1852	AB057410.RNPDE7B	RNPDE7B	cyclic nucleotide phosphodiesterase 7B3		aca	caa	increased
1853	AB057410.RNPDE7B	RNPDE7B	cyclic nucleotide phosphodiesterase 7B3		aca	caa	increased
1854	AB057411.RNPDE7B	RNPDE7B	cyclic nucleotide phosphodiesterase 7B4		aca	caa	increased
1855	AB057411.RNPDE7B	RNPDE7B	cyclic nucleotide phosphodiesterase 7B4		aca	caa	increased
1856	AB057411.RNPDE7B	RNPDE7B	cyclic nucleotide phosphodiesterase 7B4		aca	caa	increased
1857	AB057411.RNPDE7B	RNPDE7B	cyclic nucleotide phosphodiesterase 7B4		aca	caa	increased
1858	AB057411.RNPDE7B	RNPDE7B	cyclic nucleotide phosphodiesterase 7B4		aca	caa	increased
1859	AF030091.PE1	nc	cyclin ania-6a		cct	aac	increased
1860	AF030091.PE1	nc	cyclin ania-6a		cct	aac	increased
1861	AB042564.PE1	nc	cyclin D1		gta	agg	No change
1862	AB042564.PE1	nc	cyclin D1		gta	agg	No change
1863	RNCCND1.CCND1	CCND1	CYCLIN D1		gta	agg	No change
1864	RNCCND1.CCND1	CCND1	CYCLIN D1		gta	agg	No change
1865	RATCLND3.PE1	nc	cyclin D3		aac	agc	No change
1866	RATCLND3.PE1	nc	cyclin D3		ccc	tcc	No change
1867	RATCLND3.PE1	nc	cyclin D3		ccc	tcc	No change
1868	RATCLND3.PE1	nc	cyclin D3		ccc	tcc	No change
1869	RATCLND3.PE1	nc	cyclin D3		ccc	tcc	No change
1870	RNCYCG.PE1	nc	cyclin G		cac	ttt	increased
1871	RNCYCG.PE1	nc	cyclin G		cac	ttt	increased
1872	RNCYCG.PE1	nc	cyclin G		cac	ttt	increased
1873	RNCYCG.PE1	nc	cyclin G		cac	ttt	increased
1874	RNCYCG.PE1	nc	cyclin G		tgg	cca	increased
1875	RNCYCG.PE1	nc	cyclin G		tgg	cca	increased
1876	RNCYCG.PE1	nc	cyclin G		tgg	cca	increased
1877	AF474976.CDKN2A	Cdkn2a	cyclin-dependent kinase inhibitor 2a p16Ink4a	*	act	gcg	No change
1878	AF474976.CDKN2A	Cdkn2a	cyclin-dependent kinase inhibitor 2a p16Ink4a	*	act	gcg	No change
1879	AF474977.CDKN2A	Cdkn2a	cyclin-dependent kinase inhibitor 2a p16Ink4a	*	act	gcg	No change
1880	AF474977.CDKN2A	Cdkn2a	cyclin-dependent kinase inhibitor 2a p16Ink4a	*	act	gcg	No change
1881	AF474978.CDKN2B	Cdkn2b	cyclin-dependent kinase inhibitor 2b	*	aga	ctc	No change
1882	AF474978.CDKN2B	Cdkn2b	cyclin-dependent kinase inhibitor 2b	*	ggg	cgg	No change
1883	AF474979.CDKN2B	Cdkn2b	cyclin-dependent kinase inhibitor 2b	*	aga	ctc	No change
1884	AF474979.CDKN2B	Cdkn2b	cyclin-dependent kinase inhibitor 2b	*	ggg	cgg	No change
1885	RNO488291.PE1	p57kip2	cyclin-dependent kinase inhibitor p57		ctg	atc	increased
1886	RNO488291.PE1	p57kip2	cyclin-dependent kinase inhibitor p57		ctg	atc	increased
1887	RNO488291.PE1	p57kip2	cyclin-dependent kinase inhibitor p57		agg	cca	increased
1888	RNO488291.PE1	p57kip2	cyclin-dependent kinase inhibitor p57		tgt	ctc	increased
1889	RNO488291.PE1	p57kip2	cyclin-dependent kinase inhibitor p57		tgt	ctc	increased
1890	RNO488291.PE1	p57kip2	cyclin-dependent kinase inhibitor p57		ctg	ccc	increased
1891	RNO488291.PE1	p57kip2	cyclin-dependent kinase inhibitor p57		ctg	ccc	increased
1892	RNO488291.PE1	p57kip2	cyclin-dependent kinase inhibitor p57		aga	ttg	increased
1893	RNO488291.PE1	p57kip2	cyclin-dependent kinase inhibitor p57		aga	ttg	increased
1894	RNO488291.PE1	p57kip2	cyclin-dependent kinase inhibitor p57		ctc	ccg	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
1895	Hha1	15	tac	135.407	136	135.34	135.47	135.41	22 200 000	10 000 000	3 600 000	-=	\ (-)		\(2)
1896	Hha1	15	tac	135.473	136	135.54	135.47	135.41	4 324.4	2 575.32	782.94	==	-		\(2)
1897	Hha1	15	tac	136.54	136	136.54	0	0	598.53	0	0	-=	\		\(2)
1898	Hha1	33	agc	135.22	136	0	135.32	135.12	0	3 000 000	3 600 000	+=	/		\(2)
1899	Taq1	39	agg	191.385	192	191.6	191.17	0	8 300 000	27 900 000	0	+-	A		\(2)
1900	Taq1	39	agg	192.71	192	192.71	0	0	10 400 000	0	0	-=	\		\(2)
1901	Taq1	39	agg	191.385	192	191.6	191.17	0	308.22	280.4	0	=-	\		\(2)
1902	Taq1	39	agg	192.71	192	192.71	0	0	386.21	0	0	-=	\		\(2)
1903	Hha1	15	tac	135.407	136	135.34	135.47	135.41	22 200 000	10 000 000	3 600 000	-=	\ (-)		\(2)
1904	Hha1	15	tac	135.473	136	135.54	135.47	135.41	4 324.4	2 575.32	782.94	==	-		\(2)
1905	Hha1	15	tac	136.54	136	136.54	0	0	598.53	0	0	-=	\		\(2)
1906	Hha1	33	agc	135.22	136	0	135.32	135.12	0	3 000 000	3 600 000	+=	/		\(2)
1907	Taq1	39	agg	191.385	192	191.6	191.17	0	8 300 000	27 900 000	0	+-	A		\(2)
1908	Taq1	39	agg	192.71	192	192.71	0	0	10 400 000	0	0	-=	\		\(2)
1909	Taq1	39	agg	191.385	192	191.6	191.17	0	308.22	280.4	0	=-	\		\(2)
1910	Taq1	39	agg	192.71	192	192.71	0	0	386.21	0	0	-=	\		\(2)
1911	Taq1	22	tcc	108.59	109	0	0	108.59	0	0	3 700 000	=+	/	/	/(4)
1912	Hha1	22	tcc	108.61	109	0	0	108.61	0	0	8 500 000	=+	/	/	/(4)
1913	Taq1	22	tcc	109.587	109	109.54	109.63	109.59	7 500 000	6 900 000	8 100 000	==	-		/(4)
1914	Hha1	25	cag	108.9	109	108.89	0	108.91	20 300 000	0	7 100 000	-=(-)	\		/(4)
1915	Hha1	9	atc	208.77	210	0	208.93	208.61	0	3 300 000	3 900 000	+=	/		/(4)
1916	Hha1	9	atc	210.94	210	210.93	210.95	0	7 800 000	3 500 000	0	-=	\		/(4)
1917	Taq1	12	agt	209.28	210	0	209.28	209.28	0	3 600 000	3 500 000	+=	/		/(4)
1918	Taq1	12	agt	210.343	210	210.43	210.24	210.36	4 000 000	4 500 000	3 000 000	==	-		/(4)
1919	Hha1	6	aga	126.475	127	126.51	0	126.44	89 200 000	0	7 100 000	-=(-)	\		/(3)
1920	Hha1	6	aga	127.097	127	127.18	127.06	127.05	30 600 000	3 500 000	5 400 000	-=	\ (-)		/(3)
1921	Hha1	6	aga	127.6	127	0	127.54	127.66	0	3 100 000	6 300 000	++	/		/(3)
1922	Hha1	9	atc	126.45	127	0	0	126.45	0	0	4 400 000	=+	/		/(3)
1923	Taq1	9	atc	127.09	127	0	0	127.09	0	0	12 500 000	=+	/		/(3)
1924	Hha1	9	atc	127.14	127	127.14	0	0	6 500 000	0	0	-=	\		/(3)
1925	Hha1	4	aag	98.515	99	98.75	98.28	0	4 300 000	6 600 000	0	=-	\		\(2)
1926	Hha1	4	aag	98.99	99	0	98.99	0	0	4 500 000	0	+-	A		\(2)
1927	Hha1	3	aac	281.67	280	281.67	0	0	3 000 000	0	0	-=	\		\(2)
1928	Hha1	39	agg	63.33	63	63.42	63.39	63.18	1 656.89	674.66	1 318.35	-=	\ (-)		\(4)
1929	Taq1	21	acc	214.61	215	214.61	0	0	7 500 000	0	0	-=	\		\(4)
1930	Hha1	21	acc	214.53	215	214.53	0	0	4 100 000	0	0	-=	\		\(4)
1931	Hha1	21	acc	215.23	215	0	215.23	0	0	3 200 000	0	+-	A		\(4)
1932	Hha1	21	acc	216	215	0	0	216	0	0	3 500 000	=+	/		\(4)
1933	Taq1	21	acc	216.27	215	216.27	0	0	7 200 000	0	0	-=	\		\(4)
1934	Hha1	39	agg	63.33	63	63.42	63.39	63.18	1 656.89	674.66	1 318.35	-=	\ (-)		\(4)
1935	Taq1	21	acc	214.61	215	214.61	0	0	7 500 000	0	0	-=	\		\(4)
1936	Hha1	21	acc	214.53	215	214.53	0	0	4 100 000	0	0	-=	\		\(4)
1937	Hha1	21	acc	215.23	215	0	215.23	0	0	3 200 000	0	+-	A		\(4)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
1895	RRU03388.PE1	nc	cyclooxygenase 1		tac	agc	increased
1896	RRU03388.PE1	nc	cyclooxygenase 1		tac	agc	increased
1897	RRU03388.PE1	nc	cyclooxygenase 1		tac	agc	increased
1898	RRU03388.PE1	nc	cyclooxygenase 1		tac	agc	increased
1899	RRU03388.PE1	nc	cyclooxygenase 1		agg	ggc	increased
1900	RRU03388.PE1	nc	cyclooxygenase 1		agg	ggc	increased
1901	RRU03388.PE1	nc	cyclooxygenase 1		agg	ggc	increased
1902	RRU03388.PE1	nc	cyclooxygenase 1		agg	ggc	increased
1903	S67721.COX-1	COX-1	cyclooxygenase isoform		tac	agc	increased
1904	S67721.COX-1	COX-1	cyclooxygenase isoform		tac	agc	increased
1905	S67721.COX-1	COX-1	cyclooxygenase isoform		tac	agc	increased
1906	S67721.COX-1	COX-1	cyclooxygenase isoform		tac	agc	increased
1907	S67721.COX-1	COX-1	cyclooxygenase isoform		agg	ggc	increased
1908	S67721.COX-1	COX-1	cyclooxygenase isoform		agg	ggc	increased
1909	S67721.COX-1	COX-1	cyclooxygenase isoform		agg	ggc	increased
1910	S67721.COX-1	COX-1	cyclooxygenase isoform		agg	ggc	increased
1911	RNU41164.RKR1	rKr1	Cys2/His2 zinc finger protein		cag	tcc	decreased
1912	RNU41164.RKR1	rKr1	Cys2/His2 zinc finger protein		cag	tcc	decreased
1913	RNU41164.RKR1	rKr1	Cys2/His2 zinc finger protein		cag	tcc	decreased
1914	RNU41164.RKR1	rKr1	Cys2/His2 zinc finger protein		cag	tcc	decreased
1915	RNU41164.RKR1	rKr1	Cys2/His2 zinc finger protein		agt	atc	decreased
1916	RNU41164.RKR1	rKr1	Cys2/His2 zinc finger protein		agt	atc	decreased
1917	RNU41164.RKR1	rKr1	Cys2/His2 zinc finger protein		agt	atc	decreased
1918	RNU41164.RKR1	rKr1	Cys2/His2 zinc finger protein		agt	atc	decreased
1919	S48988.CRP-1	CRP-1	cystatin-related protein		aga	atc	decreased
1920	S48988.CRP-1	CRP-1	cystatin-related protein		aga	atc	decreased
1921	S48988.CRP-1	CRP-1	cystatin-related protein		aga	atc	decreased
1922	S48988.CRP-1	CRP-1	cystatin-related protein		aga	atc	decreased
1923	S48988.CRP-1	CRP-1	cystatin-related protein		aga	atc	decreased
1924	S48988.CRP-1	CRP-1	cystatin-related protein		aga	atc	decreased
1925	D83479S3.PE1	nc	cysteine dioxygenase		gta	aag	increased
1926	D83479S3.PE1	nc	cysteine dioxygenase		gta	aag	increased
1927	D83479S3.PE1	nc	cysteine dioxygenase		aac	tgt	increased
1928	RNCSD.CSD	CSD	cysteine sulfinate decarboxylase		agg	cac	increased
1929	RNCSD.CSD	CSD	cysteine sulfinate decarboxylase		acc	tgc	increased
1930	RNCSD.CSD	CSD	cysteine sulfinate decarboxylase		acc	tgc	increased
1931	RNCSD.CSD	CSD	cysteine sulfinate decarboxylase		acc	tgc	increased
1932	RNCSD.CSD	CSD	cysteine sulfinate decarboxylase		acc	tgc	increased
1933	RNCSD.CSD	CSD	cysteine sulfinate decarboxylase		acc	tgc	increased
1934	RATCSADC.PE1	nc	cysteine sulfinic acid decarboxylase		agg	cac	increased
1935	RATCSADC.PE1	nc	cysteine sulfinic acid decarboxylase		acc	tgc	increased
1936	RATCSADC.PE1	nc	cysteine sulfinic acid decarboxylase		acc	tgc	increased
1937	RATCSADC.PE1	nc	cysteine sulfinic acid decarboxylase		acc	tgc	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
1938	Hha1	21	acc	216	215	0	0	216	0	0	3 500 000	=+	/		\(4)
1939	Taq1	21	acc	216.27	215	216.27	0	0	7 200 000	0	0	-=	\		\(4)
1940	Hha1	39	agg	63.33	63	63.42	63.39	63.18	1 656.89	674.66	1 318.35	-=	\ (-)		\(4)
1941	Taq1	21	acc	214.61	215	214.61	0	0	7 500 000	0	0	-=	\		\(4)
1942	Hha1	21	acc	214.53	215	214.53	0	0	4 100 000	0	0	-=	\		\(4)
1943	Hha1	21	acc	215.23	215	0	215.23	0	0	3 200 000	0	+-	A		\(4)
1944	Hha1	21	acc	216	215	0	0	216	0	0	3 500 000	=+	/		\(4)
1945	Taq1	21	acc	216.27	215	216.27	0	0	7 200 000	0	0	-=	\		\(4)
1946	Hha1	4	aag	184.14	185	0	184.18	184.1	0	3 700 000	5 200 000	+=	/	/	/(2)
1947	Hha1	4	aag	185.06	185	0	185.06	0	0	3 000 000	0	+-	A		/(2)
1948	Hha1	4	aag	186.1	185	0	186.14	186.06	0	4 500 000	4 700 000	+=	/		/(2)
1949	Taq1	14	gat	184.14	185	0	0	184.14	0	0	4 100 000	=+	/	/	/(2)
1950	Taq1	14	gat	185.15	185	0	0	185.15	0	0	3 000 000	=+	/		/(2)
1951	Hha1	6	aga	221.83	223	221.83	0	0	9 100 000	0	0	-=	\		\(2)
1952	Hha1	25	cag	222	223	0	222	0	0	3 100 000	0	+-	A		\(2)
1953	Hha1	25	cag	222.81	223	222.89	222.76	222.78	19 200 000	9 400 000	10 600 000	-=	\ (-)		\(2)
1954	Hha1	25	cag	223.873	223	223.9	223.86	223.86	293 900 000	127 000 000	238 000 000	-=	\ (-)		\(2)
1955	Hha1	6	aga	221.83	223	221.83	0	0	9 100 000	0	0	-=	\		\(2)
1956	Hha1	25	cag	222	223	0	222	0	0	3 100 000	0	+-	A		\(2)
1957	Hha1	25	cag	222.81	223	222.89	222.76	222.78	19 200 000	9 400 000	10 600 000	-=	\ (-)		\(2)
1958	Hha1	25	cag	223.873	223	223.9	223.86	223.86	293 900 000	127 000 000	238 000 000	-=	\ (-)		\(2)
1959	Hha1	56	tga	110.023	110	110.19	110.02	109.86	155.27	1 111.84	1 206.68	+=	/ (-)		-1
1960	Hha1	26	ctg	136.21	137	0	0	136.21	0	0	3 600 000	=+	/		-1
1961	Hha1	26	ctg	137.165	137	0	137.17	137.16	0	4 000 000	3 300 000	+=	/		-1
1962	Hha1	59	ttc	165.58	165	165.44	165.5	165.8	166.4	135.1	85.37	==	-		-1
1963	Hha1	39	agg	66.61	67	0	66.57	66.65	0	1 629.94	2 937.82	+=	/		/(3)
1964	Hha1	54	ttt	68.19	68	68.18	68.28	68.11	7 500 000	3 900 000	13 100 000	=+	/ (-)		/(3)
1965	Hha1	26	ctg	223.743	225	223.77	223.71	223.75	5 400 000	3 100 000	9 800 000	=+	/ (-)		/(3)
1966	Hha1	26	ctg	224.91	225	0	0	224.91	0	0	4 000 000	=+	/		/(3)
1967	Hha1	26	ctg	225.8	225	0	0	225.8	0	0	4 300 000	=+	/		/(3)
1968	Hha1	60	ttg	224.92	225	0	224.92	0	0	3 000 000	0	+-	A		/(3)
1969	Hha1	12	agt	177.05	178	177.09	177	177.06	1 887.28	2 493.88	3 047.09	==	-		-2
1970	Hha1	61	tct	177.603	178	177.48	177.83	177.5	17 000 000	8 100 000	4 700 000	-=	\ (-)		-2
1971	Hha1	39	agg	66.61	67	0	66.57	66.65	0	1 629.94	2 937.82	+=	/		-1
1972	Hha1	54	ttt	68.19	68	68.18	68.28	68.11	7 500 000	3 900 000	13 100 000	=+	/ (-)		-1
1973	Taq1	18	cct	165.523	166	165.51	165.56	165.5	11 700 000	7 400 000	5 500 000	==	-		-1
1974	Taq1	18	cct	166.56	166	166.48	166.64	0	5 200 000	5 300 000	0	=-	\		-1
1975	Taq1	41	ccc	132.21	133	0	0	132.21	0	0	3 500 000	=+	/		/(2)
1976	Taq1	41	ccc	132.75	133	0	0	132.75	0	0	3 100 000	=+	/		/(2)
1977	Taq1	41	ccc	133.73	133	0	0	133.73	0	0	3 500 000	=+	/		/(2)
1978	Taq1	27	acg	133.27	134	0	0	133.27	0	0	7 700 000	=+	/		/(2)
1979	Taq1	27	acg	134.45	134	134.59	134.55	134.21	3 600 000	3 700 000	3 300 000	==	-		/(2)
1980	Hha1	6	aga	281.87	283	281.87	0	0	3 300 000	0	0	-=	\		/(2)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
1938	RATCSADC.PE1	nc	cysteine sulfinic acid decarboxylase		acc	tgc	increased
1939	RATCSADC.PE1	nc	cysteine sulfinic acid decarboxylase		acc	tgc	increased
1940	RNO132661.PE1	nc	cysteine-sulfinate decarboxylase		agg	cac	increased
1941	RNO132661.PE1	nc	cysteine-sulfinate decarboxylase		acc	tgc	increased
1942	RNO132661.PE1	nc	cysteine-sulfinate decarboxylase		acc	tgc	increased
1943	RNO132661.PE1	nc	cysteine-sulfinate decarboxylase		acc	tgc	increased
1944	RNO132661.PE1	nc	cysteine-sulfinate decarboxylase		acc	tgc	increased
1945	RNO132661.PE1	nc	cysteine-sulfinate decarboxylase		acc	tgc	increased
1946	RNU82623.PE1	nc	cytocentrin		gat	aag	decreased
1947	RNU82623.PE1	nc	cytocentrin		gat	aag	decreased
1948	RNU82623.PE1	nc	cytocentrin		gat	aag	decreased
1949	RNU82623.PE1	nc	cytocentrin		gat	aag	decreased
1950	RNU82623.PE1	nc	cytocentrin		gat	aag	decreased
1951	AF007108.PE1	nc	cytochrome b5	*	aga	cag	increased
1952	AF007108.PE1	nc	cytochrome b5	*	aga	cag	increased
1953	AF007108.PE1	nc	cytochrome b5	*	aga	cag	increased
1954	AF007108.PE1	nc	cytochrome b5	*	aga	cag	increased
1955	RATCYTB5.PE1	nc	cytochrome b5 precursor	*	aga	cag	increased
1956	RATCYTB5.PE1	nc	cytochrome b5 precursor	*	aga	cag	increased
1957	RATCYTB5.PE1	nc	cytochrome b5 precursor	*	aga	cag	increased
1958	RATCYTB5.PE1	nc	cytochrome b5 precursor	*	aga	cag	increased
1959	RATMTCYPCH.PE1	P450C27	cytochrome P450		tga	tag	No change
1960	RATMTCYPCH.PE1	P450C27	cytochrome P450		ctg	ctg	No change
1961	RATMTCYPCH.PE1	P450C27	cytochrome P450		ctg	ctg	No change
1962	RATMTCYPCH.PE1	P450C27	cytochrome P450		ttc	ggt	No change
1963	RATCYP45Z.PE1	nc	cytochrome P-450	*	ttt	agg	decreased
1964	RATCYP45Z.PE1	nc	cytochrome P-450	*	ttt	agg	decreased
1965	RATCYP45Z.PE1	nc	cytochrome P-450	*	ctg	ttg	decreased
1966	RATCYP45Z.PE1	nc	cytochrome P-450	*	ctg	ttg	decreased
1967	RATCYP45Z.PE1	nc	cytochrome P-450	*	ctg	ttg	decreased
1968	RATCYP45Z.PE1	nc	cytochrome P-450	*	ctg	ttg	decreased
1969	D17343S7.CYP2B15	CYP2B15	cytochrome P450 2B15		agt	tct	No change
1970	D17343S7.CYP2B15	CYP2B15	cytochrome P450 2B15		agt	tct	No change
1971	RNCYP2B5.CYP2B3	CYP2B3	cytochrome P450 2B3		ttt	agg	No change
1972	RNCYP2B5.CYP2B3	CYP2B3	cytochrome P450 2B3		ttt	agg	No change
1973	RNCYP2B5.CYP2B3	CYP2B3	cytochrome P450 2B3		cct	gga	No change
1974	RNCYP2B5.CYP2B3	CYP2B3	cytochrome P450 2B3		cct	gga	No change
1975	AF368269.PE1	nc	cytochrome P450 monooxygenase CYP2T1		acg	ccc	decreased
1976	AF368269.PE1	nc	cytochrome P450 monooxygenase CYP2T1		acg	ccc	decreased
1977	AF368269.PE1	nc	cytochrome P450 monooxygenase CYP2T1		acg	ccc	decreased
1978	AF368269.PE1	nc	cytochrome P450 monooxygenase CYP2T1		acg	ccc	decreased
1979	AF368269.PE1	nc	cytochrome P450 monooxygenase CYP2T1		acg	ccc	decreased
1980	AF368269.PE1	nc	cytochrome P450 monooxygenase CYP2T1		gct	aga	decreased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
1981	Hha1	6	aga	282.95	283	282.95	0	0	3 700 000	0	0	-=	\		/(2)
1982	Hha1	6	aga	283.56	283	283.56	0	0	3 500 000	0	0	-=	\		/(2)
1983	Hha1	6	aga	283.76	283	283.76	0	0	3 500 000	0	0	-=	\		/(2)
1984	Hha1	6	aga	283.93	283	283.93	0	0	3 400 000	0	0	-=	\		/(2)
1985	Hha1	58	gta	115.933	116	115.92	115.94	115.94	5 600 000	9 000 000	29 300 000	=+	/ (-)		-1,5
1986	Hha1	59	ttc	165.58	165	165.44	165.5	165.8	166.4	135.1	85.37	==	-		-1,5
1987	Hha1	26	ctg	182.527	183	182.41	182.64	182.53	6 200 000	5 900 000	19 200 000	=+	/ (-)		-1,5
1988	Hha1	26	ctg	183.527	183	183.5	183.54	183.54	69 500 000	75 900 000	220 900 000	=+	/ (-)		-1,5
1989	Taq1	31	gac	102.457	103	102.55	102.37	102.45	8 400 000	3 300 000	87 800 000	=+	/ (-)		\(7)
1990	Taq1	31	gac	103.36	103	0	0	103.36	0	0	17 800 000	=+	/		\(7)
1991	Hha1	8	gaa	154.255	155	154.22	154.29	0	4 400 000	7 800 000	0	=-	\		\(7)
1992	Taq1	8	gaa	154.655	155	154.83	0	154.48	3 600 000	0	3 200 000	-+(=)	V		\(7)
1993	Hha1	8	gaa	155.29	155	155.35	155.27	155.25	35 900 000	12 200 000	5 900 000	-=	\ (-)		\(7)
1994	Taq1	8	gaa	155.76	155	155.94	0	155.58	3 800 000	0	10 700 000	=+(+)	/		\(7)
1995	Taq1	20	ctc	154.583	155	154.65	154.75	154.35	44 500 000	59 500 000	11 100 000	=-	\ (-)		\(7)
1996	Taq1	20	ctc	155.33	155	0	0	155.33	0	0	10 900 000	=+	/		\(7)
1997	Taq1	49	aaa	177.99	179	178.1	177.88	0	3 800 000	4 800 000	0	=-	\		\(7)
1998	Taq1	49	aaa	178.53	179	0	178.53	0	0	4 600 000	0	+-	A		\(7)
1999	Taq1	49	aaa	179.675	179	179.62	179.73	0	30 900 000	26 500 000	0	=-	\		\(7)
2000	Taq1	50	aat	211.18	212	211.13	0	211.23	12 000 000	0	7 200 000	-+(=)	V		\(7)
2001	Taq1	50	aat	212.73	212	212.73	0	0	3 400 000	0	0	-=	\		\(7)
2002	Taq1	39	agg	299.4	300	299.45	299.35	0	330.51	177.89	0	--	\		\(7)
2003	Taq1	39	agg	299.91	300	299.91	0	0	334.22	0	0	-=	\		\(7)
2004	Taq1	49	aaa	325.52	326	325.52	0	0	16 200 000	0	0	-=	\		\(7)
2005	Taq1	49	aaa	326.1	326	0	326.1	0	0	12 400 000	0	+-	A		\(7)
2006	Taq1	49	aaa	327.79	326	327.79	0	0	20 500 000	0	0	-=	\		\(7)
2007	Hha1	26	ctg	104.535	105	104.54	104.53	0	10 900 000	3 300 000	0	-=	\		\(2)
2008	Hha1	26	ctg	105.54	105	105.54	0	0	3 100 000	0	0	-=	\		\(2)
2009	Hha1	39	agg	242.315	241	242.2	242.43	0	975.07	388.08	0	-=	\		\(2)
2010	Taq1	8	gaa	69.873	70	69.86	70.01	69.75	5 900 000	19 800 000	21 900 000	+=	/ (-)		\(8)
2011	Taq1	8	gaa	70.385	70	70.28	0	70.49	6 700 000	0	7 500 000	-+(=)	V		\(8)
2012	Hha1	20	ctc	76.92	77	77	0	76.84	371.9	0	751.43	-+(+)	V (/)		\(8)
2013	Hha1	31	gac	76.83	77	76.84	76.82	0	10 800 000	5 000 000	0	--	\		\(8)
2014	Hha1	59	ttc	94.35	94	94.22	94.34	94.49	754.03	845.11	333.73	=-	\ (-)		\(8)
2015	Taq1	10	atg	163.52	164	0	0	163.52	0	0	4 600 000	=+	/		\(8)
2016	Hha1	10	atg	163.53	164	163.45	163.61	0	7 700 000	3 100 000	0	-=	\		\(8)
2017	Hha1	10	atg	164.4	164	164.42	164.38	0	4 400 000	3 500 000	0	=-	\		\(8)
2018	Taq1	25	cat	163.817	164	163.89	163.88	163.68	1 173.74	1 387.65	1 460.45	==	-		\(8)
2019	Taq1	25	cat	164.84	164	165.01	0	164.67	1 030.43	0	881.78	-+(=)	V		\(8)
2020	Taq1	62	tgt	189.04	190	0	189.04	0	0	4 100 000	0	+-	A		\(8)
2021	Taq1	62	tgt	189.87	190	189.87	0	0	3 900 000	0	0	-=	\		\(8)
2022	Taq1	12	agt	230.745	232	230.79	230.7	0	3 100 000	4 900 000	0	=-	\		\(8)
2023	Taq1	12	agt	231.73	232	231.81	231.65	0	4 000 000	4 500 000	0	=-	\		\(8)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
1981	AF368269.PE1	nc	cytochrome P450 monooxygenase CYP2T1		gct	aga	decreased
1982	AF368269.PE1	nc	cytochrome P450 monooxygenase CYP2T1		gct	aga	decreased
1983	AF368269.PE1	nc	cytochrome P450 monooxygenase CYP2T1		gct	aga	decreased
1984	AF368269.PE1	nc	cytochrome P450 monooxygenase CYP2T1		gct	aga	decreased
1985	RNCYT27S9.PE1	nc	cytochrome P-450c27/25		gta	cca	No change
1986	RNCYT27S9.PE1	nc	cytochrome P-450c27/25		ttc	ggt	No change
1987	RNCYT27S9.PE1	nc	cytochrome P-450c27/25		ctg	tag	No change
1988	RNCYT27S9.PE1	nc	cytochrome P-450c27/25		ctg	tag	No change
1989	AB041881.DNCHC2	dnchc2	cytoplasmic dynein heavy chain		aca	gac	increased
1990	AB041881.DNCHC2	dnchc2	cytoplasmic dynein heavy chain		aca	gac	increased
1991	AB041881.DNCHC2	dnchc2	cytoplasmic dynein heavy chain		gaa	ctc	increased
1992	AB041881.DNCHC2	dnchc2	cytoplasmic dynein heavy chain		gaa	ctc	increased
1993	AB041881.DNCHC2	dnchc2	cytoplasmic dynein heavy chain		gaa	ctc	increased
1994	AB041881.DNCHC2	dnchc2	cytoplasmic dynein heavy chain		gaa	ctc	increased
1995	AB041881.DNCHC2	dnchc2	cytoplasmic dynein heavy chain		gaa	ctc	increased
1996	AB041881.DNCHC2	dnchc2	cytoplasmic dynein heavy chain		gaa	ctc	increased
1997	AB041881.DNCHC2	dnchc2	cytoplasmic dynein heavy chain		aaa	tca	increased
1998	AB041881.DNCHC2	dnchc2	cytoplasmic dynein heavy chain		aaa	tca	increased
1999	AB041881.DNCHC2	dnchc2	cytoplasmic dynein heavy chain		aaa	tca	increased
2000	AB041881.DNCHC2	dnchc2	cytoplasmic dynein heavy chain		ttg	aat	increased
2001	AB041881.DNCHC2	dnchc2	cytoplasmic dynein heavy chain		ttg	aat	increased
2002	AB041881.DNCHC2	dnchc2	cytoplasmic dynein heavy chain		agg	cgt	increased
2003	AB041881.DNCHC2	dnchc2	cytoplasmic dynein heavy chain		agg	cgt	increased
2004	AB041881.DNCHC2	dnchc2	cytoplasmic dynein heavy chain		gtg	aaa	increased
2005	AB041881.DNCHC2	dnchc2	cytoplasmic dynein heavy chain		gtg	aaa	increased
2006	AB041881.DNCHC2	dnchc2	cytoplasmic dynein heavy chain		gtg	aaa	increased
2007	RNU28356.PE1	nc	cytosolic protein tyrosine phosphatase		ctg	tgc	increased
2008	RNU28356.PE1	nc	cytosolic protein tyrosine phosphatase		ctg	tgc	increased
2009	RNU28356.PE1	nc	cytosolic protein tyrosine phosphatase		tcc	agg	increased
2010	RND100.DYNAMIN-1	dynamin-1	D100		gaa	tct	increased
2011	RND100.DYNAMIN-1	dynamin-1	D100		gaa	tct	increased
2012	RND100.DYNAMIN-1	dynamin-1	D100		gac	ctc	increased
2013	RND100.DYNAMIN-1	dynamin-1	D100		gac	ctc	increased
2014	RND100.DYNAMIN-1	dynamin-1	D100		aag	ttc	increased
2015	RND100.DYNAMIN-1	dynamin-1	D100		cat	atg	increased
2016	RND100.DYNAMIN-1	dynamin-1	D100		cat	atg	increased
2017	RND100.DYNAMIN-1	dynamin-1	D100		cat	atg	increased
2018	RND100.DYNAMIN-1	dynamin-1	D100		cat	atg	increased
2019	RND100.DYNAMIN-1	dynamin-1	D100		cat	atg	increased
2020	RND100.DYNAMIN-1	dynamin-1	D100		ggc	tgt	increased
2021	RND100.DYNAMIN-1	dynamin-1	D100		ggc	tgt	increased
2022	RND100.DYNAMIN-1	dynamin-1	D100		ctt	agt	increased
2023	RND100.DYNAMIN-1	dynamin-1	D100		ctt	agt	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
2024	Taq1	12	agt	232.88	232	0	232.88	0	0	4 300 000	0	+-	A		\(8)
2025	Taq1	63	ctt	231.35	232	231.35	0	0	3 000 000	0	0	-=	\		\(8)
2026	Taq1	63	ctt	232.48	232	232.48	0	0	3 300 000	0	0	-=	\		\(8)
2027	Hha1	40	tgg	238.06	239	0	238.06	0	0	3 900 000	0	+-	A		\(8)
2028	Hha1	40	tgg	238.845	239	238.71	238.98	0	3 900 000	3 200 000	0	=-	\		\(8)
2029	Hha1	40	tgg	239.97	239	239.97	0	0	4 500 000	0	0	-=	\		\(8)
2030	Hha1	49	aaa	240.077	240	240.21	240.1	239.92	5 500 000	6 200 000	3 800 000	==	-		\(8)
2031	Hha1	49	aaa	241.26	240	241.26	0	0	3 200 000	0	0	-=	\		\(8)
2032	Hha1	6	aga	167.615	168	167.59	0	167.64	10 500 000	0	3 200 000	-=(-)	\		\(4)
2033	Hha1	6	aga	168.64	168	168.64	0	0	6 700 000	0	0	-=	\		\(4)
2034	Taq1	22	tcc	167.33	168	167.33	0	0	3 700 000	0	0	-=	\		\(4)
2035	Hha1	22	tcc	168.037	168	167.97	168.17	167.97	139 600 000	3 600 000	16 100 000	-=	\ (-)		\(4)
2036	Hha1	22	tcc	168.92	168	168.92	0	0	23 500 000	0	0	-=	\		\(4)
2037	Taq1	22	tcc	168.81	168	0	0	168.81	0	0	3 100 000	=+	/		\(4)
2038	Taq1	61	tct	169.537	170	169.48	169.68	169.45	8 600 000	6 400 000	3 200 000	==	-		\(4)
2039	Taq1	61	tct	170.42	170	170.42	0	0	4 700 000	0	0	-=	\		\(4)
2040	Hha1	44	cgg	60.04	60	0	0	60.04	0	0	92 100 000	=+	/		/(2)
2041	Hha1	59	ttc	129.96	130	0	129.96	0	0	149.47	0	+-	A		/(2)
2042	Hha1	59	ttc	130.74	130	0	130.74	0	0	238.58	0	+-	A		/(2)
2043	Hha1	54	ttt	176.893	177	177.1	176.92	176.66	9 900 000	6 200 000	6 700 000	==	-		/(2)
2044	Hha1	54	ttt	176.22	177	0	0	176.22	0	0	4 200 000	=+	/		/(2)
2045	Hha1	44	cgg	60.04	60	0	0	60.04	0	0	92 100 000	=+	/		/(2)
2046	Hha1	59	ttc	129.96	130	0	129.96	0	0	149.47	0	+-	A		/(2)
2047	Hha1	59	ttc	130.74	130	0	130.74	0	0	238.58	0	+-	A		/(2)
2048	Hha1	54	ttt	176.893	177	177.1	176.92	176.66	9 900 000	6 200 000	6 700 000	==	-		/(2)
2049	Hha1	54	ttt	176.22	177	0	0	176.22	0	0	4 200 000	=+	/		/(2)
2050	Taq1	29	gca	100.4	100	0	0	100.4	0	0	18 100 000	=+	/		\(2)
2051	Taq1	29	gca	99.41	100	0	0	99.41	0	0	11 800 000	=+	/		\(2)
2052	Taq1	56	tga	100.495	100	100.4	100.59	0	5 100 000	9 000 000	0	=-	\		\(2)
2053	Taq1	56	tga	99.73	100	0	99.73	0	0	4 600 000	0	+-	A		\(2)
2054	Taq1	7	caa	328.24	330	328.24	0	0	3 700 000	0	0	-=	\		\(2)
2055	Taq1	9	atc	90.47	91	90.43	90.48	90.5	88 300 000	48 700 000	5 200 000	=-	\ (-)		-3
2056	Taq1	9	atc	91.415	91	91.42	91.41	0	10 400 000	4 700 000	0	--	\		-3
2057	Taq1	12	agt	119.103	119	119.06	119.05	119.2	5 100 000	7 000 000	3 800 000	=-	\ (-)		-3
2058	Taq1	26	ctg	119.07	119	0	119.07	119.07	0	14 200 000	5 700 000	+-	A		-3
2059	Taq1	57	ctg	118.943	119	118.85	118.87	119.11	6 300 000	7 600 000	9 200 000	==	-		-3
2060	Hha1	4	aag	121.725	122	0	121.66	121.79	0	3 200 000	7 400 000	=+	/		/(2)
2061	Hha1	4	aag	121.99	122	0	121.99	0	0	3 400 000	0	+-	A		/(2)
2062	Taq1	56	tga	122.603	122	122.7	122.7	122.41	98 100 000	111 200 000	4 100 000	=-	\ (-)		/(2)
2063	Taq1	52	att	230.32	230	0	0	230.32	0	0	11 900 000	=+	/		/(2)
2064	Taq1	52	att	231.31	230	0	0	231.31	0	0	3 400 000	=+	/		/(2)
2065	Hha1	31	gac	60.15	60	0	60.15	0	0	4 700 000	0	+-	A		-(2) A(2)
2066	Hha1	40	tgg	101.637	102	101.34	101.84	101.73	16 300 000	13 700 000	17 400 000	==	-	-	-(2) A(2)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
2024	RND100.DYNAMIN-1	dynamin-1	D100		ctt	agt	increased
2025	RND100.DYNAMIN-1	dynamin-1	D100		ctt	agt	increased
2026	RND100.DYNAMIN-1	dynamin-1	D100		ctt	agt	increased
2027	RND100.DYNAMIN-1	dynamin-1	D100		aaa	tgg	increased
2028	RND100.DYNAMIN-1	dynamin-1	D100		aaa	tgg	increased
2029	RND100.DYNAMIN-1	dynamin-1	D100		aaa	tgg	increased
2030	RND100.DYNAMIN-1	dynamin-1	D100		aaa	tgg	increased
2031	RND100.DYNAMIN-1	dynamin-1	D100		aaa	tgg	increased
2032	AY325251.PE1	nc	Da1-12		aga	tcc	increased
2033	AY325251.PE1	nc	Da1-12		aga	tcc	increased
2034	AY325251.PE1	nc	Da1-12		aga	tcc	increased
2035	AY325251.PE1	nc	Da1-12		aga	tcc	increased
2036	AY325251.PE1	nc	Da1-12		aga	tcc	increased
2037	AY325251.PE1	nc	Da1-12		aga	tcc	increased
2038	AY325251.PE1	nc	Da1-12		tct	ttc	increased
2039	AY325251.PE1	nc	Da1-12		tct	ttc	increased
2040	AY325257.PE1	nc	Da2-27	*	ctc	cgg	decreased
2041	AY325257.PE1	nc	Da2-27	*	agt	ttc	decreased
2042	AY325257.PE1	nc	Da2-27	*	agt	ttc	decreased
2043	AY325257.PE1	nc	Da2-27	*	tca	ttt	decreased
2044	AY325257.PE1	nc	Da2-27	*	tca	ttt	decreased
2045	AY325261.PE1	nc	Da2-4	*	ctc	cgg	decreased
2046	AY325261.PE1	nc	Da2-4	*	agt	ttc	decreased
2047	AY325261.PE1	nc	Da2-4	*	agt	ttc	decreased
2048	AY325261.PE1	nc	Da2-4	*	tca	ttt	decreased
2049	AY325261.PE1	nc	Da2-4	*	tca	ttt	decreased
2050	RNO277077.DDB1	DDB1	damage-specific DNA binding protein 1		gca	tga	increased
2051	RNO277077.DDB1	DDB1	damage-specific DNA binding protein 1		gca	tga	increased
2052	RNO277077.DDB1	DDB1	damage-specific DNA binding protein 1		gca	tga	increased
2053	RNO277077.DDB1	DDB1	damage-specific DNA binding protein 1		gca	tga	increased
2054	RNO277077.DDB1	DDB1	damage-specific DNA binding protein 1		gtg	caa	increased
2055	RATCSBP.CSBP	CSBP	dC-stretch binding protein (CSBP)		atc	agt	No change
2056	RATCSBP.CSBP	CSBP	dC-stretch binding protein (CSBP)		atc	agt	No change
2057	RATCSBP.CSBP	CSBP	dC-stretch binding protein (CSBP)		ctg	agt	No change
2058	RATCSBP.CSBP	CSBP	dC-stretch binding protein (CSBP)		ctg	agt	No change
2059	RATCSBP.CSBP	CSBP	dC-stretch binding protein (CSBP)		ctg	agt	No change
2060	RNU68725.DCC	DCC	Deleted in Colorectal Cancer		tga	aag	decreased
2061	RNU68725.DCC	DCC	Deleted in Colorectal Cancer		tga	aag	decreased
2062	RNU68725.DCC	DCC	Deleted in Colorectal Cancer		tga	aag	decreased
2063	RNU68725.DCC	DCC	Deleted in Colorectal Cancer		ttc	att	decreased
2064	RNU68725.DCC	DCC	Deleted in Colorectal Cancer		ttc	att	decreased
2065	RNU00475.DOR1	dor1	delta opioid receptor	*	tgc	gac	No change
2066	RNU00475.DOR1	dor1	delta opioid receptor	*	tgg	ttg	No change

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
2067	Hha1	40	tgg	102.35	102	0	102.35	0	0	10 700 000	0	+-	A		-(2) A(2)
2068	Hha1	60	ttg	101.403	102	101.3	101.63	101.28	7 000 000	5 100 000	5 600 000	==	-	-	-(2) A(2)
2069	Hha1	41	ccc	119.87	120	0	0	119.87	0	0	6 500 000	=+	/		/(2) \(2)
2070	Hha1	26	ctg	165.435	166	165.45	165.42	0	4 100 000	5 300 000	0	=-	\		/(2) \(2)
2071	Hha1	26	ctg	165.99	166	0	0	165.99	0	0	3 800 000	=+	/		/(2) \(2)
2072	Hha1	27	acg	178.46	179	178.46	0	0	3 200 000	0	0	-=	\		/(2) \(2)
2073	Taq1	48	ggg	130.25	131	0	130.09	130.41	0	636.4	2 775.99	=+	/		-2
2074	Taq1	48	ggg	131.177	131	130.94	131.37	131.22	3 445	1 182.75	747.38	-=	\ (-)		-2
2075	Taq1	25	cat	132.31	132	132.21	132.51	132.21	941.72	980.26	1 432.9	==	-		-2
2076	Hha1	4	aag	177.077	178	176.99	177.25	176.99	13 100 000	5 600 000	6 300 000	-=	\ (-)		\(3)
2077	Hha1	4	aag	178.093	178	178.13	178.1	178.05	21 200 000	5 900 000	17 000 000	-+	V		\(3)
2078	Hha1	4	aag	179.06	178	179.07	0	179.05	6 000 000	0	5 600 000	-+(=)	V		\(3)
2079	Taq1	23	cga	199.47	200	199.47	0	0	3 500 000	0	0	-=	\		\(3)
2080	Taq1	23	cga	200.445	200	200.47	200.42	0	5 400 000	3 700 000	0	=-	\		\(3)
2081	Hha1	16	tag	271.8	272	271.8	0	0	3 400 000	0	0	-=	\		\(3)
2082	Hha1	21	acc	179.96	181	0	0	179.96	0	0	6 200 000	=+	/	/	
2083	Taq1	21	acc	180.16	181	0	0	180.16	0	0	4 400 000	=+	/	/	
2084	Hha1	21	acc	179.96	181	0	0	179.96	0	0	6 200 000	=+	/	/	
2085	Taq1	21	acc	180.16	181	0	0	180.16	0	0	4 400 000	=+	/	/	
2086	Taq1	12	agt	236.03	236	0	0	236.03	0	0	3 100 000	=+	/	/	
2087	Taq1	26	ctg	235.85	236	0	0	235.85	0	0	4 000 000	=+	/	/	
2088	Hha1	41	ccc	148.19	148	147.96	148.26	148.35	6 200 000	12 000 000	22 900 000	=+	/ (-)	(-)	
2089	Hha1	31	gac	148.343	149	148.4	148.37	148.26	7 300 000	4 900 000	5 100 000	==	-	(-)	
2090	Hha1	33	agc	60.667	61	60.61	60.65	60.74	8 100 000	13 200 000	3 900 000	=-	\ (-)		/(6)
2091	Hha1	33	agc	66.89	67	66.93	66.98	66.76	12 300 000	23 100 000	248 400 000	=+	/ (-)		/(6)
2092	Hha1	20	ctc	76.92	77	77	0	76.84	371.9	0	751.43	-+(+)	V (/)		/(6)
2093	Hha1	33	agc	79.76	80	79.76	0	0	7 400 000	0	0	-=	\		/(6)
2094	Hha1	33	agc	79.76	80	79.76	0	0	7 400 000	0	0	-=	\		/(6)
2095	Hha1	20	ctc	86.105	86	0	86.13	86.08	0	1 180.17	1 693.7	+=	/		/(6)
2096	Hha1	26	ctg	120.87	121	0	120.81	120.93	0	8 500 000	4 900 000	+=	/		/(6)
2097	Hha1	59	ttc	120.7	121	120.7	0	0	956.83	0	0	-=	\		/(6)
2098	Hha1	59	ttc	121.365	121	0	121.51	121.22	0	175.34	150.05	+=	/		/(6)
2099	Taq1	23	cga	212.87	214	0	0	212.87	0	0	3 300 000	=+	/		/(6)
2100	Taq1	23	cga	214.66	214	214.68	214.64	0	8 200 000	3 600 000	0	-=	\		/(6)
2101	Hha1	60	ttg	272.37	274	0	272.37	0	0	4 900 000	0	+-	A		/(6)
2102	Taq1	62	tgt	109.525	110	0	109.69	109.36	0	4 800 000	27 500 000	=+	/		\(2)
2103	Taq1	62	tgt	110.46	110	0	110.59	110.33	0	5 500 000	16 000 000	=+	/		\(2)
2104	Taq1	23	cga	195.287	196	195.4	195.35	195.11	4 300 000	4 000 000	4 600 000	==	-		\(2)
2105	Taq1	23	cga	196.375	196	196.4	196.35	0	10 500 000	8 900 000	0	=-	\		\(2)
2106	Hha1	25	cag	195.98	196	195.98	0	0	3 800 000	0	0	-=	\		\(2)
2107	Taq1	55	tca	60.73	61	60.73	0	0	3 700 000	0	0	-=	\		\(7)
2108	Taq1	45	gcc	65.8	66	65.84	65.76	0	19 900 000	27 600 000	0	=-	\		\(7)
2109	Hha1	31	gac	73.007	73	72.98	73	73.04	18 900 000	9 600 000	8 500 000	-=	\ (-)		\(7)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
2067	RNU00475.DOR1	dor1	delta opioid receptor	*	tgg	ttg	No change
2068	RNU00475.DOR1	dor1	delta opioid receptor	*	tgg	ttg	No change
2069	RNU78889.PE1	nc	Delta1		ccc	act	decreased
2070	RNU78889.PE1	nc	Delta1		ctg	cat	decreased
2071	RNU78889.PE1	nc	Delta1		ctg	cat	decreased
2072	RNU78889.PE1	nc	Delta1		tag	acg	decreased
2073	AB021980.PE1	nc	delta-6 fatty acid desaturase		cat	ggg	No change
2074	AB021980.PE1	nc	delta-6 fatty acid desaturase		cat	ggg	No change
2075	AB021980.PE1	nc	delta-6 fatty acid desaturase		cat	ggg	No change
2076	RNAJ6855.PE1	nc	DeltaSAC-synaptojanin1		aag	ttg	increased
2077	RNAJ6855.PE1	nc	DeltaSAC-synaptojanin1		aag	ttg	increased
2078	RNAJ6855.PE1	nc	DeltaSAC-synaptojanin1		aag	ttg	increased
2079	RNAJ6855.PE1	nc	DeltaSAC-synaptojanin1		cga	cta	increased
2080	RNAJ6855.PE1	nc	DeltaSAC-synaptojanin1		cga	cta	increased
2081	RNAJ6855.PE1	nc	DeltaSAC-synaptojanin1		tac	tag	increased
2082	RNDENDR.PE1	nc	dendrin		acc	ctg	decreased
2083	RNDENDR.PE1	nc	dendrin		acc	ctg	decreased
2084	RNDENDRIN.PE1	nc	dendrin		acc	ctg	decreased
2085	RNDENDRIN.PE1	nc	dendrin		acc	ctg	decreased
2086	RNU66707.PE1	nc	densin-180		ctg	agt	decreased
2087	RNU66707.PE1	nc	densin-180		ctg	agt	decreased
2088	RNDES.PE1	nc	desmin		ccc	gac	No change
2089	RNDES.PE1	nc	desmin		ccc	gac	No change
2090	AB091769.DMN	DMN	desmuslin		agc	ctc	decreased
2091	AB091769.DMN	DMN	desmuslin		gag	agc	decreased
2092	AB091769.DMN	DMN	desmuslin		cgc	ctc	decreased
2093	AB091769.DMN	DMN	desmuslin		agc	ttg	decreased
2094	AB091769.DMN	DMN	desmuslin		agc	ttg	decreased
2095	AB091769.DMN	DMN	desmuslin		tcc	ctc	decreased
2096	AB091769.DMN	DMN	desmuslin		ctg	acc	decreased
2097	AB091769.DMN	DMN	desmuslin		tgc	ttc	decreased
2098	AB091769.DMN	DMN	desmuslin		tgc	ttc	decreased
2099	AB091769.DMN	DMN	desmuslin		cga	ggg	decreased
2100	AB091769.DMN	DMN	desmuslin		cga	ggg	decreased
2101	AB091769.DMN	DMN	desmuslin		atg	ttg	decreased
2102	RATDRP.TPO1	TPO1	developmentally regulated protein		gat	tgt	increased
2103	RATDRP.TPO1	TPO1	developmentally regulated protein		gat	tgt	increased
2104	RATDRP.TPO1	TPO1	developmentally regulated protein		cag	cga	increased
2105	RATDRP.TPO1	TPO1	developmentally regulated protein		cag	cga	increased
2106	RATDRP.TPO1	TPO1	developmentally regulated protein		cag	cga	increased
2107	D78588.DGK-IV	DGK-IV	diacylglycerol kinase		tca	gga	increased
2108	D78588.DGK-IV	DGK-IV	diacylglycerol kinase		gcc	ggt	increased
2109	D78588.DGK-IV	DGK-IV	diacylglycerol kinase		gac	cgc	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
2110	Hha1	59	ttc	116.49	117	0	116.49	0	0	117.85	0	+-	A		\(7)
2111	Hha1	59	ttc	117.215	117	0	117.03	117.4	0	143.72	1 360.82	=+	/		\(7)
2112	Hha1	33	agc	131.333	132	131.13	131.45	131.42	12 100 000	69 700 000	46 800 000	+=	/ (-)		\(7)
2113	Hha1	33	agc	132.16	132	132.16	0	0	4 600 000	0	0	-=	\		\(7)
2114	Hha1	9	atc	193.52	194	0	193.52	0	0	3 000 000	0	+-	A		\(7)
2115	Hha1	9	atc	194.455	194	194.27	194.64	0	4 400 000	3 500 000	0	=-	\		\(7)
2116	Hha1	59	ttc	283.08	284	283.08	0	0	416.01	0	0	-=	\		\(7)
2117	Taq1	8	gaa	283.44	285	0	0	283.44	0	0	8 400 000	=+	/		\(7)
2118	Hha1	8	gaa	284.86	285	0	284.86	0	0	3 400 000	0	+-	A		\(7)
2119	Hha1	8	gaa	286.61	285	286.61	0	0	3 100 000	0	0	-=	\		\(7)
2120	Taq1	39	agg	90.495	91	90.7	0	90.29	125 800 000	0	23 600 000	-=(-)	\		\(6)
2121	Taq1	39	agg	90.957	91	90.7	90.97	91.2	4 671.71	172 200 000	3 800 000	+-	A		\(6)
2122	Taq1	39	agg	91.085	91	0	90.97	91.2	0	1 730.67	111.92	+-	A		\(6)
2123	Taq1	47	ggc	95.27	95	0	95.15	95.39	0	4 646.72	4 103.67	+=	/		\(6)
2124	Taq1	39	agg	95.64	96	95.64	0	0	7 400 000	0	0	-=	\		\(6)
2125	Taq1	39	agg	96.15	96	96.14	96.16	0	15 100 000	32 300 000	0	+-	A		\(6)
2126	Taq1	39	agg	95.64	96	95.64	0	0	274.8	0	0	-=	\		\(6)
2127	Taq1	39	agg	96.15	96	96.14	96.16	0	560.75	324.62	0	=-	\		\(6)
2128	Hha1	59	ttc	165.58	165	165.44	165.5	165.8	166.4	135.1	85.37	==	-		\(6)
2129	Taq1	7	caa	250.34	251	250.34	0	0	5 000 000	0	0	-=	\		\(6)
2130	Hha1	7	caa	251.52	251	251.52	0	0	4 500 000	0	0	-=	\	\	\(6)
2131	Taq1	7	caa	251.62	251	251.62	0	0	3 900 000	0	0	-=	\	\	\(6)
2132	Hha1	7	caa	252.07	251	252.07	0	0	5 900 000	0	0	-=	\		\(6)
2133	Taq1	9	atc	73.93	74	73.9	73.96	0	18 200 000	28 400 000	0	=-	\		\(6)
2134	Hha1	8	gaa	120.66	121	120.66	0	0	10 700 000	0	0	-=	\		\(6)
2135	Taq1	8	gaa	120.82	121	0	0	120.82	0	0	8 800 000	=+	/		\(6)
2136	Taq1	22	tcc	120.69	121	120.82	0	120.56	5 400 000	0	9 500 000	-+(=)	V		\(6)
2137	Taq1	22	tcc	121.36	121	0	121.24	121.48	0	6 000 000	7 100 000	+=	/		\(6)
2138	Hha1	22	tcc	121.59	121	121.59	0	0	8 500 000	0	0	-=	\		\(6)
2139	Taq1	22	tcc	121.66	121	0	121.66	0	0	6 200 000	0	+-	A		\(6)
2140	Taq1	50	aat	127.66	128	127.64	127.68	127.66	7 100 000	6 800 000	15 700 000	=+	/ (-)		\(6)
2141	Taq1	50	aat	128.71	128	128.86	0	128.56	4 600 000	0	20 800 000	=+(+)	/		\(6)
2142	Taq1	54	ttt	128.3	128	128.3	0	0	852.14	0	0	-=	\		\(6)
2143	Taq1	61	tct	143.72	144	143.51	0	143.93	3 100 000	0	11 900 000	=+(+)	/		\(6)
2144	Taq1	61	tct	144.21	144	144.21	0	0	3 900 000	0	0	-=	\		\(6)
2145	Hha1	6	aga	174.96	176	0	0	174.96	0	0	5 400 000	=+	/		\(6)
2146	Hha1	6	aga	175.995	176	175.96	0	176.03	4 500 000	0	9 800 000	-+(+)	V (/)		\(6)
2147	Hha1	6	aga	177.05	176	0	0	177.05	0	0	9 400 000	=+	/		\(6)
2148	Taq1	54	ttt	176.213	177	176.14	176.26	176.24	1 449.38	952.6	856.53	==	-		\(6)
2149	Taq1	54	ttt	177.54	177	177.64	177.44	0	1 973.78	517.46	0	-=	\		\(6)
2150	Taq1	48	ggg	110.46	111	0	110.46	0	0	954.61	0	+-	A		\(2) A(2)
2151	Taq1	48	ggg	111.175	111	110.97	0	111.38	1 611.88	0	1 217.16	-+(=)	V		\(2) A(2)
2152	Taq1	49	aaa	113.075	113	113.31	112.84	0	61 400 000	19 400 000	0	-=	\		\(2) A(2)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
2110	D78588.DGK-IV	DGK-IV	diacylglycerol kinase		taa	ttc	increased
2111	D78588.DGK-IV	DGK-IV	diacylglycerol kinase		taa	ttc	increased
2112	D78588.DGK-IV	DGK-IV	diacylglycerol kinase		tgg	agc	increased
2113	D78588.DGK-IV	DGK-IV	diacylglycerol kinase		tgg	agc	increased
2114	D78588.DGK-IV	DGK-IV	diacylglycerol kinase		ggt	atc	increased
2115	D78588.DGK-IV	DGK-IV	diacylglycerol kinase		ggt	atc	increased
2116	D78588.DGK-IV	DGK-IV	diacylglycerol kinase		ttc	tga	increased
2117	D78588.DGK-IV	DGK-IV	diacylglycerol kinase		gaa	agt	increased
2118	D78588.DGK-IV	DGK-IV	diacylglycerol kinase		gaa	agt	increased
2119	D78588.DGK-IV	DGK-IV	diacylglycerol kinase		gaa	agt	increased
2120	RATVDCCA.PE1	nc	dihydropryridine-sensitive calcium channel		ctt	agg	increased
2121	RATVDCCA.PE1	nc	dihydropryridine-sensitive calcium channel		ctt	agg	increased
2122	RATVDCCA.PE1	nc	dihydropryridine-sensitive calcium channel		ctt	agg	increased
2123	RATVDCCA.PE1	nc	dihydropryridine-sensitive calcium channel		agg	ggc	increased
2124	RATVDCCA.PE1	nc	dihydropryridine-sensitive calcium channel		agg	ggc	increased
2125	RATVDCCA.PE1	nc	dihydropryridine-sensitive calcium channel		agg	ggc	increased
2126	RATVDCCA.PE1	nc	dihydropryridine-sensitive calcium channel		agg	ggc	increased
2127	RATVDCCA.PE1	nc	dihydropryridine-sensitive calcium channel		agg	ggc	increased
2128	RATVDCCA.PE1	nc	dihydropryridine-sensitive calcium channel		cca	ttc	increased
2129	RATVDCCA.PE1	nc	dihydropryridine-sensitive calcium channel		caa	gct	increased
2130	RATVDCCA.PE1	nc	dihydropryridine-sensitive calcium channel		caa	gct	increased
2131	RATVDCCA.PE1	nc	dihydropryridine-sensitive calcium channel		caa	gct	increased
2132	RATVDCCA.PE1	nc	dihydropryridine-sensitive calcium channel		caa	gct	increased
2133	RATDHSCCA.CCHL2A	CCHL2A	dihydropyridine-sesitive L-type calcium channel		tgc	atc	increased
2134	RATDHSCCA.CCHL2A	CCHL2A	dihydropyridine-sesitive L-type calcium channel		tcc	gaa	increased
2135	RATDHSCCA.CCHL2A	CCHL2A	dihydropyridine-sesitive L-type calcium channel		tcc	gaa	increased
2136	RATDHSCCA.CCHL2A	CCHL2A	dihydropyridine-sesitive L-type calcium channel		tcc	gaa	increased
2137	RATDHSCCA.CCHL2A	CCHL2A	dihydropyridine-sesitive L-type calcium channel		tcc	gaa	increased
2138	RATDHSCCA.CCHL2A	CCHL2A	dihydropyridine-sesitive L-type calcium channel		tcc	gaa	increased
2139	RATDHSCCA.CCHL2A	CCHL2A	dihydropyridine-sesitive L-type calcium channel		tcc	gaa	increased
2140	RATDHSCCA.CCHL2A	CCHL2A	dihydropyridine-sesitive L-type calcium channel		aat	ttt	increased
2141	RATDHSCCA.CCHL2A	CCHL2A	dihydropyridine-sesitive L-type calcium channel		aat	ttt	increased
2142	RATDHSCCA.CCHL2A	CCHL2A	dihydropyridine-sesitive L-type calcium channel		aat	ttt	increased
2143	RATDHSCCA.CCHL2A	CCHL2A	dihydropyridine-sesitive L-type calcium channel		gat	tct	increased
2144	RATDHSCCA.CCHL2A	CCHL2A	dihydropyridine-sesitive L-type calcium channel		gat	tct	increased
2145	RATDHSCCA.CCHL2A	CCHL2A	dihydropyridine-sesitive L-type calcium channel		aga	ttt	increased
2146	RATDHSCCA.CCHL2A	CCHL2A	dihydropyridine-sesitive L-type calcium channel		aga	ttt	increased
2147	RATDHSCCA.CCHL2A	CCHL2A	dihydropyridine-sesitive L-type calcium channel		aga	ttt	increased
2148	RATDHSCCA.CCHL2A	CCHL2A	dihydropyridine-sesitive L-type calcium channel		aga	ttt	increased
2149	RATDHSCCA.CCHL2A	CCHL2A	dihydropyridine-sesitive L-type calcium channel		aga	ttt	increased
2150	RATDA.PE1	nc	dihydropyrimidinase		ggg	aaa	increased
2151	RATDA.PE1	nc	dihydropyrimidinase		ggg	aaa	increased
2152	RATDA.PE1	nc	dihydropyrimidinase		ggg	aaa	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
2153	Taq1	49	aaa	113.55	113	0	113.7	113.4	0	25 100 000	3 000 000	+-	A		\(2) A(2)
2154	Taq1	49	aaa	265.3	266	265.3	0	0	12 500 000	0	0	-=	\		\(2) A(2)
2155	Taq1	49	aaa	265.865	266	265.85	265.88	0	21 400 000	10 900 000	0	--	\		\(2) A(2)
2156	Taq1	49	aaa	267.18	266	267.22	267.14	0	14 300 000	5 400 000	0	-=	\		\(2) A(2)
2157	Taq1	24	cgt	106.22	106	106.25	106.19	106.22	5 600 000	7 200 000	30 100 000	=+	/ (-)	(-)	
2158	Taq1	30	cgt	106.407	106	106.39	106.43	106.4	6 000 000	4 800 000	8 200 000	==	-	(-)	
2159	Hha1	41	ccc	113.853	114	113.72	113.82	114.02	20 700 000	4 700 000	4 100 000	-=	\ (-)		-(2) \(2)
2160	Hha1	26	ctg	114.717	115	114.71	114.63	114.81	12 300 000	6 500 000	4 700 000	-=	\ (-)		-(2) \(2)
2161	Hha1	44	cgg	107.93	108	0	107.93	0	0	3 700 000	0	+-	A		A(4)
2162	Hha1	44	cgg	108.59	108	108.6	108.58	0	3 200 000	5 000 000	0	=-	\		A(4)
2163	Hha1	17	cca	127.363	127	127.38	127.38	127.33	4 041.64	7 361.96	3 525.48	+-	A		A(4)
2164	Hha1	40	tgg	126.3	127	0	126.3	0	0	3 300 000	0	+-	A		A(4)
2165	Hha1	44	cgg	136.783	137	136.85	136.67	136.83	9 500 000	10 600 000	3 900 000	=-	\ (-)		A(4)
2166	Hha1	44	cgg	137.27	137	0	0	137.27	0	0	3 400 000	=+	/		A(4)
2167	Hha1	59	ttc	137.785	138	137.71	0	137.86	166.4	0	103.48	-+(=)	V		A(4)
2168	Hha1	59	ttc	138.405	138	0	138.29	138.52	0	468.55	106.07	+-	A		A(4)
2169	Taq1	47	ggc	140.863	141	140.76	140.89	140.94	3 446.15	1 973.26	2 159.82	==	-		\(3)
2170	Taq1	47	ggc	144.98	145	144.98	0	0	3 076.92	0	0	-=	\		\(3)
2171	Taq1	39	agg	145.807	146	146.07	145.65	145.7	23 800 000	54 100 000	5 100 000	+-	A		\(3)
2172	Taq1	39	agg	145.885	146	146.07	0	145.7	883.83	0	150.22	-=(-)	\		\(3)
2173	Taq1	39	agg	146.33	146	0	146.33	0	0	46 200 000	0	+-	A		\(3)
2174	Taq1	39	agg	145.65	146	0	145.65	0	0	543.72	0	+-	A		\(3)
2175	Taq1	39	agg	146.33	146	0	146.33	0	0	464.32	0	+-	A		\(3)
2176	Hha1	39	agg	216.617	217	216.63	216.72	216.5	461.87	220.9	236	-=	\ (-)		\(3)
2177	Taq1	45	gcc	81.755	82	81.62	0	81.89	14 000 000	0	7 400 000	-+(-)	V (\)		\(2)
2178	Taq1	45	gcc	82.24	82	82.18	82.3	0	5 200 000	4 300 000	0	=-	\		\(2)
2179	Hha1	40	tgg	139.54	140	139.54	0	0	5 600 000	0	0	-=	\		\(2)
2180	Hha1	40	tgg	140.665	140	140.67	140.66	0	13 800 000	9 700 000	0	=-	\		\(2)
2181	Hha1	6	aga	175.995	177	175.96	0	176.03	4 500 000	0	9 800 000	-+(+)	V (/)		/(2)
2182	Hha1	6	aga	177.05	177	0	0	177.05	0	0	9 400 000	=+	/		/(2)
2183	Hha1	6	aga	177.935	177	177.81	0	178.06	3 900 000	0	10 900 000	=+(+)	/		/(2)
2184	Taq1	54	ttt	177.54	178	177.64	177.44	0	1 973.78	517.46	0	-=	\		/(2)
2185	Taq1	54	ttt	178.38	178	178.48	178.25	178.41	655.49	364.57	770.87	=+	/ (-)		/(2)
2186	Hha1	56	tga	107.625	108	107.49	0	107.76	1 683.48	0	1 051.54	-+(=)	V	V	\(2) V(2)
2187	Hha1	56	tga	108.47	108	108.72	108.22	0	531.19	236.67	0	-=	\	\	\(2) V(2)
2188	Hha1	61	tct	107.585	108	107.59	0	107.58	7 100 000	0	3 200 000	-+(-)	V (\)	V	\(2) V(2)
2189	Hha1	61	tct	108.5	108	108.43	108.77	108.3	13 700 000	3 100 000	4 300 000	-=	\ (-)	\	\(2) V(2)
2190	Hha1	39	agg	134.885	135	134.82	0	134.95	454.54	0	227.86	-+(-)	V (\)		\(2)
2191	Hha1	39	agg	135.25	135	0	0	135.25	0	0	236	=+	/		\(2)
2192	Hha1	3	aac	162.525	163	162.57	162.48	0	6 100 000	4 100 000	0	=-	\		\(2)
2193	Hha1	20	ctc	62	62	0	61.95	62.05	0	694.99	453.24	+=	/		-4
2194	Hha1	15	tac	109.643	109	109.65	109.64	109.64	59 600 000	40 500 000	60 200 000	==	-		-4
2195	Hha1	15	tac	108.73	109	108.73	0	0	673.35	0	0	-=	\		-4

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
2153	RATDA.PE1	nc	dihydropyrimidinase		ggg	aaa	increased
2154	RATDA.PE1	nc	dihydropyrimidinase		gga	aaa	increased
2155	RATDA.PE1	nc	dihydropyrimidinase		gga	aaa	increased
2156	RATDA.PE1	nc	dihydropyrimidinase		gga	aaa	increased
2157	RATDHNPBMT.PE1	nc	dihydroxypolyprenylbenzoate methyltransferase		cgt	ttc	No change
2158	RATDHNPBMT.PE1	nc	dihydroxypolyprenylbenzoate methyltransferase		cgt	ttc	No change
2159	RATDAPRP.DPP6	dpp6	dipeptidyl aminopeptidase-related protein		ccc	ctg	No change
2160	RATDAPRP.DPP6	dpp6	dipeptidyl aminopeptidase-related protein		ccc	ctg	No change
2161	RATGATGT2X.PE1	GATA-GT2	DNA binding protein		cgg	cac	increased by mild
2162	RATGATGT2X.PE1	GATA-GT2	DNA binding protein		cgg	cac	increased by mild
2163	RATGATGT2X.PE1	GATA-GT2	DNA binding protein		tgg	cca	increased by mild
2164	RATGATGT2X.PE1	GATA-GT2	DNA binding protein		tgg	cca	increased by mild
2165	RATGATGT2X.PE1	GATA-GT2	DNA binding protein		ttc	cgg	increased by mild
2166	RATGATGT2X.PE1	GATA-GT2	DNA binding protein		ttc	cgg	increased by mild
2167	RATGATGT2X.PE1	GATA-GT2	DNA binding protein		ttc	cgg	increased by mild
2168	RATGATGT2X.PE1	GATA-GT2	DNA binding protein		ttc	cgg	increased by mild
2169	RNO245648.PE1	pol alpha	DNA polymerase alpha		ggc	gga	increased
2170	RNO245648.PE1	pol alpha	DNA polymerase alpha		agg	ggc	increased
2171	RNO245648.PE1	pol alpha	DNA polymerase alpha		agg	ggc	increased
2172	RNO245648.PE1	pol alpha	DNA polymerase alpha		agg	ggc	increased
2173	RNO245648.PE1	pol alpha	DNA polymerase alpha		agg	ggc	increased
2174	RNO245648.PE1	pol alpha	DNA polymerase alpha		agg	ggc	increased
2175	RNO245648.PE1	pol alpha	DNA polymerase alpha		agg	ggc	increased
2176	RNO245648.PE1	pol alpha	DNA polymerase alpha		agg	tca	increased
2177	RNO011605.PE1	nc	DNA polymerase alpha subunit I		cac	gcc	increased
2178	RNO011605.PE1	nc	DNA polymerase alpha subunit I		cac	gcc	increased
2179	RNO011605.PE1	nc	DNA polymerase alpha subunit I		tgg	atg	increased
2180	RNO011605.PE1	nc	DNA polymerase alpha subunit I		tgg	atg	increased
2181	AF154849.PE1	nc	dnaj-like protein		aga	ttt	decreased
2182	AF154849.PE1	nc	dnaj-like protein		aga	ttt	decreased
2183	AF154849.PE1	nc	dnaj-like protein		aga	ttt	decreased
2184	AF154849.PE1	nc	dnaj-like protein		aga	ttt	decreased
2185	AF154849.PE1	nc	dnaj-like protein		aga	ttt	decreased
2186	RNU70779.PE1	nc	Doc2A		tga	tct	decreased by mild
2187	RNU70779.PE1	nc	Doc2A		tga	tct	increased
2188	RNU70779.PE1	nc	Doc2A		tga	tct	decreased by mild
2189	RNU70779.PE1	nc	Doc2A		tga	tct	increased
2190	RATD1BR.PE1	nc	dopamine D1B receptor		agg	aga	increased
2191	RATD1BR.PE1	nc	dopamine D1B receptor		agg	aga	increased
2192	RATD1BR.PE1	nc	dopamine D1B receptor		tca	aac	increased
2193	RNU03551.PE1	nc	dopamine D4 receptor		cgt	ctc	No change
2194	RNU03551.PE1	nc	dopamine D4 receptor		tac	ccc	No change
2195	RNU03551.PE1	nc	dopamine D4 receptor		tac	ccc	No change

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
2196	Hha1	15	tac	109.643	110	109.65	109.64	109.64	59 600 000	40 500 000	60 200 000	==	-	-	-4
2197	Hha1	15	tac	109.683	110	109.77	109.64	109.64	11 491.84	10 430.07	13 092.64	==	-	-	-4
2198	Hha1	33	agc	109.83	110	109.86	109.86	109.77	6 400 000	4 300 000	6 200 000	==	-	-	-4
2199	Hha1	28	tcg	113.85	114	113.64	113.99	113.92	32 300 000	27 100 000	18 300 000	==	-		-4
2200	Hha1	28	tcg	114.553	114	114.28	114.72	114.66	47 800 000	39 300 000	28 500 000	==	-		-4
2201	Hha1	40	tgg	113.48	114	113.23	113.73	0	46 700 000	9 600 000	0	-=	\		-4
2202	Hha1	40	tgg	114.02	114	0	0	114.02	0	0	5 100 000	=+	/		-4
2203	Hha1	20	ctc	62	62	0	61.95	62.05	0	694.99	453.24	+=	/		-4
2204	Hha1	15	tac	109.643	109	109.65	109.64	109.64	59 600 000	40 500 000	60 200 000	==	-		-4
2205	Hha1	15	tac	108.73	109	108.73	0	0	673.35	0	0	-=	\		-4
2206	Hha1	15	tac	109.643	110	109.65	109.64	109.64	59 600 000	40 500 000	60 200 000	==	-	-	-4
2207	Hha1	15	tac	109.683	110	109.77	109.64	109.64	11 491.84	10 430.07	13 092.64	==	-	-	-4
2208	Hha1	33	agc	109.83	110	109.86	109.86	109.77	6 400 000	4 300 000	6 200 000	==	-	-	-4
2209	Hha1	28	tcg	113.85	114	113.64	113.99	113.92	32 300 000	27 100 000	18 300 000	==	-		-4
2210	Hha1	28	tcg	114.553	114	114.28	114.72	114.66	47 800 000	39 300 000	28 500 000	==	-		-4
2211	Hha1	40	tgg	113.48	114	113.23	113.73	0	46 700 000	9 600 000	0	-=	\		-4
2212	Hha1	40	tgg	114.02	114	0	0	114.02	0	0	5 100 000	=+	/		-4
2213	Hha1	39	agg	109.507	110	109.65	109.55	109.32	1 092.37	2 173.26	1 485.18	+=	/ (-)	/	-1
2214	Hha1	39	agg	110.08	110	0	0	110.08	0	0	557.45	=+	/		-1
2215	Hha1	39	agg	110.635	110	110.65	110.62	0	351.9	704.51	0	+-	A		-1
2216	Hha1	40	tgg	109.35	110	0	0	109.35	0	0	21 600 000	=+	/	/	-1
2217	Hha1	40	tgg	110.207	110	110.02	110.18	110.42	6 400 000	10 400 000	8 000 000	==	-		-1
2218	Hha1	33	agc	90.39	90	90.34	90.44	0	13 700 000	18 700 000	0	=-	\		\(2)
2219	Hha1	25	cag	154.14	155	0	154.14	0	0	6 500 000	0	+-	A		\(2)
2220	Hha1	25	cag	155.29	155	155.2	155.38	0	6 300 000	5 500 000	0	=-	\		\(2)
2221	Taq1	34	tgc	101.16	101	101.16	0	0	3 000 000	0	0	-=	\		/(2)
2222	Taq1	39	agg	123.357	124	123.5	123.11	123.46	16 600 000	48 400 000	30 400 000	+=	/ (-)	/	/(2)
2223	Taq1	39	agg	123.55	124	0	123.55	0	0	39 600 000	0	+-	A		/(2)
2224	Taq1	39	agg	124.58	124	124.64	124.48	124.62	11 500 000	33 000 000	92 300 000	=+	/ (-)		/(2)
2225	Taq1	39	agg	123.357	124	123.5	123.11	123.46	616.45	486.43	895.43	=+	/ (-)	/	/(2)
2226	Taq1	39	agg	123.55	124	0	123.55	0	0	397.99	0	+-	A		/(2)
2227	Taq1	39	agg	124.58	124	124.64	124.48	124.62	427.06	331.66	2 718.7	=+	/ (-)		/(2)
2228	Taq1	56	tga	123.35	124	0	0	123.35	0	0	5 100 000	=+	/	/	/(2)
2229	Hha1	39	agg	100.65	101	100.4	0	100.9	461.87	0	687.66	-+(=)	V		\(4)
2230	Hha1	39	agg	101.02	101	0	101.02	0	0	770.19	0	+-	A		\(4)
2231	Hha1	8	gaa	234.315	235	0	234.45	234.18	0	4 000 000	5 300 000	+=	/		\(4)
2232	Hha1	8	gaa	235.04	235	235.04	0	0	4 300 000	0	0	-=	\		\(4)
2233	Taq1	8	gaa	235.63	235	235.63	0	0	3 800 000	0	0	-=	\		\(4)
2234	Hha1	8	gaa	236.3	235	236.33	236.27	0	3 900 000	3 100 000	0	=-	\		\(4)
2235	Taq1	50	aat	276.38	278	276.38	0	0	3 600 000	0	0	-=	\		\(4)
2236	Taq1	50	aat	277.49	278	0	277.49	0	0	3 300 000	0	+-	A		\(4)
2237	Taq1	50	aat	278.3	278	278.3	0	0	3 300 000	0	0	-=	\		\(4)
2238	Taq1	50	aat	279.02	278	279.02	0	0	9 800 000	0	0	-=	\		\(4)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
2196	RNU03551.PE1	nc	dopamine D4 receptor		tac	agc	No change
2197	RNU03551.PE1	nc	dopamine D4 receptor		tac	agc	No change
2198	RNU03551.PE1	nc	dopamine D4 receptor		tac	agc	No change
2199	RNU03551.PE1	nc	dopamine D4 receptor		tgg	tcg	No change
2200	RNU03551.PE1	nc	dopamine D4 receptor		tgg	tcg	No change
2201	RNU03551.PE1	nc	dopamine D4 receptor		tgg	tcg	No change
2202	RNU03551.PE1	nc	dopamine D4 receptor		tgg	tcg	No change
2203	RATD4RA.RATD4	RATD4	dopamine receptor D4		cgt	ctc	No change
2204	RATD4RA.RATD4	RATD4	dopamine receptor D4		tac	ccc	No change
2205	RATD4RA.RATD4	RATD4	dopamine receptor D4		tac	ccc	No change
2206	RATD4RA.RATD4	RATD4	dopamine receptor D4		tac	agc	No change
2207	RATD4RA.RATD4	RATD4	dopamine receptor D4		tac	agc	No change
2208	RATD4RA.RATD4	RATD4	dopamine receptor D4		tac	agc	No change
2209	RATD4RA.RATD4	RATD4	dopamine receptor D4		tgg	tcg	No change
2210	RATD4RA.RATD4	RATD4	dopamine receptor D4		tgg	tcg	No change
2211	RATD4RA.RATD4	RATD4	dopamine receptor D4		tgg	tcg	No change
2212	RATD4RA.RATD4	RATD4	dopamine receptor D4		tgg	tcg	No change
2213	AF379608.DMRT1	Dmrt1	doublesex and mab-3 related transcription factor		agg	tgg	decreased
2214	AF379608.DMRT1	Dmrt1	doublesex and mab-3 related transcription factor		agg	tgg	No change
2215	AF379608.DMRT1	Dmrt1	doublesex and mab-3 related transcription factor		agg	tgg	No change
2216	AF379608.DMRT1	Dmrt1	doublesex and mab-3 related transcription factor		agg	tgg	decreased
2217	AF379608.DMRT1	Dmrt1	doublesex and mab-3 related transcription factor		agg	tgg	No change
2218	RNU43534.RED1	RED1	double-stranded RNA-specific editase		tgt	agc	increased
2219	RNU43534.RED1	RED1	double-stranded RNA-specific editase		cag	gct	increased
2220	RNU43534.RED1	RED1	double-stranded RNA-specific editase		cag	gct	increased
2221	AF297118.DREAM	Dream	DREAM		tgc	agc	decreased
2222	AF297118.DREAM	Dream	DREAM		tga	agg	decreased
2223	AF297118.DREAM	Dream	DREAM		tga	agg	decreased
2224	AF297118.DREAM	Dream	DREAM		tga	agg	decreased
2225	AF297118.DREAM	Dream	DREAM		tga	agg	decreased
2226	AF297118.DREAM	Dream	DREAM		tga	agg	decreased
2227	AF297118.DREAM	Dream	DREAM		tga	agg	decreased
2228	AF297118.DREAM	Dream	DREAM		tga	agg	decreased
2229	RNDREBRIN.PE1	nc	drebrin A		cat	agg	increased
2230	RNDREBRIN.PE1	nc	drebrin A		cat	agg	increased
2231	RNDREBRIN.PE1	nc	drebrin A		gaa	tat	increased
2232	RNDREBRIN.PE1	nc	drebrin A		gaa	tat	increased
2233	RNDREBRIN.PE1	nc	drebrin A		gaa	tat	increased
2234	RNDREBRIN.PE1	nc	drebrin A		gaa	tat	increased
2235	RNDREBRIN.PE1	nc	drebrin A		gac	aat	increased
2236	RNDREBRIN.PE1	nc	drebrin A		gac	aat	increased
2237	RNDREBRIN.PE1	nc	drebrin A		gac	aat	increased
2238	RNDREBRIN.PE1	nc	drebrin A		gac	aat	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
2239	Hha1	31	gac	170.567	171	170.58	170.65	170.47	6 600 000	5 400 000	5 500 000	==	-		-2
2240	Hha1	31	gac	171.61	171	171.59	171.71	171.53	3 400 000	4 100 000	3 500 000	==	-		-2
2241	Taq1	52	att	216.463	217	216.2	216.69	216.5	3 800 000	3 400 000	11 700 000	=+	/ (-)		-2
2242	Taq1	52	att	217.385	217	217.38	0	217.39	4 100 000	0	9 600 000	=+(+)	/		-2
2243	Taq1	7	caa	315.53	317	0	315.53	0	0	3 400 000	0	+-	A		-2
2244	Hha1	59	ttc	143.267	144	143.26	143.18	143.36	343.21	408.18	152.64	=-	\ (-)		-2
2245	Hha1	59	ttc	144.413	144	144.33	144.48	144.43	280.81	235.71	372.54	==	-		-2
2246	Hha1	40	tgg	156.92	156	156.76	156.92	157.08	5 700 000	6 000 000	3 800 000	==	-		-2
2247	Hha1	49	aaa	83.57	84	0	83.57	0	0	18 100 000	0	+-	A		/(2)
2248	Hha1	49	aaa	84.405	84	84.41	84.4	0	10 700 000	7 600 000	0	=-	\		/(2)
2249	Hha1	33	agc	86.35	86	0	86.44	86.26	0	3 200 000	67 900 000	=+	/		/(2)
2250	Hha1	56	tga	144.06	144	144.29	0	143.83	277.85	0	1 241.16	=+(+)	/		/(2)
2251	Hha1	20	ctc	120.853	121	120.78	120.99	120.79	2 561.98	1 114.6	512.88	-=	\ (-)	(-)	
2252	Hha1	39	agg	121.03	121	121.19	121.17	120.73	373.9	268.67	297.03	==	-	(-)	
2253	Taq1	8	gaa	123.28	124	0	0	123.28	0	0	22 900 000	=+	/		/(6)
2254	Hha1	8	gaa	123.7	124	0	0	123.7	0	0	3 900 000	=+	/		/(6)
2255	Taq1	26	ctg	124.2	124	124.24	124.25	124.11	4 200 000	7 900 000	4 600 000	+=	/ (-)		/(6)
2256	Taq1	57	ctg	124.13	124	0	0	124.13	0	0	6 200 000	=+	/		/(6)
2257	Taq1	34	tgc	125.9	126	125.9	125.9	0	9 900 000	13 700 000	0	=-	\		/(6)
2258	Taq1	52	att	127.025	127	0	126.97	127.08	0	12 600 000	4 700 000	+-	A		/(6)
2259	Taq1	52	att	127.365	127	0	127.49	127.24	0	5 500 000	4 200 000	+=	/		/(6)
2260	Taq1	52	att	127.39	127	0	0	127.39	0	0	4 200 000	=+	/		/(6)
2261	Taq1	23	cga	144.71	145	144.73	0	144.69	4 400 000	0	6 200 000	-+(=)	V		/(6)
2262	Taq1	23	cga	145.87	145	0	0	145.87	0	0	3 400 000	=+	/		/(6)
2263	Taq1	64	gtt	144.88	145	144.88	144.86	144.9	6 900 000	7 400 000	3 700 000	=-	\ (-)		/(6)
2264	Taq1	8	gaa	123.28	124	0	0	123.28	0	0	22 900 000	=+	/		/(6)
2265	Hha1	8	gaa	123.7	124	0	0	123.7	0	0	3 900 000	=+	/		/(6)
2266	Taq1	26	ctg	124.2	124	124.24	124.25	124.11	4 200 000	7 900 000	4 600 000	+=	/ (-)		/(6)
2267	Taq1	57	ctg	124.13	124	0	0	124.13	0	0	6 200 000	=+	/		/(6)
2268	Taq1	34	tgc	125.9	126	125.9	125.9	0	9 900 000	13 700 000	0	=-	\		/(6)
2269	Taq1	52	att	127.025	127	0	126.97	127.08	0	12 600 000	4 700 000	+-	A		/(6)
2270	Taq1	52	att	127.365	127	0	127.49	127.24	0	5 500 000	4 200 000	+=	/		/(6)
2271	Taq1	52	att	127.39	127	0	0	127.39	0	0	4 200 000	=+	/		/(6)
2272	Taq1	23	cga	144.71	145	144.73	0	144.69	4 400 000	0	6 200 000	-+(=)	V		/(6)
2273	Taq1	23	cga	145.87	145	0	0	145.87	0	0	3 400 000	=+	/		/(6)
2274	Taq1	64	gtt	144.88	145	144.88	144.86	144.9	6 900 000	7 400 000	3 700 000	=-	\ (-)		/(6)
2275	Taq1	31	gac	137.613	138	137.71	137.51	137.62	10 400 000	5 200 000	17 800 000	=+	/ (-)		-2
2276	Taq1	31	gac	138.627	138	138.72	138.52	138.64	5 100 000	4 700 000	30 400 000	=+	/ (-)		-2
2277	Taq1	61	tct	137.773	138	137.63	137.76	137.93	3 500 000	9 900 000	3 400 000	+-	A		-2
2278	Taq1	61	tct	137.86	138	137.86	0	0	4 000 000	0	0	-=	\		-2
2279	Taq1	12	agt	172.507	173	172.52	172.44	172.56	4 100 000	3 300 000	3 600 000	==	-		-2
2280	Taq1	12	agt	173.553	173	173.55	173.48	173.63	7 100 000	7 700 000	8 100 000	==	-		-2
2281	Taq1	56	tga	119.8	120	119.86	119.74	0	17 300 000	23 200 000	0	=-	\		\(2)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
2239	AF542180.DUOX1	Duox1	dual oxidase 1		gac	tca	No change
2240	AF542180.DUOX1	Duox1	dual oxidase 1		gac	tca	No change
2241	AF542180.DUOX1	Duox1	dual oxidase 1		att	ggt	No change
2242	AF542180.DUOX1	Duox1	dual oxidase 1		att	ggt	No change
2243	AF542180.DUOX1	Duox1	dual oxidase 1		caa	tga	No change
2244	AF347030.EPM2A	Epm2a	dual-specificity phosphatase laforin		ttc	aga	No change
2245	AF347030.EPM2A	Epm2a	dual-specificity phosphatase laforin		ttc	aga	No change
2246	AF347030.EPM2A	Epm2a	dual-specificity phosphatase laforin		tgg	tgc	No change
2247	RNU64030.PE1	nc	dUTPase		aaa	tcc	decreased
2248	RNU64030.PE1	nc	dUTPase		aaa	tcc	decreased
2249	RNU64030.PE1	nc	dUTPase		agc	gga	decreased
2250	RNU64030.PE1	nc	dUTPase		tga	gga	decreased
2251	AF190798.PE1	nc	dynactin subunit p62		ctc	agg	No change
2252	AF190798.PE1	nc	dynactin subunit p62		ctc	agg	No change
2253	AF195787.DRP2	Drp2	dystrophin-related protein 2 A-form splice	*	gaa	ctg	decreased
2254	AF195787.DRP2	Drp2	dystrophin-related protein 2 A-form splice	*	gaa	ctg	decreased
2255	AF195787.DRP2	Drp2	dystrophin-related protein 2 A-form splice	*	gaa	ctg	decreased
2256	AF195787.DRP2	Drp2	dystrophin-related protein 2 A-form splice	*	gaa	ctg	decreased
2257	AF195787.DRP2	Drp2	dystrophin-related protein 2 A-form splice	*	att	tgc	decreased
2258	AF195787.DRP2	Drp2	dystrophin-related protein 2 A-form splice	*	att	tgc	decreased
2259	AF195787.DRP2	Drp2	dystrophin-related protein 2 A-form splice	*	att	tgc	decreased
2260	AF195787.DRP2	Drp2	dystrophin-related protein 2 A-form splice	*	att	tgc	decreased
2261	AF195787.DRP2	Drp2	dystrophin-related protein 2 A-form splice	*	cga	gtt	decreased
2262	AF195787.DRP2	Drp2	dystrophin-related protein 2 A-form splice	*	cga	gtt	decreased
2263	AF195787.DRP2	Drp2	dystrophin-related protein 2 A-form splice	*	cga	gtt	decreased
2264	AF195788.DRP2	Drp2	dystrophin-related protein 2 B-form splice	*	gaa	ctg	decreased
2265	AF195788.DRP2	Drp2	dystrophin-related protein 2 B-form splice	*	gaa	ctg	decreased
2266	AF195788.DRP2	Drp2	dystrophin-related protein 2 B-form splice	*	gaa	ctg	decreased
2267	AF195788.DRP2	Drp2	dystrophin-related protein 2 B-form splice	*	gaa	ctg	decreased
2268	AF195788.DRP2	Drp2	dystrophin-related protein 2 B-form splice	*	att	tgc	decreased
2269	AF195788.DRP2	Drp2	dystrophin-related protein 2 B-form splice	*	att	tgc	decreased
2270	AF195788.DRP2	Drp2	dystrophin-related protein 2 B-form splice	*	att	tgc	decreased
2271	AF195788.DRP2	Drp2	dystrophin-related protein 2 B-form splice	*	att	tgc	decreased
2272	AF195788.DRP2	Drp2	dystrophin-related protein 2 B-form splice	*	cga	gtt	decreased
2273	AF195788.DRP2	Drp2	dystrophin-related protein 2 B-form splice	*	cga	gtt	decreased
2274	AF195788.DRP2	Drp2	dystrophin-related protein 2 B-form splice	*	cga	gtt	decreased
2275	RNU09228.PE1	nc	E-box binding factor		tct	gac	No change
2276	RNU09228.PE1	nc	E-box binding factor		tct	gac	No change
2277	RNU09228.PE1	nc	E-box binding factor		tct	gac	No change
2278	RNU09228.PE1	nc	E-box binding factor		tct	gac	No change
2279	RNU09228.PE1	nc	E-box binding factor		agt	agc	No change
2280	RNU09228.PE1	nc	E-box binding factor		agt	agc	No change
2281	AB017696.PE1	nc	E-cadherin		aat	tga	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
2282	Taq1	50	aat	121.24	121	121.52	121.09	121.11	11 900 000	19 200 000	5 400 000	=-	\ (-)		\(2)
2283	Taq1	10	atg	132.3	133	132.3	0	0	6 800 000	0	0	-=	\		\(3)
2284	Taq1	10	atg	132.83	133	0	132.83	0	0	4 300 000	0	+-	A		\(3)
2285	Hha1	10	atg	132.85	133	132.85	0	0	10 200 000	0	0	-=	\		\(3)
2286	Taq1	10	atg	133.225	133	133.35	0	133.1	20 400 000	0	4 800 000	-=(-)	\		\(3)
2287	Hha1	9	atc	197.09	198	197.3	0	196.88	3 200 000	0	3 400 000	-+(=)	V		V(2)
2288	Hha1	9	atc	198.45	198	198.27	198.63	0	3 000 000	3 800 000	0	=-	\		V(2)
2289	Taq1	50	aat	211.18	211	211.13	0	211.23	12 000 000	0	7 200 000	-+(=)	V		V(2)
2290	Hha1	39	agg	99.73	100	0	99.84	99.62	0	364.2	769.04	++	/		/(2)
2291	Hha1	25	cag	303.98	304	0	303.87	304.09	0	3 000 000	3 600 000	+=	/		/(2)
2292	Hha1	25	cag	305.22	304	305.22	0	0	3 100 000	0	0	-=	\		/(2)
2293	Taq1	44	cgg	139.79	139	139.74	0	139.84	277.74	0	986.32	=+(+)	/	/	
2294	Taq1	29	gca	139.62	140	0	0	139.62	0	0	5 300 000	=+	/	/	
2295	Hha1	11	act	184.157	184	184.17	184.11	184.19	4 500 000	4 500 000	7 800 000	==	-	(-)	
2296	Taq1	11	act	184.19	184	184.25	184.23	184.09	3 300 000	3 300 000	12 000 000	=+	/ (-)	(-)	
2297	Hha1	44	cgg	72.173	72	72.07	72.24	72.21	157 200 000	31 700 000	60 300 000	-=	\ (-)		-2
2298	Hha1	43	cgc	138.53	138	138.52	138.57	138.5	5 500 000	4 700 000	3 800 000	==	-		-2
2299	Hha1	16	tag	223.85	225	223.74	223.9	223.91	19 800 000	5 200 000	4 100 000	-=	\ (-)	\	\(2)
2300	Hha1	16	tag	224.793	225	224.76	224.76	224.86	14 700 000	22 100 000	15 400 000	==	-		\(2)
2301	Hha1	16	tag	225.96	225	225.96	0	0	3 400 000	0	0	-=	\		\(2)
2302	Taq1	21	acc	223.72	225	223.72	0	0	3 100 000	0	0	-=	\	\	\(2)
2303	Hha1	26	ctg	99.44	100	99.53	99.35	0	10 500 000	4 000 000	0	-=	\		\(2)
2304	Hha1	6	aga	228.935	230	228.92	228.95	0	74 800 000	6 100 000	0	-=	\		\(2)
2305	Hha1	6	aga	231.02	230	231.02	0	0	18 200 000	0	0	-=	\		\(2)
2306	Taq1	56	tga	269.47	271	0	0	269.47	0	0	5 400 000	=+	/		\(2)
2307	Hha1	26	ctg	99.44	100	99.53	99.35	0	10 500 000	4 000 000	0	-=	\		\(2)
2308	Hha1	6	aga	228.935	230	228.92	228.95	0	74 800 000	6 100 000	0	-=	\		\(2)
2309	Hha1	6	aga	231.02	230	231.02	0	0	18 200 000	0	0	-=	\		\(2)
2310	Taq1	56	tga	269.47	271	0	0	269.47	0	0	5 400 000	=+	/		\(2)
2311	Hha1	26	ctg	99.44	100	99.53	99.35	0	10 500 000	4 000 000	0	-=	\		\(2)
2312	Hha1	6	aga	228.935	230	228.92	228.95	0	74 800 000	6 100 000	0	-=	\		\(2)
2313	Hha1	6	aga	231.02	230	231.02	0	0	18 200 000	0	0	-=	\		\(2)
2314	Hha1	6	aga	220.75	221	220.75	0	0	12 200 000	0	0	-=	\	\	
2315	Hha1	7	caa	220.663	221	220.73	220.66	220.6	41 200 000	6 500 000	7 800 000	-=	\ (-)	\	
2316	Hha1	20	ctc	112.98	113	112.84	113.12	0	1 219	826.12	0	=-	\	\	\(2)
2317	Hha1	20	ctc	113.32	113	113.32	0	0	1 721.76	0	0	-=	\		\(2)
2318	Hha1	33	agc	112.82	113	112.83	112.81	0	17 300 000	12 900 000	0	=-	\	\	\(2)
2319	Hha1	49	aaa	100.63	101	100.82	100.44	0	31 100 000	25 500 000	0	=-	\		/(2) \(2)
2320	Hha1	49	aaa	101.18	101	0	0	101.18	0	0	3 500 000	=+	/		/(2) \(2)
2321	Hha1	43	cgc	171.52	172	171.55	171.54	171.47	16 700 000	17 200 000	4 500 000	=-	\ (-)		/(2) \(2)
2322	Hha1	43	cgc	172.56	172	172.56	0	0	11 600 000	0	0	-=	\		/(2) \(2)
2323	Hha1	39	agg	172.59	173	0	0	172.59	0	0	231.93	=+	/		/(2) \(2)
2324	Hha1	39	agg	173.35	173	0	173.12	173.58	0	250.76	162.76	+=	/		/(2) \(2)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
2282	AB017696.PE1	nc	E-cadherin		aat	tga	increased
2283	AF018261.PE1	nc	EH domain binding protein Epsin		ccg	atg	increased
2284	AF018261.PE1	nc	EH domain binding protein Epsin		ccg	atg	increased
2285	AF018261.PE1	nc	EH domain binding protein Epsin		ccg	atg	increased
2286	AF018261.PE1	nc	EH domain binding protein Epsin		ccg	atg	increased
2287	RNU21954.PE1	nc	Ehk-3, full length form		atc	atc	decreased by mild
2288	RNU21954.PE1	nc	Ehk-3, full length form		atc	atc	decreased by mild
2289	RNU21954.PE1	nc	Ehk-3, full length form		aat	gtg	decreased by mild
2290	AY149902.PE1	nc	ELAC2		acc	agg	decreased
2291	AY149902.PE1	nc	ELAC2		cag	gtg	decreased
2292	AY149902.PE1	nc	ELAC2		cag	gtg	decreased
2293	RNO7632.ELK3	elk3	ELK channel 3		cgg	gca	decreased
2294	RNO7632.ELK3	elk3	ELK channel 3		cgg	gca	decreased
2295	AF023657.ENMAN	Enman	endo-alpha-D-mannosidase		cat	act	No change
2296	AF023657.ENMAN	Enman	endo-alpha-D-mannosidase		cat	act	No change
2297	RNU94709.PE1	nc	EP4 prostanoid receptor		ctc	cgg	No change
2298	RNU94709.PE1	nc	EP4 prostanoid receptor		cgc	tgc	No change
2299	RNO515239.RE4	re4	epididymal secretory protein 4		acc	tag	increased
2300	RNO515239.RE4	re4	epididymal secretory protein 4		acc	tag	increased
2301	RNO515239.RE4	re4	epididymal secretory protein 4		acc	tag	increased
2302	RNO515239.RE4	re4	epididymal secretory protein 4		acc	tag	increased
2303	RNENACG.RENAC	rENaC	epithelial sodium channel, gamma subunit		ctg	aag	increased
2304	RNENACG.RENAC	rENaC	epithelial sodium channel, gamma subunit		aga	aga	increased
2305	RNENACG.RENAC	rENaC	epithelial sodium channel, gamma subunit		aga	aga	increased
2306	RNENACG.RENAC	rENaC	epithelial sodium channel, gamma subunit		tgg	tga	increased
2307	RNU37539.RENACG	rEnacg	epithelial sodium channel, gamma subunit		ctg	aag	increased
2308	RNU37539.RENACG	rEnacg	epithelial sodium channel, gamma subunit		aga	aga	increased
2309	RNU37539.RENACG	rEnacg	epithelial sodium channel, gamma subunit		aga	aga	increased
2310	RNU37539.RENACG	rEnacg	epithelial sodium channel, gamma subunit		tgg	tga	increased
2311	RNU37540.RENACG	rEnacg	epithelial sodium channel, gamma subunit		ctg	aag	increased
2312	RNU37540.RENACG	rEnacg	epithelial sodium channel, gamma subunit		aga	aga	increased
2313	RNU37540.RENACG	rEnacg	epithelial sodium channel, gamma subunit		aga	aga	increased
2314	AF176784.E3B1	e3B1	eps8 binding protein		aga	caa	increased
2315	AF176784.E3B1	e3B1	eps8 binding protein		aga	caa	increased
2316	RNO294544.ESU	esu	Esau protein		agc	ctc	increased
2317	RNO294544.ESU	esu	Esau protein		agc	ctc	increased
2318	RNO294544.ESU	esu	Esau protein		agc	ctc	increased
2319	RNU46007.PE1	nc	espin		gac	aaa	decreased
2320	RNU46007.PE1	nc	espin		gac	aaa	decreased
2321	RNU46007.PE1	nc	espin		agg	cgc	decreased
2322	RNU46007.PE1	nc	espin		agg	cgc	decreased
2323	RNU46007.PE1	nc	espin		agg	cgc	decreased
2324	RNU46007.PE1	nc	espin		agg	cgc	decreased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
2325	Hha1	26	ctg	160.49	161	0	0	160.49	0	0	9 400 000	=+	/		/(3) \(3)
2326	Hha1	26	ctg	161.59	161	161.59	0	0	3 000 000	0	0	-=	\		/(3) \(3)
2327	Hha1	61	tct	160.49	161	160.65	160.33	0	3 300 000	3 600 000	0	=-	\		/(3) \(3)
2328	Hha1	61	tct	161.41	161	0	161.41	0	0	13 200 000	0	+-	A		/(3) \(3)
2329	Hha1	32	gtc	164.93	165	164.93	0	0	750.64	0	0	-=	\		/(3) \(3)
2330	Hha1	32	gtc	165.45	165	0	0	165.45	0	0	469.31	=+	/		/(3) \(3)
2331	Hha1	41	ccc	181.43	181	0	0	181.43	0	0	3 400 000	=+	/		/(3) \(3)
2332	Hha1	17	cca	182.767	182	182.67	182.81	182.82	4 592.77	7 157.46	12 053.35	==	-		/(3) \(3)
2333	Hha1	39	agg	97.095	97	97.23	0	96.96	329.91	0	309.24	-+(=)	V		\(3)
2334	Taq1	39	agg	100.417	100	100.17	100.54	100.54	6 100 000	29 200 000	11 700 000	+-	A		\(3)
2335	Taq1	39	agg	100.523	100	100.49	100.54	100.54	4 700 000	293.47	344.62	-=	\ (-)	\	\(3)
2336	Taq1	39	agg	100.17	100	100.17	0	0	226.53	0	0	-=	\		\(3)
2337	Taq1	39	agg	100.49	100	100.49	0	0	174.53	0	0	-=	\	\	\(3)
2338	Taq1	56	tga	100.495	100	100.4	100.59	0	5 100 000	9 000 000	0	=-	\	\	\(3)
2339	Taq1	56	tga	99.73	100	0	99.73	0	0	4 600 000	0	+-	A		\(3)
2340	Hha1	49	aaa	125.425	126	0	125.52	125.33	0	3 900 000	4 000 000	+=	/		\(3)
2341	Hha1	49	aaa	126.207	126	126.38	126.03	126.21	23 600 000	8 000 000	3 600 000	-=	\ (-)		\(3)
2342	Taq1	54	ttt	135.905	136	135.89	135.92	0	662.78	893.8	0	=-	\		\(2) A(2)
2343	Taq1	54	ttt	136.7	136	0	136.7	0	0	388.09	0	+-	A		\(2) A(2)
2344	Taq1	50	aat	331.74	333	331.74	0	0	4 800 000	0	0	-=	\		\(2) A(2)
2345	Taq1	50	aat	334.54	333	0	334.54	0	0	3 000 000	0	+-	A		\(2) A(2)
2346	Hha1	27	acg	92.385	92	92.23	0	92.54	8 600 000	0	4 700 000	-+(-)	V (\)		\(3)
2347	Hha1	15	tac	94.75	95	94.77	94.73	94.75	45 600 000	19 800 000	7 400 000	-=	\ (-)		\(3)
2348	Hha1	15	tac	94.74	95	0	94.73	94.75	0	5 099.15	1 609.39	+-	A		\(3)
2349	Hha1	49	aaa	279.587	281	279.49	279.66	279.61	6 600 000	3 200 000	3 000 000	-=	\ (-)		\(3)
2350	Hha1	49	aaa	280.45	281	280.45	0	0	3 800 000	0	0	-=	\		\(3)
2351	Hha1	49	aaa	282.15	281	282.19	282.11	0	6 800 000	8 700 000	0	=-	\		\(3)
2352	Hha1	33	agc	78.69	79	78.69	0	0	4 200 000	0	0	-=	\		\(2)
2353	Hha1	33	agc	110.905	111	110.83	110.98	0	12 700 000	12 900 000	0	=-	\		\(2)
2354	Hha1	44	cgg	120.76	121	0	120.76	0	0	5 100 000	0	+-	A		\(2)
2355	Hha1	39	agg	76.73	77	76.8	76.51	76.88	549.85	1 540.39	329.58	+-	A		A(2)
2356	Hha1	40	tgg	196.87	198	0	196.71	197.03	0	4 900 000	4 600 000	+=	/		A(2)
2357	Hha1	40	tgg	197.52	198	0	197.52	0	0	5 300 000	0	+-	A		A(2)
2358	Hha1	40	tgg	198.35	198	198.35	0	0	4 300 000	0	0	-=	\		A(2)
2359	Hha1	27	acg	88.41	88	88.44	88.33	88.46	6 800 000	3 600 000	3 200 000	-=	\ (-)		\(3)
2360	Hha1	26	ctg	114.717	115	114.71	114.63	114.81	12 300 000	6 500 000	4 700 000	-=	\ (-)		\(3)
2361	Taq1	39	agg	141.93	142	141.93	0	0	10 900 000	0	0	-=	\		\(3)
2362	Taq1	39	agg	141.93	142	141.93	0	0	404.78	0	0	-=	\		\(3)
2363	Taq1	56	tga	183.85	184	0	183.85	0	0	4 700 000	0	+-	A		\(3)
2364	Hha1	27	acg	73.827	74	73.8	73.91	73.77	70 000 000	22 000 000	43 500 000	-=	\ (-)		\(2)
2365	Taq1	39	agg	156.95	157	0	156.95	0	0	38 200 000	0	+-	A		\(2)
2366	Taq1	39	agg	156.26	157	0	156.26	0	0	114.57	0	+-	A		\(2)
2367	Taq1	39	agg	156.95	157	0	156.95	0	0	383.92	0	+-	A		\(2)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
2325	RNAJ2556.PE1	nc	E-STOP protein		ctg	tct	decreased
2326	RNAJ2556.PE1	nc	E-STOP protein		ctg	tct	decreased
2327	RNAJ2556.PE1	nc	E-STOP protein		ctg	tct	decreased
2328	RNAJ2556.PE1	nc	E-STOP protein		ctg	tct	decreased
2329	RNAJ2556.PE1	nc	E-STOP protein		ggc	gtc	decreased
2330	RNAJ2556.PE1	nc	E-STOP protein		ggc	gtc	decreased
2331	RNAJ2556.PE1	nc	E-STOP protein		ccc	cca	decreased
2332	RNAJ2556.PE1	nc	E-STOP protein		ccc	cca	decreased
2333	RN17BHD1.PE1	nc	estradiol 17 beta-dehydrogenase	*	agg	agg	increased
2334	RN17BHD1.PE1	nc	estradiol 17 beta-dehydrogenase	*	agg	tga	increased
2335	RN17BHD1.PE1	nc	estradiol 17 beta-dehydrogenase	*	agg	tga	increased
2336	RN17BHD1.PE1	nc	estradiol 17 beta-dehydrogenase	*	agg	tga	increased
2337	RN17BHD1.PE1	nc	estradiol 17 beta-dehydrogenase	*	agg	tga	increased
2338	RN17BHD1.PE1	nc	estradiol 17 beta-dehydrogenase	*	agg	tga	increased
2339	RN17BHD1.PE1	nc	estradiol 17 beta-dehydrogenase	*	agg	tga	increased
2340	RN17BHD1.PE1	nc	estradiol 17 beta-dehydrogenase	*	cac	aaa	increased
2341	RN17BHD1.PE1	nc	estradiol 17 beta-dehydrogenase	*	cac	aaa	increased
2342	AF167170.ERG1	ERG1	estrogen-regulated protein		agc	ttt	increased
2343	AF167170.ERG1	ERG1	estrogen-regulated protein		agc	ttt	increased
2344	AF167170.ERG1	ERG1	estrogen-regulated protein		gat	aat	increased
2345	AF167170.ERG1	ERG1	estrogen-regulated protein		gat	aat	increased
2346	RNU91679.PE1	nc	ETS domain transcription factor PET-1		acg	cat	increased
2347	RNU91679.PE1	nc	ETS domain transcription factor PET-1		tac	ggg	increased
2348	RNU91679.PE1	nc	ETS domain transcription factor PET-1		tac	ggg	increased
2349	RNU91679.PE1	nc	ETS domain transcription factor PET-1		aaa	ggt	increased
2350	RNU91679.PE1	nc	ETS domain transcription factor PET-1		aaa	ggt	increased
2351	RNU91679.PE1	nc	ETS domain transcription factor PET-1		aaa	ggt	increased
2352	RNU83914.PE1	nc	eukaryotic initiation factor eIF-2B beta		agc	agc	increased
2353	RNU83914.PE1	nc	eukaryotic initiation factor eIF-2B beta		agc	cca	increased
2354	RNU83914.PE1	nc	eukaryotic initiation factor eIF-2B beta		cgg	ggc	increased
2355	AB040468.EFA6	EFA6	exchange factor for ARF6		cag	agg	increased by mild
2356	AB040468.EFA6	EFA6	exchange factor for ARF6		aca	tgg	increased by mild
2357	AB040468.EFA6	EFA6	exchange factor for ARF6		aca	tgg	increased by mild
2358	AB040468.EFA6	EFA6	exchange factor for ARF6		aca	tgg	increased by mild
2359	AF032669.PE1	nc	exo84		tca	acg	increased
2360	AF032669.PE1	nc	exo84		ggc	ctg	increased
2361	AF032669.PE1	nc	exo84		agg	agc	increased
2362	AF032669.PE1	nc	exo84		agg	agc	increased
2363	AF032669.PE1	nc	exo84		ggc	tga	increased
2364	RATERK1.PE1	nc	extracellular signal-regulated kinase 1		gta	acg	increased
2365	RATERK1.PE1	nc	extracellular signal-regulated kinase 1		cgt	agg	increased
2366	RATERK1.PE1	nc	extracellular signal-regulated kinase 1		cgt	agg	increased
2367	RATERK1.PE1	nc	extracellular signal-regulated kinase 1		cgt	agg	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
2368	Taq1	39	agg	157.71	157	157.71	0	0	4 600 000	0	0	-=	\		\(2)
2369	Taq1	39	agg	156.06	157	156.06	0	0	185.68	0	0	-=	\		\(2)
2370	Taq1	39	agg	157.71	157	157.71	0	0	170.82	0	0	-=	\		\(2)
2371	Taq1	24	cgt	127.25	128	127.29	127.17	127.29	4 000 000	3 800 000	8 900 000	=+	/ (-)	(-)	
2372	Taq1	30	cgt	127.367	128	127.38	127.43	127.29	12 700 000	8 800 000	8 200 000	==	-	(-)	
2373	Hha1	27	acg	73.827	74	73.8	73.91	73.77	70 000 000	22 000 000	43 500 000	-=	\ (-)		\(2)
2374	Taq1	39	agg	156.95	157	0	156.95	0	0	38 200 000	0	+-	A		\(2)
2375	Taq1	39	agg	156.26	157	0	156.26	0	0	114.57	0	+-	A		\(2)
2376	Taq1	39	agg	156.95	157	0	156.95	0	0	383.92	0	+-	A		\(2)
2377	Taq1	39	agg	157.71	157	157.71	0	0	4 600 000	0	0	-=	\		\(2)
2378	Taq1	39	agg	156.06	157	156.06	0	0	185.68	0	0	-=	\		\(2)
2379	Taq1	39	agg	157.71	157	157.71	0	0	170.82	0	0	-=	\		\(2)
2380	Hha1	7	caa	157.51	157	157.2	157.69	157.64	9 400 000	4 200 000	3 000 000	-=	\ (-)	(-)	
2381	Taq1	7	caa	157.64	157	157.84	157.43	157.65	3 600 000	5 500 000	3 100 000	==	-	(-)	
2382	Taq1	11	act	186.21	186	186.27	186.2	186.16	4 400 000	4 700 000	10 300 000	=+	/ (-)	(-)	
2383	Hha1	11	act	186.25	186	186.23	186.32	186.2	4 300 000	5 100 000	5 400 000	==	-	(-)	
2384	Hha1	2	tta	110.547	110	110.33	110.67	110.64	3 900 000	4 000 000	10 100 000	=+	/ (-)		-2
2385	Hha1	27	acg	109.64	110	109.7	109.62	109.6	73 000 000	17 000 000	49 400 000	-=	\ (-)		-2
2386	Hha1	31	gac	64.9	65	0	0	64.9	0	0	4 300 000	=+	/		/(2)
2387	Hha1	41	ccc	129.197	129	129.23	129.11	129.25	4 100 000	5 400 000	12 700 000	=+	/ (-)		/(2)
2388	Hha1	59	ttc	129.96	130	0	129.96	0	0	149.47	0	+-	A		/(2)
2389	Hha1	59	ttc	130.74	130	0	130.74	0	0	238.58	0	+-	A		/(2)
2390	Taq1	21	acc	223.72	223	223.72	0	0	3 100 000	0	0	-=	\	\	
2391	Taq1	39	agg	223.65	223	223.65	0	0	6 600 000	0	0	-=	\	\	
2392	Taq1	39	agg	223.65	223	223.65	0	0	245.09	0	0	-=	\	\	
2393	Hha1	6	aga	237.27	236	237.27	0	0	3 100 000	0	0	-=	\		\(4)
2394	Hha1	8	gaa	235.04	236	235.04	0	0	4 300 000	0	0	-=	\		\(4)
2395	Taq1	8	gaa	235.63	236	235.63	0	0	3 800 000	0	0	-=	\		\(4)
2396	Hha1	8	gaa	236.3	236	236.33	236.27	0	3 900 000	3 100 000	0	=-	\		\(4)
2397	Hha1	39	agg	66.61	67	0	66.57	66.65	0	1 629.94	2 937.82	+=	/		\(9)
2398	Taq1	45	gcc	107.68	108	107.48	107.75	107.81	3 300 000	5 000 000	5 700 000	==	-		\(9)
2399	Taq1	20	ctc	109.57	109	109.51	109.63	0	9 800 000	7 200 000	0	=-	\		\(9)
2400	Taq1	45	gcc	108.68	109	108.65	108.71	0	4 600 000	7 200 000	0	=-	\		\(9)
2401	Taq1	45	gcc	109.61	109	0	0	109.61	0	0	4 400 000	=+	/		\(9)
2402	Taq1	17	cca	109.613	110	109.48	109.66	109.7	812.7	365.64	526.23	-=	\ (-)		\(9)
2403	Taq1	17	cca	110.54	110	110.47	110.61	0	631.58	1 123.52	0	=-	\		\(9)
2404	Hha1	44	cgg	153.04	153	152.99	153.15	152.98	15 500 000	6 400 000	8 600 000	-=	\ (-)		\(9)
2405	Taq1	17	cca	171.903	172	171.91	171.8	172	273.99	744.58	691.62	+=	/ (-)		\(9)
2406	Taq1	17	cca	172.895	172	0	172.79	173	0	432.12	1 022.4	=+	/		\(9)
2407	Taq1	17	cca	239.72	241	239.72	0	0	404.03	0	0	-=	\		\(9)
2408	Taq1	17	cca	242.14	241	242.14	0	0	143.96	0	0	-=	\		\(9)
2409	Taq1	51	ata	244.755	244	244.66	0	244.85	26 600 000	0	9 800 000	-=(-)	\		\(9)
2410	Taq1	45	gcc	265.42	267	265.42	0	0	3 600 000	0	0	-=	\		\(9)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
2368	RATERK1.PE1	nc	extracellular signal-regulated kinase 1		cgt	agg	increased
2369	RATERK1.PE1	nc	extracellular signal-regulated kinase 1		cgt	agg	increased
2370	RATERK1.PE1	nc	extracellular signal-regulated kinase 1		cgt	agg	increased
2371	RATERK2.ERK2	ERK2	extracellular signal-related kinase 2		cgt	act	No change
2372	RATERK2.ERK2	ERK2	extracellular signal-related kinase 2		cgt	act	No change
2373	RATERK1A.ERK1	ERK1	extracellular-signal-regulated kinase 1		gta	acg	increased
2374	RATERK1A.ERK1	ERK1	extracellular-signal-regulated kinase 1		cgt	agg	increased
2375	RATERK1A.ERK1	ERK1	extracellular-signal-regulated kinase 1		cgt	agg	increased
2376	RATERK1A.ERK1	ERK1	extracellular-signal-regulated kinase 1		cgt	agg	increased
2377	RATERK1A.ERK1	ERK1	extracellular-signal-regulated kinase 1		cgt	agg	increased
2378	RATERK1A.ERK1	ERK1	extracellular-signal-regulated kinase 1		cgt	agg	increased
2379	RATERK1A.ERK1	ERK1	extracellular-signal-regulated kinase 1		cgt	agg	increased
2380	AF450298.PE1	nc	EZRIN		caa	tgg	No change
2381	AF450298.PE1	nc	EZRIN		caa	tgg	No change
2382	RNO18965.PE1	factor I	factor I protein		cct	act	No change
2383	RNO18965.PE1	factor I	factor I protein		cct	act	No change
2384	AF285078.PE1	nc	FAD-dependent sulfhydryl oxidase-2		tta	acg	No change
2385	AF285078.PE1	nc	FAD-dependent sulfhydryl oxidase-2		tta	acg	No change
2386	AF399874.FANG2	Fang2	FANG2		taa	gac	decreased
2387	AF399874.FANG2	Fang2	FANG2		ccc	ttc	decreased
2388	AF399874.FANG2	Fang2	FANG2		ccc	ttc	decreased
2389	AF399874.FANG2	Fang2	FANG2		ccc	ttc	decreased
2390	RATFTBS.PE1	nc	farnesyl-protein transferase beta-subunit		agg	acc	increased
2391	RATFTBS.PE1	nc	farnesyl-protein transferase beta-subunit		agg	acc	increased
2392	RATFTBS.PE1	nc	farnesyl-protein transferase beta-subunit		agg	acc	increased
2393	AB071986.RELO2	rELO2	fatty acid elongase 2		gaa	aga	increased
2394	AB071986.RELO2	rELO2	fatty acid elongase 2		gaa	aga	increased
2395	AB071986.RELO2	rELO2	fatty acid elongase 2		gaa	aga	increased
2396	AB071986.RELO2	rELO2	fatty acid elongase 2		gaa	aga	increased
2397	RATFASA.PE1	fatty acid syn	fatty acid synthase		ctg	agg	increased
2398	RATFASA.PE1	fatty acid syn	fatty acid synthase		ctc	gcc	increased
2399	RATFASA.PE1	fatty acid syn	fatty acid synthase		ctc	gcc	increased
2400	RATFASA.PE1	fatty acid syn	fatty acid synthase		cca	gcc	increased
2401	RATFASA.PE1	fatty acid syn	fatty acid synthase		cca	gcc	increased
2402	RATFASA.PE1	fatty acid syn	fatty acid synthase		cca	gcc	increased
2403	RATFASA.PE1	fatty acid syn	fatty acid synthase		cca	gcc	increased
2404	RATFASA.PE1	fatty acid syn	fatty acid synthase		cgg	tgt	increased
2405	RATFASA.PE1	fatty acid syn	fatty acid synthase		cca	ggg	increased
2406	RATFASA.PE1	fatty acid syn	fatty acid synthase		cca	ggg	increased
2407	RATFASA.PE1	fatty acid syn	fatty acid synthase		cat	cca	increased
2408	RATFASA.PE1	fatty acid syn	fatty acid synthase		cat	cca	increased
2409	RATFASA.PE1	fatty acid syn	fatty acid synthase		agc	ata	increased
2410	RATFASA.PE1	fatty acid syn	fatty acid synthase		gcc	ggc	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
2411	Taq1	45	gcc	265.96	267	0	265.96	0	0	3 300 000	0	+-	A		\(9)
2412	Taq1	39	agg	281.06	282	281.26	280.86	0	9 300 000	3 800 000	0	-=	\		\(9)
2413	Taq1	39	agg	282.4	282	0	282.4	0	0	7 200 000	0	+-	A		\(9)
2414	Taq1	39	agg	280.86	282	0	280.86	0	0	38.19	0	+-	A		\(9)
2415	Taq1	39	agg	282.4	282	0	282.4	0	0	72.36	0	+-	A		\(9)
2416	Taq1	39	agg	281.26	282	281.26	0	0	345.36	0	0	-=	\		\(9)
2417	Taq1	50	aat	282.41	283	282.41	0	0	7 600 000	0	0	-=	\		\(9)
2418	Hha1	39	agg	66.61	67	0	66.57	66.65	0	1 629.94	2 937.82	+=	/		\(9)
2419	Taq1	45	gcc	107.68	108	107.48	107.75	107.81	3 300 000	5 000 000	5 700 000	==	-		\(9)
2420	Taq1	20	ctc	109.57	109	109.51	109.63	0	9 800 000	7 200 000	0	=-	\		\(9)
2421	Taq1	45	gcc	108.68	109	108.65	108.71	0	4 600 000	7 200 000	0	=-	\		\(9)
2422	Taq1	45	gcc	109.61	109	0	0	109.61	0	0	4 400 000	=+	/		\(9)
2423	Taq1	17	cca	109.613	110	109.48	109.66	109.7	812.7	365.64	526.23	-=	\ (-)		\(9)
2424	Taq1	17	cca	110.54	110	110.47	110.61	0	631.58	1 123.52	0	=-	\		\(9)
2425	Hha1	44	cgg	153.04	153	152.99	153.15	152.98	15 500 000	6 400 000	8 600 000	-=	\ (-)		\(9)
2426	Taq1	17	cca	171.903	172	171.91	171.8	172	273.99	744.58	691.62	+=	/ (-)		\(9)
2427	Taq1	17	cca	172.895	172	0	172.79	173	0	432.12	1 022.4	=+	/		\(9)
2428	Taq1	17	cca	239.72	241	239.72	0	0	404.03	0	0	-=	\		\(9)
2429	Taq1	17	cca	242.14	241	242.14	0	0	143.96	0	0	-=	\		\(9)
2430	Taq1	51	ata	244.755	244	244.66	0	244.85	26 600 000	0	9 800 000	-=(-)	\		\(9)
2431	Taq1	45	gcc	265.42	267	265.42	0	0	3 600 000	0	0	-=	\		\(9)
2432	Taq1	45	gcc	265.96	267	0	265.96	0	0	3 300 000	0	+-	A		\(9)
2433	Taq1	39	agg	281.06	282	281.26	280.86	0	9 300 000	3 800 000	0	-=	\		\(9)
2434	Taq1	39	agg	282.4	282	0	282.4	0	0	7 200 000	0	+-	A		\(9)
2435	Taq1	39	agg	280.86	282	0	280.86	0	0	38.19	0	+-	A		\(9)
2436	Taq1	39	agg	282.4	282	0	282.4	0	0	72.36	0	+-	A		\(9)
2437	Taq1	39	agg	281.26	282	281.26	0	0	345.36	0	0	-=	\		\(9)
2438	Taq1	50	aat	282.41	283	282.41	0	0	7 600 000	0	0	-=	\		\(9)
2439	Hha1	39	agg	66.61	67	0	66.57	66.65	0	1 629.94	2 937.82	+=	/		\(9)
2440	Taq1	45	gcc	107.68	108	107.48	107.75	107.81	3 300 000	5 000 000	5 700 000	==	-		\(9)
2441	Taq1	20	ctc	109.57	109	109.51	109.63	0	9 800 000	7 200 000	0	=-	\		\(9)
2442	Taq1	45	gcc	108.68	109	108.65	108.71	0	4 600 000	7 200 000	0	=-	\		\(9)
2443	Taq1	45	gcc	109.61	109	0	0	109.61	0	0	4 400 000	=+	/		\(9)
2444	Taq1	17	cca	109.613	110	109.48	109.66	109.7	812.7	365.64	526.23	-=	\ (-)		\(9)
2445	Taq1	17	cca	110.54	110	110.47	110.61	0	631.58	1 123.52	0	=-	\		\(9)
2446	Hha1	44	cgg	153.04	153	152.99	153.15	152.98	15 500 000	6 400 000	8 600 000	-=	\ (-)		\(9)
2447	Taq1	17	cca	171.903	172	171.91	171.8	172	273.99	744.58	691.62	+=	/ (-)		\(9)
2448	Taq1	17	cca	172.895	172	0	172.79	173	0	432.12	1 022.4	=+	/		\(9)
2449	Taq1	17	cca	239.72	241	239.72	0	0	404.03	0	0	-=	\		\(9)
2450	Taq1	17	cca	242.14	241	242.14	0	0	143.96	0	0	-=	\		\(9)
2451	Taq1	51	ata	244.755	244	244.66	0	244.85	26 600 000	0	9 800 000	-=(-)	\		\(9)
2452	Taq1	45	gcc	265.42	267	265.42	0	0	3 600 000	0	0	-=	\		\(9)
2453	Taq1	45	gcc	265.96	267	0	265.96	0	0	3 300 000	0	+-	A		\(9)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
2411	RATFASA.PE1	fatty acid syn	fatty acid synthase		gcc	ggc	increased
2412	RATFASA.PE1	fatty acid syn	fatty acid synthase		agg	aat	increased
2413	RATFASA.PE1	fatty acid syn	fatty acid synthase		agg	aat	increased
2414	RATFASA.PE1	fatty acid syn	fatty acid synthase		agg	aat	increased
2415	RATFASA.PE1	fatty acid syn	fatty acid synthase		agg	aat	increased
2416	RATFASA.PE1	fatty acid syn	fatty acid synthase		agg	aat	increased
2417	RATFASA.PE1	fatty acid syn	fatty acid synthase		agg	aat	increased
2418	RATFASYN.PE1	fatty acid syn	fatty acid synthase		ctg	agg	increased
2419	RATFASYN.PE1	fatty acid syn	fatty acid synthase		ctc	gcc	increased
2420	RATFASYN.PE1	fatty acid syn	fatty acid synthase		ctc	gcc	increased
2421	RATFASYN.PE1	fatty acid syn	fatty acid synthase		cca	gcc	increased
2422	RATFASYN.PE1	fatty acid syn	fatty acid synthase		cca	gcc	increased
2423	RATFASYN.PE1	fatty acid syn	fatty acid synthase		cca	gcc	increased
2424	RATFASYN.PE1	fatty acid syn	fatty acid synthase		cca	gcc	increased
2425	RATFASYN.PE1	fatty acid syn	fatty acid synthase		cgg	tgt	increased
2426	RATFASYN.PE1	fatty acid syn	fatty acid synthase		cca	ggg	increased
2427	RATFASYN.PE1	fatty acid syn	fatty acid synthase		cca	ggg	increased
2428	RATFASYN.PE1	fatty acid syn	fatty acid synthase		cat	cca	increased
2429	RATFASYN.PE1	fatty acid syn	fatty acid synthase		cat	cca	increased
2430	RATFASYN.PE1	fatty acid syn	fatty acid synthase		agc	ata	increased
2431	RATFASYN.PE1	fatty acid syn	fatty acid synthase		gcc	ggc	increased
2432	RATFASYN.PE1	fatty acid syn	fatty acid synthase		gcc	ggc	increased
2433	RATFASYN.PE1	fatty acid syn	fatty acid synthase		agg	aat	increased
2434	RATFASYN.PE1	fatty acid syn	fatty acid synthase		agg	aat	increased
2435	RATFASYN.PE1	fatty acid syn	fatty acid synthase		agg	aat	increased
2436	RATFASYN.PE1	fatty acid syn	fatty acid synthase		agg	aat	increased
2437	RATFASYN.PE1	fatty acid syn	fatty acid synthase		agg	aat	increased
2438	RATFASYN.PE1	fatty acid syn	fatty acid synthase		agg	aat	increased
2439	RNFASDNA.FAS	FAS	fatty acid synthase	*	ctg	agg	increased
2440	RNFASDNA.FAS	FAS	fatty acid synthase	*	ctc	gcc	increased
2441	RNFASDNA.FAS	FAS	fatty acid synthase	*	ctc	gcc	increased
2442	RNFASDNA.FAS	FAS	fatty acid synthase	*	cca	gcc	increased
2443	RNFASDNA.FAS	FAS	fatty acid synthase	*	cca	gcc	increased
2444	RNFASDNA.FAS	FAS	fatty acid synthase	*	cca	gcc	increased
2445	RNFASDNA.FAS	FAS	fatty acid synthase	*	cca	gcc	increased
2446	RNFASDNA.FAS	FAS	fatty acid synthase	*	cgg	tgt	increased
2447	RNFASDNA.FAS	FAS	fatty acid synthase	*	cca	ggg	increased
2448	RNFASDNA.FAS	FAS	fatty acid synthase	*	cca	ggg	increased
2449	RNFASDNA.FAS	FAS	fatty acid synthase	*	cat	cca	increased
2450	RNFASDNA.FAS	FAS	fatty acid synthase	*	cat	cca	increased
2451	RNFASDNA.FAS	FAS	fatty acid synthase	*	agc	ata	increased
2452	RNFASDNA.FAS	FAS	fatty acid synthase	*	gcc	ggc	increased
2453	RNFASDNA.FAS	FAS	fatty acid synthase	*	gcc	ggc	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
2454	Taq1	39	agg	281.06	282	281.26	280.86	0	9 300 000	3 800 000	0	-=	\		\(9)
2455	Taq1	39	agg	282.4	282	0	282.4	0	0	7 200 000	0	+-	A		\(9)
2456	Taq1	39	agg	280.86	282	0	280.86	0	0	38.19	0	+-	A		\(9)
2457	Taq1	39	agg	282.4	282	0	282.4	0	0	72.36	0	+-	A		\(9)
2458	Taq1	39	agg	281.26	282	281.26	0	0	345.36	0	0	-=	\		\(9)
2459	Taq1	50	aat	282.41	283	282.41	0	0	7 600 000	0	0	-=	\		\(9)
2460	Hha1	40	tgg	133.193	133	133.22	133.26	133.1	3 800 000	8 000 000	6 900 000	+=	/ (-)	(-)	
2461	Hha1	49	aaa	133.33	134	133.26	133.16	133.57	15 600 000	20 200 000	7 500 000	=-	\ (-)	(-)	
2462	Hha1	39	agg	66.61	67	0	66.57	66.65	0	1 629.94	2 937.82	+=	/		\(9)
2463	Taq1	45	gcc	107.68	108	107.48	107.75	107.81	3 300 000	5 000 000	5 700 000	==	-		\(9)
2464	Taq1	20	ctc	109.57	109	109.51	109.63	0	9 800 000	7 200 000	0	=-	\		\(9)
2465	Taq1	45	gcc	108.68	109	108.65	108.71	0	4 600 000	7 200 000	0	=-	\		\(9)
2466	Taq1	45	gcc	109.61	109	0	0	109.61	0	0	4 400 000	=+	/		\(9)
2467	Taq1	17	cca	109.613	110	109.48	109.66	109.7	812.7	365.64	526.23	-=	\ (-)		\(9)
2468	Taq1	17	cca	110.54	110	110.47	110.61	0	631.58	1 123.52	0	=-	\		\(9)
2469	Hha1	44	cgg	153.04	153	152.99	153.15	152.98	15 500 000	6 400 000	8 600 000	-=	\ (-)		\(9)
2470	Taq1	17	cca	171.903	172	171.91	171.8	172	273.99	744.58	691.62	+=	/ (-)		\(9)
2471	Taq1	17	cca	172.895	172	0	172.79	173	0	432.12	1 022.4	=+	/		\(9)
2472	Taq1	17	cca	239.72	241	239.72	0	0	404.03	0	0	-=	\		\(9)
2473	Taq1	17	cca	242.14	241	242.14	0	0	143.96	0	0	-=	\		\(9)
2474	Taq1	51	ata	244.755	244	244.66	0	244.85	26 600 000	0	9 800 000	-=(-)	\		\(9)
2475	Taq1	45	gcc	265.42	267	265.42	0	0	3 600 000	0	0	-=	\		\(9)
2476	Taq1	45	gcc	265.96	267	0	265.96	0	0	3 300 000	0	+-	A		\(9)
2477	Taq1	39	agg	281.06	282	281.26	280.86	0	9 300 000	3 800 000	0	-=	\		\(9)
2478	Taq1	39	agg	282.4	282	0	282.4	0	0	7 200 000	0	+-	A		\(9)
2479	Taq1	39	agg	280.86	282	0	280.86	0	0	38.19	0	+-	A		\(9)
2480	Taq1	39	agg	282.4	282	0	282.4	0	0	72.36	0	+-	A		\(9)
2481	Taq1	39	agg	281.26	282	281.26	0	0	345.36	0	0	-=	\		\(9)
2482	Taq1	50	aat	282.41	283	282.41	0	0	7 600 000	0	0	-=	\		\(9)
2483	Taq1	21	acc	204.55	205	204.55	0	0	7 000 000	0	0	-=	\		\(2)
2484	Taq1	21	acc	205.73	205	205.73	0	0	4 900 000	0	0	-=	\		\(2)
2485	Taq1	64	gtt	204.165	205	204.17	204.16	0	4 200 000	4 100 000	0	=-	\		\(2)
2486	Taq1	64	gtt	205.197	205	205.3	205.08	205.21	3 800 000	3 300 000	4 000 000	==	-		\(2)
2487	Hha1	54	ttt	139.45	140	139.42	139.48	0	6 200 000	8 900 000	0	=-	\		\(2)
2488	Hha1	54	ttt	140.275	140	140.26	140.29	0	4 500 000	4 600 000	0	=-	\		\(2)
2489	Hha1	39	agg	166.445	167	0	166.44	166.45	0	244.79	227.86	+=	/		\(2)
2490	Hha1	39	agg	167.917	167	167.73	168.16	167.86	799.12	232.84	199.38	-=	\ (-)		\(2)
2491	Hha1	8	gaa	166.71	167	166.79	166.67	166.67	5 900 000	11 600 000	8 600 000	+=	/ (-)	/	
2492	Taq1	8	gaa	166.82	167	0	0	166.82	0	0	3 900 000	=+	/	/	
2493	Hha1	8	gaa	166.71	167	166.79	166.67	166.67	5 900 000	11 600 000	8 600 000	+=	/ (-)	/	
2494	Taq1	8	gaa	166.82	167	0	0	166.82	0	0	3 900 000	=+	/	/	
2495	Taq1	16	tag	111.43	112	0	111.47	111.39	0	4 600 000	7 100 000	+=	/		\(4)
2496	Hha1	16	tag	111.825	112	111.76	0	111.89	11 200 000	0	3 200 000	-=(-)	\		\(4)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
2454	RNFASDNA.FAS	FAS	fatty acid synthase	*	agg	aat	increased
2455	RNFASDNA.FAS	FAS	fatty acid synthase	*	agg	aat	increased
2456	RNFASDNA.FAS	FAS	fatty acid synthase	*	agg	aat	increased
2457	RNFASDNA.FAS	FAS	fatty acid synthase	*	agg	aat	increased
2458	RNFASDNA.FAS	FAS	fatty acid synthase	*	agg	aat	increased
2459	RNFASDNA.FAS	FAS	fatty acid synthase	*	agg	aat	increased
2460	RNU89529.PE1	nc	fatty acid transport protein		tgg	aaa	No change
2461	RNU89529.PE1	nc	fatty acid transport protein		tgg	aaa	No change
2462	RNFASRNA.FAS	FAS	fatty-acid synthase	*	ctg	agg	increased
2463	RNFASRNA.FAS	FAS	fatty-acid synthase	*	ctc	gcc	increased
2464	RNFASRNA.FAS	FAS	fatty-acid synthase	*	ctc	gcc	increased
2465	RNFASRNA.FAS	FAS	fatty-acid synthase	*	cca	gcc	increased
2466	RNFASRNA.FAS	FAS	fatty-acid synthase	*	cca	gcc	increased
2467	RNFASRNA.FAS	FAS	fatty-acid synthase	*	cca	gcc	increased
2468	RNFASRNA.FAS	FAS	fatty-acid synthase	*	cca	gcc	increased
2469	RNFASRNA.FAS	FAS	fatty-acid synthase	*	cgg	tgt	increased
2470	RNFASRNA.FAS	FAS	fatty-acid synthase	*	cca	ggg	increased
2471	RNFASRNA.FAS	FAS	fatty-acid synthase	*	cca	ggg	increased
2472	RNFASRNA.FAS	FAS	fatty-acid synthase	*	cat	cca	increased
2473	RNFASRNA.FAS	FAS	fatty-acid synthase	*	cat	cca	increased
2474	RNFASRNA.FAS	FAS	fatty-acid synthase	*	agc	ata	increased
2475	RNFASRNA.FAS	FAS	fatty-acid synthase	*	gcc	ggc	increased
2476	RNFASRNA.FAS	FAS	fatty-acid synthase	*	gcc	ggc	increased
2477	RNFASRNA.FAS	FAS	fatty-acid synthase	*	agg	aat	increased
2478	RNFASRNA.FAS	FAS	fatty-acid synthase	*	agg	aat	increased
2479	RNFASRNA.FAS	FAS	fatty-acid synthase	*	agg	aat	increased
2480	RNFASRNA.FAS	FAS	fatty-acid synthase	*	agg	aat	increased
2481	RNFASRNA.FAS	FAS	fatty-acid synthase	*	agg	aat	increased
2482	RNFASRNA.FAS	FAS	fatty-acid synthase	*	agg	aat	increased
2483	S55929.PE1	fatty-acid-bin	fatty-acid-binding protein		acc	gtt	increased
2484	S55929.PE1	fatty-acid-bin	fatty-acid-binding protein		acc	gtt	increased
2485	S55929.PE1	fatty-acid-bin	fatty-acid-binding protein		acc	gtt	increased
2486	S55929.PE1	fatty-acid-bin	fatty-acid-binding protein		acc	gtt	increased
2487	AF135060.PE1	nc	fibrillin-2		ttt	att	increased
2488	AF135060.PE1	nc	fibrillin-2		ttt	att	increased
2489	AF135060.PE1	nc	fibrillin-2		agg	cct	increased
2490	AF135060.PE1	nc	fibrillin-2		agg	cct	increased
2491	RNLFIB.PE2	nc	fibrinogen alpha subunit		gaa	gtg	decreased
2492	RNLFIB.PE2	nc	fibrinogen alpha subunit		gaa	gtg	decreased
2493	RNLFIB.PE1	nc	fibrinogen alpha-E subunit		gaa	gtg	decreased
2494	RNLFIB.PE1	nc	fibrinogen alpha-E subunit		gaa	gtg	decreased
2495	RNU05675.PE1	nc	fibrinogen B beta chain		cct	tag	increased
2496	RNU05675.PE1	nc	fibrinogen B beta chain		cct	tag	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
2497	Taq1	16	tag	112.325	112	112.39	0	112.26	3 100 000	0	6 600 000	-+(+)	V (/)		\(4)
2498	Hha1	16	tag	112.64	112	112.64	0	0	3 400 000	0	0	-=	\		\(4)
2499	Taq1	18	cct	111.553	112	111.49	111.59	111.58	25 800 000	21 800 000	5 300 000	=-	\ (-)		\(4)
2500	Taq1	18	cct	112.613	112	112.59	112.64	112.61	32 900 000	30 500 000	3 000 000	=-	\ (-)		\(4)
2501	Taq1	63	ctt	192.08	193	192.08	0	0	3 000 000	0	0	-=	\		\(4)
2502	Taq1	63	ctt	193.04	193	193.04	0	193.04	3 100 000	0	3 400 000	-+(=)	V		\(4)
2503	Taq1	63	ctt	192.08	193	192.08	0	0	3 000 000	0	0	-=	\		\(4)
2504	Taq1	63	ctt	193.04	193	193.04	0	193.04	3 100 000	0	3 400 000	-+(=)	V		\(4)
2505	Hha1	6	aga	126.475	126	126.51	0	126.44	89 200 000	0	7 100 000	-=(-)	\		\(2)
2506	Hha1	49	aaa	147.52	148	0	147.44	147.6	0	15 300 000	3 000 000	+-	A		\(2)
2507	Hha1	49	aaa	147.77	148	0	147.77	0	0	12 800 000	0	+-	A		\(2)
2508	Hha1	49	aaa	148.61	148	148.47	148.75	0	10 300 000	6 900 000	0	=-	\		\(2)
2509	Hha1	49	aaa	148.37	148	0	148.37	0	0	6 200 000	0	+-	A		\(2)
2510	Hha1	26	ctg	171.777	172	171.59	171.8	171.94	8 700 000	6 900 000	47 500 000	=+	/ (-)		/(2)
2511	Hha1	26	ctg	172.8	172	172.68	0	172.92	3 000 000	0	8 400 000	=+(+)	/	/	/(2)
2512	Hha1	39	agg	172.59	172	0	0	172.59	0	0	231.93	=+	/	/	/(2)
2513	Taq1	12	agt	171.43	172	171.43	171.35	171.51	8 900 000	7 500 000	12 400 000	==	-	-	
2514	Taq1	12	agt	172.507	172	172.52	172.44	172.56	4 100 000	3 300 000	3 600 000	==	-	-	
2515	Taq1	29	gca	171.597	172	171.57	171.61	171.61	11 800 000	7 900 000	5 400 000	==	-	-	
2516	Taq1	29	gca	172.643	172	172.69	172.62	172.62	15 100 000	11 200 000	5 400 000	==	-	-	
2517	Taq1	12	agt	171.43	172	171.43	171.35	171.51	8 900 000	7 500 000	12 400 000	==	-	-	
2518	Taq1	12	agt	172.507	172	172.52	172.44	172.56	4 100 000	3 300 000	3 600 000	==	-	-	
2519	Taq1	29	gca	171.597	172	171.57	171.61	171.61	11 800 000	7 900 000	5 400 000	==	-	-	
2520	Taq1	29	gca	172.643	172	172.69	172.62	172.62	15 100 000	11 200 000	5 400 000	==	-	-	
2521	Taq1	14	gat	174.727	175	174.64	174.64	174.9	6 400 000	6 400 000	3 200 000	=-	\ (-)		-(3) \(3)
2522	Taq1	14	gat	175.757	175	175.7	175.7	175.87	7 200 000	7 200 000	4 900 000	==	-		-(3) \(3)
2523	Hha1	20	ctc	221.91	223	221.91	0	0	867.76	0	0	-=	\		-(3) \(3)
2524	Hha1	20	ctc	222.675	223	222.7	222.65	0	323.69	1 193.28	0	+-	A		-(3) \(3)
2525	Hha1	20	ctc	223.71	223	223.67	223.76	223.7	1 887.05	2 045.63	2 242.36	==	-		-(3) \(3)
2526	Hha1	20	ctc	230.317	230	230.26	230.44	230.25	991.73	1 927.61	477.09	+-	A		-(3) \(3)
2527	Hha1	20	ctc	231.37	230	231.26	231.49	231.36	7 107.43	3 422.5	3 053.43	-=	\ (-)		-(3) \(3)
2528	Hha1	20	ctc	223.71	225	223.67	223.76	223.7	1 887.05	2 045.63	2 242.36	==	-		-2
2529	Hha1	20	ctc	224.77	225	0	0	224.77	0	0	441.31	=+	/		-2
2530	Hha1	33	agc	241.653	242	241.7	241.69	241.57	5 700 000	3 300 000	3 900 000	==	-		-2
2531	Taq1	1	tat	121.53	122	121.56	121.5	0	11 700 000	19 800 000	0	=-	\		\(4) -(3)
2532	Taq1	1	tat	122.677	122	122.65	122.57	122.81	6 800 000	5 900 000	4 200 000	==	-		\(4) -(3)
2533	Taq1	49	aaa	122.26	122	122.42	122.1	0	56 200 000	8 600 000	0	-=	\		\(4) -(3)
2534	Taq1	49	aaa	122.42	122	0	122.42	0	0	9 000 000	0	+-	A		\(4) -(3)
2535	Taq1	24	cgt	147.57	148	147.58	147.54	147.59	4 400 000	4 700 000	6 000 000	==	-	-	\(4) -(3)
2536	Taq1	24	cgt	148.59	148	148.64	148.57	148.56	6 400 000	6 300 000	3 000 000	=-	\ (-)	\	\(4) -(3)
2537	Taq1	30	cgt	147.643	148	147.77	147.59	147.57	4 300 000	3 100 000	4 000 000	==	-	-	\(4) -(3)
2538	Taq1	30	cgt	148.535	148	148.57	148.5	0	3 800 000	3 000 000	0	=-	\	\	\(4) -(3)
2539	Hha1	39	agg	71.64	72	71.65	71.55	71.72	13 563.04	1 176.18	2 046.71	-=	\ (-)		\(3)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
2497	RNU05675.PE1	nc	fibrinogen B beta chain		cct	tag	increased
2498	RNU05675.PE1	nc	fibrinogen B beta chain		cct	tag	increased
2499	RNU05675.PE1	nc	fibrinogen B beta chain		cct	tag	increased
2500	RNU05675.PE1	nc	fibrinogen B beta chain		cct	tag	increased
2501	RNU05675.PE1	nc	fibrinogen B beta chain		ctt	tta	increased
2502	RNU05675.PE1	nc	fibrinogen B beta chain		ctt	tta	increased
2503	RNU05675.PE1	nc	fibrinogen B beta chain		ctt	tta	increased
2504	RNU05675.PE1	nc	fibrinogen B beta chain		ctt	tta	increased
2505	S54008.PE1	fibroblast gro	fibroblast growth factor receptor 1		aga	gct	increased
2506	S54008.PE1	fibroblast gro	fibroblast growth factor receptor 1		cat	aaa	increased
2507	S54008.PE1	fibroblast gro	fibroblast growth factor receptor 1		cat	aaa	increased
2508	S54008.PE1	fibroblast gro	fibroblast growth factor receptor 1		cat	aaa	increased
2509	S54008.PE1	fibroblast gro	fibroblast growth factor receptor 1		cat	aaa	increased
2510	RNU82612.FN-1	fn-1	fibronectin		ctg	agg	decreased
2511	RNU82612.FN-1	fn-1	fibronectin		ctg	agg	decreased
2512	RNU82612.FN-1	fn-1	fibronectin		ctg	agg	decreased
2513	AB055759.L-FILIP	L-FILIP	filamin-interacting protein L-FILIP		gca	agt	No change
2514	AB055759.L-FILIP	L-FILIP	filamin-interacting protein L-FILIP		gca	agt	No change
2515	AB055759.L-FILIP	L-FILIP	filamin-interacting protein L-FILIP		gca	agt	No change
2516	AB055759.L-FILIP	L-FILIP	filamin-interacting protein L-FILIP		gca	agt	No change
2517	D87257.S-FILIP	S-FILIP	filamin-interacting protein S-FILIP		gca	agt	No change
2518	D87257.S-FILIP	S-FILIP	filamin-interacting protein S-FILIP		gca	agt	No change
2519	D87257.S-FILIP	S-FILIP	filamin-interacting protein S-FILIP		gca	agt	No change
2520	D87257.S-FILIP	S-FILIP	filamin-interacting protein S-FILIP		gca	agt	No change
2521	AB069907.PE1	nc	FIP-2 like protein		gat	ttc	No change
2522	AB069907.PE1	nc	FIP-2 like protein		gat	ttc	No change
2523	AB069907.PE1	nc	FIP-2 like protein		tca	ctc	No change
2524	AB069907.PE1	nc	FIP-2 like protein		tca	ctc	No change
2525	AB069907.PE1	nc	FIP-2 like protein		tca	ctc	No change
2526	AB069907.PE1	nc	FIP-2 like protein		ctc	ctc	No change
2527	AB069907.PE1	nc	FIP-2 like protein		ctc	ctc	No change
2528	AB072907.SDHA	SDHA	flavoprotein subunit of succinate-ubiquinone		ctc	aca	No change
2529	AB072907.SDHA	SDHA	flavoprotein subunit of succinate-ubiquinone		ctc	aca	No change
2530	AB072907.SDHA	SDHA	flavoprotein subunit of succinate-ubiquinone		ctc	agc	No change
2531	AF020777.FAK	FAK	focal adhesion kinase		tat	aaa	increased
2532	AF020777.FAK	FAK	focal adhesion kinase		tat	aaa	increased
2533	AF020777.FAK	FAK	focal adhesion kinase		tat	aaa	increased
2534	AF020777.FAK	FAK	focal adhesion kinase		tat	aaa	increased
2535	AF020777.FAK	FAK	focal adhesion kinase		cgt	ccg	No change
2536	AF020777.FAK	FAK	focal adhesion kinase		cgt	ccg	increased
2537	AF020777.FAK	FAK	focal adhesion kinase		cgt	ccg	No change
2538	AF020777.FAK	FAK	focal adhesion kinase		cgt	ccg	increased
2539	AB071603.FLRG	flrg	follistatin-like protein		gtc	agg	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
2540	Hha1	33	agc	150.42	151	150.39	150.45	0	5 500 000	5 500 000	0	=-	\		\(3)
2541	Hha1	33	agc	151.405	151	151.45	151.36	0	7 400 000	7 400 000	0	=-	\		\(3)
2542	Hha1	59	ttc	267.955	268	268.09	0	267.82	286.01	0	87.96	-=(-)	\		\(3)
2543	Taq1	56	tga	78.733	79	78.58	79.04	78.58	23 900 000	5 500 000	3 400 000	-=	\ (-)		-(5) \(4)
2544	Taq1	39	agg	80.563	81	80.4	80.41	80.88	22 200 000	94 400 000	14 900 000	+-	A		-(5) \(4)
2545	Taq1	39	agg	80.93	81	80.9	81.01	80.88	22 600 000	34 400 000	438.88	=-	\ (-)		-(5) \(4)
2546	Taq1	39	agg	80.955	81	80.9	81.01	0	839.27	345.73	0	-=	\		-(5) \(4)
2547	Hha1	26	ctg	104.535	105	104.54	104.53	0	10 900 000	3 300 000	0	-=	\		-(5) \(4)
2548	Hha1	26	ctg	105.54	105	105.54	0	0	3 100 000	0	0	-=	\		-(5) \(4)
2549	Hha1	44	cgg	120.76	121	0	120.76	0	0	5 100 000	0	+-	A		-(5) \(4)
2550	Hha1	32	gtc	130.85	131	130.8	130.94	130.81	3 350.42	2 797.55	5 342.96	=+	/ (-)		-(5) \(4)
2551	Taq1	17	cca	153.253	154	153.4	153.13	153.23	227.55	1 183.35	736.73	+=	/ (-)		-(5) \(4)
2552	Taq1	17	cca	154.253	154	154.31	154.15	154.3	469.04	678.1	1 428.35	=+	/ (-)		-(5) \(4)
2553	Hha1	44	cgg	240.6	242	240.6	0	240.6	12 100 000	0	7 200 000	-+(=)	V		-(5) \(4)
2554	Hha1	44	cgg	241.507	242	241.56	241.47	241.49	73 000 000	8 800 000	30 900 000	-=	\ (-)		-(5) \(4)
2555	Hha1	44	cgg	242.14	242	242.19	242.08	242.15	38 600 000	5 400 000	22 100 000	-=	\ (-)		-(5) \(4)
2556	Hha1	44	cgg	243.22	242	0	0	243.22	0	0	5 400 000	=+	/		-(5) \(4)
2557	Hha1	40	tgg	123.29	124	0	123.13	123.45	0	6 200 000	4 300 000	+=	/	/	/(2)
2558	Hha1	59	ttc	123.295	124	123.37	0	123.22	218.4	0	5 570.07	=+(+)	/	/	/(2)
2559	Hha1	59	ttc	124.185	124	0	124.09	124.28	0	416.81	571.75	+=	/		/(2)
2560	Hha1	12	agt	174.913	175	174.81	174.85	175.08	3 231.64	4 123.87	3 601.1	==	-		/(2)
2561	Hha1	39	agg	133.55	133	0	133.55	0	0	208.96	0	+-	A	A	
2562	Hha1	59	ttc	133.55	133	0	133.55	0	0	238.58	0	+-	A	A	
2563	Hha1	15	tac	115.13	115	115.15	115.19	115.05	52 100 000	17 900 000	5 900 000	-=	\ (-)	\	
2564	Hha1	33	agc	114.89	115	114.89	0	0	3 800 000	0	0	-=	\	\	
2565	Hha1	41	ccc	116.9	117	116.9	0	0	12 200 000	0	0	-=	\		\(4)
2566	Taq1	21	acc	154.29	155	154.26	0	154.32	5 500 000	0	6 900 000	-+(=)	V		\(4)
2567	Taq1	21	acc	154.81	155	154.81	0	0	11 200 000	0	0	-=	\		\(4)
2568	Taq1	21	acc	155.39	155	0	0	155.39	0	0	5 500 000	=+	/		\(4)
2569	Hha1	21	acc	155.54	155	155.54	0	0	4 100 000	0	0	-=	\		\(4)
2570	Taq1	39	agg	272.64	274	0	272.64	0	0	79 800 000	0	+-	A		\(4)
2571	Taq1	39	agg	275.01	274	274.96	275.06	0	3 000 000	38 800 000	0	+-	A		\(4)
2572	Taq1	39	agg	274.96	274	274.96	0	0	111.4	0	0	-=	\		\(4)
2573	Taq1	39	agg	272.64	274	0	272.64	0	0	802.01	0	+-	A		\(4)
2574	Taq1	39	agg	275.06	274	0	275.06	0	0	389.95	0	+-	A		\(4)
2575	Taq1	9	atc	173.785	173	173.73	173.84	0	3 500 000	6 400 000	0	+-	A	A	
2576	Hha1	9	atc	174.03	173	0	174.03	0	0	8 000 000	0	+-	A	A	
2577	Taq1	11	act	163.557	163	163.63	163.71	163.33	5 000 000	3 600 000	22 300 000	=+	/ (-)	/	
2578	Hha1	11	act	163.677	163	163.77	163.57	163.69	9 000 000	5 300 000	13 200 000	=+	/ (-)	/	
2579	Hha1	64	gtt	70.367	70	70.31	70.37	70.42	6 400 000	5 200 000	17 000 000	=+	/ (-)		/(3)
2580	Hha1	33	agc	73.643	74	73.74	73.76	73.43	3 700 000	4 300 000	7 000 000	==	-		/(3)
2581	Hha1	41	ccc	101.51	102	0	0	101.51	0	0	5 200 000	=+	/		/(3)
2582	Hha1	41	ccc	102.115	102	102.1	102.13	0	16 000 000	6 700 000	0	-=	\		/(3)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
2540	AB071603.FLRG	flrg	follistatin-like protein		cgt	agc	increased
2541	AB071603.FLRG	flrg	follistatin-like protein		cgt	agc	increased
2542	AB071603.FLRG	flrg	follistatin-like protein		ttc	cat	increased
2543	AF079233.PE1	nc	formiminotransferase-cyclodeaminase		ggg	tga	No change
2544	AF079233.PE1	nc	formiminotransferase-cyclodeaminase		ctg	agg	No change
2545	AF079233.PE1	nc	formiminotransferase-cyclodeaminase		ctg	agg	No change
2546	AF079233.PE1	nc	formiminotransferase-cyclodeaminase		ctg	agg	No change
2547	AF079233.PE1	nc	formiminotransferase-cyclodeaminase		ggg	ctg	No change
2548	AF079233.PE1	nc	formiminotransferase-cyclodeaminase		ggg	ctg	No change
2549	AF079233.PE1	nc	formiminotransferase-cyclodeaminase		aca	cgg	No change
2550	AF079233.PE1	nc	formiminotransferase-cyclodeaminase		cag	gtc	No change
2551	AF079233.PE1	nc	formiminotransferase-cyclodeaminase		tgc	cca	No change
2552	AF079233.PE1	nc	formiminotransferase-cyclodeaminase		tgc	cca	No change
2553	AF079233.PE1	nc	formiminotransferase-cyclodeaminase		cct	cgg	No change
2554	AF079233.PE1	nc	formiminotransferase-cyclodeaminase		cct	cgg	No change
2555	AF079233.PE1	nc	formiminotransferase-cyclodeaminase		cct	cgg	No change
2556	AF079233.PE1	nc	formiminotransferase-cyclodeaminase		cct	cgg	No change
2557	AF012891.PE1	nc	frizzled related protein frpAP		ttc	tgg	decreased
2558	AF012891.PE1	nc	frizzled related protein frpAP		ttc	tgg	decreased
2559	AF012891.PE1	nc	frizzled related protein frpAP		ttc	tgg	decreased
2560	AF012891.PE1	nc	frizzled related protein frpAP		atc	agt	decreased
2561	AF455054.PE1	nc	frizzled-9		ttc	agg	increased by mild
2562	AF455054.PE1	nc	frizzled-9		ttc	agg	increased by mild
2563	RNU55815.KCC1	KCC1	furosemide-sensitive K-Cl cotransporter		tac	agc	increased
2564	RNU55815.KCC1	KCC1	furosemide-sensitive K-Cl cotransporter		tac	agc	increased
2565	RNU55816.KCC2	KCC2	furosemide-sensitive K-Cl cotransporter		aat	ccc	increased
2566	RNU55816.KCC2	KCC2	furosemide-sensitive K-Cl cotransporter		acc	tgc	increased
2567	RNU55816.KCC2	KCC2	furosemide-sensitive K-Cl cotransporter		acc	tgc	increased
2568	RNU55816.KCC2	KCC2	furosemide-sensitive K-Cl cotransporter		acc	tgc	increased
2569	RNU55816.KCC2	KCC2	furosemide-sensitive K-Cl cotransporter		acc	tgc	increased
2570	RNU55816.KCC2	KCC2	furosemide-sensitive K-Cl cotransporter		gat	agg	increased
2571	RNU55816.KCC2	KCC2	furosemide-sensitive K-Cl cotransporter		gat	agg	increased
2572	RNU55816.KCC2	KCC2	furosemide-sensitive K-Cl cotransporter		gat	agg	increased
2573	RNU55816.KCC2	KCC2	furosemide-sensitive K-Cl cotransporter		gat	agg	increased
2574	RNU55816.KCC2	KCC2	furosemide-sensitive K-Cl cotransporter		gat	agg	increased
2575	AY364634.PE1	nc	FXNA		agt	atc	increased by mild
2576	AY364634.PE1	nc	FXNA		agt	atc	increased by mild
2577	RATGA12.PE1	nc	G alpha 12		cgc	act	decreased
2578	RATGA12.PE1	nc	G alpha 12		cgc	act	decreased
2579	AB015646.PE2	nc	G protein-coupled receptor		tgc	gtt	decreased
2580	AB015646.PE2	nc	G protein-coupled receptor		ggc	agc	decreased
2581	AB015646.PE2	nc	G protein-coupled receptor		cgc	ccc	decreased
2582	AB015646.PE2	nc	G protein-coupled receptor		cgc	ccc	decreased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
2583	Hha1	59	ttc	112.757	113	112.94	112.64	112.69	286.01	664.02	150.05	+-	A		/(3)
2584	Hha1	59	ttc	113.315	113	0	113.25	113.38	0	411.06	129.35	+-	A		/(3)
2585	Taq1	45	gcc	258.9	260	0	0	258.9	0	0	3 900 000	=+	/		/(3)
2586	Taq1	45	gcc	259.68	260	259.68	0	0	3 900 000	0	0	-=	\		/(3)
2587	Taq1	45	gcc	260.8	260	260.8	0	0	10 300 000	0	0	-=	\		/(3)
2588	Taq1	40	tgg	171.46	172	0	0	171.46	0	0	6 800 000	=+	/		\(2)
2589	Taq1	40	tgg	172.645	172	0	172.77	172.52	0	3 400 000	3 100 000	+=	/		\(2)
2590	Taq1	49	aaa	172.815	173	172.62	173.01	0	30 100 000	9 900 000	0	-=	\		\(2)
2591	Taq1	49	aaa	173.1	173	173.1	0	0	35 000 000	0	0	-=	\		\(2)
2592	Taq1	49	aaa	173.815	173	173.84	173.79	0	30 700 000	17 600 000	0	=-	\		\(2)
2593	Hha1	6	aga	261.68	263	261.68	0	0	7 800 000	0	0	-=	\		\(2)
2594	Hha1	6	aga	262.38	263	262.38	0	0	3 500 000	0	0	-=	\		\(2)
2595	Hha1	6	aga	263.63	263	263.63	0	0	3 900 000	0	0	-=	\		\(2)
2596	Taq1	25	cat	103.335	103	103.15	103.52	0	1 016.78	865.69	0	=-	\		\(4)
2597	Taq1	36	ggt	102.96	103	102.93	0	102.99	5 400 000	0	4 800 000	-+(=)	V		\(4)
2598	Hha1	44	cgg	144.455	145	144.66	144.25	0	4 900 000	3 900 000	0	=-	\		\(4)
2599	Hha1	44	cgg	144.72	145	0	144.72	0	0	4 100 000	0	+-	A		\(4)
2600	Hha1	26	ctg	146.06	146	0	146.06	0	0	3 800 000	0	+-	A		\(4)
2601	Hha1	41	ccc	153.07	153	153.07	0	0	3 700 000	0	0	-=	\		\(4)
2602	Hha1	41	ccc	153.785	153	153.87	0	153.7	7 800 000	0	8 300 000	-+(=)	V		\(4)
2603	Hha1	49	aaa	216.78	218	216.77	216.72	216.85	54 400 000	26 000 000	10 300 000	-=	\ (-)		\(4)
2604	Hha1	49	aaa	217.857	218	217.68	217.91	217.98	26 700 000	5 600 000	6 100 000	-=	\ (-)		\(4)
2605	Hha1	49	aaa	218.72	218	0	218.72	0	0	5 100 000	0	+-	A		\(4)
2606	Hha1	3	aac	186.37	187	186.37	0	0	3 300 000	0	0	-=	\		\(2)
2607	Taq1	61	tct	186.203	187	186.16	186.24	186.21	5 600 000	4 300 000	4 400 000	==	-		\(2)
2608	Taq1	61	tct	187.22	187	187.22	0	0	5 000 000	0	0	-=	\		\(2)
2609	Taq1	18	cct	225.94	226	0	225.94	0	0	3 500 000	0	+-	A		\(2)
2610	Taq1	31	gac	107.61	108	0	107.61	0	0	8 500 000	0	+-	A		V(3)
2611	Taq1	56	tga	108.03	108	108.01	0	108.05	3 800 000	0	6 600 000	-+(=)	V		V(3)
2612	Taq1	45	gcc	164.535	165	164.45	0	164.62	3 800 000	0	4 900 000	-+(=)	V		V(3)
2613	Hha1	6	aga	165.59	166	165.63	165.53	165.61	7 400 000	4 900 000	5 400 000	==	-		V(3)
2614	Hha1	6	aga	166.585	166	166.62	0	166.55	6 200 000	0	4 300 000	-+(=)	V		V(3)
2615	Taq1	18	cct	178.855	179	178.85	178.86	0	8 200 000	4 700 000	0	=-	\		V(3)
2616	Taq1	18	cct	179.893	179	179.93	179.92	179.83	4 000 000	3 400 000	4 000 000	==	-		V(3)
2617	Hha1	62	tgt	100.195	100	100.25	0	100.14	6 300 000	0	3 100 000	-+(-)	V (\)		\(2)
2618	Hha1	41	ccc	125.767	126	125.78	125.72	125.8	9 000 000	9 400 000	46 200 000	=+	/ (-)		\(2)
2619	Hha1	49	aaa	356.38	358	356.38	0	0	5 700 000	0	0	-=	\		\(2)
2620	Hha1	49	aaa	359.92	358	0	359.92	0	0	14 500 000	0	+-	A		\(2)
2621	Taq1	17	cca	250.98	252	250.98	0	0	213.62	0	0	-=	\		\(2)
2622	Taq1	17	cca	252.41	252	252.41	0	0	208.98	0	0	-=	\	\	\(2)
2623	Taq1	39	agg	250.95	252	0	250.95	0	0	9 100 000	0	+-	A		\(2)
2624	Taq1	39	agg	251.575	252	251.54	251.61	0	5 000 000	8 300 000	0	=-	\		\(2)
2625	Taq1	39	agg	252.59	252	252.58	252.6	0	42 900 000	108 100 000	0	+-	A		\(2)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
2583	AB015646.PE2	nc	G protein-coupled receptor		ttc	cca	decreased
2584	AB015646.PE2	nc	G protein-coupled receptor		ttc	cca	decreased
2585	AB015646.PE2	nc	G protein-coupled receptor		gcc	gtg	decreased
2586	AB015646.PE2	nc	G protein-coupled receptor		gcc	gtg	decreased
2587	AB015646.PE2	nc	G protein-coupled receptor		gcc	gtg	decreased
2588	RNGRK4PCK.GRK4	GRK4	G protein-coupled receptor kinase GRK4A		aaa	tgg	increased
2589	RNGRK4PCK.GRK4	GRK4	G protein-coupled receptor kinase GRK4A		aaa	tgg	increased
2590	RNGRK4PCK.GRK4	GRK4	G protein-coupled receptor kinase GRK4A		aaa	tgg	increased
2591	RNGRK4PCK.GRK4	GRK4	G protein-coupled receptor kinase GRK4A		aaa	tgg	increased
2592	RNGRK4PCK.GRK4	GRK4	G protein-coupled receptor kinase GRK4A		aaa	tgg	increased
2593	RNGRK4PCK.GRK4	GRK4	G protein-coupled receptor kinase GRK4A		aga	tta	increased
2594	RNGRK4PCK.GRK4	GRK4	G protein-coupled receptor kinase GRK4A		aga	tta	increased
2595	RNGRK4PCK.GRK4	GRK4	G protein-coupled receptor kinase GRK4A		aga	tta	increased
2596	AF085693.GIT1	GIT1	G protein-coupled receptor kinase-associated ADP		cat	ggt	increased
2597	AF085693.GIT1	GIT1	G protein-coupled receptor kinase-associated ADP		cat	ggt	increased
2598	AF085693.GIT1	GIT1	G protein-coupled receptor kinase-associated ADP		ctg	cgg	increased
2599	AF085693.GIT1	GIT1	G protein-coupled receptor kinase-associated ADP		ctg	cgg	increased
2600	AF085693.GIT1	GIT1	G protein-coupled receptor kinase-associated ADP		ctg	cgg	increased
2601	AF085693.GIT1	GIT1	G protein-coupled receptor kinase-associated ADP		ccc	tgt	increased
2602	AF085693.GIT1	GIT1	G protein-coupled receptor kinase-associated ADP		ccc	tgt	increased
2603	AF085693.GIT1	GIT1	G protein-coupled receptor kinase-associated ADP		aaa	aga	increased
2604	AF085693.GIT1	GIT1	G protein-coupled receptor kinase-associated ADP		aaa	aga	increased
2605	AF085693.GIT1	GIT1	G protein-coupled receptor kinase-associated ADP		aaa	aga	increased
2606	RNP2Y4REC.P2Y4	P2Y4	G protein-linked P2Y4 receptor		aac	tct	increased
2607	RNP2Y4REC.P2Y4	P2Y4	G protein-linked P2Y4 receptor		aac	tct	increased
2608	RNP2Y4REC.P2Y4	P2Y4	G protein-linked P2Y4 receptor		aac	tct	increased
2609	RNP2Y4REC.P2Y4	P2Y4	G protein-linked P2Y4 receptor		cct	gtc	increased
2610	AF058791.EDG2	edg2	G10 protein homolog		gac	tga	decreased by mild
2611	AF058791.EDG2	edg2	G10 protein homolog		gac	tga	decreased by mild
2612	AF058791.EDG2	edg2	G10 protein homolog		gcc	aga	decreased by mild
2613	AF058791.EDG2	edg2	G10 protein homolog		gcc	aga	decreased by mild
2614	AF058791.EDG2	edg2	G10 protein homolog		gcc	aga	decreased by mild
2615	AF058791.EDG2	edg2	G10 protein homolog		cct	gtc	decreased by mild
2616	AF058791.EDG2	edg2	G10 protein homolog		cct	gtc	decreased by mild
2617	AF312319.PE1	nc	GABA B receptor 1g		tgt	cat	increased
2618	AF312319.PE1	nc	GABA B receptor 1g		ccc	ccc	increased
2619	AF312319.PE1	nc	GABA B receptor 1g		aaa	cca	increased
2620	AF312319.PE1	nc	GABA B receptor 1g		aaa	cca	increased
2621	RNU29701.GABA-T	GABA-T	GABA transaminase		cca	agg	increased
2622	RNU29701.GABA-T	GABA-T	GABA transaminase		cca	agg	increased
2623	RNU29701.GABA-T	GABA-T	GABA transaminase		cca	agg	increased
2624	RNU29701.GABA-T	GABA-T	GABA transaminase		cca	agg	increased
2625	RNU29701.GABA-T	GABA-T	GABA transaminase		cca	agg	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
2626	Taq1	39	agg	253.475	252	253.39	253.56	0	8 100 000	6 100 000	0	=-	\		\(2)
2627	Taq1	39	agg	250.95	252	0	250.95	0	0	91.45	0	+-	A		\(2)
2628	Taq1	39	agg	251.575	252	251.54	251.61	0	185.68	83.41	0	-=	\		\(2)
2629	Taq1	39	agg	252.59	252	252.58	252.6	0	1 593.13	1 086.44	0	=-	\	\	\(2)
2630	Taq1	39	agg	253.475	252	253.39	253.56	0	300.8	61.3	0	-=	\		\(2)
2631	Hha1	4	aag	106.05	106	0	0	106.05	0	0	8 800 000	=+	/	/	/(6)
2632	Taq1	55	tca	105.47	106	0	105.47	0	0	7 200 000	0	+-	A		/(6)
2633	Taq1	55	tca	106.22	106	0	106.24	106.2	0	8 300 000	9 500 000	+=	/	/	/(6)
2634	Hha1	4	aag	114.94	115	115.13	114.8	114.89	6 100 000	12 500 000	8 500 000	+=	/ (-)		/(6)
2635	Taq1	39	agg	139.32	140	139.57	0	139.07	20 500 000	0	3 400 000	-=(-)	\		/(6)
2636	Taq1	39	agg	139.66	140	0	139.66	0	0	43 600 000	0	+-	A		/(6)
2637	Taq1	39	agg	140.585	140	140.52	140.65	0	11 000 000	106 400 000	0	+-	A		/(6)
2638	Taq1	39	agg	139.57	140	139.57	0	0	761.28	0	0	-=	\		/(6)
2639	Taq1	39	agg	140.52	140	140.52	0	0	408.49	0	0	-=	\		/(6)
2640	Taq1	39	agg	139.66	140	0	139.66	0	0	438.19	0	+-	A		/(6)
2641	Taq1	39	agg	140.65	140	0	140.65	0	0	1 069.35	0	+-	A		/(6)
2642	Taq1	62	tgt	139.635	140	0	139.69	139.58	0	3 100 000	6 800 000	++	/		/(6)
2643	Taq1	62	tgt	140.697	140	140.8	140.75	140.54	3 400 000	8 100 000	15 400 000	=+	/ (-)		/(6)
2644	Hha1	6	aga	306.42	308	306.42	0	0	5 300 000	0	0	-=	\		/(6)
2645	Hha1	6	aga	307.27	308	307.37	307.18	307.26	21 400 000	12 000 000	5 200 000	==	-		/(6)
2646	Hha1	6	aga	308.39	308	0	308.32	308.46	0	10 000 000	8 800 000	+=	/		/(6)
2647	Taq1	51	ata	310.78	309	0	0	310.78	0	0	3 600 000	=+	/		/(6)
2648	Hha1	56	tga	116.725	117	116.52	0	116.93	666.04	0	586.1	-+(=)	V		A(4)
2649	Hha1	56	tga	117.1	117	0	117.1	0	0	2 025.53	0	+-	A		A(4)
2650	Taq1	50	aat	149.977	150	149.97	149.82	150.14	5 200 000	8 100 000	8 500 000	==	-		A(4)
2651	Taq1	50	aat	150.51	150	0	150.51	0	0	3 700 000	0	+-	A		A(4)
2652	Taq1	39	agg	233.28	234	0	233.28	0	0	84 600 000	0	+-	A		A(4)
2653	Taq1	39	agg	234.59	234	0	234.59	0	0	30 200 000	0	+-	A		A(4)
2654	Taq1	39	agg	233.28	234	0	233.28	0	0	850.25	0	+-	A		A(4)
2655	Taq1	39	agg	234.59	234	0	234.59	0	0	303.52	0	+-	A		A(4)
2656	Taq1	49	aaa	235.325	236	235.42	0	235.23	9 100 000	0	21 500 000	=+(+)	/		A(4)
2657	Taq1	49	aaa	236.04	236	0	236.04	0	0	14 800 000	0	+-	A		A(4)
2658	Taq1	49	aaa	236.74	236	0	236.74	0	0	8 100 000	0	+-	A		A(4)
2659	Taq1	17	cca	130.707	131	130.74	130.57	130.81	31 337.939	2 526.25	796.87	-=	\ (-)		\(2)
2660	Taq1	17	cca	131.723	131	131.79	131.65	131.73	1 983	1 023.8	1 653.88	-=	\ (-)		\(2)
2661	Taq1	39	agg	276.09	277	276.09	0	0	14 200 000	0	0	-=	\		\(2)
2662	Taq1	39	agg	277	277	0	277	0	0	55 600 000	0	+-	A		\(2)
2663	Taq1	39	agg	277.71	277	0	277.71	0	0	28 700 000	0	+-	A		\(2)
2664	Taq1	39	agg	276.09	277	276.09	0	0	527.33	0	0	-=	\		\(2)
2665	Taq1	39	agg	277	277	0	277	0	0	558.79	0	+-	A		\(2)
2666	Taq1	39	agg	277.71	277	0	277.71	0	0	288.44	0	+-	A		\(2)
2667	Hha1	4	aag	106.05	106	0	0	106.05	0	0	8 800 000	=+	/	/	/(6)
2668	Taq1	55	tca	105.47	106	0	105.47	0	0	7 200 000	0	+-	A		/(6)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
2626	RNU29701.GABA-T	GABA-T	GABA transaminase		cca	agg	increased
2627	RNU29701.GABA-T	GABA-T	GABA transaminase		cca	agg	increased
2628	RNU29701.GABA-T	GABA-T	GABA transaminase		cca	agg	increased
2629	RNU29701.GABA-T	GABA-T	GABA transaminase		cca	agg	increased
2630	RNU29701.GABA-T	GABA-T	GABA transaminase		cca	agg	increased
2631	RNGABAG3.PE1	nc	GABA-A receptor gamma-3 subunit		aag	tca	decreased
2632	RNGABAG3.PE1	nc	GABA-A receptor gamma-3 subunit		aag	tca	decreased
2633	RNGABAG3.PE1	nc	GABA-A receptor gamma-3 subunit		aag	tca	decreased
2634	RNGABAG3.PE1	nc	GABA-A receptor gamma-3 subunit		ttc	aag	decreased
2635	RNGABAG3.PE1	nc	GABA-A receptor gamma-3 subunit		tgt	agg	decreased
2636	RNGABAG3.PE1	nc	GABA-A receptor gamma-3 subunit		tgt	agg	decreased
2637	RNGABAG3.PE1	nc	GABA-A receptor gamma-3 subunit		tgt	agg	decreased
2638	RNGABAG3.PE1	nc	GABA-A receptor gamma-3 subunit		tgt	agg	decreased
2639	RNGABAG3.PE1	nc	GABA-A receptor gamma-3 subunit		tgt	agg	decreased
2640	RNGABAG3.PE1	nc	GABA-A receptor gamma-3 subunit		tgt	agg	decreased
2641	RNGABAG3.PE1	nc	GABA-A receptor gamma-3 subunit		tgt	agg	decreased
2642	RNGABAG3.PE1	nc	GABA-A receptor gamma-3 subunit		tgt	agg	decreased
2643	RNGABAG3.PE1	nc	GABA-A receptor gamma-3 subunit		tgt	agg	decreased
2644	RNGABAG3.PE1	nc	GABA-A receptor gamma-3 subunit		aga	ata	decreased
2645	RNGABAG3.PE1	nc	GABA-A receptor gamma-3 subunit		aga	ata	decreased
2646	RNGABAG3.PE1	nc	GABA-A receptor gamma-3 subunit		aga	ata	decreased
2647	RNGABAG3.PE1	nc	GABA-A receptor gamma-3 subunit		aga	ata	decreased
2648	RNU95368.PE1	nc	GABA-A receptor pi subunit		tga	tgt	increased by mild
2649	RNU95368.PE1	nc	GABA-A receptor pi subunit		tga	tgt	increased by mild
2650	RNU95368.PE1	nc	GABA-A receptor pi subunit		aat	gtc	increased by mild
2651	RNU95368.PE1	nc	GABA-A receptor pi subunit		aat	gtc	increased by mild
2652	RNU95368.PE1	nc	GABA-A receptor pi subunit		agg	cag	increased by mild
2653	RNU95368.PE1	nc	GABA-A receptor pi subunit		agg	cag	increased by mild
2654	RNU95368.PE1	nc	GABA-A receptor pi subunit		agg	cag	increased by mild
2655	RNU95368.PE1	nc	GABA-A receptor pi subunit		agg	cag	increased by mild
2656	RNU95368.PE1	nc	GABA-A receptor pi subunit		aaa	gag	increased by mild
2657	RNU95368.PE1	nc	GABA-A receptor pi subunit		aaa	gag	increased by mild
2658	RNU95368.PE1	nc	GABA-A receptor pi subunit		aaa	gag	increased by mild
2659	RATGABAAJ.PE1	GABA-A recep	GABA-A receptor rho-2 subunit		cca	ggc	increased
2660	RATGABAAJ.PE1	GABA-A recep	GABA-A receptor rho-2 subunit		cca	ggc	increased
2661	RATGABAAJ.PE1	GABA-A recep	GABA-A receptor rho-2 subunit		tgt	agg	increased
2662	RATGABAAJ.PE1	GABA-A recep	GABA-A receptor rho-2 subunit		tgt	agg	increased
2663	RATGABAAJ.PE1	GABA-A recep	GABA-A receptor rho-2 subunit		tgt	agg	increased
2664	RATGABAAJ.PE1	GABA-A recep	GABA-A receptor rho-2 subunit		tgt	agg	increased
2665	RATGABAAJ.PE1	GABA-A recep	GABA-A receptor rho-2 subunit		tgt	agg	increased
2666	RATGABAAJ.PE1	GABA-A recep	GABA-A receptor rho-2 subunit		tgt	agg	increased
2667	RATGABAA.PE1	nc	GABA-alpha receptor gamma-3 subunit		aag	tca	decreased
2668	RATGABAA.PE1	nc	GABA-alpha receptor gamma-3 subunit		aag	tca	decreased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
2669	Taq1	55	tca	106.22	106	0	106.24	106.2	0	8 300 000	9 500 000	+=	/	/	/(6)
2670	Hha1	4	aag	114.94	115	115.13	114.8	114.89	6 100 000	12 500 000	8 500 000	+=	/ (-)		/(6)
2671	Taq1	39	agg	139.32	140	139.57	0	139.07	20 500 000	0	3 400 000	-=(-)	\		/(6)
2672	Taq1	39	agg	139.66	140	0	139.66	0	0	43 600 000	0	+-	A		/(6)
2673	Taq1	39	agg	140.585	140	140.52	140.65	0	11 000 000	106 400 000	0	+-	A		/(6)
2674	Taq1	39	agg	139.57	140	139.57	0	0	761.28	0	0	-=	\		/(6)
2675	Taq1	39	agg	140.52	140	140.52	0	0	408.49	0	0	-=	\		/(6)
2676	Taq1	39	agg	139.66	140	0	139.66	0	0	438.19	0	+-	A		/(6)
2677	Taq1	39	agg	140.65	140	0	140.65	0	0	1 069.35	0	+-	A		/(6)
2678	Taq1	62	tgt	139.635	140	0	139.69	139.58	0	3 100 000	6 800 000	++	/		/(6)
2679	Taq1	62	tgt	140.697	140	140.8	140.75	140.54	3 400 000	8 100 000	15 400 000	=+	/ (-)		/(6)
2680	Hha1	6	aga	306.42	308	306.42	0	0	5 300 000	0	0	-=	\		/(6)
2681	Hha1	6	aga	307.27	308	307.37	307.18	307.26	21 400 000	12 000 000	5 200 000	==	-		/(6)
2682	Hha1	6	aga	308.39	308	0	308.32	308.46	0	10 000 000	8 800 000	+=	/		/(6)
2683	Taq1	51	ata	310.78	309	0	0	310.78	0	0	3 600 000	=+	/		/(6)
2684	Hha1	39	agg	97.095	97	97.23	0	96.96	329.91	0	309.24	-+(=)	V		\(7)
2685	Hha1	6	aga	119.987	120	120	119.94	120.02	25 400 000	3 000 000	4 900 000	-=	\ (-)	\	\(7)
2686	Taq1	39	agg	119.78	120	119.93	119.63	0	19 400 000	32 300 000	0	=-	\	\	\(7)
2687	Taq1	39	agg	119.93	120	119.93	0	0	720.43	0	0	-=	\	\	\(7)
2688	Taq1	39	agg	119.63	120	0	119.63	0	0	324.62	0	+-	A		\(7)
2689	Hha1	41	ccc	123.8	124	123.8	0	0	5 400 000	0	0	-=	\		\(7)
2690	Hha1	10	atg	215.46	216	215.46	0	0	3 800 000	0	0	-=	\	\	\(7)
2691	Taq1	10	atg	215.46	216	215.46	0	0	3 400 000	0	0	-=	\	\	\(7)
2692	Taq1	10	atg	215.99	216	0	215.99	0	0	5 900 000	0	+-	A		\(7)
2693	Hha1	10	atg	216.62	216	216.62	0	0	5 100 000	0	0	-=	\		\(7)
2694	Taq1	10	atg	217.17	216	217.17	0	0	3 000 000	0	0	-=	\		\(7)
2695	Hha1	39	agg	97.095	97	97.23	0	96.96	329.91	0	309.24	-+(=)	V		\(7)
2696	Hha1	6	aga	119.987	120	120	119.94	120.02	25 400 000	3 000 000	4 900 000	-=	\ (-)	\	\(7)
2697	Taq1	39	agg	119.78	120	119.93	119.63	0	19 400 000	32 300 000	0	=-	\	\	\(7)
2698	Taq1	39	agg	119.93	120	119.93	0	0	720.43	0	0	-=	\	\	\(7)
2699	Taq1	39	agg	119.63	120	0	119.63	0	0	324.62	0	+-	A		\(7)
2700	Hha1	41	ccc	123.8	124	123.8	0	0	5 400 000	0	0	-=	\		\(7)
2701	Hha1	10	atg	215.46	216	215.46	0	0	3 800 000	0	0	-=	\	\	\(7)
2702	Taq1	10	atg	215.46	216	215.46	0	0	3 400 000	0	0	-=	\	\	\(7)
2703	Taq1	10	atg	215.99	216	0	215.99	0	0	5 900 000	0	+-	A		\(7)
2704	Hha1	10	atg	216.62	216	216.62	0	0	5 100 000	0	0	-=	\		\(7)
2705	Taq1	10	atg	217.17	216	217.17	0	0	3 000 000	0	0	-=	\		\(7)
2706	Hha1	39	agg	97.095	97	97.23	0	96.96	329.91	0	309.24	-+(=)	V		\(8)
2707	Hha1	6	aga	119.987	120	120	119.94	120.02	25 400 000	3 000 000	4 900 000	-=	\ (-)	\	\(8)
2708	Taq1	39	agg	119.78	120	119.93	119.63	0	19 400 000	32 300 000	0	=-	\	\	\(8)
2709	Taq1	39	agg	119.93	120	119.93	0	0	720.43	0	0	-=	\	\	\(8)
2710	Taq1	39	agg	119.63	120	0	119.63	0	0	324.62	0	+-	A		\(8)
2711	Hha1	41	ccc	123.8	124	123.8	0	0	5 400 000	0	0	-=	\		\(8)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
2669	RATGABAA.PE1	nc	GABA-alpha receptor gamma-3 subunit		aag	tca	decreased
2670	RATGABAA.PE1	nc	GABA-alpha receptor gamma-3 subunit		ttc	aag	decreased
2671	RATGABAA.PE1	nc	GABA-alpha receptor gamma-3 subunit		tgt	agg	decreased
2672	RATGABAA.PE1	nc	GABA-alpha receptor gamma-3 subunit		tgt	agg	decreased
2673	RATGABAA.PE1	nc	GABA-alpha receptor gamma-3 subunit		tgt	agg	decreased
2674	RATGABAA.PE1	nc	GABA-alpha receptor gamma-3 subunit		tgt	agg	decreased
2675	RATGABAA.PE1	nc	GABA-alpha receptor gamma-3 subunit		tgt	agg	decreased
2676	RATGABAA.PE1	nc	GABA-alpha receptor gamma-3 subunit		tgt	agg	decreased
2677	RATGABAA.PE1	nc	GABA-alpha receptor gamma-3 subunit		tgt	agg	decreased
2678	RATGABAA.PE1	nc	GABA-alpha receptor gamma-3 subunit		tgt	agg	decreased
2679	RATGABAA.PE1	nc	GABA-alpha receptor gamma-3 subunit		tgt	agg	decreased
2680	RATGABAA.PE1	nc	GABA-alpha receptor gamma-3 subunit		aga	ata	decreased
2681	RATGABAA.PE1	nc	GABA-alpha receptor gamma-3 subunit		aga	ata	decreased
2682	RATGABAA.PE1	nc	GABA-alpha receptor gamma-3 subunit		aga	ata	decreased
2683	RATGABAA.PE1	nc	GABA-alpha receptor gamma-3 subunit		aga	ata	decreased
2684	RNO011318.PE1	gaba-B R2	GABA-B R2 receptor		ggc	agg	increased
2685	RNO011318.PE1	gaba-B R2	GABA-B R2 receptor		aga	agg	increased
2686	RNO011318.PE1	gaba-B R2	GABA-B R2 receptor		aga	agg	increased
2687	RNO011318.PE1	gaba-B R2	GABA-B R2 receptor		aga	agg	increased
2688	RNO011318.PE1	gaba-B R2	GABA-B R2 receptor		aga	agg	increased
2689	RNO011318.PE1	gaba-B R2	GABA-B R2 receptor		ccc	ccg	increased
2690	RNO011318.PE1	gaba-B R2	GABA-B R2 receptor		atg	ggt	increased
2691	RNO011318.PE1	gaba-B R2	GABA-B R2 receptor		atg	ggt	increased
2692	RNO011318.PE1	gaba-B R2	GABA-B R2 receptor		atg	ggt	increased
2693	RNO011318.PE1	gaba-B R2	GABA-B R2 receptor		atg	ggt	increased
2694	RNO011318.PE1	gaba-B R2	GABA-B R2 receptor		atg	ggt	increased
2695	AF109405.PE1	nc	GABA-B receptor 2	*	ggc	agg	increased
2696	AF109405.PE1	nc	GABA-B receptor 2	*	aga	agg	increased
2697	AF109405.PE1	nc	GABA-B receptor 2	*	aga	agg	increased
2698	AF109405.PE1	nc	GABA-B receptor 2	*	aga	agg	increased
2699	AF109405.PE1	nc	GABA-B receptor 2	*	aga	agg	increased
2700	AF109405.PE1	nc	GABA-B receptor 2	*	ccc	ccg	increased
2701	AF109405.PE1	nc	GABA-B receptor 2	*	atg	ggt	increased
2702	AF109405.PE1	nc	GABA-B receptor 2	*	atg	ggt	increased
2703	AF109405.PE1	nc	GABA-B receptor 2	*	atg	ggt	increased
2704	AF109405.PE1	nc	GABA-B receptor 2	*	atg	ggt	increased
2705	AF109405.PE1	nc	GABA-B receptor 2	*	atg	ggt	increased
2706	AF058795.PE1	nc	GABA-B receptor gb2		ggc	agg	increased
2707	AF058795.PE1	nc	GABA-B receptor gb2		aga	agg	increased
2708	AF058795.PE1	nc	GABA-B receptor gb2		aga	agg	increased
2709	AF058795.PE1	nc	GABA-B receptor gb2		aga	agg	increased
2710	AF058795.PE1	nc	GABA-B receptor gb2		aga	agg	increased
2711	AF058795.PE1	nc	GABA-B receptor gb2		ccc	ccg	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
2712	Hha1	10	atg	215.46	216	215.46	0	0	3 800 000	0	0	-=	\	\	\(8)
2713	Taq1	10	atg	215.46	216	215.46	0	0	3 400 000	0	0	-=	\	\	\(8)
2714	Taq1	10	atg	215.99	216	0	215.99	0	0	5 900 000	0	+-	A		\(8)
2715	Hha1	10	atg	216.62	216	216.62	0	0	5 100 000	0	0	-=	\		\(8)
2716	Taq1	10	atg	217.17	216	217.17	0	0	3 000 000	0	0	-=	\		\(8)
2717	Taq1	44	cgg	238.89	240	238.89	0	0	208.31	0	0	-=	\		\(8)
2718	Taq1	44	cgg	239.27	240	239.27	0	0	256.91	0	0	-=	\		\(8)
2719	Taq1	44	cgg	240.52	240	240.34	240.7	0	701.31	315.84	0	--	\		\(8)
2720	Hha1	8	gaa	190.237	191	190.26	190.27	190.18	10 400 000	7 900 000	3 300 000	==	-		-2
2721	Taq1	8	gaa	190.59	191	0	190.37	190.81	0	3 200 000	18 700 000	=+	/		-2
2722	Hha1	8	gaa	191.127	191	191.11	191.18	191.09	8 200 000	8 000 000	3 100 000	=-	\ (-)		-2
2723	Hha1	33	agc	60.14	60	0	60.14	0	0	4 600 000	0	+-	A		-1
2724	Hha1	64	gtt	70.367	70	70.31	70.37	70.42	6 400 000	5 200 000	17 000 000	=+	/ (-)		-1
2725	Hha1	2	tta	95.73	96	95.66	95.77	95.76	116 400 000	146 100 000	174 300 000	==	-		-1
2726	Hha1	2	tta	96.563	96	96.68	96.45	96.56	172 600 000	85 700 000	50 000 000	-=	\ (-)		-1
2727	Taq1	45	gcc	136.317	137	136.21	136.62	136.12	7 500 000	4 100 000	8 100 000	=+	/ (-)		-1
2728	Taq1	45	gcc	137.01	137	137.05	136.97	0	5 900 000	4 300 000	0	=-	\		-1
2729	Taq1	45	gcc	137.62	137	137.67	0	137.57	4 100 000	0	6 800 000	-+(=)	V		-1
2730	Taq1	26	ctg	137.343	138	137.33	137.3	137.4	4 100 000	7 000 000	5 600 000	==	-		-1
2731	Taq1	26	ctg	138.52	138	0	0	138.52	0	0	4 800 000	=+	/		-1
2732	Taq1	57	ctg	137.34	138	0	137.34	0	0	4 900 000	0	+-	A		-1
2733	Taq1	57	ctg	138.16	138	138.26	0	138.06	3 900 000	0	8 600 000	-+(+)	V (/)		-1
2734	Hha1	40	tgg	151.76	152	151.76	0	0	7 700 000	0	0	-=	\		-1
2735	Hha1	40	tgg	152.725	152	152.8	152.65	0	4 000 000	10 100 000	0	+-	A		-1
2736	Hha1	3	aac	165.68	166	165.59	0	165.77	6 200 000	0	4 700 000	-+(=)	V		-1
2737	Hha1	3	aac	166.687	166	166.62	166.75	166.69	9 400 000	3 300 000	6 800 000	-=	\ (-)		-1
2738	Taq1	36	ggt	165.37	166	0	0	165.37	0	0	4 900 000	=+	/		-1
2739	Taq1	36	ggt	166.34	166	0	0	166.34	0	0	3 100 000	=+	/		-1
2740	Hha1	64	gtt	68.403	68	68.48	68.31	68.42	72 300 000	13 000 000	31 700 000	-=	\ (-)		-(2) \(2)
2741	Hha1	33	agc	149.31	150	149.36	149.36	149.21	10 900 000	13 300 000	3 500 000	=-	\ (-)		-(2) \(2)
2742	Hha1	33	agc	150.42	150	150.39	150.45	0	5 500 000	5 500 000	0	=-	\		-(2) \(2)
2743	Hha1	54	ttt	61.63	62	61.58	61.68	0	3 800 000	8 700 000	0	+-	A		A(2)
2744	Hha1	59	ttc	90.183	90	90.33	90.16	90.06	270.41	2 023.68	87.96	+-	A		A(2)
2745	Hha1	40	tgg	145.52	146	145.53	145.44	145.59	3 100 000	9 400 000	9 100 000	+=	/ (-)		A(2)
2746	Hha1	40	tgg	146.47	146	0	146.34	146.6	0	9 800 000	16 400 000	+=	/		A(2)
2747	Hha1	33	agc	60.14	60	0	60.14	0	0	4 600 000	0	+-	A		-1
2748	Hha1	64	gtt	70.367	70	70.31	70.37	70.42	6 400 000	5 200 000	17 000 000	=+	/ (-)		-1
2749	Hha1	2	tta	95.73	96	95.66	95.77	95.76	116 400 000	146 100 000	174 300 000	==	-		-1
2750	Hha1	2	tta	96.563	96	96.68	96.45	96.56	172 600 000	85 700 000	50 000 000	-=	\ (-)		-1
2751	Taq1	45	gcc	136.317	137	136.21	136.62	136.12	7 500 000	4 100 000	8 100 000	=+	/ (-)		-1
2752	Taq1	45	gcc	137.01	137	137.05	136.97	0	5 900 000	4 300 000	0	=-	\		-1
2753	Taq1	45	gcc	137.62	137	137.67	0	137.57	4 100 000	0	6 800 000	-+(=)	V		-1
2754	Taq1	26	ctg	137.343	138	137.33	137.3	137.4	4 100 000	7 000 000	5 600 000	==	-		-1

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
2712	AF058795.PE1	nc	GABA-B receptor gb2		atg	ggt	increased
2713	AF058795.PE1	nc	GABA-B receptor gb2		atg	ggt	increased
2714	AF058795.PE1	nc	GABA-B receptor gb2		atg	ggt	increased
2715	AF058795.PE1	nc	GABA-B receptor gb2		atg	ggt	increased
2716	AF058795.PE1	nc	GABA-B receptor gb2		atg	ggt	increased
2717	AF058795.PE1	nc	GABA-B receptor gb2		cgg	tga	increased
2718	AF058795.PE1	nc	GABA-B receptor gb2		cgg	tga	increased
2719	AF058795.PE1	nc	GABA-B receptor gb2		cgg	tga	increased
2720	RATGTA.GTA	GTA	galactosyltransferase-associated kinase		gaa	tgg	No change
2721	RATGTA.GTA	GTA	galactosyltransferase-associated kinase		gaa	tgg	No change
2722	RATGTA.GTA	GTA	galactosyltransferase-associated kinase		gaa	tgg	No change
2723	AF010318.GALR2	GALR2	galanin receptor	*	tgg	agc	No change
2724	AF010318.GALR2	GALR2	galanin receptor	*	tca	gtt	No change
2725	AF010318.GALR2	GALR2	galanin receptor	*	tta	aac	No change
2726	AF010318.GALR2	GALR2	galanin receptor	*	tta	aac	No change
2727	AF010318.GALR2	GALR2	galanin receptor	*	gcc	ctg	No change
2728	AF010318.GALR2	GALR2	galanin receptor	*	gcc	ctg	No change
2729	AF010318.GALR2	GALR2	galanin receptor	*	gcc	ctg	No change
2730	AF010318.GALR2	GALR2	galanin receptor	*	gcc	ctg	No change
2731	AF010318.GALR2	GALR2	galanin receptor	*	gcc	ctg	No change
2732	AF010318.GALR2	GALR2	galanin receptor	*	gcc	ctg	No change
2733	AF010318.GALR2	GALR2	galanin receptor	*	gcc	ctg	No change
2734	AF010318.GALR2	GALR2	galanin receptor	*	tgg	tcc	No change
2735	AF010318.GALR2	GALR2	galanin receptor	*	tgg	tcc	No change
2736	AF010318.GALR2	GALR2	galanin receptor	*	aac	ggt	No change
2737	AF010318.GALR2	GALR2	galanin receptor	*	aac	ggt	No change
2738	AF010318.GALR2	GALR2	galanin receptor	*	aac	ggt	No change
2739	AF010318.GALR2	GALR2	galanin receptor	*	aac	ggt	No change
2740	RNU30290.PE1	nc	galanin receptor GALR1		tcc	gtt	No change
2741	RNU30290.PE1	nc	galanin receptor GALR1		agc	cca	No change
2742	RNU30290.PE1	nc	galanin receptor GALR1		agc	cca	No change
2743	AF073798.PE1	nc	galanin receptor GALR3		ttt	gtg	increased by mild
2744	AF073798.PE1	nc	galanin receptor GALR3		ttc	ggt	increased by mild
2745	AF073798.PE1	nc	galanin receptor GALR3		tgg	ccg	increased by mild
2746	AF073798.PE1	nc	galanin receptor GALR3		tgg	ccg	increased by mild
2747	AF008548.GALR2	GALR2	galanin receptor type 2	*	tgg	agc	No change
2748	AF008548.GALR2	GALR2	galanin receptor type 2	*	tca	gtt	No change
2749	AF008548.GALR2	GALR2	galanin receptor type 2	*	tta	aac	No change
2750	AF008548.GALR2	GALR2	galanin receptor type 2	*	tta	aac	No change
2751	AF008548.GALR2	GALR2	galanin receptor type 2	*	gcc	ctg	No change
2752	AF008548.GALR2	GALR2	galanin receptor type 2	*	gcc	ctg	No change
2753	AF008548.GALR2	GALR2	galanin receptor type 2	*	gcc	ctg	No change
2754	AF008548.GALR2	GALR2	galanin receptor type 2	*	gcc	ctg	No change

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
2755	Taq1	26	ctg	138.52	138	0	0	138.52	0	0	4 800 000	=+	/		-1
2756	Taq1	57	ctg	137.34	138	0	137.34	0	0	4 900 000	0	+-	A		-1
2757	Taq1	57	ctg	138.16	138	138.26	0	138.06	3 900 000	0	8 600 000	-+(+)	V (/)		-1
2758	Hha1	40	tgg	151.76	152	151.76	0	0	7 700 000	0	0	-=	\		-1
2759	Hha1	40	tgg	152.725	152	152.8	152.65	0	4 000 000	10 100 000	0	+-	A		-1
2760	Hha1	3	aac	165.68	166	165.59	0	165.77	6 200 000	0	4 700 000	-+(=)	V		-1
2761	Hha1	3	aac	166.687	166	166.62	166.75	166.69	9 400 000	3 300 000	6 800 000	-=	\ (-)		-1
2762	Taq1	36	ggt	165.37	166	0	0	165.37	0	0	4 900 000	=+	/		-1
2763	Taq1	36	ggt	166.34	166	0	0	166.34	0	0	3 100 000	=+	/		-1
2764	Hha1	33	agc	60.14	60	0	60.14	0	0	4 600 000	0	+-	A		-1
2765	Hha1	64	gtt	70.367	70	70.31	70.37	70.42	6 400 000	5 200 000	17 000 000	=+	/ (-)		-1
2766	Hha1	2	tta	95.73	96	95.66	95.77	95.76	116 400 000	146 100 000	174 300 000	==	-		-1
2767	Hha1	2	tta	96.563	96	96.68	96.45	96.56	172 600 000	85 700 000	50 000 000	-=	\ (-)		-1
2768	Taq1	45	gcc	136.317	137	136.21	136.62	136.12	7 500 000	4 100 000	8 100 000	=+	/ (-)		-1
2769	Taq1	45	gcc	137.01	137	137.05	136.97	0	5 900 000	4 300 000	0	=-	\		-1
2770	Taq1	45	gcc	137.62	137	137.67	0	137.57	4 100 000	0	6 800 000	-+(=)	V		-1
2771	Taq1	26	ctg	137.343	138	137.33	137.3	137.4	4 100 000	7 000 000	5 600 000	==	-		-1
2772	Taq1	26	ctg	138.52	138	0	0	138.52	0	0	4 800 000	=+	/		-1
2773	Taq1	57	ctg	137.34	138	0	137.34	0	0	4 900 000	0	+-	A		-1
2774	Taq1	57	ctg	138.16	138	138.26	0	138.06	3 900 000	0	8 600 000	-+(+)	V (/)		-1
2775	Hha1	40	tgg	151.76	152	151.76	0	0	7 700 000	0	0	-=	\		-1
2776	Hha1	40	tgg	152.725	152	152.8	152.65	0	4 000 000	10 100 000	0	+-	A		-1
2777	Hha1	3	aac	165.68	166	165.59	0	165.77	6 200 000	0	4 700 000	-+(=)	V		-1
2778	Hha1	3	aac	166.687	166	166.62	166.75	166.69	9 400 000	3 300 000	6 800 000	-=	\ (-)		-1
2779	Taq1	36	ggt	165.37	166	0	0	165.37	0	0	4 900 000	=+	/		-1
2780	Taq1	36	ggt	166.34	166	0	0	166.34	0	0	3 100 000	=+	/		-1
2781	Taq1	22	tcc	205.24	206	0	205.24	0	0	6 000 000	0	+-	A		\(3) A(3)
2782	Hha1	22	tcc	205.9	206	205.9	0	0	4 100 000	0	0	-=	\		\(3) A(3)
2783	Taq1	22	tcc	205.91	206	0	205.91	0	0	4 500 000	0	+-	A		\(3) A(3)
2784	Hha1	22	tcc	206.86	206	206.86	0	0	15 400 000	0	0	-=	\		\(3) A(3)
2785	Taq1	22	tcc	206.63	206	0	206.63	0	0	4 900 000	0	+-	A		\(3) A(3)
2786	Taq1	22	tcc	207.22	206	207.22	0	0	3 700 000	0	0	-=	\		\(3) A(3)
2787	Hha1	40	tgg	117.457	118	117.51	117.29	117.57	13 300 000	10 500 000	3 100 000	=-	\ (-)		\(3)
2788	Hha1	40	tgg	118.51	118	0	118.44	118.58	0	7 000 000	7 000 000	+=	/		\(3)
2789	Hha1	26	ctg	194.26	195	194.26	0	0	3 000 000	0	0	-=	\	\	\(3)
2790	Hha1	32	gtc	193.94	195	193.92	193.96	0	549.24	457.78	0	=-	\		\(3)
2791	Hha1	32	gtc	194.13	195	194.21	194.05	0	585.86	427.26	0	=-	\	\	\(3)
2792	Hha1	32	gtc	194.585	195	194.77	194.4	0	659.09	467.95	0	=-	\		\(3)
2793	Hha1	32	gtc	194.7	195	0	194.7	0	0	478.12	0	+-	A		\(3)
2794	Hha1	32	gtc	196	195	0	196	0	0	366.22	0	+-	A		\(3)
2795	Taq1	64	gtt	254.98	256	254.98	0	0	3 300 000	0	0	-=	\		\(2)
2796	Taq1	64	gtt	256.99	256	256.99	0	0	3 000 000	0	0	-=	\		\(2)
2797	Taq1	21	acc	268.69	269	268.69	0	0	5 800 000	0	0	-=	\		\(2)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
2755	AF008548.GALR2	GALR2	galanin receptor type 2	*	gcc	ctg	No change
2756	AF008548.GALR2	GALR2	galanin receptor type 2	*	gcc	ctg	No change
2757	AF008548.GALR2	GALR2	galanin receptor type 2	*	gcc	ctg	No change
2758	AF008548.GALR2	GALR2	galanin receptor type 2	*	tgg	tcc	No change
2759	AF008548.GALR2	GALR2	galanin receptor type 2	*	tgg	tcc	No change
2760	AF008548.GALR2	GALR2	galanin receptor type 2	*	aac	ggt	No change
2761	AF008548.GALR2	GALR2	galanin receptor type 2	*	aac	ggt	No change
2762	AF008548.GALR2	GALR2	galanin receptor type 2	*	aac	ggt	No change
2763	AF008548.GALR2	GALR2	galanin receptor type 2	*	aac	ggt	No change
2764	RNU94322.PE1	nc	galanin receptor type 2	*	tgg	agc	No change
2765	RNU94322.PE1	nc	galanin receptor type 2	*	tca	gtt	No change
2766	RNU94322.PE1	nc	galanin receptor type 2	*	tta	aac	No change
2767	RNU94322.PE1	nc	galanin receptor type 2	*	tta	aac	No change
2768	RNU94322.PE1	nc	galanin receptor type 2	*	gcc	ctg	No change
2769	RNU94322.PE1	nc	galanin receptor type 2	*	gcc	ctg	No change
2770	RNU94322.PE1	nc	galanin receptor type 2	*	gcc	ctg	No change
2771	RNU94322.PE1	nc	galanin receptor type 2	*	gcc	ctg	No change
2772	RNU94322.PE1	nc	galanin receptor type 2	*	gcc	ctg	No change
2773	RNU94322.PE1	nc	galanin receptor type 2	*	gcc	ctg	No change
2774	RNU94322.PE1	nc	galanin receptor type 2	*	gcc	ctg	No change
2775	RNU94322.PE1	nc	galanin receptor type 2	*	tgg	tcc	No change
2776	RNU94322.PE1	nc	galanin receptor type 2	*	tgg	tcc	No change
2777	RNU94322.PE1	nc	galanin receptor type 2	*	aac	ggt	No change
2778	RNU94322.PE1	nc	galanin receptor type 2	*	aac	ggt	No change
2779	RNU94322.PE1	nc	galanin receptor type 2	*	aac	ggt	No change
2780	RNU94322.PE1	nc	galanin receptor type 2	*	aac	ggt	No change
2781	RATLSOR.PE1	nc	gamma-glutamylcysteine synthetase		gac	tcc	increased
2782	RATLSOR.PE1	nc	gamma-glutamylcysteine synthetase		gac	tcc	increased
2783	RATLSOR.PE1	nc	gamma-glutamylcysteine synthetase		gac	tcc	increased
2784	RATLSOR.PE1	nc	gamma-glutamylcysteine synthetase		gac	tcc	increased
2785	RATLSOR.PE1	nc	gamma-glutamylcysteine synthetase		gac	tcc	increased
2786	RATLSOR.PE1	nc	gamma-glutamylcysteine synthetase		gac	tcc	increased
2787	AF244973.PE1	nc	gamma-glutamyltranspeptidase-like protein		tgg	cgt	increased
2788	AF244973.PE1	nc	gamma-glutamyltranspeptidase-like protein		tgg	cgt	increased
2789	AF244973.PE1	nc	gamma-glutamyltranspeptidase-like protein		ctg	gtc	increased
2790	AF244973.PE1	nc	gamma-glutamyltranspeptidase-like protein		ctg	gtc	increased
2791	AF244973.PE1	nc	gamma-glutamyltranspeptidase-like protein		ctg	gtc	increased
2792	AF244973.PE1	nc	gamma-glutamyltranspeptidase-like protein		ctg	gtc	increased
2793	AF244973.PE1	nc	gamma-glutamyltranspeptidase-like protein		ctg	gtc	increased
2794	AF244973.PE1	nc	gamma-glutamyltranspeptidase-like protein		ctg	gtc	increased
2795	AF242544.PE1	nc	gamma-synergin		tga	gtt	increased
2796	AF242544.PE1	nc	gamma-synergin		tga	gtt	increased
2797	AF242544.PE1	nc	gamma-synergin		acc	tgg	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
2798	Taq1	9	atc	79.103	79	78.96	79.07	79.28	8 200 000	5 000 000	7 100 000	==	-		\(3)
2799	Hha1	8	gaa	235.04	236	235.04	0	0	4 300 000	0	0	-=	\		\(3)
2800	Taq1	8	gaa	235.63	236	235.63	0	0	3 800 000	0	0	-=	\		\(3)
2801	Hha1	8	gaa	236.3	236	236.33	236.27	0	3 900 000	3 100 000	0	=-	\		\(3)
2802	Taq1	48	ggg	210.15	210	210.15	0	0	1 137.8	0	0	-=	\	\	
2803	Hha1	6	aga	210.285	211	210.13	210.44	0	5 000 000	3 200 000	0	=-	\	\	
2804	Taq1	36	ggt	107.223	107	107.05	107.44	107.18	7 800 000	3 400 000	3 000 000	-=	\ (-)		-2
2805	Taq1	54	ttt	107.977	108	108.11	107.76	108.06	721.04	1 140.77	792.29	==	-		-2
2806	Hha1	56	tga	137.877	138	137.73	137.8	138.1	143.01	792.6	706.77	+=	/ (-)		-1
2807	Hha1	56	tga	138.753	138	138.53	138.7	139.03	228.82	379.78	551.62	==	-		-1
2808	Hha1	60	ttg	201.167	201	201.18	201.11	201.21	6 200 000	4 700 000	14 100 000	=+	/ (-)		-1
2809	Taq1	10	atg	168.41	168	168.41	0	0	4 100 000	0	0	-=	\	\	
2810	Hha1	10	atg	168.52	168	168.52	0	0	4 700 000	0	0	-=	\	\	
2811	Taq1	10	atg	168.41	168	168.41	0	0	4 100 000	0	0	-=	\	\	
2812	Hha1	10	atg	168.52	168	168.52	0	0	4 700 000	0	0	-=	\	\	
2813	Taq1	10	atg	168.41	168	168.41	0	0	4 100 000	0	0	-=	\	\	
2814	Hha1	10	atg	168.52	168	168.52	0	0	4 700 000	0	0	-=	\	\	
2815	Taq1	10	atg	168.41	168	168.41	0	0	4 100 000	0	0	-=	\	\	
2816	Hha1	10	atg	168.52	168	168.52	0	0	4 700 000	0	0	-=	\	\	
2817	Hha1	27	acg	114.05	114	114.04	0	114.06	11 200 000	0	8 100 000	-+(=)	V		V(4) /(3)
2818	Hha1	41	ccc	128.07	128	0	0	128.07	0	0	10 500 000	=+	/	/	V(4) /(3)
2819	Hha1	43	cgc	127.785	128	128.02	0	127.55	4 800 000	0	5 500 000	-+(=)	V		V(4) /(3)
2820	Hha1	43	cgc	128.07	128	0	128.1	128.04	0	8 500 000	6 700 000	+=	/	/	V(4) /(3)
2821	Hha1	26	ctg	140.475	141	140.32	0	140.63	3 700 000	0	3 100 000	-+(=)	V		V(4) /(3)
2822	Hha1	26	ctg	141.66	141	0	141.69	141.63	0	12 100 000	41 900 000	=+	/		V(4) /(3)
2823	Hha1	44	cgg	240.6	241	240.6	0	240.6	12 100 000	0	7 200 000	-+(=)	V		V(4) /(3)
2824	Hha1	44	cgg	241.507	241	241.56	241.47	241.49	73 000 000	8 800 000	30 900 000	-=	\ (-)		V(4) /(3)
2825	Hha1	44	cgg	242.14	241	242.19	242.08	242.15	38 600 000	5 400 000	22 100 000	-=	\ (-)		V(4) /(3)
2826	Hha1	49	aaa	97.777	98	97.89	97.58	97.86	14 700 000	11 100 000	12 000 000	==	-		/(6)
2827	Hha1	49	aaa	98.455	98	98.47	0	98.44	36 000 000	0	6 200 000	-=(-)	\		/(6)
2828	Hha1	27	acg	114.05	114	114.04	0	114.06	11 200 000	0	8 100 000	-+(=)	V		/(6)
2829	Taq1	26	ctg	121.24	121	0	0	121.24	0	0	4 800 000	=+	/	/	/(6)
2830	Taq1	57	ctg	121.13	121	121.15	121.15	121.09	5 700 000	4 300 000	10 600 000	=+	/ (-)	/	/(6)
2831	Taq1	62	tgt	120.55	121	120.53	120.61	120.51	4 300 000	8 300 000	9 100 000	==	-		/(6)
2832	Taq1	62	tgt	121.485	121	121.49	0	121.48	3 400 000	0	10 100 000	=+(+)	/		/(6)
2833	Hha1	41	ccc	128.07	128	0	0	128.07	0	0	10 500 000	=+	/	/	/(6)
2834	Hha1	43	cgc	127.785	128	128.02	0	127.55	4 800 000	0	5 500 000	-+(=)	V		/(6)
2835	Hha1	43	cgc	128.07	128	0	128.1	128.04	0	8 500 000	6 700 000	+=	/	/	/(6)
2836	Hha1	26	ctg	140.475	141	140.32	0	140.63	3 700 000	0	3 100 000	-+(=)	V		/(6)
2837	Hha1	26	ctg	141.66	141	0	141.69	141.63	0	12 100 000	41 900 000	=+	/		/(6)
2838	Taq1	52	att	170.607	171	170.8	170.63	170.39	3 200 000	3 300 000	4 500 000	==	-		/(6)
2839	Hha1	27	acg	114.05	114	114.04	0	114.06	11 200 000	0	8 100 000	-+(=)	V		V(2)
2840	Hha1	26	ctg	140.475	141	140.32	0	140.63	3 700 000	0	3 100 000	-+(=)	V		V(2)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
2798	RNU65656.PE1	nc	gelatinase A		atc	cca	increased
2799	RNU65656.PE1	nc	gelatinase A		gac	gaa	increased
2800	RNU65656.PE1	nc	gelatinase A		gac	gaa	increased
2801	RNU65656.PE1	nc	gelatinase A		gac	gaa	increased
2802	RNU24441.GELB	GelB	gelatinase B		ggg	aga	increased
2803	RNU24441.GELB	GelB	gelatinase B		ggg	aga	increased
2804	RATMPP.MPP-I	MPP-I	general mitochondrial matrix processing protease		ttt	ggt	No change
2805	RATMPP.MPP-I	MPP-I	general mitochondrial matrix processing protease		ttt	ggt	No change
2806	AF265360.PE1	nc	GLAST-1a		aag	tga	No change
2807	AF265360.PE1	nc	GLAST-1a		aag	tga	No change
2808	AF265360.PE1	nc	GLAST-1a		cgt	ttg	No change
2809	RNGFABEX1.GFAP	gfap	glial fibrillary acidic protein		atg	tgt	increased
2810	RNGFABEX1.GFAP	gfap	glial fibrillary acidic protein		atg	tgt	increased
2811	RNU03700.PE1	nc	glial fibrillary acidic protein		atg	tgt	increased
2812	RNU03700.PE1	nc	glial fibrillary acidic protein		atg	tgt	increased
2813	AF028784.GFAP	GFAP	glial fibrillary acidic protein alpha		atg	tgt	increased
2814	AF028784.GFAP	GFAP	glial fibrillary acidic protein alpha		atg	tgt	increased
2815	AF028784.PE2	GFAP	glial fibrillary acidic protein delta		atg	tgt	increased
2816	AF028784.PE2	GFAP	glial fibrillary acidic protein delta		atg	tgt	increased
2817	AF194994.NRG1	Nrg1	glial growth factor		cct	acg	decreased by mild
2818	AF194994.NRG1	Nrg1	glial growth factor		cgc	ccc	decreased
2819	AF194994.NRG1	Nrg1	glial growth factor		cgc	ccc	decreased by mild
2820	AF194994.NRG1	Nrg1	glial growth factor		cgc	ccc	decreased
2821	AF194994.NRG1	Nrg1	glial growth factor		ctg	ggc	decreased by mild
2822	AF194994.NRG1	Nrg1	glial growth factor		ctg	ggc	decreased by mild
2823	AF194994.NRG1	Nrg1	glial growth factor		cgg	cgg	decreased by mild
2824	AF194994.NRG1	Nrg1	glial growth factor		cgg	cgg	decreased by mild
2825	AF194994.NRG1	Nrg1	glial growth factor		cgg	cgg	decreased by mild
2826	AF194993.NRG1	Nrg1	glial growth factor beta 1a		aaa	act	decreased
2827	AF194993.NRG1	Nrg1	glial growth factor beta 1a		aaa	act	decreased
2828	AF194993.NRG1	Nrg1	glial growth factor beta 1a		cct	acg	decreased
2829	AF194993.NRG1	Nrg1	glial growth factor beta 1a		ctg	tgt	decreased
2830	AF194993.NRG1	Nrg1	glial growth factor beta 1a		ctg	tgt	decreased
2831	AF194993.NRG1	Nrg1	glial growth factor beta 1a		ctg	tgt	decreased
2832	AF194993.NRG1	Nrg1	glial growth factor beta 1a		ctg	tgt	decreased
2833	AF194993.NRG1	Nrg1	glial growth factor beta 1a		cgc	ccc	decreased
2834	AF194993.NRG1	Nrg1	glial growth factor beta 1a		cgc	ccc	decreased
2835	AF194993.NRG1	Nrg1	glial growth factor beta 1a		cgc	ccc	decreased
2836	AF194993.NRG1	Nrg1	glial growth factor beta 1a		ctg	ggc	decreased
2837	AF194993.NRG1	Nrg1	glial growth factor beta 1a		ctg	ggc	decreased
2838	AF194993.NRG1	Nrg1	glial growth factor beta 1a		att	ggc	decreased
2839	AF194996.NRG1	Nrg1	glial growth factor GGF beta 3		cct	acg	decreased by mild
2840	AF194996.NRG1	Nrg1	glial growth factor GGF beta 3		ctg	ggc	decreased by mild

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
2841	Hha1	26	ctg	141.66	141	0	141.69	141.63	0	12 100 000	41 900 000	=+	/		V(2)
2842	Taq1	52	att	170.607	171	170.8	170.63	170.39	3 200 000	3 300 000	4 500 000	==	-		V(2)
2843	Taq1	47	ggc	114.615	115	114.6	114.63	0	4 246.15	1 718.65	0	-=	\		\(2)
2844	Taq1	49	aaa	116.43	117	116.43	0	0	35 100 000	0	0	-=	\		\(2)
2845	Taq1	49	aaa	117.215	117	117.29	117.14	0	25 000 000	14 400 000	0	=-	\		\(2)
2846	Taq1	39	agg	102.46	103	0	102.46	0	0	56 100 000	0	+-	A		\(5)
2847	Taq1	39	agg	103.263	103	103.47	103.17	103.15	15 700 000	174 900 000	6 900 000	+-	A		\(5)
2848	Taq1	39	agg	102.46	103	0	102.46	0	0	563.82	0	+-	A		\(5)
2849	Taq1	39	agg	103.263	103	103.47	103.17	103.15	583.03	1 757.8	203.24	+-	A		\(5)
2850	Taq1	17	cca	149.32	150	149.32	0	0	1 170.29	0	0	-=	\		\(5)
2851	Taq1	17	cca	150.15	150	0	150.06	150.24	0	870.89	1 052.47	+=	/		\(5)
2852	Taq1	54	ttt	150.645	151	150.51	150.78	0	2 039.32	540.98	0	-=	\		\(5)
2853	Taq1	54	ttt	151.555	151	151.7	151.41	0	1 143.48	964.36	0	=-	\		\(5)
2854	Taq1	54	ttt	151.6	151	0	151.6	0	0	858.52	0	+-	A		\(5)
2855	Taq1	8	gaa	235.63	237	235.63	0	0	3 800 000	0	0	-=	\		\(5)
2856	Hha1	8	gaa	236.3	237	236.33	236.27	0	3 900 000	3 100 000	0	=-	\		\(5)
2857	Taq1	49	aaa	236.74	238	0	236.74	0	0	8 100 000	0	+-	A		\(5)
2858	Taq1	49	aaa	237.485	238	237.47	237.5	0	7 400 000	3 300 000	0	-=	\		\(5)
2859	Taq1	49	aaa	238.583	238	238.58	238.57	238.6	29 100 000	21 100 000	3 300 000	=-	\ (-)		\(5)
2860	Taq1	39	agg	102.46	103	0	102.46	0	0	56 100 000	0	+-	A		\(5)
2861	Taq1	39	agg	103.263	103	103.47	103.17	103.15	15 700 000	174 900 000	6 900 000	+-	A		\(5)
2862	Taq1	39	agg	102.46	103	0	102.46	0	0	563.82	0	+-	A		\(5)
2863	Taq1	39	agg	103.263	103	103.47	103.17	103.15	583.03	1 757.8	203.24	+-	A		\(5)
2864	Taq1	17	cca	149.32	150	149.32	0	0	1 170.29	0	0	-=	\		\(5)
2865	Taq1	17	cca	150.15	150	0	150.06	150.24	0	870.89	1 052.47	+=	/		\(5)
2866	Taq1	54	ttt	150.645	151	150.51	150.78	0	2 039.32	540.98	0	-=	\		\(5)
2867	Taq1	54	ttt	151.555	151	151.7	151.41	0	1 143.48	964.36	0	=-	\		\(5)
2868	Taq1	54	ttt	151.6	151	0	151.6	0	0	858.52	0	+-	A		\(5)
2869	Taq1	8	gaa	235.63	237	235.63	0	0	3 800 000	0	0	-=	\		\(5)
2870	Hha1	8	gaa	236.3	237	236.33	236.27	0	3 900 000	3 100 000	0	=-	\		\(5)
2871	Taq1	49	aaa	236.74	238	0	236.74	0	0	8 100 000	0	+-	A		\(5)
2872	Taq1	49	aaa	237.485	238	237.47	237.5	0	7 400 000	3 300 000	0	-=	\		\(5)
2873	Taq1	49	aaa	238.583	238	238.58	238.57	238.6	29 100 000	21 100 000	3 300 000	=-	\ (-)		\(5)
2874	Taq1	39	agg	102.46	103	0	102.46	0	0	56 100 000	0	+-	A		\(5)
2875	Taq1	39	agg	103.263	103	103.47	103.17	103.15	15 700 000	174 900 000	6 900 000	+-	A		\(5)
2876	Taq1	39	agg	102.46	103	0	102.46	0	0	563.82	0	+-	A		\(5)
2877	Taq1	39	agg	103.263	103	103.47	103.17	103.15	583.03	1 757.8	203.24	+-	A		\(5)
2878	Taq1	17	cca	149.32	150	149.32	0	0	1 170.29	0	0	-=	\		\(5)
2879	Taq1	17	cca	150.15	150	0	150.06	150.24	0	870.89	1 052.47	+=	/		\(5)
2880	Taq1	54	ttt	150.645	151	150.51	150.78	0	2 039.32	540.98	0	-=	\		\(5)
2881	Taq1	54	ttt	151.555	151	151.7	151.41	0	1 143.48	964.36	0	=-	\		\(5)
2882	Taq1	54	ttt	151.6	151	0	151.6	0	0	858.52	0	+-	A		\(5)
2883	Taq1	8	gaa	235.63	237	235.63	0	0	3 800 000	0	0	-=	\		\(5)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
2841	AF194996.NRG1	Nrg1	glial growth factor GGF beta 3		ctg	ggc	decreased by mild
2842	AF194996.NRG1	Nrg1	glial growth factor GGF beta 3		att	ggc	decreased by mild
2843	AY266116.GLDN	Gldn	gliomedin		aaa	ggc	increased
2844	AY266116.GLDN	Gldn	gliomedin		aaa	ggc	increased
2845	AY266116.GLDN	Gldn	gliomedin		aaa	ggc	increased
2846	AF455050.PE1	nc	glucocorticoid receptor		agg	gct	increased
2847	AF455050.PE1	nc	glucocorticoid receptor		agg	gct	increased
2848	AF455050.PE1	nc	glucocorticoid receptor		agg	gct	increased
2849	AF455050.PE1	nc	glucocorticoid receptor		agg	gct	increased
2850	AF455050.PE1	nc	glucocorticoid receptor		cca	ttt	increased
2851	AF455050.PE1	nc	glucocorticoid receptor		cca	ttt	increased
2852	AF455050.PE1	nc	glucocorticoid receptor		cca	ttt	increased
2853	AF455050.PE1	nc	glucocorticoid receptor		cca	ttt	increased
2854	AF455050.PE1	nc	glucocorticoid receptor		cca	ttt	increased
2855	AF455050.PE1	nc	glucocorticoid receptor		aaa	gaa	increased
2856	AF455050.PE1	nc	glucocorticoid receptor		aaa	gaa	increased
2857	AF455050.PE1	nc	glucocorticoid receptor		aaa	gaa	increased
2858	AF455050.PE1	nc	glucocorticoid receptor		aaa	gaa	increased
2859	AF455050.PE1	nc	glucocorticoid receptor		aaa	gaa	increased
2860	AY066016.PE1	nc	glucocorticoid receptor		agg	gct	increased
2861	AY066016.PE1	nc	glucocorticoid receptor		agg	gct	increased
2862	AY066016.PE1	nc	glucocorticoid receptor		agg	gct	increased
2863	AY066016.PE1	nc	glucocorticoid receptor		agg	gct	increased
2864	AY066016.PE1	nc	glucocorticoid receptor		cca	ttt	increased
2865	AY066016.PE1	nc	glucocorticoid receptor		cca	ttt	increased
2866	AY066016.PE1	nc	glucocorticoid receptor		cca	ttt	increased
2867	AY066016.PE1	nc	glucocorticoid receptor		cca	ttt	increased
2868	AY066016.PE1	nc	glucocorticoid receptor		cca	ttt	increased
2869	AY066016.PE1	nc	glucocorticoid receptor		aaa	gaa	increased
2870	AY066016.PE1	nc	glucocorticoid receptor		aaa	gaa	increased
2871	AY066016.PE1	nc	glucocorticoid receptor		aaa	gaa	increased
2872	AY066016.PE1	nc	glucocorticoid receptor		aaa	gaa	increased
2873	AY066016.PE1	nc	glucocorticoid receptor		aaa	gaa	increased
2874	RNRNAGR.PE1	nc	glucocorticoid receptor		agg	gct	increased
2875	RNRNAGR.PE1	nc	glucocorticoid receptor		agg	gct	increased
2876	RNRNAGR.PE1	nc	glucocorticoid receptor		agg	gct	increased
2877	RNRNAGR.PE1	nc	glucocorticoid receptor		agg	gct	increased
2878	RNRNAGR.PE1	nc	glucocorticoid receptor		cca	ttt	increased
2879	RNRNAGR.PE1	nc	glucocorticoid receptor		cca	ttt	increased
2880	RNRNAGR.PE1	nc	glucocorticoid receptor		cca	ttt	increased
2881	RNRNAGR.PE1	nc	glucocorticoid receptor		cca	ttt	increased
2882	RNRNAGR.PE1	nc	glucocorticoid receptor		cca	ttt	increased
2883	RNRNAGR.PE1	nc	glucocorticoid receptor		aaa	gaa	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
2884	Hha1	8	gaa	236.3	237	236.33	236.27	0	3 900 000	3 100 000	0	=-	\		\(5)
2885	Taq1	49	aaa	236.74	238	0	236.74	0	0	8 100 000	0	+-	A		\(5)
2886	Taq1	49	aaa	237.485	238	237.47	237.5	0	7 400 000	3 300 000	0	-=	\		\(5)
2887	Taq1	49	aaa	238.583	238	238.58	238.57	238.6	29 100 000	21 100 000	3 300 000	=-	\ (-)		\(5)
2888	Taq1	49	aaa	202.12	203	202.05	202.19	0	6 300 000	3 300 000	0	--	\		\(2)
2889	Taq1	49	aaa	202.825	203	202.73	202.92	0	15 400 000	10 900 000	0	=-	\		\(2)
2890	Taq1	49	aaa	203.925	203	203.9	203.95	0	34 000 000	3 200 000	0	-=	\		\(2)
2891	Taq1	50	aat	351.69	353	351.69	0	0	6 800 000	0	0	-=	\		\(2)
2892	Taq1	50	aat	353.53	353	353.53	0	0	3 500 000	0	0	-=	\		\(2)
2893	Taq1	35	gga	136.97	137	0	0	136.97	0	0	4 800 000	=+	/	/	/(2)
2894	Taq1	40	tgg	136.89	137	0	0	136.89	0	0	22 600 000	=+	/	/	/(2)
2895	Hha1	60	ttg	169.72	170	169.86	169.48	169.82	14 300 000	4 500 000	11 300 000	-+	V		/(2)
2896	Hha1	60	ttg	170.36	170	0	170.36	0	0	10 900 000	0	+-	A		/(2)
2897	Taq1	47	ggc	156.325	157	0	156.37	156.28	0	2 450.66	2 105.83	+=	/		\(2)
2898	Taq1	21	acc	293.37	295	293.37	0	0	7 200 000	0	0	-=	\		\(2)
2899	Taq1	39	agg	293.64	295	293.64	0	0	4 700 000	0	0	-=	\		\(2)
2900	Taq1	39	agg	294.57	295	0	294.57	0	0	14 900 000	0	+-	A		\(2)
2901	Taq1	39	agg	296.655	295	296.82	0	296.49	8 000 000	0	10 700 000	-+(=)	V		\(2)
2902	Taq1	39	agg	293.64	295	293.64	0	0	174.53	0	0	-=	\		\(2)
2903	Taq1	39	agg	296.655	295	296.82	0	296.49	297.08	0	315.16	-+(=)	V		\(2)
2904	Taq1	39	agg	294.57	295	0	294.57	0	0	149.75	0	+-	A		\(2)
2905	Hha1	20	ctc	120.853	121	120.78	120.99	120.79	2 561.98	1 114.6	512.88	-=	\ (-)	\	\(4)
2906	Hha1	59	ttc	120.7	121	120.7	0	0	956.83	0	0	-=	\	\	\(4)
2907	Hha1	59	ttc	121.365	121	0	121.51	121.22	0	175.34	150.05	+=	/		\(4)
2908	Hha1	39	agg	159.2	160	159.37	159.03	0	271.26	310.46	0	=-	\	\	\(4)
2909	Hha1	39	agg	160.39	160	160.39	0	0	278.59	0	0	-=	\		\(4)
2910	Hha1	40	tgg	159.24	160	159.24	0	0	4 000 000	0	0	-=	\	\	\(4)
2911	Hha1	20	ctc	120.853	121	120.78	120.99	120.79	2 561.98	1 114.6	512.88	-=	\ (-)	\	\(4)
2912	Hha1	59	ttc	120.7	121	120.7	0	0	956.83	0	0	-=	\	\	\(4)
2913	Hha1	59	ttc	121.365	121	0	121.51	121.22	0	175.34	150.05	+=	/		\(4)
2914	Hha1	39	agg	159.2	160	159.37	159.03	0	271.26	310.46	0	=-	\	\	\(4)
2915	Hha1	39	agg	160.39	160	160.39	0	0	278.59	0	0	-=	\		\(4)
2916	Hha1	40	tgg	159.24	160	159.24	0	0	4 000 000	0	0	-=	\	\	\(4)
2917	Taq1	47	ggc	96.4	96	0	0	96.4	0	0	10 799.13	=+	/	/	
2918	Hha1	22	tcc	96.535	97	0	96.55	96.52	0	6 300 000	4 100 000	+=	/	/	
2919	Hha1	59	ttc	64.92	65	64.99	64.84	64.93	442.01	549.03	548.46	==	-		-1
2920	Taq1	26	ctg	104.45	104	104.41	104.48	104.46	5 500 000	3 100 000	28 700 000	=+	/ (-)	/	-1
2921	Taq1	35	gga	104.32	104	0	104.35	104.29	0	3 400 000	9 100 000	=+	/	/	-1
2922	Taq1	57	ctg	104.027	104	103.96	103.92	104.2	8 700 000	6 500 000	14 600 000	=+	/ (-)		-1
2923	Hha1	39	agg	134.885	135	134.82	0	134.95	454.54	0	227.86	-+(-)	V (\)		-1
2924	Hha1	39	agg	135.25	135	0	0	135.25	0	0	236	=+	/		-1
2925	Taq1	64	gtt	213.44	214	213.43	213.41	213.48	3 200 000	5 100 000	3 600 000	==	-		-1
2926	Taq1	64	gtt	214.513	214	214.51	214.5	214.53	4 100 000	3 200 000	3 100 000	==	-		-1

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
2884	RNRNAGR.PE1	nc	glucocorticoid receptor		aaa	gaa	increased
2885	RNRNAGR.PE1	nc	glucocorticoid receptor		aaa	gaa	increased
2886	RNRNAGR.PE1	nc	glucocorticoid receptor		aaa	gaa	increased
2887	RNRNAGR.PE1	nc	glucocorticoid receptor		aaa	gaa	increased
2888	RNO276893.GARG16	garg16	glucocorticoid-attenuated response gene 16		aaa	tca	increased
2889	RNO276893.GARG16	garg16	glucocorticoid-attenuated response gene 16		aaa	tca	increased
2890	RNO276893.GARG16	garg16	glucocorticoid-attenuated response gene 16		aaa	tca	increased
2891	RNO276893.GARG16	garg16	glucocorticoid-attenuated response gene 16		ggg	aat	increased
2892	RNO276893.GARG16	garg16	glucocorticoid-attenuated response gene 16		ggg	aat	increased
2893	AB050717.GIS5	gis5	glucocorticoid-inducible protein		tgg	gga	decreased
2894	AB050717.GIS5	gis5	glucocorticoid-inducible protein		tgg	gga	decreased
2895	AB050717.GIS5	gis5	glucocorticoid-inducible protein		cag	ttg	decreased
2896	AB050717.GIS5	gis5	glucocorticoid-inducible protein		cag	ttg	decreased
2897	AF217233.PE1	nc	glucokinase-associated dual specificity		gtg	ggc	increased
2898	AF217233.PE1	nc	glucokinase-associated dual specificity		agg	acc	increased
2899	AF217233.PE1	nc	glucokinase-associated dual specificity		agg	acc	increased
2900	AF217233.PE1	nc	glucokinase-associated dual specificity		agg	acc	increased
2901	AF217233.PE1	nc	glucokinase-associated dual specificity		agg	acc	increased
2902	AF217233.PE1	nc	glucokinase-associated dual specificity		agg	acc	increased
2903	AF217233.PE1	nc	glucokinase-associated dual specificity		agg	acc	increased
2904	AF217233.PE1	nc	glucokinase-associated dual specificity		agg	acc	increased
2905	RNO245935.GLUTX1	GLUTX1	glucose transporter		ttc	ctc	increased
2906	RNO245935.GLUTX1	GLUTX1	glucose transporter		ttc	ctc	increased
2907	RNO245935.GLUTX1	GLUTX1	glucose transporter		ttc	ctc	increased
2908	RNO245935.GLUTX1	GLUTX1	glucose transporter		tgg	agg	increased
2909	RNO245935.GLUTX1	GLUTX1	glucose transporter		tgg	agg	increased
2910	RNO245935.GLUTX1	GLUTX1	glucose transporter		tgg	agg	increased
2911	AB033418.GLUT8	glut8	glucose transporter 8		ttc	ctc	increased
2912	AB033418.GLUT8	glut8	glucose transporter 8		ttc	ctc	increased
2913	AB033418.GLUT8	glut8	glucose transporter 8		ttc	ctc	increased
2914	AB033418.GLUT8	glut8	glucose transporter 8		tgg	agg	increased
2915	AB033418.GLUT8	glut8	glucose transporter 8		tgg	agg	increased
2916	AB033418.GLUT8	glut8	glucose transporter 8		tgg	agg	increased
2917	AF099138.PE1	nc	GLUT4 vesicle protein		ggc	tcc	decreased
2918	AF099138.PE1	nc	GLUT4 vesicle protein		ggc	tcc	decreased
2919	AF112182.PE1	nc	glutamate receptor interacting protein 2		agt	ttc	No change
2920	AF112182.PE1	nc	glutamate receptor interacting protein 2		ctg	gga	decreased
2921	AF112182.PE1	nc	glutamate receptor interacting protein 2		ctg	gga	decreased
2922	AF112182.PE1	nc	glutamate receptor interacting protein 2		ctg	gga	No change
2923	AF112182.PE1	nc	glutamate receptor interacting protein 2		aca	agg	No change
2924	AF112182.PE1	nc	glutamate receptor interacting protein 2		aca	agg	No change
2925	AF112182.PE1	nc	glutamate receptor interacting protein 2		gtt	ggg	No change
2926	AF112182.PE1	nc	glutamate receptor interacting protein 2		gtt	ggg	No change

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
2927	Hha1	44	cgg	72.173	72	72.07	72.24	72.21	157 200 000	31 700 000	60 300 000	-=	\ (-)		-8
2928	Hha1	33	agc	72.64	73	0	0	72.64	0	0	33 300 000	=+	/		-8
2929	Hha1	44	cgg	77.89	78	77.89	0	0	3 200 000	0	0	-=	\		-8
2930	Hha1	44	cgg	83.6	84	83.72	83.48	0	10 900 000	6 800 000	0	=-	\		-8
2931	Hha1	44	cgg	84.433	84	84.62	84.37	84.31	10 200 000	9 000 000	3 600 000	=-	\ (-)		-8
2932	Hha1	33	agc	88.273	88	88.16	88.2	88.46	57 000 000	40 900 000	16 400 000	==	-		-8
2933	Hha1	54	ttt	89.477	89	89.38	89.49	89.56	3 700 000	12 700 000	20 300 000	==	-		-8
2934	Hha1	39	agg	94.89	95	94.87	0	94.91	219.94	0	248.2	-+(=)	V		-8
2935	Hha1	20	ctc	106.183	106	106.14	106.28	106.13	1 342.97	813	1 073.47	==	-		-8
2936	Hha1	27	acg	105.62	106	105.62	0	0	9 100 000	0	0	-=	\		-8
2937	Hha1	32	gtc	135.94	136	136.02	136	135.8	3 863.05	2 024.41	373.04	-=	\ (-)		-8
2938	Hha1	39	agg	139.44	140	139.4	139.48	0	219.94	829.9	0	+-	A		-8
2939	Hha1	62	tgt	140.06	140	140.06	0	0	3 000 000	0	0	-=	\		-8
2940	Hha1	20	ctc	183.553	184	183.54	183.61	183.51	21 887.051	13 493.31	14 145.99	==	-	-	-8
2941	Hha1	20	ctc	184.51	184	0	184.55	184.47	0	1 101.49	1 932.25	+=	/		-8
2942	Hha1	59	ttc	183.483	184	183.53	183.45	183.47	18 627.141	12 282.97	7 932.11	==	-	-	-8
2943	Taq1	55	tca	99.785	100	99.64	99.93	0	5 400 000	3 000 000	0	=-	\		\(6)
2944	Hha1	55	tca	99.853	100	99.85	99.84	99.87	9 600 000	7 000 000	3 200 000	==	-		\(6)
2945	Taq1	56	tga	100.495	100	100.4	100.59	0	5 100 000	9 000 000	0	=-	\		\(6)
2946	Taq1	56	tga	99.73	100	0	99.73	0	0	4 600 000	0	+-	A		\(6)
2947	Hha1	6	aga	128.355	129	128.33	128.38	0	16 000 000	6 100 000	0	-=	\		\(6)
2948	Hha1	6	aga	128.907	129	128.97	128.86	128.89	35 300 000	4 300 000	9 300 000	-=	\ (-)		\(6)
2949	Hha1	6	aga	129.19	129	0	129.19	0	0	5 000 000	0	+-	A		\(6)
2950	Taq1	63	ctt	128.935	129	128.91	0	128.96	3 500 000	0	3 500 000	-+(=)	V		\(6)
2951	Taq1	64	gtt	133.773	134	133.77	133.8	133.75	9 800 000	9 500 000	7 200 000	==	-		\(6)
2952	Taq1	64	gtt	134.737	134	134.76	134.71	134.74	13 300 000	19 000 000	4 900 000	=-	\ (-)		\(6)
2953	Hha1	20	ctc	188.13	189	188.13	0	0	309.91	0	0	-=	\		\(6)
2954	Hha1	20	ctc	189.2	189	189.2	0	0	337.46	0	0	-=	\		\(6)
2955	Taq1	49	aaa	202.825	204	202.73	202.92	0	15 400 000	10 900 000	0	=-	\		\(6)
2956	Taq1	49	aaa	203.925	204	203.9	203.95	0	34 000 000	3 200 000	0	-=	\		\(6)
2957	Taq1	49	aaa	204.37	204	0	204.37	0	0	3 300 000	0	+-	A		\(6)
2958	Taq1	49	aaa	204.94	204	204.94	0	0	51 100 000	0	0	-=	\		\(6)
2959	Taq1	36	ggt	132.707	133	132.69	132.69	132.74	26 200 000	38 000 000	7 200 000	=-	\ (-)		-(2) \(2)
2960	Taq1	52	att	133.64	134	0	133.47	133.81	0	3 800 000	8 800 000	=+	/		-(2) \(2)
2961	Taq1	52	att	134.09	134	134.09	0	0	7 000 000	0	0	-=	\		-(2) \(2)
2962	Taq1	52	att	134.777	134	134.78	134.62	134.93	9 200 000	5 800 000	11 500 000	=+	/ (-)		-(2) \(2)
2963	Taq1	62	tgt	99.61	100	0	0	99.61	0	0	22 600 000	=+	/		A(3)
2964	Taq1	39	agg	105.96	106	0	105.96	0	0	64 500 000	0	+-	A		A(3)
2965	Taq1	39	agg	105.96	106	0	105.96	0	0	648.24	0	+-	A		A(3)
2966	Taq1	55	tca	105.47	106	0	105.47	0	0	7 200 000	0	+-	A		A(3)
2967	Taq1	55	tca	106.22	106	0	106.24	106.2	0	8 300 000	9 500 000	+=	/		A(3)
2968	Taq1	50	aat	175.563	176	175.46	175.72	175.51	7 300 000	6 400 000	4 300 000	==	-		A(3)
2969	Taq1	50	aat	176.687	176	176.74	176.68	176.64	30 100 000	125 900 000	16 000 000	+-	A		A(3)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
2927	RNU08258.PE1	nc	glutamate receptor KA2 subunit		cgg	tcg	No change
2928	RNU08258.PE1	nc	glutamate receptor KA2 subunit		cct	agc	No change
2929	RNU08258.PE1	nc	glutamate receptor KA2 subunit		cac	cgg	No change
2930	RNU08258.PE1	nc	glutamate receptor KA2 subunit		ggt	cgg	No change
2931	RNU08258.PE1	nc	glutamate receptor KA2 subunit		ggt	cgg	No change
2932	RNU08258.PE1	nc	glutamate receptor KA2 subunit		ttt	agc	No change
2933	RNU08258.PE1	nc	glutamate receptor KA2 subunit		ttt	agc	No change
2934	RNU08258.PE1	nc	glutamate receptor KA2 subunit		agc	agg	No change
2935	RNU08258.PE1	nc	glutamate receptor KA2 subunit		ctc	acg	No change
2936	RNU08258.PE1	nc	glutamate receptor KA2 subunit		ctc	acg	No change
2937	RNU08258.PE1	nc	glutamate receptor KA2 subunit		gtc	ccg	No change
2938	RNU08258.PE1	nc	glutamate receptor KA2 subunit		tgt	agg	No change
2939	RNU08258.PE1	nc	glutamate receptor KA2 subunit		tgt	agg	No change
2940	RNU08258.PE1	nc	glutamate receptor KA2 subunit		ctc	ttc	No change
2941	RNU08258.PE1	nc	glutamate receptor KA2 subunit		ctc	ttc	No change
2942	RNU08258.PE1	nc	glutamate receptor KA2 subunit		ctc	ttc	No change
2943	RNGLUR6MR.PE1	nc	glutamate receptor subunit (GluR6) kainate		tca	tga	increased
2944	RNGLUR6MR.PE1	nc	glutamate receptor subunit (GluR6) kainate		tca	tga	increased
2945	RNGLUR6MR.PE1	nc	glutamate receptor subunit (GluR6) kainate		tca	tga	increased
2946	RNGLUR6MR.PE1	nc	glutamate receptor subunit (GluR6) kainate		tca	tga	increased
2947	RNGLUR6MR.PE1	nc	glutamate receptor subunit (GluR6) kainate		ctt	aga	increased
2948	RNGLUR6MR.PE1	nc	glutamate receptor subunit (GluR6) kainate		ctt	aga	increased
2949	RNGLUR6MR.PE1	nc	glutamate receptor subunit (GluR6) kainate		ctt	aga	increased
2950	RNGLUR6MR.PE1	nc	glutamate receptor subunit (GluR6) kainate		ctt	aga	increased
2951	RNGLUR6MR.PE1	nc	glutamate receptor subunit (GluR6) kainate		gtt	tat	increased
2952	RNGLUR6MR.PE1	nc	glutamate receptor subunit (GluR6) kainate		gtt	tat	increased
2953	RNGLUR6MR.PE1	nc	glutamate receptor subunit (GluR6) kainate		ctc	cag	increased
2954	RNGLUR6MR.PE1	nc	glutamate receptor subunit (GluR6) kainate		ctc	cag	increased
2955	RNGLUR6MR.PE1	nc	glutamate receptor subunit (GluR6) kainate		aaa	ttg	increased
2956	RNGLUR6MR.PE1	nc	glutamate receptor subunit (GluR6) kainate		aaa	ttg	increased
2957	RNGLUR6MR.PE1	nc	glutamate receptor subunit (GluR6) kainate		aaa	ttg	increased
2958	RNGLUR6MR.PE1	nc	glutamate receptor subunit (GluR6) kainate		aaa	ttg	increased
2959	RATGLUR4A.GLUR4	GLUR4	glutamate receptor subunit 4		att	ggt	No change
2960	RATGLUR4A.GLUR4	GLUR4	glutamate receptor subunit 4		att	ggt	No change
2961	RATGLUR4A.GLUR4	GLUR4	glutamate receptor subunit 4		att	ggt	No change
2962	RATGLUR4A.GLUR4	GLUR4	glutamate receptor subunit 4		att	ggt	No change
2963	RNGLUR1.PE1	nc	glutamate receptor, AMPA subtype, GluR1		agc	tgt	increased by mild
2964	RNGLUR1.PE1	nc	glutamate receptor, AMPA subtype, GluR1		agg	tca	increased by mild
2965	RNGLUR1.PE1	nc	glutamate receptor, AMPA subtype, GluR1		agg	tca	increased by mild
2966	RNGLUR1.PE1	nc	glutamate receptor, AMPA subtype, GluR1		agg	tca	increased by mild
2967	RNGLUR1.PE1	nc	glutamate receptor, AMPA subtype, GluR1		agg	tca	increased by mild
2968	RNGLUR1.PE1	nc	glutamate receptor, AMPA subtype, GluR1		aat	gga	increased by mild
2969	RNGLUR1.PE1	nc	glutamate receptor, AMPA subtype, GluR1		aat	gga	increased by mild

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
2970	Hha1	56	tga	137.877	138	137.73	137.8	138.1	143.01	792.6	706.77	+=	/ (-)		-1
2971	Hha1	56	tga	138.753	138	138.53	138.7	139.03	228.82	379.78	551.62	==	-		-1
2972	Hha1	60	ttg	201.167	201	201.18	201.11	201.21	6 200 000	4 700 000	14 100 000	=+	/ (-)		-1
2973	Taq1	19	cac	110.63	111	110.68	110.68	110.53	24 600 000	13 600 000	23 800 000	==	-		-(2) \(2)
2974	Taq1	19	cac	111.59	111	111.53	111.62	111.62	21 300 000	25 000 000	9 700 000	=-	\ (-)	\	-(2) \(2)
2975	Taq1	62	tgt	110.46	111	0	110.59	110.33	0	5 500 000	16 000 000	=+	/		-(2) \(2)
2976	Taq1	62	tgt	111.367	111	111.29	111.61	111.2	16 100 000	6 200 000	6 700 000	-=	\ (-)	\	-(2) \(2)
2977	Taq1	45	gcc	101.505	102	101.28	101.73	0	3 700 000	5 100 000	0	=-	\		/(2) A(2)
2978	Taq1	45	gcc	102.515	102	0	102.66	102.37	0	3 500 000	11 200 000	=+	/		/(2) A(2)
2979	Taq1	51	ata	104.305	104	0	104.13	104.48	0	28 900 000	3 900 000	+-	A		/(2) A(2)
2980	Hha1	59	ttc	210.83	212	0	210.83	0	0	209.84	0	+-	A		/(2) A(2)
2981	Hha1	59	ttc	212.235	212	0	212.38	212.09	0	103.48	807.18	=+	/		/(2) A(2)
2982	Hha1	59	ttc	212.83	212	0	0	212.83	0	0	87.96	=+	/		/(2) A(2)
2983	Taq1	40	tgg	123.5	124	0	0	123.5	0	0	18 400 000	=+	/	/	/(2)
2984	Taq1	40	tgg	124.435	124	0	124.28	124.59	0	5 600 000	39 000 000	=+	/	/	/(2)
2985	Taq1	62	tgt	123.497	124	123.62	123.49	123.38	3 000 000	4 200 000	29 100 000	=+	/ (-)	/	/(2)
2986	Taq1	62	tgt	124.54	124	124.59	124.62	124.41	5 100 000	7 400 000	69 100 000	=+	/ (-)	/	/(2)
2987	Taq1	40	tgg	123.5	124	0	0	123.5	0	0	18 400 000	=+	/	/	/(2)
2988	Taq1	40	tgg	124.435	124	0	124.28	124.59	0	5 600 000	39 000 000	=+	/	/	/(2)
2989	Taq1	62	tgt	123.497	124	123.62	123.49	123.38	3 000 000	4 200 000	29 100 000	=+	/ (-)	/	/(2)
2990	Taq1	62	tgt	124.54	124	124.59	124.62	124.41	5 100 000	7 400 000	69 100 000	=+	/ (-)	/	/(2)
2991	Taq1	40	tgg	123.5	124	0	0	123.5	0	0	18 400 000	=+	/	/	/(2)
2992	Taq1	40	tgg	124.435	124	0	124.28	124.59	0	5 600 000	39 000 000	=+	/	/	/(2)
2993	Taq1	62	tgt	123.497	124	123.62	123.49	123.38	3 000 000	4 200 000	29 100 000	=+	/ (-)	/	/(2)
2994	Taq1	62	tgt	124.54	124	124.59	124.62	124.41	5 100 000	7 400 000	69 100 000	=+	/ (-)	/	/(2)
2995	Taq1	40	tgg	123.5	124	0	0	123.5	0	0	18 400 000	=+	/	/	/(2)
2996	Taq1	40	tgg	124.435	124	0	124.28	124.59	0	5 600 000	39 000 000	=+	/	/	/(2)
2997	Taq1	62	tgt	123.497	124	123.62	123.49	123.38	3 000 000	4 200 000	29 100 000	=+	/ (-)	/	/(2)
2998	Taq1	62	tgt	124.54	124	124.59	124.62	124.41	5 100 000	7 400 000	69 100 000	=+	/ (-)	/	/(2)
2999	Hha1	40	tgg	138.57	139	138.32	0	138.82	6 700 000	0	9 200 000	-+(=)	V		\(3)
3000	Hha1	40	tgg	138.93	139	138.79	139.07	0	11 500 000	4 100 000	0	-=	\		\(3)
3001	Hha1	40	tgg	139.54	139	139.54	0	0	5 600 000	0	0	-=	\		\(3)
3002	Taq1	41	ccc	165.82	166	165.76	165.88	0	3 900 000	4 900 000	0	=-	\		\(3)
3003	Taq1	39	agg	166.23	167	166.23	0	0	11 800 000	0	0	-=	\		\(3)
3004	Taq1	39	agg	167.01	167	166.81	167.21	0	8 900 000	7 800 000	0	=-	\		\(3)
3005	Taq1	39	agg	167.16	167	167.16	0	0	8 200 000	0	0	-=	\		\(3)
3006	Taq1	39	agg	166.23	167	166.23	0	0	438.2	0	0	-=	\		\(3)
3007	Taq1	39	agg	166.81	167	166.81	0	0	330.51	0	0	-=	\		\(3)
3008	Taq1	39	agg	167.16	167	167.16	0	0	304.51	0	0	-=	\		\(3)
3009	Taq1	39	agg	167.815	167	0	167.69	167.94	0	12 700 000	4 700 000	+-	A		\(3)
3010	Taq1	39	agg	167.21	167	0	167.21	0	0	78.39	0	+-	A		\(3)
3011	Taq1	39	agg	167.69	167	0	167.69	0	0	127.63	0	+-	A		\(3)
3012	Hha1	6	aga	107.747	108	107.78	107.56	107.9	11 700 000	3 600 000	5 500 000	-=	\ (-)	\	\(5)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
2970	RNGLUAS.PE1	nc	glutamate/aspartate transporter		aag	tga	No change
2971	RNGLUAS.PE1	nc	glutamate/aspartate transporter		aag	tga	No change
2972	RNGLUAS.PE1	nc	glutamate/aspartate transporter		cgt	ttg	No change
2973	RNGPLIV.PE1	nc	glycogen phosphorylase liver type		cac	tgt	No change
2974	RNGPLIV.PE1	nc	glycogen phosphorylase liver type		cac	tgt	increased
2975	RNGPLIV.PE1	nc	glycogen phosphorylase liver type		cac	tgt	No change
2976	RNGPLIV.PE1	nc	glycogen phosphorylase liver type		cac	tgt	increased
2977	RNGP56.PE1	nc	glycoprotein 56		gcc	ata	decreased
2978	RNGP56.PE1	nc	glycoprotein 56		gcc	ata	decreased
2979	RNGP56.PE1	nc	glycoprotein 56		gcc	ata	decreased
2980	RNGP56.PE1	nc	glycoprotein 56		tgc	ttc	decreased
2981	RNGP56.PE1	nc	glycoprotein 56		tgc	ttc	decreased
2982	RNGP56.PE1	nc	glycoprotein 56		tgc	ttc	decreased
2983	RATCD44A.CD44	CD44	glycoprotein CD44		tgg	tgt	decreased
2984	RATCD44A.CD44	CD44	glycoprotein CD44		tgg	tgt	decreased
2985	RATCD44A.CD44	CD44	glycoprotein CD44		tgg	tgt	decreased
2986	RATCD44A.CD44	CD44	glycoprotein CD44		tgg	tgt	decreased
2987	RATMETAA.META-1	meta-1	glycoprotein CD44		tgg	tgt	decreased
2988	RATMETAA.META-1	meta-1	glycoprotein CD44		tgg	tgt	decreased
2989	RATMETAA.META-1	meta-1	glycoprotein CD44		tgg	tgt	decreased
2990	RATMETAA.META-1	meta-1	glycoprotein CD44		tgg	tgt	decreased
2991	AF065147.PE1	nc	glycoprotein CD44s	*	tgg	tgt	decreased
2992	AF065147.PE1	nc	glycoprotein CD44s	*	tgg	tgt	decreased
2993	AF065147.PE1	nc	glycoprotein CD44s	*	tgg	tgt	decreased
2994	AF065147.PE1	nc	glycoprotein CD44s	*	tgg	tgt	decreased
2995	RNU52179.PE1	nc	glycoprotein CD44s	*	tgg	tgt	decreased
2996	RNU52179.PE1	nc	glycoprotein CD44s	*	tgg	tgt	decreased
2997	RNU52179.PE1	nc	glycoprotein CD44s	*	tgg	tgt	decreased
2998	RNU52179.PE1	nc	glycoprotein CD44s	*	tgg	tgt	decreased
2999	D88035.GLCAT-P	GlcAT-P	glycoprotein specific UDP-glucuronyltransferase		tgg	atc	increased
3000	D88035.GLCAT-P	GlcAT-P	glycoprotein specific UDP-glucuronyltransferase		tgg	atc	increased
3001	D88035.GLCAT-P	GlcAT-P	glycoprotein specific UDP-glucuronyltransferase		tgg	atc	increased
3002	D88035.GLCAT-P	GlcAT-P	glycoprotein specific UDP-glucuronyltransferase		ccc	agg	increased
3003	D88035.GLCAT-P	GlcAT-P	glycoprotein specific UDP-glucuronyltransferase		ccc	agg	increased
3004	D88035.GLCAT-P	GlcAT-P	glycoprotein specific UDP-glucuronyltransferase		ccc	agg	increased
3005	D88035.GLCAT-P	GlcAT-P	glycoprotein specific UDP-glucuronyltransferase		ccc	agg	increased
3006	D88035.GLCAT-P	GlcAT-P	glycoprotein specific UDP-glucuronyltransferase		ccc	agg	increased
3007	D88035.GLCAT-P	GlcAT-P	glycoprotein specific UDP-glucuronyltransferase		ccc	agg	increased
3008	D88035.GLCAT-P	GlcAT-P	glycoprotein specific UDP-glucuronyltransferase		ccc	agg	increased
3009	D88035.GLCAT-P	GlcAT-P	glycoprotein specific UDP-glucuronyltransferase		ccc	agg	increased
3010	D88035.GLCAT-P	GlcAT-P	glycoprotein specific UDP-glucuronyltransferase		ccc	agg	increased
3011	D88035.GLCAT-P	GlcAT-P	glycoprotein specific UDP-glucuronyltransferase		ccc	agg	increased
3012	RATRTA.RTA	RTA	G-protein coupled receptor		aga	tgc	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
3013	Hha1	6	aga	108.21	108	108.21	0	0	11 300 000	0	0	-=	\		\(5)
3014	Taq1	34	tgc	107.52	108	107.5	107.54	0	22 600 000	25 800 000	0	=-	\	\	\(5)
3015	Hha1	60	ttg	249.35	248	249.57	249.13	0	3 300 000	4 200 000	0	=-	\		\(5)
3016	Hha1	40	tgg	248.77	250	0	248.77	0	0	3 300 000	0	+-	A		\(5)
3017	Hha1	40	tgg	251.41	250	251.47	251.35	0	3 900 000	4 200 000	0	=-	\		\(5)
3018	Hha1	26	ctg	253.207	253	253.18	253.29	253.15	15 000 000	4 200 000	9 600 000	-=	\ (-)		\(5)
3019	Hha1	3	aac	186.37	187	186.37	0	0	3 300 000	0	0	-=	\		\(2)
3020	Taq1	61	tct	186.203	187	186.16	186.24	186.21	5 600 000	4 300 000	4 400 000	==	-		\(2)
3021	Taq1	61	tct	187.22	187	187.22	0	0	5 000 000	0	0	-=	\		\(2)
3022	Taq1	18	cct	225.94	226	0	225.94	0	0	3 500 000	0	+-	A		\(2)
3023	Taq1	21	acc	265.485	267	265.48	265.49	0	29 800 000	9 200 000	0	-=	\		\(2)
3024	Taq1	50	aat	268.04	268	268.04	0	0	4 700 000	0	0	-=	\		\(2)
3025	Taq1	50	aat	269.6	268	269.6	0	0	3 000 000	0	0	-=	\		\(2)
3026	Hha1	44	cgg	92.57	93	92.78	92.57	92.36	8 400 000	3 100 000	6 900 000	-+	V		-3
3027	Hha1	44	cgg	93.393	93	93.28	93.46	93.44	6 100 000	4 000 000	6 300 000	==	-		-3
3028	Hha1	39	agg	137.01	137	136.94	137.14	136.95	1 620.23	382.11	866.69	-=	\ (-)		-3
3029	Hha1	40	tgg	156.92	157	156.76	156.92	157.08	5 700 000	6 000 000	3 800 000	==	-		-3
3030	Hha1	33	agc	104.61	105	104.48	0	104.74	4 300 000	0	5 800 000	-+(=)	V		/(3) -(2)
3031	Hha1	33	agc	105.15	105	0	105.11	105.19	0	6 300 000	12 500 000	++	/		/(3) -(2)
3032	Hha1	61	tct	104.49	105	0	0	104.49	0	0	4 700 000	=+	/		/(3) -(2)
3033	Hha1	61	tct	104.81	105	0	0	104.81	0	0	4 700 000	=+	/		/(3) -(2)
3034	Hha1	61	tct	105.54	105	105.52	105.6	105.5	3 700 000	8 400 000	12 900 000	==	-		/(3) -(2)
3035	Hha1	15	tac	137.45	138	137.45	0	0	3 800 000	0	0	-=	\		/(3) -(2)
3036	Hha1	15	tac	137.857	138	137.57	138	138	1 017.5	4 100 000	14 800 000	=+	/ (-)		/(3) -(2)
3037	Hha1	15	tac	138	138	0	138	138	0	1 055.88	3 218.79	=+	/		/(3) -(2)
3038	Hha1	33	agc	104.61	105	104.48	0	104.74	4 300 000	0	5 800 000	-+(=)	V		-1
3039	Hha1	33	agc	105.15	105	0	105.11	105.19	0	6 300 000	12 500 000	++	/		-1
3040	Hha1	61	tct	104.49	105	0	0	104.49	0	0	4 700 000	=+	/		-1
3041	Hha1	61	tct	104.81	105	0	0	104.81	0	0	4 700 000	=+	/		-1
3042	Hha1	61	tct	105.54	105	105.52	105.6	105.5	3 700 000	8 400 000	12 900 000	==	-		-1
3043	Hha1	15	tac	137.45	138	137.45	0	0	3 800 000	0	0	-=	\		-1
3044	Hha1	15	tac	137.857	138	137.57	138	138	1 017.5	4 100 000	14 800 000	=+	/ (-)		-1
3045	Hha1	15	tac	138	138	0	138	138	0	1 055.88	3 218.79	=+	/		-1
3046	Hha1	61	tct	167.4	168	167.31	167.4	167.49	3 300 000	17 900 000	11 000 000	+=	/ (-)		-1
3047	Hha1	61	tct	168.495	168	0	168.48	168.51	0	4 300 000	3 400 000	+=	/		-1
3048	Hha1	61	tct	168.63	168	0	0	168.63	0	0	4 100 000	=+	/		-1
3049	Hha1	61	tct	168.6	168	0	0	168.6	0	0	3 400 000	=+	/		-1
3050	Hha1	20	ctc	231.37	232	231.26	231.49	231.36	7 107.43	3 422.5	3 053.43	-=	\ (-)		-1
3051	Hha1	20	ctc	232.347	232	232.34	232.52	232.18	833.33	485.18	500.95	==	-		-1
3052	Taq1	45	gcc	249.73	251	249.73	0	0	4 300 000	0	0	-=	\		-1
3053	Taq1	45	gcc	250.13	251	250.13	0	0	4 000 000	0	0	-=	\		-1
3054	Taq1	45	gcc	251.93	251	251.75	252.11	0	158 600 000	3 100 000	0	-=	\		-1
3055	Taq1	45	gcc	252.22	251	252.22	0	0	5 200 000	0	0	-=	\		-1

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
3013	RATRTA.RTA	RTA	G-protein coupled receptor		aga	tgc	increased
3014	RATRTA.RTA	RTA	G-protein coupled receptor		aga	tgc	increased
3015	RATRTA.RTA	RTA	G-protein coupled receptor		tga	ttg	increased
3016	RATRTA.RTA	RTA	G-protein coupled receptor		cgc	tgg	increased
3017	RATRTA.RTA	RTA	G-protein coupled receptor		cgc	tgg	increased
3018	RATRTA.RTA	RTA	G-protein coupled receptor		ctg	cgg	increased
3019	RNP2Y4RG.P2Y4	P2Y4	G-protein coupled receptor		aac	tct	increased
3020	RNP2Y4RG.P2Y4	P2Y4	G-protein coupled receptor		aac	tct	increased
3021	RNP2Y4RG.P2Y4	P2Y4	G-protein coupled receptor		aac	tct	increased
3022	RNP2Y4RG.P2Y4	P2Y4	G-protein coupled receptor		cct	gtc	increased
3023	RNO132407.GDF-9B	gdf-9B	growth differentiation factor-9B		acc	aat	increased
3024	RNO132407.GDF-9B	gdf-9B	growth differentiation factor-9B		acc	aat	increased
3025	RNO132407.GDF-9B	gdf-9B	growth differentiation factor-9B		acc	aat	increased
3026	AF115249.PE1	nc	growth factor-regulated G protein-coupled		cgg	tcc	No change
3027	AF115249.PE1	nc	growth factor-regulated G protein-coupled		cgg	tcc	No change
3028	AF115249.PE1	nc	growth factor-regulated G protein-coupled		gtg	agg	No change
3029	AF115249.PE1	nc	growth factor-regulated G protein-coupled		tgg	aca	No change
3030	AB001982.PE1	GHS-R Ia	growth hormone secretagogue receptor type 1a		tct	agc	decreased
3031	AB001982.PE1	GHS-R Ia	growth hormone secretagogue receptor type 1a		tct	agc	decreased
3032	AB001982.PE1	GHS-R Ia	growth hormone secretagogue receptor type 1a		tct	agc	decreased
3033	AB001982.PE1	GHS-R Ia	growth hormone secretagogue receptor type 1a		tct	agc	decreased
3034	AB001982.PE1	GHS-R Ia	growth hormone secretagogue receptor type 1a		tct	agc	decreased
3035	AB001982.PE1	GHS-R Ia	growth hormone secretagogue receptor type 1a		tac	tgc	decreased
3036	AB001982.PE1	GHS-R Ia	growth hormone secretagogue receptor type 1a		tac	tgc	decreased
3037	AB001982.PE1	GHS-R Ia	growth hormone secretagogue receptor type 1a		tac	tgc	decreased
3038	RNU94321.PE1	nc	growth hormone secretagogue receptor type 1a		tct	agc	No change
3039	RNU94321.PE1	nc	growth hormone secretagogue receptor type 1a		tct	agc	No change
3040	RNU94321.PE1	nc	growth hormone secretagogue receptor type 1a		tct	agc	No change
3041	RNU94321.PE1	nc	growth hormone secretagogue receptor type 1a		tct	agc	No change
3042	RNU94321.PE1	nc	growth hormone secretagogue receptor type 1a		tct	agc	No change
3043	RNU94321.PE1	nc	growth hormone secretagogue receptor type 1a		tac	tgc	No change
3044	RNU94321.PE1	nc	growth hormone secretagogue receptor type 1a		tac	tgc	No change
3045	RNU94321.PE1	nc	growth hormone secretagogue receptor type 1a		tac	tgc	No change
3046	RNU94321.PE1	nc	growth hormone secretagogue receptor type 1a		tct	cca	No change
3047	RNU94321.PE1	nc	growth hormone secretagogue receptor type 1a		tct	cca	No change
3048	RNU94321.PE1	nc	growth hormone secretagogue receptor type 1a		tct	cca	No change
3049	RNU94321.PE1	nc	growth hormone secretagogue receptor type 1a		tct	cca	No change
3050	RNU94321.PE1	nc	growth hormone secretagogue receptor type 1a		ctc	tga	No change
3051	RNU94321.PE1	nc	growth hormone secretagogue receptor type 1a		ctc	tga	No change
3052	RNU94321.PE1	nc	growth hormone secretagogue receptor type 1a		gcc	ctt	No change
3053	RNU94321.PE1	nc	growth hormone secretagogue receptor type 1a		gcc	ctt	No change
3054	RNU94321.PE1	nc	growth hormone secretagogue receptor type 1a		gcc	ctt	No change
3055	RNU94321.PE1	nc	growth hormone secretagogue receptor type 1a		gcc	ctt	No change

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
3056	Hha1	20	ctc	101.455	102	101.45	0	101.46	523.41	0	381.67	-+(=)	V		/(2)
3057	Hha1	20	ctc	102.17	102	102.17	0	0	440.77	0	0	-=	\		/(2)
3058	Hha1	26	ctg	101.59	102	0	101.49	101.69	0	3 900 000	9 000 000	=+	/		/(2)
3059	Taq1	54	ttt	143.45	144	143.41	143.5	143.44	371.44	705.63	1 991.43	=+	/ (-)		/(2)
3060	Taq1	54	ttt	144.28	144	144.09	0	144.47	269.48	0	2 976.44	=+(+)	/		/(2)
3061	Hha1	39	agg	112.38	112	112.38	0	0	410.55	0	0	-=	\		\(3)
3062	Hha1	40	tgg	111.665	112	111.74	111.59	0	15 700 000	4 400 000	0	-=	\		\(3)
3063	Hha1	40	tgg	112.24	112	0	112.24	0	0	9 700 000	0	+-	A		\(3)
3064	Hha1	15	tac	133.3	133	133.3	133.42	133.18	28 600 000	12 100 000	6 900 000	-=	\ (-)		\(3)
3065	Hha1	15	tac	132.87	133	0	0	132.87	0	0	4 300 000	=+	/		\(3)
3066	Hha1	15	tac	132.87	133	0	0	132.87	0	0	935.18	=+	/		\(3)
3067	Hha1	15	tac	133.353	133	133.46	133.42	133.18	6 045.18	3 116.14	1 500.65	-=	\ (-)		\(3)
3068	Hha1	6	aga	212	213	0	0	212	0	0	3 300 000	=+	/		\(2)
3069	Hha1	6	aga	212.985	213	213.04	0	212.93	13 800 000	0	3 900 000	-=(-)	\		\(2)
3070	Hha1	6	aga	213.49	213	0	213.49	0	0	3 100 000	0	+-	A		\(2)
3071	Taq1	20	ctc	212.42	213	212.42	0	0	3 700 000	0	0	-=	\		\(2)
3072	Hha1	44	cgg	64.027	64	64.08	63.99	64.01	41 800 000	46 500 000	111 400 000	=+	/ (-)		/(5)
3073	Hha1	26	ctg	105.54	106	105.54	0	0	3 100 000	0	0	-=	\		/(5)
3074	Hha1	26	ctg	106.53	106	0	106.53	0	0	3 100 000	0	+-	A		/(5)
3075	Hha1	39	agg	106.243	106	106.2	106.36	106.17	1 217	12 305.21	14 347.33	+=	/ (-)		/(5)
3076	Hha1	33	agc	138.373	139	138.32	138.4	138.4	3 300 000	3 100 000	6 900 000	=+	/ (-)		/(5)
3077	Hha1	33	agc	139.36	139	139.43	139.46	139.19	10 300 000	7 000 000	32 600 000	=+	/ (-)		/(5)
3078	Hha1	4	aag	163.56	164	0	163.55	163.57	0	5 000 000	13 900 000	=+	/		/(5)
3079	Taq1	36	ggt	163.21	164	0	0	163.21	0	0	5 300 000	=+	/		/(5)
3080	Taq1	36	ggt	164.21	164	164.22	0	164.2	4 600 000	0	3 500 000	-+(=)	V		/(5)
3081	Taq1	45	gcc	381.33	381	381.08	381.58	0	3 800 000	3 700 000	0	=-	\		/(5)
3082	Taq1	26	ctg	186.63	187	0	0	186.63	0	0	4 800 000	=+	/	/	A(3) /(2)
3083	Taq1	26	ctg	187.66	187	0	187.66	0	0	3 000 000	0	+-	A	A	A(3) /(2)
3084	Taq1	57	ctg	186.41	187	0	0	186.41	0	0	6 500 000	=+	/	/	A(3) /(2)
3085	Taq1	57	ctg	187.215	187	0	187.02	187.41	0	3 300 000	5 400 000	+=	/		A(3) /(2)
3086	Taq1	57	ctg	187.45	187	0	187.45	0	0	4 800 000	0	+-	A	A	A(3) /(2)
3087	Hha1	40	tgg	225.115	226	225.12	225.11	0	4 000 000	3 800 000	0	=-	\		A(3) /(2)
3088	Hha1	40	tgg	225.76	226	0	225.76	0	0	6 500 000	0	+-	A		A(3) /(2)
3089	Hha1	39	agg	68.607	69	68.64	68.57	68.61	828.44	603.02	406.9	==	-		-(3) \(3)
3090	Hha1	39	agg	71.64	72	71.65	71.55	71.72	13 563.04	1 176.18	2 046.71	-=	\ (-)		-(3) \(3)
3091	Hha1	6	aga	124.12	124	124.12	0	0	4 500 000	0	0	-=	\		-(3) \(3)
3092	Taq1	35	gga	123.8	124	0	0	123.8	0	0	3 500 000	=+	/		-(3) \(3)
3093	Taq1	35	gga	124.71	124	0	0	124.71	0	0	3 600 000	=+	/		-(3) \(3)
3094	Hha1	61	tct	132.68	133	132.57	132.69	132.78	17 200 000	40 300 000	55 400 000	==	-		-(3) \(3)
3095	Hha1	61	tct	133.78	133	133.78	0	0	5 700 000	0	0	-=	\		-(3) \(3)
3096	Hha1	33	agc	75.685	76	75.6	75.77	0	9 100 000	5 800 000	0	=-	\		\(5) A(4)
3097	Hha1	59	ttc	159.255	160	159.3	159.21	0	161.2	166.72	0	=-	\		\(5) A(4)
3098	Hha1	59	ttc	160.1	160	0	160.1	0	0	120.73	0	+-	A		\(5) A(4)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
3056	RNU54807.RAB-3C	rab 3C	GTP-binding protein		ctc	ctg	decreased
3057	RNU54807.RAB-3C	rab 3C	GTP-binding protein		ctc	ctg	decreased
3058	RNU54807.RAB-3C	rab 3C	GTP-binding protein		ctc	ctg	decreased
3059	RNU54807.RAB-3C	rab 3C	GTP-binding protein		ttt	taa	decreased
3060	RNU54807.RAB-3C	rab 3C	GTP-binding protein		ttt	taa	decreased
3061	AF286534.RAB11B	Rab11b	GTP-binding protein RAB11B		tgg	agg	increased
3062	AF286534.RAB11B	Rab11b	GTP-binding protein RAB11B		tgg	agg	increased
3063	AF286534.RAB11B	Rab11b	GTP-binding protein RAB11B		tgg	agg	increased
3064	AF286534.RAB11B	Rab11b	GTP-binding protein RAB11B		tac	tcc	increased
3065	AF286534.RAB11B	Rab11b	GTP-binding protein RAB11B		tac	tcc	increased
3066	AF286534.RAB11B	Rab11b	GTP-binding protein RAB11B		tac	tcc	increased
3067	AF286534.RAB11B	Rab11b	GTP-binding protein RAB11B		tac	tcc	increased
3068	AF084464.REM2	Rem2	GTP-binding protein REM2		ctc	aga	increased
3069	AF084464.REM2	Rem2	GTP-binding protein REM2		ctc	aga	increased
3070	AF084464.REM2	Rem2	GTP-binding protein REM2		ctc	aga	increased
3071	AF084464.REM2	Rem2	GTP-binding protein REM2		ctc	aga	increased
3072	RATGNDSA.PE1	nc	guanine nucleotide dissociation stimulator		cga	cgg	decreased
3073	RATGNDSA.PE1	nc	guanine nucleotide dissociation stimulator		ctg	agg	decreased
3074	RATGNDSA.PE1	nc	guanine nucleotide dissociation stimulator		ctg	agg	decreased
3075	RATGNDSA.PE1	nc	guanine nucleotide dissociation stimulator		ctg	agg	decreased
3076	RATGNDSA.PE1	nc	guanine nucleotide dissociation stimulator		agc	ggc	decreased
3077	RATGNDSA.PE1	nc	guanine nucleotide dissociation stimulator		agc	ggc	decreased
3078	RATGNDSA.PE1	nc	guanine nucleotide dissociation stimulator		ggt	aag	decreased
3079	RATGNDSA.PE1	nc	guanine nucleotide dissociation stimulator		ggt	aag	decreased
3080	RATGNDSA.PE1	nc	guanine nucleotide dissociation stimulator		ggt	aag	decreased
3081	RATGNDSA.PE1	nc	guanine nucleotide dissociation stimulator		gcc	tcc	decreased
3082	AF107844.PE2	XLalphas	guanine nucleotide-binding protein		ctg	aca	decreased
3083	AF107844.PE2	XLalphas	guanine nucleotide-binding protein		ctg	aca	increased by mild
3084	AF107844.PE2	XLalphas	guanine nucleotide-binding protein		ctg	aca	decreased
3085	AF107844.PE2	XLalphas	guanine nucleotide-binding protein		ctg	aca	increased by mild
3086	AF107844.PE2	XLalphas	guanine nucleotide-binding protein		ctg	aca	increased by mild
3087	AF107844.PE2	XLalphas	guanine nucleotide-binding protein		tcc	tgg	increased by mild
3088	AF107844.PE2	XLalphas	guanine nucleotide-binding protein		tcc	tgg	increased by mild
3089	RNGZAL4.GZ-ALPHA	Gz-alpha	guanine nucleotide-binding protein	*	ggc	agg	No change
3090	RNGZAL4.GZ-ALPHA	Gz-alpha	guanine nucleotide-binding protein	*	ccg	agg	No change
3091	RNGZAL4.GZ-ALPHA	Gz-alpha	guanine nucleotide-binding protein	*	gga	aga	No change
3092	RNGZAL4.GZ-ALPHA	Gz-alpha	guanine nucleotide-binding protein	*	gga	aga	No change
3093	RNGZAL4.GZ-ALPHA	Gz-alpha	guanine nucleotide-binding protein	*	gga	aga	No change
3094	RNGZAL4.GZ-ALPHA	Gz-alpha	guanine nucleotide-binding protein	*	tct	tct	No change
3095	RNGZAL4.GZ-ALPHA	Gz-alpha	guanine nucleotide-binding protein	*	tct	tct	No change
3096	RATGCM.PE1	guanylate cyc	guanylate cyclase		tcc	agc	increased
3097	RATGCM.PE1	guanylate cyc	guanylate cyclase		aag	ttc	increased
3098	RATGCM.PE1	guanylate cyc	guanylate cyclase		aag	ttc	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
3099	Hha1	59	ttc	160.46	160	0	160.31	160.61	0	89.11	85.37	+=	/		\(5) A(4)
3100	Taq1	44	cgg	178.5	179	0	178.5	0	0	861.38	0	+-	A		\(5) A(4)
3101	Taq1	44	cgg	179.575	179	179.48	179.67	0	343.71	488.12	0	=-	\		\(5) A(4)
3102	Taq1	23	cga	178.95	180	178.89	178.95	179.01	5 000 000	3 500 000	4 100 000	==	-		\(5) A(4)
3103	Taq1	23	cga	179.985	180	179.98	179.99	0	9 000 000	6 800 000	0	=-	\		\(5) A(4)
3104	Taq1	23	cga	181.025	180	181.06	180.99	0	6 000 000	11 400 000	0	+-	A		\(5) A(4)
3105	Hha1	49	aaa	377.86	380	0	377.86	0	0	11 400 000	0	+-	A		\(5) A(4)
3106	Hha1	49	aaa	379.26	380	379.26	0	0	13 100 000	0	0	-=	\		\(5) A(4)
3107	Hha1	49	aaa	380	380	380	0	0	18 600 000	0	0	-=	\		\(5) A(4)
3108	Hha1	49	aaa	381.97	380	381.97	0	0	4 200 000	0	0	-=	\		\(5) A(4)
3109	Hha1	33	agc	181.073	182	180.99	181.14	181.09	3 200 000	3 000 000	13 000 000	=+	/ (-)	(-)	
3110	Hha1	40	tgg	181.293	182	181.31	181.28	181.29	10 800 000	10 500 000	15 300 000	==	-	(-)	
3111	Hha1	32	gtc	196	197	0	196	0	0	366.22	0	+-	A	A	
3112	Hha1	40	tgg	195.975	197	0	195.9	196.05	0	7 800 000	3 800 000	+-	A	A	
3113	Taq1	8	gaa	132.82	133	132.71	132.93	0	4 400 000	6 100 000	0	=-	\	\	
3114	Hha1	8	gaa	133.017	133	133.08	133.07	132.9	34 400 000	25 100 000	9 200 000	=-	\ (-)	\	
3115	Hha1	55	tca	94.43	94	0	0	94.43	0	0	3 300 000	=+	/	/	
3116	Taq1	55	tca	94.545	94	0	94.5	94.59	0	17 500 000	10 600 000	+=	/	/	
3117	Hha1	27	acg	75.7	76	75.85	0	75.55	3 000 000	0	3 400 000	-+(=)	V		/(2)
3118	Hha1	27	acg	76.385	76	0	76.43	76.34	0	3 300 000	7 300 000	++	/		/(2)
3119	Hha1	28	tcg	159.14	160	0	159.14	0	0	3 600 000	0	+-	A		/(2)
3120	Hha1	33	agc	159.603	160	159.63	159.66	159.52	4 200 000	6 000 000	31 200 000	=+	/ (-)		/(2)
3121	Hha1	33	agc	160.593	160	160.67	160.58	160.53	4 200 000	6 100 000	26 700 000	=+	/ (-)		/(2)
3122	Hha1	39	agg	69.617	70	69.51	69.49	69.85	3 218.47	501.52	240.07	-=	\ (-)		\(2)
3123	Hha1	44	cgg	143.815	144	143.9	143.73	0	3 600 000	4 400 000	0	=-	\		\(2)
3124	Hha1	44	cgg	144.455	144	144.66	144.25	0	4 900 000	3 900 000	0	=-	\		\(2)
3125	Hha1	44	cgg	144.01	144	0	144.01	0	0	3 800 000	0	+-	A		\(2)
3126	Hha1	44	cgg	144.72	144	0	144.72	0	0	4 100 000	0	+-	A		\(2)
3127	Hha1	8	gaa	192.223	193	192.17	192.27	192.23	6 900 000	8 500 000	3 300 000	=-	\ (-)		A(3)
3128	Taq1	8	gaa	192.62	193	0	192.62	0	0	8 500 000	0	+-	A		A(3)
3129	Taq1	8	gaa	193.35	193	0	0	193.35	0	0	4 100 000	=+	/		A(3)
3130	Hha1	8	gaa	193.115	193	193.11	193.12	0	4 600 000	11 300 000	0	+-	A		A(3)
3131	Hha1	8	gaa	193.97	193	193.91	194.03	0	5 400 000	3 500 000	0	=-	\		A(3)
3132	Taq1	56	tga	192.29	193	0	0	192.29	0	0	6 500 000	=+	/		A(3)
3133	Taq1	56	tga	194.08	193	0	194.08	0	0	3 500 000	0	+-	A		A(3)
3134	Hha1	39	agg	101.907	102	101.94	101.97	101.81	263.92	1 313.51	1 192.22	+=	/ (-)		\(10)
3135	Hha1	32	gtc	142.783	142	142.67	142.64	143.04	897.1	417.09	409.14	-=	\ (-)		\(10)
3136	Taq1	61	tct	141.99	142	0	142.14	141.84	0	8 900 000	26 800 000	=+	/		\(10)
3137	Hha1	27	acg	145.58	146	145.46	145.6	145.68	9 300 000	5 700 000	5 900 000	==	-		\(10)
3138	Hha1	27	acg	146.717	146	146.81	146.69	146.65	9 500 000	3 800 000	4 000 000	-=	\ (-)		\(10)
3139	Taq1	45	gcc	148.61	149	148.61	0	0	5 300 000	0	0	-=	\		\(10)
3140	Taq1	45	gcc	149.11	149	149.11	0	0	3 800 000	0	0	-=	\		\(10)
3141	Hha1	31	gac	157.27	158	157.27	0	0	6 600 000	0	0	-=	\		\(10)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
3099	RATGCM.PE1	guanylate cyc	guanylate cyclase		aag	ttc	increased
3100	RATGCM.PE1	guanylate cyc	guanylate cyclase		cgg	cga	increased
3101	RATGCM.PE1	guanylate cyc	guanylate cyclase		cgg	cga	increased
3102	RATGCM.PE1	guanylate cyc	guanylate cyclase		cgg	cga	increased
3103	RATGCM.PE1	guanylate cyc	guanylate cyclase		cgg	cga	increased
3104	RATGCM.PE1	guanylate cyc	guanylate cyclase		cgg	cga	increased
3105	RATGCM.PE1	guanylate cyc	guanylate cyclase		aaa	aca	increased
3106	RATGCM.PE1	guanylate cyc	guanylate cyclase		aaa	aca	increased
3107	RATGCM.PE1	guanylate cyc	guanylate cyclase		aaa	aca	increased
3108	RATGCM.PE1	guanylate cyc	guanylate cyclase		aaa	aca	increased
3109	RATGCE.GC-E	GC-E	guanylyl cyclase		tgg	agc	No change
3110	RATGCE.GC-E	GC-E	guanylyl cyclase		tgg	agc	No change
3111	RATGCE.GC-E	GC-E	guanylyl cyclase		tgg	gtc	increased by mild
3112	RATGCE.GC-E	GC-E	guanylyl cyclase		tgg	gtc	increased by mild
3113	RATGCF.GC-F	GC-F	guanylyl cyclase		ata	gaa	increased
3114	RATGCF.GC-F	GC-F	guanylyl cyclase		ata	gaa	increased
3115	RATATPASEZ.PE1	H+,K+-ATPas	H+,K+-ATPase	*	ctc	tca	decreased
3116	RATATPASEZ.PE1	H+,K+-ATPas	H+,K+-ATPase	*	ctc	tca	decreased
3117	RNH2AB.PE1	nc	H2B histone		tcg	acg	decreased
3118	RNH2AB.PE1	nc	H2B histone		tcg	acg	decreased
3119	RNH2AB.PE1	nc	H2B histone		agc	tcg	decreased
3120	RNH2AB.PE1	nc	H2B histone		agc	tcg	decreased
3121	RNH2AB.PE1	nc	H2B histone		agc	tcg	decreased
3122	RATH3HISTO.PE1	nc	H3 histone		gag	agg	increased
3123	RATH3HISTO.PE1	nc	H3 histone		aag	cgg	increased
3124	RATH3HISTO.PE1	nc	H3 histone		aag	cgg	increased
3125	RATH3HISTO.PE1	nc	H3 histone		aag	cgg	increased
3126	RATH3HISTO.PE1	nc	H3 histone		aag	cgg	increased
3127	AF389348.HDGF	Hdgf	HDGF		gaa	tga	increased by mild
3128	AF389348.HDGF	Hdgf	HDGF		gaa	tga	increased by mild
3129	AF389348.HDGF	Hdgf	HDGF		gaa	tga	increased by mild
3130	AF389348.HDGF	Hdgf	HDGF		gaa	tga	increased by mild
3131	AF389348.HDGF	Hdgf	HDGF		gaa	tga	increased by mild
3132	AF389348.HDGF	Hdgf	HDGF		gaa	tga	increased by mild
3133	AF389348.HDGF	Hdgf	HDGF		gaa	tga	increased by mild
3134	RATHSP70A.HSP70	HSP70	heat shock protein 70		ggt	agg	increased
3135	RATHSP70A.HSP70	HSP70	heat shock protein 70		aac	gtc	increased
3136	RATHSP70A.HSP70	HSP70	heat shock protein 70		cgc	tct	increased
3137	RATHSP70A.HSP70	HSP70	heat shock protein 70		acg	ccg	increased
3138	RATHSP70A.HSP70	HSP70	heat shock protein 70		acg	ccg	increased
3139	RATHSP70A.HSP70	HSP70	heat shock protein 70		gga	gcc	increased
3140	RATHSP70A.HSP70	HSP70	heat shock protein 70		gga	gcc	increased
3141	RATHSP70A.HSP70	HSP70	heat shock protein 70		gac	cac	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
3142	Hha1	7	caa	189.15	190	0	189.15	0	0	4 800 000	0	+-	A		\(10)
3143	Taq1	7	caa	189.34	190	189.42	189.26	0	4 700 000	4 000 000	0	=-	\		\(10)
3144	Hha1	7	caa	189.2	190	189.2	0	0	10 900 000	0	0	-=	\	\	\(10)
3145	Hha1	7	caa	190.17	190	190.28	190.06	0	4 100 000	6 000 000	0	=-	\	\	\(10)
3146	Taq1	61	tct	189.22	190	189.22	0	0	4 700 000	0	0	-=	\	\	\(10)
3147	Taq1	61	tct	190.11	190	190.21	189.87	190.25	7 700 000	3 100 000	3 700 000	-=	\ (-)	\	\(10)
3148	Taq1	61	tct	190.42	190	0	190.42	0	0	4 800 000	0	+-	A		\(10)
3149	Taq1	18	cct	213.65	214	213.73	213.57	0	3 400 000	4 100 000	0	=-	\		\(10)
3150	Taq1	18	cct	214.52	214	0	214.52	0	0	3 200 000	0	+-	A		\(10)
3151	Hha1	59	ttc	212.83	214	0	0	212.83	0	0	87.96	=+	/		\(10)
3152	Hha1	59	ttc	213.51	214	213.52	213.5	0	416.01	333.44	0	=-	\		\(10)
3153	Hha1	59	ttc	214.04	214	0	0	214.04	0	0	85.37	=+	/		\(10)
3154	Hha1	60	ttg	231.27	232	231.27	0	0	4 000 000	0	0	-=	\		\(10)
3155	Hha1	60	ttg	233.3	232	0	233.3	0	0	3 700 000	0	+-	A		\(10)
3156	Hha1	39	agg	101.907	102	101.94	101.97	101.81	263.92	1 313.51	1 192.22	+=	/ (-)		\(11)
3157	Hha1	26	ctg	112.757	113	112.71	112.77	112.79	32 400 000	14 800 000	8 000 000	-=	\ (-)		\(11)
3158	Hha1	32	gtc	142.783	142	142.67	142.64	143.04	897.1	417.09	409.14	-=	\ (-)		\(11)
3159	Taq1	61	tct	141.99	142	0	142.14	141.84	0	8 900 000	26 800 000	=+	/		\(11)
3160	Hha1	27	acg	145.58	146	145.46	145.6	145.68	9 300 000	5 700 000	5 900 000	==	-		\(11)
3161	Hha1	27	acg	146.717	146	146.81	146.69	146.65	9 500 000	3 800 000	4 000 000	-=	\ (-)		\(11)
3162	Taq1	45	gcc	148.61	149	148.61	0	0	5 300 000	0	0	-=	\		\(11)
3163	Taq1	45	gcc	149.11	149	149.11	0	0	3 800 000	0	0	-=	\		\(11)
3164	Hha1	31	gac	157.27	158	157.27	0	0	6 600 000	0	0	-=	\		\(11)
3165	Hha1	7	caa	189.15	190	0	189.15	0	0	4 800 000	0	+-	A		\(11)
3166	Taq1	7	caa	189.34	190	189.42	189.26	0	4 700 000	4 000 000	0	=-	\		\(11)
3167	Hha1	7	caa	189.2	190	189.2	0	0	10 900 000	0	0	-=	\	\	\(11)
3168	Hha1	7	caa	190.17	190	190.28	190.06	0	4 100 000	6 000 000	0	=-	\	\	\(11)
3169	Taq1	61	tct	189.22	190	189.22	0	0	4 700 000	0	0	-=	\	\	\(11)
3170	Taq1	61	tct	190.11	190	190.21	189.87	190.25	7 700 000	3 100 000	3 700 000	-=	\ (-)	\	\(11)
3171	Taq1	61	tct	190.42	190	0	190.42	0	0	4 800 000	0	+-	A		\(11)
3172	Taq1	18	cct	213.65	214	213.73	213.57	0	3 400 000	4 100 000	0	=-	\		\(11)
3173	Taq1	18	cct	214.52	214	0	214.52	0	0	3 200 000	0	+-	A		\(11)
3174	Hha1	59	ttc	212.83	214	0	0	212.83	0	0	87.96	=+	/		\(11)
3175	Hha1	59	ttc	213.51	214	213.52	213.5	0	416.01	333.44	0	=-	\		\(11)
3176	Hha1	59	ttc	214.04	214	0	0	214.04	0	0	85.37	=+	/		\(11)
3177	Hha1	60	ttg	231.27	232	231.27	0	0	4 000 000	0	0	-=	\		\(11)
3178	Hha1	60	ttg	233.3	232	0	233.3	0	0	3 700 000	0	+-	A		\(11)
3179	Hha1	39	agg	101.907	102	101.94	101.97	101.81	263.92	1 313.51	1 192.22	+=	/ (-)		\(10)
3180	Hha1	32	gtc	142.783	142	142.67	142.64	143.04	897.1	417.09	409.14	-=	\ (-)		\(10)
3181	Taq1	61	tct	141.99	142	0	142.14	141.84	0	8 900 000	26 800 000	=+	/		\(10)
3182	Hha1	27	acg	145.58	146	145.46	145.6	145.68	9 300 000	5 700 000	5 900 000	==	-		\(10)
3183	Hha1	27	acg	146.717	146	146.81	146.69	146.65	9 500 000	3 800 000	4 000 000	-=	\ (-)		\(10)
3184	Taq1	45	gcc	148.61	149	148.61	0	0	5 300 000	0	0	-=	\		\(10)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
3142	RATHSP70A.HSP70	HSP70	heat shock protein 70		caa	tct	increased
3143	RATHSP70A.HSP70	HSP70	heat shock protein 70		caa	tct	increased
3144	RATHSP70A.HSP70	HSP70	heat shock protein 70		caa	tct	increased
3145	RATHSP70A.HSP70	HSP70	heat shock protein 70		caa	tct	increased
3146	RATHSP70A.HSP70	HSP70	heat shock protein 70		caa	tct	increased
3147	RATHSP70A.HSP70	HSP70	heat shock protein 70		caa	tct	increased
3148	RATHSP70A.HSP70	HSP70	heat shock protein 70		caa	tct	increased
3149	RATHSP70A.HSP70	HSP70	heat shock protein 70		cct	aca	increased
3150	RATHSP70A.HSP70	HSP70	heat shock protein 70		cct	aca	increased
3151	RATHSP70A.HSP70	HSP70	heat shock protein 70		ttc	tcg	increased
3152	RATHSP70A.HSP70	HSP70	heat shock protein 70		ttc	tcg	increased
3153	RATHSP70A.HSP70	HSP70	heat shock protein 70		ttc	tcg	increased
3154	RATHSP70A.HSP70	HSP70	heat shock protein 70		aac	ttg	increased
3155	RATHSP70A.HSP70	HSP70	heat shock protein 70		aac	ttg	increased
3156	RNHSP70.HSP70.1	hsp70.1	heat shock protein 70		ggt	agg	increased
3157	RNHSP70.HSP70.1	hsp70.1	heat shock protein 70		gtg	ctg	increased
3158	RNHSP70.HSP70.1	hsp70.1	heat shock protein 70		aac	gtc	increased
3159	RNHSP70.HSP70.1	hsp70.1	heat shock protein 70		cgc	tct	increased
3160	RNHSP70.HSP70.1	hsp70.1	heat shock protein 70		acg	ccg	increased
3161	RNHSP70.HSP70.1	hsp70.1	heat shock protein 70		acg	ccg	increased
3162	RNHSP70.HSP70.1	hsp70.1	heat shock protein 70		gga	gcc	increased
3163	RNHSP70.HSP70.1	hsp70.1	heat shock protein 70		gga	gcc	increased
3164	RNHSP70.HSP70.1	hsp70.1	heat shock protein 70		gac	cac	increased
3165	RNHSP70.HSP70.1	hsp70.1	heat shock protein 70		caa	tct	increased
3166	RNHSP70.HSP70.1	hsp70.1	heat shock protein 70		caa	tct	increased
3167	RNHSP70.HSP70.1	hsp70.1	heat shock protein 70		caa	tct	increased
3168	RNHSP70.HSP70.1	hsp70.1	heat shock protein 70		caa	tct	increased
3169	RNHSP70.HSP70.1	hsp70.1	heat shock protein 70		caa	tct	increased
3170	RNHSP70.HSP70.1	hsp70.1	heat shock protein 70		caa	tct	increased
3171	RNHSP70.HSP70.1	hsp70.1	heat shock protein 70		caa	tct	increased
3172	RNHSP70.HSP70.1	hsp70.1	heat shock protein 70		cct	aca	increased
3173	RNHSP70.HSP70.1	hsp70.1	heat shock protein 70		cct	aca	increased
3174	RNHSP70.HSP70.1	hsp70.1	heat shock protein 70		ttc	tcg	increased
3175	RNHSP70.HSP70.1	hsp70.1	heat shock protein 70		ttc	tcg	increased
3176	RNHSP70.HSP70.1	hsp70.1	heat shock protein 70		ttc	tcg	increased
3177	RNHSP70.HSP70.1	hsp70.1	heat shock protein 70		aac	ttg	increased
3178	RNHSP70.HSP70.1	hsp70.1	heat shock protein 70		aac	ttg	increased
3179	RNHSP701.HSP70-1	Hsp70-1	heat shock protein 70		ggt	agg	increased
3180	RNHSP701.HSP70-1	Hsp70-1	heat shock protein 70		aac	gtc	increased
3181	RNHSP701.HSP70-1	Hsp70-1	heat shock protein 70		cgc	tct	increased
3182	RNHSP701.HSP70-1	Hsp70-1	heat shock protein 70		acg	ccg	increased
3183	RNHSP701.HSP70-1	Hsp70-1	heat shock protein 70		acg	ccg	increased
3184	RNHSP701.HSP70-1	Hsp70-1	heat shock protein 70		gga	gcc	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
3185	Taq1	45	gcc	149.11	149	149.11	0	0	3 800 000	0	0	-=	\		\(10)
3186	Hha1	31	gac	157.27	158	157.27	0	0	6 600 000	0	0	-=	\		\(10)
3187	Hha1	7	caa	189.15	190	0	189.15	0	0	4 800 000	0	+-	A		\(10)
3188	Taq1	7	caa	189.34	190	189.42	189.26	0	4 700 000	4 000 000	0	=-	\		\(10)
3189	Hha1	7	caa	189.2	190	189.2	0	0	10 900 000	0	0	-=	\	\	\(10)
3190	Hha1	7	caa	190.17	190	190.28	190.06	0	4 100 000	6 000 000	0	=-	\	\	\(10)
3191	Taq1	61	tct	189.22	190	189.22	0	0	4 700 000	0	0	-=	\	\	\(10)
3192	Taq1	61	tct	190.11	190	190.21	189.87	190.25	7 700 000	3 100 000	3 700 000	-=	\ (-)	\	\(10)
3193	Taq1	61	tct	190.42	190	0	190.42	0	0	4 800 000	0	+-	A		\(10)
3194	Taq1	18	cct	213.65	214	213.73	213.57	0	3 400 000	4 100 000	0	=-	\		\(10)
3195	Taq1	18	cct	214.52	214	0	214.52	0	0	3 200 000	0	+-	A		\(10)
3196	Hha1	59	ttc	212.83	214	0	0	212.83	0	0	87.96	=+	/		\(10)
3197	Hha1	59	ttc	213.51	214	213.52	213.5	0	416.01	333.44	0	=-	\		\(10)
3198	Hha1	59	ttc	214.04	214	0	0	214.04	0	0	85.37	=+	/		\(10)
3199	Hha1	60	ttg	231.27	232	231.27	0	0	4 000 000	0	0	-=	\		\(10)
3200	Hha1	60	ttg	233.3	232	0	233.3	0	0	3 700 000	0	+-	A		\(10)
3201	Hha1	39	agg	101.907	102	101.94	101.97	101.81	263.92	1 313.51	1 192.22	+=	/ (-)		\(10)
3202	Hha1	32	gtc	142.783	142	142.67	142.64	143.04	897.1	417.09	409.14	-=	\ (-)		\(10)
3203	Taq1	61	tct	141.99	142	0	142.14	141.84	0	8 900 000	26 800 000	=+	/		\(10)
3204	Hha1	27	acg	145.58	146	145.46	145.6	145.68	9 300 000	5 700 000	5 900 000	==	-		\(10)
3205	Hha1	27	acg	146.717	146	146.81	146.69	146.65	9 500 000	3 800 000	4 000 000	-=	\ (-)		\(10)
3206	Taq1	45	gcc	148.61	149	148.61	0	0	5 300 000	0	0	-=	\		\(10)
3207	Taq1	45	gcc	149.11	149	149.11	0	0	3 800 000	0	0	-=	\		\(10)
3208	Hha1	31	gac	157.27	158	157.27	0	0	6 600 000	0	0	-=	\		\(10)
3209	Hha1	7	caa	189.15	190	0	189.15	0	0	4 800 000	0	+-	A		\(10)
3210	Taq1	7	caa	189.34	190	189.42	189.26	0	4 700 000	4 000 000	0	=-	\		\(10)
3211	Hha1	7	caa	189.2	190	189.2	0	0	10 900 000	0	0	-=	\	\	\(10)
3212	Hha1	7	caa	190.17	190	190.28	190.06	0	4 100 000	6 000 000	0	=-	\	\	\(10)
3213	Taq1	61	tct	189.22	190	189.22	0	0	4 700 000	0	0	-=	\	\	\(10)
3214	Taq1	61	tct	190.11	190	190.21	189.87	190.25	7 700 000	3 100 000	3 700 000	-=	\ (-)	\	\(10)
3215	Taq1	61	tct	190.42	190	0	190.42	0	0	4 800 000	0	+-	A		\(10)
3216	Taq1	18	cct	213.65	214	213.73	213.57	0	3 400 000	4 100 000	0	=-	\		\(10)
3217	Taq1	18	cct	214.52	214	0	214.52	0	0	3 200 000	0	+-	A		\(10)
3218	Hha1	59	ttc	212.83	214	0	0	212.83	0	0	87.96	=+	/		\(10)
3219	Hha1	59	ttc	213.51	214	213.52	213.5	0	416.01	333.44	0	=-	\		\(10)
3220	Hha1	59	ttc	214.04	214	0	0	214.04	0	0	85.37	=+	/		\(10)
3221	Hha1	60	ttg	231.27	232	231.27	0	0	4 000 000	0	0	-=	\		\(10)
3222	Hha1	60	ttg	233.3	232	0	233.3	0	0	3 700 000	0	+-	A		\(10)
3223	Hha1	61	tct	141.085	141	0	141.02	141.15	0	14 700 000	7 200 000	+-	A		\(6)
3224	Hha1	32	gtc	142.783	142	142.67	142.64	143.04	897.1	417.09	409.14	-=	\ (-)		\(6)
3225	Taq1	61	tct	141.99	142	0	142.14	141.84	0	8 900 000	26 800 000	=+	/		\(6)
3226	Hha1	7	caa	189.15	190	0	189.15	0	0	4 800 000	0	+-	A		\(6)
3227	Taq1	7	caa	189.34	190	189.42	189.26	0	4 700 000	4 000 000	0	=-	\		\(6)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
3185	RNHSP701.HSP70-1	Hsp70-1	heat shock protein 70		gga	gcc	increased
3186	RNHSP701.HSP70-1	Hsp70-1	heat shock protein 70		gac	cac	increased
3187	RNHSP701.HSP70-1	Hsp70-1	heat shock protein 70		caa	tct	increased
3188	RNHSP701.HSP70-1	Hsp70-1	heat shock protein 70		caa	tct	increased
3189	RNHSP701.HSP70-1	Hsp70-1	heat shock protein 70		caa	tct	increased
3190	RNHSP701.HSP70-1	Hsp70-1	heat shock protein 70		caa	tct	increased
3191	RNHSP701.HSP70-1	Hsp70-1	heat shock protein 70		caa	tct	increased
3192	RNHSP701.HSP70-1	Hsp70-1	heat shock protein 70		caa	tct	increased
3193	RNHSP701.HSP70-1	Hsp70-1	heat shock protein 70		caa	tct	increased
3194	RNHSP701.HSP70-1	Hsp70-1	heat shock protein 70		cct	aca	increased
3195	RNHSP701.HSP70-1	Hsp70-1	heat shock protein 70		cct	aca	increased
3196	RNHSP701.HSP70-1	Hsp70-1	heat shock protein 70		ttc	tcg	increased
3197	RNHSP701.HSP70-1	Hsp70-1	heat shock protein 70		ttc	tcg	increased
3198	RNHSP701.HSP70-1	Hsp70-1	heat shock protein 70		ttc	tcg	increased
3199	RNHSP701.HSP70-1	Hsp70-1	heat shock protein 70		aac	ttg	increased
3200	RNHSP701.HSP70-1	Hsp70-1	heat shock protein 70		aac	ttg	increased
3201	RNHSP702.HSP70-2	Hsp70-2	heat shock protein 70		ggt	agg	increased
3202	RNHSP702.HSP70-2	Hsp70-2	heat shock protein 70		aac	gtc	increased
3203	RNHSP702.HSP70-2	Hsp70-2	heat shock protein 70		cgc	tct	increased
3204	RNHSP702.HSP70-2	Hsp70-2	heat shock protein 70		acg	ccg	increased
3205	RNHSP702.HSP70-2	Hsp70-2	heat shock protein 70		acg	ccg	increased
3206	RNHSP702.HSP70-2	Hsp70-2	heat shock protein 70		gga	gcc	increased
3207	RNHSP702.HSP70-2	Hsp70-2	heat shock protein 70		gga	gcc	increased
3208	RNHSP702.HSP70-2	Hsp70-2	heat shock protein 70		gac	cac	increased
3209	RNHSP702.HSP70-2	Hsp70-2	heat shock protein 70		caa	tct	increased
3210	RNHSP702.HSP70-2	Hsp70-2	heat shock protein 70		caa	tct	increased
3211	RNHSP702.HSP70-2	Hsp70-2	heat shock protein 70		caa	tct	increased
3212	RNHSP702.HSP70-2	Hsp70-2	heat shock protein 70		caa	tct	increased
3213	RNHSP702.HSP70-2	Hsp70-2	heat shock protein 70		caa	tct	increased
3214	RNHSP702.HSP70-2	Hsp70-2	heat shock protein 70		caa	tct	increased
3215	RNHSP702.HSP70-2	Hsp70-2	heat shock protein 70		caa	tct	increased
3216	RNHSP702.HSP70-2	Hsp70-2	heat shock protein 70		cct	aca	increased
3217	RNHSP702.HSP70-2	Hsp70-2	heat shock protein 70		cct	aca	increased
3218	RNHSP702.HSP70-2	Hsp70-2	heat shock protein 70		ttc	tcg	increased
3219	RNHSP702.HSP70-2	Hsp70-2	heat shock protein 70		ttc	tcg	increased
3220	RNHSP702.HSP70-2	Hsp70-2	heat shock protein 70		ttc	tcg	increased
3221	RNHSP702.HSP70-2	Hsp70-2	heat shock protein 70		aac	ttg	increased
3222	RNHSP702.HSP70-2	Hsp70-2	heat shock protein 70		aac	ttg	increased
3223	RNHSP703.HSP70-3	Hsp70-3	heat shock protein 70		atg	tct	increased
3224	RNHSP703.HSP70-3	Hsp70-3	heat shock protein 70		aac	gtc	increased
3225	RNHSP703.HSP70-3	Hsp70-3	heat shock protein 70		cgc	tct	increased
3226	RNHSP703.HSP70-3	Hsp70-3	heat shock protein 70		caa	tct	increased
3227	RNHSP703.HSP70-3	Hsp70-3	heat shock protein 70		caa	tct	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
3228	Hha1	7	caa	189.2	190	189.2	0	0	10 900 000	0	0	-=	\	\	\(6)
3229	Hha1	7	caa	190.17	190	190.28	190.06	0	4 100 000	6 000 000	0	=-	\	\	\(6)
3230	Taq1	61	tct	189.22	190	189.22	0	0	4 700 000	0	0	-=	\	\	\(6)
3231	Taq1	61	tct	190.11	190	190.21	189.87	190.25	7 700 000	3 100 000	3 700 000	-=	\ (-)	\	\(6)
3232	Taq1	61	tct	190.42	190	0	190.42	0	0	4 800 000	0	+-	A		\(6)
3233	Hha1	54	ttt	214.22	215	214.22	0	0	3 900 000	0	0	-=	\		\(6)
3234	Hha1	54	ttt	215.035	215	215.25	214.82	0	4 600 000	4 400 000	0	=-	\		\(6)
3235	Hha1	54	ttt	214.79	215	214.79	0	0	3 900 000	0	0	-=	\		\(6)
3236	Hha1	54	ttt	215.77	215	0	215.77	0	0	3 600 000	0	+-	A		\(6)
3237	Hha1	39	agg	243.143	244	243.16	243.32	242.95	945.74	1 397.09	1 110.83	==	-		\(6)
3238	Hha1	39	agg	244.015	244	244.13	0	243.9	263.92	0	122.07	-+(-)	V (\)		\(6)
3239	Hha1	39	agg	244.99	244	0	0	244.99	0	0	146.48	=+	/		\(6)
3240	Taq1	47	ggc	139.07	139	139.06	139.08	0	2 953.84	1 623.16	0	--	\		\(3)
3241	Taq1	40	tgg	139.98	140	0	0	139.98	0	0	3 300 000	=+	/		\(3)
3242	Taq1	40	tgg	140.815	140	140.64	0	140.99	18 700 000	0	9 300 000	-+(-)	V (\)		\(3)
3243	Taq1	45	gcc	352.43	351	0	352.43	0	0	4 100 000	0	+-	A		\(3)
3244	Taq1	17	cca	350.56	352	0	350.56	0	0	8 250.23	0	+-	A		\(3)
3245	Taq1	17	cca	351.535	352	0	351.6	351.47	0	651.5	631.48	+=	/		\(3)
3246	Taq1	17	cca	352	352	352	0	0	1 657.92	0	0	-=	\		\(3)
3247	Hha1	39	agg	75.715	76	0	75.56	75.87	0	9 827.45	1 440.42	+-	A		A(2)
3248	Hha1	20	ctc	105.28	105	0	105.28	0	0	603.19	0	+-	A		A(2)
3249	Hha1	59	ttc	226.85	228	226.85	0	0	265.21	0	0	-=	\		A(2)
3250	Hha1	59	ttc	228.15	228	228.15	0	0	166.4	0	0	-=	\		A(2)
3251	Hha1	59	ttc	228.933	228	229.24	228.79	228.77	447.21	129.35	155.22	-=	\ (-)		A(2)
3252	Hha1	12	agt	103.845	104	103.9	103.79	0	1 318.51	1 173.59	0	=-	\		\(3)
3253	Hha1	26	ctg	103.745	104	103.68	0	103.81	6 400 000	0	8 300 000	-+(=)	V		\(3)
3254	Hha1	26	ctg	104.535	104	104.54	104.53	0	10 900 000	3 300 000	0	-=	\		\(3)
3255	Hha1	44	cgg	137.27	138	0	0	137.27	0	0	3 400 000	=+	/		\(3)
3256	Hha1	44	cgg	138.157	138	138.25	137.92	138.3	10 700 000	4 400 000	7 900 000	-=	\ (-)		\(3)
3257	Hha1	33	agc	139.36	140	139.43	139.46	139.19	10 300 000	7 000 000	32 600 000	=+	/ (-)		\(3)
3258	Hha1	33	agc	140.27	140	140.37	0	140.17	5 900 000	0	34 400 000	=+(+)	/		\(3)
3259	Hha1	59	ttc	196.9	198	0	196.9	0	0	106.35	0	+-	A		\(3)
3260	Taq1	56	tga	72.6	73	72.48	72.72	0	3 800 000	47 300 000	0	+-	A		A(2)
3261	Taq1	10	atg	246.48	247	0	246.48	0	0	5 500 000	0	+-	A		A(2)
3262	Hha1	33	agc	152.495	153	152.42	152.57	0	4 000 000	3 100 000	0	=-	\		\(2)
3263	Hha1	33	agc	153.6	153	153.57	153.63	0	4 100 000	4 700 000	0	=-	\		\(2)
3264	Hha1	40	tgg	170.36	171	170.46	170.26	0	7 700 000	8 800 000	0	=-	\		\(2)
3265	Hha1	40	tgg	171	171	171	0	0	6 700 000	0	0	-=	\		\(2)
3266	Hha1	33	agc	152.495	153	152.42	152.57	0	4 000 000	3 100 000	0	=-	\		\(2)
3267	Hha1	33	agc	153.6	153	153.57	153.63	0	4 100 000	4 700 000	0	=-	\		\(2)
3268	Hha1	40	tgg	170.36	171	170.46	170.26	0	7 700 000	8 800 000	0	=-	\		\(2)
3269	Hha1	40	tgg	171	171	171	0	0	6 700 000	0	0	-=	\		\(2)
3270	Hha1	26	ctg	106.53	107	0	106.53	0	0	3 100 000	0	+-	A		A(2)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
3228	RNHSP703.HSP70-3	Hsp70-3	heat shock protein 70		caa	tct	increased
3229	RNHSP703.HSP70-3	Hsp70-3	heat shock protein 70		caa	tct	increased
3230	RNHSP703.HSP70-3	Hsp70-3	heat shock protein 70		caa	tct	increased
3231	RNHSP703.HSP70-3	Hsp70-3	heat shock protein 70		caa	tct	increased
3232	RNHSP703.HSP70-3	Hsp70-3	heat shock protein 70		caa	tct	increased
3233	RNHSP703.HSP70-3	Hsp70-3	heat shock protein 70		ttt	tcg	increased
3234	RNHSP703.HSP70-3	Hsp70-3	heat shock protein 70		ttt	tcg	increased
3235	RNHSP703.HSP70-3	Hsp70-3	heat shock protein 70		ttt	tcg	increased
3236	RNHSP703.HSP70-3	Hsp70-3	heat shock protein 70		ttt	tcg	increased
3237	RNHSP703.HSP70-3	Hsp70-3	heat shock protein 70		tgt	agg	increased
3238	RNHSP703.HSP70-3	Hsp70-3	heat shock protein 70		tgt	agg	increased
3239	RNHSP703.HSP70-3	Hsp70-3	heat shock protein 70		tgt	agg	increased
3240	AF184967.HEP	Hep	heparanase		tgg	ggc	increased
3241	AF184967.HEP	Hep	heparanase		tgg	ggc	increased
3242	AF184967.HEP	Hep	heparanase		tgg	ggc	increased
3243	AF184967.HEP	Hep	heparanase		gcc	cca	increased
3244	AF184967.HEP	Hep	heparanase		gcc	cca	increased
3245	AF184967.HEP	Hep	heparanase		gcc	cca	increased
3246	AF184967.HEP	Hep	heparanase		gcc	cca	increased
3247	AB017044.HNF-3G	HNF-3G	hepatocyte nuclear factor 3 gamma		agg	cat	increased by mild
3248	AB017044.HNF-3G	HNF-3G	hepatocyte nuclear factor 3 gamma		ctc	atc	increased by mild
3249	AB017044.HNF-3G	HNF-3G	hepatocyte nuclear factor 3 gamma		ttc	agt	increased by mild
3250	AB017044.HNF-3G	HNF-3G	hepatocyte nuclear factor 3 gamma		ttc	agt	increased by mild
3251	AB017044.HNF-3G	HNF-3G	hepatocyte nuclear factor 3 gamma		ttc	agt	increased by mild
3252	RNHNF3A.PE1	nc	hepatocyte nuclear factor 3A		agt	ctg	increased
3253	RNHNF3A.PE1	nc	hepatocyte nuclear factor 3A		agt	ctg	increased
3254	RNHNF3A.PE1	nc	hepatocyte nuclear factor 3A		agt	ctg	increased
3255	RNHNF3A.PE1	nc	hepatocyte nuclear factor 3A		cgg	aga	increased
3256	RNHNF3A.PE1	nc	hepatocyte nuclear factor 3A		cgg	aga	increased
3257	RNHNF3A.PE1	nc	hepatocyte nuclear factor 3A		agc	ggc	increased
3258	RNHNF3A.PE1	nc	hepatocyte nuclear factor 3A		agc	ggc	increased
3259	RNHNF3A.PE1	nc	hepatocyte nuclear factor 3A		ttc	cct	increased
3260	RATHNF4CL.PE1	nc	hepatocyte nuclear factor 4		tga	tct	increased by mild
3261	RATHNF4CL.PE1	nc	hepatocyte nuclear factor 4		atg	gga	increased by mild
3262	RNHNF6A.HNF-6	HNF-6	hepatocyte nuclear factor 6 alpha		agc	ggt	increased
3263	RNHNF6A.HNF-6	HNF-6	hepatocyte nuclear factor 6 alpha		agc	ggt	increased
3264	RNHNF6A.HNF-6	HNF-6	hepatocyte nuclear factor 6 alpha		aga	tgg	increased
3265	RNHNF6A.HNF-6	HNF-6	hepatocyte nuclear factor 6 alpha		aga	tgg	increased
3266	RNHNF6B.HNF-6	HNF-6	hepatocyte nuclear factor 6 beta		agc	ggt	increased
3267	RNHNF6B.HNF-6	HNF-6	hepatocyte nuclear factor 6 beta		agc	ggt	increased
3268	RNHNF6B.HNF-6	HNF-6	hepatocyte nuclear factor 6 beta		aga	tgg	increased
3269	RNHNF6B.HNF-6	HNF-6	hepatocyte nuclear factor 6 beta		aga	tgg	increased
3270	RATHES1A.PE1	nc	HES-1 factor		act	ctg	increased by mild

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
3271	Hha1	44	cgg	108.59	109	108.6	108.58	0	3 200 000	5 000 000	0	=-	\		A(2)
3272	Hha1	44	cgg	109.155	109	108.95	0	109.36	3 400 000	0	5 000 000	-+(=)	V		A(2)
3273	Hha1	44	cgg	180.213	181	179.96	180.37	180.31	3 700 000	4 100 000	4 700 000	==	-		A(2)
3274	Hha1	44	cgg	180.86	181	0	180.86	0	0	5 200 000	0	+-	A		A(2)
3275	Hha1	9	atc	146.22	147	146.19	0	146.25	4 400 000	0	3 300 000	-+(=)	V	V	
3276	Taq1	9	atc	146.285	147	146.25	0	146.32	4 900 000	0	6 400 000	-+(=)	V	V	
3277	Taq1	8	gaa	90.965	91	91.08	90.85	0	3 500 000	9 700 000	0	+-	A	A	A(7) \(6)
3278	Taq1	8	gaa	91.41	91	91.41	0	0	4 200 000	0	0	-=	\		A(7) \(6)
3279	Taq1	56	tga	90.95	91	0	90.95	0	0	3 100 000	0	+-	A	A	A(7) \(6)
3280	Hha1	61	tct	97.147	97	97.14	97.21	97.09	90 300 000	8 000 000	13 200 000	-=	\ (-)		A(7) \(6)
3281	Hha1	26	ctg	105.54	106	105.54	0	0	3 100 000	0	0	-=	\		A(7) \(6)
3282	Hha1	26	ctg	106.53	106	0	106.53	0	0	3 100 000	0	+-	A		A(7) \(6)
3283	Hha1	44	cgg	107.93	108	0	107.93	0	0	3 700 000	0	+-	A		A(7) \(6)
3284	Hha1	44	cgg	108.59	108	108.6	108.58	0	3 200 000	5 000 000	0	=-	\		A(7) \(6)
3285	Hha1	20	ctc	126.45	127	126.46	126.33	126.56	557.85	498.29	1 514.79	=+	/ (-)		A(7) \(6)
3286	Hha1	20	ctc	126.57	127	0	126.57	0	0	576.97	0	+-	A		A(7) \(6)
3287	Hha1	20	ctc	127.167	127	127.11	127.19	127.2	971.07	839.23	1 705.62	=+	/ (-)		A(7) \(6)
3288	Hha1	39	agg	126.81	127	126.74	0	126.88	322.58	0	272.62	-+(=)	V		A(7) \(6)
3289	Taq1	39	agg	195.24	196	195.24	0	0	5 700 000	0	0	-=	\		A(7) \(6)
3290	Taq1	39	agg	196.265	196	0	196.04	196.49	0	54 300 000	29 200 000	+-	A		A(7) \(6)
3291	Taq1	39	agg	195.24	196	195.24	0	0	211.67	0	0	-=	\		A(7) \(6)
3292	Taq1	39	agg	196.04	196	0	196.04	0	0	545.73	0	+-	A		A(7) \(6)
3293	Taq1	39	agg	196.49	196	0	0	196.49	0	0	860.08	=+	/		A(7) \(6)
3294	Taq1	8	gaa	225.26	226	0	225.26	0	0	4 200 000	0	+-	A		A(7) \(6)
3295	Hha1	8	gaa	226.11	226	0	0	226.11	0	0	3 300 000	=+	/		A(7) \(6)
3296	Hha1	8	gaa	227.09	226	227.25	0	226.93	5 300 000	0	3 000 000	-+(=)	V		A(7) \(6)
3297	Taq1	19	cac	224.725	226	224.64	0	224.81	3 100 000	0	3 700 000	-+(=)	V		A(7) \(6)
3298	Taq1	19	cac	225.77	226	225.69	225.85	0	3 500 000	3 000 000	0	=-	\		A(7) \(6)
3299	Taq1	19	cac	226.823	226	226.79	226.82	226.86	3 200 000	3 800 000	4 600 000	==	-		A(7) \(6)
3300	Taq1	8	gaa	90.965	91	91.08	90.85	0	3 500 000	9 700 000	0	+-	A	A	A(4)
3301	Taq1	8	gaa	91.41	91	91.41	0	0	4 200 000	0	0	-=	\		A(4)
3302	Taq1	56	tga	90.95	91	0	90.95	0	0	3 100 000	0	+-	A	A	A(4)
3303	Hha1	61	tct	97.147	97	97.14	97.21	97.09	90 300 000	8 000 000	13 200 000	-=	\ (-)		A(4)
3304	Hha1	44	cgg	107.93	108	0	107.93	0	0	3 700 000	0	+-	A		A(4)
3305	Hha1	44	cgg	108.59	108	108.6	108.58	0	3 200 000	5 000 000	0	=-	\		A(4)
3306	Hha1	20	ctc	126.45	127	126.46	126.33	126.56	557.85	498.29	1 514.79	=+	/ (-)		A(4)
3307	Hha1	20	ctc	126.57	127	0	126.57	0	0	576.97	0	+-	A		A(4)
3308	Hha1	20	ctc	127.167	127	127.11	127.19	127.2	971.07	839.23	1 705.62	=+	/ (-)		A(4)
3309	Hha1	39	agg	126.81	127	126.74	0	126.88	322.58	0	272.62	-+(=)	V		A(4)
3310	Hha1	33	agc	61.923	62	61.88	61.97	61.92	37 200 000	64 600 000	37 900 000	==	-		-6
3311	Hha1	20	ctc	88.21	88	0	0	88.21	0	0	620.22	=+	/		-6
3312	Hha1	39	agg	88.14	88	88.14	0	0	755.13	0	0	-=	\		-6
3313	Hha1	43	cgc	107.03	107	106.98	107.08	0	6 700 000	8 500 000	0	=-	\		-6

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
3271	RATHES1A.PE1	nc	HES-1 factor		cgg	acc	increased by mild
3272	RATHES1A.PE1	nc	HES-1 factor		cgg	acc	increased by mild
3273	RATHES1A.PE1	nc	HES-1 factor		cgg	ccg	increased by mild
3274	RATHES1A.PE1	nc	HES-1 factor		cgg	ccg	increased by mild
3275	RATHEXOKIN.PE1	nc	hexokinase		atc	aaa	decreased by mild
3276	RATHEXOKIN.PE1	nc	hexokinase		atc	aaa	decreased by mild
3277	RATHKII.HKII	HKII	hexokinase type II		gaa	tga	increased by mild
3278	RATHKII.HKII	HKII	hexokinase type II		gaa	tga	increased by mild
3279	RATHKII.HKII	HKII	hexokinase type II		gaa	tga	increased by mild
3280	RATHKII.HKII	HKII	hexokinase type II		aac	tct	increased by mild
3281	RATHKII.HKII	HKII	hexokinase type II		ctg	gtg	increased by mild
3282	RATHKII.HKII	HKII	hexokinase type II		ctg	gtg	increased by mild
3283	RATHKII.HKII	HKII	hexokinase type II		cac	cgg	increased by mild
3284	RATHKII.HKII	HKII	hexokinase type II		cac	cgg	increased by mild
3285	RATHKII.HKII	HKII	hexokinase type II		ctc	agg	increased by mild
3286	RATHKII.HKII	HKII	hexokinase type II		ctc	agg	increased by mild
3287	RATHKII.HKII	HKII	hexokinase type II		ctc	agg	increased by mild
3288	RATHKII.HKII	HKII	hexokinase type II		ctc	agg	increased by mild
3289	RATHKII.HKII	HKII	hexokinase type II		cat	agg	increased by mild
3290	RATHKII.HKII	HKII	hexokinase type II		cat	agg	increased by mild
3291	RATHKII.HKII	HKII	hexokinase type II		cat	agg	increased by mild
3292	RATHKII.HKII	HKII	hexokinase type II		cat	agg	increased by mild
3293	RATHKII.HKII	HKII	hexokinase type II		cat	agg	increased by mild
3294	RATHKII.HKII	HKII	hexokinase type II		gaa	cac	increased by mild
3295	RATHKII.HKII	HKII	hexokinase type II		gaa	cac	increased by mild
3296	RATHKII.HKII	HKII	hexokinase type II		gaa	cac	increased by mild
3297	RATHKII.HKII	HKII	hexokinase type II		gaa	cac	increased by mild
3298	RATHKII.HKII	HKII	hexokinase type II		gaa	cac	increased by mild
3299	RATHKII.HKII	HKII	hexokinase type II		gaa	cac	increased by mild
3300	RATHKIINAH.HKII	HKII	hexokinase type II		gaa	tga	increased by mild
3301	RATHKIINAH.HKII	HKII	hexokinase type II		gaa	tga	increased by mild
3302	RATHKIINAH.HKII	HKII	hexokinase type II		gaa	tga	increased by mild
3303	RATHKIINAH.HKII	HKII	hexokinase type II		aac	tct	increased by mild
3304	RATHKIINAH.HKII	HKII	hexokinase type II		cac	cgg	increased by mild
3305	RATHKIINAH.HKII	HKII	hexokinase type II		cac	cgg	increased by mild
3306	RATHKIINAH.HKII	HKII	hexokinase type II		ctc	agg	increased by mild
3307	RATHKIINAH.HKII	HKII	hexokinase type II		ctc	agg	increased by mild
3308	RATHKIINAH.HKII	HKII	hexokinase type II		ctc	agg	increased by mild
3309	RATHKIINAH.HKII	HKII	hexokinase type II		ctc	agg	increased by mild
3310	AF031879.NF-H	NF-H	high molecular-weight neurofilament		agc	ctg	No change
3311	AF031879.NF-H	NF-H	high molecular-weight neurofilament		tca	ctc	No change
3312	AF031879.NF-H	NF-H	high molecular-weight neurofilament		agg	cga	No change
3313	AF031879.NF-H	NF-H	high molecular-weight neurofilament		cgc	cgc	No change

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
3314	Hha1	43	cgc	107.583	107	107.51	107.56	107.68	10 100 000	13 700 000	4 700 000	=-	\ (-)		-6
3315	Hha1	61	tct	138.613	139	138.54	138.59	138.71	62 000 000	9 200 000	22 400 000	-=	\ (-)		-6
3316	Hha1	61	tct	139.377	139	139.61	139.14	139.38	8 000 000	6 200 000	3 900 000	==	-		-6
3317	Hha1	61	tct	139.377	140	139.61	139.14	139.38	8 000 000	6 200 000	3 900 000	==	-		-6
3318	Hha1	61	tct	140.07	140	0	140.07	0	0	3 400 000	0	+-	A		-6
3319	Hha1	33	agc	143.23	144	143.2	143.26	0	6 800 000	5 700 000	0	=-	\		-6
3320	Hha1	33	agc	144.21	144	144.2	0	144.22	4 000 000	0	3 500 000	-+(=)	V		-6
3321	Taq1	29	gca	155.027	155	155.01	155.06	155.01	5 900 000	6 700 000	8 100 000	==	-	-	-6
3322	Taq1	62	tgt	154.92	155	155.02	154.85	154.89	4 200 000	6 200 000	4 900 000	==	-	-	-6
3323	Taq1	62	tgt	155.84	155	0	155.84	0	0	5 700 000	0	+-	A		-6
3324	Taq1	39	agg	67.183	67	67.29	67.21	67.05	3 900 000	74 300 000	6 900 000	+-	A		/(3)
3325	Taq1	39	agg	67.183	67	67.29	67.21	67.05	144.83	746.74	203.24	+-	A		/(3)
3326	Taq1	47	ggc	96.08	96	0	96.19	95.97	0	11 680.45	10 367.17	+=	/		/(3)
3327	Taq1	47	ggc	96.4	96	0	0	96.4	0	0	10 799.13	=+	/		/(3)
3328	Taq1	62	tgt	96.507	97	96.37	96.38	96.77	6 900 000	9 300 000	15 900 000	==	-		/(3)
3329	Taq1	62	tgt	97.33	97	97.16	97.5	0	5 900 000	12 100 000	0	+-	A		/(3)
3330	Taq1	62	tgt	97.34	97	97.34	0	0	5 600 000	0	0	-=	\		/(3)
3331	Taq1	29	gca	198.11	199	0	0	198.11	0	0	3 200 000	=+	/		/(3)
3332	Taq1	29	gca	199.15	199	0	0	199.15	0	0	3 300 000	=+	/		/(3)
3333	Taq1	29	gca	200.16	199	0	0	200.16	0	0	3 400 000	=+	/		/(3)
3334	Taq1	26	ctg	294.97	296	0	0	294.97	0	0	4 000 000	=+	/		/(3)
3335	Hha1	61	tct	99.33	99	0	0	99.33	0	0	6 200 000	=+	/		/(2)
3336	Hha1	56	tga	121.79	122	0	0	121.79	0	0	930.87	=+	/		/(2)
3337	Hha1	61	tct	99.33	99	0	0	99.33	0	0	6 200 000	=+	/		/(2)
3338	Hha1	56	tga	121.79	122	0	0	121.79	0	0	930.87	=+	/		/(2)
3339	Hha1	61	tct	99.33	99	0	0	99.33	0	0	6 200 000	=+	/		/(2)
3340	Hha1	56	tga	121.79	122	0	0	121.79	0	0	930.87	=+	/		/(2)
3341	Hha1	39	agg	62.237	62	62.19	62.23	62.29	1 187.68	4 901.78	655.11	+-	A		A(3)
3342	Hha1	44	cgg	86.575	87	86.59	0	86.56	3 100 000	0	4 600 000	-+(=)	V		A(3)
3343	Hha1	31	gac	88.09	88	88.11	87.84	88.32	15 300 000	5 000 000	8 800 000	-=	\ (-)		A(3)
3344	Hha1	31	gac	88.52	88	0	88.52	0	0	6 700 000	0	+-	A		A(3)
3345	Hha1	60	ttg	135.66	136	0	135.66	0	0	11 100 000	0	+-	A		A(3)
3346	Hha1	39	agg	62.237	62	62.19	62.23	62.29	1 187.68	4 901.78	655.11	+-	A		A(3)
3347	Hha1	44	cgg	86.575	87	86.59	0	86.56	3 100 000	0	4 600 000	-+(=)	V		A(3)
3348	Hha1	31	gac	88.09	88	88.11	87.84	88.32	15 300 000	5 000 000	8 800 000	-=	\ (-)		A(3)
3349	Hha1	31	gac	88.52	88	0	88.52	0	0	6 700 000	0	+-	A		A(3)
3350	Hha1	60	ttg	135.66	136	0	135.66	0	0	11 100 000	0	+-	A		A(3)
3351	Hha1	55	tca	94.43	94	0	0	94.43	0	0	3 300 000	=+	/	/	
3352	Taq1	55	tca	94.545	94	0	94.5	94.59	0	17 500 000	10 600 000	+=	/	/	
3353	Hha1	55	tca	94.43	94	0	0	94.43	0	0	3 300 000	=+	/	/	
3354	Taq1	55	tca	94.545	94	0	94.5	94.59	0	17 500 000	10 600 000	+=	/	/	
3355	Hha1	20	ctc	78.76	79	78.76	0	0	557.85	0	0	-=	\		\(2)
3356	Hha1	20	ctc	148.52	149	148.52	0	0	268.59	0	0	-=	\		\(2)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
3314	AF031879.NF-H	NF-H	high molecular-weight neurofilament		cgc	cgc	No change
3315	AF031879.NF-H	NF-H	high molecular-weight neurofilament		tct	tgc	No change
3316	AF031879.NF-H	NF-H	high molecular-weight neurofilament		tct	tgc	No change
3317	AF031879.NF-H	NF-H	high molecular-weight neurofilament		tct	ggc	No change
3318	AF031879.NF-H	NF-H	high molecular-weight neurofilament		tct	ggc	No change
3319	AF031879.NF-H	NF-H	high molecular-weight neurofilament		agc	ata	No change
3320	AF031879.NF-H	NF-H	high molecular-weight neurofilament		agc	ata	No change
3321	AF031879.NF-H	NF-H	high molecular-weight neurofilament		gca	tgt	No change
3322	AF031879.NF-H	NF-H	high molecular-weight neurofilament		gca	tgt	No change
3323	AF031879.NF-H	NF-H	high molecular-weight neurofilament		gca	tgt	No change
3324	RATHALHID.PE1	nc	histidase		ggt	agg	decreased
3325	RATHALHID.PE1	nc	histidase		ggt	agg	decreased
3326	RATHALHID.PE1	nc	histidase		ggc	tgt	decreased
3327	RATHALHID.PE1	nc	histidase		ggc	tgt	decreased
3328	RATHALHID.PE1	nc	histidase		ggc	tgt	decreased
3329	RATHALHID.PE1	nc	histidase		ggc	tgt	decreased
3330	RATHALHID.PE1	nc	histidase		ggc	tgt	decreased
3331	RATHALHID.PE1	nc	histidase		gca	tgt	decreased
3332	RATHALHID.PE1	nc	histidase		gca	tgt	decreased
3333	RATHALHID.PE1	nc	histidase		gca	tgt	decreased
3334	RATHALHID.PE1	nc	histidase		tac	ctg	decreased
3335	AB081649.PE1	ratABO2.66	histo-blood group ABO transferase		tct	tca	decreased
3336	AB081649.PE1	ratABO2.66	histo-blood group ABO transferase		ttt	tga	decreased
3337	AB081652.PE1	ratABO3.47	histo-blood group ABO transferase	*	tct	tca	decreased
3338	AB081652.PE1	ratABO3.47	histo-blood group ABO transferase	*	ttt	tga	decreased
3339	AB081650.PE1	ratABO2.61	histo-blood group ABO transferase like enzyme	*	tct	tca	decreased
3340	AB081650.PE1	ratABO2.61	histo-blood group ABO transferase like enzyme	*	ttt	tga	decreased
3341	RATH1TH4T.H4T	H4t	histone H4	*	taa	agg	increased by mild
3342	RATH1TH4T.H4T	H4t	histone H4	*	gac	cgg	increased by mild
3343	RATH1TH4T.H4T	H4t	histone H4	*	gac	cgg	increased by mild
3344	RATH1TH4T.H4T	H4t	histone H4	*	gac	cgg	increased by mild
3345	RATH1TH4T.H4T	H4t	histone H4	*	atc	ttg	increased by mild
3346	RATHIS4G.PE1	nc	histone H4	*	taa	agg	increased by mild
3347	RATHIS4G.PE1	nc	histone H4	*	gac	cgg	increased by mild
3348	RATHIS4G.PE1	nc	histone H4	*	gac	cgg	increased by mild
3349	RATHIS4G.PE1	nc	histone H4	*	gac	cgg	increased by mild
3350	RATHIS4G.PE1	nc	histone H4	*	atc	ttg	increased by mild
3351	RNU94912.PE1	HKalpha2a	H-K-ATPase alpha 2a subunit	*	ctc	tca	decreased
3352	RNU94912.PE1	HKalpha2a	H-K-ATPase alpha 2a subunit	*	ctc	tca	decreased
3353	RNU94913.PE1	HKalpha2b	H-K-ATPase alpha 2b subunit		ctc	tca	decreased
3354	RNU94913.PE1	HKalpha2b	H-K-ATPase alpha 2b subunit		ctc	tca	decreased
3355	AY157669.PE1	nc	HMG box transcription factor SRY1	*	ccc	ctc	increased
3356	AY157669.PE1	nc	HMG box transcription factor SRY1	*	aag	ctc	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
3357	Hha1	20	ctc	78.76	79	78.76	0	0	557.85	0	0	-=	\		\(2)
3358	Hha1	20	ctc	148.52	149	148.52	0	0	268.59	0	0	-=	\		\(2)
3359	Hha1	20	ctc	78.76	79	78.76	0	0	557.85	0	0	-=	\		\(2)
3360	Hha1	20	ctc	148.52	149	148.52	0	0	268.59	0	0	-=	\		\(2)
3361	Hha1	20	ctc	78.76	79	78.76	0	0	557.85	0	0	-=	\		\(2)
3362	Hha1	20	ctc	148.52	149	148.52	0	0	268.59	0	0	-=	\		\(2)
3363	Hha1	20	ctc	78.76	79	78.76	0	0	557.85	0	0	-=	\		\(2)
3364	Hha1	20	ctc	148.52	149	148.52	0	0	268.59	0	0	-=	\		\(2)
3365	Hha1	39	agg	75.715	76	0	75.56	75.87	0	9 827.45	1 440.42	+-	A		A(2)
3366	Hha1	20	ctc	105.28	105	0	105.28	0	0	603.19	0	+-	A		A(2)
3367	Hha1	59	ttc	226.85	228	226.85	0	0	265.21	0	0	-=	\		A(2)
3368	Hha1	59	ttc	228.15	228	228.15	0	0	166.4	0	0	-=	\		A(2)
3369	Hha1	59	ttc	228.933	228	229.24	228.79	228.77	447.21	129.35	155.22	-=	\ (-)		A(2)
3370	Hha1	33	agc	78.69	79	78.69	0	0	4 200 000	0	0	-=	\		\(6)
3371	Hha1	44	cgg	90.59	91	90.65	0	90.53	4 400 000	0	3 200 000	-+(=)	V		\(6)
3372	Hha1	44	cgg	91.42	91	91.44	91.63	91.19	4 500 000	7 200 000	3 300 000	=-	\ (-)		\(6)
3373	Hha1	31	gac	135.227	136	135.24	135.15	135.29	14 800 000	7 100 000	50 500 000	=+	/ (-)		\(6)
3374	Hha1	31	gac	135.94	136	135.93	135.95	0	16 300 000	11 000 000	0	=-	\		\(6)
3375	Hha1	60	ttg	135.66	136	0	135.66	0	0	11 100 000	0	+-	A		\(6)
3376	Hha1	44	cgg	153.04	153	152.99	153.15	152.98	15 500 000	6 400 000	8 600 000	-=	\ (-)		\(6)
3377	Hha1	27	acg	153.45	154	153.42	0	153.48	9 500 000	0	3 900 000	-=(-)	\		\(6)
3378	Hha1	27	acg	154.093	154	154.06	154.12	154.1	10 100 000	4 800 000	4 000 000	-=	\ (-)		\(6)
3379	Hha1	28	tcg	175.71	176	175.71	0	0	3 500 000	0	0	-=	\		\(6)
3380	Hha1	28	tcg	176.53	176	176.53	0	0	3 300 000	0	0	-=	\		\(6)
3381	Hha1	33	agc	198.51	199	0	0	198.51	0	0	6 500 000	=+	/		\(6)
3382	Hha1	33	agc	199.49	199	0	0	199.49	0	0	7 700 000	=+	/		\(6)
3383	Hha1	25	cag	299.23	300	0	0	299.23	0	0	4 500 000	=+	/		\(6)
3384	Hha1	40	tgg	97.03	97	97.14	96.93	97.02	4 100 000	11 500 000	5 300 000	+-	A		\(3)
3385	Taq1	19	cac	132.643	133	132.68	132.64	132.61	14 500 000	10 900 000	13 400 000	==	-		\(3)
3386	Taq1	19	cac	133.633	133	133.6	133.63	133.67	35 400 000	22 500 000	5 400 000	=-	\ (-)		\(3)
3387	Taq1	63	ctt	132.86	133	132.86	132.86	0	3 000 000	3 500 000	0	=-	\		\(3)
3388	Taq1	36	ggt	192.065	193	192.07	192.06	0	3 300 000	3 200 000	0	=-	\		\(3)
3389	Hha1	33	agc	62.84	63	62.76	62.92	62.84	4 400 000	18 500 000	17 900 000	+=	/ (-)		-1
3390	Hha1	27	acg	75.7	76	75.85	0	75.55	3 000 000	0	3 400 000	-+(=)	V		-1
3391	Hha1	27	acg	76.385	76	0	76.43	76.34	0	3 300 000	7 300 000	++	/		-1
3392	Hha1	33	agc	92.217	92	92.23	92.2	92.22	8 900 000	7 200 000	8 500 000	==	-		-1
3393	Hha1	39	agg	95.91	96	96.16	95.91	95.66	271.26	334.34	390.62	==	-		-1
3394	Hha1	39	agg	96.44	96	0	0	96.44	0	0	146.48	=+	/		-1
3395	Hha1	62	tgt	96.245	96	96.23	0	96.26	3 200 000	0	3 100 000	-+(=)	V		-1
3396	Taq1	20	ctc	110.395	111	0	110.29	110.5	0	5 100 000	3 500 000	+=	/		-1
3397	Taq1	20	ctc	111.32	111	0	111.32	0	0	8 000 000	0	+-	A		-1
3398	Hha1	28	tcg	132.237	133	132.18	132.27	132.26	34 600 000	20 500 000	8 000 000	==	-		-1
3399	Hha1	28	tcg	132.905	133	0	132.92	132.89	0	36 400 000	14 300 000	+-	A		-1

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
3357	AY157672.PE1	nc	HMG box transcription factor SRY3		ccc	ctc	increased
3358	AY157672.PE1	nc	HMG box transcription factor SRY3		aag	ctc	increased
3359	AY157996.PE1	nc	HMG box transcription factor Sry3B		ccc	ctc	increased
3360	AY157996.PE1	nc	HMG box transcription factor Sry3B		aag	ctc	increased
3361	AY157997.PE1	nc	HMG box transcription factor Sry3B-I		ccc	ctc	increased
3362	AY157997.PE1	nc	HMG box transcription factor Sry3B-I		aag	ctc	increased
3363	AY157671.PE1	nc	HMG box transcription factor SRY3C	*	ccc	ctc	increased
3364	AY157671.PE1	nc	HMG box transcription factor SRY3C	*	aag	ctc	increased
3365	RATHNF3G.PE1	nc	HNF-3 gamma		agg	cat	increased by mild
3366	RATHNF3G.PE1	nc	HNF-3 gamma		ctc	atc	increased by mild
3367	RATHNF3G.PE1	nc	HNF-3 gamma		ttc	agt	increased by mild
3368	RATHNF3G.PE1	nc	HNF-3 gamma		ttc	agt	increased by mild
3369	RATHNF3G.PE1	nc	HNF-3 gamma		ttc	agt	increased by mild
3370	RATHFH1.HFH-1	HFH-1	HNF-3/forkhead homolog-1		cac	agc	increased
3371	RATHFH1.HFH-1	HFH-1	HNF-3/forkhead homolog-1		ccc	cgg	increased
3372	RATHFH1.HFH-1	HFH-1	HNF-3/forkhead homolog-1		ccc	cgg	increased
3373	RATHFH1.HFH-1	HFH-1	HNF-3/forkhead homolog-1		gac	ttg	increased
3374	RATHFH1.HFH-1	HFH-1	HNF-3/forkhead homolog-1		gac	ttg	increased
3375	RATHFH1.HFH-1	HFH-1	HNF-3/forkhead homolog-1		gac	ttg	increased
3376	RATHFH1.HFH-1	HFH-1	HNF-3/forkhead homolog-1		cgg	acg	increased
3377	RATHFH1.HFH-1	HFH-1	HNF-3/forkhead homolog-1		cgg	acg	increased
3378	RATHFH1.HFH-1	HFH-1	HNF-3/forkhead homolog-1		cgg	acg	increased
3379	RATHFH1.HFH-1	HFH-1	HNF-3/forkhead homolog-1		tcg	tcc	increased
3380	RATHFH1.HFH-1	HFH-1	HNF-3/forkhead homolog-1		tcg	tcc	increased
3381	RATHFH1.HFH-1	HFH-1	HNF-3/forkhead homolog-1		agc	cag	increased
3382	RATHFH1.HFH-1	HFH-1	HNF-3/forkhead homolog-1		agc	cag	increased
3383	RATHFH1.HFH-1	HFH-1	HNF-3/forkhead homolog-1		cag	aat	increased
3384	RATHOX111A.PE1	Hox 1.11	homeobox protein		tgg	ggg	increased
3385	RATHOX111A.PE1	Hox 1.11	homeobox protein		cac	ctt	increased
3386	RATHOX111A.PE1	Hox 1.11	homeobox protein		cac	ctt	increased
3387	RATHOX111A.PE1	Hox 1.11	homeobox protein		cac	ctt	increased
3388	RATHOX111A.PE1	Hox 1.11	homeobox protein		ggt	ttg	increased
3389	AB030833.SIX3	Six3	homeobox protein Six3		act	agc	No change
3390	AB030833.SIX3	Six3	homeobox protein Six3		ggc	acg	No change
3391	AB030833.SIX3	Six3	homeobox protein Six3		ggc	acg	No change
3392	AB030833.SIX3	Six3	homeobox protein Six3		agc	atc	No change
3393	AB030833.SIX3	Six3	homeobox protein Six3		agg	tgt	No change
3394	AB030833.SIX3	Six3	homeobox protein Six3		agg	tgt	No change
3395	AB030833.SIX3	Six3	homeobox protein Six3		agg	tgt	No change
3396	AB030833.SIX3	Six3	homeobox protein Six3		gcg	ctc	No change
3397	AB030833.SIX3	Six3	homeobox protein Six3		gcg	ctc	No change
3398	AB030833.SIX3	Six3	homeobox protein Six3		tcg	tcc	No change
3399	AB030833.SIX3	Six3	homeobox protein Six3		tcg	tcc	No change

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
3400	Hha1	28	tcg	133.6	133	133.6	0	0	17 800 000	0	0	-=	\		-1
3401	Hha1	20	ctc	146.54	147	146.68	146.66	146.28	254.82	419.61	417.46	==	-		-1
3402	Hha1	20	ctc	147.35	147	0	147.49	147.21	0	498.29	620.22	+=	/		-1
3403	Taq1	45	gcc	156.07	157	156.07	0	0	3 100 000	0	0	-=	\		-1
3404	Taq1	45	gcc	157.285	157	157.45	157.12	0	3 300 000	3 000 000	0	=-	\		-1
3405	Taq1	22	tcc	157.48	158	157.37	157.73	157.34	3 300 000	4 500 000	14 200 000	=+	/ (-)		-1
3406	Taq1	22	tcc	158.37	158	0	0	158.37	0	0	18 400 000	=+	/		-1
3407	Hha1	39	agg	82.733	83	83.05	82.55	82.6	828.44	1 671.74	545.24	+-	A		A(3)
3408	Hha1	39	agg	83	83	0	83	0	0	1 492.62	0	+-	A		A(3)
3409	Hha1	40	tgg	135.63	135	0	135.41	135.85	0	10 700 000	4 300 000	+-	A		A(3)
3410	Hha1	59	ttc	195.75	196	195.88	0	195.62	187.2	0	95.72	-+(-)	V (\)		A(3)
3411	Hha1	59	ttc	196.9	196	0	196.9	0	0	106.35	0	+-	A		A(3)
3412	Hha1	27	acg	148.58	149	148.58	0	0	3 800 000	0	0	-=	\		\(4)
3413	Hha1	27	acg	149.673	149	149.7	149.66	149.66	14 200 000	5 600 000	11 700 000	-=	\ (-)		\(4)
3414	Hha1	64	gtt	148.973	149	149.11	148.9	148.91	10 800 000	4 700 000	8 900 000	-=	\ (-)		\(4)
3415	Taq1	39	agg	285.5	287	0	285.5	0	0	7 600 000	0	+-	A		\(4)
3416	Taq1	39	agg	286.22	287	0	286.22	0	0	15 600 000	0	+-	A		\(4)
3417	Taq1	39	agg	285.5	287	0	285.5	0	0	76.38	0	+-	A		\(4)
3418	Taq1	39	agg	286.22	287	0	286.22	0	0	156.78	0	+-	A		\(4)
3419	Taq1	39	agg	287.82	287	287.82	0	0	6 400 000	0	0	-=	\		\(4)
3420	Taq1	39	agg	287.82	287	287.82	0	0	237.67	0	0	-=	\		\(4)
3421	Taq1	49	aaa	286.73	288	286.73	286.73	0	26 100 000	12 200 000	0	--	\		\(4)
3422	Taq1	49	aaa	288.24	288	288.24	0	0	6 900 000	0	0	-=	\		\(4)
3423	Taq1	49	aaa	289.1	288	289.12	289.08	0	8 000 000	7 200 000	0	=-	\		\(4)
3424	Hha1	6	aga	121.875	122	0	122.04	121.71	0	3 100 000	23 600 000	=+	/		/(3)
3425	Taq1	36	ggt	121.59	122	0	0	121.59	0	0	3 000 000	=+	/		/(3)
3426	Taq1	36	ggt	122.59	122	0	0	122.59	0	0	5 100 000	=+	/		/(3)
3427	Taq1	61	tct	162.29	163	0	0	162.29	0	0	10 600 000	=+	/		/(3)
3428	Taq1	61	tct	163.33	163	0	0	163.33	0	0	19 900 000	=+	/		/(3)
3429	Taq1	64	gtt	162.073	163	162.21	162.01	162	6 300 000	7 000 000	3 200 000	=-	\ (-)		/(3)
3430	Taq1	64	gtt	163.157	163	163.17	163.09	163.21	5 200 000	5 300 000	3 700 000	==	-		/(3)
3431	Taq1	50	aat	95.223	95	95.19	95.24	95.24	68 800 000	12 500 000	27 000 000	-=	\ (-)		\(2)
3432	Hha1	26	ctg	100.685	101	100.5	100.87	0	3 700 000	5 800 000	0	=-	\		\(2)
3433	Hha1	26	ctg	101.59	101	0	101.49	101.69	0	3 900 000	9 000 000	=+	/		\(2)
3434	Hha1	33	agc	135.22	136	0	135.32	135.12	0	3 000 000	3 600 000	+=	/	/	
3435	Hha1	39	agg	135.25	136	0	0	135.25	0	0	236	=+	/	/	
3436	Taq1	39	agg	154.87	155	154.87	0	0	14 100 000	0	0	-=	\		\(2)
3437	Taq1	39	agg	154.87	155	154.87	0	0	523.61	0	0	-=	\		\(2)
3438	Taq1	61	tct	154.927	155	154.95	154.69	155.14	7 500 000	4 100 000	9 800 000	=+	/ (-)		\(2)
3439	Taq1	39	agg	171.09	172	171.09	0	0	14 500 000	0	0	-=	\		\(2)
3440	Taq1	39	agg	171.44	172	171.44	0	0	12 200 000	0	0	-=	\		\(2)
3441	Taq1	39	agg	172.98	172	173.19	172.77	0	7 500 000	35 200 000	0	+-	A		\(2)
3442	Taq1	39	agg	171.09	172	171.09	0	0	538.47	0	0	-=	\		\(2)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
3400	AB030833.SIX3	Six3	homeobox protein Six3		tcg	tcc	No change
3401	AB030833.SIX3	Six3	homeobox protein Six3		cgt	ctc	No change
3402	AB030833.SIX3	Six3	homeobox protein Six3		cgt	ctc	No change
3403	AB030833.SIX3	Six3	homeobox protein Six3		tcc	gcc	No change
3404	AB030833.SIX3	Six3	homeobox protein Six3		tcc	gcc	No change
3405	AB030833.SIX3	Six3	homeobox protein Six3		tcc	gcc	No change
3406	AB030833.SIX3	Six3	homeobox protein Six3		tcc	gcc	No change
3407	RNU93092.HOXA1	HoxA1	homeobox-plus HoxA1 protein		gag	agg	increased by mild
3408	RNU93092.HOXA1	HoxA1	homeobox-plus HoxA1 protein		gag	agg	increased by mild
3409	RNU93092.HOXA1	HoxA1	homeobox-plus HoxA1 protein		gag	tgg	increased by mild
3410	RNU93092.HOXA1	HoxA1	homeobox-plus HoxA1 protein		acc	ttc	increased by mild
3411	RNU93092.HOXA1	HoxA1	homeobox-plus HoxA1 protein		acc	ttc	increased by mild
3412	RATCART1X.CART-1	Cart-1	homeoprotein 1		gtt	acg	increased
3413	RATCART1X.CART-1	Cart-1	homeoprotein 1		gtt	acg	increased
3414	RATCART1X.CART-1	Cart-1	homeoprotein 1		gtt	acg	increased
3415	RATCART1X.CART-1	Cart-1	homeoprotein 1		agg	aaa	increased
3416	RATCART1X.CART-1	Cart-1	homeoprotein 1		agg	aaa	increased
3417	RATCART1X.CART-1	Cart-1	homeoprotein 1		agg	aaa	increased
3418	RATCART1X.CART-1	Cart-1	homeoprotein 1		agg	aaa	increased
3419	RATCART1X.CART-1	Cart-1	homeoprotein 1		agg	aaa	increased
3420	RATCART1X.CART-1	Cart-1	homeoprotein 1		agg	aaa	increased
3421	RATCART1X.CART-1	Cart-1	homeoprotein 1		agg	aaa	increased
3422	RATCART1X.CART-1	Cart-1	homeoprotein 1		agg	aaa	increased
3423	RATCART1X.CART-1	Cart-1	homeoprotein 1		agg	aaa	increased
3424	AF036537.PE1	nc	homocysteine respondent protein HCYP2		aga	ggt	decreased
3425	AF036537.PE1	nc	homocysteine respondent protein HCYP2		aga	ggt	decreased
3426	AF036537.PE1	nc	homocysteine respondent protein HCYP2		aga	ggt	decreased
3427	AF036537.PE1	nc	homocysteine respondent protein HCYP2		tct	gtt	decreased
3428	AF036537.PE1	nc	homocysteine respondent protein HCYP2		tct	gtt	decreased
3429	AF036537.PE1	nc	homocysteine respondent protein HCYP2		tct	gtt	decreased
3430	AF036537.PE1	nc	homocysteine respondent protein HCYP2		tct	gtt	decreased
3431	RNHNPCR.PE1	nc	homologue to natriuretic peptide clearance		ggg	aat	increased
3432	RNHNPCR.PE1	nc	homologue to natriuretic peptide clearance		ctg	ggc	increased
3433	RNHNPCR.PE1	nc	homologue to natriuretic peptide clearance		ctg	ggc	increased
3434	AF036344.HRS	Hrs	Hrs		agg	agc	decreased
3435	AF036344.HRS	Hrs	Hrs		agg	agc	decreased
3436	AB005052.RHIP1R	rHIP1R	huntingtin interacting protein 1 related		agg	tct	increased
3437	AB005052.RHIP1R	rHIP1R	huntingtin interacting protein 1 related		agg	tct	increased
3438	AB005052.RHIP1R	rHIP1R	huntingtin interacting protein 1 related		agg	tct	increased
3439	AB005052.RHIP1R	rHIP1R	huntingtin interacting protein 1 related		agg	ggc	increased
3440	AB005052.RHIP1R	rHIP1R	huntingtin interacting protein 1 related		agg	ggc	increased
3441	AB005052.RHIP1R	rHIP1R	huntingtin interacting protein 1 related		agg	ggc	increased
3442	AB005052.RHIP1R	rHIP1R	huntingtin interacting protein 1 related		agg	ggc	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
3443	Taq1	39	agg	171.44	172	171.44	0	0	453.06	0	0	-=	\		\(2)
3444	Taq1	39	agg	172.77	172	0	172.77	0	0	353.77	0	+-	A		\(2)
3445	Hha1	41	ccc	153.785	154	153.87	0	153.7	7 800 000	0	8 300 000	-+(=)	V		V(2)
3446	Hha1	26	ctg	154.083	155	154.07	154.1	154.08	55 500 000	17 300 000	45 300 000	-+	V		V(2)
3447	Hha1	26	ctg	155.007	155	154.99	155.02	155.01	8 900 000	3 900 000	8 500 000	-+	V		V(2)
3448	Hha1	40	tgg	195.975	197	0	195.9	196.05	0	7 800 000	3 800 000	+-	A		V(2)
3449	Hha1	40	tgg	196.87	197	0	196.71	197.03	0	4 900 000	4 600 000	+=	/		V(2)
3450	Hha1	40	tgg	197.52	197	0	197.52	0	0	5 300 000	0	+-	A		V(2)
3451	Hha1	10	atg	215.46	215	215.46	0	0	3 800 000	0	0	-=	\	\	
3452	Taq1	10	atg	215.46	215	215.46	0	0	3 400 000	0	0	-=	\	\	
3453	Hha1	25	cag	104.6	105	0	0	104.6	0	0	3 000 000	=+	/	/	-1
3454	Taq1	62	tgt	104.44	105	104.28	104.56	104.48	3 100 000	5 900 000	11 500 000	=+	/ (-)	/	-1
3455	Taq1	62	tgt	105.385	105	105.28	0	105.49	3 300 000	0	16 800 000	=+(+)	/		-1
3456	Taq1	50	aat	179.917	181	179.92	179.96	179.87	19 800 000	35 900 000	4 500 000	=-	\ (-)		-1
3457	Taq1	50	aat	181.155	181	181.28	181.03	0	3 600 000	3 700 000	0	=-	\		-1
3458	Taq1	50	aat	181.2	181	181.2	0	0	3 800 000	0	0	-=	\		-1
3459	Taq1	50	aat	182.075	181	182.32	0	181.83	9 500 000	0	3 600 000	-=(-)	\		-1
3460	Hha1	26	ctg	149.125	150	149.11	149.14	0	5 200 000	3 800 000	0	=-	\		/(2)
3461	Hha1	26	ctg	150.085	150	150.14	150.03	0	3 800 000	3 500 000	0	=-	\		/(2)
3462	Hha1	62	tgt	150.41	150	0	150.2	150.62	0	3 300 000	3 900 000	+=	/		/(2)
3463	Hha1	59	ttc	214.04	215	0	0	214.04	0	0	85.37	=+	/		/(2)
3464	Taq1	1	tat	127.79	128	0	0	127.79	0	0	14 800 000	=+	/		/(2) \(2)
3465	Taq1	1	tat	128.73	128	0	0	128.73	0	0	17 000 000	=+	/		/(2) \(2)
3466	Taq1	45	gcc	153.78	154	153.99	153.57	0	5 900 000	4 400 000	0	=-	\		/(2) \(2)
3467	Taq1	45	gcc	154.35	154	0	154.24	154.46	0	5 300 000	3 800 000	+=	/		/(2) \(2)
3468	Hha1	55	tca	154.56	155	154.56	0	0	4 200 000	0	0	-=	\		/(2) \(2)
3469	Hha1	55	tca	155.483	155	155.56	155.46	155.43	4 400 000	3 100 000	3 000 000	==	-		/(2) \(2)
3470	Hha1	62	tgt	104.79	105	0	104.79	0	0	3 000 000	0	+-	A		A(2)
3471	Taq1	34	tgc	112.86	113	0	112.86	0	0	3 900 000	0	+-	A		A(2)
3472	Hha1	61	tct	114.59	115	114.59	0	0	3 400 000	0	0	-=	\		A(2)
3473	Hha1	6	aga	138.265	139	138.34	0	138.19	8 000 000	0	23 300 000	=+(+)	/		/(5)
3474	Hha1	6	aga	138.45	139	138.45	0	0	8 100 000	0	0	-=	\		/(5)
3475	Hha1	6	aga	139.29	139	139.41	0	139.17	5 500 000	0	28 500 000	=+(+)	/		/(5)
3476	Taq1	26	ctg	150.785	151	0	150.76	150.81	0	3 200 000	14 200 000	=+	/		/(5)
3477	Taq1	26	ctg	151.67	151	0	151.67	0	0	3 500 000	0	+-	A		/(5)
3478	Taq1	57	ctg	150.17	151	0	0	150.17	0	0	3 800 000	=+	/		/(5)
3479	Taq1	57	ctg	151.277	151	151.29	151.32	151.22	5 900 000	4 100 000	4 900 000	==	-		/(5)
3480	Hha1	6	aga	174.06	175	0	0	174.06	0	0	7 800 000	=+	/		/(5)
3481	Hha1	6	aga	174.96	175	0	0	174.96	0	0	5 400 000	=+	/		/(5)
3482	Hha1	6	aga	175.995	175	175.96	0	176.03	4 500 000	0	9 800 000	-+(+)	V (/)		/(5)
3483	Taq1	36	ggt	174.59	175	0	174.59	0	0	3 100 000	0	+-	A		/(5)
3484	Taq1	36	ggt	175.555	175	0	175.58	175.53	0	3 900 000	3 800 000	+=	/		/(5)
3485	Hha1	6	aga	138.265	139	138.34	0	138.19	8 000 000	0	23 300 000	=+(+)	/		/(5)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
3443	AB005052.RHIP1R	rHIP1R	huntingtin interacting protein 1 related		agg	ggc	increased
3444	AB005052.RHIP1R	rHIP1R	huntingtin interacting protein 1 related		agg	ggc	increased
3445	RATHOM.PE1	nc	hydroxyindole-O-methyltransferase		ctg	ccc	decreased by mild
3446	RATHOM.PE1	nc	hydroxyindole-O-methyltransferase		ctg	ccc	decreased by mild
3447	RATHOM.PE1	nc	hydroxyindole-O-methyltransferase		ctg	ccc	decreased by mild
3448	RATHOM.PE1	nc	hydroxyindole-O-methyltransferase		tgg	ggg	decreased by mild
3449	RATHOM.PE1	nc	hydroxyindole-O-methyltransferase		tgg	ggg	decreased by mild
3450	RATHOM.PE1	nc	hydroxyindole-O-methyltransferase		tgg	ggg	decreased by mild
3451	AF247450.HCN1	HCN1	hyperpolarization-activated, cyclic		tga	atg	increased
3452	AF247450.HCN1	HCN1	hyperpolarization-activated, cyclic		tga	atg	increased
3453	RNU41803.PE1	nc	hypertension-related protein		cag	tgt	decreased
3454	RNU41803.PE1	nc	hypertension-related protein		cag	tgt	decreased
3455	RNU41803.PE1	nc	hypertension-related protein		cag	tgt	No change
3456	RNU41803.PE1	nc	hypertension-related protein		gct	aat	No change
3457	RNU41803.PE1	nc	hypertension-related protein		gct	aat	No change
3458	RNU41803.PE1	nc	hypertension-related protein		gct	aat	No change
3459	RNU41803.PE1	nc	hypertension-related protein		gct	aat	No change
3460	RNO297794.PE2	nc	hypothetical protein		ctg	tgt	decreased
3461	RNO297794.PE2	nc	hypothetical protein		ctg	tgt	decreased
3462	RNO297794.PE2	nc	hypothetical protein		ctg	tgt	decreased
3463	RNO297794.PE2	nc	hypothetical protein		ttc	ggg	decreased
3464	AF009921.PE1	nc	I100		tat	gag	decreased
3465	AF009921.PE1	nc	I100		tat	gag	decreased
3466	AF009921.PE1	nc	I100		gcc	tca	decreased
3467	AF009921.PE1	nc	I100		gcc	tca	decreased
3468	AF009921.PE1	nc	I100		gcc	tca	decreased
3469	AF009921.PE1	nc	I100		gcc	tca	decreased
3470	RATIRPRA.PC4	PC4	IFRD1		tgt	tca	increased by mild
3471	RATIRPRA.PC4	PC4	IFRD1		tgc	gct	increased by mild
3472	RATIRPRA.PC4	PC4	IFRD1		tct	tca	increased by mild
3473	AY055777.IAN4L1	Ian4l1	immune-associated nucleotide 4 protein, long		gtc	aga	decreased
3474	AY055777.IAN4L1	Ian4l1	immune-associated nucleotide 4 protein, long		gtc	aga	decreased
3475	AY055777.IAN4L1	Ian4l1	immune-associated nucleotide 4 protein, long		gtc	aga	decreased
3476	AY055777.IAN4L1	Ian4l1	immune-associated nucleotide 4 protein, long		gtc	ctg	decreased
3477	AY055777.IAN4L1	Ian4l1	immune-associated nucleotide 4 protein, long		gtc	ctg	decreased
3478	AY055777.IAN4L1	Ian4l1	immune-associated nucleotide 4 protein, long		gtc	ctg	decreased
3479	AY055777.IAN4L1	Ian4l1	immune-associated nucleotide 4 protein, long		gtc	ctg	decreased
3480	AY055777.IAN4L1	Ian4l1	immune-associated nucleotide 4 protein, long		aga	ggt	decreased
3481	AY055777.IAN4L1	Ian4l1	immune-associated nucleotide 4 protein, long		aga	ggt	decreased
3482	AY055777.IAN4L1	Ian4l1	immune-associated nucleotide 4 protein, long		aga	ggt	decreased
3483	AY055777.IAN4L1	Ian4l1	immune-associated nucleotide 4 protein, long		aga	ggt	decreased
3484	AY055777.IAN4L1	Ian4l1	immune-associated nucleotide 4 protein, long		aga	ggt	decreased
3485	AY055776.IAN4L1	Ian4l1	immune-associated nucleotide 4 protein, short		gtc	aga	decreased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
3486	Hha1	6	aga	138.45	139	138.45	0	0	8 100 000	0	0	-=	\		/(5)
3487	Hha1	6	aga	139.29	139	139.41	0	139.17	5 500 000	0	28 500 000	=+(+)	/		/(5)
3488	Taq1	26	ctg	150.785	151	0	150.76	150.81	0	3 200 000	14 200 000	=+	/		/(5)
3489	Taq1	26	ctg	151.67	151	0	151.67	0	0	3 500 000	0	+-	A		/(5)
3490	Taq1	57	ctg	150.17	151	0	0	150.17	0	0	3 800 000	=+	/		/(5)
3491	Taq1	57	ctg	151.277	151	151.29	151.32	151.22	5 900 000	4 100 000	4 900 000	==	-		/(5)
3492	Hha1	6	aga	174.06	175	0	0	174.06	0	0	7 800 000	=+	/		/(5)
3493	Hha1	6	aga	174.96	175	0	0	174.96	0	0	5 400 000	=+	/		/(5)
3494	Hha1	6	aga	175.995	175	175.96	0	176.03	4 500 000	0	9 800 000	-+(+)	V (/)		/(5)
3495	Taq1	36	ggt	174.59	175	0	174.59	0	0	3 100 000	0	+-	A		/(5)
3496	Taq1	36	ggt	175.555	175	0	175.58	175.53	0	3 900 000	3 800 000	+=	/		/(5)
3497	Taq1	18	cct	228.98	229	0	228.98	0	0	4 600 000	0	+-	A		A(2) \(2)
3498	Taq1	18	cct	229.98	229	230.01	229.95	0	3 400 000	4 600 000	0	=-	\		A(2) \(2)
3499	Hha1	22	tcc	229.45	229	229.45	0	0	10 300 000	0	0	-=	\		A(2) \(2)
3500	Hha1	22	tcc	230.345	229	0	230.3	230.39	0	12 300 000	3 600 000	+-	A		A(2) \(2)
3501	Taq1	18	cct	228.98	229	0	228.98	0	0	4 600 000	0	+-	A		A(2) \(2)
3502	Taq1	18	cct	229.98	229	230.01	229.95	0	3 400 000	4 600 000	0	=-	\		A(2) \(2)
3503	Hha1	22	tcc	229.45	229	229.45	0	0	10 300 000	0	0	-=	\		A(2) \(2)
3504	Hha1	22	tcc	230.345	229	0	230.3	230.39	0	12 300 000	3 600 000	+-	A		A(2) \(2)
3505	Taq1	18	cct	228.98	229	0	228.98	0	0	4 600 000	0	+-	A		A(2) \(2)
3506	Taq1	18	cct	229.98	229	230.01	229.95	0	3 400 000	4 600 000	0	=-	\		A(2) \(2)
3507	Hha1	22	tcc	229.45	229	229.45	0	0	10 300 000	0	0	-=	\		A(2) \(2)
3508	Hha1	22	tcc	230.345	229	0	230.3	230.39	0	12 300 000	3 600 000	+-	A		A(2) \(2)
3509	Taq1	17	cca	164.36	165	164.36	0	0	1 783.3	0	0	-=	\		/(2)
3510	Taq1	17	cca	165.225	165	165.43	165.02	0	5 466.02	711.34	0	-=	\		/(2)
3511	Taq1	17	cca	165.57	165	0	165.54	165.6	0	438.77	541.27	+=	/		/(2)
3512	Taq1	40	tgg	164.45	165	0	164.54	164.36	0	90 600 000	5 800 000	+-	A		/(2)
3513	Taq1	40	tgg	165.26	165	0	0	165.26	0	0	13 300 000	=+	/		/(2)
3514	Taq1	25	cat	120.315	120	120.32	120.31	0	832.53	980.26	0	=-	\		\(4)
3515	Taq1	20	ctc	122.29	123	0	122.29	0	0	17 000 000	0	+-	A		\(4)
3516	Taq1	20	ctc	123.32	123	123.1	123.54	0	10 800 000	3 400 000	0	-=	\		\(4)
3517	Taq1	34	tgc	122.65	123	122.69	122.61	0	38 400 000	23 300 000	0	=-	\		\(4)
3518	Taq1	14	gat	174.727	175	174.64	174.64	174.9	6 400 000	6 400 000	3 200 000	=-	\ (-)		\(4)
3519	Taq1	14	gat	175.757	175	175.7	175.7	175.87	7 200 000	7 200 000	4 900 000	==	-		\(4)
3520	Hha1	59	ttc	85.84	86	0	85.84	0	0	462.8	0	+-	A		A(5)
3521	Taq1	36	ggt	116.617	117	116.65	116.69	116.51	7 400 000	17 100 000	5 000 000	+-	A	A	A(5)
3522	Taq1	36	ggt	117.5	117	117.47	117.49	117.54	7 000 000	17 400 000	3 900 000	+-	A		A(5)
3523	Taq1	63	ctt	116.76	117	0	116.76	0	0	3 000 000	0	+-	A	A	A(5)
3524	Hha1	44	cgg	159.18	159	0	0	159.18	0	0	5 900 000	=+	/		A(5)
3525	Taq1	44	cgg	237.69	239	0	237.69	0	0	559.9	0	+-	A		A(5)
3526	Taq1	44	cgg	238.89	239	238.89	0	0	208.31	0	0	-=	\	\	A(5)
3527	Taq1	44	cgg	239.27	239	239.27	0	0	256.91	0	0	-=	\		A(5)
3528	Hha1	8	gaa	238.66	240	238.83	238.49	0	4 500 000	3 100 000	0	=-	\	\	A(5)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
3486	AY055776.IAN4L1	Ian4l1	immune-associated nucleotide 4 protein, short		gtc	aga	decreased
3487	AY055776.IAN4L1	Ian4l1	immune-associated nucleotide 4 protein, short		gtc	aga	decreased
3488	AY055776.IAN4L1	Ian4l1	immune-associated nucleotide 4 protein, short		gtc	ctg	decreased
3489	AY055776.IAN4L1	Ian4l1	immune-associated nucleotide 4 protein, short		gtc	ctg	decreased
3490	AY055776.IAN4L1	Ian4l1	immune-associated nucleotide 4 protein, short		gtc	ctg	decreased
3491	AY055776.IAN4L1	Ian4l1	immune-associated nucleotide 4 protein, short		gtc	ctg	decreased
3492	AY055776.IAN4L1	Ian4l1	immune-associated nucleotide 4 protein, short		aga	ggt	decreased
3493	AY055776.IAN4L1	Ian4l1	immune-associated nucleotide 4 protein, short		aga	ggt	decreased
3494	AY055776.IAN4L1	Ian4l1	immune-associated nucleotide 4 protein, short		aga	ggt	decreased
3495	AY055776.IAN4L1	Ian4l1	immune-associated nucleotide 4 protein, short		aga	ggt	decreased
3496	AY055776.IAN4L1	Ian4l1	immune-associated nucleotide 4 protein, short		aga	ggt	decreased
3497	RNIGE01.PE1	nc	immunoglobulin epsilon heavy chain		cct	tcc	increased by mild
3498	RNIGE01.PE1	nc	immunoglobulin epsilon heavy chain		cct	tcc	increased by mild
3499	RNIGE01.PE1	nc	immunoglobulin epsilon heavy chain		cct	tcc	increased by mild
3500	RNIGE01.PE1	nc	immunoglobulin epsilon heavy chain		cct	tcc	increased by mild
3501	RATIGCA.IGE	IgE	immunoglobulin epsilon-chain		cct	tcc	increased by mild
3502	RATIGCA.IGE	IgE	immunoglobulin epsilon-chain		cct	tcc	increased by mild
3503	RATIGCA.IGE	IgE	immunoglobulin epsilon-chain		cct	tcc	increased by mild
3504	RATIGCA.IGE	IgE	immunoglobulin epsilon-chain		cct	tcc	increased by mild
3505	RATIGCA.PE2	IgE	immunoglobulin epsilon-chain		cct	tcc	increased by mild
3506	RATIGCA.PE2	IgE	immunoglobulin epsilon-chain		cct	tcc	increased by mild
3507	RATIGCA.PE2	IgE	immunoglobulin epsilon-chain		cct	tcc	increased by mild
3508	RATIGCA.PE2	IgE	immunoglobulin epsilon-chain		cct	tcc	increased by mild
3509	RATIGG1Z.IGG1	IgG1	immunoglobulin gamma-1 chain		cca	tgg	decreased
3510	RATIGG1Z.IGG1	IgG1	immunoglobulin gamma-1 chain		cca	tgg	decreased
3511	RATIGG1Z.IGG1	IgG1	immunoglobulin gamma-1 chain		cca	tgg	decreased
3512	RATIGG1Z.IGG1	IgG1	immunoglobulin gamma-1 chain		cca	tgg	decreased
3513	RATIGG1Z.IGG1	IgG1	immunoglobulin gamma-1 chain		cca	tgg	decreased
3514	RNO130946.PE1	importin alpha	importin alpha		tgc	cat	increased
3515	RNO130946.PE1	importin alpha	importin alpha		ctc	tgc	increased
3516	RNO130946.PE1	importin alpha	importin alpha		ctc	tgc	increased
3517	RNO130946.PE1	importin alpha	importin alpha		ctc	tgc	increased
3518	RNO130946.PE1	importin alpha	importin alpha		gat	tca	increased
3519	RNO130946.PE1	importin alpha	importin alpha		gat	tca	increased
3520	RNU05989.PE1	nc	induced by effectors of apoptosis		cag	ttc	increased by mild
3521	RNU05989.PE1	nc	induced by effectors of apoptosis		ctt	ggt	increased by mild
3522	RNU05989.PE1	nc	induced by effectors of apoptosis		ctt	ggt	increased by mild
3523	RNU05989.PE1	nc	induced by effectors of apoptosis		ctt	ggt	increased by mild
3524	RNU05989.PE1	nc	induced by effectors of apoptosis		caa	cgg	increased by mild
3525	RNU05989.PE1	nc	induced by effectors of apoptosis		gaa	cgg	increased by mild
3526	RNU05989.PE1	nc	induced by effectors of apoptosis		gaa	cgg	increased
3527	RNU05989.PE1	nc	induced by effectors of apoptosis		gaa	cgg	increased by mild
3528	RNU05989.PE1	nc	induced by effectors of apoptosis		gaa	cgg	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
3529	Hha1	8	gaa	244.36	243	244.36	0	0	3 700 000	0	0	-=	\		A(5)
3530	Taq1	39	agg	241.875	243	242	241.75	0	4 900 000	32 100 000	0	+-	A		A(5)
3531	Taq1	39	agg	243.37	243	0	243.37	0	0	16 700 000	0	+-	A		A(5)
3532	Taq1	39	agg	241.75	243	0	241.75	0	0	322.61	0	+-	A		A(5)
3533	Taq1	39	agg	243.37	243	0	243.37	0	0	167.84	0	+-	A		A(5)
3534	Taq1	39	agg	242	243	242	0	0	181.96	0	0	-=	\		A(5)
3535	Taq1	17	cca	165.57	166	0	165.54	165.6	0	438.77	541.27	+=	/	/	
3536	Taq1	17	cca	166.77	166	0	0	166.77	0	0	466.09	=+	/	/	
3537	Taq1	27	acg	165.77	166	165.75	165.74	165.82	5 500 000	3 500 000	9 900 000	=+	/ (-)	/	
3538	Taq1	27	acg	166.76	166	0	0	166.76	0	0	4 700 000	=+	/	/	
3539	Taq1	17	cca	165.57	166	0	165.54	165.6	0	438.77	541.27	+=	/	/	
3540	Taq1	17	cca	166.77	166	0	0	166.77	0	0	466.09	=+	/	/	
3541	Taq1	27	acg	165.77	166	165.75	165.74	165.82	5 500 000	3 500 000	9 900 000	=+	/ (-)	/	
3542	Taq1	27	acg	166.76	166	0	0	166.76	0	0	4 700 000	=+	/	/	
3543	Hha1	6	aga	114.53	115	0	114.53	0	0	11 200 000	0	+-	A		A(2)
3544	Hha1	6	aga	115.065	115	115.05	0	115.08	16 900 000	0	4 400 000	-=(-)	\		A(2)
3545	Hha1	6	aga	115.65	115	115.64	115.66	0	9 500 000	3 500 000	0	-=	\		A(2)
3546	Taq1	17	cca	346.51	348	0	346.51	0	0	239.32	0	+-	A		A(2)
3547	Taq1	17	cca	349.53	348	0	349.53	0	0	850.95	0	+-	A		A(2)
3548	Hha1	44	cgg	76.835	77	76.71	76.96	0	6 200 000	16 600 000	0	+-	A		/(2) \(2) A(2)
3549	Hha1	44	cgg	77.32	77	0	0	77.32	0	0	4 200 000	=+	/		/(2) \(2) A(2)
3550	Hha1	39	agg	152.55	152	152.55	0	0	469.2	0	0	-=	\		/(2) \(2) A(2)
3551	Taq1	49	aaa	281.57	282	0	281.57	0	0	11 000 000	0	+-	A		/(2) \(2) A(2)
3552	Taq1	49	aaa	282.35	282	0	282.35	0	0	4 800 000	0	+-	A		/(2) \(2) A(2)
3553	Taq1	49	aaa	283.13	282	0	283.35	282.91	0	10 900 000	41 000 000	=+	/		/(2) \(2) A(2)
3554	Taq1	49	aaa	283.44	282	283.44	0	0	9 600 000	0	0	-=	\		/(2) \(2) A(2)
3555	Hha1	44	cgg	76.835	77	76.71	76.96	0	6 200 000	16 600 000	0	+-	A		/(2) \(2) A(2)
3556	Hha1	44	cgg	77.32	77	0	0	77.32	0	0	4 200 000	=+	/		/(2) \(2) A(2)
3557	Hha1	39	agg	152.55	152	152.55	0	0	469.2	0	0	-=	\		/(2) \(2) A(2)
3558	Taq1	49	aaa	281.57	282	0	281.57	0	0	11 000 000	0	+-	A		/(2) \(2) A(2)
3559	Taq1	49	aaa	282.35	282	0	282.35	0	0	4 800 000	0	+-	A		/(2) \(2) A(2)
3560	Taq1	49	aaa	283.13	282	0	283.35	282.91	0	10 900 000	41 000 000	=+	/		/(2) \(2) A(2)
3561	Taq1	49	aaa	283.44	282	283.44	0	0	9 600 000	0	0	-=	\		/(2) \(2) A(2)
3562	Hha1	49	aaa	70.745	71	0	70.56	70.93	0	31 500 000	3 400 000	+-	A		\(9)
3563	Hha1	49	aaa	71.09	71	71.09	0	0	54 300 000	0	0	-=	\		\(9)
3564	Hha1	20	ctc	73.83	74	73.76	73.99	73.74	392.56	655.65	369.75	==	-		\(9)
3565	Hha1	20	ctc	74.44	74	0	74.49	74.39	0	773.66	763.35	+=	/		\(9)
3566	Hha1	20	ctc	86.105	86	0	86.13	86.08	0	1 180.17	1 693.7	+=	/		\(9)
3567	Hha1	33	agc	113.725	114	113.86	113.59	0	6 500 000	9 600 000	0	=-	\		\(9)
3568	Hha1	32	gtc	157.153	158	157.17	157.23	157.06	3 570.12	2 502.54	469.31	=-	\ (-)		\(9)
3569	Hha1	32	gtc	158.09	158	158.18	158	0	952.03	681.58	0	=-	\		\(9)
3570	Hha1	33	agc	157.62	158	0	157.68	157.56	0	3 500 000	14 400 000	=+	/		\(9)
3571	Hha1	33	agc	158.6	158	0	0	158.6	0	0	20 700 000	=+	/		\(9)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
3529	RNU05989.PE1	nc	induced by effectors of apoptosis		gaa	agg	increased by mild
3530	RNU05989.PE1	nc	induced by effectors of apoptosis		gaa	agg	increased by mild
3531	RNU05989.PE1	nc	induced by effectors of apoptosis		gaa	agg	increased by mild
3532	RNU05989.PE1	nc	induced by effectors of apoptosis		gaa	agg	increased by mild
3533	RNU05989.PE1	nc	induced by effectors of apoptosis		gaa	agg	increased by mild
3534	RNU05989.PE1	nc	induced by effectors of apoptosis		gaa	agg	increased by mild
3535	RATNWUT.PE1	nc	inducible nitric oxide synthase		cca	acg	decreased
3536	RATNWUT.PE1	nc	inducible nitric oxide synthase		cca	acg	decreased
3537	RATNWUT.PE1	nc	inducible nitric oxide synthase		cca	acg	decreased
3538	RATNWUT.PE1	nc	inducible nitric oxide synthase		cca	acg	decreased
3539	RNO230462.INOS	iNOS	inducible nitric oxide synthase		cca	acg	decreased
3540	RNO230462.INOS	iNOS	inducible nitric oxide synthase		cca	acg	decreased
3541	RNO230462.INOS	iNOS	inducible nitric oxide synthase		cca	acg	decreased
3542	RNO230462.INOS	iNOS	inducible nitric oxide synthase		cca	acg	decreased
3543	RNU38253.PE1	eIF-2B gamm	initiation factor eIF-2B gamma subunit		aga	gag	increased by mild
3544	RNU38253.PE1	eIF-2B gamm	initiation factor eIF-2B gamma subunit		aga	gag	increased by mild
3545	RNU38253.PE1	eIF-2B gamm	initiation factor eIF-2B gamma subunit		aga	gag	increased by mild
3546	RNU38253.PE1	eIF-2B gamm	initiation factor eIF-2B gamma subunit		gta	cca	increased by mild
3547	RNU38253.PE1	eIF-2B gamm	initiation factor eIF-2B gamma subunit		gta	cca	increased by mild
3548	RNO440782.IP3K-C	ip3k-c	inositol 1,4,5-trisphosphate 3-kinase	*	tgc	cgg	decreased
3549	RNO440782.IP3K-C	ip3k-c	inositol 1,4,5-trisphosphate 3-kinase	*	tgc	cgg	decreased
3550	RNO440782.IP3K-C	ip3k-c	inositol 1,4,5-trisphosphate 3-kinase	*	cct	agg	decreased
3551	RNO440782.IP3K-C	ip3k-c	inositol 1,4,5-trisphosphate 3-kinase	*	ggg	aaa	decreased
3552	RNO440782.IP3K-C	ip3k-c	inositol 1,4,5-trisphosphate 3-kinase	*	ggg	aaa	decreased
3553	RNO440782.IP3K-C	ip3k-c	inositol 1,4,5-trisphosphate 3-kinase	*	ggg	aaa	decreased
3554	RNO440782.IP3K-C	ip3k-c	inositol 1,4,5-trisphosphate 3-kinase	*	ggg	aaa	decreased
3555	AY160770.IP3KC	Ip3kc	inositol 1,4,5-trisphosphate 3-kinase C	*	tgc	cgg	decreased
3556	AY160770.IP3KC	Ip3kc	inositol 1,4,5-trisphosphate 3-kinase C	*	tgc	cgg	decreased
3557	AY160770.IP3KC	Ip3kc	inositol 1,4,5-trisphosphate 3-kinase C	*	cct	agg	decreased
3558	AY160770.IP3KC	Ip3kc	inositol 1,4,5-trisphosphate 3-kinase C	*	ggg	aaa	decreased
3559	AY160770.IP3KC	Ip3kc	inositol 1,4,5-trisphosphate 3-kinase C	*	ggg	aaa	decreased
3560	AY160770.IP3KC	Ip3kc	inositol 1,4,5-trisphosphate 3-kinase C	*	ggg	aaa	decreased
3561	AY160770.IP3KC	Ip3kc	inositol 1,4,5-trisphosphate 3-kinase C	*	ggg	aaa	decreased
3562	RNO242781.IP3K-B	ip3K-B	inositol 1,4,5-trisphosphate 3-kinase, isoform		aaa	ttg	increased
3563	RNO242781.IP3K-B	ip3K-B	inositol 1,4,5-trisphosphate 3-kinase, isoform		aaa	ttg	increased
3564	RNO242781.IP3K-B	ip3K-B	inositol 1,4,5-trisphosphate 3-kinase, isoform		tga	ctc	increased
3565	RNO242781.IP3K-B	ip3K-B	inositol 1,4,5-trisphosphate 3-kinase, isoform		tga	ctc	increased
3566	RNO242781.IP3K-B	ip3K-B	inositol 1,4,5-trisphosphate 3-kinase, isoform		gaa	ctc	increased
3567	RNO242781.IP3K-B	ip3K-B	inositol 1,4,5-trisphosphate 3-kinase, isoform		agc	tgc	increased
3568	RNO242781.IP3K-B	ip3K-B	inositol 1,4,5-trisphosphate 3-kinase, isoform		agc	gtc	increased
3569	RNO242781.IP3K-B	ip3K-B	inositol 1,4,5-trisphosphate 3-kinase, isoform		agc	gtc	increased
3570	RNO242781.IP3K-B	ip3K-B	inositol 1,4,5-trisphosphate 3-kinase, isoform		agc	gtc	increased
3571	RNO242781.IP3K-B	ip3K-B	inositol 1,4,5-trisphosphate 3-kinase, isoform		agc	gtc	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
3572	Hha1	10	atg	181.13	182	181.13	0	0	4 700 000	0	0	-=	\		\(9)
3573	Taq1	10	atg	181.19	182	0	181.19	0	0	3 500 000	0	+-	A		\(9)
3574	Taq1	10	atg	181.74	182	181.74	0	0	3 200 000	0	0	-=	\		\(9)
3575	Hha1	10	atg	181.97	182	181.97	0	0	4 200 000	0	0	-=	\		\(9)
3576	Taq1	10	atg	182.87	182	182.87	0	0	8 200 000	0	0	-=	\		\(9)
3577	Hha1	10	atg	182.99	182	182.99	0	0	4 100 000	0	0	-=	\		\(9)
3578	Hha1	8	gaa	251.45	252	0	251.45	0	0	3 600 000	0	+-	A		\(9)
3579	Hha1	8	gaa	251.07	252	0	251.07	0	0	3 500 000	0	+-	A		\(9)
3580	Hha1	8	gaa	252.2	252	252.2	0	0	3 200 000	0	0	-=	\		\(9)
3581	Taq1	8	gaa	251.63	252	0	251.63	0	0	3 500 000	0	+-	A		\(9)
3582	Hha1	59	ttc	210.393	211	210.62	210.27	210.29	187.2	497.29	173.33	+-	A		A(2)
3583	Hha1	59	ttc	210.795	211	0	210.83	210.76	0	209.84	137.11	+=	/		A(2)
3584	Hha1	59	ttc	212.235	211	0	212.38	212.09	0	103.48	807.18	=+	/		A(2)
3585	Hha1	49	aaa	249.51	251	249.52	249.5	0	4 000 000	8 700 000	0	+-	A		A(2)
3586	Hha1	49	aaa	251.18	251	251.1	251.26	0	24 500 000	3 900 000	0	-=	\		A(2)
3587	Hha1	49	aaa	252.22	251	0	252.22	0	0	7 600 000	0	+-	A		A(2)
3588	Taq1	56	tga	119.8	120	119.86	119.74	0	17 300 000	23 200 000	0	=-	\		\(3)
3589	Taq1	49	aaa	120.84	121	120.64	121.04	0	34 100 000	12 100 000	0	-=	\		\(3)
3590	Taq1	49	aaa	381.8	384	0	381.8	0	0	9 100 000	0	+-	A		\(3)
3591	Taq1	49	aaa	383.05	384	383.05	0	0	30 700 000	0	0	-=	\		\(3)
3592	Taq1	49	aaa	384.68	384	384.68	0	0	6 800 000	0	0	-=	\		\(3)
3593	Taq1	10	atg	70.603	71	70.68	70.67	70.46	40 600 000	61 700 000	7 800 000	=-	\ (-)		\(2)
3594	Taq1	48	ggg	133.415	134	133.19	133.64	0	1 011.37	1 795.14	0	=-	\		\(2)
3595	Taq1	48	ggg	134.31	134	134.23	134.39	0	1 390.64	2 479.58	0	=-	\		\(2)
3596	Taq1	61	tct	230.64	232	0	230.64	0	0	3 100 000	0	+-	A		\(2)
3597	Taq1	61	tct	231.07	232	0	231.07	0	0	3 000 000	0	+-	A		\(2)
3598	Taq1	61	tct	231.53	232	0	231.53	0	0	4 200 000	0	+-	A		\(2)
3599	Taq1	20	ctc	106.49	107	0	106.49	0	0	3 800 000	0	+-	A		\(3)
3600	Taq1	39	agg	106.905	107	106.72	107.09	0	25 600 000	41 000 000	0	=-	\		\(3)
3601	Taq1	39	agg	107.245	107	107.4	107.09	0	20 800 000	412.06	0	-=	\		\(3)
3602	Taq1	39	agg	106.72	107	106.72	0	0	950.68	0	0	-=	\		\(3)
3603	Taq1	39	agg	107.4	107	107.4	0	0	772.43	0	0	-=	\		\(3)
3604	Hha1	6	aga	107.747	108	107.78	107.56	107.9	11 700 000	3 600 000	5 500 000	-=	\ (-)		\(3)
3605	Hha1	6	aga	108.21	108	108.21	0	0	11 300 000	0	0	-=	\		\(3)
3606	Taq1	31	gac	107.61	108	0	107.61	0	0	8 500 000	0	+-	A		\(3)
3607	Taq1	45	gcc	310.32	311	310.32	0	0	3 300 000	0	0	-=	\		\(3)
3608	Taq1	45	gcc	311.33	311	311.33	0	0	3 700 000	0	0	-=	\		\(3)
3609	Taq1	18	cct	112.613	113	112.59	112.64	112.61	32 900 000	30 500 000	3 000 000	=-	\ (-)	(-)	-(4) /(3) \(3)
3610	Taq1	18	cct	113.567	113	113.4	113.59	113.71	10 100 000	9 800 000	6 400 000	==	-		-(4) /(3) \(3)
3611	Taq1	62	tgt	112.4	113	112.49	112.53	112.18	4 000 000	13 500 000	27 100 000	=+	/ (-)	(-)	-(4) /(3) \(3)
3612	Taq1	62	tgt	113.46	113	0	113.66	113.26	0	4 900 000	102 300 000	=+	/		-(4) /(3) \(3)
3613	Hha1	25	cag	141.58	142	141.59	141.53	141.62	13 900 000	8 600 000	24 300 000	=+	/ (-)	/	-(4) /(3) \(3)
3614	Hha1	25	cag	142.65	142	142.65	0	0	5 700 000	0	0	-=	\		-(4) /(3) \(3)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
3572	RNO242781.IP3K-B	ip3K-B	inositol 1,4,5-trisphosphate 3-kinase, isoform		ggg	atg	increased
3573	RNO242781.IP3K-B	ip3K-B	inositol 1,4,5-trisphosphate 3-kinase, isoform		ggg	atg	increased
3574	RNO242781.IP3K-B	ip3K-B	inositol 1,4,5-trisphosphate 3-kinase, isoform		ggg	atg	increased
3575	RNO242781.IP3K-B	ip3K-B	inositol 1,4,5-trisphosphate 3-kinase, isoform		ggg	atg	increased
3576	RNO242781.IP3K-B	ip3K-B	inositol 1,4,5-trisphosphate 3-kinase, isoform		ggg	atg	increased
3577	RNO242781.IP3K-B	ip3K-B	inositol 1,4,5-trisphosphate 3-kinase, isoform		ggg	atg	increased
3578	RNO242781.IP3K-B	ip3K-B	inositol 1,4,5-trisphosphate 3-kinase, isoform		gaa	tga	increased
3579	RNO242781.IP3K-B	ip3K-B	inositol 1,4,5-trisphosphate 3-kinase, isoform		gaa	tga	increased
3580	RNO242781.IP3K-B	ip3K-B	inositol 1,4,5-trisphosphate 3-kinase, isoform		gaa	tga	increased
3581	RNO242781.IP3K-B	ip3K-B	inositol 1,4,5-trisphosphate 3-kinase, isoform		gaa	tga	increased
3582	AB049151.PE1	nc	inositol hexakisphosphate kinase		ttc	cga	increased by mild
3583	AB049151.PE1	nc	inositol hexakisphosphate kinase		ttc	cga	increased by mild
3584	AB049151.PE1	nc	inositol hexakisphosphate kinase		ttc	cga	increased by mild
3585	AB049151.PE1	nc	inositol hexakisphosphate kinase		aaa	agg	increased by mild
3586	AB049151.PE1	nc	inositol hexakisphosphate kinase		aaa	agg	increased by mild
3587	AB049151.PE1	nc	inositol hexakisphosphate kinase		aaa	agg	increased by mild
3588	RNU26397.PE1	nc	inositol polyphosphate 4-phosphatase		aaa	tga	increased
3589	RNU26397.PE1	nc	inositol polyphosphate 4-phosphatase		aaa	tga	increased
3590	RNU26397.PE1	nc	inositol polyphosphate 4-phosphatase		aaa	ggt	increased
3591	RNU26397.PE1	nc	inositol polyphosphate 4-phosphatase		aaa	ggt	increased
3592	RNU26397.PE1	nc	inositol polyphosphate 4-phosphatase		aaa	ggt	increased
3593	RNITPR2R.ITPR2	ITPR2	inositol triphosphate receptor type 2		atg	tgc	increased
3594	RNITPR2R.ITPR2	ITPR2	inositol triphosphate receptor type 2		gag	ggg	increased
3595	RNITPR2R.ITPR2	ITPR2	inositol triphosphate receptor type 2		gag	ggg	increased
3596	RNITPR2R.ITPR2	ITPR2	inositol triphosphate receptor type 2		taa	tct	increased
3597	RNITPR2R.ITPR2	ITPR2	inositol triphosphate receptor type 2		taa	tct	increased
3598	RNITPR2R.ITPR2	ITPR2	inositol triphosphate receptor type 2		taa	tct	increased
3599	RATIRRB.PE1	nc	insulin receptor-related receptor-alpha subunit		ctc	agg	increased
3600	RATIRRB.PE1	nc	insulin receptor-related receptor-alpha subunit		ctc	agg	increased
3601	RATIRRB.PE1	nc	insulin receptor-related receptor-alpha subunit		ctc	agg	increased
3602	RATIRRB.PE1	nc	insulin receptor-related receptor-alpha subunit		ctc	agg	increased
3603	RATIRRB.PE1	nc	insulin receptor-related receptor-alpha subunit		ctc	agg	increased
3604	RATIRRB.PE1	nc	insulin receptor-related receptor-alpha subunit		gac	aga	increased
3605	RATIRRB.PE1	nc	insulin receptor-related receptor-alpha subunit		gac	aga	increased
3606	RATIRRB.PE1	nc	insulin receptor-related receptor-alpha subunit		gac	aga	increased
3607	RATIRRB.PE1	nc	insulin receptor-related receptor-alpha subunit		gcc	tgg	increased
3608	RATIRRB.PE1	nc	insulin receptor-related receptor-alpha subunit		gcc	tgg	increased
3609	RNINSDEGM.PE1	nc	insulin-degrading enzyme		tgt	cct	No change
3610	RNINSDEGM.PE1	nc	insulin-degrading enzyme		tgt	cct	No change
3611	RNINSDEGM.PE1	nc	insulin-degrading enzyme		tgt	cct	No change
3612	RNINSDEGM.PE1	nc	insulin-degrading enzyme		tgt	cct	No change
3613	RNINSDEGM.PE1	nc	insulin-degrading enzyme		tgt	cag	decreased
3614	RNINSDEGM.PE1	nc	insulin-degrading enzyme		tgt	cag	No change

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
3615	Taq1	62	tgt	141.58	142	0	141.63	141.53	0	4 700 000	29 100 000	=+	/	/	-(4) /(3) \(3)
3616	Taq1	62	tgt	142.67	142	142.75	142.75	142.51	5 200 000	9 500 000	70 300 000	=+	/ (-)		-(4) /(3) \(3)
3617	Taq1	50	aat	220.405	221	220.39	0	220.42	4 800 000	0	7 100 000	-+(=)	V		-(4) /(3) \(3)
3618	Taq1	50	aat	221.175	221	221.19	221.16	0	5 200 000	4 700 000	0	=-	\		-(4) /(3) \(3)
3619	Hha1	59	ttc	114.603	114	114.73	114.55	114.53	218.4	526.04	488.96	+=	/ (-)		-4
3620	Hha1	61	tct	114.59	114	114.59	0	0	3 400 000	0	0	-=	\		-4
3621	Hha1	6	aga	117.44	118	0	0	117.44	0	0	9 400 000	=+	/		-4
3622	Hha1	6	aga	118.04	118	118.11	0	117.97	49 700 000	0	40 700 000	-+(=)	V		-4
3623	Taq1	48	ggg	135.38	136	135.33	135.45	135.36	3 666.24	2 101.34	1 558.82	==	-		-4
3624	Hha1	3	aac	137.2	137	137.21	137.05	137.34	9 800 000	10 400 000	7 300 000	==	-		-4
3625	Taq1	56	tga	157.19	157	157.19	0	0	3 300 000	0	0	-=	\		-4
3626	Hha1	40	tgg	242.917	244	242.9	242.91	242.94	33 800 000	14 700 000	13 400 000	-=	\ (-)		-4
3627	Hha1	40	tgg	243.765	244	243.61	243.92	0	7 100 000	5 000 000	0	=-	\		-4
3628	Hha1	60	ttg	117.71	118	117.87	117.49	117.77	4 900 000	4 100 000	3 800 000	==	-		-2
3629	Taq1	19	cac	126.637	127	126.66	126.65	126.6	3 100 000	5 000 000	20 700 000	=+	/ (-)		-2
3630	Taq1	19	cac	127.64	127	127.65	127.6	127.67	3 700 000	5 100 000	6 200 000	==	-		-2
3631	Taq1	52	att	361.25	363	361.25	0	0	3 800 000	0	0	-=	\		-2
3632	Taq1	52	att	361.95	363	361.95	0	0	3 800 000	0	0	-=	\		-2
3633	Hha1	60	ttg	117.71	118	117.87	117.49	117.77	4 900 000	4 100 000	3 800 000	==	-		-2
3634	Taq1	19	cac	126.637	127	126.66	126.65	126.6	3 100 000	5 000 000	20 700 000	=+	/ (-)		-2
3635	Taq1	19	cac	127.64	127	127.65	127.6	127.67	3 700 000	5 100 000	6 200 000	==	-		-2
3636	Taq1	52	att	361.25	363	361.25	0	0	3 800 000	0	0	-=	\		-2
3637	Taq1	52	att	361.95	363	361.95	0	0	3 800 000	0	0	-=	\		-2
3638	Hha1	60	ttg	117.71	118	117.87	117.49	117.77	4 900 000	4 100 000	3 800 000	==	-		-2
3639	Taq1	19	cac	126.637	127	126.66	126.65	126.6	3 100 000	5 000 000	20 700 000	=+	/ (-)		-2
3640	Taq1	19	cac	127.64	127	127.65	127.6	127.67	3 700 000	5 100 000	6 200 000	==	-		-2
3641	Taq1	25	cat	110.43	111	0	110.43	0	0	827.49	0	+-	A		\(4) A(4)
3642	Taq1	25	cat	111.293	111	111.29	111.32	111.27	586.87	1 273.07	1 019.56	+=	/ (-)		\(4) A(4)
3643	Hha1	25	cag	151.42	152	151.53	151.27	151.46	11 800 000	9 200 000	9 600 000	==	-		\(4) A(4)
3644	Hha1	25	cag	152.38	152	152.34	152.36	152.44	5 000 000	9 500 000	4 000 000	+-	A		\(4) A(4)
3645	Taq1	31	gac	151.82	152	151.97	151.67	0	6 200 000	9 800 000	0	=-	\		\(4) A(4)
3646	Taq1	31	gac	152.9	152	153.08	152.72	0	4 300 000	10 900 000	0	+-	A		\(4) A(4)
3647	Hha1	41	ccc	171.5	172	171.5	0	0	4 900 000	0	0	-=	\		\(4) A(4)
3648	Hha1	41	ccc	172.593	172	172.5	172.61	172.67	9 500 000	3 600 000	3 500 000	-=	\ (-)		\(4) A(4)
3649	Hha1	39	agg	176.94	177	0	177.1	176.78	0	310.46	236	+=	/		\(4) A(4)
3650	Hha1	26	ctg	248.75	250	248.75	0	0	3 600 000	0	0	-=	\		\(4) A(4)
3651	Hha1	49	aaa	249.51	251	249.52	249.5	0	4 000 000	8 700 000	0	+-	A		\(4) A(4)
3652	Hha1	49	aaa	251.18	251	251.1	251.26	0	24 500 000	3 900 000	0	-=	\		\(4) A(4)
3653	Hha1	49	aaa	252.22	251	0	252.22	0	0	7 600 000	0	+-	A		\(4) A(4)
3654	Hha1	41	ccc	97.215	97	97.25	97.18	0	7 100 000	7 300 000	0	=-	\		/(2) \(2)
3655	Hha1	39	agg	172.59	172	0	0	172.59	0	0	231.93	=+	/		/(2) \(2)
3656	Taq1	29	gca	227.715	228	227.65	227.78	0	3 000 000	3 100 000	0	=-	\		/(2) \(2)
3657	Taq1	29	gca	228.87	228	0	0	228.87	0	0	3 100 000	=+	/		/(2) \(2)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
3615	RNINSDEGM.PE1	nc	insulin-degrading enzyme		tgt	cag	decreased
3616	RNINSDEGM.PE1	nc	insulin-degrading enzyme		tgt	cag	No change
3617	RNINSDEGM.PE1	nc	insulin-degrading enzyme		cgt	aat	No change
3618	RNINSDEGM.PE1	nc	insulin-degrading enzyme		cgt	aat	No change
3619	RATIGFIRT.PE1	nc	insulin-like growth factor I receptor precursor		tct	ttc	No change
3620	RATIGFIRT.PE1	nc	insulin-like growth factor I receptor precursor		tct	ttc	No change
3621	RATIGFIRT.PE1	nc	insulin-like growth factor I receptor precursor		gag	aga	No change
3622	RATIGFIRT.PE1	nc	insulin-like growth factor I receptor precursor		gag	aga	No change
3623	RATIGFIRT.PE1	nc	insulin-like growth factor I receptor precursor		ggg	aac	No change
3624	RATIGFIRT.PE1	nc	insulin-like growth factor I receptor precursor		ggg	aac	No change
3625	RATIGFIRT.PE1	nc	insulin-like growth factor I receptor precursor		ttc	tga	No change
3626	RATIGFIRT.PE1	nc	insulin-like growth factor I receptor precursor		tgg	ata	No change
3627	RATIGFIRT.PE1	nc	insulin-like growth factor I receptor precursor		tgg	ata	No change
3628	RATIGFII5.IGFII	IGFII	insulin-like growth factor II	*	aga	ttg	No change
3629	RATIGFII5.IGFII	IGFII	insulin-like growth factor II	*	cac	gct	No change
3630	RATIGFII5.IGFII	IGFII	insulin-like growth factor II	*	cac	gct	No change
3631	RATIGFII5.IGFII	IGFII	insulin-like growth factor II	*	tgt	att	No change
3632	RATIGFII5.IGFII	IGFII	insulin-like growth factor II	*	tgt	att	No change
3633	RATIGFIIA3.IGFII	IGFII	insulin-like growth factor II	*	aga	ttg	No change
3634	RATIGFIIA3.IGFII	IGFII	insulin-like growth factor II	*	cac	gct	No change
3635	RATIGFIIA3.IGFII	IGFII	insulin-like growth factor II	*	cac	gct	No change
3636	RATIGFIIA3.IGFII	IGFII	insulin-like growth factor II	*	tgt	att	No change
3637	RATIGFIIA3.IGFII	IGFII	insulin-like growth factor II	*	tgt	att	No change
3638	RNIGFIIAA.IGFII	IGFII	insulin-like growth factor II gene	*	aga	ttg	No change
3639	RNIGFIIAA.IGFII	IGFII	insulin-like growth factor II gene	*	cac	gct	No change
3640	RNIGFIIAA.IGFII	IGFII	insulin-like growth factor II gene	*	cac	gct	No change
3641	RNIAC.PE1	nc	integrin alpha chain		tac	cat	increased
3642	RNIAC.PE1	nc	integrin alpha chain		tac	cat	increased
3643	RNIAC.PE1	nc	integrin alpha chain		cag	gac	increased
3644	RNIAC.PE1	nc	integrin alpha chain		cag	gac	increased
3645	RNIAC.PE1	nc	integrin alpha chain		cag	gac	increased
3646	RNIAC.PE1	nc	integrin alpha chain		cag	gac	increased
3647	RNIAC.PE1	nc	integrin alpha chain		ccc	aca	increased
3648	RNIAC.PE1	nc	integrin alpha chain		ccc	aca	increased
3649	RNIAC.PE1	nc	integrin alpha chain		agg	atg	increased
3650	RNIAC.PE1	nc	integrin alpha chain		ctg	aaa	increased
3651	RNIAC.PE1	nc	integrin alpha chain		ctg	aaa	increased
3652	RNIAC.PE1	nc	integrin alpha chain		ctg	aaa	increased
3653	RNIAC.PE1	nc	integrin alpha chain		ctg	aaa	increased
3654	RNU60096.PE1	RATINTB4R	integrin beta 4 subunit precursor		ccc	tcc	decreased
3655	RNU60096.PE1	RATINTB4R	integrin beta 4 subunit precursor		aac	agg	decreased
3656	RNU60096.PE1	RATINTB4R	integrin beta 4 subunit precursor		gca	tgg	decreased
3657	RNU60096.PE1	RATINTB4R	integrin beta 4 subunit precursor		gca	tgg	decreased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
3658	Taq1	45	gcc	104.085	104	104.09	104.08	0	14 200 000	24 700 000	0	=-	\		\(2)
3659	Taq1	21	acc	104.81	105	0	104.81	0	0	6 400 000	0	+-	A		\(2)
3660	Taq1	21	acc	105.44	105	105.35	105.44	105.53	108 600 000	93 300 000	16 000 000	=-	\ (-)		\(2)
3661	Taq1	12	agt	97.363	97	97.39	97.43	97.27	9 900 000	11 900 000	3 100 000	=-	\ (-)		-3
3662	Hha1	33	agc	122.127	122	122.29	122.07	122.02	3 600 000	5 300 000	7 000 000	==	-		-3
3663	Taq1	56	tga	214.755	216	214.8	214.71	0	5 900 000	5 600 000	0	=-	\		-3
3664	Taq1	56	tga	215.765	216	215.8	215.73	0	3 300 000	7 600 000	0	+-	A		-3
3665	Taq1	56	tga	216.81	216	0	216.81	0	0	9 200 000	0	+-	A		-3
3666	Taq1	64	gtt	215.51	216	215.47	215.63	215.43	4 100 000	3 400 000	3 200 000	==	-		-3
3667	Taq1	64	gtt	216.533	216	216.5	216.51	216.59	4 200 000	4 000 000	3 500 000	==	-		-3
3668	Hha1	26	ctg	126.61	127	126.75	126.75	126.33	29 700 000	8 000 000	5 600 000	-=	\ (-)		\(2)
3669	Hha1	26	ctg	127.69	127	127.69	0	0	3 600 000	0	0	-=	\		\(2)
3670	Hha1	33	agc	126.97	127	127.07	0	126.87	3 000 000	0	9 600 000	=+(+)	/		\(2)
3671	Hha1	40	tgg	238.06	239	0	238.06	0	0	3 900 000	0	+-	A		\(2)
3672	Hha1	40	tgg	238.845	239	238.71	238.98	0	3 900 000	3 200 000	0	=-	\		\(2)
3673	Hha1	40	tgg	239.97	239	239.97	0	0	4 500 000	0	0	-=	\		\(2)
3674	Taq1	56	tga	87.863	88	87.7	87.87	88.02	6 500 000	7 900 000	15 400 000	=+	/ (-)		-(3) \(2)
3675	Hha1	6	aga	162.405	163	162.45	0	162.36	4 500 000	0	5 900 000	-+(=)	V		-(3) \(2)
3676	Hha1	6	aga	163.67	163	163.92	163.51	163.58	15 700 000	3 600 000	3 000 000	-=	\ (-)	(-)	-(3) \(2)
3677	Taq1	17	cca	162.45	163	162.45	0	0	218.26	0	0	-=	\		-(3) \(2)
3678	Taq1	17	cca	163.46	163	163.15	163.63	163.6	190.4	339.05	586.37	==	-	(-)	-(3) \(2)
3679	Hha1	10	atg	181.13	182	181.13	0	0	4 700 000	0	0	-=	\		\(6)
3680	Taq1	10	atg	181.19	182	0	181.19	0	0	3 500 000	0	+-	A		\(6)
3681	Taq1	10	atg	181.74	182	181.74	0	0	3 200 000	0	0	-=	\		\(6)
3682	Hha1	10	atg	181.97	182	181.97	0	0	4 200 000	0	0	-=	\		\(6)
3683	Taq1	10	atg	182.87	182	182.87	0	0	8 200 000	0	0	-=	\		\(6)
3684	Hha1	10	atg	182.99	182	182.99	0	0	4 100 000	0	0	-=	\		\(6)
3685	Hha1	8	gaa	251.45	252	0	251.45	0	0	3 600 000	0	+-	A		\(6)
3686	Hha1	8	gaa	251.07	252	0	251.07	0	0	3 500 000	0	+-	A		\(6)
3687	Hha1	8	gaa	252.2	252	252.2	0	0	3 200 000	0	0	-=	\		\(6)
3688	Taq1	8	gaa	251.63	252	0	251.63	0	0	3 500 000	0	+-	A		\(6)
3689	Taq1	39	agg	69.613	70	69.38	69.64	69.82	24 900 000	67 800 000	84 500 000	+=	/ (-)		/(3) -(2)
3690	Taq1	39	agg	70.4	70	70.42	70.26	70.52	9 400 000	87 500 000	138 100 000	+=	/ (-)		/(3) -(2)
3691	Taq1	39	agg	69.613	70	69.38	69.64	69.82	924.68	681.41	2 488.95	=+	/ (-)		/(3) -(2)
3692	Taq1	39	agg	70.4	70	70.42	70.26	70.52	349.07	879.4	4 067.74	=+	/ (-)		/(3) -(2)
3693	Taq1	47	ggc	106.71	107	0	0	106.71	0	0	2 915.76	=+	/		/(3) -(2)
3694	Taq1	17	cca	107.653	108	107.65	107.71	107.6	775.55	472.01	1 774.16	=+	/ (-)		/(3) -(2)
3695	Taq1	45	gcc	64.753	65	64.91	64.6	64.75	13 900 000	6 600 000	3 300 000	-=	\ (-)		-(2) \(2)
3696	Taq1	9	atc	65.75	66	65.77	65.73	0	7 100 000	3 900 000	0	--	\		-(2) \(2)
3697	Hha1	44	cgg	69.333	69	69.35	69.13	69.52	6 600 000	6 300 000	4 600 000	==	-		-(2) \(2)
3698	Taq1	44	cgg	147.347	148	147.47	147.4	147.17	607.57	1 292.08	762.16	+=	/ (-)		A(3)
3699	Taq1	44	cgg	148.21	148	0	0	148.21	0	0	1 120.82	=+	/		A(3)
3700	Taq1	44	cgg	148.845	148	148.74	148.95	0	642.29	1 327.97	0	+-	A	A	A(3)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
3658	RNINT3REC.PE1	nc	interleukin-3 receptor beta-subunit		gcc	acc	increased
3659	RNINT3REC.PE1	nc	interleukin-3 receptor beta-subunit		gcc	acc	increased
3660	RNINT3REC.PE1	nc	interleukin-3 receptor beta-subunit		gcc	acc	increased
3661	AB022331.PE1	nc	ion channel		gga	agt	No change
3662	AB022331.PE1	nc	ion channel		att	agc	No change
3663	AB022331.PE1	nc	ion channel		tga	gtt	No change
3664	AB022331.PE1	nc	ion channel		tga	gtt	No change
3665	AB022331.PE1	nc	ion channel		tga	gtt	No change
3666	AB022331.PE1	nc	ion channel		tga	gtt	No change
3667	AB022331.PE1	nc	ion channel		tga	gtt	No change
3668	AB022332.PE1	nc	ion channel		ctg	agc	increased
3669	AB022332.PE1	nc	ion channel		ctg	agc	increased
3670	AB022332.PE1	nc	ion channel		ctg	agc	increased
3671	AB022332.PE1	nc	ion channel		tgg	act	increased
3672	AB022332.PE1	nc	ion channel		tgg	act	increased
3673	AB022332.PE1	nc	ion channel		tgg	act	increased
3674	RNO309926.PE1	asic 1b	ion channel		agc	tga	No change
3675	RNO309926.PE1	asic 1b	ion channel		cca	aga	No change
3676	RNO309926.PE1	asic 1b	ion channel		cca	aga	No change
3677	RNO309926.PE1	asic 1b	ion channel		cca	aga	No change
3678	RNO309926.PE1	asic 1b	ion channel		cca	aga	No change
3679	RNIP3.PE1	nc	IP3 3-kinase		ggg	atg	increased
3680	RNIP3.PE1	nc	IP3 3-kinase		ggg	atg	increased
3681	RNIP3.PE1	nc	IP3 3-kinase		ggg	atg	increased
3682	RNIP3.PE1	nc	IP3 3-kinase		ggg	atg	increased
3683	RNIP3.PE1	nc	IP3 3-kinase		ggg	atg	increased
3684	RNIP3.PE1	nc	IP3 3-kinase		ggg	atg	increased
3685	RNIP3.PE1	nc	IP3 3-kinase		gaa	tga	increased
3686	RNIP3.PE1	nc	IP3 3-kinase		gaa	tga	increased
3687	RNIP3.PE1	nc	IP3 3-kinase		gaa	tga	increased
3688	RNIP3.PE1	nc	IP3 3-kinase		gaa	tga	increased
3689	AF118818.PE1	nc	IPR328 protein		agg	ttt	decreased
3690	AF118818.PE1	nc	IPR328 protein		agg	ttt	decreased
3691	AF118818.PE1	nc	IPR328 protein		agg	ttt	decreased
3692	AF118818.PE1	nc	IPR328 protein		agg	ttt	decreased
3693	AF118818.PE1	nc	IPR328 protein		cca	ggc	decreased
3694	AF118818.PE1	nc	IPR328 protein		cca	ggc	decreased
3695	AF108959.IB1	IB1	islet-brain 1		atc	gcc	No change
3696	AF108959.IB1	IB1	islet-brain 1		atc	gcc	No change
3697	AF108959.IB1	IB1	islet-brain 1		cgg	tac	No change
3698	RATJAPR.PE1	nc	jagged protein		cgg	cat	increased by mild
3699	RATJAPR.PE1	nc	jagged protein		cgg	cat	increased by mild
3700	RATJAPR.PE1	nc	jagged protein		cgg	cat	increased by mild

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
3701	Taq1	25	cat	148.815	149	148.78	148.85	0	511.8	1 871.41	0	+-	A	A	A(3)
3702	Taq1	25	cat	149.51	149	149.72	0	149.3	1 235.15	0	1 350.23	-+(=)	V		A(3)
3703	Taq1	25	cat	149.87	149	0	149.87	0	0	649.26	0	+-	A		A(3)
3704	Taq1	56	tga	151.42	151	0	0	151.42	0	0	3 000 000	=+	/		A(3)
3705	Taq1	62	tgt	150.873	151	150.89	150.91	150.82	6 000 000	13 600 000	5 600 000	+-	A		A(3)
3706	Hha1	40	tgg	252.785	253	252.6	0	252.97	6 600 000	0	5 200 000	-+(=)	V		A(3)
3707	Hha1	40	tgg	253.49	253	253.49	0	0	7 300 000	0	0	-=	\		A(3)
3708	Hha1	40	tgg	254.44	253	254.41	254.47	0	3 900 000	6 300 000	0	=-	\		A(3)
3709	Taq1	45	gcc	64.753	65	64.91	64.6	64.75	13 900 000	6 600 000	3 300 000	-=	\ (-)		-(2) \(2)
3710	Taq1	9	atc	65.75	66	65.77	65.73	0	7 100 000	3 900 000	0	--	\		-(2) \(2)
3711	Hha1	44	cgg	69.333	69	69.35	69.13	69.52	6 600 000	6 300 000	4 600 000	==	-		-(2) \(2)
3712	Taq1	45	gcc	64.753	65	64.91	64.6	64.75	13 900 000	6 600 000	3 300 000	-=	\ (-)		-(2) \(2)
3713	Taq1	9	atc	65.75	66	65.77	65.73	0	7 100 000	3 900 000	0	--	\		-(2) \(2)
3714	Hha1	44	cgg	69.333	69	69.35	69.13	69.52	6 600 000	6 300 000	4 600 000	==	-		-(2) \(2)
3715	Taq1	45	gcc	64.753	65	64.91	64.6	64.75	13 900 000	6 600 000	3 300 000	-=	\ (-)		\(3)
3716	Taq1	9	atc	65.75	66	65.77	65.73	0	7 100 000	3 900 000	0	--	\		\(3)
3717	Hha1	44	cgg	69.333	69	69.35	69.13	69.52	6 600 000	6 300 000	4 600 000	==	-		\(3)
3718	Taq1	45	gcc	273.6	274	273.6	0	0	7 500 000	0	0	-=	\		\(3)
3719	Taq1	45	gcc	274.97	274	274.97	0	0	6 300 000	0	0	-=	\		\(3)
3720	Hha1	26	ctg	103.745	104	103.68	0	103.81	6 400 000	0	8 300 000	-+(=)	V		\(2)
3721	Hha1	26	ctg	104.535	104	104.54	104.53	0	10 900 000	3 300 000	0	-=	\		\(2)
3722	Hha1	26	ctg	118.97	119	118.97	118.97	118.97	9 400 000	7 800 000	5 400 000	==	-		\(2)
3723	Hha1	59	ttc	133.55	134	0	133.55	0	0	238.58	0	+-	A		\(2)
3724	Hha1	59	ttc	134.335	134	134.37	134.3	0	166.4	103.48	0	=-	\		\(2)
3725	Hha1	20	ctc	86.105	86	0	86.13	86.08	0	1 180.17	1 693.7	+=	/	/	/(3)
3726	Hha1	39	agg	85.905	86	0	86.1	85.71	0	991.1	895.18	+=	/	/	/(3)
3727	Hha1	39	agg	86.31	86	86.31	0	0	791.78	0	0	-=	\		/(3)
3728	Hha1	33	agc	197.52	198	0	0	197.52	0	0	5 600 000	=+	/		/(3)
3729	Hha1	33	agc	198.51	198	0	0	198.51	0	0	6 500 000	=+	/		/(3)
3730	Hha1	40	tgg	102.66	103	102.77	102.55	0	17 300 000	10 800 000	0	=-	\		/(4) \(4)
3731	Hha1	26	ctg	105.54	106	105.54	0	0	3 100 000	0	0	-=	\		/(4) \(4)
3732	Hha1	26	ctg	106.53	106	0	106.53	0	0	3 100 000	0	+-	A		/(4) \(4)
3733	Hha1	33	agc	105.77	106	0	0	105.77	0	0	22 500 000	=+	/		/(4) \(4)
3734	Hha1	56	tga	108.47	109	108.72	108.22	0	531.19	236.67	0	-=	\		/(4) \(4)
3735	Hha1	56	tga	108.93	109	0	109.03	108.83	0	886.17	741.25	+=	/		/(4) \(4)
3736	Hha1	56	tga	110.727	111	110.67	110.86	110.65	404.52	4 023.55	5 378.38	+=	/ (-)		/(4) \(4)
3737	Hha1	56	tga	111.28	111	111.28	0	0	645.6	0	0	-=	\		/(4) \(4)
3738	Hha1	41	ccc	218.12	218	0	0	218.12	0	0	3 000 000	=+	/		/(4) \(4)
3739	Hha1	41	ccc	218.96	218	0	0	218.96	0	0	3 000 000	=+	/		/(4) \(4)
3740	Taq1	48	ggg	113.37	114	0	113.37	0	0	2 563.64	0	+-	A		A(3) \(3)
3741	Taq1	48	ggg	114.2	114	114.2	114.2	0	1 485.46	1 464.93	0	=-	\		A(3) \(3)
3742	Hha1	6	aga	114.53	115	0	114.53	0	0	11 200 000	0	+-	A		A(3) \(3)
3743	Hha1	6	aga	114.53	115	0	114.53	0	0	11 200 000	0	+-	A		A(3) \(3)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
3701	RATJAPR.PE1	nc	jagged protein		cgg	cat	increased by mild
3702	RATJAPR.PE1	nc	jagged protein		cgg	cat	increased by mild
3703	RATJAPR.PE1	nc	jagged protein		cgg	cat	increased by mild
3704	RATJAPR.PE1	nc	jagged protein		tga	tgt	increased by mild
3705	RATJAPR.PE1	nc	jagged protein		tga	tgt	increased by mild
3706	RATJAPR.PE1	nc	jagged protein		gaa	tgg	increased by mild
3707	RATJAPR.PE1	nc	jagged protein		gaa	tgg	increased by mild
3708	RATJAPR.PE1	nc	jagged protein		gaa	tgg	increased by mild
3709	AF109772.PE1	nc	JIP-1b		atc	gcc	No change
3710	AF109772.PE1	nc	JIP-1b		atc	gcc	No change
3711	AF109772.PE1	nc	JIP-1b		cgg	tac	No change
3712	AF109773.PE1	nc	JIP-1c		atc	gcc	No change
3713	AF109773.PE1	nc	JIP-1c		atc	gcc	No change
3714	AF109773.PE1	nc	JIP-1c		cgg	tac	No change
3715	AF109774.PE1	nc	JIP-2a		atc	gcc	increased
3716	AF109774.PE1	nc	JIP-2a		atc	gcc	increased
3717	AF109774.PE1	nc	JIP-2a		cgg	tac	increased
3718	AF109774.PE1	nc	JIP-2a		gcc	tca	increased
3719	AF109774.PE1	nc	JIP-2a		gcc	tca	increased
3720	RNPJUNB.PJUNB	pJunB	Jun B protein		ggg	ctg	increased
3721	RNPJUNB.PJUNB	pJunB	Jun B protein		ggg	ctg	increased
3722	RNPJUNB.PJUNB	pJunB	Jun B protein		ctg	cac	increased
3723	RNPJUNB.PJUNB	pJunB	Jun B protein		ttc	tcc	increased
3724	RNPJUNB.PJUNB	pJunB	Jun B protein		ttc	tcc	increased
3725	RNU53450.JDP-1	jdp-1	Jun dimerization protein 1 JDP-1		agg	ctc	decreased
3726	RNU53450.JDP-1	jdp-1	Jun dimerization protein 1 JDP-1		agg	ctc	decreased
3727	RNU53450.JDP-1	jdp-1	Jun dimerization protein 1 JDP-1		agg	ctc	decreased
3728	RNU53450.JDP-1	jdp-1	Jun dimerization protein 1 JDP-1		ctg	agc	decreased
3729	RNU53450.JDP-1	jdp-1	Jun dimerization protein 1 JDP-1		ctg	agc	decreased
3730	RATJUND.JUN-D	jun-D	Jun-D		tgg	ggg	decreased
3731	RATJUND.JUN-D	jun-D	Jun-D		ctg	agc	decreased
3732	RATJUND.JUN-D	jun-D	Jun-D		ctg	agc	decreased
3733	RATJUND.JUN-D	jun-D	Jun-D		ctg	agc	decreased
3734	RATJUND.JUN-D	jun-D	Jun-D		tga	gaa	decreased
3735	RATJUND.JUN-D	jun-D	Jun-D		tga	gaa	decreased
3736	RATJUND.JUN-D	jun-D	Jun-D		tga	aat	decreased
3737	RATJUND.JUN-D	jun-D	Jun-D		tga	aat	decreased
3738	RATJUND.JUN-D	jun-D	Jun-D		ccc	ctt	decreased
3739	RATJUND.JUN-D	jun-D	Jun-D		ccc	ctt	decreased
3740	RATSHIIIA.PE1	KShIIIa	K+ channel protein		ggg	aga	increased by mild
3741	RATSHIIIA.PE1	KShIIIa	K+ channel protein		ggg	aga	increased by mild
3742	RATSHIIIA.PE1	KShIIIa	K+ channel protein		ggg	aga	increased by mild
3743	RATSHIIIA.PE1	KShIIIa	K+ channel protein		ggg	aga	increased by mild

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
3744	Hha1	6	aga	115.065	115	115.05	0	115.08	16 900 000	0	4 400 000	-=(-)	\		A(3) \(3)
3745	Hha1	6	aga	115.065	115	115.05	0	115.08	16 900 000	0	4 400 000	-=(-)	\		A(3) \(3)
3746	Hha1	6	aga	115.65	115	115.64	115.66	0	9 500 000	3 500 000	0	-=	\		A(3) \(3)
3747	Hha1	6	aga	115.65	115	115.64	115.66	0	9 500 000	3 500 000	0	-=	\		A(3) \(3)
3748	Hha1	6	aga	126.475	127	126.51	0	126.44	89 200 000	0	7 100 000	-=(-)	\		A(3) \(3)
3749	Hha1	6	aga	127.097	127	127.18	127.06	127.05	30 600 000	3 500 000	5 400 000	-=	\ (-)		A(3) \(3)
3750	Hha1	6	aga	127.6	127	0	127.54	127.66	0	3 100 000	6 300 000	++	/		A(3) \(3)
3751	Taq1	8	gaa	259.31	259	0	259.31	0	0	3 100 000	0	+-	A		A(3) \(3)
3752	Taq1	48	ggg	113.37	114	0	113.37	0	0	2 563.64	0	+-	A		A(4)
3753	Taq1	48	ggg	114.2	114	114.2	114.2	0	1 485.46	1 464.93	0	=-	\		A(4)
3754	Hha1	6	aga	114.53	115	0	114.53	0	0	11 200 000	0	+-	A		A(4)
3755	Hha1	6	aga	114.53	115	0	114.53	0	0	11 200 000	0	+-	A		A(4)
3756	Hha1	6	aga	115.065	115	115.05	0	115.08	16 900 000	0	4 400 000	-=(-)	\		A(4)
3757	Hha1	6	aga	115.065	115	115.05	0	115.08	16 900 000	0	4 400 000	-=(-)	\		A(4)
3758	Hha1	6	aga	115.65	115	115.64	115.66	0	9 500 000	3 500 000	0	-=	\		A(4)
3759	Hha1	6	aga	115.65	115	115.64	115.66	0	9 500 000	3 500 000	0	-=	\		A(4)
3760	Hha1	6	aga	126.475	127	126.51	0	126.44	89 200 000	0	7 100 000	-=(-)	\		A(4)
3761	Hha1	6	aga	127.097	127	127.18	127.06	127.05	30 600 000	3 500 000	5 400 000	-=	\ (-)		A(4)
3762	Hha1	6	aga	127.6	127	0	127.54	127.66	0	3 100 000	6 300 000	++	/		A(4)
3763	Hha1	20	ctc	166.875	167	166.87	166.88	0	268.59	747.44	0	+-	A		A(4)
3764	Hha1	20	ctc	167.745	167	0	167.76	167.73	0	524.52	489.02	+=	/		A(4)
3765	Hha1	59	ttc	167.38	167	0	167.38	167.38	0	215.59	2 054.17	=+	/		A(4)
3766	Taq1	8	gaa	259.31	259	0	259.31	0	0	3 100 000	0	+-	A		A(4)
3767	Taq1	55	tca	99.785	100	99.64	99.93	0	5 400 000	3 000 000	0	=-	\		\(6)
3768	Hha1	55	tca	99.853	100	99.85	99.84	99.87	9 600 000	7 000 000	3 200 000	==	-		\(6)
3769	Taq1	56	tga	100.495	100	100.4	100.59	0	5 100 000	9 000 000	0	=-	\		\(6)
3770	Taq1	56	tga	99.73	100	0	99.73	0	0	4 600 000	0	+-	A		\(6)
3771	Hha1	6	aga	128.355	129	128.33	128.38	0	16 000 000	6 100 000	0	-=	\		\(6)
3772	Hha1	6	aga	128.907	129	128.97	128.86	128.89	35 300 000	4 300 000	9 300 000	-=	\ (-)		\(6)
3773	Hha1	6	aga	129.19	129	0	129.19	0	0	5 000 000	0	+-	A		\(6)
3774	Taq1	63	ctt	128.935	129	128.91	0	128.96	3 500 000	0	3 500 000	-+(=)	V		\(6)
3775	Taq1	64	gtt	133.773	134	133.77	133.8	133.75	9 800 000	9 500 000	7 200 000	==	-		\(6)
3776	Taq1	64	gtt	134.737	134	134.76	134.71	134.74	13 300 000	19 000 000	4 900 000	=-	\ (-)		\(6)
3777	Hha1	20	ctc	188.13	189	188.13	0	0	309.91	0	0	-=	\		\(6)
3778	Hha1	20	ctc	189.2	189	189.2	0	0	337.46	0	0	-=	\		\(6)
3779	Taq1	49	aaa	202.825	204	202.73	202.92	0	15 400 000	10 900 000	0	=-	\		\(6)
3780	Taq1	49	aaa	203.925	204	203.9	203.95	0	34 000 000	3 200 000	0	-=	\		\(6)
3781	Taq1	49	aaa	204.37	204	0	204.37	0	0	3 300 000	0	+-	A		\(6)
3782	Taq1	49	aaa	204.94	204	204.94	0	0	51 100 000	0	0	-=	\		\(6)
3783	Hha1	44	cgg	72.173	72	72.07	72.24	72.21	157 200 000	31 700 000	60 300 000	-=	\ (-)		-8
3784	Hha1	33	agc	72.64	73	0	0	72.64	0	0	33 300 000	=+	/		-8
3785	Hha1	44	cgg	77.89	78	77.89	0	0	3 200 000	0	0	-=	\		-8
3786	Hha1	44	cgg	83.6	84	83.72	83.48	0	10 900 000	6 800 000	0	=-	\		-8

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
3744	RATSHIIIA.PE1	KShIIIa	K+ channel protein		ggg	aga	increased by mild
3745	RATSHIIIA.PE1	KShIIIa	K+ channel protein		ggg	aga	increased by mild
3746	RATSHIIIA.PE1	KShIIIa	K+ channel protein		ggg	aga	increased by mild
3747	RATSHIIIA.PE1	KShIIIa	K+ channel protein		ggg	aga	increased by mild
3748	RATSHIIIA.PE1	KShIIIa	K+ channel protein		tcg	aga	increased by mild
3749	RATSHIIIA.PE1	KShIIIa	K+ channel protein		tcg	aga	increased by mild
3750	RATSHIIIA.PE1	KShIIIa	K+ channel protein		tcg	aga	increased by mild
3751	RATSHIIIA.PE1	KShIIIa	K+ channel protein		gaa	agc	increased by mild
3752	RATSHIIIC.PE1	KSHIIIA3	K+ channel protein	*	ggg	aga	increased by mild
3753	RATSHIIIC.PE1	KSHIIIA3	K+ channel protein	*	ggg	aga	increased by mild
3754	RATSHIIIC.PE1	KSHIIIA3	K+ channel protein	*	ggg	aga	increased by mild
3755	RATSHIIIC.PE1	KSHIIIA3	K+ channel protein	*	ggg	aga	increased by mild
3756	RATSHIIIC.PE1	KSHIIIA3	K+ channel protein	*	ggg	aga	increased by mild
3757	RATSHIIIC.PE1	KSHIIIA3	K+ channel protein	*	ggg	aga	increased by mild
3758	RATSHIIIC.PE1	KSHIIIA3	K+ channel protein	*	ggg	aga	increased by mild
3759	RATSHIIIC.PE1	KSHIIIA3	K+ channel protein	*	ggg	aga	increased by mild
3760	RATSHIIIC.PE1	KSHIIIA3	K+ channel protein	*	tcg	aga	increased by mild
3761	RATSHIIIC.PE1	KSHIIIA3	K+ channel protein	*	tcg	aga	increased by mild
3762	RATSHIIIC.PE1	KSHIIIA3	K+ channel protein	*	tcg	aga	increased by mild
3763	RATSHIIIC.PE1	KSHIIIA3	K+ channel protein	*	ttc	ctc	increased by mild
3764	RATSHIIIC.PE1	KSHIIIA3	K+ channel protein	*	ttc	ctc	increased by mild
3765	RATSHIIIC.PE1	KSHIIIA3	K+ channel protein	*	ttc	ctc	increased by mild
3766	RATSHIIIC.PE1	KSHIIIA3	K+ channel protein	*	gaa	agc	increased by mild
3767	RNGLUR6.PE1	nc	kainate receptor		tca	tga	increased
3768	RNGLUR6.PE1	nc	kainate receptor		tca	tga	increased
3769	RNGLUR6.PE1	nc	kainate receptor		tca	tga	increased
3770	RNGLUR6.PE1	nc	kainate receptor		tca	tga	increased
3771	RNGLUR6.PE1	nc	kainate receptor		ctt	aga	increased
3772	RNGLUR6.PE1	nc	kainate receptor		ctt	aga	increased
3773	RNGLUR6.PE1	nc	kainate receptor		ctt	aga	increased
3774	RNGLUR6.PE1	nc	kainate receptor		ctt	aga	increased
3775	RNGLUR6.PE1	nc	kainate receptor		gtt	tat	increased
3776	RNGLUR6.PE1	nc	kainate receptor		gtt	tat	increased
3777	RNGLUR6.PE1	nc	kainate receptor		ctc	cag	increased
3778	RNGLUR6.PE1	nc	kainate receptor		ctc	cag	increased
3779	RNGLUR6.PE1	nc	kainate receptor		aaa	ttg	increased
3780	RNGLUR6.PE1	nc	kainate receptor		aaa	ttg	increased
3781	RNGLUR6.PE1	nc	kainate receptor		aaa	ttg	increased
3782	RNGLUR6.PE1	nc	kainate receptor		aaa	ttg	increased
3783	RNKA2.PE1	nc	kainate receptor		cgg	tcg	No change
3784	RNKA2.PE1	nc	kainate receptor		cct	agc	No change
3785	RNKA2.PE1	nc	kainate receptor		cac	cgg	No change
3786	RNKA2.PE1	nc	kainate receptor		ggt	cgg	No change

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
3787	Hha1	44	cgg	84.433	84	84.62	84.37	84.31	10 200 000	9 000 000	3 600 000	=-	\ (-)		-8
3788	Hha1	33	agc	88.273	88	88.16	88.2	88.46	57 000 000	40 900 000	16 400 000	==	-		-8
3789	Hha1	54	ttt	89.477	89	89.38	89.49	89.56	3 700 000	12 700 000	20 300 000	==	-		-8
3790	Hha1	39	agg	94.89	95	94.87	0	94.91	219.94	0	248.2	-+(=)	V		-8
3791	Hha1	20	ctc	106.183	106	106.14	106.28	106.13	1 342.97	813	1 073.47	==	-		-8
3792	Hha1	27	acg	105.62	106	105.62	0	0	9 100 000	0	0	-=	\		-8
3793	Hha1	32	gtc	135.94	136	136.02	136	135.8	3 863.05	2 024.41	373.04	-=	\ (-)		-8
3794	Hha1	39	agg	139.44	140	139.4	139.48	0	219.94	829.9	0	+-	A		-8
3795	Hha1	62	tgt	140.06	140	140.06	0	0	3 000 000	0	0	-=	\		-8
3796	Hha1	20	ctc	183.553	184	183.54	183.61	183.51	21 887.051	13 493.31	14 145.99	==	-	-	-8
3797	Hha1	20	ctc	184.51	184	0	184.55	184.47	0	1 101.49	1 932.25	+=	/		-8
3798	Hha1	59	ttc	183.483	184	183.53	183.45	183.47	18 627.141	12 282.97	7 932.11	==	-	-	-8
3799	Taq1	61	tct	147.96	148	148.04	147.78	148.06	3 000 000	12 800 000	5 500 000	+-	A	A	A(2)
3800	Taq1	62	tgt	147.845	148	147.88	147.81	0	5 500 000	10 900 000	0	+-	A	A	A(2)
3801	Taq1	62	tgt	148.743	148	148.83	148.75	148.65	11 800 000	22 000 000	5 400 000	+-	A		A(2)
3802	Taq1	61	tct	147.96	148	148.04	147.78	148.06	3 000 000	12 800 000	5 500 000	+-	A	A	A(2)
3803	Taq1	62	tgt	147.845	148	147.88	147.81	0	5 500 000	10 900 000	0	+-	A	A	A(2)
3804	Taq1	62	tgt	148.743	148	148.83	148.75	148.65	11 800 000	22 000 000	5 400 000	+-	A		A(2)
3805	Taq1	61	tct	147.96	148	148.04	147.78	148.06	3 000 000	12 800 000	5 500 000	+-	A	A	A(2)
3806	Taq1	62	tgt	147.845	148	147.88	147.81	0	5 500 000	10 900 000	0	+-	A	A	A(2)
3807	Taq1	62	tgt	148.743	148	148.83	148.75	148.65	11 800 000	22 000 000	5 400 000	+-	A		A(2)
3808	Hha1	22	tcc	114.313	115	114.13	114.38	114.43	8 700 000	9 400 000	12 200 000	==	-	-	
3809	Taq1	22	tcc	114.36	115	114.26	114.34	114.48	11 500 000	12 200 000	9 500 000	==	-	-	
3810	Hha1	26	ctg	123.06	123	123.17	122.89	123.12	6 100 000	8 400 000	3 000 000	=-	\ (-)		\(9)
3811	Hha1	26	ctg	123.06	123	123.17	122.89	123.12	6 100 000	8 400 000	3 000 000	=-	\ (-)		\(9)
3812	Hha1	40	tgg	122.55	123	0	122.55	0	0	3 900 000	0	+-	A		\(9)
3813	Hha1	40	tgg	123.29	123	0	123.13	123.45	0	6 200 000	4 300 000	+=	/		\(9)
3814	Hha1	64	gtt	122.74	123	122.73	122.75	0	17 200 000	3 700 000	0	-=	\		\(9)
3815	Hha1	64	gtt	123.62	123	123.62	0	0	3 600 000	0	0	-=	\		\(9)
3816	Taq1	40	tgg	141.19	142	141.39	0	140.99	7 000 000	0	9 300 000	-+(=)	V		\(9)
3817	Taq1	40	tgg	142.03	142	0	0	142.03	0	0	10 400 000	=+	/		\(9)
3818	Taq1	56	tga	142.833	142	142.99	142.94	142.57	27 400 000	33 000 000	9 400 000	=-	\ (-)		\(9)
3819	Taq1	25	cat	171.74	172	171.84	171.64	0	771.12	445.57	0	=-	\		\(9)
3820	Taq1	41	ccc	182.87	183	0	182.87	0	0	21 100 000	0	+-	A		\(9)
3821	Taq1	41	ccc	183.885	183	183.84	183.93	0	4 400 000	4 800 000	0	=-	\		\(9)
3822	Taq1	62	tgt	183.84	184	0	184.04	183.64	0	3 800 000	9 000 000	=+	/		\(9)
3823	Taq1	18	cct	216.67	217	0	0	216.67	0	0	3 700 000	=+	/		\(9)
3824	Hha1	26	ctg	225.8	227	0	0	225.8	0	0	4 300 000	=+	/		\(9)
3825	Hha1	26	ctg	228.08	227	228.08	0	0	7 500 000	0	0	-=	\		\(9)
3826	Taq1	10	atg	279.235	278	279.29	279.18	0	4 900 000	4 400 000	0	=-	\		\(9)
3827	Hha1	7	caa	293.42	292	293.42	0	0	3 800 000	0	0	-=	\		\(9)
3828	Taq1	7	caa	293.52	292	0	293.52	0	0	3 200 000	0	+-	A		\(9)
3829	Hha1	3	aac	295.39	297	295.39	0	0	4 100 000	0	0	-=	\		\(9)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
3787	RNKA2.PE1	nc	kainate receptor		ggt	cgg	No change
3788	RNKA2.PE1	nc	kainate receptor		ttt	agc	No change
3789	RNKA2.PE1	nc	kainate receptor		ttt	agc	No change
3790	RNKA2.PE1	nc	kainate receptor		agc	agg	No change
3791	RNKA2.PE1	nc	kainate receptor		ctc	acg	No change
3792	RNKA2.PE1	nc	kainate receptor		ctc	acg	No change
3793	RNKA2.PE1	nc	kainate receptor		gtc	ccg	No change
3794	RNKA2.PE1	nc	kainate receptor		tgt	agg	No change
3795	RNKA2.PE1	nc	kainate receptor		tgt	agg	No change
3796	RNKA2.PE1	nc	kainate receptor		ctc	ttc	No change
3797	RNKA2.PE1	nc	kainate receptor		ctc	ttc	No change
3798	RNKA2.PE1	nc	kainate receptor		ctc	ttc	No change
3799	RATKALLA.PE1	nc	kallikrein		tct	tgt	increased by mild
3800	RATKALLA.PE1	nc	kallikrein		tct	tgt	increased by mild
3801	RATKALLA.PE1	nc	kallikrein		tct	tgt	increased by mild
3802	RNTKALRC.PE1	nc	kallikrein		tct	tgt	increased by mild
3803	RNTKALRC.PE1	nc	kallikrein		tct	tgt	increased by mild
3804	RNTKALRC.PE1	nc	kallikrein		tct	tgt	increased by mild
3805	D00446S3.PE1	nc	kallikrein precursor	*	tct	tgt	increased by mild
3806	D00446S3.PE1	nc	kallikrein precursor	*	tct	tgt	increased by mild
3807	D00446S3.PE1	nc	kallikrein precursor	*	tct	tgt	increased by mild
3808	AY342389.PE1	nc	keratin 5		tcc	tga	No change
3809	AY342389.PE1	nc	keratin 5		tcc	tga	No change
3810	AB053447.PE1	KIAA1774	KIAA1774 protein		tgg	ctg	increased
3811	AB053447.PE1	KIAA1774	KIAA1774 protein		tgg	ctg	increased
3812	AB053447.PE1	KIAA1774	KIAA1774 protein		tgg	ctg	increased
3813	AB053447.PE1	KIAA1774	KIAA1774 protein		tgg	ctg	increased
3814	AB053447.PE1	KIAA1774	KIAA1774 protein		gtt	ctg	increased
3815	AB053447.PE1	KIAA1774	KIAA1774 protein		gtt	ctg	increased
3816	AB053447.PE1	KIAA1774	KIAA1774 protein		tga	tgg	increased
3817	AB053447.PE1	KIAA1774	KIAA1774 protein		tga	tgg	increased
3818	AB053447.PE1	KIAA1774	KIAA1774 protein		tga	tgg	increased
3819	AB053447.PE1	KIAA1774	KIAA1774 protein		cat	aca	increased
3820	AB053447.PE1	KIAA1774	KIAA1774 protein		ccc	tgt	increased
3821	AB053447.PE1	KIAA1774	KIAA1774 protein		ccc	tgt	increased
3822	AB053447.PE1	KIAA1774	KIAA1774 protein		ccc	tgt	increased
3823	AB053447.PE1	KIAA1774	KIAA1774 protein		cct	tta	increased
3824	AB053447.PE1	KIAA1774	KIAA1774 protein		cag	ctg	increased
3825	AB053447.PE1	KIAA1774	KIAA1774 protein		cag	ctg	increased
3826	AB053447.PE1	KIAA1774	KIAA1774 protein		tgg	atg	increased
3827	AB053447.PE1	KIAA1774	KIAA1774 protein		caa	gct	increased
3828	AB053447.PE1	KIAA1774	KIAA1774 protein		caa	gct	increased
3829	AB053447.PE1	KIAA1774	KIAA1774 protein		aac	agg	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
3830	Taq1	39	agg	296.655	297	296.82	0	296.49	8 000 000	0	10 700 000	-+(=)	V		\(9)
3831	Taq1	39	agg	296.655	297	296.82	0	296.49	297.08	0	315.16	-+(=)	V		\(9)
3832	Taq1	39	agg	297.29	297	0	297.29	0	0	15 600 000	0	+-	A		\(9)
3833	Taq1	39	agg	297.29	297	0	297.29	0	0	156.78	0	+-	A		\(9)
3834	Hha1	6	aga	308.39	310	0	308.32	308.46	0	10 000 000	8 800 000	+=	/		\(9)
3835	Taq1	45	gcc	142.145	143	142.1	0	142.19	11 100 000	0	7 000 000	-+(=)	V		\(8)
3836	Taq1	45	gcc	143.37	143	143.53	0	143.21	5 200 000	0	3 000 000	-+(=)	V		\(8)
3837	Hha1	6	aga	143.277	144	143.37	143.3	143.16	10 800 000	5 000 000	3 900 000	-=	\ (-)		\(8)
3838	Hha1	6	aga	144.09	144	144.29	143.89	0	23 700 000	6 000 000	0	-=	\		\(8)
3839	Taq1	34	tgc	159.255	160	159.31	159.2	0	11 500 000	3 000 000	0	-=	\	\	\(8)
3840	Taq1	56	tga	159.2	160	159.28	159.12	0	19 700 000	15 700 000	0	=-	\	\	\(8)
3841	Taq1	56	tga	160.065	160	160.08	160.05	0	9 600 000	6 200 000	0	=-	\		\(8)
3842	Taq1	39	agg	161.31	162	0	161.31	0	0	8 500 000	0	+-	A		\(8)
3843	Taq1	39	agg	162.23	162	162.23	0	0	6 900 000	0	0	-=	\		\(8)
3844	Taq1	39	agg	162.23	162	162.23	0	0	256.23	0	0	-=	\		\(8)
3845	Taq1	39	agg	162.87	162	0	162.87	0	0	19 600 000	0	+-	A		\(8)
3846	Taq1	39	agg	161.31	162	0	161.31	0	0	85.42	0	+-	A		\(8)
3847	Taq1	39	agg	162.87	162	0	162.87	0	0	196.98	0	+-	A		\(8)
3848	Taq1	56	tga	176.74	177	176.74	0	0	4 000 000	0	0	-=	\		\(8)
3849	Taq1	56	tga	177.855	177	177.91	177.8	0	10 000 000	6 800 000	0	=-	\		\(8)
3850	Hha1	7	caa	248.82	250	248.82	0	0	4 500 000	0	0	-=	\		\(8)
3851	Taq1	7	caa	250.34	250	250.34	0	0	5 000 000	0	0	-=	\		\(8)
3852	Taq1	52	att	286.26	286	286.26	0	0	3 000 000	0	0	-=	\		\(8)
3853	Taq1	39	agg	86.555	87	86.62	86.49	0	17 400 000	39 900 000	0	+-	A		\(3)
3854	Taq1	39	agg	86.49	87	0	86.49	0	0	401	0	+-	A		\(3)
3855	Taq1	39	agg	87.285	87	87.28	0	87.29	10 100 000	0	86 600 000	=+(+)	/		\(3)
3856	Taq1	39	agg	86.62	87	86.62	0	0	646.16	0	0	-=	\		\(3)
3857	Taq1	39	agg	87.285	87	87.28	0	87.29	375.07	0	2 550.81	=+(+)	/		\(3)
3858	Taq1	17	cca	201.29	202	201.29	0	0	283.28	0	0	-=	\		\(3)
3859	Taq1	17	cca	228.665	230	228.47	228.86	0	408.67	272.57	0	=-	\		\(3)
3860	Taq1	17	cca	229.95	230	0	229.95	0	0	285.86	0	+-	A		\(3)
3861	Taq1	17	cca	230.823	230	230.71	230.85	230.91	413.31	1 515.75	706.66	+-	A		\(3)
3862	Hha1	49	aaa	231.417	232	231.49	231.36	231.4	17 200 000	34 300 000	25 000 000	+=	/ (-)		\(3)
3863	Hha1	49	aaa	232.39	232	232.41	232.38	232.38	4 100 000	41 000 000	22 900 000	+=	/ (-)		\(3)
3864	Hha1	33	agc	62.84	63	62.76	62.92	62.84	4 400 000	18 500 000	17 900 000	+=	/ (-)		-2
3865	Hha1	31	gac	70.873	71	70.86	70.86	70.9	14 500 000	13 200 000	11 900 000	==	-		-2
3866	Hha1	33	agc	88.273	88	88.16	88.2	88.46	57 000 000	40 900 000	16 400 000	==	-		\(5)
3867	Taq1	52	att	97.615	98	97.55	97.68	0	10 000 000	6 400 000	0	=-	\		\(5)
3868	Taq1	52	att	98.317	98	98.47	98.4	98.08	9 900 000	5 900 000	11 700 000	=+	/ (-)		\(5)
3869	Taq1	64	gtt	106.693	107	106.62	106.65	106.81	6 700 000	6 400 000	3 400 000	==	-		\(5)
3870	Taq1	64	gtt	107.613	107	107.54	107.6	107.7	9 800 000	9 900 000	5 900 000	==	-		\(5)
3871	Taq1	39	agg	192.71	193	192.71	0	0	10 400 000	0	0	-=	\		\(5)
3872	Taq1	39	agg	193.545	193	193.39	193.7	0	5 900 000	31 200 000	0	+-	A		\(5)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
3830	AB053447.PE1	KIAA1774	KIAA1774 protein		aac	agg	increased
3831	AB053447.PE1	KIAA1774	KIAA1774 protein		aac	agg	increased
3832	AB053447.PE1	KIAA1774	KIAA1774 protein		aac	agg	increased
3833	AB053447.PE1	KIAA1774	KIAA1774 protein		aac	agg	increased
3834	AB053447.PE1	KIAA1774	KIAA1774 protein		aga	tga	increased
3835	AF239045.PE1	Kidins220	KIDINS220		aga	gcc	increased
3836	AF239045.PE1	Kidins220	KIDINS220		aga	gcc	increased
3837	AF239045.PE1	Kidins220	KIDINS220		aga	gcc	increased
3838	AF239045.PE1	Kidins220	KIDINS220		aga	gcc	increased
3839	AF239045.PE1	Kidins220	KIDINS220		tga	tgc	increased
3840	AF239045.PE1	Kidins220	KIDINS220		tga	tgc	increased
3841	AF239045.PE1	Kidins220	KIDINS220		tga	tgc	increased
3842	AF239045.PE1	Kidins220	KIDINS220		agg	aca	increased
3843	AF239045.PE1	Kidins220	KIDINS220		agg	aca	increased
3844	AF239045.PE1	Kidins220	KIDINS220		agg	aca	increased
3845	AF239045.PE1	Kidins220	KIDINS220		agg	aca	increased
3846	AF239045.PE1	Kidins220	KIDINS220		agg	aca	increased
3847	AF239045.PE1	Kidins220	KIDINS220		agg	aca	increased
3848	AF239045.PE1	Kidins220	KIDINS220		tga	gag	increased
3849	AF239045.PE1	Kidins220	KIDINS220		tga	gag	increased
3850	AF239045.PE1	Kidins220	KIDINS220		gtc	caa	increased
3851	AF239045.PE1	Kidins220	KIDINS220		gtc	caa	increased
3852	AF239045.PE1	Kidins220	KIDINS220		gct	att	increased
3853	RNU10354.PE1	nc	kidney extracellular calcium-sensing receptor		ttc	agg	increased
3854	RNU10354.PE1	nc	kidney extracellular calcium-sensing receptor		ttc	agg	increased
3855	RNU10354.PE1	nc	kidney extracellular calcium-sensing receptor		ttc	agg	increased
3856	RNU10354.PE1	nc	kidney extracellular calcium-sensing receptor		ttc	agg	increased
3857	RNU10354.PE1	nc	kidney extracellular calcium-sensing receptor		ttc	agg	increased
3858	RNU10354.PE1	nc	kidney extracellular calcium-sensing receptor		gta	cca	increased
3859	RNU10354.PE1	nc	kidney extracellular calcium-sensing receptor		cca	tga	increased
3860	RNU10354.PE1	nc	kidney extracellular calcium-sensing receptor		cca	tga	increased
3861	RNU10354.PE1	nc	kidney extracellular calcium-sensing receptor		cca	tga	increased
3862	RNU10354.PE1	nc	kidney extracellular calcium-sensing receptor		aaa	aat	increased
3863	RNU10354.PE1	nc	kidney extracellular calcium-sensing receptor		aaa	aat	increased
3864	AF302091.PE1	nc	kidney-type glutaminase		agc	cgg	No change
3865	AF302091.PE1	nc	kidney-type glutaminase		gac	ggc	No change
3866	AB070355.PE1	KIF1Bp204	kinesin-family protein 1Bp204		tca	agc	increased
3867	AB070355.PE1	KIF1Bp204	kinesin-family protein 1Bp204		gtg	att	increased
3868	AB070355.PE1	KIF1Bp204	kinesin-family protein 1Bp204		gtg	att	increased
3869	AB070355.PE1	KIF1Bp204	kinesin-family protein 1Bp204		gtg	gtt	increased
3870	AB070355.PE1	KIF1Bp204	kinesin-family protein 1Bp204		gtg	gtt	increased
3871	AB070355.PE1	KIF1Bp204	kinesin-family protein 1Bp204		tta	agg	increased
3872	AB070355.PE1	KIF1Bp204	kinesin-family protein 1Bp204		tta	agg	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
3873	Taq1	39	agg	193.7	193	0	193.7	0	0	313.57	0	+-	A		\(5)
3874	Taq1	39	agg	192.71	193	192.71	0	0	386.21	0	0	-=	\		\(5)
3875	Taq1	39	agg	193.39	193	193.39	0	0	219.1	0	0	-=	\		\(5)
3876	Taq1	17	cca	193.275	194	193.25	193.3	0	664.09	339.05	0	--	\	\	\(5)
3877	Taq1	17	cca	194.45	194	194.61	194.21	194.53	631.58	578.38	526.23	==	-		\(5)
3878	Taq1	39	agg	193.545	194	193.39	193.7	0	5 900 000	31 200 000	0	+-	A		\(5)
3879	Taq1	39	agg	193.7	194	0	193.7	0	0	313.57	0	+-	A		\(5)
3880	Taq1	39	agg	194.44	194	0	0	194.44	0	0	3 000 000	=+	/		\(5)
3881	Taq1	39	agg	194.44	194	0	0	194.44	0	0	88.36	=+	/		\(5)
3882	Taq1	39	agg	193.39	194	193.39	0	0	219.1	0	0	-=	\	\	\(5)
3883	Hha1	25	cag	201.375	202	201.32	0	201.43	5 600 000	0	11 300 000	-+(+)	V (/)		\(5)
3884	Hha1	25	cag	201.95	202	0	201.95	0	0	4 400 000	0	+-	A		\(5)
3885	Hha1	25	cag	201.63	202	0	201.63	0	0	4 900 000	0	+-	A		\(5)
3886	Hha1	25	cag	202.59	202	0	0	202.59	0	0	4 200 000	=+	/		\(5)
3887	Hha1	8	gaa	268.07	267	268.07	0	0	4 600 000	0	0	-=	\		\(5)
3888	Hha1	22	tcc	129.3	130	0	0	129.3	0	0	3 700 000	=+	/		/(5)
3889	Hha1	22	tcc	129.85	130	129.85	0	0	3 300 000	0	0	-=	\		/(5)
3890	Taq1	22	tcc	129.68	130	0	0	129.68	0	0	14 500 000	=+	/		/(5)
3891	Taq1	22	tcc	130.72	130	0	0	130.72	0	0	10 200 000	=+	/		/(5)
3892	Taq1	64	gtt	129.74	130	129.77	129.71	129.74	7 500 000	9 600 000	6 600 000	==	-		/(5)
3893	Taq1	64	gtt	130.757	130	130.75	130.72	130.8	12 400 000	12 600 000	3 700 000	=-	\ (-)		/(5)
3894	Taq1	62	tgt	135.63	136	135.74	135.61	135.54	3 100 000	3 200 000	8 200 000	=+	/ (-)		/(5)
3895	Taq1	62	tgt	136.76	136	0	0	136.76	0	0	5 100 000	=+	/		/(5)
3896	Taq1	39	agg	265.03	266	0	265.03	0	0	67 300 000	0	+-	A		/(5)
3897	Taq1	39	agg	266.05	266	0	266.05	0	0	49 500 000	0	+-	A		/(5)
3898	Taq1	39	agg	266.93	266	0	266.84	267.02	0	7 000 000	13 900 000	++	/		/(5)
3899	Taq1	39	agg	267.02	266	0	0	267.02	0	0	409.42	=+	/		/(5)
3900	Taq1	39	agg	265.03	266	0	265.03	0	0	676.38	0	+-	A		/(5)
3901	Taq1	39	agg	266.05	266	0	266.05	0	0	497.49	0	+-	A		/(5)
3902	Taq1	39	agg	266.84	266	0	266.84	0	0	70.35	0	+-	A		/(5)
3903	Hha1	6	aga	308.39	310	0	308.32	308.46	0	10 000 000	8 800 000	+=	/		/(5)
3904	Hha1	33	agc	87.413	87	87.37	87.58	87.29	8 100 000	13 600 000	18 100 000	==	-		-3
3905	Hha1	41	ccc	109.51	109	109.75	109.29	109.49	11 900 000	3 000 000	5 900 000	-=	\ (-)	(-)	-3
3906	Hha1	39	agg	109.507	110	109.65	109.55	109.32	1 092.37	2 173.26	1 485.18	+=	/ (-)	(-)	-3
3907	Hha1	39	agg	110.08	110	0	0	110.08	0	0	557.45	=+	/		-3
3908	Hha1	39	agg	110.635	110	110.65	110.62	0	351.9	704.51	0	+-	A		-3
3909	Taq1	39	agg	119.78	120	119.93	119.63	0	19 400 000	32 300 000	0	=-	\		-3
3910	Taq1	39	agg	119.93	120	119.93	0	0	720.43	0	0	-=	\		-3
3911	Taq1	39	agg	119.63	120	0	119.63	0	0	324.62	0	+-	A		-3
3912	Taq1	9	atc	104.5	105	104.51	104.54	104.45	20 600 000	3 100 000	11 400 000	-=	\ (-)		-1
3913	Hha1	9	atc	105.12	105	105.1	105.09	105.17	5 000 000	7 600 000	16 100 000	=+	/ (-)		-1
3914	Taq1	9	atc	105.447	105	105.42	105.45	105.47	10 400 000	4 700 000	18 200 000	=+	/ (-)		-1
3915	Taq1	51	ata	105.37	106	0	0	105.37	0	0	6 800 000	=+	/		-1

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
3873	AB070355.PE1	KIF1Bp204	kinesin-family protein 1Bp204		tta	agg	increased
3874	AB070355.PE1	KIF1Bp204	kinesin-family protein 1Bp204		tta	agg	increased
3875	AB070355.PE1	KIF1Bp204	kinesin-family protein 1Bp204		tta	agg	increased
3876	AB070355.PE1	KIF1Bp204	kinesin-family protein 1Bp204		cca	agg	increased
3877	AB070355.PE1	KIF1Bp204	kinesin-family protein 1Bp204		cca	agg	increased
3878	AB070355.PE1	KIF1Bp204	kinesin-family protein 1Bp204		cca	agg	increased
3879	AB070355.PE1	KIF1Bp204	kinesin-family protein 1Bp204		cca	agg	increased
3880	AB070355.PE1	KIF1Bp204	kinesin-family protein 1Bp204		cca	agg	increased
3881	AB070355.PE1	KIF1Bp204	kinesin-family protein 1Bp204		cca	agg	increased
3882	AB070355.PE1	KIF1Bp204	kinesin-family protein 1Bp204		cca	agg	increased
3883	AB070355.PE1	KIF1Bp204	kinesin-family protein 1Bp204		cag	ttg	increased
3884	AB070355.PE1	KIF1Bp204	kinesin-family protein 1Bp204		cag	ttg	increased
3885	AB070355.PE1	KIF1Bp204	kinesin-family protein 1Bp204		cag	ttg	increased
3886	AB070355.PE1	KIF1Bp204	kinesin-family protein 1Bp204		cag	ttg	increased
3887	AB070355.PE1	KIF1Bp204	kinesin-family protein 1Bp204		gaa	taa	increased
3888	RNU44979.KRP2	KRP2	kinesin-related protein 2		tcc	gtt	decreased
3889	RNU44979.KRP2	KRP2	kinesin-related protein 2		tcc	gtt	decreased
3890	RNU44979.KRP2	KRP2	kinesin-related protein 2		tcc	gtt	decreased
3891	RNU44979.KRP2	KRP2	kinesin-related protein 2		tcc	gtt	decreased
3892	RNU44979.KRP2	KRP2	kinesin-related protein 2		tcc	gtt	decreased
3893	RNU44979.KRP2	KRP2	kinesin-related protein 2		tcc	gtt	decreased
3894	RNU44979.KRP2	KRP2	kinesin-related protein 2		tgt	agc	decreased
3895	RNU44979.KRP2	KRP2	kinesin-related protein 2		tgt	agc	decreased
3896	RNU44979.KRP2	KRP2	kinesin-related protein 2		gat	agg	decreased
3897	RNU44979.KRP2	KRP2	kinesin-related protein 2		gat	agg	decreased
3898	RNU44979.KRP2	KRP2	kinesin-related protein 2		gat	agg	decreased
3899	RNU44979.KRP2	KRP2	kinesin-related protein 2		gat	agg	decreased
3900	RNU44979.KRP2	KRP2	kinesin-related protein 2		gat	agg	decreased
3901	RNU44979.KRP2	KRP2	kinesin-related protein 2		gat	agg	decreased
3902	RNU44979.KRP2	KRP2	kinesin-related protein 2		gat	agg	decreased
3903	RNU44979.KRP2	KRP2	kinesin-related protein 2		ctt	aga	decreased
3904	AB017820.PE1	nc	Klotho		ggg	agc	No change
3905	AB017820.PE1	nc	Klotho		ccc	agg	No change
3906	AB017820.PE1	nc	Klotho		ccc	agg	No change
3907	AB017820.PE1	nc	Klotho		ccc	agg	No change
3908	AB017820.PE1	nc	Klotho		ccc	agg	No change
3909	AB017820.PE1	nc	Klotho		agg	taa	No change
3910	AB017820.PE1	nc	Klotho		agg	taa	No change
3911	AB017820.PE1	nc	Klotho		agg	taa	No change
3912	AF102129.KPL2	Kpl2	KPL2		ata	atc	No change
3913	AF102129.KPL2	Kpl2	KPL2		ata	atc	No change
3914	AF102129.KPL2	Kpl2	KPL2		ata	atc	No change
3915	AF102129.KPL2	Kpl2	KPL2		ata	atc	No change

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
3916	Taq1	51	ata	106.435	106	106.23	106.64	0	8 300 000	50 500 000	0	+-	A		-1
3917	Hha1	35	gga	94.91	95	94.87	95.05	94.81	10 377.9	3 016.24	1 822.37	-=	\ (-)		-(2) \(2)
3918	Hha1	44	cgg	180.213	181	179.96	180.37	180.31	3 700 000	4 100 000	4 700 000	==	-		-(2) \(2)
3919	Hha1	44	cgg	180.86	181	0	180.86	0	0	5 200 000	0	+-	A		-(2) \(2)
3920	Hha1	26	ctg	217.95	219	217.95	0	0	4 400 000	0	0	-=	\		-(2) \(2)
3921	Hha1	33	agc	66.89	67	66.93	66.98	66.76	12 300 000	23 100 000	248 400 000	=+	/ (-)		/(4)
3922	Hha1	20	ctc	88.76	89	0	0	88.76	0	0	369.75	=+	/		/(4)
3923	Hha1	54	ttt	89.477	90	89.38	89.49	89.56	3 700 000	12 700 000	20 300 000	==	-		/(4)
3924	Hha1	54	ttt	90.523	90	90.49	90.49	90.59	3 700 000	4 700 000	6 000 000	==	-		/(4)
3925	Hha1	39	agg	142.785	143	0	142.99	142.58	0	310.46	272.62	+=	/		/(4)
3926	Hha1	33	agc	144.21	145	144.2	0	144.22	4 000 000	0	3 500 000	-+(=)	V		/(4)
3927	Hha1	33	agc	145.22	145	0	0	145.22	0	0	7 200 000	=+	/		/(4)
3928	Hha1	26	ctg	220.85	220	220.85	0	0	5 000 000	0	0	-=	\		/(4)
3929	Taq1	45	gcc	66.68	67	66.86	66.68	66.5	33 500 000	13 000 000	7 900 000	-=	\ (-)		\(3)
3930	Hha1	6	aga	160.585	161	160.81	0	160.36	10 900 000	0	8 000 000	-+(=)	V		\(3)
3931	Hha1	6	aga	161.59	161	161.71	0	161.47	8 900 000	0	4 000 000	-=(-)	\		\(3)
3932	Hha1	49	aaa	254.89	256	254.89	0	0	3 900 000	0	0	-=	\		\(3)
3933	Hha1	49	aaa	255.84	256	0	255.84	0	0	7 200 000	0	+-	A		\(3)
3934	Hha1	49	aaa	256.69	256	0	256.69	0	0	12 800 000	0	+-	A		\(3)
3935	Hha1	41	ccc	103.02	103	0	103.02	103.02	0	3 700 000	3 000 000	+=	/		/(2)
3936	Hha1	64	gtt	152.933	153	152.99	152.91	152.9	12 300 000	8 500 000	15 200 000	==	-		/(2)
3937	Hha1	64	gtt	153.91	153	0	0	153.91	0	0	6 100 000	=+	/		/(2)
3938	Hha1	44	cgg	228.85	230	228.85	0	0	3 300 000	0	0	-=	\		/(2)
3939	Hha1	44	cgg	229.31	230	229.19	229.43	0	3 300 000	10 500 000	0	+-	A		/(2)
3940	Taq1	44	cgg	142.4	143	142.4	0	0	1 051.97	0	0	-=	\		/(2)
3941	Taq1	44	cgg	143.02	143	0	0	143.02	0	0	874.24	=+	/		/(2)
3942	Taq1	44	cgg	143.71	143	143.55	143.58	144	708.25	538.36	762.16	==	-		/(2)
3943	Taq1	29	gca	143.71	144	0	0	143.71	0	0	7 600 000	=+	/		/(2)
3944	Taq1	29	gca	144.72	144	144.71	0	144.73	3 200 000	0	8 300 000	=+(+)	/		/(2)
3945	Taq1	44	cgg	142.4	143	142.4	0	0	1 051.97	0	0	-=	\		/(2)
3946	Taq1	44	cgg	143.02	143	0	0	143.02	0	0	874.24	=+	/		/(2)
3947	Taq1	44	cgg	143.71	143	143.55	143.58	144	708.25	538.36	762.16	==	-		/(2)
3948	Taq1	29	gca	143.71	144	0	0	143.71	0	0	7 600 000	=+	/		/(2)
3949	Taq1	29	gca	144.72	144	144.71	0	144.73	3 200 000	0	8 300 000	=+(+)	/		/(2)
3950	Taq1	44	cgg	142.4	143	142.4	0	0	1 051.97	0	0	-=	\		/(2)
3951	Taq1	44	cgg	143.02	143	0	0	143.02	0	0	874.24	=+	/		/(2)
3952	Taq1	44	cgg	143.71	143	143.55	143.58	144	708.25	538.36	762.16	==	-		/(2)
3953	Taq1	29	gca	143.71	144	0	0	143.71	0	0	7 600 000	=+	/		/(2)
3954	Taq1	29	gca	144.72	144	144.71	0	144.73	3 200 000	0	8 300 000	=+(+)	/		/(2)
3955	Hha1	20	ctc	68	68	68	0	0	426.99	0	0	-=	\		\(2)
3956	Taq1	47	ggc	119.735	120	119.73	119.74	0	2 215.38	1 750.47	0	=-	\		\(2)
3957	Taq1	47	ggc	120.71	120	120.68	120.74	0	2 830.76	1 241.24	0	-=	\		\(2)
3958	Hha1	44	cgg	134.697	135	134.72	134.74	134.63	10 900 000	10 200 000	4 800 000	=-	\ (-)		-3

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
3916	AF102129.KPL2	Kpl2	KPL2		ata	atc	No change
3917	AB020759.PE1	nc	Kruppel-like transcription factor		gga	ggc	No change
3918	AB020759.PE1	nc	Kruppel-like transcription factor		cgg	gaa	No change
3919	AB020759.PE1	nc	Kruppel-like transcription factor		cgg	gaa	No change
3920	AB020759.PE1	nc	Kruppel-like transcription factor		ctg	agg	No change
3921	RNLAMA.LAMIN-A	lamin A	lamin A		tcc	agc	decreased
3922	RNLAMA.LAMIN-A	lamin A	lamin A		ctc	ttt	decreased
3923	RNLAMA.LAMIN-A	lamin A	lamin A		ctc	ttt	decreased
3924	RNLAMA.LAMIN-A	lamin A	lamin A		ctc	ttt	decreased
3925	RNLAMA.LAMIN-A	lamin A	lamin A		agg	acg	decreased
3926	RNLAMA.LAMIN-A	lamin A	lamin A		aag	agc	decreased
3927	RNLAMA.LAMIN-A	lamin A	lamin A		aag	agc	decreased
3928	RNLAMA.LAMIN-A	lamin A	lamin A		ctg	tgc	decreased
3929	RNU07971.PE1	nc	L-arginine:glycine amidinotransferase		gcc	atg	increased
3930	RNU07971.PE1	nc	L-arginine:glycine amidinotransferase		aga	ggc	increased
3931	RNU07971.PE1	nc	L-arginine:glycine amidinotransferase		aga	ggc	increased
3932	RNU07971.PE1	nc	L-arginine:glycine amidinotransferase		ata	aaa	increased
3933	RNU07971.PE1	nc	L-arginine:glycine amidinotransferase		ata	aaa	increased
3934	RNU07971.PE1	nc	L-arginine:glycine amidinotransferase		ata	aaa	increased
3935	RNLTBP2.PE1	nc	latent TGF-beta binding protein-2 like protein		ccc	gtc	decreased
3936	RNLTBP2.PE1	nc	latent TGF-beta binding protein-2 like protein		gtt	cac	decreased
3937	RNLTBP2.PE1	nc	latent TGF-beta binding protein-2 like protein		gtt	cac	decreased
3938	RNLTBP2.PE1	nc	latent TGF-beta binding protein-2 like protein		cgg	acg	decreased
3939	RNLTBP2.PE1	nc	latent TGF-beta binding protein-2 like protein		cgg	acg	decreased
3940	RNLCAR.PE4	nc	L-CA variant 1		cgg	gca	decreased
3941	RNLCAR.PE4	nc	L-CA variant 1		cgg	gca	decreased
3942	RNLCAR.PE4	nc	L-CA variant 1		cgg	gca	decreased
3943	RNLCAR.PE4	nc	L-CA variant 1		cgg	gca	decreased
3944	RNLCAR.PE4	nc	L-CA variant 1		cgg	gca	decreased
3945	RNLCAR.PE3	nc	L-CA variant 2		cgg	gca	decreased
3946	RNLCAR.PE3	nc	L-CA variant 2		cgg	gca	decreased
3947	RNLCAR.PE3	nc	L-CA variant 2		cgg	gca	decreased
3948	RNLCAR.PE3	nc	L-CA variant 2		cgg	gca	decreased
3949	RNLCAR.PE3	nc	L-CA variant 2		cgg	gca	decreased
3950	RNLCAR.PE2	nc	L-CA variant 3		cgg	gca	decreased
3951	RNLCAR.PE2	nc	L-CA variant 3		cgg	gca	decreased
3952	RNLCAR.PE2	nc	L-CA variant 3		cgg	gca	decreased
3953	RNLCAR.PE2	nc	L-CA variant 3		cgg	gca	decreased
3954	RNLCAR.PE2	nc	L-CA variant 3		cgg	gca	decreased
3955	AB003104.PE1	CP94 or filens	lens fiber cell beaded-filament		ctg	ctc	increased
3956	AB003104.PE1	CP94 or filens	lens fiber cell beaded-filament		ggc	gcg	increased
3957	AB003104.PE1	CP94 or filens	lens fiber cell beaded-filament		ggc	gcg	increased
3958	RATMP19A.MP19	MP19	lens intrinsic membrane protein 19	*	ttt	cgg	No change

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
3959	Hha1	44	cgg	135.66	135	135.85	135.49	135.64	5 600 000	4 600 000	4 100 000	==	-		-3
3960	Hha1	54	ttt	136.483	137	136.55	136.4	136.5	15 300 000	13 400 000	7 200 000	==	-		-3
3961	Hha1	54	ttt	137.21	137	137.26	137.33	137.04	26 200 000	18 700 000	8 800 000	==	-		-3
3962	Hha1	33	agc	180.145	180	0	180.17	180.12	0	4 400 000	16 700 000	=+	/		-3
3963	Hha1	33	agc	181.073	180	180.99	181.14	181.09	3 200 000	3 000 000	13 000 000	=+	/ (-)		-3
3964	Hha1	44	cgg	134.697	135	134.72	134.74	134.63	10 900 000	10 200 000	4 800 000	=-	\ (-)		-3
3965	Hha1	44	cgg	135.66	135	135.85	135.49	135.64	5 600 000	4 600 000	4 100 000	==	-		-3
3966	Hha1	54	ttt	136.483	137	136.55	136.4	136.5	15 300 000	13 400 000	7 200 000	==	-		-3
3967	Hha1	54	ttt	137.21	137	137.26	137.33	137.04	26 200 000	18 700 000	8 800 000	==	-		-3
3968	Hha1	33	agc	180.145	180	0	180.17	180.12	0	4 400 000	16 700 000	=+	/		-3
3969	Hha1	33	agc	181.073	180	180.99	181.14	181.09	3 200 000	3 000 000	13 000 000	=+	/ (-)		-3
3970	Hha1	33	agc	79.76	80	79.76	0	0	7 400 000	0	0	-=	\		\(5)
3971	Taq1	61	tct	217.88	219	217.88	0	0	3 900 000	0	0	-=	\		\(5)
3972	Taq1	61	tct	218.87	219	0	0	218.87	0	0	3 900 000	=+	/		\(5)
3973	Taq1	61	tct	219.7	219	0	219.7	0	0	3 000 000	0	+-	A		\(5)
3974	Hha1	16	tag	253.16	254	253.16	0	0	21 900 000	0	0	-=	\		\(5)
3975	Hha1	16	tag	254.97	254	254.89	254.97	255.05	3 600 000	4 100 000	5 800 000	==	-		\(5)
3976	Hha1	8	gaa	263.67	265	263.67	0	0	7 000 000	0	0	-=	\		\(5)
3977	Hha1	8	gaa	264.4	265	0	264.4	0	0	3 700 000	0	+-	A		\(5)
3978	Taq1	8	gaa	264.34	265	0	0	264.34	0	0	3 500 000	=+	/		\(5)
3979	Taq1	8	gaa	264.92	265	264.92	264.92	0	11 000 000	10 100 000	0	=-	\		\(5)
3980	Taq1	39	agg	89.565	90	89.76	89.37	0	30 800 000	7 372.93	0	-=	\		\(2)
3981	Taq1	39	agg	90.495	90	90.7	0	90.29	125 800 000	0	23 600 000	-=(-)	\		\(2)
3982	Taq1	39	agg	89.76	90	89.76	0	0	1 143.79	0	0	-=	\		\(2)
3983	Taq1	39	agg	90.495	90	90.7	0	90.29	4 671.71	0	695.13	-=(-)	\		\(2)
3984	Hha1	9	atc	194.455	195	194.27	194.64	0	4 400 000	3 500 000	0	=-	\		\(2)
3985	Hha1	9	atc	195.36	195	195.36	0	0	4 600 000	0	0	-=	\		\(2)
3986	Taq1	8	gaa	200.94	200	0	200.94	0	0	3 700 000	0	+-	A		\(2)
3987	Taq1	44	cgg	142.4	143	142.4	0	0	1 051.97	0	0	-=	\		/(2)
3988	Taq1	44	cgg	143.02	143	0	0	143.02	0	0	874.24	=+	/		/(2)
3989	Taq1	44	cgg	143.71	143	143.55	143.58	144	708.25	538.36	762.16	==	-		/(2)
3990	Taq1	29	gca	143.71	144	0	0	143.71	0	0	7 600 000	=+	/		/(2)
3991	Taq1	29	gca	144.72	144	144.71	0	144.73	3 200 000	0	8 300 000	=+(+)	/		/(2)
3992	Hha1	61	tct	132.68	133	132.57	132.69	132.78	17 200 000	40 300 000	55 400 000	==	-		A(4)
3993	Hha1	61	tct	133.78	133	133.78	0	0	5 700 000	0	0	-=	\		A(4)
3994	Hha1	43	cgc	157.54	158	157.54	0	0	4 400 000	0	0	-=	\		A(4)
3995	Hha1	43	cgc	158.18	158	0	158.18	0	0	5 500 000	0	+-	A		A(4)
3996	Taq1	29	gca	205.34	206	0	0	205.34	0	0	3 300 000	=+	/		A(4)
3997	Hha1	59	ttc	210.393	211	210.62	210.27	210.29	187.2	497.29	173.33	+-	A		A(4)
3998	Hha1	59	ttc	210.795	211	0	210.83	210.76	0	209.84	137.11	+=	/		A(4)
3999	Hha1	59	ttc	212.235	211	0	212.38	212.09	0	103.48	807.18	=+	/		A(4)
4000	Hha1	3	aac	222.09	223	0	222.09	0	0	5 900 000	0	+-	A		A(4)
4001	Hha1	40	tgg	247.96	249	247.96	0	0	6 100 000	0	0	-=	\		A(4)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
3959	RATMP19A.MP19	MP19	lens intrinsic membrane protein 19	*	ttt	cgg	No change
3960	RATMP19A.MP19	MP19	lens intrinsic membrane protein 19	*	ttt	cgg	No change
3961	RATMP19A.MP19	MP19	lens intrinsic membrane protein 19	*	ttt	cgg	No change
3962	RATMP19A.MP19	MP19	lens intrinsic membrane protein 19	*	agc	cag	No change
3963	RATMP19A.MP19	MP19	lens intrinsic membrane protein 19	*	agc	cag	No change
3964	RATMP20A.MP20	MP20	lens membrane protein	*	ttt	cgg	No change
3965	RATMP20A.MP20	MP20	lens membrane protein	*	ttt	cgg	No change
3966	RATMP20A.MP20	MP20	lens membrane protein	*	ttt	cgg	No change
3967	RATMP20A.MP20	MP20	lens membrane protein	*	ttt	cgg	No change
3968	RATMP20A.MP20	MP20	lens membrane protein	*	agc	cag	No change
3969	RATMP20A.MP20	MP20	lens membrane protein	*	agc	cag	No change
3970	AF087433.LEPRE1	lepre1	leprecan		tgc	agc	increased
3971	AF087433.LEPRE1	lepre1	leprecan		agc	tct	increased
3972	AF087433.LEPRE1	lepre1	leprecan		agc	tct	increased
3973	AF087433.LEPRE1	lepre1	leprecan		agc	tct	increased
3974	AF087433.LEPRE1	lepre1	leprecan		gac	tag	increased
3975	AF087433.LEPRE1	lepre1	leprecan		gac	tag	increased
3976	AF087433.LEPRE1	lepre1	leprecan		gaa	tgt	increased
3977	AF087433.LEPRE1	lepre1	leprecan		gaa	tgt	increased
3978	AF087433.LEPRE1	lepre1	leprecan		gaa	tgt	increased
3979	AF087433.LEPRE1	lepre1	leprecan		gaa	tgt	increased
3980	D86345.PE1	nc	leukemia inhibitor factor receptor alpha-chain		tat	agg	increased
3981	D86345.PE1	nc	leukemia inhibitor factor receptor alpha-chain		tat	agg	increased
3982	D86345.PE1	nc	leukemia inhibitor factor receptor alpha-chain		tat	agg	increased
3983	D86345.PE1	nc	leukemia inhibitor factor receptor alpha-chain		tat	agg	increased
3984	D86345.PE1	nc	leukemia inhibitor factor receptor alpha-chain		gtc	atc	increased
3985	D86345.PE1	nc	leukemia inhibitor factor receptor alpha-chain		gtc	atc	increased
3986	D86345.PE1	nc	leukemia inhibitor factor receptor alpha-chain		cta	gaa	increased
3987	RATLCA1.L-CA	L-CA	leukocyte common antigen		cgg	gca	decreased
3988	RATLCA1.L-CA	L-CA	leukocyte common antigen		cgg	gca	decreased
3989	RATLCA1.L-CA	L-CA	leukocyte common antigen		cgg	gca	decreased
3990	RATLCA1.L-CA	L-CA	leukocyte common antigen		cgg	gca	decreased
3991	RATLCA1.L-CA	L-CA	leukocyte common antigen		cgg	gca	decreased
3992	RATLARA.LAR	LAR	leukocyte common antigen-related phosphatase		atg	tct	increased by mild
3993	RATLARA.LAR	LAR	leukocyte common antigen-related phosphatase		atg	tct	increased by mild
3994	RATLARA.LAR	LAR	leukocyte common antigen-related phosphatase		cgc	cca	increased by mild
3995	RATLARA.LAR	LAR	leukocyte common antigen-related phosphatase		cgc	cca	increased by mild
3996	RATLARA.LAR	LAR	leukocyte common antigen-related phosphatase		cgc	gca	increased by mild
3997	RATLARA.LAR	LAR	leukocyte common antigen-related phosphatase		caa	ttc	increased by mild
3998	RATLARA.LAR	LAR	leukocyte common antigen-related phosphatase		caa	ttc	increased by mild
3999	RATLARA.LAR	LAR	leukocyte common antigen-related phosphatase		caa	ttc	increased by mild
4000	RATLARA.LAR	LAR	leukocyte common antigen-related phosphatase		aac	gtc	increased by mild
4001	RATLARA.LAR	LAR	leukocyte common antigen-related phosphatase		cag	tgg	increased by mild

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
4002	Hha1	40	tgg	247.54	249	247.54	0	0	4 500 000	0	0	-=	\		A(4)
4003	Hha1	40	tgg	248.77	249	0	248.77	0	0	3 300 000	0	+-	A		A(4)
4004	Hha1	33	agc	108.77	109	108.83	108.8	108.68	11 600 000	9 300 000	8 800 000	==	-		-2
4005	Hha1	61	tct	108.5	109	108.43	108.77	108.3	13 700 000	3 100 000	4 300 000	-=	\ (-)		-2
4006	Hha1	61	tct	109.345	109	109.11	0	109.58	7 200 000	0	6 100 000	-+(=)	V		-2
4007	Hha1	61	tct	109.65	109	109.66	109.64	0	10 200 000	7 100 000	0	=-	\		-2
4008	Hha1	3	aac	188.41	188	188.41	0	0	3 100 000	0	0	-=	\		\(5)
4009	Hha1	3	aac	189.12	188	189.13	189.21	189.02	6 300 000	4 500 000	5 200 000	==	-		\(5)
4010	Hha1	10	atg	187.15	188	187.15	0	0	4 000 000	0	0	-=	\		\(5)
4011	Hha1	10	atg	188.085	188	188.04	188.13	0	8 000 000	3 900 000	0	--	\		\(5)
4012	Taq1	10	atg	188.83	188	188.73	188.93	0	4 900 000	9 900 000	0	+-	A		\(5)
4013	Hha1	10	atg	189.1	188	189.1	0	0	4 400 000	0	0	-=	\		\(5)
4014	Taq1	44	cgg	251.5	253	0	251.59	251.41	0	660.39	672.49	+=	/		\(5)
4015	Taq1	44	cgg	251.97	253	251.97	0	0	184	0	0	-=	\	\	\(5)
4016	Taq1	45	gcc	251.93	253	251.75	252.11	0	158 600 000	3 100 000	0	-=	\	\	\(5)
4017	Taq1	45	gcc	252.22	253	252.22	0	0	5 200 000	0	0	-=	\	\	\(5)
4018	Taq1	45	gcc	254.26	253	0	254.26	0	0	3 700 000	0	+-	A		\(5)
4019	Hha1	27	acg	75.7	76	75.85	0	75.55	3 000 000	0	3 400 000	-+(=)	V		\(5)
4020	Hha1	27	acg	76.385	76	0	76.43	76.34	0	3 300 000	7 300 000	++	/		\(5)
4021	Hha1	33	agc	94.285	94	94.26	94.31	0	4 500 000	3 800 000	0	=-	\		\(5)
4022	Hha1	26	ctg	104.535	105	104.54	104.53	0	10 900 000	3 300 000	0	-=	\		\(5)
4023	Hha1	26	ctg	105.54	105	105.54	0	0	3 100 000	0	0	-=	\		\(5)
4024	Hha1	61	tct	120.8	121	0	120.8	0	0	4 300 000	0	+-	A		\(5)
4025	Taq1	56	tga	138.535	139	138.58	138.49	0	14 300 000	14 300 000	0	=-	\		\(5)
4026	Taq1	56	tga	139.383	139	139.51	139.44	139.2	37 300 000	35 400 000	4 700 000	=-	\ (-)		\(5)
4027	Taq1	61	tct	138.855	139	0	138.77	138.94	0	8 700 000	8 100 000	+=	/		\(5)
4028	Hha1	56	tga	174.61	175	174.43	174.79	0	298.28	231.17	0	=-	\		\(5)
4029	Hha1	56	tga	175.17	175	175.17	0	0	228.82	0	0	-=	\		\(5)
4030	Taq1	18	cct	218.52	218	218.52	0	0	3 700 000	0	0	-=	\		\(5)
4031	Taq1	17	cca	126.693	127	126.77	126.64	126.67	227.55	904.13	1 308.07	+=	/ (-)	/	
4032	Taq1	62	tgt	126.573	127	126.54	126.64	126.54	5 600 000	10 400 000	6 400 000	+=	/ (-)	/	
4033	Taq1	41	ccc	207.22	207	207.22	0	0	4 700 000	0	0	-=	\	\	
4034	Taq1	61	tct	207.45	208	207.45	0	0	4 000 000	0	0	-=	\	\	
4035	Hha1	20	ctc	165.705	166	0	165.87	165.54	0	511.4	405.53	+=	/		/(2) \(2)
4036	Hha1	20	ctc	166.875	166	166.87	166.88	0	268.59	747.44	0	+-	A		/(2) \(2)
4037	Hha1	26	ctg	165.435	166	165.45	165.42	0	4 100 000	5 300 000	0	=-	\		/(2) \(2)
4038	Hha1	26	ctg	165.99	166	0	0	165.99	0	0	3 800 000	=+	/		/(2) \(2)
4039	Hha1	40	tgg	251.41	251	251.47	251.35	0	3 900 000	4 200 000	0	=-	\		/(2) \(2)
4040	Hha1	20	ctc	165.705	166	0	165.87	165.54	0	511.4	405.53	+=	/		/(2) \(2)
4041	Hha1	20	ctc	166.875	166	166.87	166.88	0	268.59	747.44	0	+-	A		/(2) \(2)
4042	Hha1	26	ctg	165.435	166	165.45	165.42	0	4 100 000	5 300 000	0	=-	\		/(2) \(2)
4043	Hha1	26	ctg	165.99	166	0	0	165.99	0	0	3 800 000	=+	/		/(2) \(2)
4044	Hha1	40	tgg	251.41	251	251.47	251.35	0	3 900 000	4 200 000	0	=-	\		/(2) \(2)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
4002	RATLARA.LAR	LAR	leukocyte common antigen-related phosphatase		cag	tgg	increased by mild
4003	RATLARA.LAR	LAR	leukocyte common antigen-related phosphatase		cag	tgg	increased by mild
4004	AB048790.LTC4	LTC4	leukotriene C4 synthase		tct	agc	No change
4005	AB048790.LTC4	LTC4	leukotriene C4 synthase		tct	agc	No change
4006	AB048790.LTC4	LTC4	leukotriene C4 synthase		tct	agc	No change
4007	AB048790.LTC4	LTC4	leukotriene C4 synthase		tct	agc	No change
4008	RNSDHMR.PE1	nc	L-iditol 2-dehydrogenase		atg	aac	increased
4009	RNSDHMR.PE1	nc	L-iditol 2-dehydrogenase		atg	aac	increased
4010	RNSDHMR.PE1	nc	L-iditol 2-dehydrogenase		atg	aac	increased
4011	RNSDHMR.PE1	nc	L-iditol 2-dehydrogenase		atg	aac	increased
4012	RNSDHMR.PE1	nc	L-iditol 2-dehydrogenase		atg	aac	increased
4013	RNSDHMR.PE1	nc	L-iditol 2-dehydrogenase		atg	aac	increased
4014	RNSDHMR.PE1	nc	L-iditol 2-dehydrogenase		gcc	cgg	increased
4015	RNSDHMR.PE1	nc	L-iditol 2-dehydrogenase		gcc	cgg	increased
4016	RNSDHMR.PE1	nc	L-iditol 2-dehydrogenase		gcc	cgg	increased
4017	RNSDHMR.PE1	nc	L-iditol 2-dehydrogenase		gcc	cgg	increased
4018	RNSDHMR.PE1	nc	L-iditol 2-dehydrogenase		gcc	cgg	increased
4019	AF031880.NF-L	NF-L	light molecular-weight neurofilament		tac	acg	increased
4020	AF031880.NF-L	NF-L	light molecular-weight neurofilament		tac	acg	increased
4021	AF031880.NF-L	NF-L	light molecular-weight neurofilament		gtg	agc	increased
4022	AF031880.NF-L	NF-L	light molecular-weight neurofilament		cct	ctg	increased
4023	AF031880.NF-L	NF-L	light molecular-weight neurofilament		cct	ctg	increased
4024	AF031880.NF-L	NF-L	light molecular-weight neurofilament		tca	tct	increased
4025	AF031880.NF-L	NF-L	light molecular-weight neurofilament		tct	tga	increased
4026	AF031880.NF-L	NF-L	light molecular-weight neurofilament		tct	tga	increased
4027	AF031880.NF-L	NF-L	light molecular-weight neurofilament		tct	tga	increased
4028	AF031880.NF-L	NF-L	light molecular-weight neurofilament		tgc	tga	increased
4029	AF031880.NF-L	NF-L	light molecular-weight neurofilament		tgc	tga	increased
4030	AF031880.NF-L	NF-L	light molecular-weight neurofilament		cct	ggt	increased
4031	RATLIMK1.LIMK-1	limk-1	LIMK-1		cca	tgt	decreased
4032	RATLIMK1.LIMK-1	limk-1	LIMK-1		cca	tgt	decreased
4033	RATLIMK1.LIMK-1	limk-1	LIMK-1		ccc	tct	increased
4034	RATLIMK1.LIMK-1	limk-1	LIMK-1		ccc	tct	increased
4035	RATLIMK2A.PE1	limk-2a	LIMK-2a		ctg	ctc	decreased
4036	RATLIMK2A.PE1	limk-2a	LIMK-2a		ctg	ctc	decreased
4037	RATLIMK2A.PE1	limk-2a	LIMK-2a		ctg	ctc	decreased
4038	RATLIMK2A.PE1	limk-2a	LIMK-2a		ctg	ctc	decreased
4039	RATLIMK2A.PE1	limk-2a	LIMK-2a		ctc	tgg	decreased
4040	RATLIMK2B.PE1	limk-2b	LIMK-2b		ctg	ctc	decreased
4041	RATLIMK2B.PE1	limk-2b	LIMK-2b		ctg	ctc	decreased
4042	RATLIMK2B.PE1	limk-2b	LIMK-2b		ctg	ctc	decreased
4043	RATLIMK2B.PE1	limk-2b	LIMK-2b		ctg	ctc	decreased
4044	RATLIMK2B.PE1	limk-2b	LIMK-2b		ctc	tgg	decreased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
4045	Hha1	20	ctc	165.705	166	0	165.87	165.54	0	511.4	405.53	+=	/		/(2) \(2)
4046	Hha1	20	ctc	166.875	166	166.87	166.88	0	268.59	747.44	0	+-	A		/(2) \(2)
4047	Hha1	26	ctg	165.435	166	165.45	165.42	0	4 100 000	5 300 000	0	=-	\		/(2) \(2)
4048	Hha1	26	ctg	165.99	166	0	0	165.99	0	0	3 800 000	=+	/		/(2) \(2)
4049	Hha1	40	tgg	251.41	251	251.47	251.35	0	3 900 000	4 200 000	0	=-	\		/(2) \(2)
4050	Hha1	31	gac	103.37	103	103.37	0	0	7 000 000	0	0	-=	\		\(5)
4051	Hha1	59	ttc	103.43	103	0	103.43	0	0	937.1	0	+-	A		\(5)
4052	Hha1	28	tcg	118.04	118	118.04	0	0	3 700 000	0	0	-=	\		\(5)
4053	Taq1	44	cgg	177.595	178	177.37	177.82	0	1 024.19	602.97	0	=-	\		\(5)
4054	Taq1	44	cgg	178.5	178	0	178.5	0	0	861.38	0	+-	A		\(5)
4055	Taq1	17	cca	177.93	179	177.96	177.9	0	176.47	438.77	0	+-	A		\(5)
4056	Taq1	17	cca	179.57	179	179.57	0	0	348.3	0	0	-=	\		\(5)
4057	Hha1	26	ctg	225.8	227	0	0	225.8	0	0	4 300 000	=+	/		\(5)
4058	Hha1	26	ctg	228.08	227	228.08	0	0	7 500 000	0	0	-=	\		\(5)
4059	Taq1	10	atg	246.48	247	0	246.48	0	0	5 500 000	0	+-	A	A	A(2)
4060	Taq1	50	aat	246.545	248	246.34	246.75	0	3 200 000	8 300 000	0	+-	A	A	A(2)
4061	Taq1	50	aat	247.46	248	247.45	247.47	0	6 900 000	7 700 000	0	=-	\		A(2)
4062	Taq1	50	aat	248.04	248	248.04	0	0	13 800 000	0	0	-=	\		A(2)
4063	Taq1	50	aat	249.1	248	249.1	0	0	7 800 000	0	0	-=	\		A(2)
4064	Taq1	50	aat	249.26	248	249.26	0	0	7 400 000	0	0	-=	\		A(2)
4065	Hha1	33	agc	69.835	70	69.78	69.89	0	36 000 000	32 900 000	0	=-	\		\(2)
4066	Hha1	33	agc	113.725	114	113.86	113.59	0	6 500 000	9 600 000	0	=-	\		\(2)
4067	Hha1	39	agg	69.617	70	69.51	69.49	69.85	3 218.47	501.52	240.07	-=	\ (-)		\(7)
4068	Taq1	45	gcc	86.003	86	85.99	85.93	86.09	14 600 000	21 500 000	4 600 000	=-	\ (-)		\(7)
4069	Taq1	45	gcc	86.44	86	86.44	0	0	12 700 000	0	0	-=	\		\(7)
4070	Hha1	40	tgg	100.52	101	100.28	0	100.76	3 400 000	0	9 300 000	=+(+)	/		\(7)
4071	Hha1	32	gtc	112.67	113	0	112.68	112.66	0	9 654.12	12 539.1	+=	/		\(7)
4072	Taq1	22	tcc	124.525	125	0	124.63	124.42	0	10 400 000	54 800 000	=+	/		\(7)
4073	Hha1	22	tcc	124.863	125	124.69	125.12	124.78	32 500 000	3 200 000	3 600 000	-=	\ (-)		\(7)
4074	Taq1	22	tcc	125.597	125	125.44	125.82	125.53	5 300 000	4 700 000	13 300 000	=+	/ (-)	/	\(7)
4075	Taq1	23	cga	124.375	125	124.33	0	124.42	5 900 000	0	12 400 000	-+(+)	V (/)		\(7)
4076	Taq1	23	cga	125.45	125	125.33	0	125.57	3 500 000	0	13 700 000	=+(+)	/	/	\(7)
4077	Taq1	45	gcc	147.485	148	147.68	147.29	0	6 500 000	4 800 000	0	=-	\		\(7)
4078	Taq1	45	gcc	148.61	148	148.61	0	0	5 300 000	0	0	-=	\		\(7)
4079	Taq1	27	acg	148.973	149	149.16	149.08	148.68	24 700 000	20 700 000	7 800 000	=-	\ (-)		\(7)
4080	Taq1	27	acg	149.8	149	0	149.91	149.69	0	10 900 000	21 500 000	++	/		\(7)
4081	Hha1	59	ttc	170.07	171	170.07	0	0	364.01	0	0	-=	\		\(7)
4082	Hha1	59	ttc	171.283	171	171.1	171.42	171.33	535.62	181.09	150.05	-=	\ (-)		\(7)
4083	Taq1	45	gcc	310.32	311	310.32	0	0	3 300 000	0	0	-=	\		\(7)
4084	Taq1	45	gcc	311.33	311	311.33	0	0	3 700 000	0	0	-=	\		\(7)
4085	Hha1	60	ttg	125.49	126	0	0	125.49	0	0	3 300 000	=+	/		-1
4086	Hha1	60	ttg	126.477	126	126.57	126.57	126.29	9 000 000	9 800 000	5 500 000	==	-	(-)	-1
4087	Hha1	61	tct	125.783	126	125.74	125.82	125.79	48 900 000	11 800 000	18 100 000	-=	\ (-)		-1

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
4045	RATLIMK2C.PE1	limk-2c	LIMK-2c		ctg	ctc	decreased
4046	RATLIMK2C.PE1	limk-2c	LIMK-2c		ctg	ctc	decreased
4047	RATLIMK2C.PE1	limk-2c	LIMK-2c		ctg	ctc	decreased
4048	RATLIMK2C.PE1	limk-2c	LIMK-2c		ctg	ctc	decreased
4049	RATLIMK2C.PE1	limk-2c	LIMK-2c		ctc	tgg	decreased
4050	AY057064.PE1	nc	liprin alpha 4		gac	ttc	increased
4051	AY057064.PE1	nc	liprin alpha 4		gac	ttc	increased
4052	AY057064.PE1	nc	liprin alpha 4		cag	tcg	increased
4053	AY057064.PE1	nc	liprin alpha 4		cca	cgg	increased
4054	AY057064.PE1	nc	liprin alpha 4		cca	cgg	increased
4055	AY057064.PE1	nc	liprin alpha 4		cca	cgg	increased
4056	AY057064.PE1	nc	liprin alpha 4		cca	cgg	increased
4057	AY057064.PE1	nc	liprin alpha 4		ctg	ggc	increased
4058	AY057064.PE1	nc	liprin alpha 4		ctg	ggc	increased
4059	AY327504.PE1	nc	liver regeneration-related protein LRRG03		aat	atg	increased by mild
4060	AY327504.PE1	nc	liver regeneration-related protein LRRG03		aat	atg	increased by mild
4061	AY327504.PE1	nc	liver regeneration-related protein LRRG03		aat	atg	increased by mild
4062	AY327504.PE1	nc	liver regeneration-related protein LRRG03		aat	atg	increased by mild
4063	AY327504.PE1	nc	liver regeneration-related protein LRRG03		aat	atg	increased by mild
4064	AY327504.PE1	nc	liver regeneration-related protein LRRG03		aat	atg	increased by mild
4065	AB064323.LON	Lon	Lon		aac	agc	increased
4066	AB064323.LON	Lon	Lon		ggt	agc	increased
4067	RATLTPBCA.PE1	nc	long type PB-cadherin		agg	cgt	increased
4068	RATLTPBCA.PE1	nc	long type PB-cadherin		ggg	gcc	increased
4069	RATLTPBCA.PE1	nc	long type PB-cadherin		ggg	gcc	increased
4070	RATLTPBCA.PE1	nc	long type PB-cadherin		tgg	cct	increased
4071	RATLTPBCA.PE1	nc	long type PB-cadherin		gtg	gtc	increased
4072	RATLTPBCA.PE1	nc	long type PB-cadherin		cga	tcc	increased
4073	RATLTPBCA.PE1	nc	long type PB-cadherin		cga	tcc	increased
4074	RATLTPBCA.PE1	nc	long type PB-cadherin		cga	tcc	decreased
4075	RATLTPBCA.PE1	nc	long type PB-cadherin		cga	tcc	increased
4076	RATLTPBCA.PE1	nc	long type PB-cadherin		cga	tcc	decreased
4077	RATLTPBCA.PE1	nc	long type PB-cadherin		gcc	acg	increased
4078	RATLTPBCA.PE1	nc	long type PB-cadherin		gcc	acg	increased
4079	RATLTPBCA.PE1	nc	long type PB-cadherin		gcc	acg	increased
4080	RATLTPBCA.PE1	nc	long type PB-cadherin		gcc	acg	increased
4081	RATLTPBCA.PE1	nc	long type PB-cadherin		tgt	ttc	increased
4082	RATLTPBCA.PE1	nc	long type PB-cadherin		tgt	ttc	increased
4083	RATLTPBCA.PE1	nc	long type PB-cadherin		gcc	ggt	increased
4084	RATLTPBCA.PE1	nc	long type PB-cadherin		gcc	ggt	increased
4085	AB070849.PE1	sglt2 beta	low affinity Na-dependent glucose transporter		tct	ttg	No change
4086	AB070849.PE1	sglt2 beta	low affinity Na-dependent glucose transporter		tct	ttg	No change
4087	AB070849.PE1	sglt2 beta	low affinity Na-dependent glucose transporter		tct	ttg	No change

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
4088	Hha1	61	tct	126.727	126	126.65	126.76	126.77	8 200 000	28 700 000	27 500 000	+=	/ (-)	(-)	-1
4089	Hha1	61	tct	125.783	126	125.74	125.82	125.79	48 900 000	11 800 000	18 100 000	-=	\ (-)		-1
4090	Hha1	61	tct	126.727	126	126.65	126.76	126.77	8 200 000	28 700 000	27 500 000	+=	/ (-)	(-)	-1
4091	Hha1	60	ttg	125.49	126	0	0	125.49	0	0	3 300 000	=+	/		-1
4092	Hha1	60	ttg	126.477	126	126.57	126.57	126.29	9 000 000	9 800 000	5 500 000	==	-	(-)	-1
4093	Hha1	61	tct	125.783	126	125.74	125.82	125.79	48 900 000	11 800 000	18 100 000	-=	\ (-)		-1
4094	Hha1	61	tct	126.727	126	126.65	126.76	126.77	8 200 000	28 700 000	27 500 000	+=	/ (-)	(-)	-1
4095	Hha1	33	agc	79.76	80	79.76	0	0	7 400 000	0	0	-=	\		\(2)
4096	Hha1	49	aaa	92.243	92	92.45	92.24	92.04	38 300 000	19 200 000	5 900 000	-=	\ (-)		\(2)
4097	Hha1	6	aga	150.743	151	150.74	150.79	150.7	63 700 000	38 400 000	13 400 000	==	-	-	
4098	Taq1	29	gca	150.953	151	150.99	151	150.87	9 600 000	8 600 000	6 900 000	==	-	-	
4099	Hha1	44	cgg	71.307	71	71.21	71.39	71.32	26 500 000	4 100 000	9 300 000	-=	\ (-)		\(6)
4100	Hha1	39	agg	144.21	145	0	144.41	144.01	0	191.05	211.58	+=	/		\(6)
4101	Hha1	39	agg	144.63	145	0	0	144.63	0	0	215.65	=+	/		\(6)
4102	Hha1	39	agg	145.82	145	0	146	145.64	0	770.19	797.52	+=	/		\(6)
4103	Taq1	39	agg	147.14	148	0	147.14	0	0	45 500 000	0	+-	A		\(6)
4104	Taq1	39	agg	148.14	148	148.24	148.04	0	11 300 000	15 600 000	0	=-	\		\(6)
4105	Taq1	39	agg	147.14	148	0	147.14	0	0	457.29	0	+-	A		\(6)
4106	Taq1	39	agg	148.14	148	148.24	148.04	0	419.63	156.78	0	-=	\		\(6)
4107	Taq1	44	cgg	177.595	178	177.37	177.82	0	1 024.19	602.97	0	=-	\		\(6)
4108	Taq1	44	cgg	178.5	178	0	178.5	0	0	861.38	0	+-	A		\(6)
4109	Taq1	21	acc	178.015	179	177.93	0	178.1	4 900 000	0	4 000 000	-+(=)	V		\(6)
4110	Taq1	21	acc	179.055	179	178.84	179.27	0	8 600 000	3 200 000	0	-=	\		\(6)
4111	Hha1	21	acc	179.96	179	0	0	179.96	0	0	6 200 000	=+	/		\(6)
4112	Hha1	40	tgg	209.925	210	0	210.06	209.79	0	3 000 000	4 400 000	+=	/		\(6)
4113	Hha1	40	tgg	210.2	210	0	0	210.2	0	0	4 100 000	=+	/		\(6)
4114	Hha1	40	tgg	210.95	210	210.85	211.05	0	5 400 000	7 700 000	0	=-	\		\(6)
4115	Taq1	50	aat	472.41	470	472.41	0	0	3 200 000	0	0	-=	\		\(6)
4116	Taq1	39	agg	90.495	91	90.7	0	90.29	125 800 000	0	23 600 000	-=(-)	\		\(5)
4117	Taq1	39	agg	90.957	91	90.7	90.97	91.2	4 671.71	172 200 000	3 800 000	+-	A		\(5)
4118	Taq1	39	agg	91.085	91	0	90.97	91.2	0	1 730.67	111.92	+-	A		\(5)
4119	Hha1	59	ttc	165.58	165	165.44	165.5	165.8	166.4	135.1	85.37	==	-		\(5)
4120	Taq1	7	caa	250.34	251	250.34	0	0	5 000 000	0	0	-=	\		\(5)
4121	Hha1	7	caa	251.52	251	251.52	0	0	4 500 000	0	0	-=	\	\	\(5)
4122	Taq1	7	caa	251.62	251	251.62	0	0	3 900 000	0	0	-=	\	\	\(5)
4123	Hha1	7	caa	252.07	251	252.07	0	0	5 900 000	0	0	-=	\		\(5)
4124	Taq1	39	agg	90.495	91	90.7	0	90.29	125 800 000	0	23 600 000	-=(-)	\		\(5)
4125	Taq1	39	agg	90.957	91	90.7	90.97	91.2	4 671.71	172 200 000	3 800 000	+-	A		\(5)
4126	Taq1	39	agg	91.085	91	0	90.97	91.2	0	1 730.67	111.92	+-	A		\(5)
4127	Hha1	59	ttc	165.58	165	165.44	165.5	165.8	166.4	135.1	85.37	==	-		\(5)
4128	Taq1	7	caa	250.34	251	250.34	0	0	5 000 000	0	0	-=	\		\(5)
4129	Hha1	7	caa	251.52	251	251.52	0	0	4 500 000	0	0	-=	\	\	\(5)
4130	Taq1	7	caa	251.62	251	251.62	0	0	3 900 000	0	0	-=	\	\	\(5)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
4088	AB070849.PE1	sglt2 beta	low affinity Na-dependent glucose transporter		tct	ttg	No change
4089	AB070849.PE1	sglt2 beta	low affinity Na-dependent glucose transporter		tct	ttg	No change
4090	AB070849.PE1	sglt2 beta	low affinity Na-dependent glucose transporter		tct	ttg	No change
4091	RNU29881.SGLT2	SGLT2	low affinity sodium-glucose cotransporter		tct	ttg	No change
4092	RNU29881.SGLT2	SGLT2	low affinity sodium-glucose cotransporter		tct	ttg	No change
4093	RNU29881.SGLT2	SGLT2	low affinity sodium-glucose cotransporter		tct	ttg	No change
4094	RNU29881.SGLT2	SGLT2	low affinity sodium-glucose cotransporter		tct	ttg	No change
4095	AY323237.QPC	Qpc	low molecular mass ubiquinone-binding protein		ctt	agc	increased
4096	AY323237.QPC	Qpc	low molecular mass ubiquinone-binding protein		cgc	aaa	increased
4097	AF086827.CACNA1I	CACNA1I	low voltage-activated T-type calcium channel		gca	aga	No change
4098	AF086827.CACNA1I	CACNA1I	low voltage-activated T-type calcium channel		gca	aga	No change
4099	RNCAA1G.CACNA1G	CACNA1G	low voltage-activated, T-type calcium channel	*	gga	cgg	increased
4100	RNCAA1G.CACNA1G	CACNA1G	low voltage-activated, T-type calcium channel	*	atc	agg	increased
4101	RNCAA1G.CACNA1G	CACNA1G	low voltage-activated, T-type calcium channel	*	atc	agg	increased
4102	RNCAA1G.CACNA1G	CACNA1G	low voltage-activated, T-type calcium channel	*	atc	agg	increased
4103	RNCAA1G.CACNA1G	CACNA1G	low voltage-activated, T-type calcium channel	*	gcg	agg	increased
4104	RNCAA1G.CACNA1G	CACNA1G	low voltage-activated, T-type calcium channel	*	gcg	agg	increased
4105	RNCAA1G.CACNA1G	CACNA1G	low voltage-activated, T-type calcium channel	*	gcg	agg	increased
4106	RNCAA1G.CACNA1G	CACNA1G	low voltage-activated, T-type calcium channel	*	gcg	agg	increased
4107	RNCAA1G.CACNA1G	CACNA1G	low voltage-activated, T-type calcium channel	*	cgg	acc	increased
4108	RNCAA1G.CACNA1G	CACNA1G	low voltage-activated, T-type calcium channel	*	cgg	acc	increased
4109	RNCAA1G.CACNA1G	CACNA1G	low voltage-activated, T-type calcium channel	*	cgg	acc	increased
4110	RNCAA1G.CACNA1G	CACNA1G	low voltage-activated, T-type calcium channel	*	cgg	acc	increased
4111	RNCAA1G.CACNA1G	CACNA1G	low voltage-activated, T-type calcium channel	*	cgg	acc	increased
4112	RNCAA1G.CACNA1G	CACNA1G	low voltage-activated, T-type calcium channel	*	tag	tgg	increased
4113	RNCAA1G.CACNA1G	CACNA1G	low voltage-activated, T-type calcium channel	*	tag	tgg	increased
4114	RNCAA1G.CACNA1G	CACNA1G	low voltage-activated, T-type calcium channel	*	tag	tgg	increased
4115	RNCAA1G.CACNA1G	CACNA1G	low voltage-activated, T-type calcium channel	*	gta	aat	increased
4116	AF394938.PE1	nc	L-type calcium channel alpha-1c subunit		ctt	agg	increased
4117	AF394938.PE1	nc	L-type calcium channel alpha-1c subunit		ctt	agg	increased
4118	AF394938.PE1	nc	L-type calcium channel alpha-1c subunit		ctt	agg	increased
4119	AF394938.PE1	nc	L-type calcium channel alpha-1c subunit		cca	ttc	increased
4120	AF394938.PE1	nc	L-type calcium channel alpha-1c subunit		caa	gct	increased
4121	AF394938.PE1	nc	L-type calcium channel alpha-1c subunit		caa	gct	increased
4122	AF394938.PE1	nc	L-type calcium channel alpha-1c subunit		caa	gct	increased
4123	AF394938.PE1	nc	L-type calcium channel alpha-1c subunit		caa	gct	increased
4124	AF394939.PE1	nc	L-type calcium channel alpha-1c subunit		ctt	agg	increased
4125	AF394939.PE1	nc	L-type calcium channel alpha-1c subunit		ctt	agg	increased
4126	AF394939.PE1	nc	L-type calcium channel alpha-1c subunit		ctt	agg	increased
4127	AF394939.PE1	nc	L-type calcium channel alpha-1c subunit		cca	ttc	increased
4128	AF394939.PE1	nc	L-type calcium channel alpha-1c subunit		caa	gct	increased
4129	AF394939.PE1	nc	L-type calcium channel alpha-1c subunit		caa	gct	increased
4130	AF394939.PE1	nc	L-type calcium channel alpha-1c subunit		caa	gct	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
4131	Hha1	7	caa	252.07	251	252.07	0	0	5 900 000	0	0	-=	\		\(5)
4132	Taq1	39	agg	90.495	91	90.7	0	90.29	125 800 000	0	23 600 000	-=(-)	\		\(5)
4133	Taq1	39	agg	90.957	91	90.7	90.97	91.2	4 671.71	172 200 000	3 800 000	+-	A		\(5)
4134	Taq1	39	agg	91.085	91	0	90.97	91.2	0	1 730.67	111.92	+-	A		\(5)
4135	Hha1	59	ttc	165.58	165	165.44	165.5	165.8	166.4	135.1	85.37	==	-		\(5)
4136	Taq1	7	caa	250.34	251	250.34	0	0	5 000 000	0	0	-=	\		\(5)
4137	Hha1	7	caa	251.52	251	251.52	0	0	4 500 000	0	0	-=	\	\	\(5)
4138	Taq1	7	caa	251.62	251	251.62	0	0	3 900 000	0	0	-=	\	\	\(5)
4139	Hha1	7	caa	252.07	251	252.07	0	0	5 900 000	0	0	-=	\		\(5)
4140	Hha1	8	gaa	106.345	106	0	106.18	106.51	0	5 600 000	6 200 000	+=	/	/	
4141	Taq1	8	gaa	106.5	106	0	0	106.5	0	0	30 800 000	=+	/	/	
4142	Hha1	22	tcc	135.305	136	0	135.43	135.18	0	8 700 000	5 000 000	+=	/		/(3) \(3)
4143	Taq1	22	tcc	135.645	136	135.57	0	135.72	6 100 000	0	38 300 000	=+(+)	/		/(3) \(3)
4144	Taq1	22	tcc	136.1	136	136.1	0	0	5 700 000	0	0	-=	\		/(3) \(3)
4145	Taq1	22	tcc	136.737	136	136.64	136.88	136.69	4 400 000	7 800 000	35 600 000	=+	/ (-)		/(3) \(3)
4146	Taq1	61	tct	135.837	136	135.78	135.92	135.81	3 700 000	12 300 000	15 600 000	+=	/ (-)		/(3) \(3)
4147	Taq1	45	gcc	237.79	238	237.79	0	0	3 100 000	0	0	-=	\		/(3) \(3)
4148	Hha1	8	gaa	238.66	239	238.83	238.49	0	4 500 000	3 100 000	0	=-	\		/(3) \(3)
4149	Taq1	39	agg	282.4	283	0	282.4	0	0	7 200 000	0	+-	A		\(2)
4150	Taq1	39	agg	283.73	283	283.73	0	0	4 300 000	0	0	-=	\		\(2)
4151	Taq1	39	agg	283.73	283	283.73	0	0	159.68	0	0	-=	\		\(2)
4152	Taq1	39	agg	282.4	283	0	282.4	0	0	72.36	0	+-	A		\(2)
4153	Taq1	8	gaa	374.78	375	374.78	0	0	3 200 000	0	0	-=	\		\(2)
4154	Hha1	40	tgg	179.9	180	0	179.9	0	0	6 400 000	0	+-	A		A(2)
4155	Hha1	59	ttc	179.45	180	0	179.45	0	0	160.97	0	+-	A		A(2)
4156	Hha1	41	ccc	228.457	229	228.5	228.44	228.43	4 000 000	5 200 000	14 400 000	=+	/ (-)		A(2)
4157	Hha1	41	ccc	229.483	229	229.5	229.47	229.48	8 100 000	38 800 000	140 800 000	=+	/ (-)		A(2)
4158	Hha1	20	ctc	84.1	84	0	84.12	84.08	0	8 811.95	894.56	+-	A		A(2)
4159	Hha1	39	agg	124.655	125	124.74	0	124.57	344.57	0	256.34	-+(=)	V		A(2)
4160	Hha1	39	agg	125.1	125	0	125.1	0	0	298.52	0	+-	A		A(2)
4161	Hha1	20	ctc	84.1	84	0	84.12	84.08	0	8 811.95	894.56	+-	A		A(2)
4162	Hha1	39	agg	124.655	125	124.74	0	124.57	344.57	0	256.34	-+(=)	V		A(2)
4163	Hha1	39	agg	125.1	125	0	125.1	0	0	298.52	0	+-	A		A(2)
4164	Hha1	40	tgg	172.767	173	172.84	172.73	172.73	13 200 000	4 600 000	4 100 000	-=	\ (-)		-(2) \(2)
4165	Hha1	40	tgg	173.72	173	0	0	173.72	0	0	4 200 000	=+	/		-(2) \(2)
4166	Taq1	14	gat	195.33	196	195.33	195.33	0	3 500 000	3 500 000	0	=-	\		-(2) \(2)
4167	Taq1	14	gat	196.483	196	196.49	196.49	196.47	3 300 000	3 300 000	3 000 000	==	-		-(2) \(2)
4168	Hha1	33	agc	67.933	68	67.9	68.03	67.87	4 300 000	8 100 000	32 400 000	=+	/ (-)		/(5)
4169	Hha1	44	cgg	86.575	87	86.59	0	86.56	3 100 000	0	4 600 000	-+(=)	V		/(5)
4170	Hha1	20	ctc	93.51	94	93.44	93.58	0	1 494.49	576.97	0	-=	\		/(5)
4171	Hha1	20	ctc	94.37	94	94.37	0	0	530.3	0	0	-=	\		/(5)
4172	Hha1	44	cgg	111.61	112	0	111.64	111.58	0	7 300 000	5 200 000	+=	/		/(5)
4173	Hha1	44	cgg	112.525	112	0	112.65	112.4	0	3 300 000	4 600 000	+=	/		/(5)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
4131	AF394939.PE1	nc	L-type calcium channel alpha-1c subunit		caa	gct	increased
4132	AF394940.PE1	nc	L-type calcium channel alpha-1c subunit		ctt	agg	increased
4133	AF394940.PE1	nc	L-type calcium channel alpha-1c subunit		ctt	agg	increased
4134	AF394940.PE1	nc	L-type calcium channel alpha-1c subunit		ctt	agg	increased
4135	AF394940.PE1	nc	L-type calcium channel alpha-1c subunit		cca	ttc	increased
4136	AF394940.PE1	nc	L-type calcium channel alpha-1c subunit		caa	gct	increased
4137	AF394940.PE1	nc	L-type calcium channel alpha-1c subunit		caa	gct	increased
4138	AF394940.PE1	nc	L-type calcium channel alpha-1c subunit		caa	gct	increased
4139	AF394940.PE1	nc	L-type calcium channel alpha-1c subunit		caa	gct	increased
4140	AF400662.PE1	nc	L-type calcium channel alpha2/delta subunit		tcc	gaa	decreased
4141	AF400662.PE1	nc	L-type calcium channel alpha2/delta subunit		tcc	gaa	decreased
4142	RNLPKG.PE1	nc	L-type pyruvate kinase		tct	tcc	decreased
4143	RNLPKG.PE1	nc	L-type pyruvate kinase		tct	tcc	decreased
4144	RNLPKG.PE1	nc	L-type pyruvate kinase		tct	tcc	decreased
4145	RNLPKG.PE1	nc	L-type pyruvate kinase		tct	tcc	decreased
4146	RNLPKG.PE1	nc	L-type pyruvate kinase		tct	tcc	decreased
4147	RNLPKG.PE1	nc	L-type pyruvate kinase		gaa	gcc	decreased
4148	RNLPKG.PE1	nc	L-type pyruvate kinase		gaa	gcc	decreased
4149	AB035510.LU	LU	Lutheran antigen		ctc	agg	increased
4150	AB035510.LU	LU	Lutheran antigen		ctc	agg	increased
4151	AB035510.LU	LU	Lutheran antigen		ctc	agg	increased
4152	AB035510.LU	LU	Lutheran antigen		ctc	agg	increased
4153	AB035510.LU	LU	Lutheran antigen		gaa	agg	increased
4154	RNO301677.F52	F52	Mac-MARCKS protein		ttc	tgg	increased by mild
4155	RNO301677.F52	F52	Mac-MARCKS protein		ttc	tgg	increased by mild
4156	RNO301677.F52	F52	Mac-MARCKS protein		ccc	tga	increased by mild
4157	RNO301677.F52	F52	Mac-MARCKS protein		ccc	tga	increased by mild
4158	RNU20999.PE1	nc	macrophage migration inhibitory factor		ctc	cag	increased by mild
4159	RNU20999.PE1	nc	macrophage migration inhibitory factor		agg	agg	increased by mild
4160	RNU20999.PE1	nc	macrophage migration inhibitory factor		agg	agg	increased by mild
4161	RNU62326.MIF	Mif	macrophage migration inhibitory factor		ctc	cag	increased by mild
4162	RNU62326.MIF	Mif	macrophage migration inhibitory factor		agg	agg	increased by mild
4163	RNU62326.MIF	Mif	macrophage migration inhibitory factor		agg	agg	increased by mild
4164	RNU56241.PE1	nc	Maf1		acc	tgg	No change
4165	RNU56241.PE1	nc	Maf1		acc	tgg	No change
4166	RNU56241.PE1	nc	Maf1		cgt	gat	No change
4167	RNU56241.PE1	nc	Maf1		cgt	gat	No change
4168	RNU56242.PE1	nc	Maf2		agc	cgg	decreased
4169	RNU56242.PE1	nc	Maf2		cgg	ccc	decreased
4170	RNU56242.PE1	nc	Maf2		acc	ctc	decreased
4171	RNU56242.PE1	nc	Maf2		acc	ctc	decreased
4172	RNU56242.PE1	nc	Maf2		aga	cgg	decreased
4173	RNU56242.PE1	nc	Maf2		aga	cgg	decreased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
4174	Hha1	20	ctc	113.32	114	113.32	0	0	1 721.76	0	0	-=	\		/(5)
4175	Hha1	20	ctc	114.24	114	0	0	114.24	0	0	500.95	=+	/		/(5)
4176	Taq1	17	cca	137.747	138	137.72	137.69	137.83	283.28	478.65	932.19	=+	/ (-)	(-)	/(5)
4177	Taq1	17	cca	138.79	138	138.65	138.81	138.91	283.28	265.92	2 044.8	=+	/ (-)		/(5)
4178	Taq1	29	gca	137.51	138	137.51	137.47	137.55	7 600 000	3 500 000	6 600 000	-=	\ (-)	(-)	/(5)
4179	Taq1	29	gca	138.537	138	138.49	138.52	138.6	5 300 000	6 100 000	5 400 000	==	-		/(5)
4180	Hha1	33	agc	139.36	140	139.43	139.46	139.19	10 300 000	7 000 000	32 600 000	=+	/ (-)		/(5)
4181	Hha1	33	agc	140.27	140	140.37	0	140.17	5 900 000	0	34 400 000	=+(+)	/		/(5)
4182	Hha1	27	acg	87.243	87	87.23	87.26	87.24	71 300 000	19 700 000	10 100 000	-=	\ (-)		\(2)
4183	Hha1	39	agg	134.885	135	134.82	0	134.95	454.54	0	227.86	-+(-)	V (\)		\(2)
4184	Hha1	39	agg	135.25	135	0	0	135.25	0	0	236	=+	/		\(2)
4185	Hha1	20	ctc	73.83	74	73.76	73.99	73.74	392.56	655.65	369.75	==	-		-3
4186	Hha1	20	ctc	74.44	74	0	74.49	74.39	0	773.66	763.35	+=	/		-3
4187	Hha1	59	ttc	73.915	74	0	73.97	73.86	0	1 069.33	721.8	+=	/		-3
4188	Hha1	33	agc	92.217	92	92.23	92.2	92.22	8 900 000	7 200 000	8 500 000	==	-		-3
4189	Hha1	26	ctg	113.7	114	113.66	113.69	113.75	8 500 000	5 900 000	5 200 000	==	-		-3
4190	Hha1	20	ctc	73.83	74	73.76	73.99	73.74	392.56	655.65	369.75	==	-		-3
4191	Hha1	20	ctc	74.44	74	0	74.49	74.39	0	773.66	763.35	+=	/		-3
4192	Hha1	59	ttc	73.915	74	0	73.97	73.86	0	1 069.33	721.8	+=	/		-3
4193	Hha1	33	agc	92.217	92	92.23	92.2	92.22	8 900 000	7 200 000	8 500 000	==	-		-3
4194	Hha1	26	ctg	113.7	114	113.66	113.69	113.75	8 500 000	5 900 000	5 200 000	==	-		-3
4195	Taq1	45	gcc	72.893	73	72.81	72.84	73.03	71 800 000	45 600 000	9 500 000	=-	\ (-)		-3
4196	Hha1	15	tac	146.31	147	146.27	146.34	146.32	10 000 000	7 900 000	11 900 000	==	-		-3
4197	Hha1	15	tac	146.333	147	146.34	146.34	146.32	2 020.05	2 034.5	2 588.08	==	-		-3
4198	Hha1	59	ttc	147.013	147	147.11	147.01	146.92	176.8	215.59	349.26	==	-		-3
4199	Hha1	6	aga	205.605	206	205.45	205.76	0	3 800 000	3 800 000	0	=-	\		-3
4200	Hha1	6	aga	206.72	206	206.72	0	0	10 500 000	0	0	-=	\		-3
4201	Taq1	36	ggt	120.61	121	120.6	0	120.62	3 800 000	0	5 400 000	-+(=)	V		\(3)
4202	Taq1	36	ggt	121.59	121	0	0	121.59	0	0	3 000 000	=+	/	/	\(3)
4203	Taq1	40	tgg	120.38	121	120.22	120.32	120.6	5 900 000	107 000 000	9 700 000	+-	A		\(3)
4204	Taq1	40	tgg	120.94	121	120.79	121.09	0	22 800 000	13 300 000	0	=-	\		\(3)
4205	Taq1	40	tgg	121.58	121	0	0	121.58	0	0	8 700 000	=+	/	/	\(3)
4206	Hha1	40	tgg	222.635	223	222.71	222.56	0	4 400 000	4 800 000	0	=-	\		\(3)
4207	Taq1	17	cca	247.325	247	247.19	247.46	0	181.11	239.32	0	=-	\		\(3)
4208	Taq1	17	cca	247.92	247	247.92	0	0	297.21	0	0	-=	\		\(3)
4209	Taq1	17	cca	248.33	247	248.33	0	0	236.84	0	0	-=	\		\(3)
4210	Hha1	27	acg	73.827	74	73.8	73.91	73.77	70 000 000	22 000 000	43 500 000	-=	\ (-)		\(2)
4211	Taq1	39	agg	156.95	157	0	156.95	0	0	38 200 000	0	+-	A		\(2)
4212	Taq1	39	agg	156.26	157	0	156.26	0	0	114.57	0	+-	A		\(2)
4213	Taq1	39	agg	156.95	157	0	156.95	0	0	383.92	0	+-	A		\(2)
4214	Taq1	39	agg	157.71	157	157.71	0	0	4 600 000	0	0	-=	\		\(2)
4215	Taq1	39	agg	156.06	157	156.06	0	0	185.68	0	0	-=	\		\(2)
4216	Taq1	39	agg	157.71	157	157.71	0	0	170.82	0	0	-=	\		\(2)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
4174	RNU56242.PE1	nc	Maf2		ctc	ggc	decreased
4175	RNU56242.PE1	nc	Maf2		ctc	ggc	decreased
4176	RNU56242.PE1	nc	Maf2		cca	gca	No change
4177	RNU56242.PE1	nc	Maf2		cca	gca	decreased
4178	RNU56242.PE1	nc	Maf2		cca	gca	No change
4179	RNU56242.PE1	nc	Maf2		cca	gca	decreased
4180	RNU56242.PE1	nc	Maf2		cct	agc	decreased
4181	RNU56242.PE1	nc	Maf2		cct	agc	decreased
4182	RNTR1AUAG.PE1	RT1.Alu	major histocompatibility complex class I		acg	ggg	increased
4183	RNTR1AUAG.PE1	RT1.Alu	major histocompatibility complex class I		ggt	agg	increased
4184	RNTR1AUAG.PE1	RT1.Alu	major histocompatibility complex class I		ggt	agg	increased
4185	AF304865.PE1	nc	malonyl-CoA decarboxylase		ttc	ctc	No change
4186	AF304865.PE1	nc	malonyl-CoA decarboxylase		ttc	ctc	No change
4187	AF304865.PE1	nc	malonyl-CoA decarboxylase		ttc	ctc	No change
4188	AF304865.PE1	nc	malonyl-CoA decarboxylase		cat	agc	No change
4189	AF304865.PE1	nc	malonyl-CoA decarboxylase		ctg	tag	No change
4190	RNO7704.PE1	nc	malonyl-Coa decarboxylase		ttc	ctc	No change
4191	RNO7704.PE1	nc	malonyl-Coa decarboxylase		ttc	ctc	No change
4192	RNO7704.PE1	nc	malonyl-Coa decarboxylase		ttc	ctc	No change
4193	RNO7704.PE1	nc	malonyl-Coa decarboxylase		cat	agc	No change
4194	RNO7704.PE1	nc	malonyl-Coa decarboxylase		ctg	tag	No change
4195	AY371924.MDGA2	Mdga2	MAM domain-containing		gac	gcc	No change
4196	AY371924.MDGA2	Mdga2	MAM domain-containing		tac	ttc	No change
4197	AY371924.MDGA2	Mdga2	MAM domain-containing		tac	ttc	No change
4198	AY371924.MDGA2	Mdga2	MAM domain-containing		tac	ttc	No change
4199	AY371924.MDGA2	Mdga2	MAM domain-containing		ctt	aga	No change
4200	AY371924.MDGA2	Mdga2	MAM domain-containing		ctt	aga	No change
4201	RNU59809.M6P	M6P/IGF2r	mannose 6-phosphate/insulin-like growth factor		ggt	tgg	increased
4202	RNU59809.M6P	M6P/IGF2r	mannose 6-phosphate/insulin-like growth factor		ggt	tgg	decreased
4203	RNU59809.M6P	M6P/IGF2r	mannose 6-phosphate/insulin-like growth factor		ggt	tgg	increased
4204	RNU59809.M6P	M6P/IGF2r	mannose 6-phosphate/insulin-like growth factor		ggt	tgg	increased
4205	RNU59809.M6P	M6P/IGF2r	mannose 6-phosphate/insulin-like growth factor		ggt	tgg	decreased
4206	RNU59809.M6P	M6P/IGF2r	mannose 6-phosphate/insulin-like growth factor		ttc	tgg	increased
4207	RNU59809.M6P	M6P/IGF2r	mannose 6-phosphate/insulin-like growth factor		tat	cca	increased
4208	RNU59809.M6P	M6P/IGF2r	mannose 6-phosphate/insulin-like growth factor		tat	cca	increased
4209	RNU59809.M6P	M6P/IGF2r	mannose 6-phosphate/insulin-like growth factor		tat	cca	increased
4210	RNMAPKIN.PE1	nc	MAP kinase		gta	acg	increased
4211	RNMAPKIN.PE1	nc	MAP kinase		cgt	agg	increased
4212	RNMAPKIN.PE1	nc	MAP kinase		cgt	agg	increased
4213	RNMAPKIN.PE1	nc	MAP kinase		cgt	agg	increased
4214	RNMAPKIN.PE1	nc	MAP kinase		cgt	agg	increased
4215	RNMAPKIN.PE1	nc	MAP kinase		cgt	agg	increased
4216	RNMAPKIN.PE1	nc	MAP kinase		cgt	agg	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
4217	Hha1	26	ctg	98.155	98	98.13	98.18	0	5 200 000	3 900 000	0	=-	\	\	
4218	Hha1	33	agc	98.18	98	98.15	98.21	0	3 100 000	3 100 000	0	=-	\	\	
4219	Taq1	17	cca	138.79	139	138.65	138.81	138.91	283.28	265.92	2 044.8	=+	/ (-)		-1
4220	Taq1	17	cca	139.775	139	139.67	0	139.88	171.82	0	1 037.43	=+(+)	/	/	-1
4221	Taq1	29	gca	138.537	139	138.49	138.52	138.6	5 300 000	6 100 000	5 400 000	==	-		-1
4222	Taq1	29	gca	139.62	139	0	0	139.62	0	0	5 300 000	=+	/	/	-1
4223	Hha1	20	ctc	65.19	65	65.1	65.11	65.36	495.86	3 606.08	8 826.33	=+	/ (-)		-3
4224	Taq1	44	cgg	96	96	0	96.03	95.97	0	1 521.78	4 303.96	=+	/		-3
4225	Taq1	29	gca	97.373	97	97.38	97.33	97.41	34 200 000	15 300 000	5 200 000	-=	\ (-)		-3
4226	Hha1	28	tcg	134.287	135	134.25	134.3	134.31	22 900 000	12 300 000	5 200 000	-=	\ (-)		-3
4227	Hha1	28	tcg	135.117	135	135.41	134.98	134.96	4 800 000	16 700 000	7 700 000	+-	A		-3
4228	Taq1	27	acg	109.523	110	109.41	109.55	109.61	15 400 000	17 200 000	15 000 000	==	-	-	-2
4229	Taq1	27	acg	110.55	110	110.45	110.53	110.67	57 500 000	67 500 000	47 400 000	==	-		-2
4230	Taq1	36	ggt	109.51	110	109.52	109.46	109.55	9 000 000	6 200 000	3 000 000	==	-	-	-2
4231	Taq1	36	ggt	110.59	110	0	110.59	0	0	3 600 000	0	+-	A		-2
4232	Taq1	64	gtt	275.93	276	0	275.93	0	0	3 900 000	0	+-	A		A(2)
4233	Taq1	49	aaa	288.24	289	288.24	0	0	6 900 000	0	0	-=	\		A(2)
4234	Taq1	49	aaa	289.1	289	289.12	289.08	0	8 000 000	7 200 000	0	=-	\		A(2)
4235	Taq1	49	aaa	289.78	289	0	289.78	0	0	5 500 000	0	+-	A		A(2)
4236	Taq1	49	aaa	290.615	289	290.39	290.84	0	16 600 000	7 000 000	0	-=	\		A(2)
4237	Taq1	39	agg	71.635	72	71.65	71.62	0	21 000 000	36 900 000	0	=-	\		\(14)
4238	Taq1	39	agg	72.38	72	72.48	72.3	72.36	58 700 000	5 800 000	10 200 000	-=	\ (-)		\(14)
4239	Taq1	39	agg	71.635	72	71.65	71.62	0	779.85	370.85	0	--	\		\(14)
4240	Taq1	39	agg	72.38	72	72.48	72.3	72.36	2 179.88	58.29	300.44	-=	\ (-)		\(14)
4241	Hha1	10	atg	100.15	100	100.34	99.96	0	5 900 000	7 800 000	0	=-	\		\(14)
4242	Taq1	10	atg	99.693	100	99.83	99.79	99.46	152 900 000	53 000 000	3 300 000	-=	\ (-)		\(14)
4243	Taq1	19	cac	99.56	100	99.56	0	0	7 300 000	0	0	-=	\		\(14)
4244	Taq1	19	cac	100.46	100	0	0	100.46	0	0	13 300 000	=+	/		\(14)
4245	Hha1	12	agt	123.87	124	123.87	0	0	2 507.75	0	0	-=	\		\(14)
4246	Hha1	6	aga	151.28	152	151.28	0	0	25 900 000	0	0	-=	\		\(14)
4247	Hha1	6	aga	151.84	152	0	151.84	0	0	5 700 000	0	+-	A		\(14)
4248	Hha1	11	act	151.207	152	151.21	151.29	151.12	11 300 000	12 700 000	9 000 000	==	-		\(14)
4249	Taq1	11	act	151.385	152	151.44	151.33	0	9 500 000	14 700 000	0	=-	\		\(14)
4250	Taq1	11	act	152.02	152	0	0	152.02	0	0	7 600 000	=+	/		\(14)
4251	Hha1	11	act	152.18	152	0	152.18	0	0	3 500 000	0	+-	A		\(14)
4252	Taq1	11	act	152.4	152	152.42	152.38	0	9 600 000	5 900 000	0	=-	\		\(14)
4253	Taq1	40	tgg	153.42	154	0	153.42	0	0	314 800 000	0	+-	A		\(14)
4254	Taq1	40	tgg	154.225	154	0	154.28	154.17	0	65 000 000	11 300 000	+-	A		\(14)
4255	Taq1	54	ttt	154.675	155	154.61	154.74	0	1 194.46	1 493.59	0	=-	\		\(14)
4256	Taq1	54	ttt	155.557	155	155.53	155.56	155.58	8 761.83	11 654.71	1 199.14	=-	\ (-)		\(14)
4257	Taq1	25	cat	187.575	188	187.73	187.42	0	791.59	509.22	0	=-	\		\(14)
4258	Taq1	25	cat	188.605	188	188.8	188.41	0	1 296.57	1 654.99	0	=-	\		\(14)
4259	Taq1	18	cct	190.3	191	190.41	190.19	0	3 000 000	4 900 000	0	=-	\		\(14)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
4217	RNU48596.MEKK1	MEKK1	MAP kinase kinase kinase 1		ctg	agc	increased
4218	RNU48596.MEKK1	MEKK1	MAP kinase kinase kinase 1		ctg	agc	increased
4219	RNMAP2D.MAP2	MAP2	MAP2d		cca	gca	No change
4220	RNMAP2D.MAP2	MAP2	MAP2d		cca	gca	decreased
4221	RNMAP2D.MAP2	MAP2	MAP2d		cca	gca	No change
4222	RNMAP2D.MAP2	MAP2	MAP2d		cca	gca	decreased
4223	AF013144.CPG21	cpg21	MAP-kinase phosphatase		aag	ctc	No change
4224	AF013144.CPG21	cpg21	MAP-kinase phosphatase		cgg	gca	No change
4225	AF013144.CPG21	cpg21	MAP-kinase phosphatase		cgg	gca	No change
4226	AF013144.CPG21	cpg21	MAP-kinase phosphatase		tcg	ggc	No change
4227	AF013144.CPG21	cpg21	MAP-kinase phosphatase		tcg	ggc	No change
4228	RNU58857.PE1	nc	maspin		ggt	acg	No change
4229	RNU58857.PE1	nc	maspin		ggt	acg	No change
4230	RNU58857.PE1	nc	maspin		ggt	acg	No change
4231	RNU58857.PE1	nc	maspin		ggt	acg	No change
4232	AF043642.PE1	matrin-cyp	matrin cyclophilin		ttc	gtt	increased by mild
4233	AF043642.PE1	matrin-cyp	matrin cyclophilin		aaa	tcc	increased by mild
4234	AF043642.PE1	matrin-cyp	matrin cyclophilin		aaa	tcc	increased by mild
4235	AF043642.PE1	matrin-cyp	matrin cyclophilin		aaa	tcc	increased by mild
4236	AF043642.PE1	matrin-cyp	matrin cyclophilin		aaa	tcc	increased by mild
4237	RATMEGA.GP330	nc	megalin		gtg	agg	increased
4238	RATMEGA.GP330	nc	megalin		gtg	agg	increased
4239	RATMEGA.GP330	nc	megalin		gtg	agg	increased
4240	RATMEGA.GP330	nc	megalin		gtg	agg	increased
4241	RATMEGA.GP330	nc	megalin		atg	cac	increased
4242	RATMEGA.GP330	nc	megalin		atg	cac	increased
4243	RATMEGA.GP330	nc	megalin		atg	cac	increased
4244	RATMEGA.GP330	nc	megalin		atg	cac	increased
4245	RATMEGA.GP330	nc	megalin		caa	agt	increased
4246	RATMEGA.GP330	nc	megalin		aga	act	increased
4247	RATMEGA.GP330	nc	megalin		aga	act	increased
4248	RATMEGA.GP330	nc	megalin		aga	act	increased
4249	RATMEGA.GP330	nc	megalin		aga	act	increased
4250	RATMEGA.GP330	nc	megalin		aga	act	increased
4251	RATMEGA.GP330	nc	megalin		aga	act	increased
4252	RATMEGA.GP330	nc	megalin		aga	act	increased
4253	RATMEGA.GP330	nc	megalin		tgg	ttt	increased
4254	RATMEGA.GP330	nc	megalin		tgg	ttt	increased
4255	RATMEGA.GP330	nc	megalin		tgg	ttt	increased
4256	RATMEGA.GP330	nc	megalin		tgg	ttt	increased
4257	RATMEGA.GP330	nc	megalin		cat	agc	increased
4258	RATMEGA.GP330	nc	megalin		cat	agc	increased
4259	RATMEGA.GP330	nc	megalin		gtt	cct	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
4260	Taq1	18	cct	191.205	191	191.16	191.25	0	3 300 000	5 000 000	0	=-	\		\(14)
4261	Taq1	64	gtt	189.95	191	189.96	189.86	190.03	5 500 000	7 100 000	3 200 000	=-	\ (-)		\(14)
4262	Taq1	64	gtt	190.96	191	191.06	190.93	190.89	4 600 000	5 700 000	3 800 000	==	-		\(14)
4263	Taq1	64	gtt	191.993	191	191.98	191.96	192.04	4 700 000	4 700 000	5 300 000	==	-		\(14)
4264	Taq1	51	ata	217.995	219	217.94	218.05	0	7 100 000	5 900 000	0	=-	\		\(14)
4265	Taq1	51	ata	219.84	219	219.84	0	0	6 400 000	0	0	-=	\		\(14)
4266	Hha1	6	aga	248.48	247	248.48	0	0	4 600 000	0	0	-=	\		\(14)
4267	Hha1	26	ctg	147.13	148	147.09	147.06	147.24	7 700 000	4 900 000	4 100 000	==	-		/(3)
4268	Hha1	26	ctg	148.08	148	0	0	148.08	0	0	3 900 000	=+	/		/(3)
4269	Hha1	28	tcg	147.46	148	0	147.35	147.57	0	4 500 000	3 700 000	+=	/		/(3)
4270	Taq1	34	tgc	384.57	385	0	0	384.57	0	0	6 100 000	=+	/		/(3)
4271	Hha1	33	agc	158.6	159	0	0	158.6	0	0	20 700 000	=+	/		-1
4272	Hha1	33	agc	159.603	159	159.63	159.66	159.52	4 200 000	6 000 000	31 200 000	=+	/ (-)		-1
4273	Hha1	39	agg	164.92	165	0	0	164.92	0	0	268.55	=+	/		-1
4274	Hha1	39	agg	165.565	165	0	165.46	165.67	0	322.4	236	+=	/		-1
4275	Taq1	14	gat	168.6	169	168.6	168.6	0	5 400 000	5 400 000	0	=-	\		-1
4276	Taq1	14	gat	169.6	169	169.58	169.58	169.64	5 900 000	5 900 000	4 800 000	==	-		-1
4277	Hha1	15	tac	130.033	130	130.01	130.03	130.06	23 000 000	26 600 000	38 100 000	==	-	(-)	
4278	Hha1	15	tac	130.067	130	130.11	130.03	130.06	5 207.24	6 850.37	8 286.21	==	-	(-)	
4279	Hha1	33	agc	130.103	130	129.97	130.2	130.14	5 800 000	9 900 000	4 400 000	=-	\ (-)	(-)	
4280	Hha1	44	cgg	71.307	71	71.21	71.39	71.32	26 500 000	4 100 000	9 300 000	-=	\ (-)		\(2)
4281	Hha1	39	agg	73.733	74	73.74	73.57	73.89	4 428.15	12 096.24	4 785.15	+-	A		\(2)
4282	Taq1	50	aat	229.445	230	229.59	229.3	0	6 700 000	5 600 000	0	=-	\		\(2)
4283	Taq1	50	aat	230.565	230	230.43	230.7	0	9 600 000	7 600 000	0	=-	\		\(2)
4284	Hha1	44	cgg	144.455	145	144.66	144.25	0	4 900 000	3 900 000	0	=-	\		\(4)
4285	Hha1	44	cgg	144.72	145	0	144.72	0	0	4 100 000	0	+-	A		\(4)
4286	Hha1	26	ctg	146.06	146	0	146.06	0	0	3 800 000	0	+-	A		\(4)
4287	Hha1	27	acg	168.955	169	168.86	0	169.05	7 500 000	0	4 000 000	-+(-)	V (\)		\(4)
4288	Hha1	27	acg	169.835	169	169.79	0	169.88	6 800 000	0	4 700 000	-+(=)	V		\(4)
4289	Hha1	56	tga	181.72	182	181.52	181.73	181.91	780.45	220.16	551.62	-=	\ (-)		\(4)
4290	Hha1	56	tga	182.52	182	182.57	182.47	0	179.78	209.15	0	=-	\		\(4)
4291	Hha1	56	tga	183.085	182	0	183.14	183.03	0	335.75	741.25	++	/		\(4)
4292	Hha1	40	tgg	243.765	245	243.61	243.92	0	7 100 000	5 000 000	0	=-	\		\(4)
4293	Hha1	40	tgg	246.45	245	246.41	0	246.49	4 400 000	0	3 900 000	-+(=)	V		\(4)
4294	Hha1	32	gtc	190.163	191	190.1	190.17	190.22	952.03	661.24	782.19	==	-		\(3)
4295	Hha1	32	gtc	190.78	191	0	0	190.78	0	0	361.01	=+	/		\(3)
4296	Hha1	33	agc	190.18	191	190.1	190.26	0	4 300 000	3 300 000	0	=-	\		\(3)
4297	Taq1	45	gcc	194.35	195	0	194.35	0	0	4 300 000	0	+-	A		\(3)
4298	Hha1	6	aga	256.33	256	256.33	0	0	3 800 000	0	0	-=	\		\(3)
4299	Hha1	6	aga	257.24	256	257.24	0	0	6 000 000	0	0	-=	\	\	\(3)
4300	Taq1	64	gtt	254.98	256	254.98	0	0	3 300 000	0	0	-=	\		\(3)
4301	Taq1	64	gtt	256.99	256	256.99	0	0	3 000 000	0	0	-=	\	\	\(3)
4302	Hha1	4	aag	171.585	171	0	171.51	171.66	0	6 900 000	6 600 000	+=	/	/	

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
4260	RATMEGA.GP330	nc	megalin		gtt	cct	increased
4261	RATMEGA.GP330	nc	megalin		gtt	cct	increased
4262	RATMEGA.GP330	nc	megalin		gtt	cct	increased
4263	RATMEGA.GP330	nc	megalin		gtt	cct	increased
4264	RATMEGA.GP330	nc	megalin		ttg	ata	increased
4265	RATMEGA.GP330	nc	megalin		ttg	ata	increased
4266	RATMEGA.GP330	nc	megalin		gtc	aga	increased
4267	AB011530.MEGF4	MEGF4	MEGF4		ctg	tcg	decreased
4268	AB011530.MEGF4	MEGF4	MEGF4		ctg	tcg	decreased
4269	AB011530.MEGF4	MEGF4	MEGF4		ctg	tcg	decreased
4270	AB011530.MEGF4	MEGF4	MEGF4		tgc	agg	decreased
4271	AB011532.MEGF6	MEGF6	MEGF6		ccg	agc	No change
4272	AB011532.MEGF6	MEGF6	MEGF6		ccg	agc	No change
4273	AB011532.MEGF6	MEGF6	MEGF6		agg	att	No change
4274	AB011532.MEGF6	MEGF6	MEGF6		agg	att	No change
4275	AB011532.MEGF6	MEGF6	MEGF6		gat	tac	No change
4276	AB011532.MEGF6	MEGF6	MEGF6		gat	tac	No change
4277	AB040807.MLS2S	MLS2s	melastatin like 2		tac	agc	No change
4278	AB040807.MLS2S	MLS2s	melastatin like 2		tac	agc	No change
4279	AB040807.MLS2S	MLS2s	melastatin like 2		tac	agc	No change
4280	AB06968S27.ATRN	Atrn	membrane attractin	*	cgg	ccg	increased
4281	AB06968S27.ATRN	Atrn	membrane attractin	*	ccg	agg	increased
4282	AB06968S27.ATRN	Atrn	membrane attractin	*	aat	agc	increased
4283	AB06968S27.ATRN	Atrn	membrane attractin	*	aat	agc	increased
4284	AB049189.PE1	nc	membrane bound arginine specific serine		cgg	ctg	increased
4285	AB049189.PE1	nc	membrane bound arginine specific serine		cgg	ctg	increased
4286	AB049189.PE1	nc	membrane bound arginine specific serine		cgg	ctg	increased
4287	AB049189.PE1	nc	membrane bound arginine specific serine		agt	acg	increased
4288	AB049189.PE1	nc	membrane bound arginine specific serine		agt	acg	increased
4289	AB049189.PE1	nc	membrane bound arginine specific serine		tga	gat	increased
4290	AB049189.PE1	nc	membrane bound arginine specific serine		tga	gat	increased
4291	AB049189.PE1	nc	membrane bound arginine specific serine		tga	gat	increased
4292	AB049189.PE1	nc	membrane bound arginine specific serine		tgg	ttc	increased
4293	AB049189.PE1	nc	membrane bound arginine specific serine		tgg	ttc	increased
4294	AF212861.MIR16	Mir16	membrane interacting protein of RGS16		agc	gtc	increased
4295	AF212861.MIR16	Mir16	membrane interacting protein of RGS16		agc	gtc	increased
4296	AF212861.MIR16	Mir16	membrane interacting protein of RGS16		agc	gtc	increased
4297	AF212861.MIR16	Mir16	membrane interacting protein of RGS16		gcc	tgt	increased
4298	AF212861.MIR16	Mir16	membrane interacting protein of RGS16		gtt	aga	increased
4299	AF212861.MIR16	Mir16	membrane interacting protein of RGS16		gtt	aga	increased
4300	AF212861.MIR16	Mir16	membrane interacting protein of RGS16		gtt	aga	increased
4301	AF212861.MIR16	Mir16	membrane interacting protein of RGS16		gtt	aga	increased
4302	AF102854.PE1	nc	membrane-associated guanylate kinase-interacting		aag	ctg	decreased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
4303	Taq1	26	ctg	171.56	171	0	0	171.56	0	0	3 500 000	=+	/	/	
4304	Taq1	29	gca	98.353	98	98.39	98.28	98.39	19 100 000	8 200 000	10 300 000	-=	\ (-)		V(3)
4305	Taq1	61	tct	98.24	98	98.19	0	98.29	12 500 000	0	12 300 000	-+(=)	V		V(3)
4306	Hha1	6	aga	175.995	177	175.96	0	176.03	4 500 000	0	9 800 000	-+(+)	V (/)		V(3)
4307	Hha1	6	aga	177.05	177	0	0	177.05	0	0	9 400 000	=+	/		V(3)
4308	Hha1	6	aga	177.935	177	177.81	0	178.06	3 900 000	0	10 900 000	=+(+)	/		V(3)
4309	Taq1	40	tgg	177.575	177	177.51	0	177.64	4 400 000	0	5 200 000	-+(=)	V		V(3)
4310	Hha1	59	ttc	100.097	100	99.97	100.31	100.01	171.6	494.42	952.06	=+	/ (-)		-2
4311	Hha1	12	agt	177.05	178	177.09	177	177.06	1 887.28	2 493.88	3 047.09	==	-		-2
4312	Taq1	25	cat	151.097	151	151.13	150.89	151.27	443.56	1 336.72	1 240.01	+=	/ (-)	(-)	-4
4313	Taq1	29	gca	150.953	151	150.99	151	150.87	9 600 000	8 600 000	6 900 000	==	-	(-)	-4
4314	Taq1	29	gca	151.897	151	151.87	151.92	151.9	15 000 000	11 300 000	6 800 000	==	-		-4
4315	Hha1	20	ctc	161.05	162	161.26	160.95	160.94	213.49	458.95	596.37	==	-		-4
4316	Hha1	20	ctc	161.51	162	0	0	161.51	0	0	417.46	=+	/		-4
4317	Hha1	61	tct	189.98	190	190.02	189.96	189.96	4 700 000	4 900 000	3 900 000	==	-		-4
4318	Taq1	52	att	211.475	212	211.56	211.39	0	6 400 000	4 500 000	0	=-	\		-4
4319	Hha1	59	ttc	115.51	116	0	115.28	115.74	0	201.21	152.64	+=	/	/	
4320	Hha1	60	ttg	115.495	116	0	115.48	115.51	0	3 200 000	7 100 000	++	/	/	
4321	Hha1	12	agt	119.207	119	119.09	119.16	119.37	7 988.62	6 308.06	4 801.47	==	-	-	
4322	Hha1	26	ctg	118.97	119	118.97	118.97	118.97	9 400 000	7 800 000	5 400 000	==	-	-	
4323	Taq1	25	cat	151.097	151	151.13	150.89	151.27	443.56	1 336.72	1 240.01	+=	/ (-)	(-)	-4
4324	Taq1	29	gca	150.953	151	150.99	151	150.87	9 600 000	8 600 000	6 900 000	==	-	(-)	-4
4325	Taq1	29	gca	151.897	151	151.87	151.92	151.9	15 000 000	11 300 000	6 800 000	==	-		-4
4326	Hha1	20	ctc	161.05	162	161.26	160.95	160.94	213.49	458.95	596.37	==	-		-4
4327	Hha1	20	ctc	161.51	162	0	0	161.51	0	0	417.46	=+	/		-4
4328	Hha1	61	tct	189.98	190	190.02	189.96	189.96	4 700 000	4 900 000	3 900 000	==	-		-4
4329	Taq1	52	att	211.475	212	211.56	211.39	0	6 400 000	4 500 000	0	=-	\		-4
4330	Hha1	12	agt	119.207	119	119.09	119.16	119.37	7 988.62	6 308.06	4 801.47	==	-	-	
4331	Hha1	26	ctg	118.97	119	118.97	118.97	118.97	9 400 000	7 800 000	5 400 000	==	-	-	
4332	Hha1	54	ttt	90.523	91	90.49	90.49	90.59	3 700 000	4 700 000	6 000 000	==	-		-2
4333	Hha1	32	gtc	120.58	120	120.53	120.63	0	1 501.28	579.85	0	-=	\		-2
4334	Taq1	64	gtt	182.69	183	182.72	182.7	182.65	4 400 000	4 000 000	3 100 000	==	-		-2
4335	Taq1	64	gtt	183.73	183	183.77	183.7	183.72	4 600 000	6 300 000	3 500 000	==	-		-2
4336	Taq1	17	cca	121.493	121	121.29	121.59	121.6	306.5	219.38	631.48	=+	/ (-)	/	
4337	Taq1	36	ggt	121.59	121	0	0	121.59	0	0	3 000 000	=+	/	/	
4338	Hha1	44	cgg	83.6	84	83.72	83.48	0	10 900 000	6 800 000	0	=-	\		\(2)
4339	Hha1	44	cgg	84.433	84	84.62	84.37	84.31	10 200 000	9 000 000	3 600 000	=-	\ (-)		\(2)
4340	Hha1	59	ttc	85.28	85	85.4	85.16	0	962.03	94.86	0	-=	\		\(2)
4341	Hha1	26	ctg	177.995	178	0	177.99	178	0	3 600 000	5 400 000	+=	/		\(2)
4342	Hha1	15	tac	179.05	178	0	0	179.05	0	0	3 900 000	=+	/		/(2)
4343	Hha1	39	agg	176.94	178	0	177.1	176.78	0	310.46	236	+=	/		/(2)
4344	Hha1	39	agg	178.22	178	0	178.4	178.04	0	220.9	183.1	+=	/		/(2)
4345	Hha1	27	acg	87.243	87	87.23	87.26	87.24	71 300 000	19 700 000	10 100 000	-=	\ (-)		/(2)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
4303	AF102854.PE1	nc	membrane-associated guanylate kinase-interacting		aag	ctg	decreased
4304	AF359355.PE1	nc	membrane-bound aminopeptidase P		tct	gca	decreased by mild
4305	AF359355.PE1	nc	membrane-bound aminopeptidase P		tct	gca	decreased by mild
4306	AF359355.PE1	nc	membrane-bound aminopeptidase P		aga	tgg	decreased by mild
4307	AF359355.PE1	nc	membrane-bound aminopeptidase P		aga	tgg	decreased by mild
4308	AF359355.PE1	nc	membrane-bound aminopeptidase P		aga	tgg	decreased by mild
4309	AF359355.PE1	nc	membrane-bound aminopeptidase P		aga	tgg	decreased by mild
4310	RNMTMMPGN.MT-MMP	mt-mmp	membrane-type metalloproteinase		cct	ttc	No change
4311	RNMTMMPGN.MT-MMP	mt-mmp	membrane-type metalloproteinase		tat	agt	No change
4312	RATGPCGR.MGLUR1	MGLUR1	metabotropic glutamate receptor		cat	gca	No change
4313	RATGPCGR.MGLUR1	MGLUR1	metabotropic glutamate receptor		cat	gca	No change
4314	RATGPCGR.MGLUR1	MGLUR1	metabotropic glutamate receptor		cat	gca	No change
4315	RATGPCGR.MGLUR1	MGLUR1	metabotropic glutamate receptor		ctc	tca	No change
4316	RATGPCGR.MGLUR1	MGLUR1	metabotropic glutamate receptor		ctc	tca	No change
4317	RATGPCGR.MGLUR1	MGLUR1	metabotropic glutamate receptor		tct	tcg	No change
4318	RATGPCGR.MGLUR1	MGLUR1	metabotropic glutamate receptor		att	aca	No change
4319	RATMGLUR4A.GLUR4	GLUR4	metabotropic glutamate receptor		ttc	ttg	decreased
4320	RATMGLUR4A.GLUR4	GLUR4	metabotropic glutamate receptor		ttc	ttg	decreased
4321	RATMGLUR4A.GLUR4	GLUR4	metabotropic glutamate receptor		agt	ctg	No change
4322	RATMGLUR4A.GLUR4	GLUR4	metabotropic glutamate receptor		agt	ctg	No change
4323	RNMGRRN.PE1	nc	metabotropic glutamate receptor		cat	gca	No change
4324	RNMGRRN.PE1	nc	metabotropic glutamate receptor		cat	gca	No change
4325	RNMGRRN.PE1	nc	metabotropic glutamate receptor		cat	gca	No change
4326	RNMGRRN.PE1	nc	metabotropic glutamate receptor		ctc	tca	No change
4327	RNMGRRN.PE1	nc	metabotropic glutamate receptor		ctc	tca	No change
4328	RNMGRRN.PE1	nc	metabotropic glutamate receptor		tct	tcg	No change
4329	RNMGRRN.PE1	nc	metabotropic glutamate receptor		att	aca	No change
4330	RNU47331.PE1	nc	metabotropic glutamate receptor 4b		agt	ctg	No change
4331	RNU47331.PE1	nc	metabotropic glutamate receptor 4b		agt	ctg	No change
4332	RATMGLUR.PE1	nc	metabotropic glutamate receptor mGluR5		ttt	ggc	No change
4333	RATMGLUR.PE1	nc	metabotropic glutamate receptor mGluR5		cgt	gtc	No change
4334	RATMGLUR.PE1	nc	metabotropic glutamate receptor mGluR5		gtt	gct	No change
4335	RATMGLUR.PE1	nc	metabotropic glutamate receptor mGluR5		gtt	gct	No change
4336	AF525467.MLN51	Mln51	metastatic lymph node 51		ggt	cca	decreased
4337	AF525467.MLN51	Mln51	metastatic lymph node 51		ggt	cca	decreased
4338	RNU53706.PE1	nc	mevalonate pyrophosphate decarboxylase		cgg	ttc	increased
4339	RNU53706.PE1	nc	mevalonate pyrophosphate decarboxylase		cgg	ttc	increased
4340	RNU53706.PE1	nc	mevalonate pyrophosphate decarboxylase		cgg	ttc	increased
4341	RNU53706.PE1	nc	mevalonate pyrophosphate decarboxylase		atg	ctg	increased
4342	AF074609.RT1.EC3	RT1.EC3	MHC class I antigen		tac	agg	decreased
4343	AF074609.RT1.EC3	RT1.EC3	MHC class I antigen		tac	agg	decreased
4344	AF074609.RT1.EC3	RT1.EC3	MHC class I antigen		tac	agg	decreased
4345	RNO306619.RT1-E	rt1-E	MHC class I antigen		acg	gaa	decreased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
4346	Hha1	15	tac	179.05	178	0	0	179.05	0	0	3 900 000	=+	/		/(2)
4347	Hha1	39	agg	176.94	178	0	177.1	176.78	0	310.46	236	+=	/		/(2)
4348	Hha1	39	agg	178.22	178	0	178.4	178.04	0	220.9	183.1	+=	/		/(2)
4349	Hha1	59	ttc	79.593	80	79.5	79.64	79.64	4 362.97	2 230.65	2 129.2	-=	\ (-)		\(3) -(2)
4350	Hha1	59	ttc	80.225	80	80.31	0	80.14	2 028.08	0	1 836.85	-+(=)	V		\(3) -(2)
4351	Hha1	27	acg	87.243	87	87.23	87.26	87.24	71 300 000	19 700 000	10 100 000	-=	\ (-)		\(3) -(2)
4352	Taq1	25	cat	120.315	121	120.32	120.31	0	832.53	980.26	0	=-	\		\(3) -(2)
4353	Taq1	25	cat	121.21	121	121.19	121.23	0	1 044.08	954.8	0	=-	\		\(3) -(2)
4354	Hha1	59	ttc	79.593	80	79.5	79.64	79.64	4 362.97	2 230.65	2 129.2	-=	\ (-)		-4
4355	Hha1	59	ttc	80.225	80	80.31	0	80.14	2 028.08	0	1 836.85	-+(=)	V		-4
4356	Taq1	25	cat	120.315	121	120.32	120.31	0	832.53	980.26	0	=-	\		-4
4357	Taq1	25	cat	121.21	121	121.19	121.23	0	1 044.08	954.8	0	=-	\		-4
4358	Hha1	33	agc	158.6	159	0	0	158.6	0	0	20 700 000	=+	/		-4
4359	Hha1	33	agc	159.603	159	159.63	159.66	159.52	4 200 000	6 000 000	31 200 000	=+	/ (-)		-4
4360	Taq1	29	gca	169.503	170	169.49	169.53	169.49	4 100 000	3 400 000	5 000 000	==	-	(-)	-4
4361	Taq1	29	gca	170.577	170	170.51	170.59	170.63	9 400 000	6 300 000	4 900 000	==	-		-4
4362	Taq1	62	tgt	169.26	170	169.32	169.28	169.18	3 800 000	7 900 000	4 600 000	+=	/ (-)	(-)	-4
4363	Taq1	62	tgt	170.31	170	0	170.31	0	0	5 000 000	0	+-	A		-4
4364	Hha1	59	ttc	79.593	80	79.5	79.64	79.64	4 362.97	2 230.65	2 129.2	-=	\ (-)		/(3)
4365	Hha1	59	ttc	80.225	80	80.31	0	80.14	2 028.08	0	1 836.85	-+(=)	V		/(3)
4366	Hha1	27	acg	108.07	108	0	108.07	0	0	4 100 000	0	+-	A		/(3)
4367	Hha1	27	acg	108.1	108	0	108.1	0	0	3 100 000	0	+-	A		/(3)
4368	Hha1	62	tgt	108.04	108	0	0	108.04	0	0	26 500 000	=+	/		/(3)
4369	Hha1	33	agc	158.6	159	0	0	158.6	0	0	20 700 000	=+	/		/(3)
4370	Hha1	33	agc	159.603	159	159.63	159.66	159.52	4 200 000	6 000 000	31 200 000	=+	/ (-)		/(3)
4371	Hha1	33	agc	214.93	214	0	0	214.93	0	0	3 000 000	=+	/		/(3)
4372	Hha1	39	agg	134.885	135	134.82	0	134.95	454.54	0	227.86	-+(-)	V (\)		/(2)
4373	Hha1	39	agg	135.25	135	0	0	135.25	0	0	236	=+	/		/(2)
4374	Hha1	40	tgg	142.665	143	0	142.82	142.51	0	3 200 000	3 800 000	+=	/		/(2)
4375	Hha1	40	tgg	143.785	143	0	143.72	143.85	0	5 200 000	3 000 000	+=	/		/(2)
4376	Hha1	40	tgg	142.665	143	0	142.82	142.51	0	3 200 000	3 800 000	+=	/		/(2)
4377	Hha1	40	tgg	143.785	143	0	143.72	143.85	0	5 200 000	3 000 000	+=	/		/(2)
4378	Hha1	33	agc	158.6	159	0	0	158.6	0	0	20 700 000	=+	/		/(2)
4379	Hha1	33	agc	159.603	159	159.63	159.66	159.52	4 200 000	6 000 000	31 200 000	=+	/ (-)		/(2)
4380	Hha1	27	acg	87.243	87	87.23	87.26	87.24	71 300 000	19 700 000	10 100 000	-=	\ (-)		\(2)
4381	Hha1	39	agg	134.885	135	134.82	0	134.95	454.54	0	227.86	-+(-)	V (\)		\(2)
4382	Hha1	39	agg	135.25	135	0	0	135.25	0	0	236	=+	/		\(2)
4383	Hha1	27	acg	87.243	87	87.23	87.26	87.24	71 300 000	19 700 000	10 100 000	-=	\ (-)		\(2)
4384	Hha1	39	agg	134.885	135	134.82	0	134.95	454.54	0	227.86	-+(-)	V (\)		\(2)
4385	Hha1	39	agg	135.25	135	0	0	135.25	0	0	236	=+	/		\(2)
4386	Hha1	59	ttc	79.593	80	79.5	79.64	79.64	4 362.97	2 230.65	2 129.2	-=	\ (-)		\(3)
4387	Hha1	59	ttc	80.225	80	80.31	0	80.14	2 028.08	0	1 836.85	-+(=)	V		\(3)
4388	Hha1	27	acg	87.243	87	87.23	87.26	87.24	71 300 000	19 700 000	10 100 000	-=	\ (-)		\(3)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
4346	RNO306619.RT1-E	rt1-E	MHC class I antigen		tac	agg	decreased
4347	RNO306619.RT1-E	rt1-E	MHC class I antigen		tac	agg	decreased
4348	RNO306619.RT1-E	rt1-E	MHC class I antigen		tac	agg	decreased
4349	RATCMHCI.PE1	nc	MHC class I protein		ttc	ccg	increased
4350	RATCMHCI.PE1	nc	MHC class I protein		ttc	ccg	increased
4351	RATCMHCI.PE1	nc	MHC class I protein		acg	ggg	increased
4352	RATCMHCI.PE1	nc	MHC class I protein		cat	agc	increased
4353	RATCMHCI.PE1	nc	MHC class I protein		cat	agc	increased
4354	RNO277139.RT1-A3	RT1-A3	MHC class I protein		ttc	ccg	No change
4355	RNO277139.RT1-A3	RT1-A3	MHC class I protein		ttc	ccg	No change
4356	RNO277139.RT1-A3	RT1-A3	MHC class I protein		cat	agc	No change
4357	RNO277139.RT1-A3	RT1-A3	MHC class I protein		cat	agc	No change
4358	RNO277139.RT1-A3	RT1-A3	MHC class I protein		aga	agc	No change
4359	RNO277139.RT1-A3	RT1-A3	MHC class I protein		aga	agc	No change
4360	RNO277139.RT1-A3	RT1-A3	MHC class I protein		tgt	gca	No change
4361	RNO277139.RT1-A3	RT1-A3	MHC class I protein		tgt	gca	No change
4362	RNO277139.RT1-A3	RT1-A3	MHC class I protein		tgt	gca	No change
4363	RNO277139.RT1-A3	RT1-A3	MHC class I protein		tgt	gca	No change
4364	RNO314857.PE10	RT1-C/E7	MHC class I protein		ttc	ccg	decreased
4365	RNO314857.PE10	RT1-C/E7	MHC class I protein		ttc	ccg	decreased
4366	RNO314857.PE10	RT1-C/E7	MHC class I protein		tgt	acg	decreased
4367	RNO314857.PE10	RT1-C/E7	MHC class I protein		tgt	acg	decreased
4368	RNO314857.PE10	RT1-C/E7	MHC class I protein		tgt	acg	decreased
4369	RNO314857.PE10	RT1-C/E7	MHC class I protein		aga	agc	decreased
4370	RNO314857.PE10	RT1-C/E7	MHC class I protein		aga	agc	decreased
4371	RNO314857.PE10	RT1-C/E7	MHC class I protein		tcc	agc	decreased
4372	RNO314857.PE11	RT1-C/E8	MHC class I protein		cct	agg	decreased
4373	RNO314857.PE11	RT1-C/E8	MHC class I protein		cct	agg	decreased
4374	RNO314857.PE11	RT1-C/E8	MHC class I protein		tgg	acg	decreased
4375	RNO314857.PE11	RT1-C/E8	MHC class I protein		tgg	acg	decreased
4376	RNO314857.RT1-C	RT1-C/E1	MHC class I protein		tgg	acg	decreased
4377	RNO314857.RT1-C	RT1-C/E1	MHC class I protein		tgg	acg	decreased
4378	RNO314857.RT1-C	RT1-C/E1	MHC class I protein		aga	agc	decreased
4379	RNO314857.RT1-C	RT1-C/E1	MHC class I protein		aga	agc	decreased
4380	RNU38970.PE1	nc	MHC class I RT1.Ab heavy chain precursor		acg	ggg	increased
4381	RNU38970.PE1	nc	MHC class I RT1.Ab heavy chain precursor		ggt	agg	increased
4382	RNU38970.PE1	nc	MHC class I RT1.Ab heavy chain precursor		ggt	agg	increased
4383	RNU38972.PE1	nc	MHC class I RT1.Au heavy chain precursor		acg	ggg	increased
4384	RNU38972.PE1	nc	MHC class I RT1.Au heavy chain precursor		ggt	agg	increased
4385	RNU38972.PE1	nc	MHC class I RT1.Au heavy chain precursor		ggt	agg	increased
4386	RATMHCIMRA.PE1	nc	MHC class I RT1.Aw3 protein		ttc	ccg	increased
4387	RATMHCIMRA.PE1	nc	MHC class I RT1.Aw3 protein		ttc	ccg	increased
4388	RATMHCIMRA.PE1	nc	MHC class I RT1.Aw3 protein		acg	ggg	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
4389	Taq1	25	cat	99.77	100	0	99.53	100.01	0	445.57	1 267.56	=+	/		\(3)
4390	Taq1	25	cat	100.19	100	100.19	0	0	1 323.87	0	0	-=	\		\(3)
4391	Hha1	27	acg	121.525	122	121.53	0	121.52	3 800 000	0	11 500 000	=+(+)	/		\(3)
4392	Hha1	39	agg	142.785	143	0	142.99	142.58	0	310.46	272.62	+=	/		/(2)
4393	Hha1	33	agc	158.6	159	0	0	158.6	0	0	20 700 000	=+	/		/(2)
4394	Hha1	33	agc	159.603	159	159.63	159.66	159.52	4 200 000	6 000 000	31 200 000	=+	/ (-)		/(2)
4395	Hha1	27	acg	87.243	87	87.23	87.26	87.24	71 300 000	19 700 000	10 100 000	-=	\ (-)		/(2)
4396	Hha1	15	tac	179.05	178	0	0	179.05	0	0	3 900 000	=+	/		/(2)
4397	Hha1	39	agg	176.94	178	0	177.1	176.78	0	310.46	236	+=	/		/(2)
4398	Hha1	39	agg	178.22	178	0	178.4	178.04	0	220.9	183.1	+=	/		/(2)
4399	Hha1	27	acg	87.243	87	87.23	87.26	87.24	71 300 000	19 700 000	10 100 000	-=	\ (-)		\(2)
4400	Taq1	25	cat	120.315	121	120.32	120.31	0	832.53	980.26	0	=-	\		\(2)
4401	Taq1	25	cat	121.21	121	121.19	121.23	0	1 044.08	954.8	0	=-	\		\(2)
4402	Hha1	39	agg	142.785	143	0	142.99	142.58	0	310.46	272.62	+=	/		-2
4403	Hha1	15	tac	146.31	146	146.27	146.34	146.32	10 000 000	7 900 000	11 900 000	==	-		-2
4404	Hha1	15	tac	146.333	146	146.34	146.34	146.32	2 020.05	2 034.5	2 588.08	==	-		-2
4405	Hha1	60	ttg	145.557	146	145.4	145.86	145.41	5 100 000	7 700 000	4 100 000	=-	\ (-)		-2
4406	Hha1	60	ttg	145.9	146	145.87	0	145.93	6 800 000	0	4 400 000	-+(=)	V		-2
4407	Hha1	59	ttc	79.593	80	79.5	79.64	79.64	4 362.97	2 230.65	2 129.2	-=	\ (-)		\(3) -(2) V(2)
4408	Hha1	59	ttc	80.225	80	80.31	0	80.14	2 028.08	0	1 836.85	-+(=)	V		\(3) -(2) V(2)
4409	Hha1	27	acg	87.243	87	87.23	87.26	87.24	71 300 000	19 700 000	10 100 000	-=	\ (-)		\(3) -(2) V(2)
4410	Hha1	39	agg	134.885	135	134.82	0	134.95	454.54	0	227.86	-+(-)	V (\)		\(3) -(2) V(2)
4411	Hha1	39	agg	135.25	135	0	0	135.25	0	0	236	=+	/		\(3) -(2) V(2)
4412	Taq1	19	cac	115.403	116	115.38	115.38	115.45	48 700 000	27 900 000	4 800 000	=-	\ (-)		/(5)
4413	Taq1	19	cac	116.35	116	116.38	116.3	116.37	8 100 000	24 000 000	14 600 000	+=	/ (-)	/	/(5)
4414	Taq1	40	tgg	115.43	116	0	0	115.43	0	0	7 900 000	=+	/		/(5)
4415	Taq1	40	tgg	116.5	116	0	0	116.5	0	0	19 300 000	=+	/	/	/(5)
4416	Taq1	17	cca	138.79	139	138.65	138.81	138.91	283.28	265.92	2 044.8	=+	/ (-)		/(5)
4417	Taq1	17	cca	139.775	139	139.67	0	139.88	171.82	0	1 037.43	=+(+)	/	/	/(5)
4418	Taq1	29	gca	138.537	139	138.49	138.52	138.6	5 300 000	6 100 000	5 400 000	==	-		/(5)
4419	Taq1	29	gca	139.62	139	0	0	139.62	0	0	5 300 000	=+	/	/	/(5)
4420	Hha1	6	aga	159.6	160	159.64	0	159.56	5 600 000	0	20 300 000	=+(+)	/		/(5)
4421	Hha1	6	aga	160.585	160	160.81	0	160.36	10 900 000	0	8 000 000	-+(=)	V		/(5)
4422	Taq1	40	tgg	180.51	181	180.51	0	0	6 100 000	0	0	-=	\		/(5)
4423	Taq1	40	tgg	181.71	181	181.63	0	181.79	3 800 000	0	3 500 000	-+(=)	V		/(5)
4424	Hha1	27	acg	73.827	74	73.8	73.91	73.77	70 000 000	22 000 000	43 500 000	-=	\ (-)		\(2)
4425	Taq1	39	agg	156.95	157	0	156.95	0	0	38 200 000	0	+-	A		\(2)
4426	Taq1	39	agg	156.26	157	0	156.26	0	0	114.57	0	+-	A		\(2)
4427	Taq1	39	agg	156.95	157	0	156.95	0	0	383.92	0	+-	A		\(2)
4428	Taq1	39	agg	157.71	157	157.71	0	0	4 600 000	0	0	-=	\		\(2)
4429	Taq1	39	agg	156.06	157	156.06	0	0	185.68	0	0	-=	\		\(2)
4430	Taq1	39	agg	157.71	157	157.71	0	0	170.82	0	0	-=	\		\(2)
4431	Hha1	28	tcg	113.85	114	113.64	113.99	113.92	32 300 000	27 100 000	18 300 000	==	-		-4

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
4389	RATMHCIMRA.PE1	nc	MHC class I RT1.Aw3 protein		cat	agc	increased
4390	RATMHCIMRA.PE1	nc	MHC class I RT1.Aw3 protein		cat	agc	increased
4391	RATMHCIMRA.PE1	nc	MHC class I RT1.Aw3 protein		ggg	acg	increased
4392	RATMHRT1C.PE1	nc	MHC class I RT1.C-type protein		agg	acg	decreased
4393	RATMHRT1C.PE1	nc	MHC class I RT1.C-type protein		aga	agc	decreased
4394	RATMHRT1C.PE1	nc	MHC class I RT1.C-type protein		aga	agc	decreased
4395	RATMHCIMRC.PE1	nc	MHC class I RT1.E		acg	gaa	decreased
4396	RATMHCIMRC.PE1	nc	MHC class I RT1.E		tac	agg	decreased
4397	RATMHCIMRC.PE1	nc	MHC class I RT1.E		tac	agg	decreased
4398	RATMHCIMRC.PE1	nc	MHC class I RT1.E		tac	agg	decreased
4399	AF025309.RT1.AL	RT1.Al	MHC class Ia protein		acg	ggg	increased
4400	AF025309.RT1.AL	RT1.Al	MHC class Ia protein		cat	agc	increased
4401	AF025309.RT1.AL	RT1.Al	MHC class Ia protein		cat	agc	increased
4402	AF457139.RT1.L	Rt1.L	MHC class Ib RT1.L		agg	acg	No change
4403	AF457139.RT1.L	Rt1.L	MHC class Ib RT1.L		tac	ttg	No change
4404	AF457139.RT1.L	Rt1.L	MHC class Ib RT1.L		tac	ttg	No change
4405	AF457139.RT1.L	Rt1.L	MHC class Ib RT1.L		tac	ttg	No change
4406	AF457139.RT1.L	Rt1.L	MHC class Ib RT1.L		tac	ttg	No change
4407	RATMHCRT.PE1	nc	MHC RT1.Aa alpha-chain precursor		ttc	ccg	increased
4408	RATMHCRT.PE1	nc	MHC RT1.Aa alpha-chain precursor		ttc	ccg	increased
4409	RATMHCRT.PE1	nc	MHC RT1.Aa alpha-chain precursor		acg	ggg	increased
4410	RATMHCRT.PE1	nc	MHC RT1.Aa alpha-chain precursor		ggt	agg	increased
4411	RATMHCRT.PE1	nc	MHC RT1.Aa alpha-chain precursor		ggt	agg	increased
4412	RNMAP2R.PE1	nc	microtubule associated protein 2		cac	tgg	decreased
4413	RNMAP2R.PE1	nc	microtubule associated protein 2		cac	tgg	decreased
4414	RNMAP2R.PE1	nc	microtubule associated protein 2		cac	tgg	decreased
4415	RNMAP2R.PE1	nc	microtubule associated protein 2		cac	tgg	decreased
4416	RNMAP2R.PE1	nc	microtubule associated protein 2		cca	gca	decreased
4417	RNMAP2R.PE1	nc	microtubule associated protein 2		cca	gca	decreased
4418	RNMAP2R.PE1	nc	microtubule associated protein 2		cca	gca	decreased
4419	RNMAP2R.PE1	nc	microtubule associated protein 2		cca	gca	decreased
4420	RNMAP2R.PE1	nc	microtubule associated protein 2		aga	ttg	decreased
4421	RNMAP2R.PE1	nc	microtubule associated protein 2		aga	ttg	decreased
4422	RNMAP2R.PE1	nc	microtubule associated protein 2		agc	tgg	decreased
4423	RNMAP2R.PE1	nc	microtubule associated protein 2		agc	tgg	decreased
4424	RNU12008.PE1	nc	microtubule-associated protein-2 kinase		gta	acg	increased
4425	RNU12008.PE1	nc	microtubule-associated protein-2 kinase		cgt	agg	increased
4426	RNU12008.PE1	nc	microtubule-associated protein-2 kinase		cgt	agg	increased
4427	RNU12008.PE1	nc	microtubule-associated protein-2 kinase		cgt	agg	increased
4428	RNU12008.PE1	nc	microtubule-associated protein-2 kinase		cgt	agg	increased
4429	RNU12008.PE1	nc	microtubule-associated protein-2 kinase		cgt	agg	increased
4430	RNU12008.PE1	nc	microtubule-associated protein-2 kinase		cgt	agg	increased
4431	AF029109.MINT-3	mint 3	mint 3		tgg	tcg	No change

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
4432	Hha1	28	tcg	114.553	114	114.28	114.72	114.66	47 800 000	39 300 000	28 500 000	==	-		-4
4433	Hha1	40	tgg	113.48	114	113.23	113.73	0	46 700 000	9 600 000	0	-=	\		-4
4434	Hha1	40	tgg	114.02	114	0	0	114.02	0	0	5 100 000	=+	/		-4
4435	Hha1	2	tta	119.597	120	119.52	119.62	119.65	5 700 000	8 300 000	3 100 000	=-	\ (-)		-4
4436	Hha1	2	tta	120.155	120	120.1	120.21	0	3 100 000	5 500 000	0	=-	\		-4
4437	Hha1	39	agg	119.58	120	0	119.61	119.55	0	274.64	146.48	+-	A		-4
4438	Hha1	27	acg	124.597	124	124.48	124.69	124.62	9 500 000	6 300 000	4 800 000	==	-		-4
4439	Hha1	39	agg	137.01	137	136.94	137.14	136.95	1 620.23	382.11	866.69	-=	\ (-)		-4
4440	Hha1	31	gac	66.86	67	0	0	66.86	0	0	32 400 000	=+	/		\(5)
4441	Hha1	31	gac	74.787	75	74.79	74.8	74.77	195 900 000	82 000 000	39 500 000	-=	\ (-)		\(5)
4442	Hha1	43	cgc	109.76	110	109.76	109.79	109.73	8 600 000	20 800 000	10 900 000	+-	A		\(5)
4443	Hha1	32	gtc	116.607	117	116.54	116.7	116.58	22 409.369	11 068.15	4 440.43	-=	\ (-)		\(5)
4444	Hha1	7	caa	251.52	253	251.52	0	0	4 500 000	0	0	-=	\	\	\(5)
4445	Taq1	7	caa	251.62	253	251.62	0	0	3 900 000	0	0	-=	\	\	\(5)
4446	Hha1	7	caa	252.07	253	252.07	0	0	5 900 000	0	0	-=	\		\(5)
4447	Taq1	31	gac	96.42	97	96.37	96.33	96.56	55 000 000	43 400 000	3 100 000	=-	\ (-)		\(2)
4448	Taq1	31	gac	97.437	97	97.4	97.32	97.59	62 800 000	57 200 000	11 100 000	=-	\ (-)		\(2)
4449	Hha1	61	tct	204.33	205	204.26	204.4	0	3 200 000	3 400 000	0	=-	\		\(2)
4450	Hha1	61	tct	205.365	205	0	205.43	205.3	0	3 300 000	3 000 000	+=	/		\(2)
4451	Hha1	26	ctg	121.91	122	0	121.95	121.87	0	8 100 000	10 200 000	+=	/		/(2)
4452	Hha1	33	agc	197.52	198	0	0	197.52	0	0	5 600 000	=+	/		/(2)
4453	Hha1	33	agc	198.51	198	0	0	198.51	0	0	6 500 000	=+	/		/(2)
4454	Hha1	33	agc	69.835	70	69.78	69.89	0	36 000 000	32 900 000	0	=-	\		\(3)
4455	Hha1	27	acg	110.98	111	111.02	110.89	111.03	26 500 000	9 300 000	29 400 000	-+	V		\(3)
4456	Hha1	40	tgg	110.9	111	0	110.9	0	0	11 200 000	0	+-	A		\(3)
4457	Hha1	40	tgg	111.665	111	111.74	111.59	0	15 700 000	4 400 000	0	-=	\		\(3)
4458	Hha1	43	cgc	156.85	156	0	156.85	0	0	6 300 000	0	+-	A		\(3)
4459	Hha1	31	gac	156.29	157	156.26	156.32	0	8 400 000	3 800 000	0	--	\		\(3)
4460	Hha1	31	gac	157.27	157	157.27	0	0	6 600 000	0	0	-=	\		\(3)
4461	Hha1	7	caa	212.78	214	212.78	0	0	6 600 000	0	0	-=	\		\(2)
4462	Taq1	7	caa	213.25	214	0	213.25	0	0	4 500 000	0	+-	A		\(2)
4463	Hha1	7	caa	213.78	214	213.78	0	0	4 700 000	0	0	-=	\		\(2)
4464	Taq1	8	gaa	141.22	142	141.22	0	0	3 800 000	0	0	-=	\		\(2)
4465	Taq1	8	gaa	142.755	142	142.97	142.54	0	7 200 000	7 700 000	0	=-	\		\(2)
4466	Taq1	1	tat	142.98	143	142.98	0	0	5 500 000	0	0	-=	\		\(2)
4467	Taq1	8	gaa	141.22	142	141.22	0	0	3 800 000	0	0	-=	\		\(2)
4468	Taq1	8	gaa	142.755	142	142.97	142.54	0	7 200 000	7 700 000	0	=-	\		\(2)
4469	Taq1	1	tat	142.98	143	142.98	0	0	5 500 000	0	0	-=	\		\(2)
4470	Hha1	26	ctg	109.847	110	109.83	109.83	109.88	4 200 000	6 200 000	4 100 000	==	-		-5
4471	Hha1	60	ttg	110.32	110	110.48	110.44	110.04	8 800 000	19 300 000	18 200 000	+=	/ (-)		-5
4472	Hha1	54	ttt	116.14	116	116.14	116.2	116.08	16 800 000	10 900 000	11 600 000	==	-		-5
4473	Hha1	31	gac	135.227	136	135.24	135.15	135.29	14 800 000	7 100 000	50 500 000	=+	/ (-)		-5
4474	Hha1	31	gac	135.94	136	135.93	135.95	0	16 300 000	11 000 000	0	=-	\	\	-5

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
4432	AF029109.MINT-3	mint 3	mint 3		tgg	tcg	No change
4433	AF029109.MINT-3	mint 3	mint 3		tgg	tcg	No change
4434	AF029109.MINT-3	mint 3	mint 3		tgg	tcg	No change
4435	AF029109.MINT-3	mint 3	mint 3		agg	tta	No change
4436	AF029109.MINT-3	mint 3	mint 3		agg	tta	No change
4437	AF029109.MINT-3	mint 3	mint 3		agg	tta	No change
4438	AF029109.MINT-3	mint 3	mint 3		gag	acg	No change
4439	AF029109.MINT-3	mint 3	mint 3		agg	aat	No change
4440	AF029105.MINT-1	mint 1	Mint1		gac	tcc	increased
4441	AF029105.MINT-1	mint 1	Mint1		gac	cta	increased
4442	AF029105.MINT-1	mint 1	Mint1		cta	cgc	increased
4443	AF029105.MINT-1	mint 1	Mint1		cga	gtc	increased
4444	AF029105.MINT-1	mint 1	Mint1		caa	tgg	increased
4445	AF029105.MINT-1	mint 1	Mint1		caa	tgg	increased
4446	AF029105.MINT-1	mint 1	Mint1		caa	tgg	increased
4447	AF029107.MINT-2	mint 2	Mint2		gac	aca	increased
4448	AF029107.MINT-2	mint 2	Mint2		gac	aca	increased
4449	AF029107.MINT-2	mint 2	Mint2		tct	tca	increased
4450	AF029107.MINT-2	mint 2	Mint2		tct	tca	increased
4451	RNU42427.RATMRII	RATMRII	MIS type II receptor		ctg	tgc	decreased
4452	RNU42427.RATMRII	RATMRII	MIS type II receptor		agc	agc	decreased
4453	RNU42427.RATMRII	RATMRII	MIS type II receptor		agc	agc	decreased
4454	RNVLCACT.PE1	nc	mitochondrial very-long-chain acyl-CoA		ggc	agc	increased
4455	RNVLCACT.PE1	nc	mitochondrial very-long-chain acyl-CoA		gga	acg	increased
4456	RNVLCACT.PE1	nc	mitochondrial very-long-chain acyl-CoA		tgg	cag	increased
4457	RNVLCACT.PE1	nc	mitochondrial very-long-chain acyl-CoA		tgg	cag	increased
4458	RNVLCACT.PE1	nc	mitochondrial very-long-chain acyl-CoA		gac	cgc	increased
4459	RNVLCACT.PE1	nc	mitochondrial very-long-chain acyl-CoA		gac	cgc	increased
4460	RNVLCACT.PE1	nc	mitochondrial very-long-chain acyl-CoA		gac	cgc	increased
4461	AY197741.PE1	nc	mitogen-activated protein kinase-activated		caa	gac	increased
4462	AY197741.PE1	nc	mitogen-activated protein kinase-activated		caa	gac	increased
4463	AY197741.PE1	nc	mitogen-activated protein kinase-activated		caa	gac	increased
4464	RNU62316.MCT2	MCT2	monocarboxylate transporter 2		tat	gaa	increased
4465	RNU62316.MCT2	MCT2	monocarboxylate transporter 2		tat	gaa	increased
4466	RNU62316.MCT2	MCT2	monocarboxylate transporter 2		tat	gaa	increased
4467	RNMOCATR2.PE1	nc	monocarboxylate transporter MCT2		tat	gaa	increased
4468	RNMOCATR2.PE1	nc	monocarboxylate transporter MCT2		tat	gaa	increased
4469	RNMOCATR2.PE1	nc	monocarboxylate transporter MCT2		tat	gaa	increased
4470	AF059258.PE1	nc	monocarboxylate transporter MCT3		ctg	ttg	No change
4471	AF059258.PE1	nc	monocarboxylate transporter MCT3		ctg	ttg	No change
4472	AF059258.PE1	nc	monocarboxylate transporter MCT3		ttt	gag	No change
4473	AF059258.PE1	nc	monocarboxylate transporter MCT3		gac	gtc	No change
4474	AF059258.PE1	nc	monocarboxylate transporter MCT3		gac	gtc	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
4475	Hha1	32	gtc	135.94	136	136.02	136	135.8	3 863.05	2 024.41	373.04	-=	\ (-)	\	-5
4476	Hha1	20	ctc	224.77	226	0	0	224.77	0	0	441.31	=+	/		-5
4477	Hha1	40	tgg	201.08	202	0	201.08	0	0	6 200 000	0	+-	A		A(2) \(2)
4478	Hha1	40	tgg	202.96	202	202.96	0	0	4 200 000	0	0	-=	\		A(2) \(2)
4479	Hha1	59	ttc	201.44	202	0	201.44	0	0	212.71	0	+-	A		A(2) \(2)
4480	Hha1	59	ttc	202.71	202	202.9	202.52	0	228.8	160.97	0	=-	\		A(2) \(2)
4481	Taq1	11	act	124.26	125	124.24	0	124.28	3 500 000	0	65 000 000	=+(+)	/	/	
4482	Hha1	11	act	124.33	125	0	0	124.33	0	0	3 100 000	=+	/	/	
4483	Hha1	56	tga	155.015	155	154.98	0	155.05	281.94	0	2 223.75	=+(+)	/		/(2)
4484	Hha1	9	atc	197.09	198	197.3	0	196.88	3 200 000	0	3 400 000	-+(=)	V		/(2)
4485	Hha1	9	atc	198.45	198	198.27	198.63	0	3 000 000	3 800 000	0	=-	\		/(2)
4486	Taq1	63	ctt	197.17	198	0	0	197.17	0	0	3 100 000	=+	/		/(2)
4487	Hha1	59	ttc	100.097	100	99.97	100.31	100.01	171.6	494.42	952.06	=+	/ (-)		-2
4488	Hha1	12	agt	177.05	178	177.09	177	177.06	1 887.28	2 493.88	3 047.09	==	-		-2
4489	Taq1	48	ggg	98.92	99	98.86	99.17	98.73	1 580.27	354.22	640.61	-=	\ (-)		-(2) \(2)
4490	Taq1	39	agg	100.417	100	100.17	100.54	100.54	6 100 000	29 200 000	11 700 000	+-	A		-(2) \(2)
4491	Taq1	39	agg	100.523	100	100.49	100.54	100.54	4 700 000	293.47	344.62	-=	\ (-)		-(2) \(2)
4492	Taq1	39	agg	100.17	100	100.17	0	0	226.53	0	0	-=	\		-(2) \(2)
4493	Taq1	39	agg	100.49	100	100.49	0	0	174.53	0	0	-=	\		-(2) \(2)
4494	Taq1	39	agg	98.48	99	0	0	98.48	0	0	94 100 000	=+	/		/(6) \(5)
4495	Taq1	39	agg	99.153	99	99.03	99.16	99.27	23 200 000	39 900 000	4 800 000	=-	\ (-)		/(6) \(5)
4496	Taq1	39	agg	98.48	99	0	0	98.48	0	0	2 771.72	=+	/		/(6) \(5)
4497	Taq1	39	agg	99.153	99	99.03	99.16	99.27	861.55	401	141.38	-=	\ (-)		/(6) \(5)
4498	Taq1	45	gcc	162.66	162	0	162.66	0	0	6 800 000	0	+-	A		/(6) \(5)
4499	Taq1	61	tct	162.29	163	0	0	162.29	0	0	10 600 000	=+	/		/(6) \(5)
4500	Taq1	61	tct	163.33	163	0	0	163.33	0	0	19 900 000	=+	/		/(6) \(5)
4501	Taq1	31	gac	173.89	174	173.85	173.93	0	5 000 000	3 100 000	0	=-	\		/(6) \(5)
4502	Taq1	31	gac	174.933	174	174.86	174.82	175.12	6 700 000	3 800 000	4 000 000	==	-		/(6) \(5)
4503	Taq1	40	tgg	173.5	174	0	0	173.5	0	0	8 700 000	=+	/		/(6) \(5)
4504	Taq1	22	tcc	202.33	203	0	0	202.33	0	0	3 900 000	=+	/		/(6) \(5)
4505	Taq1	22	tcc	204.03	203	204.03	0	0	3 600 000	0	0	-=	\		/(6) \(5)
4506	Taq1	56	tga	202.23	203	0	202.23	0	0	5 700 000	0	+-	A		/(6) \(5)
4507	Taq1	39	agg	237.155	238	237.19	237.12	0	9 700 000	35 600 000	0	+-	A		/(6) \(5)
4508	Taq1	39	agg	237.885	238	237.68	0	238.09	3 900 000	0	4 500 000	-+(=)	V		/(6) \(5)
4509	Taq1	39	agg	238.24	238	0	238.24	0	0	100 400 000	0	+-	A		/(6) \(5)
4510	Taq1	39	agg	237.12	238	0	237.12	0	0	357.79	0	+-	A		/(6) \(5)
4511	Taq1	39	agg	238.24	238	0	238.24	0	0	1 009.05	0	+-	A		/(6) \(5)
4512	Taq1	39	agg	239.18	238	239.24	0	239.12	9 400 000	0	46 900 000	=+(+)	/		/(6) \(5)
4513	Taq1	39	agg	237.19	238	237.19	0	0	360.21	0	0	-=	\		/(6) \(5)
4514	Taq1	39	agg	237.885	238	237.68	0	238.09	144.83	0	132.54	-+(=)	V		/(6) \(5)
4515	Taq1	39	agg	239.18	238	239.24	0	239.12	349.07	0	1 381.44	=+(+)	/		/(6) \(5)
4516	Hha1	39	agg	243.143	244	243.16	243.32	242.95	945.74	1 397.09	1 110.83	==	-		/(6) \(5)
4517	Hha1	39	agg	244.015	244	244.13	0	243.9	263.92	0	122.07	-+(-)	V (\)		/(6) \(5)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
4475	AF059258.PE1	nc	monocarboxylate transporter MCT3		gac	gtc	increased
4476	AF059258.PE1	nc	monocarboxylate transporter MCT3		ctc	tcc	No change
4477	RNU66479.MAD3	Mad3	mothers against dpp 3 homolog		ttc	tgg	increased by mild
4478	RNU66479.MAD3	Mad3	mothers against dpp 3 homolog		ttc	tgg	increased by mild
4479	RNU66479.MAD3	Mad3	mothers against dpp 3 homolog		ttc	tgg	increased by mild
4480	RNU66479.MAD3	Mad3	mothers against dpp 3 homolog		ttc	tgg	increased by mild
4481	AF218574.MRE11	MRE11	MRE11		tgc	act	decreased
4482	AF218574.MRE11	MRE11	MRE11		tgc	act	decreased
4483	RNMSH2.MSH2	msh2	MSH2 protein		tga	act	decreased
4484	RNMSH2.MSH2	msh2	MSH2 protein		ctt	atc	decreased
4485	RNMSH2.MSH2	msh2	MSH2 protein		ctt	atc	decreased
4486	RNMSH2.MSH2	msh2	MSH2 protein		ctt	atc	decreased
4487	RNMTMMP.RAT-29	rat 29	MT-MMP		cct	ttc	No change
4488	RNMTMMP.RAT-29	rat 29	MT-MMP		tat	agt	No change
4489	RRU92072.PE1	nc	m-tomosyn		agg	ggg	No change
4490	RRU92072.PE1	nc	m-tomosyn		agg	ggg	No change
4491	RRU92072.PE1	nc	m-tomosyn		agg	ggg	No change
4492	RRU92072.PE1	nc	m-tomosyn		agg	ggg	No change
4493	RRU92072.PE1	nc	m-tomosyn		agg	ggg	No change
4494	RNU53858.CLS1	cls1	mu-calpain large subunit		gag	agg	decreased
4495	RNU53858.CLS1	cls1	mu-calpain large subunit		gag	agg	decreased
4496	RNU53858.CLS1	cls1	mu-calpain large subunit		gag	agg	decreased
4497	RNU53858.CLS1	cls1	mu-calpain large subunit		gag	agg	decreased
4498	RNU53858.CLS1	cls1	mu-calpain large subunit		gcc	tct	decreased
4499	RNU53858.CLS1	cls1	mu-calpain large subunit		gcc	tct	decreased
4500	RNU53858.CLS1	cls1	mu-calpain large subunit		gcc	tct	decreased
4501	RNU53858.CLS1	cls1	mu-calpain large subunit		gac	tgg	decreased
4502	RNU53858.CLS1	cls1	mu-calpain large subunit		gac	tgg	decreased
4503	RNU53858.CLS1	cls1	mu-calpain large subunit		gac	tgg	decreased
4504	RNU53858.CLS1	cls1	mu-calpain large subunit		tga	tcc	decreased
4505	RNU53858.CLS1	cls1	mu-calpain large subunit		tga	tcc	decreased
4506	RNU53858.CLS1	cls1	mu-calpain large subunit		tga	tcc	decreased
4507	RNU53858.CLS1	cls1	mu-calpain large subunit		gag	agg	decreased
4508	RNU53858.CLS1	cls1	mu-calpain large subunit		gag	agg	decreased
4509	RNU53858.CLS1	cls1	mu-calpain large subunit		gag	agg	decreased
4510	RNU53858.CLS1	cls1	mu-calpain large subunit		gag	agg	decreased
4511	RNU53858.CLS1	cls1	mu-calpain large subunit		gag	agg	decreased
4512	RNU53858.CLS1	cls1	mu-calpain large subunit		gag	agg	decreased
4513	RNU53858.CLS1	cls1	mu-calpain large subunit		gag	agg	decreased
4514	RNU53858.CLS1	cls1	mu-calpain large subunit		gag	agg	decreased
4515	RNU53858.CLS1	cls1	mu-calpain large subunit		gag	agg	decreased
4516	RNU53858.CLS1	cls1	mu-calpain large subunit		ttc	agg	decreased
4517	RNU53858.CLS1	cls1	mu-calpain large subunit		ttc	agg	decreased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
4518	Hha1	39	agg	244.99	244	0	0	244.99	0	0	146.48	=+	/		/(6) \(5)
4519	Taq1	39	agg	74.71	75	74.51	74.92	74.7	14 400 000	28 400 000	18 600 000	+=	/ (-)		\(3)
4520	Taq1	39	agg	74.81	75	0	74.92	74.7	0	285.43	547.86	++	/		\(3)
4521	Taq1	39	agg	75.37	75	75.37	0	0	45 000 000	0	0	-=	\		\(3)
4522	Taq1	39	agg	75.37	75	75.37	0	0	1 671.12	0	0	-=	\		\(3)
4523	Taq1	64	gtt	107.613	108	107.54	107.6	107.7	9 800 000	9 900 000	5 900 000	==	-		\(3)
4524	Taq1	50	aat	230.565	231	230.43	230.7	0	9 600 000	7 600 000	0	=-	\		\(3)
4525	Taq1	50	aat	232.295	231	232.27	232.32	0	7 300 000	4 000 000	0	--	\		\(3)
4526	Taq1	45	gcc	259.68	261	259.68	0	0	3 900 000	0	0	-=	\		\(3)
4527	Taq1	45	gcc	260.8	261	260.8	0	0	10 300 000	0	0	-=	\		\(3)
4528	Taq1	9	atc	70.91	71	70.93	70.89	0	26 600 000	26 900 000	0	=-	\		/(6)
4529	Hha1	16	tag	70.645	71	0	70.55	70.74	0	6 000 000	5 500 000	+=	/		/(6)
4530	Hha1	16	tag	71.22	71	0	71.22	0	0	4 200 000	0	+-	A		/(6)
4531	Hha1	11	act	145.28	146	0	0	145.28	0	0	9 000 000	=+	/		/(6)
4532	Taq1	11	act	145.563	146	145.42	145.4	145.87	3 800 000	3 800 000	8 400 000	=+	/ (-)		/(6)
4533	Hha1	11	act	146.17	146	0	0	146.17	0	0	4 400 000	=+	/		/(6)
4534	Taq1	11	act	146.62	146	146.51	0	146.73	3 000 000	0	20 200 000	=+(+)	/		/(6)
4535	Taq1	17	cca	145.953	146	145.74	146	146.12	185.76	372.29	511.2	==	-		/(6)
4536	Taq1	17	cca	146.28	146	146.28	0	0	329.72	0	0	-=	\		/(6)
4537	Taq1	57	ctg	202.79	202	0	0	202.79	0	0	4 800 000	=+	/		/(6)
4538	Taq1	10	atg	166.48	167	166.48	0	0	5 600 000	0	0	-=	\	\	
4539	Hha1	10	atg	166.54	167	166.54	0	0	4 000 000	0	0	-=	\	\	
4540	Taq1	10	atg	166.48	167	166.48	0	0	5 600 000	0	0	-=	\	\	
4541	Hha1	10	atg	166.54	167	166.54	0	0	4 000 000	0	0	-=	\	\	
4542	Taq1	45	gcc	190.08	191	190.08	0	0	5 100 000	0	0	-=	\		/(2)
4543	Taq1	45	gcc	191.3	191	0	0	191.3	0	0	3 700 000	=+	/	/	/(2)
4544	Taq1	17	cca	191.373	192	191.43	191.21	191.48	157.89	279.21	571.34	=+	/ (-)	/	/(2)
4545	Taq1	17	cca	192.3	192	192.37	192.23	0	222.91	565.08	0	+-	A		/(2)
4546	Hha1	35	gga	114.66	114	114.53	114.85	114.6	3 798.19	3 634.95	5 767.01	==	-	(-)	
4547	Hha1	59	ttc	114.603	114	114.73	114.55	114.53	218.4	526.04	488.96	+=	/ (-)	(-)	
4548	Hha1	39	agg	81.873	82	81.97	81.6	82.05	1 392.96	2 161.32	789.38	=-	\ (-)		\(3)
4549	Hha1	61	tct	181.92	183	0	181.96	181.88	0	12 000 000	5 600 000	+-	A		\(3)
4550	Hha1	61	tct	183.85	183	0	0	183.85	0	0	4 900 000	=+	/		\(3)
4551	Hha1	40	tgg	251.41	252	251.47	251.35	0	3 900 000	4 200 000	0	=-	\		\(3)
4552	Hha1	40	tgg	252.785	252	252.6	0	252.97	6 600 000	0	5 200 000	-+(=)	V		\(3)
4553	Hha1	40	tgg	253.49	252	253.49	0	0	7 300 000	0	0	-=	\		\(3)
4554	Taq1	17	cca	273.94	274	273.94	0	0	167.18	0	0	-=	\		\(3)
4555	Hha1	39	agg	81.873	82	81.97	81.6	82.05	1 392.96	2 161.32	789.38	=-	\ (-)		\(3)
4556	Hha1	61	tct	181.92	183	0	181.96	181.88	0	12 000 000	5 600 000	+-	A		\(3)
4557	Hha1	61	tct	183.85	183	0	0	183.85	0	0	4 900 000	=+	/		\(3)
4558	Hha1	40	tgg	251.41	252	251.47	251.35	0	3 900 000	4 200 000	0	=-	\		\(3)
4559	Hha1	40	tgg	252.785	252	252.6	0	252.97	6 600 000	0	5 200 000	-+(=)	V		\(3)
4560	Hha1	40	tgg	253.49	252	253.49	0	0	7 300 000	0	0	-=	\		\(3)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
4518	RNU53858.CLS1	cls1	mu-calpain large subunit		ttc	agg	decreased
4519	RNU07615.PE1	nc	mucin		gct	agg	increased
4520	RNU07615.PE1	nc	mucin		gct	agg	increased
4521	RNU07615.PE1	nc	mucin		gct	agg	increased
4522	RNU07615.PE1	nc	mucin		gct	agg	increased
4523	RNU07615.PE1	nc	mucin		gag	gtt	increased
4524	RNU07615.PE1	nc	mucin		aat	tca	increased
4525	RNU07615.PE1	nc	mucin		aat	tca	increased
4526	RNU07615.PE1	nc	mucin		gga	gcc	increased
4527	RNU07615.PE1	nc	mucin		gga	gcc	increased
4528	RNMUPP1.MUPP1	MUPP1	multi PDZ domain protein 1		atc	tag	decreased
4529	RNMUPP1.MUPP1	MUPP1	multi PDZ domain protein 1		atc	tag	decreased
4530	RNMUPP1.MUPP1	MUPP1	multi PDZ domain protein 1		atc	tag	decreased
4531	RNMUPP1.MUPP1	MUPP1	multi PDZ domain protein 1		act	cca	decreased
4532	RNMUPP1.MUPP1	MUPP1	multi PDZ domain protein 1		act	cca	decreased
4533	RNMUPP1.MUPP1	MUPP1	multi PDZ domain protein 1		act	cca	decreased
4534	RNMUPP1.MUPP1	MUPP1	multi PDZ domain protein 1		act	cca	decreased
4535	RNMUPP1.MUPP1	MUPP1	multi PDZ domain protein 1		act	cca	decreased
4536	RNMUPP1.MUPP1	MUPP1	multi PDZ domain protein 1		act	cca	decreased
4537	RNMUPP1.MUPP1	MUPP1	multi PDZ domain protein 1		tgt	ctg	decreased
4538	AF138789.PE1	nc	multidomain presynaptic cytomatrix protein		aga	atg	increased
4539	AF138789.PE1	nc	multidomain presynaptic cytomatrix protein		aga	atg	increased
4540	AF227534.PE1	nc	multidomain presynaptic cytomatrix protein		aga	atg	increased
4541	AF227534.PE1	nc	multidomain presynaptic cytomatrix protein		aga	atg	increased
4542	AB020209.MRP5	MRP5	multidrug resistance protein (MRP5)		gcc	cca	decreased
4543	AB020209.MRP5	MRP5	multidrug resistance protein (MRP5)		gcc	cca	decreased
4544	AB020209.MRP5	MRP5	multidrug resistance protein (MRP5)		gcc	cca	decreased
4545	AB020209.MRP5	MRP5	multidrug resistance protein (MRP5)		gcc	cca	decreased
4546	AF257746.PGY1	Pgy1	multidrug resistance protein 1a		ttc	gga	No change
4547	AF257746.PGY1	Pgy1	multidrug resistance protein 1a		ttc	gga	No change
4548	AB010466.PE1	nc	multidrug resistance-associated protein	*	tgg	agg	increased
4549	AB010466.PE1	nc	multidrug resistance-associated protein	*	aga	tct	increased
4550	AB010466.PE1	nc	multidrug resistance-associated protein	*	aga	tct	increased
4551	AB010466.PE1	nc	multidrug resistance-associated protein	*	tgg	tcg	increased
4552	AB010466.PE1	nc	multidrug resistance-associated protein	*	tgg	tcg	increased
4553	AB010466.PE1	nc	multidrug resistance-associated protein	*	tgg	tcg	increased
4554	AB010466.PE1	nc	multidrug resistance-associated protein	*	gtc	cca	increased
4555	RNU73038.MRP6	mrp6	multidrug resistance-associated protein 6	*	tgg	agg	increased
4556	RNU73038.MRP6	mrp6	multidrug resistance-associated protein 6	*	aga	tct	increased
4557	RNU73038.MRP6	mrp6	multidrug resistance-associated protein 6	*	aga	tct	increased
4558	RNU73038.MRP6	mrp6	multidrug resistance-associated protein 6	*	tgg	tcg	increased
4559	RNU73038.MRP6	mrp6	multidrug resistance-associated protein 6	*	tgg	tcg	increased
4560	RNU73038.MRP6	mrp6	multidrug resistance-associated protein 6	*	tgg	tcg	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
4561	Taq1	17	cca	273.94	274	273.94	0	0	167.18	0	0	-=	\		\(3)
4562	Taq1	11	act	144.575	145	144.5	0	144.65	5 900 000	0	32 000 000	=+(+)	/		/(3)
4563	Hha1	11	act	145.28	145	0	0	145.28	0	0	9 000 000	=+	/		/(3)
4564	Taq1	11	act	145.563	145	145.42	145.4	145.87	3 800 000	3 800 000	8 400 000	=+	/ (-)		/(3)
4565	Taq1	52	att	146.08	146	0	146.08	0	0	3 200 000	0	+-	A		/(3)
4566	Taq1	52	att	146.75	146	146.6	146.9	0	4 300 000	3 600 000	0	=-	\		/(3)
4567	Taq1	11	act	144.575	145	144.5	0	144.65	5 900 000	0	32 000 000	=+(+)	/		/(3)
4568	Hha1	11	act	145.28	145	0	0	145.28	0	0	9 000 000	=+	/		/(3)
4569	Taq1	11	act	145.563	145	145.42	145.4	145.87	3 800 000	3 800 000	8 400 000	=+	/ (-)		/(3)
4570	Taq1	52	att	146.08	146	0	146.08	0	0	3 200 000	0	+-	A		/(3)
4571	Taq1	52	att	146.75	146	146.6	146.9	0	4 300 000	3 600 000	0	=-	\		/(3)
4572	Taq1	45	gcc	108.68	109	108.65	108.71	0	4 600 000	7 200 000	0	=-	\		\(7)
4573	Taq1	45	gcc	109.61	109	0	0	109.61	0	0	4 400 000	=+	/		\(7)
4574	Taq1	56	tga	110.12	110	0	0	110.12	0	0	7 000 000	=+	/		\(7)
4575	Hha1	62	tgt	137.11	137	137.11	0	0	4 800 000	0	0	-=	\		\(7)
4576	Hha1	7	caa	145.19	146	0	145.16	145.22	0	43 900 000	51 200 000	+=	/		\(7)
4577	Taq1	7	caa	145.41	146	145.25	0	145.57	3 800 000	0	4 100 000	-+(=)	V		\(7)
4578	Taq1	7	caa	146.29	146	0	146.29	0	0	6 500 000	0	+-	A		\(7)
4579	Hha1	7	caa	146.205	146	0	146.26	146.15	0	13 000 000	21 900 000	+=	/		\(7)
4580	Hha1	7	caa	146.73	146	146.73	0	0	8 000 000	0	0	-=	\		\(7)
4581	Hha1	25	cag	145.45	146	0	145.52	145.38	0	7 100 000	3 200 000	+-	A		\(7)
4582	Hha1	25	cag	145.96	146	146.08	0	145.84	18 400 000	0	5 800 000	-=(-)	\		\(7)
4583	Taq1	39	agg	153.567	154	153.47	153.65	153.58	77 000 000	535 700 000	431 400 000	+=	/ (-)		\(7)
4584	Taq1	39	agg	153.615	154	0	153.65	153.58	0	5 383.97	12 706.92	=+	/		\(7)
4585	Taq1	39	agg	154.87	154	154.87	0	0	14 100 000	0	0	-=	\		\(7)
4586	Taq1	39	agg	153.47	154	153.47	0	0	2 859.47	0	0	-=	\		\(7)
4587	Taq1	39	agg	154.87	154	154.87	0	0	523.61	0	0	-=	\		\(7)
4588	Taq1	51	ata	154.09	155	0	0	154.09	0	0	4 800 000	=+	/		\(7)
4589	Taq1	51	ata	155.34	155	155.34	0	0	4 800 000	0	0	-=	\		\(7)
4590	Taq1	39	agg	263.915	265	263.88	263.95	0	10 600 000	5 000 000	0	--	\		\(7)
4591	Taq1	39	agg	263.88	265	263.88	0	0	393.64	0	0	-=	\		\(7)
4592	Taq1	39	agg	265.03	265	0	265.03	0	0	67 300 000	0	+-	A		\(7)
4593	Taq1	39	agg	266.05	265	0	266.05	0	0	49 500 000	0	+-	A		\(7)
4594	Taq1	39	agg	263.95	265	0	263.95	0	0	50.25	0	+-	A		\(7)
4595	Taq1	39	agg	265.03	265	0	265.03	0	0	676.38	0	+-	A		\(7)
4596	Taq1	39	agg	266.05	265	0	266.05	0	0	497.49	0	+-	A		\(7)
4597	Hha1	7	caa	165.61	165	165.84	165.52	165.47	10 300 000	27 900 000	25 600 000	+=	/ (-)	/	
4598	Taq1	7	caa	165.84	165	0	0	165.84	0	0	3 400 000	=+	/	/	
4599	Taq1	39	agg	76.68	77	76.57	76.72	76.75	26 000 000	38 400 000	11 700 000	=-	\ (-)		\(2)
4600	Taq1	39	agg	77.453	77	77.62	77.4	77.34	45 900 000	61 500 000	17 100 000	=-	\ (-)		\(2)
4601	Taq1	39	agg	76.68	77	76.57	76.72	76.75	965.53	385.93	344.62	-=	\ (-)		\(2)
4602	Taq1	39	agg	77.453	77	77.62	77.4	77.34	1 704.54	618.09	503.68	-=	\ (-)		\(2)
4603	Taq1	8	gaa	142.755	143	142.97	142.54	0	7 200 000	7 700 000	0	=-	\		\(2)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
4561	RNU73038.MRP6	mrp6	multidrug resistance-associated protein 6	*	gtc	cca	increased
4562	RNU24071.PE1	nc	Munc13-2		att	act	decreased
4563	RNU24071.PE1	nc	Munc13-2		att	act	decreased
4564	RNU24071.PE1	nc	Munc13-2		att	act	decreased
4565	RNU24071.PE1	nc	Munc13-2		att	act	decreased
4566	RNU24071.PE1	nc	Munc13-2		att	act	decreased
4567	AF159706.PE1	nc	Munc13-2 protein		att	act	decreased
4568	AF159706.PE1	nc	Munc13-2 protein		att	act	decreased
4569	AF159706.PE1	nc	Munc13-2 protein		att	act	decreased
4570	AF159706.PE1	nc	Munc13-2 protein		att	act	decreased
4571	AF159706.PE1	nc	Munc13-2 protein		att	act	decreased
4572	RNU75361.PE1	nc	Munc13-3		tga	gcc	increased
4573	RNU75361.PE1	nc	Munc13-3		tga	gcc	increased
4574	RNU75361.PE1	nc	Munc13-3		tga	gcc	increased
4575	RNU75361.PE1	nc	Munc13-3		tca	tgt	increased
4576	RNU75361.PE1	nc	Munc13-3		cag	caa	increased
4577	RNU75361.PE1	nc	Munc13-3		cag	caa	increased
4578	RNU75361.PE1	nc	Munc13-3		cag	caa	increased
4579	RNU75361.PE1	nc	Munc13-3		cag	caa	increased
4580	RNU75361.PE1	nc	Munc13-3		cag	caa	increased
4581	RNU75361.PE1	nc	Munc13-3		cag	caa	increased
4582	RNU75361.PE1	nc	Munc13-3		cag	caa	increased
4583	RNU75361.PE1	nc	Munc13-3		ata	agg	increased
4584	RNU75361.PE1	nc	Munc13-3		ata	agg	increased
4585	RNU75361.PE1	nc	Munc13-3		ata	agg	increased
4586	RNU75361.PE1	nc	Munc13-3		ata	agg	increased
4587	RNU75361.PE1	nc	Munc13-3		ata	agg	increased
4588	RNU75361.PE1	nc	Munc13-3		ata	agg	increased
4589	RNU75361.PE1	nc	Munc13-3		ata	agg	increased
4590	RNU75361.PE1	nc	Munc13-3		agg	ggt	increased
4591	RNU75361.PE1	nc	Munc13-3		agg	ggt	increased
4592	RNU75361.PE1	nc	Munc13-3		agg	ggt	increased
4593	RNU75361.PE1	nc	Munc13-3		agg	ggt	increased
4594	RNU75361.PE1	nc	Munc13-3		agg	ggt	increased
4595	RNU75361.PE1	nc	Munc13-3		agg	ggt	increased
4596	RNU75361.PE1	nc	Munc13-3		agg	ggt	increased
4597	RNRNAMCP.PE1	nc	muscle C-protein		caa	ggc	decreased
4598	RNRNAMCP.PE1	nc	muscle C-protein		caa	ggc	decreased
4599	AF478683.PE1	nc	MYH		agg	gcg	increased
4600	AF478683.PE1	nc	MYH		agg	gcg	increased
4601	AF478683.PE1	nc	MYH		agg	gcg	increased
4602	AF478683.PE1	nc	MYH		agg	gcg	increased
4603	AF478683.PE1	nc	MYH		cta	gaa	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
4604	Taq1	8	gaa	143.07	143	0	0	143.07	0	0	5 000 000	=+	/		\(2)
4605	Hha1	8	gaa	143.13	143	0	143.13	0	0	6 100 000	0	+-	A		\(2)
4606	Taq1	47	ggc	114.615	114	114.6	114.63	0	4 246.15	1 718.65	0	-=	\	\	\(2)
4607	Taq1	18	cct	114.52	115	114.5	114.54	114.52	21 700 000	29 300 000	7 500 000	=-	\ (-)	\	\(2)
4608	Taq1	18	cct	115.39	115	115.34	115.38	115.45	58 000 000	74 100 000	4 000 000	=-	\ (-)		\(2)
4609	Hha1	62	tgt	104.79	105	0	104.79	0	0	3 000 000	0	+-	A		A(3)
4610	Hha1	39	agg	129.775	130	129.85	129.7	0	285.92	298.52	0	=-	\		A(3)
4611	Hha1	39	agg	130.465	130	0	130.65	130.28	0	191.05	280.76	+=	/		A(3)
4612	Taq1	45	gcc	248.04	249	0	248.04	0	0	3 500 000	0	+-	A		A(3)
4613	Taq1	45	gcc	249.12	249	249.12	0	0	4 600 000	0	0	-=	\		A(3)
4614	Taq1	45	gcc	249.73	249	249.73	0	0	4 300 000	0	0	-=	\		A(3)
4615	Taq1	45	gcc	250.13	249	250.13	0	0	4 000 000	0	0	-=	\		A(3)
4616	Taq1	39	agg	249.09	250	0	249.09	0	0	38 700 000	0	+-	A		A(3)
4617	Taq1	39	agg	249.96	250	0	249.96	0	0	9 400 000	0	+-	A		A(3)
4618	Taq1	39	agg	250.95	250	0	250.95	0	0	9 100 000	0	+-	A		A(3)
4619	Taq1	39	agg	249.09	250	0	249.09	0	0	388.94	0	+-	A		A(3)
4620	Taq1	39	agg	249.96	250	0	249.96	0	0	94.47	0	+-	A		A(3)
4621	Taq1	39	agg	250.95	250	0	250.95	0	0	91.45	0	+-	A		A(3)
4622	Taq1	31	gac	110.557	111	110.36	110.6	110.71	16 700 000	37 900 000	3 100 000	+-	A	A	A(4)
4623	Taq1	31	gac	111.515	111	111.36	111.67	0	4 100 000	28 000 000	0	+-	A		A(4)
4624	Taq1	36	ggt	110.59	111	0	110.59	0	0	3 600 000	0	+-	A	A	A(4)
4625	Taq1	36	ggt	111.507	111	111.35	111.52	111.65	3 000 000	5 000 000	3 500 000	==	-		A(4)
4626	Taq1	23	cga	202.34	203	0	202.34	0	0	3 400 000	0	+-	A	A	A(4)
4627	Taq1	56	tga	202.23	203	0	202.23	0	0	5 700 000	0	+-	A	A	A(4)
4628	Hha1	7	caa	100.26	100	100.26	0	0	4 500 000	0	0	-=	\	\	
4629	Taq1	7	caa	100.29	100	100.29	100.29	0	5 000 000	4 700 000	0	=-	\	\	
4630	Hha1	39	agg	110.635	111	110.65	110.62	0	351.9	704.51	0	+-	A	A	
4631	Hha1	62	tgt	110.69	111	0	110.69	0	0	4 000 000	0	+-	A	A	
4632	Hha1	62	tgt	128.45	128	0	0	128.45	0	0	9 800 000	=+	/		/(4)
4633	Hha1	17	cca	130.26	130	130.22	130.33	130.23	5 572.56	13 496.93	12 863.26	+=	/ (-)		/(4)
4634	Hha1	40	tgg	135.63	135	0	135.41	135.85	0	10 700 000	4 300 000	+-	A		/(4)
4635	Hha1	33	agc	214.93	214	0	0	214.93	0	0	3 000 000	=+	/		/(4)
4636	Hha1	59	ttc	212.83	214	0	0	212.83	0	0	87.96	=+	/		/(4)
4637	Hha1	59	ttc	213.51	214	213.52	213.5	0	416.01	333.44	0	=-	\		/(4)
4638	Hha1	59	ttc	214.04	214	0	0	214.04	0	0	85.37	=+	/		/(4)
4639	Hha1	40	tgg	135.63	136	0	135.41	135.85	0	10 700 000	4 300 000	+-	A		\(2)
4640	Hha1	40	tgg	136.03	136	136.03	0	0	11 400 000	0	0	-=	\		\(2)
4641	Hha1	43	cgc	170.535	171	170.57	170.5	0	4 300 000	5 600 000	0	=-	\		\(2)
4642	Hha1	43	cgc	171.52	171	171.55	171.54	171.47	16 700 000	17 200 000	4 500 000	=-	\ (-)		\(2)
4643	Hha1	40	tgg	135.63	136	0	135.41	135.85	0	10 700 000	4 300 000	+-	A		\(2)
4644	Hha1	40	tgg	136.03	136	136.03	0	0	11 400 000	0	0	-=	\		\(2)
4645	Hha1	43	cgc	170.535	171	170.57	170.5	0	4 300 000	5 600 000	0	=-	\		\(2)
4646	Hha1	43	cgc	171.52	171	171.55	171.54	171.47	16 700 000	17 200 000	4 500 000	=-	\ (-)		\(2)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
4604	AF478683.PE1	nc	MYH		cta	gaa	increased
4605	AF478683.PE1	nc	MYH		cta	gaa	increased
4606	AF191769.PE1	nc	myodulin	*	ggc	cct	increased
4607	AF191769.PE1	nc	myodulin	*	ggc	cct	increased
4608	AF191769.PE1	nc	myodulin	*	ggc	cct	increased
4609	AF054894.PE1	nc	myogenin		gat	tgt	increased by mild
4610	AF054894.PE1	nc	myogenin		agg	agg	increased by mild
4611	AF054894.PE1	nc	myogenin		agg	agg	increased by mild
4612	AF054894.PE1	nc	myogenin		gcc	agg	increased by mild
4613	AF054894.PE1	nc	myogenin		gcc	agg	increased by mild
4614	AF054894.PE1	nc	myogenin		gcc	agg	increased by mild
4615	AF054894.PE1	nc	myogenin		gcc	agg	increased by mild
4616	AF054894.PE1	nc	myogenin		gcc	agg	increased by mild
4617	AF054894.PE1	nc	myogenin		gcc	agg	increased by mild
4618	AF054894.PE1	nc	myogenin		gcc	agg	increased by mild
4619	AF054894.PE1	nc	myogenin		gcc	agg	increased by mild
4620	AF054894.PE1	nc	myogenin		gcc	agg	increased by mild
4621	AF054894.PE1	nc	myogenin		gcc	agg	increased by mild
4622	AY160191.IMPA2	Impa2	myo-inositol monophosphatase 2		ggt	gac	increased by mild
4623	AY160191.IMPA2	Impa2	myo-inositol monophosphatase 2		ggt	gac	increased by mild
4624	AY160191.IMPA2	Impa2	myo-inositol monophosphatase 2		ggt	gac	increased by mild
4625	AY160191.IMPA2	Impa2	myo-inositol monophosphatase 2		ggt	gac	increased by mild
4626	AY160191.IMPA2	Impa2	myo-inositol monophosphatase 2		cga	tga	increased by mild
4627	AY160191.IMPA2	Impa2	myo-inositol monophosphatase 2		cga	tga	increased by mild
4628	RNMHCG.MHC	MHC	myosin heavy chain		caa	tct	increased
4629	RNMHCG.MHC	MHC	myosin heavy chain		caa	tct	increased
4630	RNMHCG.MHC	MHC	myosin heavy chain		agg	tgt	increased by mild
4631	RNMHCG.MHC	MHC	myosin heavy chain		agg	tgt	increased by mild
4632	RNMYR5.MYR5	myr5	myosin heavy chain		aag	tgt	decreased
4633	RNMYR5.MYR5	myr5	myosin heavy chain		caa	cca	decreased
4634	RNMYR5.MYR5	myr5	myosin heavy chain		tgg	agt	decreased
4635	RNMYR5.MYR5	myr5	myosin heavy chain		ttc	agc	decreased
4636	RNMYR5.MYR5	myr5	myosin heavy chain		ttc	agc	decreased
4637	RNMYR5.MYR5	myr5	myosin heavy chain		ttc	agc	decreased
4638	RNMYR5.MYR5	myr5	myosin heavy chain		ttc	agc	decreased
4639	RNMHC15.PE1	nc	myosin heavy chain (AA 279)		aag	tgg	increased
4640	RNMHC15.PE1	nc	myosin heavy chain (AA 279)		aag	tgg	increased
4641	RNMHC15.PE1	nc	myosin heavy chain (AA 279)		cgc	tca	increased
4642	RNMHC15.PE1	nc	myosin heavy chain (AA 279)		cgc	tca	increased
4643	RNMHC21.PE1	nc	myosin heavy chain 21 (AA 621)		aag	tgg	increased
4644	RNMHC21.PE1	nc	myosin heavy chain 21 (AA 621)		aag	tgg	increased
4645	RNMHC21.PE1	nc	myosin heavy chain 21 (AA 621)		cgc	tca	increased
4646	RNMHC21.PE1	nc	myosin heavy chain 21 (AA 621)		cgc	tca	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
4647	Taq1	24	cgt	105.24	105	105.21	105.19	105.32	7 300 000	12 400 000	25 400 000	=+	/ (-)		/(5)
4648	Hha1	25	cag	104.6	105	0	0	104.6	0	0	3 000 000	=+	/		/(5)
4649	Taq1	30	cgt	104.387	105	104.42	104.39	104.35	5 500 000	6 400 000	9 800 000	==	-		/(5)
4650	Taq1	30	cgt	105.44	105	105.53	105.43	105.36	42 400 000	29 200 000	27 600 000	==	-		/(5)
4651	Taq1	39	agg	129.73	130	129.59	129.87	0	17 200 000	71 300 000	0	+-	A		/(5)
4652	Taq1	39	agg	130.39	130	130.53	130.47	130.17	11 500 000	64 400 000	5 500 000	+-	A		/(5)
4653	Taq1	39	agg	130.17	130	0	0	130.17	0	0	162	=+	/		/(5)
4654	Taq1	39	agg	129.73	130	129.59	129.87	0	638.74	716.59	0	=-	\		/(5)
4655	Taq1	39	agg	130.5	130	130.53	130.47	0	427.06	647.24	0	=-	\		/(5)
4656	Taq1	55	tca	129.32	130	0	129.45	129.19	0	8 600 000	7 800 000	+=	/		/(5)
4657	Taq1	55	tca	130.105	130	0	130	130.21	0	10 400 000	5 100 000	+-	A		/(5)
4658	Taq1	55	tca	130.65	130	0	130.65	0	0	21 000 000	0	+-	A		/(5)
4659	Hha1	40	tgg	159.24	160	159.24	0	0	4 000 000	0	0	-=	\	\	/(5)
4660	Hha1	59	ttc	159.255	160	159.3	159.21	0	161.2	166.72	0	=-	\	\	/(5)
4661	Hha1	59	ttc	160.1	160	0	160.1	0	0	120.73	0	+-	A		/(5)
4662	Hha1	59	ttc	160.46	160	0	160.31	160.61	0	89.11	85.37	+=	/		/(5)
4663	Taq1	24	cgt	105.24	105	105.21	105.19	105.32	7 300 000	12 400 000	25 400 000	=+	/ (-)		/(5)
4664	Hha1	25	cag	104.6	105	0	0	104.6	0	0	3 000 000	=+	/		/(5)
4665	Taq1	30	cgt	104.387	105	104.42	104.39	104.35	5 500 000	6 400 000	9 800 000	==	-		/(5)
4666	Taq1	30	cgt	105.44	105	105.53	105.43	105.36	42 400 000	29 200 000	27 600 000	==	-		/(5)
4667	Taq1	39	agg	129.73	130	129.59	129.87	0	17 200 000	71 300 000	0	+-	A		/(5)
4668	Taq1	39	agg	130.39	130	130.53	130.47	130.17	11 500 000	64 400 000	5 500 000	+-	A		/(5)
4669	Taq1	39	agg	130.17	130	0	0	130.17	0	0	162	=+	/		/(5)
4670	Taq1	39	agg	129.73	130	129.59	129.87	0	638.74	716.59	0	=-	\		/(5)
4671	Taq1	39	agg	130.5	130	130.53	130.47	0	427.06	647.24	0	=-	\		/(5)
4672	Taq1	55	tca	129.32	130	0	129.45	129.19	0	8 600 000	7 800 000	+=	/		/(5)
4673	Taq1	55	tca	130.105	130	0	130	130.21	0	10 400 000	5 100 000	+-	A		/(5)
4674	Taq1	55	tca	130.65	130	0	130.65	0	0	21 000 000	0	+-	A		/(5)
4675	Hha1	40	tgg	159.24	160	159.24	0	0	4 000 000	0	0	-=	\	\	/(5)
4676	Hha1	59	ttc	159.255	160	159.3	159.21	0	161.2	166.72	0	=-	\	\	/(5)
4677	Hha1	59	ttc	160.1	160	0	160.1	0	0	120.73	0	+-	A		/(5)
4678	Hha1	59	ttc	160.46	160	0	160.31	160.61	0	89.11	85.37	+=	/		/(5)
4679	Taq1	64	gtt	129.74	130	129.77	129.71	129.74	7 500 000	9 600 000	6 600 000	==	-		\(5)
4680	Taq1	64	gtt	130.757	130	130.75	130.72	130.8	12 400 000	12 600 000	3 700 000	=-	\ (-)		\(5)
4681	Taq1	9	atc	134.24	135	134.34	134.14	0	9 500 000	6 900 000	0	=-	\		\(5)
4682	Hha1	9	atc	135.125	135	135.07	135.18	0	7 800 000	5 500 000	0	=-	\	\	\(5)
4683	Taq1	9	atc	135.247	135	135.22	135.19	135.33	16 100 000	12 500 000	3 200 000	=-	\ (-)	\	\(5)
4684	Taq1	39	agg	296.655	298	296.82	0	296.49	8 000 000	0	10 700 000	-+(=)	V		\(5)
4685	Taq1	39	agg	296.655	298	296.82	0	296.49	297.08	0	315.16	-+(=)	V		\(5)
4686	Taq1	39	agg	297.29	298	0	297.29	0	0	15 600 000	0	+-	A		\(5)
4687	Taq1	39	agg	297.29	298	0	297.29	0	0	156.78	0	+-	A		\(5)
4688	Taq1	39	agg	299.4	298	299.45	299.35	0	330.51	177.89	0	--	\		\(5)
4689	Hha1	6	aga	130.145	130	130.36	129.93	0	28 200 000	3 400 000	0	-=	\		\(4) -(3)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
4647	AF209114.PE1	nc	myosin heavy chain Myr 8		cag	cgt	decreased
4648	AF209114.PE1	nc	myosin heavy chain Myr 8		cag	cgt	decreased
4649	AF209114.PE1	nc	myosin heavy chain Myr 8		cag	cgt	decreased
4650	AF209114.PE1	nc	myosin heavy chain Myr 8		cag	cgt	decreased
4651	AF209114.PE1	nc	myosin heavy chain Myr 8		tca	agg	decreased
4652	AF209114.PE1	nc	myosin heavy chain Myr 8		tca	agg	decreased
4653	AF209114.PE1	nc	myosin heavy chain Myr 8		tca	agg	decreased
4654	AF209114.PE1	nc	myosin heavy chain Myr 8		tca	agg	decreased
4655	AF209114.PE1	nc	myosin heavy chain Myr 8		tca	agg	decreased
4656	AF209114.PE1	nc	myosin heavy chain Myr 8		tca	agg	decreased
4657	AF209114.PE1	nc	myosin heavy chain Myr 8		tca	agg	decreased
4658	AF209114.PE1	nc	myosin heavy chain Myr 8		tca	agg	decreased
4659	AF209114.PE1	nc	myosin heavy chain Myr 8		ttc	tgg	increased
4660	AF209114.PE1	nc	myosin heavy chain Myr 8		ttc	tgg	increased
4661	AF209114.PE1	nc	myosin heavy chain Myr 8		ttc	tgg	decreased
4662	AF209114.PE1	nc	myosin heavy chain Myr 8		ttc	tgg	decreased
4663	AY004215.PE1	nc	myosin heavy chain Myr 8b		cag	cgt	decreased
4664	AY004215.PE1	nc	myosin heavy chain Myr 8b		cag	cgt	decreased
4665	AY004215.PE1	nc	myosin heavy chain Myr 8b		cag	cgt	decreased
4666	AY004215.PE1	nc	myosin heavy chain Myr 8b		cag	cgt	decreased
4667	AY004215.PE1	nc	myosin heavy chain Myr 8b		tca	agg	decreased
4668	AY004215.PE1	nc	myosin heavy chain Myr 8b		tca	agg	decreased
4669	AY004215.PE1	nc	myosin heavy chain Myr 8b		tca	agg	decreased
4670	AY004215.PE1	nc	myosin heavy chain Myr 8b		tca	agg	decreased
4671	AY004215.PE1	nc	myosin heavy chain Myr 8b		tca	agg	decreased
4672	AY004215.PE1	nc	myosin heavy chain Myr 8b		tca	agg	decreased
4673	AY004215.PE1	nc	myosin heavy chain Myr 8b		tca	agg	decreased
4674	AY004215.PE1	nc	myosin heavy chain Myr 8b		tca	agg	decreased
4675	AY004215.PE1	nc	myosin heavy chain Myr 8b		ttc	tgg	increased
4676	AY004215.PE1	nc	myosin heavy chain Myr 8b		ttc	tgg	increased
4677	AY004215.PE1	nc	myosin heavy chain Myr 8b		ttc	tgg	decreased
4678	AY004215.PE1	nc	myosin heavy chain Myr 8b		ttc	tgg	decreased
4679	RNMYR1A.MYR1	MYR1	myosin I heavy chain		gtt	tgc	increased
4680	RNMYR1A.MYR1	MYR1	myosin I heavy chain		gtt	tgc	increased
4681	RNMYR1A.MYR1	MYR1	myosin I heavy chain		atc	agc	increased
4682	RNMYR1A.MYR1	MYR1	myosin I heavy chain		atc	agc	increased
4683	RNMYR1A.MYR1	MYR1	myosin I heavy chain		atc	agc	increased
4684	RNMYR1A.MYR1	MYR1	myosin I heavy chain		agg	atc	increased
4685	RNMYR1A.MYR1	MYR1	myosin I heavy chain		agg	atc	increased
4686	RNMYR1A.MYR1	MYR1	myosin I heavy chain		agg	atc	increased
4687	RNMYR1A.MYR1	MYR1	myosin I heavy chain		agg	atc	increased
4688	RNMYR1A.MYR1	MYR1	myosin I heavy chain		agg	atc	increased
4689	RATMLC138.PE1	MLC1-f	myosin light chain		gtt	aga	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
4690	Taq1	64	gtt	129.74	130	129.77	129.71	129.74	7 500 000	9 600 000	6 600 000	==	-		\(4) -(3)
4691	Taq1	64	gtt	130.757	130	130.75	130.72	130.8	12 400 000	12 600 000	3 700 000	=-	\ (-)		\(4) -(3)
4692	Hha1	25	cag	174.66	175	174.66	0	0	6 700 000	0	0	-=	\		\(4) -(3)
4693	Hha1	25	cag	175.753	175	175.72	175.75	175.79	89 200 000	58 200 000	14 800 000	=-	\ (-)		\(4) -(3)
4694	Taq1	54	ttt	175.21	176	175.21	0	0	1 485.79	0	0	-=	\		\(4) -(3)
4695	Taq1	54	ttt	176.213	176	176.14	176.26	176.24	1 449.38	952.6	856.53	==	-		\(4) -(3)
4696	Hha1	6	aga	130.145	130	130.36	129.93	0	28 200 000	3 400 000	0	-=	\		\(4) -(3)
4697	Taq1	64	gtt	129.74	130	129.77	129.71	129.74	7 500 000	9 600 000	6 600 000	==	-		\(4) -(3)
4698	Taq1	64	gtt	130.757	130	130.75	130.72	130.8	12 400 000	12 600 000	3 700 000	=-	\ (-)		\(4) -(3)
4699	Hha1	25	cag	174.66	175	174.66	0	0	6 700 000	0	0	-=	\		\(4) -(3)
4700	Hha1	25	cag	175.753	175	175.72	175.75	175.79	89 200 000	58 200 000	14 800 000	=-	\ (-)		\(4) -(3)
4701	Taq1	54	ttt	175.21	176	175.21	0	0	1 485.79	0	0	-=	\		\(4) -(3)
4702	Taq1	54	ttt	176.213	176	176.14	176.26	176.24	1 449.38	952.6	856.53	==	-		\(4) -(3)
4703	Taq1	40	tgg	150.207	151	150.09	150.41	150.12	5 300 000	10 100 000	3 600 000	+-	A		/(2)
4704	Taq1	40	tgg	151.16	151	0	0	151.16	0	0	10 100 000	=+	/		/(2)
4705	Taq1	56	tga	151.42	151	0	0	151.42	0	0	3 000 000	=+	/		/(2)
4706	Taq1	17	cca	244.42	244	244.42	0	0	422.6	0	0	-=	\		/(2)
4707	Taq1	40	tgg	150.207	151	150.09	150.41	150.12	5 300 000	10 100 000	3 600 000	+-	A		/(2)
4708	Taq1	40	tgg	151.16	151	0	0	151.16	0	0	10 100 000	=+	/		/(2)
4709	Taq1	56	tga	151.42	151	0	0	151.42	0	0	3 000 000	=+	/		/(2)
4710	Taq1	17	cca	244.42	244	244.42	0	0	422.6	0	0	-=	\		/(2)
4711	Hha1	33	agc	64.945	65	0	65.19	64.7	0	4 100 000	31 500 000	=+	/		/(2)
4712	Hha1	33	agc	199.49	200	0	0	199.49	0	0	7 700 000	=+	/		/(2)
4713	Hha1	33	agc	200.51	200	0	0	200.51	0	0	6 800 000	=+	/		/(2)
4714	Hha1	64	gtt	70.367	70	70.31	70.37	70.42	6 400 000	5 200 000	17 000 000	=+	/ (-)		\(11)
4715	Taq1	47	ggc	108.45	108	108.45	0	0	1 969.23	0	0	-=	\		\(11)
4716	Taq1	39	agg	108.75	109	108.92	108.58	0	13 900 000	56 000 000	0	+-	A		\(11)
4717	Taq1	39	agg	109.455	109	109.31	109.6	0	12 800 000	59 600 000	0	+-	A		\(11)
4718	Taq1	39	agg	108.75	109	108.92	108.58	0	516.19	562.81	0	=-	\		\(11)
4719	Taq1	39	agg	109.455	109	109.31	109.6	0	475.34	599	0	=-	\		\(11)
4720	Taq1	39	agg	117.575	118	0	117.49	117.66	0	53 300 000	4 600 000	+-	A		\(11)
4721	Taq1	39	agg	117.875	118	118.09	0	117.66	17 600 000	0	135.49	-=(-)	\		\(11)
4722	Taq1	39	agg	117.49	118	0	117.49	0	0	535.68	0	+-	A		\(11)
4723	Taq1	39	agg	118.09	118	118.09	0	0	653.59	0	0	-=	\		\(11)
4724	Hha1	61	tct	177.603	178	177.48	177.83	177.5	17 000 000	8 100 000	4 700 000	-=	\ (-)		\(11)
4725	Hha1	59	ttc	207.49	208	207.5	207.3	207.67	166.4	399.56	124.18	+-	A		\(11)
4726	Hha1	59	ttc	208.45	208	0	208.45	0	0	169.59	0	+-	A		\(11)
4727	Hha1	59	ttc	208.945	208	209.09	208.8	0	306.81	250.08	0	=-	\		\(11)
4728	Taq1	61	tct	215.85	217	0	0	215.85	0	0	3 300 000	=+	/		\(11)
4729	Taq1	61	tct	216.9	217	0	0	216.9	0	0	6 300 000	=+	/		\(11)
4730	Taq1	61	tct	217.88	217	217.88	0	0	3 900 000	0	0	-=	\		\(11)
4731	Taq1	50	aat	217.5	218	217.42	217.59	217.49	34 800 000	8 000 000	7 500 000	-=	\ (-)		\(11)
4732	Taq1	50	aat	218.655	218	218.44	218.87	0	6 000 000	4 400 000	0	=-	\		\(11)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
4690	RATMLC138.PE1	MLC1-f	myosin light chain		gtt	aga	increased
4691	RATMLC138.PE1	MLC1-f	myosin light chain		gtt	aga	increased
4692	RATMLC138.PE1	MLC1-f	myosin light chain		cag	ttt	increased
4693	RATMLC138.PE1	MLC1-f	myosin light chain		cag	ttt	increased
4694	RATMLC138.PE1	MLC1-f	myosin light chain		cag	ttt	increased
4695	RATMLC138.PE1	MLC1-f	myosin light chain		cag	ttt	increased
4696	RATMLC138.PE2	MLC3-f	myosin light chain		gtt	aga	increased
4697	RATMLC138.PE2	MLC3-f	myosin light chain		gtt	aga	increased
4698	RATMLC138.PE2	MLC3-f	myosin light chain		gtt	aga	increased
4699	RATMLC138.PE2	MLC3-f	myosin light chain		cag	ttt	increased
4700	RATMLC138.PE2	MLC3-f	myosin light chain		cag	ttt	increased
4701	RATMLC138.PE2	MLC3-f	myosin light chain		cag	ttt	increased
4702	RATMLC138.PE2	MLC3-f	myosin light chain		cag	ttt	increased
4703	RATMRLC.PE1	nc	myosin regulatory light chain		tga	tgg	decreased
4704	RATMRLC.PE1	nc	myosin regulatory light chain		tga	tgg	decreased
4705	RATMRLC.PE1	nc	myosin regulatory light chain		tga	tgg	decreased
4706	RATMRLC.PE1	nc	myosin regulatory light chain		cca	agc	decreased
4707	RNMRLCB.PE1	nc	myosin RLC-B		tga	tgg	decreased
4708	RNMRLCB.PE1	nc	myosin RLC-B		tga	tgg	decreased
4709	RNMRLCB.PE1	nc	myosin RLC-B		tga	tgg	decreased
4710	RNMRLCB.PE1	nc	myosin RLC-B		cca	agc	decreased
4711	AB035736.MYO5A	Myo5a	myosin-Va		cat	agc	decreased
4712	AB035736.MYO5A	Myo5a	myosin-Va		agc	att	decreased
4713	AB035736.MYO5A	Myo5a	myosin-Va		agc	att	decreased
4714	AF021936.PE1	MRCK-beta	myotonic dystrophy kinase-related Cdc42-binding		gtt	tgt	increased
4715	AF021936.PE1	MRCK-beta	myotonic dystrophy kinase-related Cdc42-binding		ggc	agg	increased
4716	AF021936.PE1	MRCK-beta	myotonic dystrophy kinase-related Cdc42-binding		ggc	agg	increased
4717	AF021936.PE1	MRCK-beta	myotonic dystrophy kinase-related Cdc42-binding		ggc	agg	increased
4718	AF021936.PE1	MRCK-beta	myotonic dystrophy kinase-related Cdc42-binding		ggc	agg	increased
4719	AF021936.PE1	MRCK-beta	myotonic dystrophy kinase-related Cdc42-binding		ggc	agg	increased
4720	AF021936.PE1	MRCK-beta	myotonic dystrophy kinase-related Cdc42-binding		gct	agg	increased
4721	AF021936.PE1	MRCK-beta	myotonic dystrophy kinase-related Cdc42-binding		gct	agg	increased
4722	AF021936.PE1	MRCK-beta	myotonic dystrophy kinase-related Cdc42-binding		gct	agg	increased
4723	AF021936.PE1	MRCK-beta	myotonic dystrophy kinase-related Cdc42-binding		gct	agg	increased
4724	AF021936.PE1	MRCK-beta	myotonic dystrophy kinase-related Cdc42-binding		gag	tct	increased
4725	AF021936.PE1	MRCK-beta	myotonic dystrophy kinase-related Cdc42-binding		ttc	acg	increased
4726	AF021936.PE1	MRCK-beta	myotonic dystrophy kinase-related Cdc42-binding		ttc	acg	increased
4727	AF021936.PE1	MRCK-beta	myotonic dystrophy kinase-related Cdc42-binding		ttc	acg	increased
4728	AF021936.PE1	MRCK-beta	myotonic dystrophy kinase-related Cdc42-binding		aat	tct	increased
4729	AF021936.PE1	MRCK-beta	myotonic dystrophy kinase-related Cdc42-binding		aat	tct	increased
4730	AF021936.PE1	MRCK-beta	myotonic dystrophy kinase-related Cdc42-binding		aat	tct	increased
4731	AF021936.PE1	MRCK-beta	myotonic dystrophy kinase-related Cdc42-binding		aat	tct	increased
4732	AF021936.PE1	MRCK-beta	myotonic dystrophy kinase-related Cdc42-binding		aat	tct	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**		**size**			**fluorescence**		**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
4733	Hha1	6	aga	225.19	226	225.19	0	0	7 000 000	0	0	-=	\		\(11)
4734	Taq1	8	gaa	235.63	237	235.63	0	0	3 800 000	0	0	-=	\		\(11)
4735	Hha1	8	gaa	236.3	237	236.33	236.27	0	3 900 000	3 100 000	0	=-	\		\(11)
4736	Taq1	45	gcc	237.79	237	237.79	0	0	3 100 000	0	0	-=	\		\(11)
4737	Hha1	56	tga	122.82	123	122.55	123	122.91	5 168.96	660.5	672.29	-=	\ (-)		\(2)
4738	Hha1	56	tga	123.58	123	123.54	123.62	0	739.59	616.46	0	=-	\		\(2)
4739	Hha1	54	ttt	124.03	124	124.17	123.89	0	7 500 000	5 400 000	0	=-	\		\(2)
4740	Hha1	39	agg	87.397	87	87.19	87.6	87.4	1 312.31	447.78	545.24	-=	\ (-)		\(5)
4741	Taq1	41	ccc	95.76	96	95.76	0	0	3 700 000	0	0	-=	\		\(5)
4742	Taq1	41	ccc	96.43	96	0	96.43	0	0	5 600 000	0	+-	A		\(5)
4743	Hha1	6	aga	187.02	188	187.02	0	0	4 800 000	0	0	-=	\		\(5)
4744	Hha1	6	aga	188.12	188	188.12	0	0	10 100 000	0	0	-=	\		\(5)
4745	Taq1	21	acc	187.65	188	187.65	0	0	6 000 000	0	0	-=	\		\(5)
4746	Hha1	21	acc	188.35	188	0	188.45	188.25	0	3 400 000	5 200 000	+=	/		\(5)
4747	Taq1	49	aaa	284.435	286	284.42	284.45	0	223 200 000	92 100 000	0	-=	\		\(5)
4748	Taq1	49	aaa	285.51	286	285.35	285.67	0	26 700 000	18 600 000	0	=-	\		\(5)
4749	Taq1	49	aaa	286.73	286	286.73	286.73	0	26 100 000	12 200 000	0	--	\		\(5)
4750	Hha1	20	ctc	126.45	126	126.46	126.33	126.56	557.85	498.29	1 514.79	=+	/ (-)		-1
4751	Hha1	20	ctc	126.57	126	0	126.57	0	0	576.97	0	+-	A		-1
4752	Hha1	62	tgt	146.79	146	0	0	146.79	0	0	7 100 000	=+	/		-1
4753	Hha1	54	ttt	150.39	151	150.39	0	0	4 800 000	0	0	-=	\		-1
4754	Hha1	54	ttt	151.537	151	151.52	151.59	151.5	5 700 000	4 700 000	4 100 000	==	-		-1
4755	Hha1	39	agg	91.76	92	91.76	0	0	483.87	0	0	-=	\		\(10)
4756	Hha1	26	ctg	114.717	115	114.71	114.63	114.81	12 300 000	6 500 000	4 700 000	-=	\ (-)		\(10)
4757	Taq1	44	cgg	134.19	135	134.04	134.34	0	847.13	445.05	0	--	\		\(10)
4758	Taq1	44	cgg	135.227	135	135.42	135.29	134.97	1 597.05	1 406.93	1 412.23	==	-		\(10)
4759	Taq1	29	gca	135.507	136	135.56	135.44	135.52	24 600 000	19 200 000	8 000 000	=-	\ (-)		\(10)
4760	Taq1	29	gca	136.547	136	136.54	136.49	136.61	6 000 000	3 900 000	8 100 000	=+	/ (-)		\(10)
4761	Hha1	39	agg	147.545	148	147.33	0	147.76	256.59	0	264.48	-+(=)	V		\(10)
4762	Hha1	39	agg	148.44	148	148.38	148.5	0	373.9	262.7	0	=-	\		\(10)
4763	Taq1	18	cct	168.705	169	168.65	168.76	0	5 300 000	5 500 000	0	=-	\		\(10)
4764	Taq1	18	cct	169.87	169	169.98	169.76	0	16 300 000	12 600 000	0	=-	\		\(10)
4765	Taq1	39	agg	168.1	169	0	168.26	167.94	0	43 800 000	138.43	+-	A		\(10)
4766	Taq1	39	agg	168.975	169	169.12	168.83	0	9 200 000	19 400 000	0	+-	A		\(10)
4767	Taq1	39	agg	169.875	169	169.95	169.8	0	6 500 000	83 000 000	0	+-	A		\(10)
4768	Taq1	39	agg	168.26	169	0	168.26	0	0	440.2	0	+-	A		\(10)
4769	Taq1	39	agg	168.975	169	169.12	168.83	0	341.65	194.97	0	=-	\		\(10)
4770	Taq1	39	agg	169.875	169	169.95	169.8	0	241.38	834.17	0	+-	A		\(10)
4771	Taq1	56	tga	195.14	196	0	195.14	0	0	7 700 000	0	+-	A		\(10)
4772	Taq1	56	tga	196.315	196	196.32	196.31	0	3 700 000	4 300 000	0	=-	\		\(10)
4773	Taq1	21	acc	254.92	255	254.92	0	0	3 900 000	0	0	-=	\		\(10)
4774	Hha1	25	cag	254.24	255	254.24	0	0	3 200 000	0	0	-=	\		\(10)
4775	Hha1	4	aag	139.233	140	139.25	139.24	139.21	79 200 000	14 200 000	43 900 000	-=	\ (-)		/(3)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
4733	AF021936.PE1	MRCK-beta	myotonic dystrophy kinase-related Cdc42-binding		tgc	aga	increased
4734	AF021936.PE1	MRCK-beta	myotonic dystrophy kinase-related Cdc42-binding		gaa	tgg	increased
4735	AF021936.PE1	MRCK-beta	myotonic dystrophy kinase-related Cdc42-binding		gaa	tgg	increased
4736	AF021936.PE1	MRCK-beta	myotonic dystrophy kinase-related Cdc42-binding		agc	gcc	increased
4737	RRU45986.PE1	nc	Myx		ttt	tga	increased
4738	RRU45986.PE1	nc	Myx		ttt	tga	increased
4739	RRU45986.PE1	nc	Myx		ttt	tga	increased
4740	RATNACHI.PE1	nc	Na+ channel	*	caa	agg	increased
4741	RATNACHI.PE1	nc	Na+ channel	*	ccc	gag	increased
4742	RATNACHI.PE1	nc	Na+ channel	*	ccc	gag	increased
4743	RATNACHI.PE1	nc	Na+ channel	*	acc	aga	increased
4744	RATNACHI.PE1	nc	Na+ channel	*	acc	aga	increased
4745	RATNACHI.PE1	nc	Na+ channel	*	acc	aga	increased
4746	RATNACHI.PE1	nc	Na+ channel	*	acc	aga	increased
4747	RATNACHI.PE1	nc	Na+ channel	*	cct	aaa	increased
4748	RATNACHI.PE1	nc	Na+ channel	*	cct	aaa	increased
4749	RATNACHI.PE1	nc	Na+ channel	*	cct	aaa	increased
4750	AY125814.PE1	nc	Na+-dependent amino acid transporter ASCT2		caa	ctc	No change
4751	AY125814.PE1	nc	Na+-dependent amino acid transporter ASCT2		caa	ctc	No change
4752	AY125814.PE1	nc	Na+-dependent amino acid transporter ASCT2		tgt	cca	No change
4753	AY125814.PE1	nc	Na+-dependent amino acid transporter ASCT2		ttt	tag	No change
4754	AY125814.PE1	nc	Na+-dependent amino acid transporter ASCT2		ttt	tag	No change
4755	RATNAT.PE1	nc	N-acetylglucosaminyltransferase III		aac	agg	increased
4756	RATNAT.PE1	nc	N-acetylglucosaminyltransferase III		ctg	aca	increased
4757	RATNAT.PE1	nc	N-acetylglucosaminyltransferase III		cgg	gca	increased
4758	RATNAT.PE1	nc	N-acetylglucosaminyltransferase III		cgg	gca	increased
4759	RATNAT.PE1	nc	N-acetylglucosaminyltransferase III		cgg	gca	increased
4760	RATNAT.PE1	nc	N-acetylglucosaminyltransferase III		cgg	gca	increased
4761	RATNAT.PE1	nc	N-acetylglucosaminyltransferase III		aag	agg	increased
4762	RATNAT.PE1	nc	N-acetylglucosaminyltransferase III		aag	agg	increased
4763	RATNAT.PE1	nc	N-acetylglucosaminyltransferase III		cct	agg	increased
4764	RATNAT.PE1	nc	N-acetylglucosaminyltransferase III		cct	agg	increased
4765	RATNAT.PE1	nc	N-acetylglucosaminyltransferase III		cct	agg	increased
4766	RATNAT.PE1	nc	N-acetylglucosaminyltransferase III		cct	agg	increased
4767	RATNAT.PE1	nc	N-acetylglucosaminyltransferase III		cct	agg	increased
4768	RATNAT.PE1	nc	N-acetylglucosaminyltransferase III		cct	agg	increased
4769	RATNAT.PE1	nc	N-acetylglucosaminyltransferase III		cct	agg	increased
4770	RATNAT.PE1	nc	N-acetylglucosaminyltransferase III		cct	agg	increased
4771	RATNAT.PE1	nc	N-acetylglucosaminyltransferase III		gta	tga	increased
4772	RATNAT.PE1	nc	N-acetylglucosaminyltransferase III		gta	tga	increased
4773	RATNAT.PE1	nc	N-acetylglucosaminyltransferase III		cag	acc	increased
4774	RATNAT.PE1	nc	N-acetylglucosaminyltransferase III		cag	acc	increased
4775	RATNACE.PE1	nc	N-acetylglucosaminyltransferase V		aag	cca	decreased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
4776	Hha1	4	aag	140.12	140	140.27	0	139.97	6 400 000	0	6 500 000	-+(=)	V		/(3)
4777	Taq1	17	cca	139.775	140	139.67	0	139.88	171.82	0	1 037.43	=+(+)	/		/(3)
4778	Taq1	17	cca	140.73	140	140.48	140.82	140.89	208.98	292.51	1 187.79	=+	/ (-)		/(3)
4779	Taq1	26	ctg	164.11	165	0	164.11	0	0	3 700 000	0	+-	A		/(3)
4780	Taq1	26	ctg	165	165	0	0	165	0	0	10 600 000	=+	/		/(3)
4781	Taq1	57	ctg	164.54	165	0	0	164.54	0	0	6 200 000	=+	/		/(3)
4782	Taq1	57	ctg	165.61	165	0	0	165.61	0	0	13 000 000	=+	/		/(3)
4783	Taq1	49	aaa	238.583	240	238.58	238.57	238.6	29 100 000	21 100 000	3 300 000	=-	\ (-)		\(2)
4784	Taq1	49	aaa	239.467	240	239.44	239.44	239.52	627 100 032	308 600 000	49 400 000	-=	\ (-)		\(2)
4785	Taq1	49	aaa	240.21	240	0	240.21	0	0	19 600 000	0	+-	A		\(2)
4786	Taq1	49	aaa	241.02	240	241.08	240.96	0	51 800 000	15 300 000	0	-=	\	\	\(2)
4787	Taq1	51	ata	240.28	240	240.28	0	0	4 100 000	0	0	-=	\		\(2)
4788	Taq1	51	ata	241.225	240	241.25	241.2	0	83 400 000	32 800 000	0	-=	\	\	\(2)
4789	Hha1	9	atc	218.87	218	218.87	0	0	3 000 000	0	0	-=	\		\(2)
4790	Taq1	51	ata	217.995	219	217.94	218.05	0	7 100 000	5 900 000	0	=-	\		\(2)
4791	Taq1	51	ata	219.84	219	219.84	0	0	6 400 000	0	0	-=	\		\(2)
4792	Taq1	49	aaa	238.583	240	238.58	238.57	238.6	29 100 000	21 100 000	3 300 000	=-	\ (-)		\(2)
4793	Taq1	49	aaa	239.467	240	239.44	239.44	239.52	627 100 032	308 600 000	49 400 000	-=	\ (-)		\(2)
4794	Taq1	49	aaa	240.21	240	0	240.21	0	0	19 600 000	0	+-	A		\(2)
4795	Taq1	49	aaa	241.02	240	241.08	240.96	0	51 800 000	15 300 000	0	-=	\	\	\(2)
4796	Taq1	51	ata	240.28	240	240.28	0	0	4 100 000	0	0	-=	\		\(2)
4797	Taq1	51	ata	241.225	240	241.25	241.2	0	83 400 000	32 800 000	0	-=	\	\	\(2)
4798	Hha1	9	atc	218.87	218	218.87	0	0	3 000 000	0	0	-=	\		\(2)
4799	Taq1	51	ata	217.995	219	217.94	218.05	0	7 100 000	5 900 000	0	=-	\		\(2)
4800	Taq1	51	ata	219.84	219	219.84	0	0	6 400 000	0	0	-=	\		\(2)
4801	Taq1	22	tcc	107.623	108	107.61	107.67	107.59	5 000 000	7 200 000	7 200 000	==	-		/(4)
4802	Hha1	22	tcc	107.72	108	107.72	0	0	5 600 000	0	0	-=	\		/(4)
4803	Taq1	22	tcc	108.59	108	0	0	108.59	0	0	3 700 000	=+	/	/	/(4)
4804	Hha1	22	tcc	108.61	108	0	0	108.61	0	0	8 500 000	=+	/	/	/(4)
4805	Taq1	29	gca	107.45	108	0	0	107.45	0	0	7 700 000	=+	/		/(4)
4806	Taq1	29	gca	108.537	108	108.54	108.57	108.5	11 700 000	8 300 000	8 900 000	==	-		/(4)
4807	Taq1	51	ata	111.57	112	111.57	0	0	9 100 000	0	0	-=	\		/(4)
4808	Taq1	51	ata	112.41	112	0	112.52	112.3	0	13 300 000	15 300 000	+=	/		/(4)
4809	Taq1	54	ttt	112.42	112	0	112.42	0	0	446.9	0	+-	A		/(4)
4810	Taq1	54	ttt	112.67	112	0	112.67	0	0	540.98	0	+-	A		/(4)
4811	Hha1	61	tct	107.585	107	107.59	0	107.58	7 100 000	0	3 200 000	-+(-)	V (\)		\(4)
4812	Hha1	60	ttg	176.86	177	176.86	0	0	4 600 000	0	0	-=	\		\(4)
4813	Hha1	60	ttg	177.81	177	177.85	177.67	177.91	7 300 000	5 600 000	6 800 000	==	-		\(4)
4814	Hha1	40	tgg	220.38	221	220.38	0	0	11 800 000	0	0	-=	\		\(4)
4815	Hha1	40	tgg	221.135	221	221.22	221.05	0	8 700 000	5 100 000	0	=-	\		\(4)
4816	Hha1	25	cag	250.76	251	0	0	250.76	0	0	4 500 000	=+	/		\(4)
4817	Hha1	44	cgg	275.98	276	275.98	0	0	3 000 000	0	0	-=	\		\(4)
4818	Hha1	44	cgg	276.79	276	276.79	0	0	3 100 000	0	0	-=	\		\(4)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
4776	RATNACE.PE1	nc	N-acetylglucosaminyltransferase V		aag	cca	decreased
4777	RATNACE.PE1	nc	N-acetylglucosaminyltransferase V		aag	cca	decreased
4778	RATNACE.PE1	nc	N-acetylglucosaminyltransferase V		aag	cca	decreased
4779	RATNACE.PE1	nc	N-acetylglucosaminyltransferase V		tat	ctg	decreased
4780	RATNACE.PE1	nc	N-acetylglucosaminyltransferase V		tat	ctg	decreased
4781	RATNACE.PE1	nc	N-acetylglucosaminyltransferase V		tat	ctg	decreased
4782	RATNACE.PE1	nc	N-acetylglucosaminyltransferase V		tat	ctg	decreased
4783	AY172581.ND1	ND1	NADH dehydrogenase subunit 1		ata	aaa	increased
4784	AY172581.ND1	ND1	NADH dehydrogenase subunit 1		ata	aaa	increased
4785	AY172581.ND1	ND1	NADH dehydrogenase subunit 1		ata	aaa	increased
4786	AY172581.ND1	ND1	NADH dehydrogenase subunit 1		ata	aaa	increased
4787	AY172581.ND1	ND1	NADH dehydrogenase subunit 1		ata	aaa	increased
4788	AY172581.ND1	ND1	NADH dehydrogenase subunit 1		ata	aaa	increased
4789	MIRNND1.ND1	ND1	NADH dehydrogenase subunit 1		ata	atc	increased
4790	MIRNND1.ND1	ND1	NADH dehydrogenase subunit 1		ata	atc	increased
4791	MIRNND1.ND1	ND1	NADH dehydrogenase subunit 1		ata	atc	increased
4792	RNO428514.NADH1	NADH1	NADH dehydrogenase subunit 1		ata	aaa	increased
4793	RNO428514.NADH1	NADH1	NADH dehydrogenase subunit 1		ata	aaa	increased
4794	RNO428514.NADH1	NADH1	NADH dehydrogenase subunit 1		ata	aaa	increased
4795	RNO428514.NADH1	NADH1	NADH dehydrogenase subunit 1		ata	aaa	increased
4796	RNO428514.NADH1	NADH1	NADH dehydrogenase subunit 1		ata	aaa	increased
4797	RNO428514.NADH1	NADH1	NADH dehydrogenase subunit 1		ata	aaa	increased
4798	MIRNXX.PE1	nc	NADH subunit 1		ata	atc	increased
4799	MIRNXX.PE1	nc	NADH subunit 1		ata	atc	increased
4800	MIRNXX.PE1	nc	NADH subunit 1		ata	atc	increased
4801	AF152963.PE1	nc	NADH/NADPH mitogenic oxidase subunit p65-mox		gca	tcc	decreased
4802	AF152963.PE1	nc	NADH/NADPH mitogenic oxidase subunit p65-mox		gca	tcc	decreased
4803	AF152963.PE1	nc	NADH/NADPH mitogenic oxidase subunit p65-mox		gca	tcc	decreased
4804	AF152963.PE1	nc	NADH/NADPH mitogenic oxidase subunit p65-mox		gca	tcc	decreased
4805	AF152963.PE1	nc	NADH/NADPH mitogenic oxidase subunit p65-mox		gca	tcc	decreased
4806	AF152963.PE1	nc	NADH/NADPH mitogenic oxidase subunit p65-mox		gca	tcc	decreased
4807	AF152963.PE1	nc	NADH/NADPH mitogenic oxidase subunit p65-mox		ttt	ata	decreased
4808	AF152963.PE1	nc	NADH/NADPH mitogenic oxidase subunit p65-mox		ttt	ata	decreased
4809	AF152963.PE1	nc	NADH/NADPH mitogenic oxidase subunit p65-mox		ttt	ata	decreased
4810	AF152963.PE1	nc	NADH/NADPH mitogenic oxidase subunit p65-mox		ttt	ata	decreased
4811	AF237962.PE1	nc	NADH/NADPH thyroid oxidase THOX2		tct	tgc	increased
4812	AF237962.PE1	nc	NADH/NADPH thyroid oxidase THOX2		aca	ttg	increased
4813	AF237962.PE1	nc	NADH/NADPH thyroid oxidase THOX2		aca	ttg	increased
4814	AF237962.PE1	nc	NADH/NADPH thyroid oxidase THOX2		cat	tgg	increased
4815	AF237962.PE1	nc	NADH/NADPH thyroid oxidase THOX2		cat	tgg	increased
4816	AF237962.PE1	nc	NADH/NADPH thyroid oxidase THOX2		gat	cag	increased
4817	AF237962.PE1	nc	NADH/NADPH thyroid oxidase THOX2		gac	cgg	increased
4818	AF237962.PE1	nc	NADH/NADPH thyroid oxidase THOX2		gac	cgg	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
4819	Hha1	8	gaa	106.345	106	0	106.18	106.51	0	5 600 000	6 200 000	+=	/	/	
4820	Taq1	8	gaa	106.5	106	0	0	106.5	0	0	30 800 000	=+	/	/	
4821	Hha1	8	gaa	106.345	106	0	106.18	106.51	0	5 600 000	6 200 000	+=	/	/	
4822	Taq1	8	gaa	106.5	106	0	0	106.5	0	0	30 800 000	=+	/	/	
4823	Taq1	18	cct	156.12	157	156.1	156.14	0	15 200 000	16 300 000	0	=-	\	\	
4824	Taq1	39	agg	156.06	157	156.06	0	0	185.68	0	0	-=	\	\	
4825	Hha1	39	agg	74.737	75	74.7	74.52	74.99	1 158.35	4 167.41	8 748.37	=+	/ (-)		/(2)
4826	Hha1	39	agg	75.345	75	75.13	75.56	0	608.5	9 827.45	0	+-	A		/(2)
4827	Hha1	6	aga	153.31	154	153.31	0	0	8 700 000	0	0	-=	\		/(2)
4828	Hha1	6	aga	154.4	154	154.27	0	154.53	14 200 000	0	12 300 000	-+(=)	V		/(2)
4829	Hha1	39	agg	197.13	198	0	197.22	197.04	0	238.82	260.41	+=	/		/(2)
4830	Hha1	39	agg	97.095	97	97.23	0	96.96	329.91	0	309.24	-+(=)	V		\(7)
4831	Hha1	6	aga	119.987	120	120	119.94	120.02	25 400 000	3 000 000	4 900 000	-=	\ (-)	\	\(7)
4832	Taq1	39	agg	119.78	120	119.93	119.63	0	19 400 000	32 300 000	0	=-	\	\	\(7)
4833	Taq1	39	agg	119.93	120	119.93	0	0	720.43	0	0	-=	\	\	\(7)
4834	Taq1	39	agg	119.63	120	0	119.63	0	0	324.62	0	+-	A		\(7)
4835	Hha1	41	ccc	123.8	124	123.8	0	0	5 400 000	0	0	-=	\		\(7)
4836	Hha1	10	atg	215.46	216	215.46	0	0	3 800 000	0	0	-=	\	\	\(7)
4837	Taq1	10	atg	215.46	216	215.46	0	0	3 400 000	0	0	-=	\	\	\(7)
4838	Taq1	10	atg	215.99	216	0	215.99	0	0	5 900 000	0	+-	A		\(7)
4839	Hha1	10	atg	216.62	216	216.62	0	0	5 100 000	0	0	-=	\		\(7)
4840	Taq1	10	atg	217.17	216	217.17	0	0	3 000 000	0	0	-=	\		\(7)
4841	Taq1	40	tgg	131.82	132	0	0	131.82	0	0	4 300 000	=+	/		/(2)
4842	Hha1	61	tct	147.073	147	147.05	147.04	147.13	8 600 000	27 600 000	17 800 000	+=	/ (-)		/(2)
4843	Hha1	26	ctg	231.04	232	0	231.04	0	0	3 600 000	0	+-	A		/(2)
4844	Hha1	59	ttc	87.205	87	0	87.12	87.29	0	687.01	357.02	+-	A		A(4) \(3)
4845	Hha1	25	cag	158.25	159	0	0	158.25	0	0	8 000 000	=+	/		A(4) \(3)
4846	Hha1	25	cag	158.96	159	0	158.96	0	0	3 400 000	0	+-	A		A(4) \(3)
4847	Taq1	56	tga	160.065	161	160.08	160.05	0	9 600 000	6 200 000	0	=-	\		A(4) \(3)
4848	Taq1	56	tga	161.31	161	161.39	161.23	0	19 700 000	12 200 000	0	=-	\		A(4) \(3)
4849	Taq1	17	cca	228.665	229	228.47	228.86	0	408.67	272.57	0	=-	\		A(4) \(3)
4850	Taq1	17	cca	229.95	229	0	229.95	0	0	285.86	0	+-	A		A(4) \(3)
4851	Taq1	39	agg	228.995	229	228.85	229.14	0	15 000 000	29 200 000	0	+-	A		A(4) \(3)
4852	Taq1	39	agg	228.995	229	228.85	229.14	0	557.04	293.47	0	--	\		A(4) \(3)
4853	Hha1	39	agg	78.64	79	78.87	78.41	0	2 023.46	728.4	0	-=	\		/(3) -(2)
4854	Hha1	39	agg	78.96	79	0	0	78.96	0	0	960.28	=+	/		/(3) -(2)
4855	Taq1	45	gcc	135.293	136	135.33	135.33	135.22	5 900 000	4 700 000	6 200 000	==	-		/(3) -(2)
4856	Taq1	45	gcc	136.317	136	136.21	136.62	136.12	7 500 000	4 100 000	8 100 000	=+	/ (-)	/	/(3) -(2)
4857	Taq1	56	tga	136.38	137	0	0	136.38	0	0	27 700 000	=+	/	/	/(3) -(2)
4858	Taq1	56	tga	137.043	137	137.02	136.95	137.16	3 500 000	3 900 000	8 500 000	=+	/ (-)		/(3) -(2)
4859	Taq1	9	atc	124.52	125	124.52	0	0	8 800 000	0	0	-=	\		\(8)
4860	Hha1	9	atc	124.995	125	124.94	125.05	0	13 600 000	6 200 000	0	--	\		\(8)
4861	Taq1	9	atc	125.075	125	125.09	0	125.06	5 500 000	0	19 600 000	=+(+)	/		\(8)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
4819	AF070475.NBC2	NBC2	NBC-like protein 2		gaa	acg	decreased
4820	AF070475.NBC2	NBC2	NBC-like protein 2		gaa	acg	decreased
4821	AF080106.NBC3	NBC3	NBC-like protein 3		gaa	acg	decreased
4822	AF080106.NBC3	NBC3	NBC-like protein 3		gaa	acg	decreased
4823	A75684.PE1	nc	nc		agg	cct	increased
4824	A75684.PE1	nc	nc		agg	cct	increased
4825	AB075005S9.DLST	DLST	nc		atc	agg	decreased
4826	AB075005S9.DLST	DLST	nc		atc	agg	decreased
4827	AB075005S9.DLST	DLST	nc		aga	aga	decreased
4828	AB075005S9.DLST	DLST	nc		aga	aga	decreased
4829	AB075005S9.DLST	DLST	nc		ctg	agg	decreased
4830	AX023740.PE1	nc	nc	*	ggc	agg	increased
4831	AX023740.PE1	nc	nc	*	aga	agg	increased
4832	AX023740.PE1	nc	nc	*	aga	agg	increased
4833	AX023740.PE1	nc	nc	*	aga	agg	increased
4834	AX023740.PE1	nc	nc	*	aga	agg	increased
4835	AX023740.PE1	nc	nc	*	ccc	ccg	increased
4836	AX023740.PE1	nc	nc	*	atg	ggt	increased
4837	AX023740.PE1	nc	nc	*	atg	ggt	increased
4838	AX023740.PE1	nc	nc	*	atg	ggt	increased
4839	AX023740.PE1	nc	nc	*	atg	ggt	increased
4840	AX023740.PE1	nc	nc	*	atg	ggt	increased
4841	AX137596.PE1	nc	nc	*	tgg	gct	decreased
4842	AX137596.PE1	nc	nc	*	ggt	tct	decreased
4843	AX137596.PE1	nc	nc	*	ctg	tgc	decreased
4844	AX287046.PE1	nc	nc		ttc	ctg	increased by mild
4845	AX287046.PE1	nc	nc		gtg	cag	increased by mild
4846	AX287046.PE1	nc	nc		gtg	cag	increased by mild
4847	AX287046.PE1	nc	nc		tga	aca	increased by mild
4848	AX287046.PE1	nc	nc		tga	aca	increased by mild
4849	AX287046.PE1	nc	nc		agg	cca	increased by mild
4850	AX287046.PE1	nc	nc		agg	cca	increased by mild
4851	AX287046.PE1	nc	nc		agg	cca	increased by mild
4852	AX287046.PE1	nc	nc		agg	cca	increased by mild
4853	AX418615.PE1	nc	nc	*	agg	agt	decreased
4854	AX418615.PE1	nc	nc	*	agg	agt	decreased
4855	AX418615.PE1	nc	nc	*	tga	gcc	decreased
4856	AX418615.PE1	nc	nc	*	tga	gcc	decreased
4857	AX418615.PE1	nc	nc	*	tga	gcc	decreased
4858	AX418615.PE1	nc	nc	*	tga	gcc	decreased
4859	AX492861.PE1	nc	nc	*	cct	atc	increased
4860	AX492861.PE1	nc	nc	*	cct	atc	increased
4861	AX492861.PE1	nc	nc	*	cct	atc	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
4862	Taq1	18	cct	124.58	125	124.51	124.78	124.45	10 700 000	7 400 000	17 100 000	=+	/ (-)		\(8)
4863	Taq1	18	cct	125.427	125	125.38	125.43	125.47	5 200 000	4 700 000	5 200 000	==	-		\(8)
4864	Taq1	9	atc	135.247	136	135.22	135.19	135.33	16 100 000	12 500 000	3 200 000	=-	\ (-)		\(8)
4865	Hha1	9	atc	136.12	136	135.96	136.28	0	4 400 000	3 000 000	0	=-	\	\	\(8)
4866	Taq1	9	atc	136.215	136	136.26	136.17	0	5 300 000	6 900 000	0	=-	\	\	\(8)
4867	Taq1	31	gac	135.577	136	135.72	135.49	135.52	11 900 000	8 500 000	6 100 000	==	-		\(8)
4868	Taq1	31	gac	136.6	136	136.69	136.54	136.57	9 200 000	8 100 000	6 800 000	==	-		\(8)
4869	Hha1	3	aac	154.31	155	154.28	154.34	0	38 200 000	6 800 000	0	-=	\		\(8)
4870	Hha1	3	aac	155.577	155	155.46	155.53	155.74	5 600 000	7 500 000	4 800 000	==	-		\(8)
4871	Taq1	20	ctc	154.583	155	154.65	154.75	154.35	44 500 000	59 500 000	11 100 000	=-	\ (-)		\(8)
4872	Taq1	20	ctc	155.33	155	0	0	155.33	0	0	10 900 000	=+	/		\(8)
4873	Taq1	50	aat	241.79	242	241.57	242.01	0	4 200 000	3 400 000	0	=-	\		\(8)
4874	Hha1	60	ttg	272.37	274	0	272.37	0	0	4 900 000	0	+-	A		\(8)
4875	Hha1	28	tcg	109.673	110	109.63	109.74	109.65	22 900 000	11 800 000	28 300 000	=+	/ (-)	/	
4876	Hha1	39	agg	109.507	110	109.65	109.55	109.32	1 092.37	2 173.26	1 485.18	+=	/ (-)	/	
4877	Taq1	12	agt	119.103	119	119.06	119.05	119.2	5 100 000	7 000 000	3 800 000	=-	\ (-)	\	
4878	Taq1	23	cga	119.32	119	119.32	0	0	4 800 000	0	0	-=	\	\	
4879	Hha1	39	agg	152.55	152	152.55	0	0	469.2	0	0	-=	\		\(2)
4880	Hha1	25	cag	174.66	175	174.66	0	0	6 700 000	0	0	-=	\		\(2)
4881	Hha1	25	cag	175.753	175	175.72	175.75	175.79	89 200 000	58 200 000	14 800 000	=-	\ (-)		\(2)
4882	Taq1	62	tgt	174.315	175	0	174.44	174.19	0	4 000 000	3 300 000	+=	/		\(2)
4883	Taq1	62	tgt	175.4	175	0	175.48	175.32	0	6 400 000	3 900 000	+=	/		\(2)
4884	Taq1	49	aaa	174.62	175	174.62	0	0	25 700 000	0	0	-=	\		\(2)
4885	Taq1	49	aaa	175.89	175	175.69	176.09	0	20 900 000	13 900 000	0	=-	\		\(2)
4886	Taq1	51	ata	254.21	255	254.21	0	0	3 400 000	0	0	-=	\		\(2)
4887	Taq1	51	ata	256.15	255	256.15	0	0	6 400 000	0	0	-=	\		\(2)
4888	Taq1	49	aaa	174.62	175	174.62	0	0	25 700 000	0	0	-=	\		\(2)
4889	Taq1	49	aaa	175.89	175	175.69	176.09	0	20 900 000	13 900 000	0	=-	\		\(2)
4890	Taq1	51	ata	254.21	255	254.21	0	0	3 400 000	0	0	-=	\		\(2)
4891	Taq1	51	ata	256.15	255	256.15	0	0	6 400 000	0	0	-=	\		\(2)
4892	Hha1	3	aac	127.283	127	127.22	127.33	127.3	9 000 000	3 600 000	11 700 000	-+	V		-2
4893	Hha1	6	aga	126.475	127	126.51	0	126.44	89 200 000	0	7 100 000	-=(-)	\		-2
4894	Hha1	6	aga	127.097	127	127.18	127.06	127.05	30 600 000	3 500 000	5 400 000	-=	\ (-)		-2
4895	Hha1	6	aga	127.6	127	0	127.54	127.66	0	3 100 000	6 300 000	++	/		-2
4896	Taq1	19	cac	154.097	154	154.09	154.08	154.12	8 200 000	5 300 000	4 100 000	==	-		-2
4897	Taq1	8	gaa	138.59	139	138.49	138.69	0	3 500 000	4 800 000	0	=-	\		\(3)
4898	Hha1	8	gaa	138.857	139	138.89	138.94	138.74	9 100 000	11 400 000	5 800 000	=-	\ (-)		\(3)
4899	Taq1	8	gaa	139.07	139	0	139.07	0	0	4 200 000	0	+-	A		\(3)
4900	Taq1	18	cct	138.69	139	0	0	138.69	0	0	3 900 000	=+	/		\(3)
4901	Taq1	18	cct	139.81	139	0	0	139.81	0	0	6 100 000	=+	/		\(3)
4902	Hha1	40	tgg	200.105	200	199.94	200.27	0	4 100 000	4 000 000	0	=-	\		\(3)
4903	Hha1	40	tgg	201.08	200	0	201.08	0	0	6 200 000	0	+-	A		\(3)
4904	Hha1	39	agg	74.737	75	74.7	74.52	74.99	1 158.35	4 167.41	8 748.37	=+	/ (-)		/(2)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
4862	AX492861.PE1	nc	nc	*	cct	atc	increased
4863	AX492861.PE1	nc	nc	*	cct	atc	increased
4864	AX492861.PE1	nc	nc	*	atc	gac	increased
4865	AX492861.PE1	nc	nc	*	atc	gac	increased
4866	AX492861.PE1	nc	nc	*	atc	gac	increased
4867	AX492861.PE1	nc	nc	*	atc	gac	increased
4868	AX492861.PE1	nc	nc	*	atc	gac	increased
4869	AX492861.PE1	nc	nc	*	ctc	aac	increased
4870	AX492861.PE1	nc	nc	*	ctc	aac	increased
4871	AX492861.PE1	nc	nc	*	ctc	aac	increased
4872	AX492861.PE1	nc	nc	*	ctc	aac	increased
4873	AX492861.PE1	nc	nc	*	cgt	aat	increased
4874	AX492861.PE1	nc	nc	*	cag	ttg	increased
4875	AX710158.PE1	nc	nc	*	agg	tcg	decreased
4876	AX710158.PE1	nc	nc	*	agg	tcg	decreased
4877	AX710158.PE1	nc	nc	*	cga	agt	increased
4878	AX710158.PE1	nc	nc	*	cga	agt	increased
4879	D42012S4.RT1.HA	RT1.Ha	nc		agg	aga	increased
4880	D42012S4.RT1.HA	RT1.Ha	nc		cag	tgt	increased
4881	D42012S4.RT1.HA	RT1.Ha	nc		cag	tgt	increased
4882	D42012S4.RT1.HA	RT1.Ha	nc		cag	tgt	increased
4883	D42012S4.RT1.HA	RT1.Ha	nc		cag	tgt	increased
4884	RAT33DPPT.PE1	nc	nc		aaa	agc	increased
4885	RAT33DPPT.PE1	nc	nc		aaa	agc	increased
4886	RAT33DPPT.PE1	nc	nc		ata	tat	increased
4887	RAT33DPPT.PE1	nc	nc		ata	tat	increased
4888	RAT33DPTP.PE1	nc	nc		aaa	agc	increased
4889	RAT33DPTP.PE1	nc	nc		aaa	agc	increased
4890	RAT33DPTP.PE1	nc	nc		ata	tat	increased
4891	RAT33DPTP.PE1	nc	nc		ata	tat	increased
4892	RAT5RPHP.PE1	nc	nc		aga	aac	No change
4893	RAT5RPHP.PE1	nc	nc		aga	aac	No change
4894	RAT5RPHP.PE1	nc	nc		aga	aac	No change
4895	RAT5RPHP.PE1	nc	nc		aga	aac	No change
4896	RAT5RPHP.PE1	nc	nc		tat	cac	No change
4897	RATACHRMD.PE1	nc	nc		cct	gaa	increased
4898	RATACHRMD.PE1	nc	nc		cct	gaa	increased
4899	RATACHRMD.PE1	nc	nc		cct	gaa	increased
4900	RATACHRMD.PE1	nc	nc		cct	gaa	increased
4901	RATACHRMD.PE1	nc	nc		cct	gaa	increased
4902	RATACHRMD.PE1	nc	nc		aat	tgg	increased
4903	RATACHRMD.PE1	nc	nc		aat	tgg	increased
4904	RATAKGE2.PE1	nc	nc		atc	agg	decreased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
4905	Hha1	39	agg	75.345	75	75.13	75.56	0	608.5	9 827.45	0	+-	A		/(2)
4906	Hha1	6	aga	153.31	154	153.31	0	0	8 700 000	0	0	-=	\		/(2)
4907	Hha1	6	aga	154.4	154	154.27	0	154.53	14 200 000	0	12 300 000	-+(=)	V		/(2)
4908	Hha1	39	agg	197.13	198	0	197.22	197.04	0	238.82	260.41	+=	/		/(2)
4909	Hha1	59	ttc	192.56	193	192.56	0	0	306.81	0	0	-=	\		\(2)
4910	Hha1	59	ttc	267.955	268	268.09	0	267.82	286.01	0	87.96	-=(-)	\		\(2)
4911	Hha1	59	ttc	192.56	193	192.56	0	0	306.81	0	0	-=	\		\(2)
4912	Hha1	59	ttc	267.955	268	268.09	0	267.82	286.01	0	87.96	-=(-)	\		\(2)
4913	Hha1	25	cag	95.76	96	95.76	95.73	95.79	236 200 000	210 800 000	38 200 000	=-	\ (-)		-(2) \(2)
4914	Hha1	25	cag	96.24	96	0	0	96.24	0	0	26 000 000	=+	/		-(2) \(2)
4915	Taq1	51	ata	96.46	97	96.46	96.48	96.44	51 900 000	5 100 000	20 000 000	-=	\ (-)		-(2) \(2)
4916	Taq1	51	ata	97.483	97	97.54	97.42	97.49	92 500 000	35 900 000	44 800 000	-=	\ (-)		-(2) \(2)
4917	Hha1	6	aga	126.475	127	126.51	0	126.44	89 200 000	0	7 100 000	-=(-)	\		/(3)
4918	Hha1	6	aga	127.097	127	127.18	127.06	127.05	30 600 000	3 500 000	5 400 000	-=	\ (-)		/(3)
4919	Hha1	6	aga	127.6	127	0	127.54	127.66	0	3 100 000	6 300 000	++	/		/(3)
4920	Hha1	9	atc	126.45	127	0	0	126.45	0	0	4 400 000	=+	/		/(3)
4921	Taq1	9	atc	127.09	127	0	0	127.09	0	0	12 500 000	=+	/		/(3)
4922	Hha1	9	atc	127.14	127	127.14	0	0	6 500 000	0	0	-=	\		/(3)
4923	Hha1	10	atg	191.97	193	191.97	0	0	16 300 000	0	0	-=	\		\(2)
4924	Hha1	10	atg	192.95	193	192.95	0	0	4 400 000	0	0	-=	\		\(2)
4925	Taq1	10	atg	193.64	193	0	193.64	0	0	5 200 000	0	+-	A		\(2)
4926	Taq1	12	agt	192.023	193	192.01	191.98	192.08	4 800 000	5 700 000	5 500 000	==	-		\(2)
4927	Taq1	12	agt	192.965	193	193	192.93	0	3 400 000	4 400 000	0	=-	\		\(2)
4928	Taq1	12	agt	194.03	193	194.03	193.96	194.1	4 900 000	7 600 000	3 900 000	=-	\ (-)		\(2)
4929	Hha1	49	aaa	69.087	69	68.93	69.38	68.95	15 400 000	17 900 000	3 500 000	=-	\ (-)		-(4) \(4)
4930	Hha1	26	ctg	130.91	131	130.91	0	0	7 800 000	0	0	-=	\		-(4) \(4)
4931	Hha1	3	aac	133.207	134	133.21	133.02	133.39	5 800 000	3 800 000	3 700 000	==	-		-(4) \(4)
4932	Hha1	3	aac	134.06	134	134.06	0	0	5 500 000	0	0	-=	\		-(4) \(4)
4933	Taq1	31	gac	155.917	156	156.15	155.73	155.87	9 200 000	3 700 000	7 000 000	-=	\ (-)		-(4) \(4)
4934	Hha1	55	tca	155.483	156	155.56	155.46	155.43	4 400 000	3 100 000	3 000 000	==	-		-(4) \(4)
4935	Hha1	49	aaa	69.087	69	68.93	69.38	68.95	15 400 000	17 900 000	3 500 000	=-	\ (-)		-(4) \(4)
4936	Hha1	26	ctg	130.91	131	130.91	0	0	7 800 000	0	0	-=	\		-(4) \(4)
4937	Hha1	3	aac	133.207	134	133.21	133.02	133.39	5 800 000	3 800 000	3 700 000	==	-		-(4) \(4)
4938	Hha1	3	aac	134.06	134	134.06	0	0	5 500 000	0	0	-=	\		-(4) \(4)
4939	Taq1	31	gac	155.917	156	156.15	155.73	155.87	9 200 000	3 700 000	7 000 000	-=	\ (-)		-(4) \(4)
4940	Hha1	55	tca	155.483	156	155.56	155.46	155.43	4 400 000	3 100 000	3 000 000	==	-		-(4) \(4)
4941	Hha1	10	atg	191.97	193	191.97	0	0	16 300 000	0	0	-=	\		\(2)
4942	Hha1	10	atg	192.95	193	192.95	0	0	4 400 000	0	0	-=	\		\(2)
4943	Taq1	10	atg	193.64	193	0	193.64	0	0	5 200 000	0	+-	A		\(2)
4944	Taq1	12	agt	192.023	193	192.01	191.98	192.08	4 800 000	5 700 000	5 500 000	==	-		\(2)
4945	Taq1	12	agt	192.965	193	193	192.93	0	3 400 000	4 400 000	0	=-	\		\(2)
4946	Taq1	12	agt	194.03	193	194.03	193.96	194.1	4 900 000	7 600 000	3 900 000	=-	\ (-)		\(2)
4947	Taq1	45	gcc	126.075	126	0	126.14	126.01	0	4 400 000	3 400 000	+=	/		-2

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
4905	RATAKGE2.PE1	nc	nc		atc	agg	decreased
4906	RATAKGE2.PE1	nc	nc		aga	aga	decreased
4907	RATAKGE2.PE1	nc	nc		aga	aga	decreased
4908	RATAKGE2.PE1	nc	nc		ctg	agg	decreased
4909	RATALDA.PE1	nc	nc		tgt	ttc	increased
4910	RATALDA.PE1	nc	nc		ttc	tca	increased
4911	RATALDA2.PE1	nc	nc		tgt	ttc	increased
4912	RATALDA2.PE1	nc	nc		ttc	tca	increased
4913	RATAMPDA.PE1	nc	nc		ata	cag	No change
4914	RATAMPDA.PE1	nc	nc		ata	cag	No change
4915	RATAMPDA.PE1	nc	nc		ata	cag	No change
4916	RATAMPDA.PE1	nc	nc		ata	cag	No change
4917	RATANDPRO.PE1	nc	nc	*	aga	atc	decreased
4918	RATANDPRO.PE1	nc	nc	*	aga	atc	decreased
4919	RATANDPRO.PE1	nc	nc	*	aga	atc	decreased
4920	RATANDPRO.PE1	nc	nc	*	aga	atc	decreased
4921	RATANDPRO.PE1	nc	nc	*	aga	atc	decreased
4922	RATANDPRO.PE1	nc	nc	*	aga	atc	decreased
4923	RATANDREC.PE1	nc	nc		atg	agt	increased
4924	RATANDREC.PE1	nc	nc		atg	agt	increased
4925	RATANDREC.PE1	nc	nc		atg	agt	increased
4926	RATANDREC.PE1	nc	nc		atg	agt	increased
4927	RATANDREC.PE1	nc	nc		atg	agt	increased
4928	RATANDREC.PE1	nc	nc		atg	agt	increased
4929	RATAPOA01.PE1	nc	nc	*	aaa	atc	No change
4930	RATAPOA01.PE1	nc	nc	*	ctg	ggg	No change
4931	RATAPOA01.PE1	nc	nc	*	ggc	aac	No change
4932	RATAPOA01.PE1	nc	nc	*	ggc	aac	No change
4933	RATAPOA01.PE1	nc	nc	*	gac	tca	No change
4934	RATAPOA01.PE1	nc	nc	*	gac	tca	No change
4935	RATAPOAI.PE1	nc	nc	*	aaa	atc	No change
4936	RATAPOAI.PE1	nc	nc	*	ctg	ggg	No change
4937	RATAPOAI.PE1	nc	nc	*	ggc	aac	No change
4938	RATAPOAI.PE1	nc	nc	*	ggc	aac	No change
4939	RATAPOAI.PE1	nc	nc	*	gac	tca	No change
4940	RATAPOAI.PE1	nc	nc	*	gac	tca	No change
4941	RATARB.PE1	nc	nc		atg	agt	increased
4942	RATARB.PE1	nc	nc		atg	agt	increased
4943	RATARB.PE1	nc	nc		atg	agt	increased
4944	RATARB.PE1	nc	nc		atg	agt	increased
4945	RATARB.PE1	nc	nc		atg	agt	increased
4946	RATARB.PE1	nc	nc		atg	agt	increased
4947	RATATPA1.PE1	nc	nc		gca	gcc	No change

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
4948	Taq1	45	gcc	126.66	126	126.66	0	0	6 400 000	0	0	-=	\		-2
4949	Taq1	29	gca	126.473	127	126.52	126.46	126.44	6 300 000	5 600 000	9 500 000	==	-		-2
4950	Taq1	29	gca	127.51	127	127.52	127.49	127.52	5 600 000	3 400 000	5 300 000	==	-		-2
4951	Hha1	61	tct	200.247	200	200.01	200.35	200.38	3 300 000	4 500 000	4 700 000	==	-		-2
4952	Hha1	41	ccc	160.71	161	0	0	160.71	0	0	3 400 000	=+	/		/(2)
4953	Hha1	56	tga	162.093	162	161.85	162.1	162.33	710.98	286.21	930.87	-+	V		/(2)
4954	Taq1	23	cga	212.87	214	0	0	212.87	0	0	3 300 000	=+	/		/(2)
4955	Taq1	23	cga	214.66	214	214.68	214.64	0	8 200 000	3 600 000	0	-=	\		/(2)
4956	Hha1	7	caa	183.7	184	183.69	183.71	183.7	273 700 000	30 200 000	48 600 000	-=	\ (-)		\(2)
4957	Hha1	7	caa	184.9	184	184.58	185.08	185.04	10 200 000	9 700 000	12 800 000	==	-		\(2)
4958	Taq1	34	tgc	183.96	184	183.96	0	0	4 300 000	0	0	-=	\		\(2)
4959	Hha1	31	gac	60.763	61	60.78	60.77	60.74	11 300 000	7 200 000	27 300 000	=+	/ (-)		-1
4960	Hha1	20	ctc	65.19	65	65.1	65.11	65.36	495.86	3 606.08	8 826.33	=+	/ (-)		-1
4961	Hha1	20	ctc	68.973	69	68.95	69.09	68.88	550.96	485.18	1 145.03	=+	/ (-)		-1
4962	Hha1	59	ttc	94.35	94	94.22	94.34	94.49	754.03	845.11	333.73	=-	\ (-)		-1
4963	Hha1	56	tga	113.573	114	113.53	113.49	113.7	429.04	726.55	3 464.91	=+	/ (-)		-1
4964	Hha1	56	tga	114.53	114	114.39	114.45	114.75	2 202.42	308.23	896.39	-=	\ (-)		-1
4965	Hha1	20	ctc	129.17	129	0	129.32	129.02	0	406.5	584.44	+=	/		-1
4966	Hha1	40	tgg	145.52	146	145.53	145.44	145.59	3 100 000	9 400 000	9 100 000	+=	/ (-)		-1
4967	Hha1	40	tgg	146.47	146	0	146.34	146.6	0	9 800 000	16 400 000	+=	/		-1
4968	Hha1	40	tgg	238.06	237	0	238.06	0	0	3 900 000	0	+-	A		-1
4969	Hha1	59	ttc	68.59	69	0	68.61	68.57	0	12 182.36	2 196.46	+-	A		A(4)
4970	Taq1	55	tca	75.61	76	0	75.61	0	0	6 000 000	0	+-	A		A(4)
4971	Taq1	55	tca	76.24	76	76.15	76.33	0	3 300 000	35 400 000	0	+-	A		A(4)
4972	Taq1	12	agt	155.7	156	155.78	155.62	0	5 200 000	11 200 000	0	+-	A		A(4)
4973	Taq1	12	agt	156.843	156	156.85	156.73	156.95	12 500 000	31 700 000	7 400 000	+-	A		A(4)
4974	Taq1	36	ggt	155.127	156	155.15	155.19	155.04	12 900 000	21 200 000	6 700 000	=-	\ (-)		A(4)
4975	Taq1	36	ggt	156.02	156	155.99	156.07	156	3 300 000	10 000 000	3 500 000	+-	A		A(4)
4976	Hha1	41	ccc	167.49	168	0	0	167.49	0	0	3 300 000	=+	/		\(2)
4977	Hha1	41	ccc	168.595	168	168.57	168.62	0	5 600 000	4 000 000	0	=-	\	\	\(2)
4978	Hha1	39	agg	168.81	169	168.81	0	0	2 536.65	0	0	-=	\	\	\(2)
4979	Hha1	39	agg	169.657	169	169.84	169.79	169.34	2 126.09	555.25	524.9	-=	\ (-)		\(2)
4980	Taq1	39	agg	196.265	197	0	196.04	196.49	0	54 300 000	29 200 000	+-	A		\(3)
4981	Taq1	39	agg	197.23	197	197.04	197.42	0	6 100 000	35 600 000	0	+-	A		\(3)
4982	Taq1	39	agg	198.005	197	198.21	0	197.8	10 400 000	0	4 200 000	-=(-)	\		\(3)
4983	Taq1	39	agg	196.49	197	0	0	196.49	0	0	860.08	=+	/		\(3)
4984	Taq1	39	agg	197.04	197	197.04	0	0	226.53	0	0	-=	\		\(3)
4985	Taq1	39	agg	198.005	197	198.21	0	197.8	386.21	0	123.71	-=(-)	\		\(3)
4986	Taq1	39	agg	196.04	197	0	196.04	0	0	545.73	0	+-	A		\(3)
4987	Taq1	39	agg	197.42	197	0	197.42	0	0	357.79	0	+-	A		\(3)
4988	Hha1	6	aga	215.98	217	0	0	215.98	0	0	3 100 000	=+	/		\(3)
4989	Hha1	6	aga	216.94	217	216.94	0	0	74 800 000	0	0	-=	\		\(3)
4990	Hha1	6	aga	285.5	286	285.5	0	0	4 200 000	0	0	-=	\		\(3)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
4948	RATATPA1.PE1	nc	nc		gca	gcc	No change
4949	RATATPA1.PE1	nc	nc		gca	gcc	No change
4950	RATATPA1.PE1	nc	nc		gca	gcc	No change
4951	RATATPA1.PE1	nc	nc		tct	cct	No change
4952	RATATPA2.PE1	nc	nc		tga	ccc	decreased
4953	RATATPA2.PE1	nc	nc		tga	ccc	decreased
4954	RATATPA2.PE1	nc	nc		cga	tgc	decreased
4955	RATATPA2.PE1	nc	nc		cga	tgc	decreased
4956	RATATPA3.PE1	nc	nc		caa	tgc	increased
4957	RATATPA3.PE1	nc	nc		caa	tgc	increased
4958	RATATPA3.PE1	nc	nc		caa	tgc	increased
4959	RATB1AR.PE1	nc	nc		tcc	gac	No change
4960	RATB1AR.PE1	nc	nc		ctc	ctt	No change
4961	RATB1AR.PE1	nc	nc		ctc	ggc	No change
4962	RATB1AR.PE1	nc	nc		tgg	ttc	No change
4963	RATB1AR.PE1	nc	nc		ggc	tga	No change
4964	RATB1AR.PE1	nc	nc		ggc	tga	No change
4965	RATB1AR.PE1	nc	nc		ctc	ggg	No change
4966	RATB1AR.PE1	nc	nc		tca	tgg	No change
4967	RATB1AR.PE1	nc	nc		tca	tgg	No change
4968	RATB1AR.PE1	nc	nc		tca	tgg	No change
4969	RATBAND33E.PE1	nc	nc		ttc	tgc	increased by mild
4970	RATBAND33E.PE1	nc	nc		tca	cca	increased by mild
4971	RATBAND33E.PE1	nc	nc		tca	cca	increased by mild
4972	RATBAND33E.PE1	nc	nc		agt	ggt	increased by mild
4973	RATBAND33E.PE1	nc	nc		agt	ggt	increased by mild
4974	RATBAND33E.PE1	nc	nc		agt	ggt	increased by mild
4975	RATBAND33E.PE1	nc	nc		agt	ggt	increased by mild
4976	RATBCL2A.BCL-2	bcl-2	nc		ccc	agg	increased
4977	RATBCL2A.BCL-2	bcl-2	nc		ccc	agg	increased
4978	RATBCL2A.BCL-2	bcl-2	nc		ccc	agg	increased
4979	RATBCL2A.BCL-2	bcl-2	nc		ccc	agg	increased
4980	RATBIP.PE1	nc	nc		agg	gta	increased
4981	RATBIP.PE1	nc	nc		agg	gta	increased
4982	RATBIP.PE1	nc	nc		agg	gta	increased
4983	RATBIP.PE1	nc	nc		agg	gta	increased
4984	RATBIP.PE1	nc	nc		agg	gta	increased
4985	RATBIP.PE1	nc	nc		agg	gta	increased
4986	RATBIP.PE1	nc	nc		agg	gta	increased
4987	RATBIP.PE1	nc	nc		agg	gta	increased
4988	RATBIP.PE1	nc	nc		ctt	aga	increased
4989	RATBIP.PE1	nc	nc		ctt	aga	increased
4990	RATBIP.PE1	nc	nc		tgt	aga	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
4991	Hha1	3	aac	98.427	98	98.48	98.4	98.4	13 000 000	5 800 000	5 600 000	-=	\ (-)	(-)	-(2) \(2)
4992	Taq1	31	gac	97.437	98	97.4	97.32	97.59	62 800 000	57 200 000	11 100 000	=-	\ (-)		-(2) \(2)
4993	Taq1	31	gac	98.43	98	98.41	98.36	98.52	10 400 000	15 700 000	18 300 000	==	-	(-)	-(2) \(2)
4994	Taq1	26	ctg	186.63	187	0	0	186.63	0	0	4 800 000	=+	/	/	A(3) /(2)
4995	Taq1	26	ctg	187.66	187	0	187.66	0	0	3 000 000	0	+-	A	A	A(3) /(2)
4996	Taq1	57	ctg	186.41	187	0	0	186.41	0	0	6 500 000	=+	/	/	A(3) /(2)
4997	Taq1	57	ctg	187.215	187	0	187.02	187.41	0	3 300 000	5 400 000	+=	/		A(3) /(2)
4998	Taq1	57	ctg	187.45	187	0	187.45	0	0	4 800 000	0	+-	A	A	A(3) /(2)
4999	Hha1	40	tgg	225.115	226	225.12	225.11	0	4 000 000	3 800 000	0	=-	\		A(3) /(2)
5000	Hha1	40	tgg	225.76	226	0	225.76	0	0	6 500 000	0	+-	A		A(3) /(2)
5001	Taq1	51	ata	97.483	98	97.54	97.42	97.49	92 500 000	35 900 000	44 800 000	-=	\ (-)		/(2)
5002	Taq1	51	ata	98.365	98	0	98.41	98.32	0	3 700 000	3 700 000	+=	/		/(2)
5003	Taq1	56	tga	147.835	148	0	147.59	148.08	0	3 200 000	20 000 000	=+	/		/(2)
5004	Taq1	63	ctt	148.03	148	147.9	0	148.16	3 800 000	0	4 200 000	-+(=)	V		/(2)
5005	Hha1	44	cgg	104.397	105	104.37	104.38	104.44	3 500 000	11 100 000	12 300 000	+=	/ (-)		-1
5006	Hha1	39	agg	106.243	106	106.2	106.36	106.17	1 217	12 305.21	14 347.33	+=	/ (-)		-1
5007	Hha1	44	cgg	71.307	71	71.21	71.39	71.32	26 500 000	4 100 000	9 300 000	-=	\ (-)		\(3)
5008	Hha1	43	cgc	99.97	100	99.92	100.02	0	25 600 000	8 600 000	0	-=	\		\(3)
5009	Hha1	33	agc	100.705	101	100.71	100.7	0	6 700 000	11 200 000	0	=-	\		\(3)
5010	Hha1	41	ccc	218.96	220	0	0	218.96	0	0	3 000 000	=+	/		\(3)
5011	Hha1	61	tct	220.78	221	0	220.78	0	0	3 200 000	0	+-	A		\(3)
5012	Hha1	61	tct	221.88	221	221.88	221.88	221.88	10 000 000	8 200 000	6 100 000	==	-		\(3)
5013	Hha1	44	cgg	71.307	71	71.21	71.39	71.32	26 500 000	4 100 000	9 300 000	-=	\ (-)		\(3)
5014	Hha1	43	cgc	99.97	100	99.92	100.02	0	25 600 000	8 600 000	0	-=	\		\(3)
5015	Hha1	33	agc	100.705	101	100.71	100.7	0	6 700 000	11 200 000	0	=-	\		\(3)
5016	Hha1	41	ccc	218.96	220	0	0	218.96	0	0	3 000 000	=+	/		\(3)
5017	Hha1	61	tct	220.78	221	0	220.78	0	0	3 200 000	0	+-	A		\(3)
5018	Hha1	61	tct	221.88	221	221.88	221.88	221.88	10 000 000	8 200 000	6 100 000	==	-		\(3)
5019	Hha1	44	cgg	71.307	71	71.21	71.39	71.32	26 500 000	4 100 000	9 300 000	-=	\ (-)		\(3)
5020	Hha1	43	cgc	99.97	100	99.92	100.02	0	25 600 000	8 600 000	0	-=	\		\(3)
5021	Hha1	33	agc	100.705	101	100.71	100.7	0	6 700 000	11 200 000	0	=-	\		\(3)
5022	Hha1	41	ccc	218.96	220	0	0	218.96	0	0	3 000 000	=+	/		\(3)
5023	Hha1	61	tct	220.78	221	0	220.78	0	0	3 200 000	0	+-	A		\(3)
5024	Hha1	61	tct	221.88	221	221.88	221.88	221.88	10 000 000	8 200 000	6 100 000	==	-		\(3)
5025	Taq1	19	cac	231.985	233	0	231.98	231.99	0	4 000 000	3 200 000	+=	/		/(2)
5026	Taq1	19	cac	232.94	233	232.92	0	232.96	3 300 000	0	4 600 000	-+(=)	V		/(2)
5027	Taq1	19	cac	234.02	233	233.98	234.06	234.02	4 300 000	3 200 000	3 500 000	==	-		/(2)
5028	Taq1	56	tga	269.47	268	0	0	269.47	0	0	5 400 000	=+	/		/(2)
5029	Hha1	20	ctc	93.51	94	93.44	93.58	0	1 494.49	576.97	0	-=	\		\(3)
5030	Hha1	20	ctc	94.37	94	94.37	0	0	530.3	0	0	-=	\	\	\(3)
5031	Hha1	33	agc	94.285	94	94.26	94.31	0	4 500 000	3 800 000	0	=-	\	\	\(3)
5032	Hha1	44	cgg	174.45	175	0	174.45	0	0	3 800 000	0	+-	A		\(3)
5033	Hha1	44	cgg	175.29	175	175.29	0	0	12 200 000	0	0	-=	\		\(3)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
4991	RATBP2A.PE1	nc	nc		gac	aac	No change
4992	RATBP2A.PE1	nc	nc		gac	aac	No change
4993	RATBP2A.PE1	nc	nc		gac	aac	No change
4994	RATBPGTPD.PE1	nc	nc	*	ctg	aca	decreased
4995	RATBPGTPD.PE1	nc	nc	*	ctg	aca	increased by mild
4996	RATBPGTPD.PE1	nc	nc	*	ctg	aca	decreased
4997	RATBPGTPD.PE1	nc	nc	*	ctg	aca	increased by mild
4998	RATBPGTPD.PE1	nc	nc	*	ctg	aca	increased by mild
4999	RATBPGTPD.PE1	nc	nc	*	tcc	tgg	increased by mild
5000	RATBPGTPD.PE1	nc	nc	*	tcc	tgg	increased by mild
5001	RATCACH3B.PE1	nc	nc		gcg	ata	decreased
5002	RATCACH3B.PE1	nc	nc		gcg	ata	decreased
5003	RATCACH3B.PE1	nc	nc		ctt	tga	decreased
5004	RATCACH3B.PE1	nc	nc		ctt	tga	decreased
5005	RATCALB.PE1	nc	nc		agg	cgg	No change
5006	RATCALB.PE1	nc	nc		agg	cgg	No change
5007	RATCAR1.PE1	nc	nc		cgg	caa	increased
5008	RATCAR1.PE1	nc	nc		agc	cgc	increased
5009	RATCAR1.PE1	nc	nc		agc	cgc	increased
5010	RATCAR1.PE1	nc	nc		ccc	tct	increased
5011	RATCAR1.PE1	nc	nc		ccc	tct	increased
5012	RATCAR1.PE1	nc	nc		ccc	tct	increased
5013	RATCAR2.PE1	nc	nc		cgg	caa	increased
5014	RATCAR2.PE1	nc	nc		agc	cgc	increased
5015	RATCAR2.PE1	nc	nc		agc	cgc	increased
5016	RATCAR2.PE1	nc	nc		ccc	tct	increased
5017	RATCAR2.PE1	nc	nc		ccc	tct	increased
5018	RATCAR2.PE1	nc	nc		ccc	tct	increased
5019	RATCAR3.PE1	nc	nc		cgg	caa	increased
5020	RATCAR3.PE1	nc	nc		agc	cgc	increased
5021	RATCAR3.PE1	nc	nc		agc	cgc	increased
5022	RATCAR3.PE1	nc	nc		ccc	tct	increased
5023	RATCAR3.PE1	nc	nc		ccc	tct	increased
5024	RATCAR3.PE1	nc	nc		ccc	tct	increased
5025	RATCBXPA.PE1	nc	nc	*	cac	gtc	decreased
5026	RATCBXPA.PE1	nc	nc	*	cac	gtc	decreased
5027	RATCBXPA.PE1	nc	nc	*	cac	gtc	decreased
5028	RATCBXPA.PE1	nc	nc	*	tga	tcc	decreased
5029	RATCCK.PE1	nc	nc	*	agc	ctc	increased
5030	RATCCK.PE1	nc	nc	*	agc	ctc	increased
5031	RATCCK.PE1	nc	nc	*	agc	ctc	increased
5032	RATCCK.PE1	nc	nc	*	act	cgg	increased
5033	RATCCK.PE1	nc	nc	*	act	cgg	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
5034	Hha1	20	ctc	93.51	94	93.44	93.58	0	1 494.49	576.97	0	-=	\		\(3)
5035	Hha1	20	ctc	94.37	94	94.37	0	0	530.3	0	0	-=	\	\	\(3)
5036	Hha1	33	agc	94.285	94	94.26	94.31	0	4 500 000	3 800 000	0	=-	\	\	\(3)
5037	Hha1	44	cgg	174.45	175	0	174.45	0	0	3 800 000	0	+-	A		\(3)
5038	Hha1	44	cgg	175.29	175	175.29	0	0	12 200 000	0	0	-=	\		\(3)
5039	Hha1	33	agc	117.93	118	0	117.93	0	0	3 000 000	0	+-	A		/(2)
5040	Hha1	33	agc	118.38	118	0	118.38	0	0	4 000 000	0	+-	A		/(2)
5041	Taq1	18	cct	123.28	124	123.14	0	123.42	3 300 000	0	5 700 000	-+(=)	V		/(2)
5042	Taq1	18	cct	124.58	124	124.51	124.78	124.45	10 700 000	7 400 000	17 100 000	=+	/ (-)	/	/(2)
5043	Taq1	35	gga	123.8	124	0	0	123.8	0	0	3 500 000	=+	/		/(2)
5044	Taq1	35	gga	124.71	124	0	0	124.71	0	0	3 600 000	=+	/	/	/(2)
5045	Hha1	44	cgg	90.59	91	90.65	0	90.53	4 400 000	0	3 200 000	-+(=)	V		-3
5046	Hha1	44	cgg	91.42	91	91.44	91.63	91.19	4 500 000	7 200 000	3 300 000	=-	\ (-)		-3
5047	Hha1	59	ttc	115.51	116	0	115.28	115.74	0	201.21	152.64	+=	/		-3
5048	Hha1	59	ttc	116.287	116	116.49	116	116.37	447.21	580.65	155.22	=-	\ (-)		-3
5049	Hha1	59	ttc	116.49	116	0	116.49	0	0	117.85	0	+-	A		-3
5050	Hha1	44	cgg	131.54	132	0	131.48	131.6	0	8 100 000	7 200 000	+=	/		-3
5051	Hha1	57	cta	132.93	133	132.87	133.02	132.9	970.45	1 225.09	1 022.94	==	-		-3
5052	Hha1	61	tct	165.387	166	165.28	165.41	165.47	3 000 000	17 800 000	8 300 000	+-	A		-3
5053	Hha1	61	tct	166.38	166	0	166.38	0	0	5 400 000	0	+-	A		-3
5054	Taq1	39	agg	90.495	91	90.7	0	90.29	125 800 000	0	23 600 000	-=(-)	\		A(2)
5055	Taq1	39	agg	90.957	91	90.7	90.97	91.2	4 671.71	172 200 000	3 800 000	+-	A	A	A(2)
5056	Taq1	39	agg	91.085	91	0	90.97	91.2	0	1 730.67	111.92	+-	A	A	A(2)
5057	Taq1	56	tga	90.95	91	0	90.95	0	0	3 100 000	0	+-	A	A	A(2)
5058	Hha1	8	gaa	157.313	157	157.36	157.31	157.27	22 700 000	11 900 000	5 600 000	-=	\ (-)	\	
5059	Taq1	8	gaa	157.43	157	157.43	0	0	3 200 000	0	0	-=	\	\	
5060	Hha1	8	gaa	157.313	157	157.36	157.31	157.27	22 700 000	11 900 000	5 600 000	-=	\ (-)	\	
5061	Taq1	8	gaa	157.43	157	157.43	0	0	3 200 000	0	0	-=	\	\	
5062	Hha1	61	tct	94.46	94	94.46	0	0	24 100 000	0	0	-=	\		/(3)
5063	Taq1	40	tgg	114.37	115	0	0	114.37	0	0	17 700 000	=+	/		/(3)
5064	Taq1	40	tgg	115.43	115	0	0	115.43	0	0	7 900 000	=+	/		/(3)
5065	Hha1	59	ttc	120.7	121	120.7	0	0	956.83	0	0	-=	\		/(3)
5066	Hha1	59	ttc	121.365	121	0	121.51	121.22	0	175.34	150.05	+=	/		/(3)
5067	Hha1	39	agg	180.56	180	0	0	180.56	0	0	126.13	=+	/		/(3)
5068	Hha1	61	tct	94.46	94	94.46	0	0	24 100 000	0	0	-=	\		/(3)
5069	Taq1	40	tgg	114.37	115	0	0	114.37	0	0	17 700 000	=+	/		/(3)
5070	Taq1	40	tgg	115.43	115	0	0	115.43	0	0	7 900 000	=+	/		/(3)
5071	Hha1	59	ttc	120.7	121	120.7	0	0	956.83	0	0	-=	\		/(3)
5072	Hha1	59	ttc	121.365	121	0	121.51	121.22	0	175.34	150.05	+=	/		/(3)
5073	Hha1	39	agg	180.56	180	0	0	180.56	0	0	126.13	=+	/		/(3)
5074	Hha1	10	atg	201.445	202	201.33	201.56	0	9 200 000	3 400 000	0	-=	\		\(4)
5075	Taq1	10	atg	201.73	202	201.73	0	0	3 700 000	0	0	-=	\		\(4)
5076	Hha1	10	atg	202.34	202	202.34	0	0	3 200 000	0	0	-=	\		\(4)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
5034	RATCCKA.PE1	nc	nc	*	agc	ctc	increased
5035	RATCCKA.PE1	nc	nc	*	agc	ctc	increased
5036	RATCCKA.PE1	nc	nc	*	agc	ctc	increased
5037	RATCCKA.PE1	nc	nc	*	act	cgg	increased
5038	RATCCKA.PE1	nc	nc	*	act	cgg	increased
5039	RATCDS37.PE1	nc	nc		aag	agc	decreased
5040	RATCDS37.PE1	nc	nc		aag	agc	decreased
5041	RATCDS37.PE1	nc	nc		gga	cct	decreased
5042	RATCDS37.PE1	nc	nc		gga	cct	decreased
5043	RATCDS37.PE1	nc	nc		gga	cct	decreased
5044	RATCDS37.PE1	nc	nc		gga	cct	decreased
5045	RATCELF.CELF	CELF	nc		cgg	tcg	No change
5046	RATCELF.CELF	CELF	nc		cgg	tcg	No change
5047	RATCELF.CELF	CELF	nc		ggg	ttc	No change
5048	RATCELF.CELF	CELF	nc		ggg	ttc	No change
5049	RATCELF.CELF	CELF	nc		ggg	ttc	No change
5050	RATCELF.CELF	CELF	nc		cta	cgg	No change
5051	RATCELF.CELF	CELF	nc		cta	cgg	No change
5052	RATCELF.CELF	CELF	nc		acc	tct	No change
5053	RATCELF.CELF	CELF	nc		acc	tct	No change
5054	RATCIIDBPR.PE1	CIIDBP	nc		tga	agg	increased by mild
5055	RATCIIDBPR.PE1	CIIDBP	nc		tga	agg	increased by mild
5056	RATCIIDBPR.PE1	CIIDBP	nc		tga	agg	increased by mild
5057	RATCIIDBPR.PE1	CIIDBP	nc		tga	agg	increased by mild
5058	RATCKB.PE1	nc	nc		gaa	aga	increased
5059	RATCKB.PE1	nc	nc		gaa	aga	increased
5060	RATCKBR.PE1	nc	nc		gaa	aga	increased
5061	RATCKBR.PE1	nc	nc		gaa	aga	increased
5062	RATCKM.PE1	nc	nc		act	tct	decreased
5063	RATCKM.PE1	nc	nc		aca	tgg	decreased
5064	RATCKM.PE1	nc	nc		aca	tgg	decreased
5065	RATCKM.PE1	nc	nc		gga	ttc	decreased
5066	RATCKM.PE1	nc	nc		gga	ttc	decreased
5067	RATCKM.PE1	nc	nc		cgt	agg	decreased
5068	RATCKMA.PE1	nc	nc		act	tct	decreased
5069	RATCKMA.PE1	nc	nc		aca	tgg	decreased
5070	RATCKMA.PE1	nc	nc		aca	tgg	decreased
5071	RATCKMA.PE1	nc	nc		gga	ttc	decreased
5072	RATCKMA.PE1	nc	nc		gga	ttc	decreased
5073	RATCKMA.PE1	nc	nc		cgt	agg	decreased
5074	RATCNRA.PE1	nc	nc	*	atg	agg	increased
5075	RATCNRA.PE1	nc	nc	*	atg	agg	increased
5076	RATCNRA.PE1	nc	nc	*	atg	agg	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
5077	Taq1	39	agg	201.075	202	201.22	200.93	0	11 500 000	11 100 000	0	=-	\		\(4)
5078	Taq1	39	agg	201.935	202	201.96	201.91	0	8 700 000	38 600 000	0	+-	A		\(4)
5079	Taq1	39	agg	202.85	202	202.85	0	0	8 800 000	0	0	-=	\		\(4)
5080	Taq1	39	agg	201.075	202	201.22	200.93	0	427.06	111.55	0	-=	\		\(4)
5081	Taq1	39	agg	201.935	202	201.96	201.91	0	323.08	387.94	0	=-	\		\(4)
5082	Taq1	39	agg	202.85	202	202.85	0	0	326.79	0	0	-=	\		\(4)
5083	Taq1	19	cac	231.985	233	0	231.98	231.99	0	4 000 000	3 200 000	+=	/		/(2)
5084	Taq1	19	cac	232.94	233	232.92	0	232.96	3 300 000	0	4 600 000	-+(=)	V		/(2)
5085	Taq1	19	cac	234.02	233	233.98	234.06	234.02	4 300 000	3 200 000	3 500 000	==	-		/(2)
5086	Taq1	56	tga	269.47	268	0	0	269.47	0	0	5 400 000	=+	/		/(2)
5087	Hha1	39	agg	66.61	67	0	66.57	66.65	0	1 629.94	2 937.82	+=	/		/(4)
5088	Hha1	54	ttt	68.19	68	68.18	68.28	68.11	7 500 000	3 900 000	13 100 000	=+	/ (-)		/(4)
5089	Taq1	19	cac	95.585	96	95.53	0	95.64	5 900 000	0	11 400 000	-+(+)	V (/)		/(4)
5090	Taq1	19	cac	96.55	96	96.58	96.58	96.49	16 100 000	7 600 000	8 200 000	-=	\ (-)		/(4)
5091	Taq1	63	ctt	96.275	96	96.22	0	96.33	4 000 000	0	4 000 000	-+(=)	V		/(4)
5092	Hha1	26	ctg	223.743	225	223.77	223.71	223.75	5 400 000	3 100 000	9 800 000	=+	/ (-)		/(4)
5093	Hha1	26	ctg	224.91	225	0	0	224.91	0	0	4 000 000	=+	/		/(4)
5094	Hha1	26	ctg	225.8	225	0	0	225.8	0	0	4 300 000	=+	/		/(4)
5095	Hha1	40	tgg	225.115	225	225.12	225.11	0	4 000 000	3 800 000	0	=-	\		/(4)
5096	Hha1	40	tgg	225.76	225	0	225.76	0	0	6 500 000	0	+-	A		/(4)
5097	Hha1	39	agg	66.61	67	0	66.57	66.65	0	1 629.94	2 937.82	+=	/		-1
5098	Hha1	54	ttt	68.19	68	68.18	68.28	68.11	7 500 000	3 900 000	13 100 000	=+	/ (-)		-1
5099	Taq1	18	cct	165.523	166	165.51	165.56	165.5	11 700 000	7 400 000	5 500 000	==	-		-1
5100	Taq1	18	cct	166.56	166	166.48	166.64	0	5 200 000	5 300 000	0	=-	\		-1
5101	Taq1	12	agt	155.7	156	155.78	155.62	0	5 200 000	11 200 000	0	+-	A		A(3)
5102	Taq1	12	agt	156.843	156	156.85	156.73	156.95	12 500 000	31 700 000	7 400 000	+-	A		A(3)
5103	Taq1	39	agg	156.053	156	156.06	156.26	155.84	5 000 000	11 400 000	3 700 000	+-	A		A(3)
5104	Taq1	39	agg	155.84	156	0	0	155.84	0	0	108.98	=+	/		A(3)
5105	Taq1	39	agg	156.26	156	0	156.26	0	0	114.57	0	+-	A		A(3)
5106	Taq1	39	agg	156.06	156	156.06	0	0	185.68	0	0	-=	\		A(3)
5107	Hha1	26	ctg	231.04	232	0	231.04	0	0	3 600 000	0	+-	A		A(3)
5108	Taq1	56	tga	72.6	73	72.48	72.72	0	3 800 000	47 300 000	0	+-	A		/(3)
5109	Hha1	4	aag	128.23	129	128.33	128.15	128.21	3 000 000	10 700 000	6 300 000	+=	/ (-)		/(3)
5110	Hha1	4	aag	128.983	129	128.92	129.05	128.98	5 600 000	33 000 000	23 800 000	+=	/ (-)		/(3)
5111	Taq1	26	ctg	150.785	151	0	150.76	150.81	0	3 200 000	14 200 000	=+	/		/(3)
5112	Taq1	26	ctg	151.67	151	0	151.67	0	0	3 500 000	0	+-	A		/(3)
5113	Taq1	57	ctg	150.17	151	0	0	150.17	0	0	3 800 000	=+	/		/(3)
5114	Taq1	57	ctg	151.277	151	151.29	151.32	151.22	5 900 000	4 100 000	4 900 000	==	-		/(3)
5115	Taq1	10	atg	233.32	234	233.32	0	0	3 300 000	0	0	-=	\		/(3)
5116	Hha1	39	agg	66.61	67	0	66.57	66.65	0	1 629.94	2 937.82	+=	/		/(3)
5117	Hha1	54	ttt	68.19	68	68.18	68.28	68.11	7 500 000	3 900 000	13 100 000	=+	/ (-)		/(3)
5118	Hha1	26	ctg	223.743	225	223.77	223.71	223.75	5 400 000	3 100 000	9 800 000	=+	/ (-)		/(3)
5119	Hha1	26	ctg	224.91	225	0	0	224.91	0	0	4 000 000	=+	/		/(3)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
5077	RATCNRA.PE1	nc	nc	*	atg	agg	increased
5078	RATCNRA.PE1	nc	nc	*	atg	agg	increased
5079	RATCNRA.PE1	nc	nc	*	atg	agg	increased
5080	RATCNRA.PE1	nc	nc	*	atg	agg	increased
5081	RATCNRA.PE1	nc	nc	*	atg	agg	increased
5082	RATCNRA.PE1	nc	nc	*	atg	agg	increased
5083	RATCPA7.PE1	nc	nc		cac	gtc	decreased
5084	RATCPA7.PE1	nc	nc		cac	gtc	decreased
5085	RATCPA7.PE1	nc	nc		cac	gtc	decreased
5086	RATCPA7.PE1	nc	nc		tga	tcc	decreased
5087	RATCY45EL.PE1	nc	nc		ttt	agg	decreased
5088	RATCY45EL.PE1	nc	nc		ttt	agg	decreased
5089	RATCY45EL.PE1	nc	nc		cac	ctt	decreased
5090	RATCY45EL.PE1	nc	nc		cac	ctt	decreased
5091	RATCY45EL.PE1	nc	nc		cac	ctt	decreased
5092	RATCY45EL.PE1	nc	nc		ctg	tgg	decreased
5093	RATCY45EL.PE1	nc	nc		ctg	tgg	decreased
5094	RATCY45EL.PE1	nc	nc		ctg	tgg	decreased
5095	RATCY45EL.PE1	nc	nc		ctg	tgg	decreased
5096	RATCY45EL.PE1	nc	nc		ctg	tgg	decreased
5097	RATCY45II.PE1	nc	nc		ttt	agg	No change
5098	RATCY45II.PE1	nc	nc		ttt	agg	No change
5099	RATCY45II.PE1	nc	nc		cct	gga	No change
5100	RATCY45II.PE1	nc	nc		cct	gga	No change
5101	RATCYP2A1.PE1	nc	nc		agg	agt	increased by mild
5102	RATCYP2A1.PE1	nc	nc		agg	agt	increased by mild
5103	RATCYP2A1.PE1	nc	nc		agg	agt	increased by mild
5104	RATCYP2A1.PE1	nc	nc		agg	agt	increased by mild
5105	RATCYP2A1.PE1	nc	nc		agg	agt	increased by mild
5106	RATCYP2A1.PE1	nc	nc		agg	agt	increased by mild
5107	RATCYP2A1.PE1	nc	nc		tat	ctg	increased by mild
5108	RATCYP2A3A.PE1	nc	nc		gga	tga	decreased
5109	RATCYP2A3A.PE1	nc	nc		aag	agc	decreased
5110	RATCYP2A3A.PE1	nc	nc		aag	agc	decreased
5111	RATCYP2A3A.PE1	nc	nc		ctg	tgc	decreased
5112	RATCYP2A3A.PE1	nc	nc		ctg	tgc	decreased
5113	RATCYP2A3A.PE1	nc	nc		ctg	tgc	decreased
5114	RATCYP2A3A.PE1	nc	nc		ctg	tgc	decreased
5115	RATCYP2A3A.PE1	nc	nc		atg	tga	decreased
5116	RATCYP450.PE1	nc	nc	*	ttt	agg	decreased
5117	RATCYP450.PE1	nc	nc	*	ttt	agg	decreased
5118	RATCYP450.PE1	nc	nc	*	ctg	ttg	decreased
5119	RATCYP450.PE1	nc	nc	*	ctg	ttg	decreased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
5120	Hha1	26	ctg	225.8	225	0	0	225.8	0	0	4 300 000	=+	/		/(3)
5121	Hha1	60	ttg	224.92	225	0	224.92	0	0	3 000 000	0	+-	A		/(3)
5122	Hha1	39	agg	66.61	67	0	66.57	66.65	0	1 629.94	2 937.82	+=	/		/(3)
5123	Hha1	54	ttt	68.19	68	68.18	68.28	68.11	7 500 000	3 900 000	13 100 000	=+	/ (-)		/(3)
5124	Hha1	26	ctg	223.743	225	223.77	223.71	223.75	5 400 000	3 100 000	9 800 000	=+	/ (-)		/(3)
5125	Hha1	26	ctg	224.91	225	0	0	224.91	0	0	4 000 000	=+	/		/(3)
5126	Hha1	26	ctg	225.8	225	0	0	225.8	0	0	4 300 000	=+	/		/(3)
5127	Hha1	60	ttg	224.92	225	0	224.92	0	0	3 000 000	0	+-	A		/(3)
5128	Taq1	12	agt	155.7	156	155.78	155.62	0	5 200 000	11 200 000	0	+-	A		A(3)
5129	Taq1	12	agt	156.843	156	156.85	156.73	156.95	12 500 000	31 700 000	7 400 000	+-	A		A(3)
5130	Taq1	39	agg	156.053	156	156.06	156.26	155.84	5 000 000	11 400 000	3 700 000	+-	A		A(3)
5131	Taq1	39	agg	155.84	156	0	0	155.84	0	0	108.98	=+	/		A(3)
5132	Taq1	39	agg	156.26	156	0	156.26	0	0	114.57	0	+-	A		A(3)
5133	Taq1	39	agg	156.06	156	156.06	0	0	185.68	0	0	-=	\		A(3)
5134	Hha1	26	ctg	231.04	232	0	231.04	0	0	3 600 000	0	+-	A		A(3)
5135	Hha1	39	agg	66.61	67	0	66.57	66.65	0	1 629.94	2 937.82	+=	/		/(3)
5136	Hha1	54	ttt	68.19	68	68.18	68.28	68.11	7 500 000	3 900 000	13 100 000	=+	/ (-)		/(3)
5137	Hha1	26	ctg	223.743	225	223.77	223.71	223.75	5 400 000	3 100 000	9 800 000	=+	/ (-)		/(3)
5138	Hha1	26	ctg	224.91	225	0	0	224.91	0	0	4 000 000	=+	/		/(3)
5139	Hha1	26	ctg	225.8	225	0	0	225.8	0	0	4 300 000	=+	/		/(3)
5140	Hha1	60	ttg	224.92	225	0	224.92	0	0	3 000 000	0	+-	A		/(3)
5141	Hha1	39	agg	66.61	67	0	66.57	66.65	0	1 629.94	2 937.82	+=	/		/(3)
5142	Hha1	54	ttt	68.19	68	68.18	68.28	68.11	7 500 000	3 900 000	13 100 000	=+	/ (-)		/(3)
5143	Hha1	26	ctg	223.743	225	223.77	223.71	223.75	5 400 000	3 100 000	9 800 000	=+	/ (-)		/(3)
5144	Hha1	26	ctg	224.91	225	0	0	224.91	0	0	4 000 000	=+	/		/(3)
5145	Hha1	26	ctg	225.8	225	0	0	225.8	0	0	4 300 000	=+	/		/(3)
5146	Hha1	40	tgg	225.115	225	225.12	225.11	0	4 000 000	3 800 000	0	=-	\		/(3)
5147	Hha1	40	tgg	225.76	225	0	225.76	0	0	6 500 000	0	+-	A		/(3)
5148	Hha1	40	tgg	122.55	123	0	122.55	0	0	3 900 000	0	+-	A		A(2)
5149	Hha1	40	tgg	123.29	123	0	123.13	123.45	0	6 200 000	4 300 000	+=	/		A(2)
5150	Hha1	3	aac	207.68	208	207.75	0	207.61	4 200 000	0	3 100 000	-+(=)	V		A(2)
5151	Hha1	3	aac	208.74	208	208.76	208.72	0	5 500 000	4 400 000	0	=-	\		A(2)
5152	Taq1	45	gcc	316.47	317	0	316.47	0	0	3 000 000	0	+-	A		A(2)
5153	Hha1	40	tgg	100.52	101	100.28	0	100.76	3 400 000	0	9 300 000	=+(+)	/		/(5)
5154	Hha1	16	tag	141.177	142	140.98	141.31	141.24	3 100 000	3 700 000	8 900 000	=+	/ (-)		/(5)
5155	Taq1	16	tag	141.455	142	0	141.29	141.62	0	5 000 000	7 100 000	+=	/		/(5)
5156	Hha1	16	tag	141.965	142	0	141.87	142.06	0	7 000 000	3 200 000	+-	A		/(5)
5157	Taq1	16	tag	142.63	142	0	142.64	142.62	0	3 000 000	19 500 000	=+	/		/(5)
5158	Hha1	26	ctg	179.43	180	179.41	0	179.45	4 900 000	0	4 300 000	-+(=)	V		/(5)
5159	Hha1	26	ctg	180.61	180	0	0	180.61	0	0	6 800 000	=+	/		/(5)
5160	Hha1	49	aaa	191.23	192	191.3	191.16	0	31 700 000	7 300 000	0	-=	\		/(5)
5161	Hha1	49	aaa	192.317	192	192.11	192.42	192.42	6 300 000	9 000 000	3 900 000	=-	\ (-)		/(5)
5162	Hha1	39	agg	159.2	160	159.37	159.03	0	271.26	310.46	0	=-	\	\	\(2)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
5120	RATCYP450.PE1	nc	nc	*	ctg	ttg	decreased
5121	RATCYP450.PE1	nc	nc	*	ctg	ttg	decreased
5122	RATCYP45A.PE1	nc	nc		ttt	agg	decreased
5123	RATCYP45A.PE1	nc	nc		ttt	agg	decreased
5124	RATCYP45A.PE1	nc	nc		ctg	ttg	decreased
5125	RATCYP45A.PE1	nc	nc		ctg	ttg	decreased
5126	RATCYP45A.PE1	nc	nc		ctg	ttg	decreased
5127	RATCYP45A.PE1	nc	nc		ctg	ttg	decreased
5128	RATCYP45F.PE1	nc	nc		agg	agt	increased by mild
5129	RATCYP45F.PE1	nc	nc		agg	agt	increased by mild
5130	RATCYP45F.PE1	nc	nc		agg	agt	increased by mild
5131	RATCYP45F.PE1	nc	nc		agg	agt	increased by mild
5132	RATCYP45F.PE1	nc	nc		agg	agt	increased by mild
5133	RATCYP45F.PE1	nc	nc		agg	agt	increased by mild
5134	RATCYP45F.PE1	nc	nc		tat	ctg	increased by mild
5135	RATCYPB9.PE1	nc	nc		ttt	agg	decreased
5136	RATCYPB9.PE1	nc	nc		ttt	agg	decreased
5137	RATCYPB9.PE1	nc	nc		ctg	ttg	decreased
5138	RATCYPB9.PE1	nc	nc		ctg	ttg	decreased
5139	RATCYPB9.PE1	nc	nc		ctg	ttg	decreased
5140	RATCYPB9.PE1	nc	nc		ctg	ttg	decreased
5141	RATCYPE9.PE1	nc	nc		ttt	agg	decreased
5142	RATCYPE9.PE1	nc	nc		ttt	agg	decreased
5143	RATCYPE9.PE1	nc	nc		ctg	tgg	decreased
5144	RATCYPE9.PE1	nc	nc		ctg	tgg	decreased
5145	RATCYPE9.PE1	nc	nc		ctg	tgg	decreased
5146	RATCYPE9.PE1	nc	nc		ctg	tgg	decreased
5147	RATCYPE9.PE1	nc	nc		ctg	tgg	decreased
5148	RATDRS.DRS	drs	nc		tgg	cat	increased by mild
5149	RATDRS.DRS	drs	nc		tgg	cat	increased by mild
5150	RATDRS.DRS	drs	nc		aac	agc	increased by mild
5151	RATDRS.DRS	drs	nc		aac	agc	increased by mild
5152	RATDRS.DRS	drs	nc		tgg	gcc	increased by mild
5153	RATESP1A.R-ESP1	R-esp1	nc		tgg	tga	decreased
5154	RATESP1A.R-ESP1	R-esp1	nc		gat	tag	decreased
5155	RATESP1A.R-ESP1	R-esp1	nc		gat	tag	decreased
5156	RATESP1A.R-ESP1	R-esp1	nc		gat	tag	decreased
5157	RATESP1A.R-ESP1	R-esp1	nc		gat	tag	decreased
5158	RATESP1A.R-ESP1	R-esp1	nc		cca	ctg	decreased
5159	RATESP1A.R-ESP1	R-esp1	nc		cca	ctg	decreased
5160	RATESP1A.R-ESP1	R-esp1	nc		agt	aaa	decreased
5161	RATESP1A.R-ESP1	R-esp1	nc		agt	aaa	decreased
5162	RATFERL.PE1	nc	nc		agg	tgg	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
5163	Hha1	39	agg	160.39	160	160.39	0	0	278.59	0	0	-=	\		\(2)
5164	Hha1	40	tgg	159.24	160	159.24	0	0	4 000 000	0	0	-=	\	\	\(2)
5165	Hha1	8	gaa	166.71	167	166.79	166.67	166.67	5 900 000	11 600 000	8 600 000	+=	/ (-)	/	-1
5166	Taq1	8	gaa	166.82	167	0	0	166.82	0	0	3 900 000	=+	/	/	-1
5167	Hha1	8	gaa	167.627	167	167.55	167.67	167.66	9 900 000	7 800 000	4 300 000	==	-		-1
5168	Hha1	20	ctc	68.973	69	68.95	69.09	68.88	550.96	485.18	1 145.03	=+	/ (-)		\(5)
5169	Hha1	39	agg	87.397	87	87.19	87.6	87.4	1 312.31	447.78	545.24	-=	\ (-)		\(5)
5170	Taq1	47	ggc	119.735	120	119.73	119.74	0	2 215.38	1 750.47	0	=-	\		\(5)
5171	Taq1	47	ggc	120.71	120	120.68	120.74	0	2 830.76	1 241.24	0	-=	\		\(5)
5172	Hha1	59	ttc	119.5	120	119.76	119.46	119.28	410.81	376.56	250.95	==	-		\(5)
5173	Hha1	59	ttc	120.06	120	0	120.06	0	0	218.46	0	+-	A		\(5)
5174	Hha1	59	ttc	120.7	120	120.7	0	0	956.83	0	0	-=	\		\(5)
5175	Hha1	64	gtt	119.49	120	0	0	119.49	0	0	3 000 000	=+	/		\(5)
5176	Hha1	64	gtt	120.365	120	0	120.41	120.32	0	3 800 000	3 000 000	+=	/		\(5)
5177	Taq1	61	tct	120.51	121	0	120.27	120.75	0	9 800 000	6 500 000	+=	/		\(5)
5178	Taq1	61	tct	121.523	121	121.35	121.4	121.82	5 000 000	15 100 000	10 900 000	+=	/ (-)		\(5)
5179	Hha1	33	agc	137.335	137	137.26	137.41	0	3 400 000	4 500 000	0	=-	\		\(5)
5180	Hha1	59	ttc	175.055	176	0	174.93	175.18	0	91.98	116.42	+=	/		\(5)
5181	Hha1	59	ttc	176.415	176	176.39	176.44	0	202.8	146.6	0	=-	\		\(5)
5182	Taq1	17	cca	201.29	202	201.29	0	0	283.28	0	0	-=	\		\(2)
5183	Hha1	6	aga	272.09	273	272.09	0	0	7 100 000	0	0	-=	\		\(2)
5184	Taq1	39	agg	102.46	103	0	102.46	0	0	56 100 000	0	+-	A		\(6) A(4)
5185	Taq1	39	agg	103.263	103	103.47	103.17	103.15	15 700 000	174 900 000	6 900 000	+-	A		\(6) A(4)
5186	Taq1	39	agg	102.46	103	0	102.46	0	0	563.82	0	+-	A		\(6) A(4)
5187	Taq1	39	agg	103.263	103	103.47	103.17	103.15	583.03	1 757.8	203.24	+-	A		\(6) A(4)
5188	Taq1	17	cca	149.32	150	149.32	0	0	1 170.29	0	0	-=	\		\(6) A(4)
5189	Taq1	17	cca	150.15	150	0	150.06	150.24	0	870.89	1 052.47	+=	/		\(6) A(4)
5190	Taq1	54	ttt	150.645	151	150.51	150.78	0	2 039.32	540.98	0	-=	\		\(6) A(4)
5191	Taq1	54	ttt	151.555	151	151.7	151.41	0	1 143.48	964.36	0	=-	\		\(6) A(4)
5192	Taq1	54	ttt	151.6	151	0	151.6	0	0	858.52	0	+-	A		\(6) A(4)
5193	Taq1	8	gaa	235.63	237	235.63	0	0	3 800 000	0	0	-=	\		\(6) A(4)
5194	Hha1	8	gaa	236.3	237	236.33	236.27	0	3 900 000	3 100 000	0	=-	\		\(6) A(4)
5195	Taq1	49	aaa	236.74	238	0	236.74	0	0	8 100 000	0	+-	A		\(6) A(4)
5196	Taq1	49	aaa	237.485	238	237.47	237.5	0	7 400 000	3 300 000	0	-=	\		\(6) A(4)
5197	Taq1	49	aaa	238.583	238	238.58	238.57	238.6	29 100 000	21 100 000	3 300 000	=-	\ (-)		\(6) A(4)
5198	Taq1	49	aaa	330.16	331	330.16	0	0	9 300 000	0	0	-=	\		\(6) A(4)
5199	Taq1	49	aaa	331.57	331	0	331.57	0	0	5 200 000	0	+-	A		\(6) A(4)
5200	Taq1	49	aaa	332.29	331	332.29	0	0	22 700 000	0	0	-=	\		\(6) A(4)
5201	Taq1	49	aaa	331.64	331	331.64	0	0	13 500 000	0	0	-=	\		\(6) A(4)
5202	Hha1	8	gaa	157.313	157	157.36	157.31	157.27	22 700 000	11 900 000	5 600 000	-=	\ (-)	\	
5203	Taq1	8	gaa	157.43	157	157.43	0	0	3 200 000	0	0	-=	\	\	
5204	Hha1	39	agg	103.52	104	0	103.55	103.49	0	179.11	122.07	+=	/		\(2)
5205	Hha1	39	agg	104.08	104	104.08	0	0	469.2	0	0	-=	\		\(2)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
5163	RATFERL.PE1	nc	nc		agg	tgg	increased
5164	RATFERL.PE1	nc	nc		agg	tgg	increased
5165	RATFIBAA.PE1	nc	nc		gaa	gtg	decreased
5166	RATFIBAA.PE1	nc	nc		gaa	gtg	decreased
5167	RATFIBAA.PE1	nc	nc		gaa	gtg	No change
5168	RATFRZH.PE1	nc	nc		ctc	cgt	increased
5169	RATFRZH.PE1	nc	nc		gga	agg	increased
5170	RATFRZH.PE1	nc	nc		ggc	tct	increased
5171	RATFRZH.PE1	nc	nc		ggc	tct	increased
5172	RATFRZH.PE1	nc	nc		ttc	gtt	increased
5173	RATFRZH.PE1	nc	nc		ttc	gtt	increased
5174	RATFRZH.PE1	nc	nc		ttc	gtt	increased
5175	RATFRZH.PE1	nc	nc		ttc	gtt	increased
5176	RATFRZH.PE1	nc	nc		ttc	gtt	increased
5177	RATFRZH.PE1	nc	nc		ggc	tct	increased
5178	RATFRZH.PE1	nc	nc		ggc	tct	increased
5179	RATFRZH.PE1	nc	nc		cct	agc	increased
5180	RATFRZH.PE1	nc	nc		ttc	tcc	increased
5181	RATFRZH.PE1	nc	nc		ttc	tcc	increased
5182	RATGASB.PE1	nc	nc		gac	cca	increased
5183	RATGASB.PE1	nc	nc		gag	aga	increased
5184	RATGCR.PE1	nc	nc		agg	gct	increased
5185	RATGCR.PE1	nc	nc		agg	gct	increased
5186	RATGCR.PE1	nc	nc		agg	gct	increased
5187	RATGCR.PE1	nc	nc		agg	gct	increased
5188	RATGCR.PE1	nc	nc		cca	ttt	increased
5189	RATGCR.PE1	nc	nc		cca	ttt	increased
5190	RATGCR.PE1	nc	nc		cca	ttt	increased
5191	RATGCR.PE1	nc	nc		cca	ttt	increased
5192	RATGCR.PE1	nc	nc		cca	ttt	increased
5193	RATGCR.PE1	nc	nc		aaa	gaa	increased
5194	RATGCR.PE1	nc	nc		aaa	gaa	increased
5195	RATGCR.PE1	nc	nc		aaa	gaa	increased
5196	RATGCR.PE1	nc	nc		aaa	gaa	increased
5197	RATGCR.PE1	nc	nc		aaa	gaa	increased
5198	RATGCR.PE1	nc	nc		aaa	ggt	increased
5199	RATGCR.PE1	nc	nc		aaa	ggt	increased
5200	RATGCR.PE1	nc	nc		aaa	ggt	increased
5201	RATGCR.PE1	nc	nc		aaa	ggt	increased
5202	RATGCSA.PE1	nc	nc		ccc	gaa	increased
5203	RATGCSA.PE1	nc	nc		ccc	gaa	increased
5204	RATGLK10.PE1	nc	nc	*	agg	ggc	increased
5205	RATGLK10.PE1	nc	nc	*	agg	ggc	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
5206	Hha1	27	acg	165.945	166	165.91	0	165.98	4 000 000	0	3 400 000	-+(=)	V		\(2)
5207	Hha1	27	acg	166.62	166	166.62	0	0	3 100 000	0	0	-=	\		\(2)
5208	Hha1	39	agg	103.52	104	0	103.55	103.49	0	179.11	122.07	+=	/		\(2)
5209	Hha1	39	agg	104.08	104	104.08	0	0	469.2	0	0	-=	\		\(2)
5210	Hha1	27	acg	165.945	166	165.91	0	165.98	4 000 000	0	3 400 000	-+(=)	V		\(2)
5211	Hha1	27	acg	166.62	166	166.62	0	0	3 100 000	0	0	-=	\		\(2)
5212	Taq1	26	ctg	186.63	187	0	0	186.63	0	0	4 800 000	=+	/	/	A(3) /(2)
5213	Taq1	26	ctg	187.66	187	0	187.66	0	0	3 000 000	0	+-	A	A	A(3) /(2)
5214	Taq1	57	ctg	186.41	187	0	0	186.41	0	0	6 500 000	=+	/	/	A(3) /(2)
5215	Taq1	57	ctg	187.215	187	0	187.02	187.41	0	3 300 000	5 400 000	+=	/		A(3) /(2)
5216	Taq1	57	ctg	187.45	187	0	187.45	0	0	4 800 000	0	+-	A	A	A(3) /(2)
5217	Hha1	40	tgg	225.115	226	225.12	225.11	0	4 000 000	3 800 000	0	=-	\		A(3) /(2)
5218	Hha1	40	tgg	225.76	226	0	225.76	0	0	6 500 000	0	+-	A		A(3) /(2)
5219	Taq1	48	ggg	100.837	101	100.98	100.93	100.6	4 551.2	612.39	2 114.02	-=	\ (-)		\(2)
5220	Taq1	49	aaa	102.575	103	102.67	102.48	0	44 100 000	13 400 000	0	-=	\		\(2)
5221	Taq1	49	aaa	103.135	103	103.13	103.14	0	29 300 000	3 300 000	0	-=	\		\(2)
5222	Hha1	39	agg	68.607	69	68.64	68.57	68.61	828.44	603.02	406.9	==	-		-(3) \(3)
5223	Hha1	39	agg	71.64	72	71.65	71.55	71.72	13 563.04	1 176.18	2 046.71	-=	\ (-)		-(3) \(3)
5224	Hha1	6	aga	124.12	124	124.12	0	0	4 500 000	0	0	-=	\		-(3) \(3)
5225	Taq1	35	gga	123.8	124	0	0	123.8	0	0	3 500 000	=+	/		-(3) \(3)
5226	Taq1	35	gga	124.71	124	0	0	124.71	0	0	3 600 000	=+	/		-(3) \(3)
5227	Hha1	61	tct	132.68	133	132.57	132.69	132.78	17 200 000	40 300 000	55 400 000	==	-		-(3) \(3)
5228	Hha1	61	tct	133.78	133	133.78	0	0	5 700 000	0	0	-=	\		-(3) \(3)
5229	Hha1	49	aaa	100.63	101	100.82	100.44	0	31 100 000	25 500 000	0	=-	\		\(2)
5230	Hha1	49	aaa	101.18	101	0	0	101.18	0	0	3 500 000	=+	/		\(2)
5231	Hha1	26	ctg	108.8	109	108.86	108.8	108.74	5 700 000	5 700 000	4 900 000	==	-		\(2)
5232	Hha1	59	ttc	110.77	111	110.89	110.65	0	343.21	434.05	0	=-	\		\(2)
5233	Hha1	15	tac	133.3	134	133.3	133.42	133.18	28 600 000	12 100 000	6 900 000	-=	\ (-)		\(2)
5234	Hha1	15	tac	134.565	134	134.58	134.55	0	6 100 000	4 700 000	0	=-	\	\	\(2)
5235	Hha1	15	tac	133.44	134	133.46	133.42	0	6 045.18	3 116.14	0	--	\		\(2)
5236	Hha1	15	tac	134.545	134	134.54	134.55	0	1 167.14	1 210.4	0	=-	\	\	\(2)
5237	Hha1	61	tct	133.78	134	133.78	0	0	5 700 000	0	0	-=	\		\(2)
5238	Hha1	61	tct	134.76	134	134.76	0	0	4 000 000	0	0	-=	\	\	\(2)
5239	Hha1	15	tac	133.3	134	133.3	133.42	133.18	28 600 000	12 100 000	6 900 000	-=	\ (-)		\(2)
5240	Hha1	15	tac	134.565	134	134.58	134.55	0	6 100 000	4 700 000	0	=-	\	\	\(2)
5241	Hha1	15	tac	133.44	134	133.46	133.42	0	6 045.18	3 116.14	0	--	\		\(2)
5242	Hha1	15	tac	134.545	134	134.54	134.55	0	1 167.14	1 210.4	0	=-	\	\	\(2)
5243	Hha1	61	tct	133.78	134	133.78	0	0	5 700 000	0	0	-=	\		\(2)
5244	Hha1	61	tct	134.76	134	134.76	0	0	4 000 000	0	0	-=	\	\	\(2)
5245	Taq1	56	tga	67.115	67	0	66.93	67.3	0	8 500 000	55 300 000	=+	/		/(4)
5246	Taq1	12	agt	141.41	142	141.42	141.42	141.39	4 800 000	4 100 000	5 300 000	==	-		/(4)
5247	Taq1	12	agt	142.413	142	142.43	142.44	142.37	13 800 000	10 600 000	20 500 000	=+	/ (-)	/	/(4)
5248	Taq1	51	ata	142.45	143	0	0	142.45	0	0	4 100 000	=+	/	/	/(4)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
5206	RATGLK10.PE1	nc	nc	*	acg	aca	increased
5207	RATGLK10.PE1	nc	nc	*	acg	aca	increased
5208	RATGLUKB.PE1	nc	nc		agg	ggc	increased
5209	RATGLUKB.PE1	nc	nc		agg	ggc	increased
5210	RATGLUKB.PE1	nc	nc		acg	aca	increased
5211	RATGLUKB.PE1	nc	nc		acg	aca	increased
5212	RATGNPAS.PE1	nc	nc	*	ctg	aca	decreased
5213	RATGNPAS.PE1	nc	nc	*	ctg	aca	increased by mild
5214	RATGNPAS.PE1	nc	nc	*	ctg	aca	decreased
5215	RATGNPAS.PE1	nc	nc	*	ctg	aca	increased by mild
5216	RATGNPAS.PE1	nc	nc	*	ctg	aca	increased by mild
5217	RATGNPAS.PE1	nc	nc	*	tcc	tgg	increased by mild
5218	RATGNPAS.PE1	nc	nc	*	tcc	tgg	increased by mild
5219	RATGSTAA.PE1	nc	nc		ggg	aaa	increased
5220	RATGSTAA.PE1	nc	nc		ggg	aaa	increased
5221	RATGSTAA.PE1	nc	nc		ggg	aaa	increased
5222	RATGXA.PE1	nc	nc	*	ggc	agg	No change
5223	RATGXA.PE1	nc	nc	*	ccg	agg	No change
5224	RATGXA.PE1	nc	nc	*	gga	aga	No change
5225	RATGXA.PE1	nc	nc	*	gga	aga	No change
5226	RATGXA.PE1	nc	nc	*	gga	aga	No change
5227	RATGXA.PE1	nc	nc	*	tct	tct	No change
5228	RATGXA.PE1	nc	nc	*	tct	tct	No change
5229	RATHIS1D.PE1	nc	nc		aaa	tcc	increased
5230	RATHIS1D.PE1	nc	nc		aaa	tcc	increased
5231	RATHIS1D.PE1	nc	nc		ctc	ctg	increased
5232	RATHIS1D.PE1	nc	nc		ccg	ttc	increased
5233	RATHPA3.PE1	nc	nc		tct	tac	increased
5234	RATHPA3.PE1	nc	nc		tct	tac	increased
5235	RATHPA3.PE1	nc	nc		tct	tac	increased
5236	RATHPA3.PE1	nc	nc		tct	tac	increased
5237	RATHPA3.PE1	nc	nc		tct	tac	increased
5238	RATHPA3.PE1	nc	nc		tct	tac	increased
5239	RATHPAB.PE1	nc	nc		tct	tac	increased
5240	RATHPAB.PE1	nc	nc		tct	tac	increased
5241	RATHPAB.PE1	nc	nc		tct	tac	increased
5242	RATHPAB.PE1	nc	nc		tct	tac	increased
5243	RATHPAB.PE1	nc	nc		tct	tac	increased
5244	RATHPAB.PE1	nc	nc		tct	tac	increased
5245	RATI145TR.PE1	nc	nc		caa	tga	decreased
5246	RATI145TR.PE1	nc	nc		ata	agt	decreased
5247	RATI145TR.PE1	nc	nc		ata	agt	decreased
5248	RATI145TR.PE1	nc	nc		ata	agt	decreased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
5249	Taq1	51	ata	143.11	143	0	143.14	143.08	0	23 500 000	5 000 000	+-	A		/(4)
5250	Taq1	18	cct	196.225	197	0	196.23	196.22	0	3 600 000	3 500 000	+=	/		/(4)
5251	Taq1	18	cct	197.25	197	197.25	197.25	0	4 700 000	5 000 000	0	=-	\		/(4)
5252	Taq1	50	aat	336.52	337	0	336.52	0	0	3 700 000	0	+-	A		/(4)
5253	Taq1	56	tga	67.115	67	0	66.93	67.3	0	8 500 000	55 300 000	=+	/		/(4)
5254	Taq1	12	agt	141.41	142	141.42	141.42	141.39	4 800 000	4 100 000	5 300 000	==	-		/(4)
5255	Taq1	12	agt	142.413	142	142.43	142.44	142.37	13 800 000	10 600 000	20 500 000	=+	/ (-)	/	/(4)
5256	Taq1	51	ata	142.45	143	0	0	142.45	0	0	4 100 000	=+	/	/	/(4)
5257	Taq1	51	ata	143.11	143	0	143.14	143.08	0	23 500 000	5 000 000	+-	A		/(4)
5258	Taq1	18	cct	196.225	197	0	196.23	196.22	0	3 600 000	3 500 000	+=	/		/(4)
5259	Taq1	18	cct	197.25	197	197.25	197.25	0	4 700 000	5 000 000	0	=-	\		/(4)
5260	Taq1	50	aat	336.52	337	0	336.52	0	0	3 700 000	0	+-	A		/(4)
5261	Taq1	18	cct	228.98	229	0	228.98	0	0	4 600 000	0	+-	A		A(2) \(2)
5262	Taq1	18	cct	229.98	229	230.01	229.95	0	3 400 000	4 600 000	0	=-	\		A(2) \(2)
5263	Hha1	22	tcc	229.45	229	229.45	0	0	10 300 000	0	0	-=	\		A(2) \(2)
5264	Hha1	22	tcc	230.345	229	0	230.3	230.39	0	12 300 000	3 600 000	+-	A		A(2) \(2)
5265	Hha1	59	ttc	114.603	114	114.73	114.55	114.53	218.4	526.04	488.96	+=	/ (-)		-3
5266	Hha1	61	tct	114.59	114	114.59	0	0	3 400 000	0	0	-=	\		-3
5267	Hha1	6	aga	117.44	118	0	0	117.44	0	0	9 400 000	=+	/		-3
5268	Hha1	6	aga	118.04	118	118.11	0	117.97	49 700 000	0	40 700 000	-+(=)	V		-3
5269	Taq1	48	ggg	135.38	136	135.33	135.45	135.36	3 666.24	2 101.34	1 558.82	==	-		-3
5270	Hha1	3	aac	137.2	137	137.21	137.05	137.34	9 800 000	10 400 000	7 300 000	==	-		-3
5271	Hha1	60	ttg	117.71	118	117.87	117.49	117.77	4 900 000	4 100 000	3 800 000	==	-		-2
5272	Taq1	19	cac	126.637	127	126.66	126.65	126.6	3 100 000	5 000 000	20 700 000	=+	/ (-)		-2
5273	Taq1	19	cac	127.64	127	127.65	127.6	127.67	3 700 000	5 100 000	6 200 000	==	-		-2
5274	Hha1	60	ttg	117.71	118	117.87	117.49	117.77	4 900 000	4 100 000	3 800 000	==	-		-2
5275	Taq1	19	cac	126.637	127	126.66	126.65	126.6	3 100 000	5 000 000	20 700 000	=+	/ (-)		-2
5276	Taq1	19	cac	127.64	127	127.65	127.6	127.67	3 700 000	5 100 000	6 200 000	==	-		-2
5277	Taq1	40	tgg	119.665	120	119.69	119.64	0	8 000 000	13 700 000	0	=-	\		\(3)
5278	Taq1	40	tgg	120.38	120	120.22	120.32	120.6	5 900 000	107 000 000	9 700 000	+-	A		\(3)
5279	Taq1	45	gcc	264.465	266	264.47	264.46	0	46 500 000	41 900 000	0	=-	\		\(3)
5280	Taq1	45	gcc	265.42	266	265.42	0	0	3 600 000	0	0	-=	\	\	\(3)
5281	Taq1	45	gcc	265.96	266	0	265.96	0	0	3 300 000	0	+-	A		\(3)
5282	Hha1	6	aga	265.59	267	265.59	0	0	3 200 000	0	0	-=	\	\	\(3)
5283	Hha1	6	aga	268.5	267	268.5	0	0	13 500 000	0	0	-=	\		\(3)
5284	Hha1	33	agc	62.84	63	62.76	62.92	62.84	4 400 000	18 500 000	17 900 000	+=	/ (-)		/(2) \(2)
5285	Hha1	43	cgc	164.33	165	164.33	0	0	5 300 000	0	0	-=	\		/(2) \(2)
5286	Hha1	40	tgg	165.64	166	165.47	0	165.81	7 900 000	0	3 100 000	-=(-)	\		/(2) \(2)
5287	Hha1	40	tgg	166.36	166	0	0	166.36	0	0	3 000 000	=+	/		/(2) \(2)
5288	Taq1	40	tgg	119.665	120	119.69	119.64	0	8 000 000	13 700 000	0	=-	\		\(3)
5289	Taq1	40	tgg	120.38	120	120.22	120.32	120.6	5 900 000	107 000 000	9 700 000	+-	A		\(3)
5290	Taq1	45	gcc	264.465	266	264.47	264.46	0	46 500 000	41 900 000	0	=-	\		\(3)
5291	Taq1	45	gcc	265.42	266	265.42	0	0	3 600 000	0	0	-=	\	\	\(3)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
5249	RATI145TR.PE1	nc	nc		ata	agt	decreased
5250	RATI145TR.PE1	nc	nc		cct	tcg	decreased
5251	RATI145TR.PE1	nc	nc		cct	tcg	decreased
5252	RATI145TR.PE1	nc	nc		aat	gcg	decreased
5253	RATI145TR.PE2	nc	nc		caa	tga	decreased
5254	RATI145TR.PE2	nc	nc		ata	agt	decreased
5255	RATI145TR.PE2	nc	nc		ata	agt	decreased
5256	RATI145TR.PE2	nc	nc		ata	agt	decreased
5257	RATI145TR.PE2	nc	nc		ata	agt	decreased
5258	RATI145TR.PE2	nc	nc		cct	tcg	decreased
5259	RATI145TR.PE2	nc	nc		cct	tcg	decreased
5260	RATI145TR.PE2	nc	nc		aat	gcg	decreased
5261	RATIGEM.PE1	nc	nc		cct	tcc	increased by mild
5262	RATIGEM.PE1	nc	nc		cct	tcc	increased by mild
5263	RATIGEM.PE1	nc	nc		cct	tcc	increased by mild
5264	RATIGEM.PE1	nc	nc		cct	tcc	increased by mild
5265	RATIGFI.PE1	nc	nc		tct	ttc	No change
5266	RATIGFI.PE1	nc	nc		tct	ttc	No change
5267	RATIGFI.PE1	nc	nc		gag	aga	No change
5268	RATIGFI.PE1	nc	nc		gag	aga	No change
5269	RATIGFI.PE1	nc	nc		ggg	aac	No change
5270	RATIGFI.PE1	nc	nc		ggg	aac	No change
5271	RATILGF2A.PE1	nc	nc		aga	ttg	No change
5272	RATILGF2A.PE1	nc	nc		cac	gct	No change
5273	RATILGF2A.PE1	nc	nc		cac	gct	No change
5274	RATILGFII.PE1	nc	nc		aga	ttg	No change
5275	RATILGFII.PE1	nc	nc		cac	gct	No change
5276	RATILGFII.PE1	nc	nc		cac	gct	No change
5277	RATINHA.PE1	nc	nc	*	tgc	tgg	increased
5278	RATINHA.PE1	nc	nc	*	tgc	tgg	increased
5279	RATINHA.PE1	nc	nc	*	aga	gcc	increased
5280	RATINHA.PE1	nc	nc	*	aga	gcc	increased
5281	RATINHA.PE1	nc	nc	*	aga	gcc	increased
5282	RATINHA.PE1	nc	nc	*	aga	gcc	increased
5283	RATINHA.PE1	nc	nc	*	aga	gcc	increased
5284	RATINHB.PE1	nc	nc		agc	aca	decreased
5285	RATINHB.PE1	nc	nc		tgg	cgc	decreased
5286	RATINHB.PE1	nc	nc		tgg	cgc	decreased
5287	RATINHB.PE1	nc	nc		tgg	cgc	decreased
5288	RATINHBAB2.PE1	nc	nc	*	tgc	tgg	increased
5289	RATINHBAB2.PE1	nc	nc	*	tgc	tgg	increased
5290	RATINHBAB2.PE1	nc	nc	*	aga	gcc	increased
5291	RATINHBAB2.PE1	nc	nc	*	aga	gcc	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
5292	Taq1	45	gcc	265.96	266	0	265.96	0	0	3 300 000	0	+-	A		\(3)
5293	Hha1	6	aga	265.59	267	265.59	0	0	3 200 000	0	0	-=	\	\	\(3)
5294	Hha1	6	aga	268.5	267	268.5	0	0	13 500 000	0	0	-=	\		\(3)
5295	Taq1	8	gaa	72.803	73	72.97	72.82	72.62	3 000 000	22 500 000	17 300 000	+=	/ (-)		\(6)
5296	Hha1	16	tag	72.57	73	72.39	72.66	72.66	4 900 000	12 400 000	3 800 000	+-	A		\(6)
5297	Taq1	34	tgc	105.7	106	105.69	105.71	0	3 300 000	4 000 000	0	=-	\		\(6)
5298	Taq1	34	tgc	106.605	106	106.55	106.66	0	3 700 000	5 900 000	0	=-	\		\(6)
5299	Hha1	6	aga	174.06	175	0	0	174.06	0	0	7 800 000	=+	/		\(6)
5300	Hha1	6	aga	174.96	175	0	0	174.96	0	0	5 400 000	=+	/		\(6)
5301	Hha1	6	aga	175.995	175	175.96	0	176.03	4 500 000	0	9 800 000	-+(+)	V (/)		\(6)
5302	Taq1	18	cct	210.51	210	210.54	210.48	0	3 200 000	5 000 000	0	=-	\		\(6)
5303	Taq1	39	agg	224.67	226	224.67	0	0	19 500 000	0	0	-=	\		\(6)
5304	Taq1	39	agg	226.075	226	226.06	226.09	0	23 000 000	51 200 000	0	+-	A		\(6)
5305	Taq1	39	agg	224.67	226	224.67	0	0	724.15	0	0	-=	\		\(6)
5306	Taq1	39	agg	226.06	226	226.06	0	0	854.12	0	0	-=	\	\	\(6)
5307	Taq1	39	agg	226.91	226	0	226.91	0	0	23 000 000	0	+-	A		\(6)
5308	Taq1	39	agg	226.09	226	0	226.09	0	0	514.57	0	+-	A		\(6)
5309	Taq1	39	agg	226.91	226	0	226.91	0	0	231.15	0	+-	A		\(6)
5310	Taq1	64	gtt	224.97	226	224.97	0	0	3 700 000	0	0	-=	\		\(6)
5311	Taq1	64	gtt	225.9	226	225.83	225.97	0	3 100 000	3 600 000	0	=-	\	\	\(6)
5312	Taq1	64	gtt	227.007	226	226.96	226.93	227.13	3 400 000	3 800 000	3 400 000	==	-		\(6)
5313	Hha1	9	atc	255.81	257	255.63	255.83	255.97	4 900 000	4 100 000	6 300 000	==	-		\(6)
5314	Taq1	39	agg	255.6	257	0	255.6	0	0	50 300 000	0	+-	A		\(6)
5315	Taq1	39	agg	256.83	257	0	256.83	0	0	11 900 000	0	+-	A		\(6)
5316	Taq1	39	agg	257.89	257	258.11	257.67	0	7 900 000	3 400 000	0	-=	\		\(6)
5317	Taq1	39	agg	255.6	257	0	255.6	0	0	505.53	0	+-	A		\(6)
5318	Taq1	39	agg	256.83	257	0	256.83	0	0	119.59	0	+-	A		\(6)
5319	Taq1	39	agg	257.67	257	0	257.67	0	0	34.17	0	+-	A		\(6)
5320	Taq1	39	agg	258.11	257	258.11	0	0	293.37	0	0	-=	\		\(6)
5321	Hha1	3	aac	295.39	297	295.39	0	0	4 100 000	0	0	-=	\		\(6)
5322	Hha1	33	agc	114.89	115	114.89	0	0	3 800 000	0	0	-=	\		-(3) \(3)
5323	Hha1	27	acg	148.58	149	148.58	0	0	3 800 000	0	0	-=	\		-(3) \(3)
5324	Hha1	27	acg	149.673	149	149.7	149.66	149.66	14 200 000	5 600 000	11 700 000	-=	\ (-)		-(3) \(3)
5325	Hha1	32	gtc	149.13	149	149.14	149.17	149.08	1 537.89	1 414.03	3 128.76	=+	/ (-)		-(3) \(3)
5326	Hha1	56	tga	185.11	186	0	185.2	185.02	0	181.63	999.82	=+	/		-(3) \(3)
5327	Hha1	56	tga	186	186	185.91	186.09	186	424.95	176.13	982.58	=+	/ (-)		-(3) \(3)
5328	Hha1	56	tga	187.11	186	187.14	187.08	0	343.23	264.2	0	=-	\		-(3) \(3)
5329	Hha1	6	aga	210.285	211	210.13	210.44	0	5 000 000	3 200 000	0	=-	\		\(2)
5330	Hha1	6	aga	211.18	211	211.4	0	210.96	16 400 000	0	4 500 000	-=(-)	\		\(2)
5331	Hha1	6	aga	212	211	0	0	212	0	0	3 300 000	=+	/		\(2)
5332	Hha1	25	cag	210.6	211	210.58	210.62	0	3 700 000	3 300 000	0	=-	\		\(2)
5333	Hha1	25	cag	211.76	211	211.76	0	0	4 200 000	0	0	-=	\		\(2)
5334	Taq1	61	tct	147.96	148	148.04	147.78	148.06	3 000 000	12 800 000	5 500 000	+-	A	A	A(2)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
5292	RATINHBAB2.PE1	nc	nc	*	aga	gcc	increased
5293	RATINHBAB2.PE1	nc	nc	*	aga	gcc	increased
5294	RATINHBAB2.PE1	nc	nc	*	aga	gcc	increased
5295	RATINSAB.PE1	nc	nc		gaa	tag	increased
5296	RATINSAB.PE1	nc	nc		gaa	tag	increased
5297	RATINSAB.PE1	nc	nc		gat	tgc	increased
5298	RATINSAB.PE1	nc	nc		gat	tgc	increased
5299	RATINSAB.PE1	nc	nc		gag	aga	increased
5300	RATINSAB.PE1	nc	nc		gag	aga	increased
5301	RATINSAB.PE1	nc	nc		gag	aga	increased
5302	RATINSAB.PE1	nc	nc		gga	cct	increased
5303	RATINSAB.PE1	nc	nc		gtt	agg	increased
5304	RATINSAB.PE1	nc	nc		gtt	agg	increased
5305	RATINSAB.PE1	nc	nc		gtt	agg	increased
5306	RATINSAB.PE1	nc	nc		gtt	agg	increased
5307	RATINSAB.PE1	nc	nc		gtt	agg	increased
5308	RATINSAB.PE1	nc	nc		gtt	agg	increased
5309	RATINSAB.PE1	nc	nc		gtt	agg	increased
5310	RATINSAB.PE1	nc	nc		gtt	agg	increased
5311	RATINSAB.PE1	nc	nc		gtt	agg	increased
5312	RATINSAB.PE1	nc	nc		gtt	agg	increased
5313	RATINSAB.PE1	nc	nc		agg	atc	increased
5314	RATINSAB.PE1	nc	nc		agg	atc	increased
5315	RATINSAB.PE1	nc	nc		agg	atc	increased
5316	RATINSAB.PE1	nc	nc		agg	atc	increased
5317	RATINSAB.PE1	nc	nc		agg	atc	increased
5318	RATINSAB.PE1	nc	nc		agg	atc	increased
5319	RATINSAB.PE1	nc	nc		agg	atc	increased
5320	RATINSAB.PE1	nc	nc		agg	atc	increased
5321	RATINSAB.PE1	nc	nc		aac	gga	increased
5322	RATIS2A.ISLET-2	islet-2	nc		agc	agt	No change
5323	RATIS2A.ISLET-2	islet-2	nc		acg	gtc	No change
5324	RATIS2A.ISLET-2	islet-2	nc		acg	gtc	No change
5325	RATIS2A.ISLET-2	islet-2	nc		acg	gtc	No change
5326	RATIS2A.ISLET-2	islet-2	nc		tga	ccg	No change
5327	RATIS2A.ISLET-2	islet-2	nc		tga	ccg	No change
5328	RATIS2A.ISLET-2	islet-2	nc		tga	ccg	No change
5329	RATISCOAD.PE1	nc	nc		cag	aga	increased
5330	RATISCOAD.PE1	nc	nc		cag	aga	increased
5331	RATISCOAD.PE1	nc	nc		cag	aga	increased
5332	RATISCOAD.PE1	nc	nc		cag	aga	increased
5333	RATISCOAD.PE1	nc	nc		cag	aga	increased
5334	RATKALGK3.PE1	nc	nc		tct	tgt	increased by mild

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
5335	Taq1	62	tgt	147.845	148	147.88	147.81	0	5 500 000	10 900 000	0	+-	A	A	A(2)
5336	Taq1	62	tgt	148.743	148	148.83	148.75	148.65	11 800 000	22 000 000	5 400 000	+-	A		A(2)
5337	Taq1	61	tct	147.96	148	148.04	147.78	148.06	3 000 000	12 800 000	5 500 000	+-	A	A	A(2)
5338	Taq1	62	tgt	147.845	148	147.88	147.81	0	5 500 000	10 900 000	0	+-	A	A	A(2)
5339	Taq1	62	tgt	148.743	148	148.83	148.75	148.65	11 800 000	22 000 000	5 400 000	+-	A		A(2)
5340	Hha1	3	aac	111.99	112	112.03	112.09	111.85	12 800 000	14 100 000	3 600 000	=-	\ (-)	(-)	-2
5341	Taq1	12	agt	112.097	112	112.11	112.08	112.1	11 900 000	6 200 000	73 600 000	=+	/ (-)	(-)	-2
5342	Hha1	59	ttc	218.29	219	218.29	0	0	187.2	0	0	-=	\		\(2)
5343	Taq1	19	cac	238.08	239	238.08	0	0	3 400 000	0	0	-=	\		\(2)
5344	Taq1	19	cac	239.115	239	239.08	0	239.15	4 000 000	0	3 100 000	-+(=)	V		\(2)
5345	Taq1	19	cac	240.17	239	0	0	240.17	0	0	3 600 000	=+	/		\(2)
5346	Taq1	31	gac	131.425	132	131.49	131.36	0	4 800 000	12 200 000	0	+-	A		A(2) \(2)
5347	Taq1	31	gac	132.45	132	132.57	132.33	0	14 200 000	8 500 000	0	=-	\		A(2) \(2)
5348	Taq1	36	ggt	131.78	132	131.74	131.82	0	12 300 000	28 700 000	0	+-	A		A(2) \(2)
5349	Taq1	36	ggt	132.707	132	132.69	132.69	132.74	26 200 000	38 000 000	7 200 000	=-	\ (-)		A(2) \(2)
5350	Hha1	27	acg	118.767	119	118.75	118.76	118.79	3 700 000	3 700 000	11 000 000	=+	/ (-)		-1,5
5351	Hha1	26	ctg	142.84	143	143.16	142.67	142.69	3 300 000	181 900 000	762 800 000	=+	/ (-)		-1,5
5352	Hha1	26	ctg	143.585	143	0	143.56	143.61	0	25 200 000	89 600 000	=+	/		-1,5
5353	Taq1	64	gtt	187.887	189	187.86	187.94	187.86	4 100 000	5 300 000	3 200 000	==	-		-1,5
5354	Taq1	64	gtt	188.893	189	188.94	188.86	188.88	4 800 000	5 800 000	4 100 000	==	-		-1,5
5355	Taq1	64	gtt	189.95	189	189.96	189.86	190.03	5 500 000	7 100 000	3 200 000	=-	\ (-)		-1,5
5356	Hha1	39	agg	117.867	118	118	117.99	117.61	373.9	352.25	410.97	==	-		-2
5357	Hha1	15	tac	130.033	130	130.01	130.03	130.06	23 000 000	26 600 000	38 100 000	==	-		-2
5358	Hha1	15	tac	130.067	130	130.11	130.03	130.06	5 207.24	6 850.37	8 286.21	==	-		-2
5359	Hha1	20	ctc	183.553	184	183.54	183.61	183.51	21 887.051	13 493.31	14 145.99	==	-		A(3)
5360	Hha1	20	ctc	184.51	184	0	184.55	184.47	0	1 101.49	1 932.25	+=	/		A(3)
5361	Taq1	45	gcc	184.95	186	184.95	0	0	4 700 000	0	0	-=	\		A(3)
5362	Taq1	45	gcc	185.625	186	0	185.49	185.76	0	8 600 000	3 100 000	+-	A		A(3)
5363	Taq1	45	gcc	186.905	186	186.86	186.95	0	10 000 000	4 500 000	0	--	\		A(3)
5364	Hha1	26	ctg	200.6	201	0	200.6	0	0	4 600 000	0	+-	A		A(3)
5365	Hha1	26	ctg	201.407	201	201.34	201.48	201.4	7 300 000	4 000 000	8 100 000	=+	/ (-)		A(3)
5366	Taq1	49	aaa	457.63	458	0	457.63	0	0	3 300 000	0	+-	A		A(3)
5367	Taq1	49	aaa	458.63	458	458.63	0	0	10 600 000	0	0	-=	\		A(3)
5368	Taq1	8	gaa	112.65	113	112.65	112.65	0	3 000 000	15 500 000	0	+-	A		A(3)
5369	Hha1	8	gaa	112.73	113	112.63	112.8	112.76	72 100 000	41 700 000	21 200 000	==	-		A(3)
5370	Taq1	39	agg	226.91	228	0	226.91	0	0	23 000 000	0	+-	A		A(3)
5371	Taq1	39	agg	228.995	228	228.85	229.14	0	15 000 000	29 200 000	0	+-	A		A(3)
5372	Taq1	39	agg	226.91	228	0	226.91	0	0	231.15	0	+-	A		A(3)
5373	Taq1	39	agg	228.995	228	228.85	229.14	0	557.04	293.47	0	--	\		A(3)
5374	Taq1	50	aat	246.545	248	246.34	246.75	0	3 200 000	8 300 000	0	+-	A		A(3)
5375	Taq1	50	aat	247.46	248	247.45	247.47	0	6 900 000	7 700 000	0	=-	\		A(3)
5376	Taq1	50	aat	248.04	248	248.04	0	0	13 800 000	0	0	-=	\		A(3)
5377	Taq1	50	aat	249.1	248	249.1	0	0	7 800 000	0	0	-=	\		A(3)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
5335	RATKALGK3.PE1	nc	nc		tct	tgt	increased by mild
5336	RATKALGK3.PE1	nc	nc		tct	tgt	increased by mild
5337	RATKALPS.PE1	nc	nc	*	tct	tgt	increased by mild
5338	RATKALPS.PE1	nc	nc	*	tct	tgt	increased by mild
5339	RATKALPS.PE1	nc	nc	*	tct	tgt	increased by mild
5340	RATKCHAN.PE1	nc	nc		aac	agt	No change
5341	RATKCHAN.PE1	nc	nc		aac	agt	No change
5342	RATKZPA.PE1	nc	nc		aga	ttc	increased
5343	RATKZPA.PE1	nc	nc		cac	gca	increased
5344	RATKZPA.PE1	nc	nc		cac	gca	increased
5345	RATKZPA.PE1	nc	nc		cac	gca	increased
5346	RATLGP120.PE1	nc	nc		ggt	gac	increased by mild
5347	RATLGP120.PE1	nc	nc		ggt	gac	increased by mild
5348	RATLGP120.PE1	nc	nc		ggt	gac	increased by mild
5349	RATLGP120.PE1	nc	nc		ggt	gac	increased by mild
5350	RATLIM2A.LIM-2	lim-2	nc		acg	caa	No change
5351	RATLIM2A.LIM-2	lim-2	nc		gtg	ctg	No change
5352	RATLIM2A.LIM-2	lim-2	nc		gtg	ctg	No change
5353	RATLIM2A.LIM-2	lim-2	nc		cga	gtt	No change
5354	RATLIM2A.LIM-2	lim-2	nc		cga	gtt	No change
5355	RATLIM2A.LIM-2	lim-2	nc		cga	gtt	No change
5356	RATMBPM.PE1	nc	nc		agg	ttc	No change
5357	RATMBPM.PE1	nc	nc		tac	tcc	No change
5358	RATMBPM.PE1	nc	nc		tac	tcc	No change
5359	RATMCR.PE1	nc	nc		ctc	tgt	increased by mild
5360	RATMCR.PE1	nc	nc		ctc	tgt	increased by mild
5361	RATMCR.PE1	nc	nc		gcc	gag	increased by mild
5362	RATMCR.PE1	nc	nc		gcc	gag	increased by mild
5363	RATMCR.PE1	nc	nc		gcc	gag	increased by mild
5364	RATMCR.PE1	nc	nc		tcc	ctg	increased by mild
5365	RATMCR.PE1	nc	nc		tcc	ctg	increased by mild
5366	RATMCR.PE1	nc	nc		aaa	ctt	increased by mild
5367	RATMCR.PE1	nc	nc		aaa	ctt	increased by mild
5368	RATMEH8.PE1	nc	nc		gaa	tat	increased by mild
5369	RATMEH8.PE1	nc	nc		gaa	tat	increased by mild
5370	RATMEH8.PE1	nc	nc		agg	ggg	increased by mild
5371	RATMEH8.PE1	nc	nc		agg	ggg	increased by mild
5372	RATMEH8.PE1	nc	nc		agg	ggg	increased by mild
5373	RATMEH8.PE1	nc	nc		agg	ggg	increased by mild
5374	RATMEH8.PE1	nc	nc		ttc	aat	increased by mild
5375	RATMEH8.PE1	nc	nc		ttc	aat	increased by mild
5376	RATMEH8.PE1	nc	nc		ttc	aat	increased by mild
5377	RATMEH8.PE1	nc	nc		ttc	aat	increased by mild

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
5378	Taq1	50	aat	249.26	248	249.26	0	0	7 400 000	0	0	-=	\		A(3)
5379	Hha1	15	tac	179.05	178	0	0	179.05	0	0	3 900 000	=+	/		/(2)
5380	Hha1	39	agg	176.94	178	0	177.1	176.78	0	310.46	236	+=	/		/(2)
5381	Hha1	39	agg	178.22	178	0	178.4	178.04	0	220.9	183.1	+=	/		/(2)
5382	Hha1	26	ctg	130	130	130	0	0	3 500 000	0	0	-=	\	\	\(2)
5383	Hha1	39	agg	129.775	130	129.85	129.7	0	285.92	298.52	0	=-	\	\	\(2)
5384	Hha1	39	agg	130.465	130	0	130.65	130.28	0	191.05	280.76	+=	/		\(2)
5385	Hha1	6	aga	130.145	130	130.36	129.93	0	28 200 000	3 400 000	0	-=	\		\(4) -(3)
5386	Taq1	64	gtt	129.74	130	129.77	129.71	129.74	7 500 000	9 600 000	6 600 000	==	-		\(4) -(3)
5387	Taq1	64	gtt	130.757	130	130.75	130.72	130.8	12 400 000	12 600 000	3 700 000	=-	\ (-)		\(4) -(3)
5388	Hha1	25	cag	174.66	175	174.66	0	0	6 700 000	0	0	-=	\		\(4) -(3)
5389	Hha1	25	cag	175.753	175	175.72	175.75	175.79	89 200 000	58 200 000	14 800 000	=-	\ (-)		\(4) -(3)
5390	Taq1	54	ttt	175.21	176	175.21	0	0	1 485.79	0	0	-=	\		\(4) -(3)
5391	Taq1	54	ttt	176.213	176	176.14	176.26	176.24	1 449.38	952.6	856.53	==	-		\(4) -(3)
5392	Hha1	6	aga	130.145	130	130.36	129.93	0	28 200 000	3 400 000	0	-=	\		\(4) -(3)
5393	Taq1	64	gtt	129.74	130	129.77	129.71	129.74	7 500 000	9 600 000	6 600 000	==	-		\(4) -(3)
5394	Taq1	64	gtt	130.757	130	130.75	130.72	130.8	12 400 000	12 600 000	3 700 000	=-	\ (-)		\(4) -(3)
5395	Hha1	25	cag	174.66	175	174.66	0	0	6 700 000	0	0	-=	\		\(4) -(3)
5396	Hha1	25	cag	175.753	175	175.72	175.75	175.79	89 200 000	58 200 000	14 800 000	=-	\ (-)		\(4) -(3)
5397	Taq1	54	ttt	175.21	176	175.21	0	0	1 485.79	0	0	-=	\		\(4) -(3)
5398	Taq1	54	ttt	176.213	176	176.14	176.26	176.24	1 449.38	952.6	856.53	==	-		\(4) -(3)
5399	Taq1	12	agt	131.217	132	131.2	131.21	131.24	8 300 000	5 400 000	8 600 000	==	-		-1,5
5400	Taq1	12	agt	132.203	132	132.2	132.17	132.24	11 600 000	7 200 000	31 700 000	=+	/ (-)		-1,5
5401	Taq1	17	cca	131.723	132	131.79	131.65	131.73	1 983	1 023.8	1 653.88	-=	\ (-)		-1,5
5402	Taq1	17	cca	132.685	132	0	132.57	132.8	0	2 047.6	661.55	+-	A		-1,5
5403	Taq1	54	ttt	178.38	179	178.48	178.25	178.41	655.49	364.57	770.87	=+	/ (-)		-1,5
5404	Taq1	54	ttt	179.44	179	0	179.52	179.36	0	1 517.11	1 284.79	+=	/		-1,5
5405	Hha1	56	tga	119.6	120	119.85	119.35	0	9 704.57	225.67	0	-=	\		\(2) A(2)
5406	Hha1	56	tga	119.71	120	0	119.71	0	0	297.22	0	+-	A		\(2) A(2)
5407	Hha1	59	ttc	119.5	120	119.76	119.46	119.28	410.81	376.56	250.95	==	-		\(2) A(2)
5408	Hha1	59	ttc	120.06	120	0	120.06	0	0	218.46	0	+-	A		\(2) A(2)
5409	Hha1	59	ttc	120.7	120	120.7	0	0	956.83	0	0	-=	\		\(2) A(2)
5410	Hha1	60	ttg	138.24	139	138.26	0	138.22	6 100 000	0	10 800 000	-+(=)	V		\(2)
5411	Hha1	60	ttg	139.01	139	139.01	0	0	5 700 000	0	0	-=	\		\(2)
5412	Hha1	60	ttg	139.747	139	139.91	139.73	139.6	3 000 000	10 600 000	4 400 000	+-	A		\(2)
5413	Hha1	59	ttc	189.127	190	189.18	189.08	189.12	509.62	129.35	183.68	-=	\ (-)		\(2)
5414	Hha1	59	ttc	189.69	190	0	189.52	189.86	0	152.35	1 249.57	=+	/		\(2)
5415	Hha1	59	ttc	190.04	190	190.04	0	0	327.61	0	0	-=	\		\(2)
5416	Taq1	55	tca	60.73	61	60.73	0	0	3 700 000	0	0	-=	\		\(8)
5417	Hha1	41	ccc	101.02	101	101.06	101.22	100.78	40 900 000	5 400 000	4 600 000	-=	\ (-)		\(8)
5418	Hha1	41	ccc	101.51	101	0	0	101.51	0	0	5 200 000	=+	/		\(8)
5419	Hha1	56	tga	110.727	111	110.67	110.86	110.65	404.52	4 023.55	5 378.38	+=	/ (-)		\(8)
5420	Hha1	56	tga	111.28	111	111.28	0	0	645.6	0	0	-=	\		\(8)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
5378	RATMEH8.PE1	nc	nc		ttc	aat	increased by mild
5379	RATMHCIAB.PE1	nc	nc		tac	agg	decreased
5380	RATMHCIAB.PE1	nc	nc		tac	agg	decreased
5381	RATMHCIAB.PE1	nc	nc		tac	agg	decreased
5382	RATMHREC.PE1	nc	nc		ctg	agg	increased
5383	RATMHREC.PE1	nc	nc		ctg	agg	increased
5384	RATMHREC.PE1	nc	nc		ctg	agg	increased
5385	RATMLCA5.PE1	nc	nc		gtt	aga	increased
5386	RATMLCA5.PE1	nc	nc		gtt	aga	increased
5387	RATMLCA5.PE1	nc	nc		gtt	aga	increased
5388	RATMLCA5.PE1	nc	nc		cag	ttt	increased
5389	RATMLCA5.PE1	nc	nc		cag	ttt	increased
5390	RATMLCA5.PE1	nc	nc		cag	ttt	increased
5391	RATMLCA5.PE1	nc	nc		cag	ttt	increased
5392	RATMLCA5.PE2	nc	nc		gtt	aga	increased
5393	RATMLCA5.PE2	nc	nc		gtt	aga	increased
5394	RATMLCA5.PE2	nc	nc		gtt	aga	increased
5395	RATMLCA5.PE2	nc	nc		cag	ttt	increased
5396	RATMLCA5.PE2	nc	nc		cag	ttt	increased
5397	RATMLCA5.PE2	nc	nc		cag	ttt	increased
5398	RATMLCA5.PE2	nc	nc		cag	ttt	increased
5399	RATMTCYOR.PE1	cytochrome o	nc		cca	agt	No change
5400	RATMTCYOR.PE1	cytochrome o	nc		cca	agt	No change
5401	RATMTCYOR.PE1	cytochrome o	nc		cca	agt	No change
5402	RATMTCYOR.PE1	cytochrome o	nc		cca	agt	No change
5403	RATMTCYOR.PE1	cytochrome o	nc		gta	ttt	No change
5404	RATMTCYOR.PE1	cytochrome o	nc		gta	ttt	No change
5405	RATMYH.PE1	nc	nc		tga	ttc	increased
5406	RATMYH.PE1	nc	nc		tga	ttc	increased
5407	RATMYH.PE1	nc	nc		tga	ttc	increased
5408	RATMYH.PE1	nc	nc		tga	ttc	increased
5409	RATMYH.PE1	nc	nc		tga	ttc	increased
5410	RATMYHCB.PE1	nc	nc		atc	ttg	increased
5411	RATMYHCB.PE1	nc	nc		atc	ttg	increased
5412	RATMYHCB.PE1	nc	nc		atc	ttg	increased
5413	RATMYHCB.PE1	nc	nc		atg	ttc	increased
5414	RATMYHCB.PE1	nc	nc		atg	ttc	increased
5415	RATMYHCB.PE1	nc	nc		atg	ttc	increased
5416	RATNESTIN.PE1	nc	nc		tca	gct	increased
5417	RATNESTIN.PE1	nc	nc		gtg	ccc	increased
5418	RATNESTIN.PE1	nc	nc		gtg	ccc	increased
5419	RATNESTIN.PE1	nc	nc		agt	tga	increased
5420	RATNESTIN.PE1	nc	nc		agt	tga	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
5421	Hha1	20	ctc	126.45	126	126.46	126.33	126.56	557.85	498.29	1 514.79	=+	/ (-)		\(8)
5422	Hha1	20	ctc	126.57	126	0	126.57	0	0	576.97	0	+-	A		\(8)
5423	Hha1	44	cgg	134.697	135	134.72	134.74	134.63	10 900 000	10 200 000	4 800 000	=-	\ (-)		\(8)
5424	Hha1	44	cgg	135.66	135	135.85	135.49	135.64	5 600 000	4 600 000	4 100 000	==	-		\(8)
5425	Hha1	31	gac	135.227	136	135.24	135.15	135.29	14 800 000	7 100 000	50 500 000	=+	/ (-)		\(8)
5426	Hha1	31	gac	135.94	136	135.93	135.95	0	16 300 000	11 000 000	0	=-	\		\(8)
5427	Taq1	47	ggc	158.34	159	158.34	0	0	1 969.23	0	0	-=	\		\(8)
5428	Hha1	7	caa	186.09	187	0	186.06	186.12	0	9 200 000	12 500 000	+=	/		\(8)
5429	Taq1	7	caa	186.42	187	186.42	0	0	3 100 000	0	0	-=	\		\(8)
5430	Hha1	7	caa	187.055	187	0	187.08	187.03	0	4 300 000	6 400 000	+=	/		\(8)
5431	Hha1	7	caa	187.67	187	187.67	0	0	5 200 000	0	0	-=	\		\(8)
5432	Taq1	7	caa	187.39	187	0	187.39	0	0	5 200 000	0	+-	A		\(8)
5433	Taq1	64	gtt	186.947	187	186.97	186.95	186.92	6 000 000	5 200 000	3 500 000	==	-		\(8)
5434	Taq1	64	gtt	187.887	187	187.86	187.94	187.86	4 100 000	5 300 000	3 200 000	==	-		\(8)
5435	Hha1	60	ttg	122.305	123	0	122.55	122.06	0	20 300 000	3 500 000	+-	A		A(2)
5436	Hha1	60	ttg	122.59	123	122.59	0	0	18 500 000	0	0	-=	\		A(2)
5437	Hha1	60	ttg	123.095	123	123.08	0	123.11	39 900 000	0	29 400 000	-+(=)	V		A(2)
5438	Hha1	61	tct	122.83	123	0	122.84	122.82	0	28 400 000	14 800 000	+-	A		A(2)
5439	Hha1	40	tgg	123.29	124	0	123.13	123.45	0	6 200 000	4 300 000	+=	/		A(2)
5440	Hha1	39	agg	88.14	88	88.14	0	0	755.13	0	0	-=	\		\(3)
5441	Hha1	61	tct	138.613	139	138.54	138.59	138.71	62 000 000	9 200 000	22 400 000	-=	\ (-)		\(3)
5442	Hha1	61	tct	139.377	139	139.61	139.14	139.38	8 000 000	6 200 000	3 900 000	==	-		\(3)
5443	Hha1	61	tct	139.377	140	139.61	139.14	139.38	8 000 000	6 200 000	3 900 000	==	-		\(3)
5444	Hha1	61	tct	140.07	140	0	140.07	0	0	3 400 000	0	+-	A		\(3)
5445	Hha1	33	agc	143.23	144	143.2	143.26	0	6 800 000	5 700 000	0	=-	\		\(3)
5446	Hha1	33	agc	144.21	144	144.2	0	144.22	4 000 000	0	3 500 000	-+(=)	V		\(3)
5447	Hha1	61	tct	138.613	139	138.54	138.59	138.71	62 000 000	9 200 000	22 400 000	-=	\ (-)		-(2) \(2)
5448	Hha1	61	tct	139.377	139	139.61	139.14	139.38	8 000 000	6 200 000	3 900 000	==	-		-(2) \(2)
5449	Hha1	61	tct	139.377	140	139.61	139.14	139.38	8 000 000	6 200 000	3 900 000	==	-		-(2) \(2)
5450	Hha1	61	tct	140.07	140	0	140.07	0	0	3 400 000	0	+-	A		-(2) \(2)
5451	Hha1	33	agc	143.23	144	143.2	143.26	0	6 800 000	5 700 000	0	=-	\		-(2) \(2)
5452	Hha1	33	agc	144.21	144	144.2	0	144.22	4 000 000	0	3 500 000	-+(=)	V		-(2) \(2)
5453	Taq1	14	gat	175.757	175	175.7	175.7	175.87	7 200 000	7 200 000	4 900 000	==	-	-	
5454	Taq1	63	ctt	175.553	175	175.54	175.49	175.63	3 000 000	3 300 000	3 200 000	==	-	-	
5455	Hha1	61	tct	189.98	190	190.02	189.96	189.96	4 700 000	4 900 000	3 900 000	==	-	(-)	
5456	Hha1	49	aaa	189.967	191	189.91	189.98	190.01	22 700 000	39 700 000	5 300 000	=-	\ (-)	(-)	
5457	Hha1	33	agc	126.01	126	126.01	0	0	5 100 000	0	0	-=	\		\(2)
5458	Hha1	59	ttc	125.685	126	125.59	125.78	0	213.2	218.46	0	=-	\		\(2)
5459	Hha1	59	ttc	126.15	126	126.16	0	126.14	161.2	0	95.72	-+(=)	V		\(2)
5460	Hha1	44	cgg	89.545	90	89.53	89.56	0	6 000 000	18 100 000	0	+-	A		/(4)
5461	Taq1	50	aat	95.223	95	95.19	95.24	95.24	68 800 000	12 500 000	27 000 000	-=	\ (-)		/(4)
5462	Hha1	26	ctg	100.685	101	100.5	100.87	0	3 700 000	5 800 000	0	=-	\		/(4)
5463	Hha1	26	ctg	101.59	101	0	101.49	101.69	0	3 900 000	9 000 000	=+	/		/(4)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
5421	RATNESTIN.PE1	nc	nc		ctc	cac	increased
5422	RATNESTIN.PE1	nc	nc		ctc	cac	increased
5423	RATNESTIN.PE1	nc	nc		gac	cgg	increased
5424	RATNESTIN.PE1	nc	nc		gac	cgg	increased
5425	RATNESTIN.PE1	nc	nc		gac	cgg	increased
5426	RATNESTIN.PE1	nc	nc		gac	cgg	increased
5427	RATNESTIN.PE1	nc	nc		ggc	gtg	increased
5428	RATNESTIN.PE1	nc	nc		caa	gtt	increased
5429	RATNESTIN.PE1	nc	nc		caa	gtt	increased
5430	RATNESTIN.PE1	nc	nc		caa	gtt	increased
5431	RATNESTIN.PE1	nc	nc		caa	gtt	increased
5432	RATNESTIN.PE1	nc	nc		caa	gtt	increased
5433	RATNESTIN.PE1	nc	nc		caa	gtt	increased
5434	RATNESTIN.PE1	nc	nc		caa	gtt	increased
5435	RATNEURA.PE1	nc	nc		tct	ttg	increased by mild
5436	RATNEURA.PE1	nc	nc		tct	ttg	increased by mild
5437	RATNEURA.PE1	nc	nc		tct	ttg	increased by mild
5438	RATNEURA.PE1	nc	nc		tct	ttg	increased by mild
5439	RATNEURA.PE1	nc	nc		tgg	gat	increased by mild
5440	RATNFHPEP.PE1	nc	nc		agg	cga	increased
5441	RATNFHPEP.PE1	nc	nc		tct	tgc	increased
5442	RATNFHPEP.PE1	nc	nc		tct	tgc	increased
5443	RATNFHPEP.PE1	nc	nc		tct	ggc	increased
5444	RATNFHPEP.PE1	nc	nc		tct	ggc	increased
5445	RATNFHPEP.PE1	nc	nc		agc	ata	increased
5446	RATNFHPEP.PE1	nc	nc		agc	ata	increased
5447	RATNFLH.PE1	nc	nc		tct	tgc	No change
5448	RATNFLH.PE1	nc	nc		tct	tgc	No change
5449	RATNFLH.PE1	nc	nc		tct	ggc	No change
5450	RATNFLH.PE1	nc	nc		tct	ggc	No change
5451	RATNFLH.PE1	nc	nc		agc	ata	No change
5452	RATNFLH.PE1	nc	nc		agc	ata	No change
5453	RATNFM.PE1	nc	nc		gat	ctt	No change
5454	RATNFM.PE1	nc	nc		gat	ctt	No change
5455	RATNFM.PE1	nc	nc		aaa	tct	No change
5456	RATNFM.PE1	nc	nc		aaa	tct	No change
5457	RATNKBNT4.PE1	nc	nc		agc	ttc	increased
5458	RATNKBNT4.PE1	nc	nc		agc	ttc	increased
5459	RATNKBNT4.PE1	nc	nc		agc	ttc	increased
5460	RATNPRC.NPR-C	NPR-C	nc		cgg	tcc	decreased
5461	RATNPRC.NPR-C	NPR-C	nc		ggg	aat	decreased
5462	RATNPRC.NPR-C	NPR-C	nc		ctg	ggc	decreased
5463	RATNPRC.NPR-C	NPR-C	nc		ctg	ggc	decreased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
5464	Taq1	40	tgg	105.95	106	0	0	105.95	0	0	39 700 000	=+	/		/(4)
5465	Hha1	40	tgg	133.193	133	133.22	133.26	133.1	3 800 000	8 000 000	6 900 000	+=	/ (-)	/	/(4)
5466	Hha1	58	gta	133.24	133	0	0	133.24	0	0	6 700 000	=+	/	/	/(4)
5467	Hha1	27	acg	136.03	136	135.97	136.09	0	3 200 000	3 600 000	0	=-	\		/(4)
5468	Taq1	8	gaa	108.56	109	0	0	108.56	0	0	3 500 000	=+	/		/(4)
5469	Hha1	8	gaa	108.69	109	108.71	108.68	108.68	32 100 000	14 200 000	11 800 000	-=	\ (-)		/(4)
5470	Hha1	8	gaa	109.37	109	0	0	109.37	0	0	14 800 000	=+	/		/(4)
5471	Taq1	17	cca	108.69	109	108.73	108.67	108.67	622.3	963.96	526.23	=-	\ (-)		/(4)
5472	Taq1	17	cca	109.613	109	109.48	109.66	109.7	812.7	365.64	526.23	-=	\ (-)		/(4)
5473	Hha1	11	act	238.51	239	0	0	238.51	0	0	3 200 000	=+	/		/(4)
5474	Taq1	11	act	239.28	239	0	0	239.28	0	0	3 000 000	=+	/		/(4)
5475	Taq1	8	gaa	108.56	109	0	0	108.56	0	0	3 500 000	=+	/		\(3)
5476	Hha1	8	gaa	108.69	109	108.71	108.68	108.68	32 100 000	14 200 000	11 800 000	-=	\ (-)		\(3)
5477	Hha1	8	gaa	109.37	109	0	0	109.37	0	0	14 800 000	=+	/		\(3)
5478	Taq1	17	cca	108.69	109	108.73	108.67	108.67	622.3	963.96	526.23	=-	\ (-)		\(3)
5479	Taq1	17	cca	109.613	109	109.48	109.66	109.7	812.7	365.64	526.23	-=	\ (-)		\(3)
5480	Taq1	12	agt	227.73	228	227.69	0	227.77	3 300 000	0	3 100 000	-+(=)	V		\(3)
5481	Taq1	12	agt	228.705	228	228.83	228.58	0	3 000 000	4 000 000	0	=-	\		\(3)
5482	Hha1	33	agc	62.84	63	62.76	62.92	62.84	4 400 000	18 500 000	17 900 000	+=	/ (-)		-(2) /(2) \(2)
5483	Hha1	20	ctc	74.577	75	74.85	74.49	74.39	3 567.49	773.66	763.35	-=	\ (-)		-(2) /(2) \(2)
5484	Hha1	20	ctc	74.93	75	0	75.01	74.85	0	1 363.75	894.56	+=	/		-(2) /(2) \(2)
5485	Hha1	33	agc	110.905	111	110.83	110.98	0	12 700 000	12 900 000	0	=-	\		-(2) /(2) \(2)
5486	Hha1	54	ttt	97.447	98	97.55	97.59	97.2	11 500 000	5 600 000	5 000 000	-=	\ (-)		\(2)
5487	Hha1	54	ttt	98.527	98	98.56	98.49	98.53	43 400 000	26 600 000	11 400 000	==	-		\(2)
5488	Hha1	54	ttt	169.61	170	0	0	169.61	0	0	3 800 000	=+	/		\(2)
5489	Hha1	54	ttt	170.915	170	170.89	170.94	0	3 800 000	4 400 000	0	=-	\		\(2)
5490	Taq1	12	agt	110.147	110	110.1	110.17	110.17	12 500 000	16 200 000	8 400 000	=-	\ (-)	\	
5491	Taq1	26	ctg	110.285	110	110.21	110.36	0	6 000 000	5 300 000	0	=-	\	\	
5492	Hha1	4	aag	139.233	139	139.25	139.24	139.21	79 200 000	14 200 000	43 900 000	-=	\ (-)	\	
5493	Taq1	12	agt	139.36	139	139.39	139.28	139.41	4 900 000	7 600 000	3 500 000	=-	\ (-)	\	
5494	Taq1	47	ggc	128.817	129	128.78	128.88	128.79	2 092.3	1 686.82	1 781.85	==	-		A(3)
5495	Taq1	17	cca	129.817	130	129.76	129.96	129.73	9 213.76	20 216.721	1 232.89	+-	A		A(3)
5496	Taq1	17	cca	130.707	130	130.74	130.57	130.81	31 337.939	2 526.25	796.87	-=	\ (-)		A(3)
5497	Taq1	39	agg	183.253	184	182.95	183.38	183.43	13 800 000	55 500 000	5 800 000	+-	A		A(3)
5498	Taq1	39	agg	183.535	184	183.64	0	183.43	5 400 000	0	170.83	-=(-)	\		A(3)
5499	Taq1	39	agg	184.48	184	184.38	184.58	0	7 100 000	8 600 000	0	=-	\		A(3)
5500	Taq1	39	agg	183.165	184	182.95	183.38	0	512.47	557.79	0	=-	\		A(3)
5501	Taq1	39	agg	183.64	184	183.64	0	0	200.53	0	0	-=	\		A(3)
5502	Taq1	39	agg	184.48	184	184.38	184.58	0	263.66	86.43	0	-=	\		A(3)
5503	Taq1	62	tgt	183.84	184	0	184.04	183.64	0	3 800 000	9 000 000	=+	/		A(3)
5504	Taq1	18	cct	252.35	253	0	252.35	0	0	3 300 000	0	+-	A		A(3)
5505	Hha1	33	agc	75.685	76	75.6	75.77	0	9 100 000	5 800 000	0	=-	\		\(3)
5506	Hha1	20	ctc	106.183	106	106.14	106.28	106.13	1 342.97	813	1 073.47	==	-		\(3)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
5464	RATNPRC.NPR-C	NPR-C	nc		ggt	tgg	decreased
5465	RATNPRC.NPR-C	NPR-C	nc		tgg	gta	decreased
5466	RATNPRC.NPR-C	NPR-C	nc		tgg	gta	decreased
5467	RATNPRC.NPR-C	NPR-C	nc		tgc	acg	decreased
5468	RATOAT2.OAT-2	OAT-2	nc		gaa	cca	decreased
5469	RATOAT2.OAT-2	OAT-2	nc		gaa	cca	decreased
5470	RATOAT2.OAT-2	OAT-2	nc		gaa	cca	decreased
5471	RATOAT2.OAT-2	OAT-2	nc		gaa	cca	decreased
5472	RATOAT2.OAT-2	OAT-2	nc		gaa	cca	decreased
5473	RATOAT2.OAT-2	OAT-2	nc		acg	act	decreased
5474	RATOAT2.OAT-2	OAT-2	nc		acg	act	decreased
5475	RATOTA.PE1	nc	nc		gaa	cca	increased
5476	RATOTA.PE1	nc	nc		gaa	cca	increased
5477	RATOTA.PE1	nc	nc		gaa	cca	increased
5478	RATOTA.PE1	nc	nc		gaa	cca	increased
5479	RATOTA.PE1	nc	nc		gaa	cca	increased
5480	RATOTA.PE1	nc	nc		gga	agt	increased
5481	RATOTA.PE1	nc	nc		gga	agt	increased
5482	RATOTCD.PE1	nc	nc		tgc	agc	No change
5483	RATOTCD.PE1	nc	nc		gga	ctc	No change
5484	RATOTCD.PE1	nc	nc		gga	ctc	No change
5485	RATOTCD.PE1	nc	nc		tgc	agc	No change
5486	RATP4505.PE1	nc	nc		ttt	aag	increased
5487	RATP4505.PE1	nc	nc		ttt	aag	increased
5488	RATP4505.PE1	nc	nc		ttt	agt	increased
5489	RATP4505.PE1	nc	nc		ttt	agt	increased
5490	RATPACE4A.PACE4	PACE4	nc		ctg	agt	increased
5491	RATPACE4A.PACE4	PACE4	nc		ctg	agt	increased
5492	RATPECG6.GTP	GTP	nc		aag	agt	increased
5493	RATPECG6.GTP	GTP	nc		aag	agt	increased
5494	RATPKCA.PE1	nc	nc		ggc	cca	increased by mild
5495	RATPKCA.PE1	nc	nc		ggc	cca	increased by mild
5496	RATPKCA.PE1	nc	nc		ggc	cca	increased by mild
5497	RATPKCA.PE1	nc	nc		agg	tgt	increased by mild
5498	RATPKCA.PE1	nc	nc		agg	tgt	increased by mild
5499	RATPKCA.PE1	nc	nc		agg	tgt	increased by mild
5500	RATPKCA.PE1	nc	nc		agg	tgt	increased by mild
5501	RATPKCA.PE1	nc	nc		agg	tgt	increased by mild
5502	RATPKCA.PE1	nc	nc		agg	tgt	increased by mild
5503	RATPKCA.PE1	nc	nc		agg	tgt	increased by mild
5504	RATPKCA.PE1	nc	nc		cct	tgg	increased by mild
5505	RATPKCI.PE1	nc	nc		agc	tct	increased
5506	RATPKCI.PE1	nc	nc		ctc	tgc	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
5507	Hha1	26	ctg	130.91	131	130.91	0	0	7 800 000	0	0	-=	\		\(3)
5508	Taq1	34	tgc	181.86	181	181.86	0	0	3 500 000	0	0	-=	\		\(3)
5509	Taq1	12	agt	100.297	100	100.31	100.28	100.3	8 100 000	5 300 000	13 800 000	=+	/ (-)		A(3)
5510	Taq1	52	att	118.39	119	0	0	118.39	0	0	5 000 000	=+	/		A(3)
5511	Taq1	52	att	118.9	119	118.9	118.9	0	4 000 000	7 700 000	0	+-	A		A(3)
5512	Taq1	52	att	119.57	119	0	0	119.57	0	0	8 500 000	=+	/		A(3)
5513	Hha1	60	ttg	193.14	194	0	193.14	0	0	4 900 000	0	+-	A		A(3)
5514	Hha1	60	ttg	195.08	194	0	195.08	0	0	3 200 000	0	+-	A		A(3)
5515	Hha1	26	ctg	231.04	232	0	231.04	0	0	3 600 000	0	+-	A		A(3)
5516	Taq1	45	gcc	237.79	238	237.79	0	0	3 100 000	0	0	-=	\		\(2)
5517	Hha1	8	gaa	238.66	239	238.83	238.49	0	4 500 000	3 100 000	0	=-	\		\(2)
5518	Hha1	22	tcc	135.305	136	0	135.43	135.18	0	8 700 000	5 000 000	+=	/		/(3) \(3)
5519	Taq1	22	tcc	135.645	136	135.57	0	135.72	6 100 000	0	38 300 000	=+(+)	/		/(3) \(3)
5520	Taq1	22	tcc	136.1	136	136.1	0	0	5 700 000	0	0	-=	\		/(3) \(3)
5521	Taq1	22	tcc	136.737	136	136.64	136.88	136.69	4 400 000	7 800 000	35 600 000	=+	/ (-)		/(3) \(3)
5522	Taq1	61	tct	135.837	136	135.78	135.92	135.81	3 700 000	12 300 000	15 600 000	+=	/ (-)		/(3) \(3)
5523	Taq1	45	gcc	237.79	238	237.79	0	0	3 100 000	0	0	-=	\		/(3) \(3)
5524	Hha1	8	gaa	238.66	239	238.83	238.49	0	4 500 000	3 100 000	0	=-	\		/(3) \(3)
5525	Hha1	22	tcc	135.305	136	0	135.43	135.18	0	8 700 000	5 000 000	+=	/		/(3) \(3)
5526	Taq1	22	tcc	135.645	136	135.57	0	135.72	6 100 000	0	38 300 000	=+(+)	/		/(3) \(3)
5527	Taq1	22	tcc	136.1	136	136.1	0	0	5 700 000	0	0	-=	\		/(3) \(3)
5528	Taq1	22	tcc	136.737	136	136.64	136.88	136.69	4 400 000	7 800 000	35 600 000	=+	/ (-)		/(3) \(3)
5529	Taq1	61	tct	135.837	136	135.78	135.92	135.81	3 700 000	12 300 000	15 600 000	+=	/ (-)		/(3) \(3)
5530	Taq1	45	gcc	237.79	238	237.79	0	0	3 100 000	0	0	-=	\		/(3) \(3)
5531	Hha1	8	gaa	238.66	239	238.83	238.49	0	4 500 000	3 100 000	0	=-	\		/(3) \(3)
5532	Hha1	22	tcc	135.305	136	0	135.43	135.18	0	8 700 000	5 000 000	+=	/		/(3) \(3)
5533	Taq1	22	tcc	135.645	136	135.57	0	135.72	6 100 000	0	38 300 000	=+(+)	/		/(3) \(3)
5534	Taq1	22	tcc	136.1	136	136.1	0	0	5 700 000	0	0	-=	\		/(3) \(3)
5535	Taq1	22	tcc	136.737	136	136.64	136.88	136.69	4 400 000	7 800 000	35 600 000	=+	/ (-)		/(3) \(3)
5536	Taq1	61	tct	135.837	136	135.78	135.92	135.81	3 700 000	12 300 000	15 600 000	+=	/ (-)		/(3) \(3)
5537	Taq1	45	gcc	237.79	238	237.79	0	0	3 100 000	0	0	-=	\		/(3) \(3)
5538	Hha1	8	gaa	238.66	239	238.83	238.49	0	4 500 000	3 100 000	0	=-	\		/(3) \(3)
5539	Hha1	6	aga	231.02	232	231.02	0	0	18 200 000	0	0	-=	\	\	
5540	Taq1	18	cct	230.87	232	230.87	0	0	3 200 000	0	0	-=	\	\	
5541	Hha1	49	aaa	273.86	274	0	273.86	0	0	5 200 000	0	+-	A		\(2)
5542	Hha1	49	aaa	274.57	274	0	274.57	0	0	8 600 000	0	+-	A		\(2)
5543	Hha1	49	aaa	275.36	274	275.36	0	0	3 600 000	0	0	-=	\		\(2)
5544	Hha1	49	aaa	328.75	329	328.73	328.77	0	17 900 000	9 100 000	0	--	\		\(2)
5545	Hha1	49	aaa	329.62	329	329.62	0	0	15 700 000	0	0	-=	\		\(2)
5546	Hha1	49	aaa	330.41	329	330.41	0	0	4 300 000	0	0	-=	\		\(2)
5547	Hha1	49	aaa	273.86	274	0	273.86	0	0	5 200 000	0	+-	A		\(2)
5548	Hha1	49	aaa	274.57	274	0	274.57	0	0	8 600 000	0	+-	A		\(2)
5549	Hha1	49	aaa	275.36	274	275.36	0	0	3 600 000	0	0	-=	\		\(2)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
5507	RATPKCI.PE1	nc	nc		ctg	aat	increased
5508	RATPKCI.PE1	nc	nc		ttg	tgc	increased
5509	RATPKCII.PE1	nc	nc		acg	agt	increased by mild
5510	RATPKCII.PE1	nc	nc		ccg	att	increased by mild
5511	RATPKCII.PE1	nc	nc		ccg	att	increased by mild
5512	RATPKCII.PE1	nc	nc		ccg	att	increased by mild
5513	RATPKCII.PE1	nc	nc		cct	ttg	increased by mild
5514	RATPKCII.PE1	nc	nc		cct	ttg	increased by mild
5515	RATPKCII.PE1	nc	nc		tgc	ctg	increased by mild
5516	RATPKL.PE1	nc	nc		gaa	gcc	increased
5517	RATPKL.PE1	nc	nc		gaa	gcc	increased
5518	RATPKLR.PE1	nc	nc	*	tct	tcc	decreased
5519	RATPKLR.PE1	nc	nc	*	tct	tcc	decreased
5520	RATPKLR.PE1	nc	nc	*	tct	tcc	decreased
5521	RATPKLR.PE1	nc	nc	*	tct	tcc	decreased
5522	RATPKLR.PE1	nc	nc	*	tct	tcc	decreased
5523	RATPKLR.PE1	nc	nc	*	gaa	gcc	decreased
5524	RATPKLR.PE1	nc	nc	*	gaa	gcc	decreased
5525	RATPKRL4.PE1	nc	nc		tct	tcc	decreased
5526	RATPKRL4.PE1	nc	nc		tct	tcc	decreased
5527	RATPKRL4.PE1	nc	nc		tct	tcc	decreased
5528	RATPKRL4.PE1	nc	nc		tct	tcc	decreased
5529	RATPKRL4.PE1	nc	nc		tct	tcc	decreased
5530	RATPKRL4.PE1	nc	nc		gaa	gcc	decreased
5531	RATPKRL4.PE1	nc	nc		gaa	gcc	decreased
5532	RATPKRL4.PE2	nc	nc		tct	tcc	decreased
5533	RATPKRL4.PE2	nc	nc		tct	tcc	decreased
5534	RATPKRL4.PE2	nc	nc		tct	tcc	decreased
5535	RATPKRL4.PE2	nc	nc		tct	tcc	decreased
5536	RATPKRL4.PE2	nc	nc		tct	tcc	decreased
5537	RATPKRL4.PE2	nc	nc		gaa	gcc	decreased
5538	RATPKRL4.PE2	nc	nc		gaa	gcc	decreased
5539	RATPPLCA.PE1	nc	nc		cct	aga	increased
5540	RATPPLCA.PE1	nc	nc		cct	aga	increased
5541	RATRAFA.PE1	nc	nc		cag	aaa	increased
5542	RATRAFA.PE1	nc	nc		cag	aaa	increased
5543	RATRAFA.PE1	nc	nc		cag	aaa	increased
5544	RATRAFA.PE1	nc	nc		aaa	gac	increased
5545	RATRAFA.PE1	nc	nc		aaa	gac	increased
5546	RATRAFA.PE1	nc	nc		aaa	gac	increased
5547	RATRAFB.PE1	nc	nc		cag	aaa	increased
5548	RATRAFB.PE1	nc	nc		cag	aaa	increased
5549	RATRAFB.PE1	nc	nc		cag	aaa	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
5550	Hha1	49	aaa	328.75	329	328.73	328.77	0	17 900 000	9 100 000	0	--	\		\(2)
5551	Hha1	49	aaa	329.62	329	329.62	0	0	15 700 000	0	0	-=	\		\(2)
5552	Hha1	49	aaa	330.41	329	330.41	0	0	4 300 000	0	0	-=	\		\(2)
5553	Hha1	60	ttg	117.71	118	117.87	117.49	117.77	4 900 000	4 100 000	3 800 000	==	-		-2
5554	Taq1	19	cac	126.637	127	126.66	126.65	126.6	3 100 000	5 000 000	20 700 000	=+	/ (-)		-2
5555	Taq1	19	cac	127.64	127	127.65	127.6	127.67	3 700 000	5 100 000	6 200 000	==	-		-2
5556	Hha1	11	act	190.187	190	190.1	190.23	190.23	5 600 000	5 800 000	4 300 000	==	-	-	
5557	Taq1	11	act	190.21	190	190.23	190.23	190.17	7 700 000	9 500 000	9 700 000	==	-	-	
5558	Hha1	44	cgg	242.14	243	242.19	242.08	242.15	38 600 000	5 400 000	22 100 000	-=	\ (-)		\(2)
5559	Hha1	44	cgg	243.22	243	0	0	243.22	0	0	5 400 000	=+	/		\(2)
5560	Hha1	54	ttt	244.455	245	244.49	0	244.42	30 800 000	0	11 200 000	-=(-)	\		\(2)
5561	Hha1	54	ttt	245.35	245	245.35	0	0	4 900 000	0	0	-=	\		\(2)
5562	Hha1	60	ttg	125.49	126	0	0	125.49	0	0	3 300 000	=+	/		/(2)
5563	Hha1	60	ttg	126.477	126	126.57	126.57	126.29	9 000 000	9 800 000	5 500 000	==	-		/(2)
5564	Hha1	54	ttt	217.985	218	0	217.83	218.14	0	4 100 000	3 900 000	+=	/		/(2)
5565	Hha1	54	ttt	218.97	218	218.97	0	0	3 700 000	0	0	-=	\		/(2)
5566	Hha1	26	ctg	97.47	97	0	97.47	0	0	4 100 000	0	+-	A		/(2)
5567	Hha1	59	ttc	97.02	97	0	97.18	96.86	0	114.98	385.48	=+	/		/(2)
5568	Hha1	59	ttc	188.09	189	188.19	188.04	188.04	1 180.44	741.63	388.06	==	-		/(2)
5569	Hha1	59	ttc	189.127	189	189.18	189.08	189.12	509.62	129.35	183.68	-=	\ (-)		/(2)
5570	Hha1	59	ttc	189.69	189	0	189.52	189.86	0	152.35	1 249.57	=+	/		/(2)
5571	Hha1	59	ttc	190.04	189	190.04	0	0	327.61	0	0	-=	\		/(2)
5572	Taq1	39	agg	61.033	61	61.09	61.22	60.79	83 000 000	79 000 000	10 400 000	=-	\ (-)		-5
5573	Taq1	39	agg	61.273	61	61.09	61.22	61.51	3 082.29	793.97	8 400 000	=+	/ (-)		-5
5574	Taq1	39	agg	60.79	61	0	0	60.79	0	0	306.33	=+	/		-5
5575	Taq1	39	agg	88.127	88	87.95	88.23	88.2	40 700 000	231 100 000	28 700 000	+-	A		-5
5576	Taq1	39	agg	88.127	88	87.95	88.23	88.2	1 511.43	2 322.63	845.36	=-	\ (-)		-5
5577	Hha1	8	gaa	94.14	94	94.11	94.17	94.14	38 500 000	28 500 000	13 400 000	==	-		-5
5578	Taq1	8	gaa	94.485	94	0	94.53	94.44	0	8 300 000	7 000 000	+=	/		-5
5579	Taq1	12	agt	94.09	94	94.19	94	94.08	4 500 000	5 100 000	27 200 000	=+	/ (-)		-5
5580	Hha1	39	agg	118.747	119	118.62	119	118.62	241.93	555.25	512.69	+=	/ (-)		-5
5581	Hha1	39	agg	119.115	119	118.93	0	119.3	234.6	0	146.48	-+(=)	V		-5
5582	Hha1	39	agg	119.21	119	119.01	0	119.41	234.6	0	130.2	-+(=)	V		-5
5583	Hha1	39	agg	119.58	119	0	119.61	119.55	0	274.64	146.48	+-	A		-5
5584	Hha1	28	tcg	159.14	160	0	159.14	0	0	3 600 000	0	+-	A		-5
5585	Hha1	6	aga	228.03	229	228.03	0	0	4 100 000	0	0	-=	\		-5
5586	Hha1	6	aga	228.935	229	228.92	228.95	0	74 800 000	6 100 000	0	-=	\		-5
5587	Taq1	56	tga	289.71	289	0	289.71	0	0	3 100 000	0	+-	A		-5
5588	Hha1	33	agc	182.18	183	0	0	182.18	0	0	6 800 000	=+	/		A(2)
5589	Hha1	33	agc	224.23	224	0	224.23	0	0	3 000 000	0	+-	A		A(2)
5590	Hha1	49	aaa	291.85	293	291.79	291.91	0	15 000 000	17 800 000	0	=-	\		A(2)
5591	Hha1	49	aaa	293.39	293	0	293.39	0	0	3 700 000	0	+-	A		A(2)
5592	Hha1	8	gaa	235.04	236	235.04	0	0	4 300 000	0	0	-=	\		\(4)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
5550	RATRAFB.PE1	nc	nc		aaa	gac	increased
5551	RATRAFB.PE1	nc	nc		aaa	gac	increased
5552	RATRAFB.PE1	nc	nc		aaa	gac	increased
5553	RATRIGF.PE1	nc	nc	*	aga	ttg	No change
5554	RATRIGF.PE1	nc	nc	*	cac	gct	No change
5555	RATRIGF.PE1	nc	nc	*	cac	gct	No change
5556	RATRPL18A.PE1	nc	nc		cca	act	No change
5557	RATRPL18A.PE1	nc	nc		cca	act	No change
5558	RATRPL19.PE1	nc	nc	*	cgg	ttt	increased
5559	RATRPL19.PE1	nc	nc	*	cgg	ttt	increased
5560	RATRPL19.PE1	nc	nc	*	cgg	ttt	increased
5561	RATRPL19.PE1	nc	nc	*	cgg	ttt	increased
5562	RATRPL7.PE1	nc	nc		tag	ttg	decreased
5563	RATRPL7.PE1	nc	nc		tag	ttg	decreased
5564	RATRPL7.PE1	nc	nc		aag	ttt	decreased
5565	RATRPL7.PE1	nc	nc		aag	ttt	decreased
5566	RATRPS6.PE1	nc	nc		ctg	ttc	decreased
5567	RATRPS6.PE1	nc	nc		ctg	ttc	decreased
5568	RATRPS6.PE1	nc	nc		cca	ttc	decreased
5569	RATRPS6.PE1	nc	nc		cca	ttc	decreased
5570	RATRPS6.PE1	nc	nc		cca	ttc	decreased
5571	RATRPS6.PE1	nc	nc		cca	ttc	decreased
5572	RATSCAL.PE1	nc	nc		cat	agg	No change
5573	RATSCAL.PE1	nc	nc		cat	agg	No change
5574	RATSCAL.PE1	nc	nc		cat	agg	No change
5575	RATSCAL.PE1	nc	nc		gac	agg	No change
5576	RATSCAL.PE1	nc	nc		gac	agg	No change
5577	RATSCAL.PE1	nc	nc		gaa	agt	No change
5578	RATSCAL.PE1	nc	nc		gaa	agt	No change
5579	RATSCAL.PE1	nc	nc		gaa	agt	No change
5580	RATSCAL.PE1	nc	nc		aga	agg	No change
5581	RATSCAL.PE1	nc	nc		aga	agg	No change
5582	RATSCAL.PE1	nc	nc		aga	agg	No change
5583	RATSCAL.PE1	nc	nc		aga	agg	No change
5584	RATSCAL.PE1	nc	nc		tcg	cga	No change
5585	RATSCAL.PE1	nc	nc		tgt	aga	No change
5586	RATSCAL.PE1	nc	nc		tgt	aga	No change
5587	RATSCAL.PE1	nc	nc		tga	gga	No change
5588	RATTAG1.PE1	nc	nc		agc	cac	increased by mild
5589	RATTAG1.PE1	nc	nc		agc	acg	increased by mild
5590	RATTAG1.PE1	nc	nc		aaa	acc	increased by mild
5591	RATTAG1.PE1	nc	nc		aaa	acc	increased by mild
5592	RATTDR.PE1	nc	nc		gaa	aaa	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
5593	Taq1	8	gaa	235.63	236	235.63	0	0	3 800 000	0	0	-=	\		\(4)
5594	Hha1	8	gaa	236.3	236	236.33	236.27	0	3 900 000	3 100 000	0	=-	\		\(4)
5595	Taq1	49	aaa	236.04	237	0	236.04	0	0	14 800 000	0	+-	A		\(4)
5596	Taq1	49	aaa	236.74	237	0	236.74	0	0	8 100 000	0	+-	A		\(4)
5597	Taq1	49	aaa	237.485	237	237.47	237.5	0	7 400 000	3 300 000	0	-=	\		\(4)
5598	Hha1	8	gaa	192.223	193	192.17	192.27	192.23	6 900 000	8 500 000	3 300 000	=-	\ (-)		\(3)
5599	Taq1	8	gaa	192.62	193	0	192.62	0	0	8 500 000	0	+-	A		\(3)
5600	Taq1	8	gaa	193.35	193	0	0	193.35	0	0	4 100 000	=+	/		\(3)
5601	Hha1	8	gaa	193.115	193	193.11	193.12	0	4 600 000	11 300 000	0	+-	A		\(3)
5602	Hha1	8	gaa	193.97	193	193.91	194.03	0	5 400 000	3 500 000	0	=-	\		\(3)
5603	Taq1	63	ctt	192.08	193	192.08	0	0	3 000 000	0	0	-=	\		\(3)
5604	Taq1	63	ctt	193.04	193	193.04	0	193.04	3 100 000	0	3 400 000	-+(=)	V		\(3)
5605	Hha1	27	acg	105.62	106	105.62	0	0	9 100 000	0	0	-=	\	\	-(2) \(2)
5606	Hha1	59	ttc	105.495	106	105.47	105.52	0	452.41	641.02	0	=-	\	\	-(2) \(2)
5607	Hha1	59	ttc	106.19	106	106.48	106.04	106.05	2 142.48	2 489.36	814.94	=-	\ (-)		-(2) \(2)
5608	Hha1	40	tgg	109.003	109	109.05	109.17	108.79	4 200 000	7 400 000	27 300 000	=+	/ (-)		-(2) \(2)
5609	Hha1	40	tgg	109.35	109	0	0	109.35	0	0	21 600 000	=+	/		-(2) \(2)
5610	Taq1	10	atg	269.56	270	269.56	0	0	3 400 000	0	0	-=	\		\(2)
5611	Taq1	10	atg	270.29	270	270.29	0	0	4 100 000	0	0	-=	\		\(2)
5612	Taq1	10	atg	271.23	270	271.23	0	0	7 000 000	0	0	-=	\		\(2)
5613	Taq1	52	att	269.97	271	269.97	0	0	3 100 000	0	0	-=	\		\(2)
5614	Taq1	52	att	271.23	271	0	0	271.23	0	0	8 300 000	=+	/		\(2)
5615	Taq1	49	aaa	431.27	431	0	431.27	0	0	3 100 000	0	+-	A		\(2)
5616	Taq1	8	gaa	87.73	88	87.91	87.49	87.79	5 300 000	38 700 000	32 000 000	+=	/ (-)		/(3)
5617	Taq1	11	act	118.163	118	118.16	118.03	118.3	3 300 000	4 500 000	29 900 000	=+	/ (-)		/(3)
5618	Taq1	17	cca	117.567	118	117.87	117.43	117.4	167.18	1 070.33	1 984.66	++	/		/(3)
5619	Taq1	17	cca	118.43	118	0	118.37	118.49	0	1 303.01	1 157.72	+=	/		/(3)
5620	Taq1	49	aaa	317.54	317	317.54	0	0	16 600 000	0	0	-=	\		/(3)
5621	Taq1	49	aaa	318.31	317	318.24	318.38	0	23 700 000	4 900 000	0	-=	\		/(3)
5622	Hha1	41	ccc	123.8	124	123.8	0	0	5 400 000	0	0	-=	\		A(2) \(2)
5623	Taq1	45	gcc	246.65	247	0	246.65	0	0	3 300 000	0	+-	A		A(2) \(2)
5624	Taq1	45	gcc	248.04	247	0	248.04	0	0	3 500 000	0	+-	A		A(2) \(2)
5625	Taq1	51	ata	278.34	280	278.34	0	0	3 500 000	0	0	-=	\		A(2) \(2)
5626	Taq1	51	ata	279.41	280	279.41	0	0	38 800 000	0	0	-=	\		A(2) \(2)
5627	Taq1	51	ata	281.25	280	0	281.25	0	0	21 000 000	0	+-	A		A(2) \(2)
5628	Hha1	39	agg	63.33	63	63.42	63.39	63.18	1 656.89	674.66	1 318.35	-=	\ (-)		\(9)
5629	Taq1	16	tag	100.56	100	0	100.56	100.56	0	3 600 000	5 300 000	+=	/		\(9)
5630	Hha1	43	cgc	99.97	100	99.92	100.02	0	25 600 000	8 600 000	0	-=	\		\(9)
5631	Taq1	56	tga	100.495	100	100.4	100.59	0	5 100 000	9 000 000	0	=-	\		\(9)
5632	Taq1	56	tga	99.73	100	0	99.73	0	0	4 600 000	0	+-	A		\(9)
5633	Hha1	26	ctg	109.847	110	109.83	109.83	109.88	4 200 000	6 200 000	4 100 000	==	-		\(9)
5634	Hha1	61	tct	120.8	121	0	120.8	0	0	4 300 000	0	+-	A		\(9)
5635	Hha1	2	tta	155.785	156	0	155.61	155.96	0	14 700 000	16 700 000	+=	/		\(9)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
5593	RATTDR.PE1	nc	nc		gaa	aaa	increased
5594	RATTDR.PE1	nc	nc		gaa	aaa	increased
5595	RATTDR.PE1	nc	nc		gaa	aaa	increased
5596	RATTDR.PE1	nc	nc		gaa	aaa	increased
5597	RATTDR.PE1	nc	nc		gaa	aaa	increased
5598	RATTHR.PE1	nc	nc		gaa	ctt	increased
5599	RATTHR.PE1	nc	nc		gaa	ctt	increased
5600	RATTHR.PE1	nc	nc		gaa	ctt	increased
5601	RATTHR.PE1	nc	nc		gaa	ctt	increased
5602	RATTHR.PE1	nc	nc		gaa	ctt	increased
5603	RATTHR.PE1	nc	nc		gaa	ctt	increased
5604	RATTHR.PE1	nc	nc		gaa	ctt	increased
5605	RATTOHA.PE1	nc	nc	*	ttc	acg	increased
5606	RATTOHA.PE1	nc	nc	*	ttc	acg	increased
5607	RATTOHA.PE1	nc	nc	*	ttc	acg	No change
5608	RATTOHA.PE1	nc	nc	*	cca	tgg	No change
5609	RATTOHA.PE1	nc	nc	*	cca	tgg	No change
5610	RATTPA14.PE1	nc	nc		att	atg	increased
5611	RATTPA14.PE1	nc	nc		att	atg	increased
5612	RATTPA14.PE1	nc	nc		att	atg	increased
5613	RATTPA14.PE1	nc	nc		att	atg	increased
5614	RATTPA14.PE1	nc	nc		att	atg	increased
5615	RATTPA14.PE1	nc	nc		aaa	tca	increased
5616	RATTROTB.PE1	nc	nc		gaa	tcc	decreased
5617	RATTROTB.PE1	nc	nc		cca	act	decreased
5618	RATTROTB.PE1	nc	nc		cca	act	decreased
5619	RATTROTB.PE1	nc	nc		cca	act	decreased
5620	RATTROTB.PE1	nc	nc		aaa	tgg	decreased
5621	RATTROTB.PE1	nc	nc		aaa	tgg	decreased
5622	RATUDPGT.PE1	nc	nc		ctc	ccc	increased by mild
5623	RATUDPGT.PE1	nc	nc		gcc	ccc	increased by mild
5624	RATUDPGT.PE1	nc	nc		gcc	ccc	increased by mild
5625	RATUDPGT.PE1	nc	nc		ata	tgg	increased by mild
5626	RATUDPGT.PE1	nc	nc		ata	tgg	increased by mild
5627	RATUDPGT.PE1	nc	nc		ata	tgg	increased by mild
5628	RATVGFA.VGF	VGF	nc		agg	tcc	increased
5629	RATVGFA.VGF	VGF	nc		tag	tga	increased
5630	RATVGFA.VGF	VGF	nc		aag	cgc	increased
5631	RATVGFA.VGF	VGF	nc		tag	tga	increased
5632	RATVGFA.VGF	VGF	nc		tag	tga	increased
5633	RATVGFA.VGF	VGF	nc		ctg	tgc	increased
5634	RATVGFA.VGF	VGF	nc		cag	tct	increased
5635	RATVGFA.VGF	VGF	nc		ccc	tta	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
5636	Hha1	2	tta	156.285	156	156.36	156.21	0	27 200 000	14 600 000	0	--	\		\(9)
5637	Hha1	27	acg	155.415	156	155.39	155.44	0	7 300 000	5 400 000	0	=-	\		\(9)
5638	Hha1	27	acg	156.153	156	155.98	156.15	156.33	7 500 000	3 100 000	9 300 000	-+	V		\(9)
5639	Hha1	40	tgg	156.92	156	156.76	156.92	157.08	5 700 000	6 000 000	3 800 000	==	-		\(9)
5640	Taq1	45	gcc	180.93	182	180.79	181.07	0	4 400 000	8 900 000	0	+-	A		\(9)
5641	Taq1	45	gcc	182.54	182	0	182.54	0	0	5 900 000	0	+-	A		\(9)
5642	Hha1	10	atg	181.97	183	181.97	0	0	4 200 000	0	0	-=	\		\(9)
5643	Taq1	10	atg	182.87	183	182.87	0	0	8 200 000	0	0	-=	\		\(9)
5644	Hha1	10	atg	182.99	183	182.99	0	0	4 100 000	0	0	-=	\		\(9)
5645	Taq1	45	gcc	237.79	237	237.79	0	0	3 100 000	0	0	-=	\		\(9)
5646	Taq1	41	ccc	98.63	99	0	0	98.63	0	0	3 400 000	=+	/		\(7)
5647	Hha1	43	cgc	107.03	107	106.98	107.08	0	6 700 000	8 500 000	0	=-	\		\(7)
5648	Hha1	43	cgc	107.583	107	107.51	107.56	107.68	10 100 000	13 700 000	4 700 000	=-	\ (-)		\(7)
5649	Hha1	41	ccc	111.88	112	111.85	111.91	0	30 900 000	15 000 000	0	--	\		\(7)
5650	Hha1	40	tgg	113.48	113	113.23	113.73	0	46 700 000	9 600 000	0	-=	\		\(7)
5651	Hha1	9	atc	116.84	117	116.77	116.91	0	11 800 000	3 800 000	0	-=	\	\	\(7)
5652	Taq1	9	atc	116.957	117	116.81	117.11	116.95	9 200 000	9 700 000	3 200 000	=-	\ (-)	\	\(7)
5653	Taq1	29	gca	117.307	117	117.28	117.32	117.32	11 500 000	6 300 000	11 400 000	-=	\ (-)		\(7)
5654	Hha1	43	cgc	131.81	132	131.81	0	0	23 000 000	0	0	-=	\		\(7)
5655	Hha1	43	cgc	132.783	132	132.94	132.9	132.51	35 700 000	56 900 000	9 400 000	=-	\ (-)		\(7)
5656	Hha1	58	gta	133.24	134	0	0	133.24	0	0	6 700 000	=+	/		\(7)
5657	Hha1	58	gta	134.137	134	134.18	134.07	134.16	4 800 000	4 600 000	17 900 000	=+	/ (-)		\(7)
5658	Hha1	33	agc	62.84	63	62.76	62.92	62.84	4 400 000	18 500 000	17 900 000	+=	/ (-)		-(2) /(2) \(2)
5659	Hha1	20	ctc	74.577	75	74.85	74.49	74.39	3 567.49	773.66	763.35	-=	\ (-)		-(2) /(2) \(2)
5660	Hha1	20	ctc	74.93	75	0	75.01	74.85	0	1 363.75	894.56	+=	/		-(2) /(2) \(2)
5661	Hha1	33	agc	110.905	111	110.83	110.98	0	12 700 000	12 900 000	0	=-	\		-(2) /(2) \(2)
5662	Taq1	8	gaa	112.65	113	112.65	112.65	0	3 000 000	15 500 000	0	+-	A		A(3)
5663	Hha1	8	gaa	112.73	113	112.63	112.8	112.76	72 100 000	41 700 000	21 200 000	==	-		A(3)
5664	Taq1	39	agg	226.91	228	0	226.91	0	0	23 000 000	0	+-	A		A(3)
5665	Taq1	39	agg	228.995	228	228.85	229.14	0	15 000 000	29 200 000	0	+-	A		A(3)
5666	Taq1	39	agg	226.91	228	0	226.91	0	0	231.15	0	+-	A		A(3)
5667	Taq1	39	agg	228.995	228	228.85	229.14	0	557.04	293.47	0	--	\		A(3)
5668	Taq1	50	aat	246.545	248	246.34	246.75	0	3 200 000	8 300 000	0	+-	A		A(3)
5669	Taq1	50	aat	247.46	248	247.45	247.47	0	6 900 000	7 700 000	0	=-	\		A(3)
5670	Taq1	50	aat	248.04	248	248.04	0	0	13 800 000	0	0	-=	\		A(3)
5671	Taq1	50	aat	249.1	248	249.1	0	0	7 800 000	0	0	-=	\		A(3)
5672	Taq1	50	aat	249.26	248	249.26	0	0	7 400 000	0	0	-=	\		A(3)
5673	Taq1	56	tga	131.19	131	0	0	131.19	0	0	4 700 000	=+	/		\(2)
5674	Taq1	54	ttt	131.605	132	131.49	131.72	0	1 369.26	870.28	0	=-	\		\(2)
5675	Taq1	54	ttt	132.08	132	132.08	0	0	859.43	0	0	-=	\		\(2)
5676	Taq1	54	ttt	132.51	132	132.51	0	0	677.34	0	0	-=	\		\(2)
5677	Hha1	26	ctg	239.63	239	239.63	0	0	12 600 000	0	0	-=	\		\(2)
5678	Taq1	56	tga	131.19	131	0	0	131.19	0	0	4 700 000	=+	/		\(2)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
5636	RATVGFA.VGF	VGF	nc		ccc	tta	increased
5637	RATVGFA.VGF	VGF	nc		tgg	acg	increased
5638	RATVGFA.VGF	VGF	nc		tgg	acg	increased
5639	RATVGFA.VGF	VGF	nc		tgg	acg	increased
5640	RATVGFA.VGF	VGF	nc		atg	gcc	increased
5641	RATVGFA.VGF	VGF	nc		atg	gcc	increased
5642	RATVGFA.VGF	VGF	nc		atg	gcc	increased
5643	RATVGFA.VGF	VGF	nc		atg	gcc	increased
5644	RATVGFA.VGF	VGF	nc		atg	gcc	increased
5645	RATVGFA.VGF	VGF	nc		gat	gcc	increased
5646	RATVHH1X.VHH-1	vhh-1	nc		gtg	ccc	increased
5647	RATVHH1X.VHH-1	vhh-1	nc		cgc	tgc	increased
5648	RATVHH1X.VHH-1	vhh-1	nc		cgc	tgc	increased
5649	RATVHH1X.VHH-1	vhh-1	nc		tgg	ccc	increased
5650	RATVHH1X.VHH-1	vhh-1	nc		tgg	ccc	increased
5651	RATVHH1X.VHH-1	vhh-1	nc		gca	atc	increased
5652	RATVHH1X.VHH-1	vhh-1	nc		gca	atc	increased
5653	RATVHH1X.VHH-1	vhh-1	nc		gca	atc	increased
5654	RATVHH1X.VHH-1	vhh-1	nc		cgc	gaa	increased
5655	RATVHH1X.VHH-1	vhh-1	nc		cgc	gaa	increased
5656	RATVHH1X.VHH-1	vhh-1	nc		gtg	gta	increased
5657	RATVHH1X.VHH-1	vhh-1	nc		gtg	gta	increased
5658	RATVPC.PE1	nc	nc		tgc	agc	No change
5659	RATVPC.PE1	nc	nc		gga	ctc	No change
5660	RATVPC.PE1	nc	nc		gga	ctc	No change
5661	RATVPC.PE1	nc	nc		tgc	agc	No change
5662	RATXEH.PE1	nc	nc		gaa	tat	increased by mild
5663	RATXEH.PE1	nc	nc		gaa	tat	increased by mild
5664	RATXEH.PE1	nc	nc		agg	ggg	increased by mild
5665	RATXEH.PE1	nc	nc		agg	ggg	increased by mild
5666	RATXEH.PE1	nc	nc		agg	ggg	increased by mild
5667	RATXEH.PE1	nc	nc		agg	ggg	increased by mild
5668	RATXEH.PE1	nc	nc		ttc	aat	increased by mild
5669	RATXEH.PE1	nc	nc		ttc	aat	increased by mild
5670	RATXEH.PE1	nc	nc		ttc	aat	increased by mild
5671	RATXEH.PE1	nc	nc		ttc	aat	increased by mild
5672	RATXEH.PE1	nc	nc		ttc	aat	increased by mild
5673	RN2258.PRX3A	Prx3A	nc		tga	ttt	increased
5674	RN2258.PRX3A	Prx3A	nc		tga	ttt	increased
5675	RN2258.PRX3A	Prx3A	nc		tga	ttt	increased
5676	RN2258.PRX3A	Prx3A	nc		tga	ttt	increased
5677	RN2258.PRX3A	Prx3A	nc		gag	ctg	increased
5678	RN2260.PRX3B	Prx3B	nc		tga	ttt	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
5679	Taq1	54	ttt	131.605	132	131.49	131.72	0	1 369.26	870.28	0	=-	\		\(2)
5680	Taq1	54	ttt	132.08	132	132.08	0	0	859.43	0	0	-=	\		\(2)
5681	Taq1	54	ttt	132.51	132	132.51	0	0	677.34	0	0	-=	\		\(2)
5682	Hha1	26	ctg	239.63	239	239.63	0	0	12 600 000	0	0	-=	\		\(2)
5683	Taq1	17	cca	98.473	99	98.22	98.62	98.58	376.16	1 369.49	3 638.55	=+	/ (-)		-4
5684	Taq1	63	ctt	99.183	99	99.12	99.35	99.08	3 300 000	4 000 000	3 000 000	==	-		-4
5685	Taq1	49	aaa	108.483	108	108.71	108.31	108.43	38 200 000	22 700 000	56 800 000	=+	/ (-)		-4
5686	Taq1	63	ctt	155.077	156	155.04	155.11	155.08	4 400 000	3 200 000	3 900 000	==	-		-4
5687	Taq1	63	ctt	156.055	156	156.03	0	156.08	3 600 000	0	3 200 000	-+(=)	V		-4
5688	Hha1	39	agg	106.243	106	106.2	106.36	106.17	1 217	12 305.21	14 347.33	+=	/ (-)		/(4)
5689	Taq1	31	gac	134.527	135	134.67	134.44	134.47	10 200 000	16 000 000	3 200 000	=-	\ (-)		/(4)
5690	Taq1	31	gac	135.577	135	135.72	135.49	135.52	11 900 000	8 500 000	6 100 000	==	-		/(4)
5691	Taq1	35	gga	134.85	135	0	0	134.85	0	0	7 700 000	=+	/		/(4)
5692	Hha1	2	tta	212.14	211	0	0	212.14	0	0	3 700 000	=+	/		/(4)
5693	Hha1	41	ccc	218.96	220	0	0	218.96	0	0	3 000 000	=+	/		/(4)
5694	Hha1	44	cgg	99.107	99	99.18	99	99.14	15 800 000	7 100 000	8 700 000	-=	\ (-)		-3
5695	Hha1	40	tgg	118.51	119	0	118.44	118.58	0	7 000 000	7 000 000	+=	/		-3
5696	Hha1	40	tgg	119.34	119	0	119.59	119.09	0	10 300 000	4 300 000	+-	A		-3
5697	Taq1	47	ggc	140.863	141	140.76	140.89	140.94	3 446.15	1 973.26	2 159.82	==	-		-3
5698	Taq1	62	tgt	141.58	142	0	141.63	141.53	0	4 700 000	29 100 000	=+	/		-3
5699	Taq1	62	tgt	142.67	142	142.75	142.75	142.51	5 200 000	9 500 000	70 300 000	=+	/ (-)		-3
5700	Hha1	7	caa	183.7	184	183.69	183.71	183.7	273 700 000	30 200 000	48 600 000	-=	\ (-)		\(2)
5701	Hha1	7	caa	184.9	184	184.58	185.08	185.04	10 200 000	9 700 000	12 800 000	==	-		\(2)
5702	Taq1	34	tgc	183.96	184	183.96	0	0	4 300 000	0	0	-=	\		\(2)
5703	Hha1	20	ctc	93.51	94	93.44	93.58	0	1 494.49	576.97	0	-=	\		\(3)
5704	Hha1	20	ctc	94.37	94	94.37	0	0	530.3	0	0	-=	\	\	\(3)
5705	Hha1	33	agc	94.285	94	94.26	94.31	0	4 500 000	3 800 000	0	=-	\	\	\(3)
5706	Hha1	44	cgg	174.45	175	0	174.45	0	0	3 800 000	0	+-	A		\(3)
5707	Hha1	44	cgg	175.29	175	175.29	0	0	12 200 000	0	0	-=	\		\(3)
5708	Hha1	39	agg	93.733	94	93.74	93.78	93.68	469.2	370.17	1 013.18	=+	/ (-)		-5
5709	Hha1	39	agg	94.175	94	94.17	0	94.18	300.58	0	203.45	-+(=)	V		-5
5710	Hha1	39	agg	94.28	94	0	0	94.28	0	0	276.69	=+	/		-5
5711	Hha1	40	tgg	106.01	106	106.04	105.8	106.19	81 800 000	135 500 000	216 000 000	==	-		-5
5712	Hha1	27	acg	110.98	111	111.02	110.89	111.03	26 500 000	9 300 000	29 400 000	-+	V		-5
5713	Hha1	28	tcg	110.803	111	110.66	110.9	110.85	4 200 000	8 900 000	17 200 000	=+	/ (-)		-5
5714	Hha1	43	cgc	112.583	112	112.63	112.59	112.53	98 500 000	133 800 000	31 700 000	=-	\ (-)	(-)	-5
5715	Hha1	56	tga	112.657	113	112.5	112.77	112.7	363.66	671.51	2 637.47	=+	/ (-)	(-)	-5
5716	Hha1	56	tga	113.573	113	113.53	113.49	113.7	429.04	726.55	3 464.91	=+	/ (-)		-5
5717	Hha1	44	cgg	144.455	145	144.66	144.25	0	4 900 000	3 900 000	0	=-	\		-5
5718	Hha1	44	cgg	144.72	145	0	144.72	0	0	4 100 000	0	+-	A		-5
5719	Hha1	26	ctg	146.06	146	0	146.06	0	0	3 800 000	0	+-	A		-5
5720	Taq1	31	gac	146.86	147	146.86	0	0	3 800 000	0	0	-=	\		A(3)
5721	Taq1	31	gac	147.65	147	0	147.65	0	0	4 500 000	0	+-	A		A(3)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
5679	RN2260.PRX3B	Prx3B	nc		tga	ttt	increased
5680	RN2260.PRX3B	Prx3B	nc		tga	ttt	increased
5681	RN2260.PRX3B	Prx3B	nc		tga	ttt	increased
5682	RN2260.PRX3B	Prx3B	nc		gag	ctg	increased
5683	RN2B1ANGN.PE1	2B1 antigen	nc		cca	ctt	No change
5684	RN2B1ANGN.PE1	2B1 antigen	nc		cca	ctt	No change
5685	RN2B1ANGN.PE1	2B1 antigen	nc		aaa	ttc	No change
5686	RN2B1ANGN.PE1	2B1 antigen	nc		taa	ctt	No change
5687	RN2B1ANGN.PE1	2B1 antigen	nc		taa	ctt	No change
5688	RNA1B.PE1	nc	nc		tcc	agg	decreased
5689	RNA1B.PE1	nc	nc		gga	gac	decreased
5690	RNA1B.PE1	nc	nc		gga	gac	decreased
5691	RNA1B.PE1	nc	nc		gga	gac	decreased
5692	RNA1B.PE1	nc	nc		tta	aca	decreased
5693	RNA1B.PE1	nc	nc		ctt	ccc	decreased
5694	RNALP.PE1	nc	nc		cgg	tca	No change
5695	RNALP.PE1	nc	nc		tgg	ata	No change
5696	RNALP.PE1	nc	nc		tgg	ata	No change
5697	RNALP.PE1	nc	nc		tgt	ggc	No change
5698	RNALP.PE1	nc	nc		tgt	ggc	No change
5699	RNALP.PE1	nc	nc		tgt	ggc	No change
5700	RNATPAHO.PE1	nc	nc		caa	tgc	increased
5701	RNATPAHO.PE1	nc	nc		caa	tgc	increased
5702	RNATPAHO.PE1	nc	nc		caa	tgc	increased
5703	RNCCKR.PE1	nc	nc	*	agc	ctc	increased
5704	RNCCKR.PE1	nc	nc	*	agc	ctc	increased
5705	RNCCKR.PE1	nc	nc	*	agc	ctc	increased
5706	RNCCKR.PE1	nc	nc	*	act	cgg	increased
5707	RNCCKR.PE1	nc	nc	*	act	cgg	increased
5708	RNCEBP.PE1	nc	nc		aac	agg	No change
5709	RNCEBP.PE1	nc	nc		aac	agg	No change
5710	RNCEBP.PE1	nc	nc		aac	agg	No change
5711	RNCEBP.PE1	nc	nc		tgg	ggg	No change
5712	RNCEBP.PE1	nc	nc		acg	tcg	No change
5713	RNCEBP.PE1	nc	nc		acg	tcg	No change
5714	RNCEBP.PE1	nc	nc		cgc	tga	No change
5715	RNCEBP.PE1	nc	nc		cgc	tga	No change
5716	RNCEBP.PE1	nc	nc		cgc	tga	No change
5717	RNCEBP.PE1	nc	nc		ctg	cgg	No change
5718	RNCEBP.PE1	nc	nc		ctg	cgg	No change
5719	RNCEBP.PE1	nc	nc		ctg	cgg	No change
5720	RNCMG1.PE1	nc	nc		gac	agg	increased by mild
5721	RNCMG1.PE1	nc	nc		gac	agg	increased by mild

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
5722	Taq1	39	agg	146.33	147	0	146.33	0	0	46 200 000	0	+-	A		A(3)
5723	Taq1	39	agg	147.14	147	0	147.14	0	0	45 500 000	0	+-	A		A(3)
5724	Taq1	39	agg	146.33	147	0	146.33	0	0	464.32	0	+-	A		A(3)
5725	Taq1	39	agg	147.14	147	0	147.14	0	0	457.29	0	+-	A		A(3)
5726	Hha1	27	acg	172.57	173	172.57	0	0	3 700 000	0	0	-=	\		A(3)
5727	Hha1	27	acg	173.78	173	173.78	0	0	3 300 000	0	0	-=	\		A(3)
5728	Hha1	32	gtc	172.36	173	0	172.36	0	0	366.22	0	+-	A		A(3)
5729	Hha1	32	gtc	173.56	173	173.55	173.54	173.59	860.49	773.14	529.48	==	-		A(3)
5730	Taq1	19	cac	231.985	233	0	231.98	231.99	0	4 000 000	3 200 000	+=	/		/(2)
5731	Taq1	19	cac	232.94	233	232.92	0	232.96	3 300 000	0	4 600 000	-+(=)	V		/(2)
5732	Taq1	19	cac	234.02	233	233.98	234.06	234.02	4 300 000	3 200 000	3 500 000	==	-		/(2)
5733	Taq1	56	tga	269.47	268	0	0	269.47	0	0	5 400 000	=+	/		/(2)
5734	Hha1	39	agg	85.905	86	0	86.1	85.71	0	991.1	895.18	+=	/		-3
5735	Hha1	39	agg	86.31	86	86.31	0	0	791.78	0	0	-=	\		-3
5736	Hha1	33	agc	88.273	88	88.16	88.2	88.46	57 000 000	40 900 000	16 400 000	==	-		-3
5737	Hha1	59	ttc	87.55	88	0	87.55	0	0	649.64	0	+-	A		-3
5738	Hha1	59	ttc	88.253	88	88.57	88.11	88.08	249.6	1 954.69	139.7	+-	A		-3
5739	Taq1	61	tct	97.33	97	97.22	97.46	97.31	10 400 000	16 700 000	28 600 000	==	-		-3
5740	Taq1	62	tgt	96.507	97	96.37	96.38	96.77	6 900 000	9 300 000	15 900 000	==	-		-3
5741	Taq1	62	tgt	97.33	97	97.16	97.5	0	5 900 000	12 100 000	0	+-	A		-3
5742	Taq1	62	tgt	97.34	97	97.34	0	0	5 600 000	0	0	-=	\		-3
5743	Hha1	39	agg	66.61	67	0	66.57	66.65	0	1 629.94	2 937.82	+=	/		\(9)
5744	Taq1	45	gcc	107.68	108	107.48	107.75	107.81	3 300 000	5 000 000	5 700 000	==	-		\(9)
5745	Taq1	20	ctc	109.57	109	109.51	109.63	0	9 800 000	7 200 000	0	=-	\		\(9)
5746	Taq1	45	gcc	108.68	109	108.65	108.71	0	4 600 000	7 200 000	0	=-	\		\(9)
5747	Taq1	45	gcc	109.61	109	0	0	109.61	0	0	4 400 000	=+	/		\(9)
5748	Taq1	17	cca	109.613	110	109.48	109.66	109.7	812.7	365.64	526.23	-=	\ (-)		\(9)
5749	Taq1	17	cca	110.54	110	110.47	110.61	0	631.58	1 123.52	0	=-	\		\(9)
5750	Hha1	44	cgg	153.04	153	152.99	153.15	152.98	15 500 000	6 400 000	8 600 000	-=	\ (-)		\(9)
5751	Taq1	17	cca	171.903	172	171.91	171.8	172	273.99	744.58	691.62	+=	/ (-)		\(9)
5752	Taq1	17	cca	172.895	172	0	172.79	173	0	432.12	1 022.4	=+	/		\(9)
5753	Taq1	17	cca	239.72	241	239.72	0	0	404.03	0	0	-=	\		\(9)
5754	Taq1	17	cca	242.14	241	242.14	0	0	143.96	0	0	-=	\		\(9)
5755	Taq1	51	ata	244.755	244	244.66	0	244.85	26 600 000	0	9 800 000	-=(-)	\		\(9)
5756	Taq1	45	gcc	265.42	267	265.42	0	0	3 600 000	0	0	-=	\		\(9)
5757	Taq1	45	gcc	265.96	267	0	265.96	0	0	3 300 000	0	+-	A		\(9)
5758	Taq1	39	agg	281.06	282	281.26	280.86	0	9 300 000	3 800 000	0	-=	\		\(9)
5759	Taq1	39	agg	282.4	282	0	282.4	0	0	7 200 000	0	+-	A		\(9)
5760	Taq1	39	agg	280.86	282	0	280.86	0	0	38.19	0	+-	A		\(9)
5761	Taq1	39	agg	282.4	282	0	282.4	0	0	72.36	0	+-	A		\(9)
5762	Taq1	39	agg	281.26	282	281.26	0	0	345.36	0	0	-=	\		\(9)
5763	Taq1	50	aat	282.41	283	282.41	0	0	7 600 000	0	0	-=	\		\(9)
5764	Hha1	44	cgg	99.107	99	99.18	99	99.14	15 800 000	7 100 000	8 700 000	-=	\ (-)		\(4)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
5722	RNCMG1.PE1	nc	nc		gac	agg	increased by mild
5723	RNCMG1.PE1	nc	nc		gac	agg	increased by mild
5724	RNCMG1.PE1	nc	nc		gac	agg	increased by mild
5725	RNCMG1.PE1	nc	nc		gac	agg	increased by mild
5726	RNCMG1.PE1	nc	nc		acg	gtc	increased by mild
5727	RNCMG1.PE1	nc	nc		acg	gtc	increased by mild
5728	RNCMG1.PE1	nc	nc		acg	gtc	increased by mild
5729	RNCMG1.PE1	nc	nc		acg	gtc	increased by mild
5730	RNCPPA.PE1	nc	nc	*	cac	gtc	decreased
5731	RNCPPA.PE1	nc	nc	*	cac	gtc	decreased
5732	RNCPPA.PE1	nc	nc	*	cac	gtc	decreased
5733	RNCPPA.PE1	nc	nc	*	tga	tcc	decreased
5734	RNDRPLA.DRPLA	DRPLA	nc		tgt	agg	No change
5735	RNDRPLA.DRPLA	DRPLA	nc		tgt	agg	No change
5736	RNDRPLA.DRPLA	DRPLA	nc		agc	ttc	No change
5737	RNDRPLA.DRPLA	DRPLA	nc		agc	ttc	No change
5738	RNDRPLA.DRPLA	DRPLA	nc		agc	ttc	No change
5739	RNDRPLA.DRPLA	DRPLA	nc		tgt	tct	No change
5740	RNDRPLA.DRPLA	DRPLA	nc		tgt	tct	No change
5741	RNDRPLA.DRPLA	DRPLA	nc		tgt	tct	No change
5742	RNDRPLA.DRPLA	DRPLA	nc		tgt	tct	No change
5743	RNFAS.PE1	nc	nc		ctg	agg	increased
5744	RNFAS.PE1	nc	nc		ctc	gcc	increased
5745	RNFAS.PE1	nc	nc		ctc	gcc	increased
5746	RNFAS.PE1	nc	nc		cca	gcc	increased
5747	RNFAS.PE1	nc	nc		cca	gcc	increased
5748	RNFAS.PE1	nc	nc		cca	gcc	increased
5749	RNFAS.PE1	nc	nc		cca	gcc	increased
5750	RNFAS.PE1	nc	nc		cgg	tgt	increased
5751	RNFAS.PE1	nc	nc		cca	ggg	increased
5752	RNFAS.PE1	nc	nc		cca	ggg	increased
5753	RNFAS.PE1	nc	nc		cat	cca	increased
5754	RNFAS.PE1	nc	nc		cat	cca	increased
5755	RNFAS.PE1	nc	nc		agc	ata	increased
5756	RNFAS.PE1	nc	nc		gcc	ggc	increased
5757	RNFAS.PE1	nc	nc		gcc	ggc	increased
5758	RNFAS.PE1	nc	nc		agg	aat	increased
5759	RNFAS.PE1	nc	nc		agg	aat	increased
5760	RNFAS.PE1	nc	nc		agg	aat	increased
5761	RNFAS.PE1	nc	nc		agg	aat	increased
5762	RNFAS.PE1	nc	nc		agg	aat	increased
5763	RNFAS.PE1	nc	nc		agg	aat	increased
5764	RNGDR.PE1	nc	nc		ggc	cgg	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
5765	Hha1	43	cgc	116.557	116	116.6	116.58	116.49	14 500 000	10 500 000	4 600 000	==	-		\(4)
5766	Hha1	44	cgg	148.03	148	148.24	147.82	0	3 000 000	3 700 000	0	=-	\		\(4)
5767	Hha1	26	ctg	149.125	149	149.11	149.14	0	5 200 000	3 800 000	0	=-	\		\(4)
5768	Hha1	31	gac	154.205	155	154.18	154.23	0	12 400 000	7 200 000	0	=-	\		\(4)
5769	Hha1	31	gac	155.33	155	155.33	0	0	8 400 000	0	0	-=	\		\(4)
5770	Hha1	44	cgg	99.107	99	99.18	99	99.14	15 800 000	7 100 000	8 700 000	-=	\ (-)		\(4)
5771	Hha1	43	cgc	116.557	116	116.6	116.58	116.49	14 500 000	10 500 000	4 600 000	==	-		\(4)
5772	Hha1	44	cgg	148.03	148	148.24	147.82	0	3 000 000	3 700 000	0	=-	\		\(4)
5773	Hha1	26	ctg	149.125	149	149.11	149.14	0	5 200 000	3 800 000	0	=-	\		\(4)
5774	Hha1	31	gac	154.205	155	154.18	154.23	0	12 400 000	7 200 000	0	=-	\		\(4)
5775	Hha1	31	gac	155.33	155	155.33	0	0	8 400 000	0	0	-=	\		\(4)
5776	Hha1	39	agg	103.52	104	0	103.55	103.49	0	179.11	122.07	+=	/		\(2)
5777	Hha1	39	agg	104.08	104	104.08	0	0	469.2	0	0	-=	\		\(2)
5778	Hha1	27	acg	165.945	166	165.91	0	165.98	4 000 000	0	3 400 000	-+(=)	V		\(2)
5779	Hha1	27	acg	166.62	166	166.62	0	0	3 100 000	0	0	-=	\		\(2)
5780	Hha1	39	agg	103.52	104	0	103.55	103.49	0	179.11	122.07	+=	/		\(2)
5781	Hha1	39	agg	104.08	104	104.08	0	0	469.2	0	0	-=	\		\(2)
5782	Hha1	27	acg	165.945	166	165.91	0	165.98	4 000 000	0	3 400 000	-+(=)	V		\(2)
5783	Hha1	27	acg	166.62	166	166.62	0	0	3 100 000	0	0	-=	\		\(2)
5784	Taq1	39	agg	102.46	103	0	102.46	0	0	56 100 000	0	+-	A		\(5)
5785	Taq1	39	agg	103.263	103	103.47	103.17	103.15	15 700 000	174 900 000	6 900 000	+-	A		\(5)
5786	Taq1	39	agg	102.46	103	0	102.46	0	0	563.82	0	+-	A		\(5)
5787	Taq1	39	agg	103.263	103	103.47	103.17	103.15	583.03	1 757.8	203.24	+-	A		\(5)
5788	Taq1	17	cca	149.32	150	149.32	0	0	1 170.29	0	0	-=	\		\(5)
5789	Taq1	17	cca	150.15	150	0	150.06	150.24	0	870.89	1 052.47	+=	/		\(5)
5790	Taq1	54	ttt	150.645	151	150.51	150.78	0	2 039.32	540.98	0	-=	\		\(5)
5791	Taq1	54	ttt	151.555	151	151.7	151.41	0	1 143.48	964.36	0	=-	\		\(5)
5792	Taq1	54	ttt	151.6	151	0	151.6	0	0	858.52	0	+-	A		\(5)
5793	Taq1	8	gaa	235.63	237	235.63	0	0	3 800 000	0	0	-=	\		\(5)
5794	Hha1	8	gaa	236.3	237	236.33	236.27	0	3 900 000	3 100 000	0	=-	\		\(5)
5795	Taq1	49	aaa	236.74	238	0	236.74	0	0	8 100 000	0	+-	A		\(5)
5796	Taq1	49	aaa	237.485	238	237.47	237.5	0	7 400 000	3 300 000	0	-=	\		\(5)
5797	Taq1	49	aaa	238.583	238	238.58	238.57	238.6	29 100 000	21 100 000	3 300 000	=-	\ (-)		\(5)
5798	Taq1	48	ggg	100.837	101	100.98	100.93	100.6	4 551.2	612.39	2 114.02	-=	\ (-)		\(2)
5799	Taq1	49	aaa	102.575	103	102.67	102.48	0	44 100 000	13 400 000	0	-=	\		\(2)
5800	Taq1	49	aaa	103.135	103	103.13	103.14	0	29 300 000	3 300 000	0	-=	\		\(2)
5801	Hha1	33	agc	75.685	76	75.6	75.77	0	9 100 000	5 800 000	0	=-	\		\(5) A(4)
5802	Hha1	59	ttc	159.255	160	159.3	159.21	0	161.2	166.72	0	=-	\		\(5) A(4)
5803	Hha1	59	ttc	160.1	160	0	160.1	0	0	120.73	0	+-	A		\(5) A(4)
5804	Hha1	59	ttc	160.46	160	0	160.31	160.61	0	89.11	85.37	+=	/		\(5) A(4)
5805	Taq1	44	cgg	178.5	179	0	178.5	0	0	861.38	0	+-	A		\(5) A(4)
5806	Taq1	44	cgg	179.575	179	179.48	179.67	0	343.71	488.12	0	=-	\		\(5) A(4)
5807	Taq1	23	cga	178.95	180	178.89	178.95	179.01	5 000 000	3 500 000	4 100 000	==	-		\(5) A(4)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
5765	RNGDR.PE1	nc	nc		cac	cgc	increased
5766	RNGDR.PE1	nc	nc		cgg	ctg	increased
5767	RNGDR.PE1	nc	nc		cgg	ctg	increased
5768	RNGDR.PE1	nc	nc		gac	ctt	increased
5769	RNGDR.PE1	nc	nc		gac	ctt	increased
5770	RNGDR1.PE1	nc	nc		ggc	cgg	increased
5771	RNGDR1.PE1	nc	nc		cac	cgc	increased
5772	RNGDR1.PE1	nc	nc		cgg	ctg	increased
5773	RNGDR1.PE1	nc	nc		cgg	ctg	increased
5774	RNGDR1.PE1	nc	nc		gac	ctt	increased
5775	RNGDR1.PE1	nc	nc		gac	ctt	increased
5776	RNGK2.PE1	nc	nc	*	agg	ggc	increased
5777	RNGK2.PE1	nc	nc	*	agg	ggc	increased
5778	RNGK2.PE1	nc	nc	*	acg	aca	increased
5779	RNGK2.PE1	nc	nc	*	acg	aca	increased
5780	RNGK3.PE1	nc	nc		agg	ggc	increased
5781	RNGK3.PE1	nc	nc		agg	ggc	increased
5782	RNGK3.PE1	nc	nc		acg	aca	increased
5783	RNGK3.PE1	nc	nc		acg	aca	increased
5784	RNGRP.PE1	nc	nc		agg	gct	increased
5785	RNGRP.PE1	nc	nc		agg	gct	increased
5786	RNGRP.PE1	nc	nc		agg	gct	increased
5787	RNGRP.PE1	nc	nc		agg	gct	increased
5788	RNGRP.PE1	nc	nc		cca	ttt	increased
5789	RNGRP.PE1	nc	nc		cca	ttt	increased
5790	RNGRP.PE1	nc	nc		cca	ttt	increased
5791	RNGRP.PE1	nc	nc		cca	ttt	increased
5792	RNGRP.PE1	nc	nc		cca	ttt	increased
5793	RNGRP.PE1	nc	nc		aaa	gaa	increased
5794	RNGRP.PE1	nc	nc		aaa	gaa	increased
5795	RNGRP.PE1	nc	nc		aaa	gaa	increased
5796	RNGRP.PE1	nc	nc		aaa	gaa	increased
5797	RNGRP.PE1	nc	nc		aaa	gaa	increased
5798	RNGSTYBR.PE1	nc	nc		ggg	aaa	increased
5799	RNGSTYBR.PE1	nc	nc		ggg	aaa	increased
5800	RNGSTYBR.PE1	nc	nc		ggg	aaa	increased
5801	RNGUACYC.PE1	nc	nc		tcc	agc	increased
5802	RNGUACYC.PE1	nc	nc		aag	ttc	increased
5803	RNGUACYC.PE1	nc	nc		aag	ttc	increased
5804	RNGUACYC.PE1	nc	nc		aag	ttc	increased
5805	RNGUACYC.PE1	nc	nc		cgg	cga	increased
5806	RNGUACYC.PE1	nc	nc		cgg	cga	increased
5807	RNGUACYC.PE1	nc	nc		cgg	cga	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
5808	Taq1	23	cga	179.985	180	179.98	179.99	0	9 000 000	6 800 000	0	=-	\		\(5) A(4)
5809	Taq1	23	cga	181.025	180	181.06	180.99	0	6 000 000	11 400 000	0	+-	A		\(5) A(4)
5810	Hha1	49	aaa	377.86	380	0	377.86	0	0	11 400 000	0	+-	A		\(5) A(4)
5811	Hha1	49	aaa	379.26	380	379.26	0	0	13 100 000	0	0	-=	\		\(5) A(4)
5812	Hha1	49	aaa	380	380	380	0	0	18 600 000	0	0	-=	\		\(5) A(4)
5813	Hha1	49	aaa	381.97	380	381.97	0	0	4 200 000	0	0	-=	\		\(5) A(4)
5814	Taq1	39	agg	100.417	100	100.17	100.54	100.54	6 100 000	29 200 000	11 700 000	+-	A		\(5)
5815	Taq1	39	agg	100.523	100	100.49	100.54	100.54	4 700 000	293.47	344.62	-=	\ (-)		\(5)
5816	Taq1	39	agg	100.17	100	100.17	0	0	226.53	0	0	-=	\		\(5)
5817	Taq1	39	agg	100.49	100	100.49	0	0	174.53	0	0	-=	\		\(5)
5818	Taq1	54	ttt	101.04	101	101.11	100.97	0	1 194.46	1 705.28	0	=-	\		\(5)
5819	Taq1	56	tga	118.02	118	0	0	118.02	0	0	3 700 000	=+	/		\(5)
5820	Taq1	63	ctt	118.01	118	118.01	0	0	3 200 000	0	0	-=	\		\(5)
5821	Taq1	12	agt	231.73	233	231.81	231.65	0	4 000 000	4 500 000	0	=-	\		\(5)
5822	Taq1	12	agt	232.88	233	0	232.88	0	0	4 300 000	0	+-	A		\(5)
5823	Taq1	12	agt	233.845	233	233.9	233.79	0	4 200 000	3 400 000	0	=-	\		\(5)
5824	Taq1	51	ata	234.56	234	234.56	0	0	7 000 000	0	0	-=	\		\(5)
5825	Hha1	49	aaa	70.745	71	0	70.56	70.93	0	31 500 000	3 400 000	+-	A		\(8)
5826	Hha1	49	aaa	71.09	71	71.09	0	0	54 300 000	0	0	-=	\		\(8)
5827	Hha1	33	agc	143.23	144	143.2	143.26	0	6 800 000	5 700 000	0	=-	\		\(8)
5828	Hha1	33	agc	144.21	144	144.2	0	144.22	4 000 000	0	3 500 000	-+(=)	V		\(8)
5829	Hha1	7	caa	183.7	184	183.69	183.71	183.7	273 700 000	30 200 000	48 600 000	-=	\ (-)		\(8)
5830	Hha1	7	caa	184.9	184	184.58	185.08	185.04	10 200 000	9 700 000	12 800 000	==	-		\(8)
5831	Taq1	34	tgc	183.96	184	183.96	0	0	4 300 000	0	0	-=	\		\(8)
5832	Hha1	60	ttg	213.13	212	0	213.13	0	0	3 000 000	0	+-	A		\(8)
5833	Hha1	6	aga	212.985	214	213.04	0	212.93	13 800 000	0	3 900 000	-=(-)	\		\(8)
5834	Hha1	6	aga	213.49	214	0	213.49	0	0	3 100 000	0	+-	A		\(8)
5835	Taq1	18	cct	213.65	214	213.73	213.57	0	3 400 000	4 100 000	0	=-	\		\(8)
5836	Taq1	18	cct	214.52	214	0	214.52	0	0	3 200 000	0	+-	A		\(8)
5837	Taq1	11	act	231.315	232	231.29	231.34	0	4 700 000	6 600 000	0	=-	\	\	\(8)
5838	Hha1	11	act	231.503	232	231.44	231.51	231.56	16 300 000	10 900 000	3 000 000	=-	\ (-)	\	\(8)
5839	Hha1	11	act	232.55	232	232.52	232.55	232.58	203 600 000	116 600 000	30 700 000	==	-		\(8)
5840	Taq1	11	act	232.19	232	0	232.19	0	0	4 200 000	0	+-	A		\(8)
5841	Taq1	11	act	233.23	232	0	233.42	233.04	0	4 000 000	3 100 000	+=	/		\(8)
5842	Hha1	8	gaa	308.307	310	308.41	308.23	308.28	33 300 000	36 900 000	25 400 000	==	-		\(8)
5843	Hha1	60	ttg	117.71	118	117.87	117.49	117.77	4 900 000	4 100 000	3 800 000	==	-		-2
5844	Taq1	19	cac	126.637	127	126.66	126.65	126.6	3 100 000	5 000 000	20 700 000	=+	/ (-)		-2
5845	Taq1	19	cac	127.64	127	127.65	127.6	127.67	3 700 000	5 100 000	6 200 000	==	-		-2
5846	Taq1	52	att	361.25	363	361.25	0	0	3 800 000	0	0	-=	\		-2
5847	Taq1	52	att	361.95	363	361.95	0	0	3 800 000	0	0	-=	\		-2
5848	Hha1	60	ttg	117.71	118	117.87	117.49	117.77	4 900 000	4 100 000	3 800 000	==	-		-2
5849	Taq1	19	cac	126.637	127	126.66	126.65	126.6	3 100 000	5 000 000	20 700 000	=+	/ (-)		-2
5850	Taq1	19	cac	127.64	127	127.65	127.6	127.67	3 700 000	5 100 000	6 200 000	==	-		-2

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
5808	RNGUACYC.PE1	nc	nc		cgg	cga	increased
5809	RNGUACYC.PE1	nc	nc		cgg	cga	increased
5810	RNGUACYC.PE1	nc	nc		aaa	aca	increased
5811	RNGUACYC.PE1	nc	nc		aaa	aca	increased
5812	RNGUACYC.PE1	nc	nc		aaa	aca	increased
5813	RNGUACYC.PE1	nc	nc		aaa	aca	increased
5814	RNHSP72PS.PE1	Hsc70-ps1	nc		ttt	agg	increased
5815	RNHSP72PS.PE1	Hsc70-ps1	nc		ttt	agg	increased
5816	RNHSP72PS.PE1	Hsc70-ps1	nc		ttt	agg	increased
5817	RNHSP72PS.PE1	Hsc70-ps1	nc		ttt	agg	increased
5818	RNHSP72PS.PE1	Hsc70-ps1	nc		ttt	agg	increased
5819	RNHSP72PS.PE1	Hsc70-ps1	nc		tga	ctt	increased
5820	RNHSP72PS.PE1	Hsc70-ps1	nc		tga	ctt	increased
5821	RNHSP72PS.PE1	Hsc70-ps1	nc		ata	agt	increased
5822	RNHSP72PS.PE1	Hsc70-ps1	nc		ata	agt	increased
5823	RNHSP72PS.PE1	Hsc70-ps1	nc		ata	agt	increased
5824	RNHSP72PS.PE1	Hsc70-ps1	nc		ata	agt	increased
5825	RNHST70A.PE1	nc	nc		aaa	ttg	increased
5826	RNHST70A.PE1	nc	nc		aaa	ttg	increased
5827	RNHST70A.PE1	nc	nc		cag	agc	increased
5828	RNHST70A.PE1	nc	nc		cag	agc	increased
5829	RNHST70A.PE1	nc	nc		caa	tgc	increased
5830	RNHST70A.PE1	nc	nc		caa	tgc	increased
5831	RNHST70A.PE1	nc	nc		caa	tgc	increased
5832	RNHST70A.PE1	nc	nc		ggg	ttg	increased
5833	RNHST70A.PE1	nc	nc		cct	aga	increased
5834	RNHST70A.PE1	nc	nc		cct	aga	increased
5835	RNHST70A.PE1	nc	nc		cct	aga	increased
5836	RNHST70A.PE1	nc	nc		cct	aga	increased
5837	RNHST70A.PE1	nc	nc		cgt	act	increased
5838	RNHST70A.PE1	nc	nc		cgt	act	increased
5839	RNHST70A.PE1	nc	nc		cgt	act	increased
5840	RNHST70A.PE1	nc	nc		cgt	act	increased
5841	RNHST70A.PE1	nc	nc		cgt	act	increased
5842	RNHST70A.PE1	nc	nc		tgc	gaa	increased
5843	RNIGF236.PE1	nc	nc	*	aga	ttg	No change
5844	RNIGF236.PE1	nc	nc	*	cac	gct	No change
5845	RNIGF236.PE1	nc	nc	*	cac	gct	No change
5846	RNIGF236.PE1	nc	nc	*	tgt	att	No change
5847	RNIGF236.PE1	nc	nc	*	tgt	att	No change
5848	RNIGF238.PE1	nc	nc	*	aga	ttg	No change
5849	RNIGF238.PE1	nc	nc	*	cac	gct	No change
5850	RNIGF238.PE1	nc	nc	*	cac	gct	No change

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
5851	Taq1	52	att	361.25	363	361.25	0	0	3 800 000	0	0	-=	\		-2
5852	Taq1	52	att	361.95	363	361.95	0	0	3 800 000	0	0	-=	\		-2
5853	Hha1	60	ttg	117.71	118	117.87	117.49	117.77	4 900 000	4 100 000	3 800 000	==	-		-2
5854	Taq1	19	cac	126.637	127	126.66	126.65	126.6	3 100 000	5 000 000	20 700 000	=+	/ (-)		-2
5855	Taq1	19	cac	127.64	127	127.65	127.6	127.67	3 700 000	5 100 000	6 200 000	==	-		-2
5856	Taq1	52	att	361.25	363	361.25	0	0	3 800 000	0	0	-=	\		-2
5857	Taq1	52	att	361.95	363	361.95	0	0	3 800 000	0	0	-=	\		-2
5858	Hha1	60	ttg	117.71	118	117.87	117.49	117.77	4 900 000	4 100 000	3 800 000	==	-		-2
5859	Taq1	19	cac	126.637	127	126.66	126.65	126.6	3 100 000	5 000 000	20 700 000	=+	/ (-)		-2
5860	Taq1	19	cac	127.64	127	127.65	127.6	127.67	3 700 000	5 100 000	6 200 000	==	-		-2
5861	Taq1	52	att	361.25	363	361.25	0	0	3 800 000	0	0	-=	\		-2
5862	Taq1	52	att	361.95	363	361.95	0	0	3 800 000	0	0	-=	\		-2
5863	Taq1	48	ggg	119.545	120	119.39	119.7	0	4 646.01	1 675.07	0	-=	\		/(6)
5864	Taq1	48	ggg	120.4	120	0	0	120.4	0	0	1 900.49	=+	/		/(6)
5865	Taq1	40	tgg	120.38	121	120.22	120.32	120.6	5 900 000	107 000 000	9 700 000	+-	A		/(6)
5866	Taq1	40	tgg	120.94	121	120.79	121.09	0	22 800 000	13 300 000	0	=-	\		/(6)
5867	Taq1	40	tgg	121.58	121	0	0	121.58	0	0	8 700 000	=+	/		/(6)
5868	Taq1	9	atc	144.395	145	144.45	0	144.34	4 400 000	0	12 100 000	=+(+)	/		/(6)
5869	Hha1	9	atc	145.295	145	145.26	145.33	0	9 000 000	3 400 000	0	-=	\		/(6)
5870	Taq1	9	atc	145.4	145	145.4	0	145.4	7 100 000	0	14 000 000	-+(+)	V (/)		/(6)
5871	Taq1	18	cct	144.78	145	0	0	144.78	0	0	8 800 000	=+	/		/(6)
5872	Taq1	45	gcc	207.8	209	0	0	207.8	0	0	7 200 000	=+	/		/(6)
5873	Taq1	45	gcc	209.52	209	209.52	0	0	5 500 000	0	0	-=	\		/(6)
5874	Taq1	40	tgg	123.5	124	0	0	123.5	0	0	18 400 000	=+	/	/	
5875	Taq1	40	tgg	124.435	124	0	124.28	124.59	0	5 600 000	39 000 000	=+	/	/	
5876	Taq1	62	tgt	123.497	124	123.62	123.49	123.38	3 000 000	4 200 000	29 100 000	=+	/ (-)	/	
5877	Taq1	62	tgt	124.54	124	124.59	124.62	124.41	5 100 000	7 400 000	69 100 000	=+	/ (-)	/	
5878	Taq1	39	agg	176.81	176	176.98	176.64	0	16 600 000	73 100 000	0	+-	A	A	
5879	Taq1	49	aaa	176.89	177	0	176.89	0	0	13 100 000	0	+-	A	A	
5880	Taq1	11	act	204.33	205	0	0	204.33	0	0	5 600 000	=+	/	/	
5881	Hha1	11	act	204.5	205	0	0	204.5	0	0	3 500 000	=+	/	/	
5882	Taq1	44	cgg	142.4	143	142.4	0	0	1 051.97	0	0	-=	\		/(2)
5883	Taq1	44	cgg	143.02	143	0	0	143.02	0	0	874.24	=+	/		/(2)
5884	Taq1	44	cgg	143.71	143	143.55	143.58	144	708.25	538.36	762.16	==	-		/(2)
5885	Taq1	29	gca	143.71	144	0	0	143.71	0	0	7 600 000	=+	/		/(2)
5886	Taq1	29	gca	144.72	144	144.71	0	144.73	3 200 000	0	8 300 000	=+(+)	/		/(2)
5887	Hha1	33	agc	60.667	61	60.61	60.65	60.74	8 100 000	13 200 000	3 900 000	=-	\ (-)		\(8)
5888	Taq1	55	tca	93.58	94	0	93.48	93.68	0	5 800 000	15 600 000	=+	/		\(8)
5889	Taq1	55	tca	93.74	94	0	93.74	0	0	6 100 000	0	+-	A		\(8)
5890	Hha1	55	tca	94.43	94	0	0	94.43	0	0	3 300 000	=+	/		\(8)
5891	Taq1	55	tca	94.545	94	0	94.5	94.59	0	17 500 000	10 600 000	+=	/		\(8)
5892	Taq1	64	gtt	94.123	94	94.08	94.08	94.21	17 900 000	15 900 000	4 900 000	=-	\ (-)		\(8)
5893	Hha1	3	aac	101.88	102	101.97	101.79	0	8 800 000	4 300 000	0	--	\		\(8)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
5851	RNIGF238.PE1	nc	nc	*	tgt	att	No change
5852	RNIGF238.PE1	nc	nc	*	tgt	att	No change
5853	RNIGF246.PE1	nc	nc	*	aga	ttg	No change
5854	RNIGF246.PE1	nc	nc	*	cac	gct	No change
5855	RNIGF246.PE1	nc	nc	*	cac	gct	No change
5856	RNIGF246.PE1	nc	nc	*	tgt	att	No change
5857	RNIGF246.PE1	nc	nc	*	tgt	att	No change
5858	RNIGFIIR.PE1	nc	nc	*	aga	ttg	No change
5859	RNIGFIIR.PE1	nc	nc	*	cac	gct	No change
5860	RNIGFIIR.PE1	nc	nc	*	cac	gct	No change
5861	RNIGFIIR.PE1	nc	nc	*	tgt	att	No change
5862	RNIGFIIR.PE1	nc	nc	*	tgt	att	No change
5863	RNIGMPOR.PE1	nc	nc		tgg	ggg	decreased
5864	RNIGMPOR.PE1	nc	nc		tgg	ggg	decreased
5865	RNIGMPOR.PE1	nc	nc		tgg	ggg	decreased
5866	RNIGMPOR.PE1	nc	nc		tgg	ggg	decreased
5867	RNIGMPOR.PE1	nc	nc		tgg	ggg	decreased
5868	RNIGMPOR.PE1	nc	nc		cct	atc	decreased
5869	RNIGMPOR.PE1	nc	nc		cct	atc	decreased
5870	RNIGMPOR.PE1	nc	nc		cct	atc	decreased
5871	RNIGMPOR.PE1	nc	nc		cct	atc	decreased
5872	RNIGMPOR.PE1	nc	nc		gct	gcc	decreased
5873	RNIGMPOR.PE1	nc	nc		gct	gcc	decreased
5874	RNIGR.PE1	nc	nc		tgt	tgg	decreased
5875	RNIGR.PE1	nc	nc		tgt	tgg	decreased
5876	RNIGR.PE1	nc	nc		tgt	tgg	decreased
5877	RNIGR.PE1	nc	nc		tgt	tgg	decreased
5878	RNIGR.PE1	nc	nc		agg	aaa	increased by mild
5879	RNIGR.PE1	nc	nc		agg	aaa	increased by mild
5880	RNIRS1IRM.IRS-1	IRS-1	nc		act	tgc	decreased
5881	RNIRS1IRM.IRS-1	IRS-1	nc		act	tgc	decreased
5882	RNLCAR.PE1	nc	nc		cgg	gca	decreased
5883	RNLCAR.PE1	nc	nc		cgg	gca	decreased
5884	RNLCAR.PE1	nc	nc		cgg	gca	decreased
5885	RNLCAR.PE1	nc	nc		cgg	gca	decreased
5886	RNLCAR.PE1	nc	nc		cgg	gca	decreased
5887	RNLL5.LL5	LL5	nc		agc	tcc	increased
5888	RNLL5.LL5	LL5	nc		gtt	tca	increased
5889	RNLL5.LL5	LL5	nc		gtt	tca	increased
5890	RNLL5.LL5	LL5	nc		gtt	tca	increased
5891	RNLL5.LL5	LL5	nc		gtt	tca	increased
5892	RNLL5.LL5	LL5	nc		gtt	tca	increased
5893	RNLL5.LL5	LL5	nc		aac	cct	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
5894	Taq1	18	cct	101.49	102	101.31	0	101.67	9 100 000	0	15 600 000	-+(=)	V		\(8)
5895	Hha1	39	agg	129.775	130	129.85	129.7	0	285.92	298.52	0	=-	\		\(8)
5896	Hha1	39	agg	130.465	130	0	130.65	130.28	0	191.05	280.76	+=	/		\(8)
5897	Hha1	41	ccc	170.505	171	170.54	170.47	0	11 400 000	8 000 000	0	=-	\		\(8)
5898	Hha1	41	ccc	171.5	171	171.5	0	0	4 900 000	0	0	-=	\		\(8)
5899	Hha1	61	tct	171.42	172	171.41	171.38	171.47	6 600 000	13 300 000	9 000 000	+=	/ (-)		\(8)
5900	Hha1	61	tct	172.39	172	0	172.39	0	0	3 800 000	0	+-	A		\(8)
5901	Hha1	61	tct	214.34	214	214.34	0	0	4 900 000	0	0	-=	\		\(8)
5902	Hha1	26	ctg	228.08	229	228.08	0	0	7 500 000	0	0	-=	\		\(8)
5903	Hha1	26	ctg	229.185	229	229.14	0	229.23	14 300 000	0	3 300 000	-=(-)	\		\(8)
5904	Hha1	26	ctg	230.06	229	230.11	230.01	0	8 300 000	3 300 000	0	-=	\		\(8)
5905	Hha1	59	ttc	267.955	269	268.09	0	267.82	286.01	0	87.96	-=(-)	\		\(8)
5906	Taq1	19	cac	115.403	116	115.38	115.38	115.45	48 700 000	27 900 000	4 800 000	=-	\ (-)		/(5)
5907	Taq1	19	cac	116.35	116	116.38	116.3	116.37	8 100 000	24 000 000	14 600 000	+=	/ (-)	/	/(5)
5908	Taq1	40	tgg	115.43	116	0	0	115.43	0	0	7 900 000	=+	/		/(5)
5909	Taq1	40	tgg	116.5	116	0	0	116.5	0	0	19 300 000	=+	/	/	/(5)
5910	Taq1	17	cca	138.79	139	138.65	138.81	138.91	283.28	265.92	2 044.8	=+	/ (-)		/(5)
5911	Taq1	17	cca	139.775	139	139.67	0	139.88	171.82	0	1 037.43	=+(+)	/	/	/(5)
5912	Taq1	29	gca	138.537	139	138.49	138.52	138.6	5 300 000	6 100 000	5 400 000	==	-		/(5)
5913	Taq1	29	gca	139.62	139	0	0	139.62	0	0	5 300 000	=+	/	/	/(5)
5914	Hha1	6	aga	159.6	160	159.64	0	159.56	5 600 000	0	20 300 000	=+(+)	/		/(5)
5915	Hha1	6	aga	160.585	160	160.81	0	160.36	10 900 000	0	8 000 000	-+(=)	V		/(5)
5916	Taq1	40	tgg	180.51	181	180.51	0	0	6 100 000	0	0	-=	\		/(5)
5917	Taq1	40	tgg	181.71	181	181.63	0	181.79	3 800 000	0	3 500 000	-+(=)	V		/(5)
5918	Taq1	17	cca	138.79	139	138.65	138.81	138.91	283.28	265.92	2 044.8	=+	/ (-)		-1
5919	Taq1	17	cca	139.775	139	139.67	0	139.88	171.82	0	1 037.43	=+(+)	/	/	-1
5920	Taq1	29	gca	138.537	139	138.49	138.52	138.6	5 300 000	6 100 000	5 400 000	==	-		-1
5921	Taq1	29	gca	139.62	139	0	0	139.62	0	0	5 300 000	=+	/	/	-1
5922	Hha1	27	acg	62.015	62	61.98	62.05	0	4 900 000	3 200 000	0	=-	\		\(3)
5923	Hha1	33	agc	78.69	79	78.69	0	0	4 200 000	0	0	-=	\		\(3)
5924	Hha1	40	tgg	113.48	113	113.23	113.73	0	46 700 000	9 600 000	0	-=	\		\(3)
5925	Hha1	60	ttg	117.71	118	117.87	117.49	117.77	4 900 000	4 100 000	3 800 000	==	-		-2
5926	Taq1	19	cac	126.637	127	126.66	126.65	126.6	3 100 000	5 000 000	20 700 000	=+	/ (-)		-2
5927	Taq1	19	cac	127.64	127	127.65	127.6	127.67	3 700 000	5 100 000	6 200 000	==	-		-2
5928	Taq1	52	att	361.25	363	361.25	0	0	3 800 000	0	0	-=	\		-2
5929	Taq1	52	att	361.95	363	361.95	0	0	3 800 000	0	0	-=	\		-2
5930	Hha1	60	ttg	117.71	118	117.87	117.49	117.77	4 900 000	4 100 000	3 800 000	==	-		-2
5931	Taq1	19	cac	126.637	127	126.66	126.65	126.6	3 100 000	5 000 000	20 700 000	=+	/ (-)		-2
5932	Taq1	19	cac	127.64	127	127.65	127.6	127.67	3 700 000	5 100 000	6 200 000	==	-		-2
5933	Taq1	52	att	361.25	363	361.25	0	0	3 800 000	0	0	-=	\		-2
5934	Taq1	52	att	361.95	363	361.95	0	0	3 800 000	0	0	-=	\		-2
5935	Hha1	60	ttg	117.71	118	117.87	117.49	117.77	4 900 000	4 100 000	3 800 000	==	-		-2
5936	Taq1	19	cac	126.637	127	126.66	126.65	126.6	3 100 000	5 000 000	20 700 000	=+	/ (-)		-2

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
5894	RNLL5.LL5	LL5	nc		aac	cct	increased
5895	RNLL5.LL5	LL5	nc		acc	agg	increased
5896	RNLL5.LL5	LL5	nc		acc	agg	increased
5897	RNLL5.LL5	LL5	nc		tct	ccc	increased
5898	RNLL5.LL5	LL5	nc		tct	ccc	increased
5899	RNLL5.LL5	LL5	nc		tct	ccc	increased
5900	RNLL5.LL5	LL5	nc		tct	ccc	increased
5901	RNLL5.LL5	LL5	nc		tag	tct	increased
5902	RNLL5.LL5	LL5	nc		ctg	tgc	increased
5903	RNLL5.LL5	LL5	nc		ctg	tgc	increased
5904	RNLL5.LL5	LL5	nc		ctg	tgc	increased
5905	RNLL5.LL5	LL5	nc		ccg	ttc	increased
5906	RNMAP2.PE1	nc	nc		cac	tgg	decreased
5907	RNMAP2.PE1	nc	nc		cac	tgg	decreased
5908	RNMAP2.PE1	nc	nc		cac	tgg	decreased
5909	RNMAP2.PE1	nc	nc		cac	tgg	decreased
5910	RNMAP2.PE1	nc	nc		cca	gca	decreased
5911	RNMAP2.PE1	nc	nc		cca	gca	decreased
5912	RNMAP2.PE1	nc	nc		cca	gca	decreased
5913	RNMAP2.PE1	nc	nc		cca	gca	decreased
5914	RNMAP2.PE1	nc	nc		aga	ttg	decreased
5915	RNMAP2.PE1	nc	nc		aga	ttg	decreased
5916	RNMAP2.PE1	nc	nc		agc	tgg	decreased
5917	RNMAP2.PE1	nc	nc		agc	tgg	decreased
5918	RNMAP2C.PE1	nc	nc		cca	gca	No change
5919	RNMAP2C.PE1	nc	nc		cca	gca	decreased
5920	RNMAP2C.PE1	nc	nc		cca	gca	No change
5921	RNMAP2C.PE1	nc	nc		cca	gca	decreased
5922	RNMASH2.PE1	nc	nc		tcc	acg	increased
5923	RNMASH2.PE1	nc	nc		tgc	agc	increased
5924	RNMASH2.PE1	nc	nc		tct	tgg	increased
5925	RNMSAR.PE1	nc	nc		aga	ttg	No change
5926	RNMSAR.PE1	nc	nc		cac	gct	No change
5927	RNMSAR.PE1	nc	nc		cac	gct	No change
5928	RNMSAR.PE1	nc	nc		tgt	att	No change
5929	RNMSAR.PE1	nc	nc		tgt	att	No change
5930	RNMSAR.PE2	nc	nc	*	aga	ttg	No change
5931	RNMSAR.PE2	nc	nc	*	cac	gct	No change
5932	RNMSAR.PE2	nc	nc	*	cac	gct	No change
5933	RNMSAR.PE2	nc	nc	*	tgt	att	No change
5934	RNMSAR.PE2	nc	nc	*	tgt	att	No change
5935	RNMSAR.PE3	nc	nc		aga	ttg	No change
5936	RNMSAR.PE3	nc	nc		cac	gct	No change

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
5937	Taq1	19	cac	127.64	127	127.65	127.6	127.67	3 700 000	5 100 000	6 200 000	==	-		-2
5938	Hha1	62	tgt	140.06	140	140.06	0	0	3 000 000	0	0	-=	\		\(2)
5939	Hha1	26	ctg	230.06	231	230.11	230.01	0	8 300 000	3 300 000	0	-=	\		\(2)
5940	Hha1	26	ctg	231.04	231	0	231.04	0	0	3 600 000	0	+-	A		\(2)
5941	Hha1	57	cta	133.93	134	133.84	134.02	133.93	3 569.11	2 584.81	903.14	=-	\ (-)		-(2) \(2)
5942	Taq1	18	cct	202.25	202	202.2	202.3	0	4 100 000	3 300 000	0	=-	\		-(2) \(2)
5943	Taq1	19	cac	201.425	202	201.36	0	201.49	3 500 000	0	4 300 000	-+(=)	V		-(2) \(2)
5944	Taq1	19	cac	202.327	202	202.27	202.28	202.43	3 600 000	3 100 000	9 800 000	=+	/ (-)		-(2) \(2)
5945	Hha1	59	ttc	99.033	99	98.95	99.2	98.95	364.01	175.34	274.23	-=	\ (-)	\	\(2)
5946	Hha1	60	ttg	98.6	99	0	98.6	0	0	10 900 000	0	+-	A		\(2)
5947	Hha1	60	ttg	98.985	99	0	98.74	99.23	0	10 700 000	5 900 000	+=	/		\(2)
5948	Hha1	60	ttg	99.28	99	99.28	0	0	3 000 000	0	0	-=	\	\	\(2)
5949	Hha1	22	tcc	135.305	136	0	135.43	135.18	0	8 700 000	5 000 000	+=	/		/(3) \(3)
5950	Taq1	22	tcc	135.645	136	135.57	0	135.72	6 100 000	0	38 300 000	=+(+)	/		/(3) \(3)
5951	Taq1	22	tcc	136.1	136	136.1	0	0	5 700 000	0	0	-=	\		/(3) \(3)
5952	Taq1	22	tcc	136.737	136	136.64	136.88	136.69	4 400 000	7 800 000	35 600 000	=+	/ (-)		/(3) \(3)
5953	Taq1	61	tct	135.837	136	135.78	135.92	135.81	3 700 000	12 300 000	15 600 000	+=	/ (-)		/(3) \(3)
5954	Taq1	45	gcc	237.79	238	237.79	0	0	3 100 000	0	0	-=	\		/(3) \(3)
5955	Hha1	8	gaa	238.66	239	238.83	238.49	0	4 500 000	3 100 000	0	=-	\		/(3) \(3)
5956	Taq1	12	agt	100.297	100	100.31	100.28	100.3	8 100 000	5 300 000	13 800 000	=+	/ (-)		A(3)
5957	Taq1	52	att	118.39	119	0	0	118.39	0	0	5 000 000	=+	/		A(3)
5958	Taq1	52	att	118.9	119	118.9	118.9	0	4 000 000	7 700 000	0	+-	A		A(3)
5959	Taq1	52	att	119.57	119	0	0	119.57	0	0	8 500 000	=+	/		A(3)
5960	Hha1	60	ttg	193.14	194	0	193.14	0	0	4 900 000	0	+-	A		A(3)
5961	Hha1	60	ttg	195.08	194	0	195.08	0	0	3 200 000	0	+-	A		A(3)
5962	Hha1	60	ttg	231.27	232	231.27	0	0	4 000 000	0	0	-=	\		A(3)
5963	Hha1	60	ttg	233.3	232	0	233.3	0	0	3 700 000	0	+-	A		A(3)
5964	Taq1	8	gaa	71.595	72	0	71.54	71.65	0	9 500 000	40 300 000	=+	/		A(2)
5965	Taq1	8	gaa	72.18	72	0	72.18	0	0	7 400 000	0	+-	A		A(2)
5966	Taq1	56	tga	71.66	72	0	71.66	0	0	6 000 000	0	+-	A		A(2)
5967	Hha1	44	cgg	114.53	114	0	114.53	0	0	6 900 000	0	+-	A		\(2)
5968	Hha1	6	aga	168.64	169	168.64	0	0	6 700 000	0	0	-=	\		\(2)
5969	Hha1	6	aga	169.525	169	169.52	0	169.53	15 400 000	0	3 500 000	-=(-)	\	\	\(2)
5970	Taq1	31	gac	169.75	169	169.61	169.89	0	9 600 000	3 900 000	0	-=	\	\	\(2)
5971	Taq1	56	tga	60.875	61	61.03	0	60.72	47 900 000	0	36 900 000	-+(=)	V		/(3)
5972	Taq1	40	tgg	150.207	151	150.09	150.41	150.12	5 300 000	10 100 000	3 600 000	+-	A		/(3)
5973	Taq1	40	tgg	151.16	151	0	0	151.16	0	0	10 100 000	=+	/		/(3)
5974	Taq1	56	tga	151.42	151	0	0	151.42	0	0	3 000 000	=+	/		/(3)
5975	Hha1	7	caa	218.985	220	0	218.97	219	0	4 000 000	3 600 000	+=	/		/(3)
5976	Hha1	7	caa	219.853	220	219.78	219.86	219.92	3 700 000	3 600 000	3 900 000	==	-		/(3)
5977	Hha1	7	caa	220.663	220	220.73	220.66	220.6	41 200 000	6 500 000	7 800 000	-=	\ (-)		/(3)
5978	Hha1	7	caa	220.96	220	0	220.96	0	0	5 300 000	0	+-	A		/(3)
5979	Hha1	59	ttc	64.92	65	64.99	64.84	64.93	442.01	549.03	548.46	==	-		-3

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
5937	RNMSAR.PE3	nc	nc		cac	gct	No change
5938	RNNGFRR.PE1	nc	nc		cag	tgt	increased
5939	RNNGFRR.PE1	nc	nc		ctg	tca	increased
5940	RNNGFRR.PE1	nc	nc		ctg	tca	increased
5941	RNO6295.AF-9	AF-9	nc		cta	tag	No change
5942	RNO6295.AF-9	AF-9	nc		cac	cct	No change
5943	RNO6295.AF-9	AF-9	nc		cac	cct	No change
5944	RNO6295.AF-9	AF-9	nc		cac	cct	No change
5945	RNPAX8.PAX-8	Pax-8	nc		ttc	ttg	increased
5946	RNPAX8.PAX-8	Pax-8	nc		ttc	ttg	increased
5947	RNPAX8.PAX-8	Pax-8	nc		ttc	ttg	increased
5948	RNPAX8.PAX-8	Pax-8	nc		ttc	ttg	increased
5949	RNPKLR.PE1	nc	nc	*	tct	tcc	decreased
5950	RNPKLR.PE1	nc	nc	*	tct	tcc	decreased
5951	RNPKLR.PE1	nc	nc	*	tct	tcc	decreased
5952	RNPKLR.PE1	nc	nc	*	tct	tcc	decreased
5953	RNPKLR.PE1	nc	nc	*	tct	tcc	decreased
5954	RNPKLR.PE1	nc	nc	*	gaa	gcc	decreased
5955	RNPKLR.PE1	nc	nc	*	gaa	gcc	decreased
5956	RNPRKCR2.PE1	nc	nc		acg	agt	increased by mild
5957	RNPRKCR2.PE1	nc	nc		ccg	att	increased by mild
5958	RNPRKCR2.PE1	nc	nc		ccg	att	increased by mild
5959	RNPRKCR2.PE1	nc	nc		ccg	att	increased by mild
5960	RNPRKCR2.PE1	nc	nc		cct	ttg	increased by mild
5961	RNPRKCR2.PE1	nc	nc		cct	ttg	increased by mild
5962	RNPRKCR2.PE1	nc	nc		tgc	ttg	increased by mild
5963	RNPRKCR2.PE1	nc	nc		tgc	ttg	increased by mild
5964	RNRARL4.PE1	nc	nc		gaa	tga	increased by mild
5965	RNRARL4.PE1	nc	nc		gaa	tga	increased by mild
5966	RNRARL4.PE1	nc	nc		gaa	tga	increased by mild
5967	RNRBIRK2.RB-IRK2	RB-IRK2	nc		cgg	tgt	increased
5968	RNRBIRK2.RB-IRK2	RB-IRK2	nc		gac	aga	increased
5969	RNRBIRK2.RB-IRK2	RB-IRK2	nc		gac	aga	increased
5970	RNRBIRK2.RB-IRK2	RB-IRK2	nc		gac	aga	increased
5971	RNRLC.PE1	nc	nc		cca	tga	decreased
5972	RNRLC.PE1	nc	nc		tga	tgg	decreased
5973	RNRLC.PE1	nc	nc		tga	tgg	decreased
5974	RNRLC.PE1	nc	nc		tga	tgg	decreased
5975	RNRLC.PE1	nc	nc		caa	agc	decreased
5976	RNRLC.PE1	nc	nc		caa	agc	decreased
5977	RNRLC.PE1	nc	nc		caa	agc	decreased
5978	RNRLC.PE1	nc	nc		caa	agc	decreased
5979	RNRNUDC.RNUDC	RnudC	nc		ttc	cat	No change

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
5980	Taq1	44	cgg	114.377	115	114.23	114.3	114.6	923.51	1 048.02	1 546.73	==	-		-3
5981	Taq1	44	cgg	115.377	115	115.2	115.34	115.59	2 784.43	1 040.84	2 824.47	-+	V		-3
5982	Taq1	39	agg	115.577	116	115.45	115.64	115.64	9 100 000	26 500 000	58 400 000	=+	/ (-)		-3
5983	Taq1	39	agg	116.42	116	116.25	116.33	116.68	20 000 000	12 500 000	11 400 000	==	-		-3
5984	Taq1	39	agg	115.577	116	115.45	115.64	115.64	337.93	266.33	1 720.17	=+	/ (-)		-3
5985	Taq1	39	agg	116.42	116	116.25	116.33	116.68	742.72	125.62	335.78	-=	\ (-)		-3
5986	Hha1	39	agg	87.397	87	87.19	87.6	87.4	1 312.31	447.78	545.24	-=	\ (-)		\(4)
5987	Taq1	50	aat	127.66	128	127.64	127.68	127.66	7 100 000	6 800 000	15 700 000	=+	/ (-)		\(4)
5988	Taq1	50	aat	128.71	128	128.86	0	128.56	4 600 000	0	20 800 000	=+(+)	/		\(4)
5989	Hha1	9	atc	196.505	197	196.27	196.74	0	4 300 000	5 400 000	0	=-	\		\(4)
5990	Hha1	9	atc	197.09	197	197.3	0	196.88	3 200 000	0	3 400 000	-+(=)	V		\(4)
5991	Hha1	6	aga	248.48	248	248.48	0	0	4 600 000	0	0	-=	\		\(4)
5992	Taq1	49	aaa	262.81	264	0	262.81	0	0	12 300 000	0	+-	A		\(4)
5993	Taq1	49	aaa	263.61	264	263.61	0	0	11 900 000	0	0	-=	\		\(4)
5994	Taq1	49	aaa	264.33	264	0	264.33	0	0	20 400 000	0	+-	A		\(4)
5995	Taq1	49	aaa	265.3	264	265.3	0	0	12 500 000	0	0	-=	\		\(4)
5996	Hha1	39	agg	87.397	87	87.19	87.6	87.4	1 312.31	447.78	545.24	-=	\ (-)		\(2)
5997	Hha1	6	aga	248.48	248	248.48	0	0	4 600 000	0	0	-=	\		\(2)
5998	Hha1	39	agg	87.397	87	87.19	87.6	87.4	1 312.31	447.78	545.24	-=	\ (-)		\(5)
5999	Taq1	41	ccc	95.76	96	95.76	0	0	3 700 000	0	0	-=	\		\(5)
6000	Taq1	41	ccc	96.43	96	0	96.43	0	0	5 600 000	0	+-	A		\(5)
6001	Hha1	6	aga	187.02	188	187.02	0	0	4 800 000	0	0	-=	\		\(5)
6002	Hha1	6	aga	188.12	188	188.12	0	0	10 100 000	0	0	-=	\		\(5)
6003	Taq1	21	acc	187.65	188	187.65	0	0	6 000 000	0	0	-=	\		\(5)
6004	Hha1	21	acc	188.35	188	0	188.45	188.25	0	3 400 000	5 200 000	+=	/		\(5)
6005	Taq1	49	aaa	284.435	286	284.42	284.45	0	223 200 000	92 100 000	0	-=	\		\(5)
6006	Taq1	49	aaa	285.51	286	285.35	285.67	0	26 700 000	18 600 000	0	=-	\		\(5)
6007	Taq1	49	aaa	286.73	286	286.73	286.73	0	26 100 000	12 200 000	0	--	\		\(5)
6008	Hha1	59	ttc	82.87	83	0	82.87	0	0	339.19	0	+-	A		A(2)
6009	Hha1	59	ttc	83.34	83	83.5	83.18	0	421.21	494.42	0	=-	\		A(2)
6010	Hha1	60	ttg	149.247	150	149.18	149.11	149.45	6 200 000	7 000 000	6 900 000	==	-		A(2)
6011	Hha1	60	ttg	150.36	150	0	150.36	0	0	6 500 000	0	+-	A		A(2)
6012	Taq1	10	atg	244.24	245	0	244.24	0	0	4 900 000	0	+-	A		A(2)
6013	Taq1	10	atg	245.5	245	0	245.5	0	0	5 400 000	0	+-	A		A(2)
6014	Taq1	50	aat	245.31	246	245.31	0	0	4 700 000	0	0	-=	\		A(2)
6015	Taq1	50	aat	246.545	246	246.34	246.75	0	3 200 000	8 300 000	0	+-	A		A(2)
6016	Taq1	50	aat	247.46	246	247.45	247.47	0	6 900 000	7 700 000	0	=-	\		A(2)
6017	Taq1	16	tag	104.21	104	0	0	104.21	0	0	4 700 000	=+	/	/	/(2)
6018	Taq1	29	gca	103.48	104	0	0	103.48	0	0	6 200 000	=+	/		/(2)
6019	Taq1	29	gca	104.42	104	0	0	104.42	0	0	7 100 000	=+	/	/	/(2)
6020	Hha1	8	gaa	160.295	161	160.22	160.37	0	3 300 000	3 000 000	0	=-	\		\(5)
6021	Taq1	8	gaa	160.52	161	0	160.52	0	0	3 800 000	0	+-	A		\(5)
6022	Hha1	8	gaa	160.995	161	160.98	161.01	0	3 900 000	5 000 000	0	=-	\		\(5)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
5980	RNRNUDC.RNUDC	RnudC	nc		cgg	agg	No change
5981	RNRNUDC.RNUDC	RnudC	nc		cgg	agg	No change
5982	RNRNUDC.RNUDC	RnudC	nc		cgg	agg	No change
5983	RNRNUDC.RNUDC	RnudC	nc		cgg	agg	No change
5984	RNRNUDC.RNUDC	RnudC	nc		cgg	agg	No change
5985	RNRNUDC.RNUDC	RnudC	nc		cgg	agg	No change
5986	RNSCIII.PE1	nc	nc		caa	agg	increased
5987	RNSCIII.PE1	nc	nc		aat	tta	increased
5988	RNSCIII.PE1	nc	nc		aat	tta	increased
5989	RNSCIII.PE1	nc	nc		atc	tat	increased
5990	RNSCIII.PE1	nc	nc		atc	tat	increased
5991	RNSCIII.PE1	nc	nc		ccc	aga	increased
5992	RNSCIII.PE1	nc	nc		aaa	aaa	increased
5993	RNSCIII.PE1	nc	nc		aaa	aaa	increased
5994	RNSCIII.PE1	nc	nc		aaa	aaa	increased
5995	RNSCIII.PE1	nc	nc		aaa	aaa	increased
5996	RNSCPIIR.PE1	nc	nc		caa	agg	increased
5997	RNSCPIIR.PE1	nc	nc		ccc	aga	increased
5998	RNSCPIR.PE1	nc	nc	*	caa	agg	increased
5999	RNSCPIR.PE1	nc	nc	*	ccc	gag	increased
6000	RNSCPIR.PE1	nc	nc	*	ccc	gag	increased
6001	RNSCPIR.PE1	nc	nc	*	acc	aga	increased
6002	RNSCPIR.PE1	nc	nc	*	acc	aga	increased
6003	RNSCPIR.PE1	nc	nc	*	acc	aga	increased
6004	RNSCPIR.PE1	nc	nc	*	acc	aga	increased
6005	RNSCPIR.PE1	nc	nc	*	cct	aaa	increased
6006	RNSCPIR.PE1	nc	nc	*	cct	aaa	increased
6007	RNSCPIR.PE1	nc	nc	*	cct	aaa	increased
6008	RNSDRPL15.PE1	ribosomal pro	nc		ttc	aga	increased by mild
6009	RNSDRPL15.PE1	ribosomal pro	nc		ttc	aga	increased by mild
6010	RNSDRPL15.PE1	ribosomal pro	nc		tgc	ttg	increased by mild
6011	RNSDRPL15.PE1	ribosomal pro	nc		tgc	ttg	increased by mild
6012	RNTF.TF	TF	nc		aat	atg	increased by mild
6013	RNTF.TF	TF	nc		aat	atg	increased by mild
6014	RNTF.TF	TF	nc		aat	atg	increased by mild
6015	RNTF.TF	TF	nc		aat	atg	increased by mild
6016	RNTF.TF	TF	nc		aat	atg	increased by mild
6017	RNTRY2.PE1	nc	nc		tag	gca	decreased
6018	RNTRY2.PE1	nc	nc		tag	gca	decreased
6019	RNTRY2.PE1	nc	nc		tag	gca	decreased
6020	RNU12252.PE1	nc	nc		gaa	atg	increased
6021	RNU12252.PE1	nc	nc		gaa	atg	increased
6022	RNU12252.PE1	nc	nc		gaa	atg	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
6023	Hha1	8	gaa	161.5	161	161.5	0	0	6 900 000	0	0	-=	\		\(5)
6024	Taq1	10	atg	160.47	161	160.29	160.65	0	5 700 000	3 500 000	0	=-	\		\(5)
6025	Hha1	10	atg	160.56	161	160.56	0	0	3 600 000	0	0	-=	\		\(5)
6026	Taq1	10	atg	161.48	161	0	161.47	161.49	0	6 100 000	5 100 000	+=	/		\(5)
6027	Hha1	10	atg	161.525	161	161.56	161.49	0	6 100 000	3 000 000	0	--	\		\(5)
6028	Hha1	33	agc	73.643	74	73.74	73.76	73.43	3 700 000	4 300 000	7 000 000	==	-		-2
6029	Hha1	33	agc	82.077	82	81.92	82	82.31	23 000 000	20 100 000	4 600 000	=-	\ (-)		-2
6030	Hha1	61	tct	124.843	125	124.71	124.84	124.98	3 400 000	8 200 000	5 200 000	+=	/ (-)		/(3) \(3)
6031	Hha1	43	cgc	141.42	142	141.36	141.48	0	36 100 000	4 400 000	0	-=	\		/(3) \(3)
6032	Hha1	62	tgt	142.86	143	0	0	142.86	0	0	4 700 000	=+	/		/(3) \(3)
6033	Hha1	25	cag	173.84	174	0	174.01	173.67	0	5 500 000	4 100 000	+=	/		/(3) \(3)
6034	Hha1	25	cag	174.66	174	174.66	0	0	6 700 000	0	0	-=	\		/(3) \(3)
6035	Taq1	50	aat	539.96	543	539.96	0	0	3 300 000	0	0	-=	\		/(3) \(3)
6036	Taq1	48	ggg	119.545	119	119.39	119.7	0	4 646.01	1 675.07	0	-=	\	\	
6037	Taq1	40	tgg	119.665	120	119.69	119.64	0	8 000 000	13 700 000	0	=-	\	\	
6038	Hha1	39	agg	63.33	63	63.42	63.39	63.18	1 656.89	674.66	1 318.35	-=	\ (-)		\(9)
6039	Taq1	16	tag	100.56	100	0	100.56	100.56	0	3 600 000	5 300 000	+=	/		\(9)
6040	Hha1	43	cgc	99.97	100	99.92	100.02	0	25 600 000	8 600 000	0	-=	\		\(9)
6041	Taq1	56	tga	100.495	100	100.4	100.59	0	5 100 000	9 000 000	0	=-	\		\(9)
6042	Taq1	56	tga	99.73	100	0	99.73	0	0	4 600 000	0	+-	A		\(9)
6043	Hha1	26	ctg	109.847	110	109.83	109.83	109.88	4 200 000	6 200 000	4 100 000	==	-		\(9)
6044	Hha1	61	tct	120.8	121	0	120.8	0	0	4 300 000	0	+-	A		\(9)
6045	Hha1	2	tta	155.785	156	0	155.61	155.96	0	14 700 000	16 700 000	+=	/		\(9)
6046	Hha1	2	tta	156.285	156	156.36	156.21	0	27 200 000	14 600 000	0	--	\		\(9)
6047	Hha1	27	acg	155.415	156	155.39	155.44	0	7 300 000	5 400 000	0	=-	\		\(9)
6048	Hha1	27	acg	156.153	156	155.98	156.15	156.33	7 500 000	3 100 000	9 300 000	-+	V		\(9)
6049	Hha1	40	tgg	156.92	156	156.76	156.92	157.08	5 700 000	6 000 000	3 800 000	==	-		\(9)
6050	Taq1	45	gcc	180.93	182	180.79	181.07	0	4 400 000	8 900 000	0	+-	A		\(9)
6051	Taq1	45	gcc	182.54	182	0	182.54	0	0	5 900 000	0	+-	A		\(9)
6052	Hha1	10	atg	181.97	183	181.97	0	0	4 200 000	0	0	-=	\		\(9)
6053	Taq1	10	atg	182.87	183	182.87	0	0	8 200 000	0	0	-=	\		\(9)
6054	Hha1	10	atg	182.99	183	182.99	0	0	4 100 000	0	0	-=	\		\(9)
6055	Taq1	45	gcc	237.79	237	237.79	0	0	3 100 000	0	0	-=	\		\(9)
6056	Hha1	39	agg	63.33	63	63.42	63.39	63.18	1 656.89	674.66	1 318.35	-=	\ (-)		\(9)
6057	Taq1	16	tag	100.56	100	0	100.56	100.56	0	3 600 000	5 300 000	+=	/		\(9)
6058	Hha1	43	cgc	99.97	100	99.92	100.02	0	25 600 000	8 600 000	0	-=	\		\(9)
6059	Taq1	56	tga	100.495	100	100.4	100.59	0	5 100 000	9 000 000	0	=-	\		\(9)
6060	Taq1	56	tga	99.73	100	0	99.73	0	0	4 600 000	0	+-	A		\(9)
6061	Hha1	26	ctg	109.847	110	109.83	109.83	109.88	4 200 000	6 200 000	4 100 000	==	-		\(9)
6062	Hha1	61	tct	120.8	121	0	120.8	0	0	4 300 000	0	+-	A		\(9)
6063	Hha1	2	tta	155.785	156	0	155.61	155.96	0	14 700 000	16 700 000	+=	/		\(9)
6064	Hha1	2	tta	156.285	156	156.36	156.21	0	27 200 000	14 600 000	0	--	\		\(9)
6065	Hha1	27	acg	155.415	156	155.39	155.44	0	7 300 000	5 400 000	0	=-	\		\(9)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
6023	RNU12252.PE1	nc	nc		gaa	atg	increased
6024	RNU12252.PE1	nc	nc		gaa	atg	increased
6025	RNU12252.PE1	nc	nc		gaa	atg	increased
6026	RNU12252.PE1	nc	nc		gaa	atg	increased
6027	RNU12252.PE1	nc	nc		gaa	atg	increased
6028	S79797.PE1	enzymatic gly	nc		agc	tgc	No change
6029	S79797.PE1	enzymatic gly	nc		tct	agc	No change
6030	AB017695.PE1	nc	N-cadherin		cat	tct	decreased
6031	AB017695.PE1	nc	N-cadherin		cgc	tgt	decreased
6032	AB017695.PE1	nc	N-cadherin		cgc	tgt	decreased
6033	AB017695.PE1	nc	N-cadherin		cag	tcg	decreased
6034	AB017695.PE1	nc	N-cadherin		cag	tcg	decreased
6035	AB017695.PE1	nc	N-cadherin		tat	aat	decreased
6036	RNU68726.PE1	nc	neogenin		ggg	tgg	increased
6037	RNU68726.PE1	nc	neogenin		ggg	tgg	increased
6038	RATNGFA.VGF	VGF	nerve growth factor inducible protein	*	agg	tcc	increased
6039	RATNGFA.VGF	VGF	nerve growth factor inducible protein	*	tag	tga	increased
6040	RATNGFA.VGF	VGF	nerve growth factor inducible protein	*	aag	cgc	increased
6041	RATNGFA.VGF	VGF	nerve growth factor inducible protein	*	tag	tga	increased
6042	RATNGFA.VGF	VGF	nerve growth factor inducible protein	*	tag	tga	increased
6043	RATNGFA.VGF	VGF	nerve growth factor inducible protein	*	ctg	tgc	increased
6044	RATNGFA.VGF	VGF	nerve growth factor inducible protein	*	cag	tct	increased
6045	RATNGFA.VGF	VGF	nerve growth factor inducible protein	*	ccc	tta	increased
6046	RATNGFA.VGF	VGF	nerve growth factor inducible protein	*	ccc	tta	increased
6047	RATNGFA.VGF	VGF	nerve growth factor inducible protein	*	tgg	acg	increased
6048	RATNGFA.VGF	VGF	nerve growth factor inducible protein	*	tgg	acg	increased
6049	RATNGFA.VGF	VGF	nerve growth factor inducible protein	*	tgg	acg	increased
6050	RATNGFA.VGF	VGF	nerve growth factor inducible protein	*	atg	gcc	increased
6051	RATNGFA.VGF	VGF	nerve growth factor inducible protein	*	atg	gcc	increased
6052	RATNGFA.VGF	VGF	nerve growth factor inducible protein	*	atg	gcc	increased
6053	RATNGFA.VGF	VGF	nerve growth factor inducible protein	*	atg	gcc	increased
6054	RATNGFA.VGF	VGF	nerve growth factor inducible protein	*	atg	gcc	increased
6055	RATNGFA.VGF	VGF	nerve growth factor inducible protein	*	gat	gcc	increased
6056	RATNGFIP.VGF	VGF	nerve growth factor-inducible protein	*	agg	tcc	increased
6057	RATNGFIP.VGF	VGF	nerve growth factor-inducible protein	*	tag	tga	increased
6058	RATNGFIP.VGF	VGF	nerve growth factor-inducible protein	*	aag	cgc	increased
6059	RATNGFIP.VGF	VGF	nerve growth factor-inducible protein	*	tag	tga	increased
6060	RATNGFIP.VGF	VGF	nerve growth factor-inducible protein	*	tag	tga	increased
6061	RATNGFIP.VGF	VGF	nerve growth factor-inducible protein	*	ctg	tgc	increased
6062	RATNGFIP.VGF	VGF	nerve growth factor-inducible protein	*	cag	tct	increased
6063	RATNGFIP.VGF	VGF	nerve growth factor-inducible protein	*	ccc	tta	increased
6064	RATNGFIP.VGF	VGF	nerve growth factor-inducible protein	*	ccc	tta	increased
6065	RATNGFIP.VGF	VGF	nerve growth factor-inducible protein	*	tgg	acg	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
6066	Hha1	27	acg	156.153	156	155.98	156.15	156.33	7 500 000	3 100 000	9 300 000	-+	V		\(9)
6067	Hha1	40	tgg	156.92	156	156.76	156.92	157.08	5 700 000	6 000 000	3 800 000	==	-		\(9)
6068	Taq1	45	gcc	180.93	182	180.79	181.07	0	4 400 000	8 900 000	0	+-	A		\(9)
6069	Taq1	45	gcc	182.54	182	0	182.54	0	0	5 900 000	0	+-	A		\(9)
6070	Hha1	10	atg	181.97	183	181.97	0	0	4 200 000	0	0	-=	\		\(9)
6071	Taq1	10	atg	182.87	183	182.87	0	0	8 200 000	0	0	-=	\		\(9)
6072	Hha1	10	atg	182.99	183	182.99	0	0	4 100 000	0	0	-=	\		\(9)
6073	Taq1	45	gcc	237.79	237	237.79	0	0	3 100 000	0	0	-=	\		\(9)
6074	Taq1	29	gca	123.37	124	0	0	123.37	0	0	11 200 000	=+	/	/	
6075	Taq1	61	tct	123.585	124	0	123.45	123.72	0	4 700 000	26 700 000	=+	/	/	
6076	Taq1	39	agg	67.183	67	67.29	67.21	67.05	3 900 000	74 300 000	6 900 000	+-	A		-(3) /(3) A(3)
6077	Taq1	39	agg	67.183	67	67.29	67.21	67.05	144.83	746.74	203.24	+-	A		-(3) /(3) A(3)
6078	Taq1	61	tct	120.51	121	0	120.27	120.75	0	9 800 000	6 500 000	+=	/		-(3) /(3) A(3)
6079	Taq1	61	tct	121.523	121	121.35	121.4	121.82	5 000 000	15 100 000	10 900 000	+=	/ (-)		-(3) /(3) A(3)
6080	Taq1	20	ctc	171.573	172	171.6	171.4	171.72	6 100 000	5 500 000	11 200 000	=+	/ (-)		-(3) /(3) A(3)
6081	Taq1	20	ctc	172.47	172	0	172.47	0	0	5 500 000	0	+-	A		-(3) /(3) A(3)
6082	Taq1	20	ctc	172.99	172	0	0	172.99	0	0	3 700 000	=+	/		-(3) /(3) A(3)
6083	Taq1	62	tgt	171.29	172	171.22	171.39	171.26	4 900 000	9 300 000	3 100 000	+-	A		-(3) /(3) A(3)
6084	Taq1	62	tgt	172.215	172	0	172.35	172.08	0	3 200 000	3 400 000	+=	/		-(3) /(3) A(3)
6085	Hha1	25	cag	215.52	216	215.51	0	215.53	10 100 000	0	5 200 000	-+(-)	V (\)		-(3) /(3) A(3)
6086	Hha1	25	cag	216.557	216	216.61	216.33	216.73	64 000 000	9 800 000	18 200 000	-=	\ (-)		-(3) /(3) A(3)
6087	Taq1	39	agg	67.183	67	67.29	67.21	67.05	3 900 000	74 300 000	6 900 000	+-	A		-(3) /(3) A(3)
6088	Taq1	39	agg	67.183	67	67.29	67.21	67.05	144.83	746.74	203.24	+-	A		-(3) /(3) A(3)
6089	Taq1	61	tct	120.51	121	0	120.27	120.75	0	9 800 000	6 500 000	+=	/		-(3) /(3) A(3)
6090	Taq1	61	tct	121.523	121	121.35	121.4	121.82	5 000 000	15 100 000	10 900 000	+=	/ (-)		-(3) /(3) A(3)
6091	Taq1	20	ctc	171.573	172	171.6	171.4	171.72	6 100 000	5 500 000	11 200 000	=+	/ (-)		-(3) /(3) A(3)
6092	Taq1	20	ctc	172.47	172	0	172.47	0	0	5 500 000	0	+-	A		-(3) /(3) A(3)
6093	Taq1	20	ctc	172.99	172	0	0	172.99	0	0	3 700 000	=+	/		-(3) /(3) A(3)
6094	Taq1	62	tgt	171.29	172	171.22	171.39	171.26	4 900 000	9 300 000	3 100 000	+-	A		-(3) /(3) A(3)
6095	Taq1	62	tgt	172.215	172	0	172.35	172.08	0	3 200 000	3 400 000	+=	/		-(3) /(3) A(3)
6096	Hha1	25	cag	215.52	216	215.51	0	215.53	10 100 000	0	5 200 000	-+(-)	V (\)		-(3) /(3) A(3)
6097	Hha1	25	cag	216.557	216	216.61	216.33	216.73	64 000 000	9 800 000	18 200 000	-=	\ (-)		-(3) /(3) A(3)
6098	Hha1	6	aga	156.663	157	156.64	156.75	156.6	17 700 000	5 500 000	15 400 000	-+	V		/(2)
6099	Hha1	6	aga	157.54	157	0	0	157.54	0	0	22 000 000	=+	/	/	/(2)
6100	Taq1	27	acg	156.53	157	0	0	156.53	0	0	3 600 000	=+	/		/(2)
6101	Taq1	27	acg	157.58	157	0	0	157.58	0	0	5 700 000	=+	/	/	/(2)
6102	Taq1	35	gga	100.28	100	0	0	100.28	0	0	4 000 000	=+	/	/	
6103	Taq1	64	gtt	100.51	100	100.52	100.49	100.52	5 300 000	5 600 000	14 800 000	=+	/ (-)	/	
6104	Taq1	29	gca	170.577	171	170.51	170.59	170.63	9 400 000	6 300 000	4 900 000	==	-		-2
6105	Taq1	29	gca	171.597	171	171.57	171.61	171.61	11 800 000	7 900 000	5 400 000	==	-		-2
6106	Taq1	49	aaa	171.005	172	0	170.94	171.07	0	12 900 000	58 400 000	=+	/		-2
6107	Taq1	49	aaa	171.86	172	172	171.76	171.82	64 500 000	9 700 000	4 200 000	-=	\ (-)		-2
6108	Taq1	49	aaa	172.815	172	172.62	173.01	0	30 100 000	9 900 000	0	-=	\		-2

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
6066	RATNGFIP.VGF	VGF	nerve growth factor-inducible protein	*	tgg	acg	increased
6067	RATNGFIP.VGF	VGF	nerve growth factor-inducible protein	*	tgg	acg	increased
6068	RATNGFIP.VGF	VGF	nerve growth factor-inducible protein	*	atg	gcc	increased
6069	RATNGFIP.VGF	VGF	nerve growth factor-inducible protein	*	atg	gcc	increased
6070	RATNGFIP.VGF	VGF	nerve growth factor-inducible protein	*	atg	gcc	increased
6071	RATNGFIP.VGF	VGF	nerve growth factor-inducible protein	*	atg	gcc	increased
6072	RATNGFIP.VGF	VGF	nerve growth factor-inducible protein	*	atg	gcc	increased
6073	RATNGFIP.VGF	VGF	nerve growth factor-inducible protein	*	gat	gcc	increased
6074	AF452647.PE1	nc	nesprin-1		gca	tct	decreased
6075	AF452647.PE1	nc	nesprin-1		gca	tct	decreased
6076	AF142097.ERG1	ERG1	N-ethylmaleimide sensitive factor	*	cca	agg	No change
6077	AF142097.ERG1	ERG1	N-ethylmaleimide sensitive factor	*	cca	agg	No change
6078	AF142097.ERG1	ERG1	N-ethylmaleimide sensitive factor	*	cgc	tct	No change
6079	AF142097.ERG1	ERG1	N-ethylmaleimide sensitive factor	*	cgc	tct	No change
6080	AF142097.ERG1	ERG1	N-ethylmaleimide sensitive factor	*	ctc	tgt	No change
6081	AF142097.ERG1	ERG1	N-ethylmaleimide sensitive factor	*	ctc	tgt	No change
6082	AF142097.ERG1	ERG1	N-ethylmaleimide sensitive factor	*	ctc	tgt	No change
6083	AF142097.ERG1	ERG1	N-ethylmaleimide sensitive factor	*	ctc	tgt	No change
6084	AF142097.ERG1	ERG1	N-ethylmaleimide sensitive factor	*	ctc	tgt	No change
6085	AF142097.ERG1	ERG1	N-ethylmaleimide sensitive factor	*	cag	ttt	No change
6086	AF142097.ERG1	ERG1	N-ethylmaleimide sensitive factor	*	cag	ttt	No change
6087	AF189019.NSF	NSF	N-ethylmaleimide sensitive factor	*	cca	agg	No change
6088	AF189019.NSF	NSF	N-ethylmaleimide sensitive factor	*	cca	agg	No change
6089	AF189019.NSF	NSF	N-ethylmaleimide sensitive factor	*	cgc	tct	No change
6090	AF189019.NSF	NSF	N-ethylmaleimide sensitive factor	*	cgc	tct	No change
6091	AF189019.NSF	NSF	N-ethylmaleimide sensitive factor	*	ctc	tgt	No change
6092	AF189019.NSF	NSF	N-ethylmaleimide sensitive factor	*	ctc	tgt	No change
6093	AF189019.NSF	NSF	N-ethylmaleimide sensitive factor	*	ctc	tgt	No change
6094	AF189019.NSF	NSF	N-ethylmaleimide sensitive factor	*	ctc	tgt	No change
6095	AF189019.NSF	NSF	N-ethylmaleimide sensitive factor	*	ctc	tgt	No change
6096	AF189019.NSF	NSF	N-ethylmaleimide sensitive factor	*	cag	ttt	No change
6097	AF189019.NSF	NSF	N-ethylmaleimide sensitive factor	*	cag	ttt	No change
6098	RNU72994.PE1	nc	neurabin		acg	aga	decreased
6099	RNU72994.PE1	nc	neurabin		acg	aga	decreased
6100	RNU72994.PE1	nc	neurabin		acg	aga	decreased
6101	RNU72994.PE1	nc	neurabin		acg	aga	decreased
6102	AF027181.PE1	nc	neurabin II		gga	gtt	decreased
6103	AF027181.PE1	nc	neurabin II		gga	gtt	decreased
6104	RNU35371.BIG-2	BIG-2	neural cell adhesion protein BIG-2 precursor		gca	aaa	No change
6105	RNU35371.BIG-2	BIG-2	neural cell adhesion protein BIG-2 precursor		gca	aaa	No change
6106	RNU35371.BIG-2	BIG-2	neural cell adhesion protein BIG-2 precursor		gca	aaa	No change
6107	RNU35371.BIG-2	BIG-2	neural cell adhesion protein BIG-2 precursor		gca	aaa	No change
6108	RNU35371.BIG-2	BIG-2	neural cell adhesion protein BIG-2 precursor		gca	aaa	No change

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
6109	Hha1	10	atg	215.46	216	215.46	0	0	3 800 000	0	0	-=	\	\	
6110	Taq1	10	atg	215.46	216	215.46	0	0	3 400 000	0	0	-=	\	\	
6111	Taq1	44	cgg	162.993	163	163.09	162.77	163.12	742.97	466.58	896.65	=+	/ (-)	/	/(2)
6112	Taq1	44	cgg	163.18	163	0	0	163.18	0	0	1 120.82	=+	/	/	/(2)
6113	Taq1	44	cgg	163.745	163	163.72	163.77	0	666.59	1 270.54	0	+-	A		/(2)
6114	Taq1	62	tgt	163.065	164	0	163.14	162.99	0	7 000 000	21 900 000	=+	/	/	/(2)
6115	Taq1	62	tgt	164.075	164	0	164.19	163.96	0	3 300 000	3 000 000	+=	/		/(2)
6116	Hha1	6	aga	117.44	118	0	0	117.44	0	0	9 400 000	=+	/		\(2)
6117	Hha1	6	aga	118.04	118	118.11	0	117.97	49 700 000	0	40 700 000	-+(=)	V		\(2)
6118	Taq1	39	agg	117.575	118	0	117.49	117.66	0	53 300 000	4 600 000	+-	A		\(2)
6119	Taq1	39	agg	117.875	118	118.09	0	117.66	17 600 000	0	135.49	-=(-)	\		\(2)
6120	Taq1	39	agg	117.49	118	0	117.49	0	0	535.68	0	+-	A		\(2)
6121	Taq1	39	agg	118.09	118	118.09	0	0	653.59	0	0	-=	\		\(2)
6122	Taq1	63	ctt	171.35	172	171.35	0	0	3 100 000	0	0	-=	\		\(2)
6123	Taq1	63	ctt	172.49	172	172.49	0	0	3 000 000	0	0	-=	\		\(2)
6124	Hha1	32	gtc	120.58	121	120.53	120.63	0	1 501.28	579.85	0	-=	\		\(6)
6125	Taq1	47	ggc	127.857	128	127.78	127.88	127.91	2 092.3	2 609.8	2 699.78	==	-		\(6)
6126	Taq1	17	cca	128.67	129	128.62	128.81	128.58	352.94	1 934.58	902.11	+-	A		\(6)
6127	Taq1	48	ggg	183.03	184	0	0	183.03	0	0	4 078.58	=+	/		\(6)
6128	Taq1	48	ggg	183.75	184	183.72	183.78	0	1 074.58	324.2	0	-=	\		\(6)
6129	Hha1	56	tga	185.11	186	0	185.2	185.02	0	181.63	999.82	=+	/		\(6)
6130	Hha1	56	tga	186	186	185.91	186.09	186	424.95	176.13	982.58	=+	/ (-)		\(6)
6131	Hha1	56	tga	187.11	186	187.14	187.08	0	343.23	264.2	0	=-	\		\(6)
6132	Taq1	44	cgg	235.46	236	0	235.46	0	0	315.84	0	+-	A		\(6)
6133	Taq1	44	cgg	236.01	236	236.01	0	0	243.03	0	0	-=	\		\(6)
6134	Taq1	44	cgg	237.07	236	237.07	0	0	1 211.67	0	0	-=	\		\(6)
6135	Taq1	17	cca	236.3	237	236.3	0	0	195.04	0	0	-=	\		\(6)
6136	Taq1	17	cca	237.59	237	0	0	237.59	0	0	826.94	=+	/		\(6)
6137	Hha1	39	agg	253.2	252	253.21	253.28	253.11	315.24	334.34	378.41	==	-		\(6)
6138	Taq1	17	cca	278.7	280	278.7	0	0	171.82	0	0	-=	\		\(6)
6139	Taq1	17	cca	279.73	280	279.73	0	0	427.25	0	0	-=	\		\(6)
6140	Hha1	59	ttc	99.033	99	98.95	99.2	98.95	364.01	175.34	274.23	-=	\ (-)		\(9)
6141	Taq1	27	acg	103.68	104	103.68	0	0	9 000 000	0	0	-=	\		\(9)
6142	Taq1	27	acg	104.46	104	0	0	104.46	0	0	4 400 000	=+	/		\(9)
6143	Hha1	33	agc	104.61	104	104.48	0	104.74	4 300 000	0	5 800 000	-+(=)	V		\(9)
6144	Hha1	39	agg	103.52	104	0	103.55	103.49	0	179.11	122.07	+=	/		\(9)
6145	Hha1	39	agg	104.08	104	104.08	0	0	469.2	0	0	-=	\		\(9)
6146	Taq1	1	tat	105.257	105	105.21	105.18	105.38	13 200 000	24 500 000	5 400 000	+-	A		\(9)
6147	Hha1	25	cag	113.745	114	113.58	113.91	0	6 800 000	7 500 000	0	=-	\		\(9)
6148	Hha1	25	cag	114.25	114	0	0	114.25	0	0	3 300 000	=+	/		\(9)
6149	Hha1	26	ctg	120.87	121	0	120.81	120.93	0	8 500 000	4 900 000	+=	/		\(9)
6150	Hha1	26	ctg	130.91	131	130.91	0	0	7 800 000	0	0	-=	\	\	\(9)
6151	Hha1	40	tgg	130.81	131	130.81	0	0	4 400 000	0	0	-=	\	\	\(9)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
6109	RNJ1NRM.PE1	nc	neural recognition molecule J1-160/180		atg	gtt	increased
6110	RNJ1NRM.PE1	nc	neural recognition molecule J1-160/180		atg	gtt	increased
6111	AF475282.SDNSF	Sdnsf	neural stem cell derived neuronal survival		cgg	tgt	decreased
6112	AF475282.SDNSF	Sdnsf	neural stem cell derived neuronal survival		cgg	tgt	decreased
6113	AF475282.SDNSF	Sdnsf	neural stem cell derived neuronal survival		cgg	tgt	decreased
6114	AF475282.SDNSF	Sdnsf	neural stem cell derived neuronal survival		cgg	tgt	decreased
6115	AF475282.SDNSF	Sdnsf	neural stem cell derived neuronal survival		cgg	tgt	decreased
6116	RATNVP1.PE1	nc	neural visinin-like protein (NVP)		aga	agg	increased
6117	RATNVP1.PE1	nc	neural visinin-like protein (NVP)		aga	agg	increased
6118	RATNVP1.PE1	nc	neural visinin-like protein (NVP)		aga	agg	increased
6119	RATNVP1.PE1	nc	neural visinin-like protein (NVP)		aga	agg	increased
6120	RATNVP1.PE1	nc	neural visinin-like protein (NVP)		aga	agg	increased
6121	RATNVP1.PE1	nc	neural visinin-like protein (NVP)		aga	agg	increased
6122	RATNVP1.PE1	nc	neural visinin-like protein (NVP)		ctt	taa	increased
6123	RATNVP1.PE1	nc	neural visinin-like protein (NVP)		ctt	taa	increased
6124	AF086607.PE1	nc	neurestin alpha		gtc	ccg	increased
6125	AF086607.PE1	nc	neurestin alpha		ggc	cca	increased
6126	AF086607.PE1	nc	neurestin alpha		ggc	cca	increased
6127	AF086607.PE1	nc	neurestin alpha		ggg	gtc	increased
6128	AF086607.PE1	nc	neurestin alpha		ggg	gtc	increased
6129	AF086607.PE1	nc	neurestin alpha		aca	tga	increased
6130	AF086607.PE1	nc	neurestin alpha		aca	tga	increased
6131	AF086607.PE1	nc	neurestin alpha		aca	tga	increased
6132	AF086607.PE1	nc	neurestin alpha		cgg	cca	increased
6133	AF086607.PE1	nc	neurestin alpha		cgg	cca	increased
6134	AF086607.PE1	nc	neurestin alpha		cgg	cca	increased
6135	AF086607.PE1	nc	neurestin alpha		cgg	cca	increased
6136	AF086607.PE1	nc	neurestin alpha		cgg	cca	increased
6137	AF086607.PE1	nc	neurestin alpha		gtg	agg	increased
6138	AF086607.PE1	nc	neurestin alpha		cca	tgc	increased
6139	AF086607.PE1	nc	neurestin alpha		cca	tgc	increased
6140	RATNIAA.PE1	neurexin I-alp	neurexin I-alpha		ttc	tgc	increased
6141	RATNIAA.PE1	neurexin I-alp	neurexin I-alpha		acg	tat	increased
6142	RATNIAA.PE1	neurexin I-alp	neurexin I-alpha		acg	tat	increased
6143	RATNIAA.PE1	neurexin I-alp	neurexin I-alpha		agg	agc	increased
6144	RATNIAA.PE1	neurexin I-alp	neurexin I-alpha		agg	agc	increased
6145	RATNIAA.PE1	neurexin I-alp	neurexin I-alpha		agg	agc	increased
6146	RATNIAA.PE1	neurexin I-alp	neurexin I-alpha		acg	tat	increased
6147	RATNIAA.PE1	neurexin I-alp	neurexin I-alpha		cag	gct	increased
6148	RATNIAA.PE1	neurexin I-alp	neurexin I-alpha		cag	gct	increased
6149	RATNIAA.PE1	neurexin I-alp	neurexin I-alpha		tca	ctg	increased
6150	RATNIAA.PE1	neurexin I-alp	neurexin I-alpha		tgg	ctg	increased
6151	RATNIAA.PE1	neurexin I-alp	neurexin I-alpha		tgg	ctg	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
6152	Taq1	62	tgt	189.04	190	0	189.04	0	0	4 100 000	0	+-	A		\(9)
6153	Taq1	62	tgt	189.87	190	189.87	0	0	3 900 000	0	0	-=	\		\(9)
6154	Taq1	7	caa	247.54	249	0	247.54	0	0	4 000 000	0	+-	A		\(9)
6155	Hha1	7	caa	247.68	249	247.68	0	0	4 400 000	0	0	-=	\		\(9)
6156	Hha1	7	caa	248.82	249	248.82	0	0	4 500 000	0	0	-=	\		\(9)
6157	Taq1	7	caa	250.34	249	250.34	0	0	5 000 000	0	0	-=	\		\(9)
6158	Hha1	39	agg	84.255	84	0	84.39	84.12	0	877.66	655.11	+=	/		/(5)
6159	Hha1	41	ccc	104.95	105	104.95	0	0	4 900 000	0	0	-=	\		/(5)
6160	Hha1	41	ccc	105.48	105	0	105.48	0	0	3 200 000	0	+-	A		/(5)
6161	Hha1	28	tcg	126.443	127	126.26	126.6	126.47	3 200 000	6 200 000	4 600 000	+=	/ (-)		/(5)
6162	Hha1	28	tcg	127.14	127	0	127.08	127.2	0	11 300 000	8 900 000	+=	/		/(5)
6163	Hha1	59	ttc	126.805	127	0	126.84	126.77	0	595.03	248.36	+-	A		/(5)
6164	Taq1	12	agt	160.007	160	160.08	159.88	160.06	3 800 000	5 800 000	3 500 000	==	-		/(5)
6165	Taq1	17	cca	159.37	160	0	159.37	0	0	232.68	0	+-	A		/(5)
6166	Taq1	17	cca	160.5	160	160.51	0	160.49	190.4	0	451.05	=+(+)	/		/(5)
6167	Hha1	39	agg	193.5	194	0	0	193.5	0	0	126.13	=+	/		/(5)
6168	Hha1	39	agg	194.28	194	0	0	194.28	0	0	195.31	=+	/		/(5)
6169	Hha1	26	ctg	225.8	227	0	0	225.8	0	0	4 300 000	=+	/		/(5)
6170	Hha1	26	ctg	228.08	227	228.08	0	0	7 500 000	0	0	-=	\		/(5)
6171	Hha1	33	agc	110.905	111	110.83	110.98	0	12 700 000	12 900 000	0	=-	\		\(3)
6172	Hha1	12	agt	174.913	174	174.81	174.85	175.08	3 231.64	4 123.87	3 601.1	==	-		\(3)
6173	Hha1	26	ctg	229.185	230	229.14	0	229.23	14 300 000	0	3 300 000	-=(-)	\		\(3)
6174	Hha1	26	ctg	230.06	230	230.11	230.01	0	8 300 000	3 300 000	0	-=	\		\(3)
6175	Hha1	26	ctg	231.04	230	0	231.04	0	0	3 600 000	0	+-	A		\(3)
6176	Hha1	59	ttc	228.933	230	229.24	228.79	228.77	447.21	129.35	155.22	-=	\ (-)		\(3)
6177	Hha1	33	agc	110.905	111	110.83	110.98	0	12 700 000	12 900 000	0	=-	\		\(3)
6178	Hha1	12	agt	174.913	174	174.81	174.85	175.08	3 231.64	4 123.87	3 601.1	==	-		\(3)
6179	Hha1	26	ctg	229.185	230	229.14	0	229.23	14 300 000	0	3 300 000	-=(-)	\		\(3)
6180	Hha1	26	ctg	230.06	230	230.11	230.01	0	8 300 000	3 300 000	0	-=	\		\(3)
6181	Hha1	26	ctg	231.04	230	0	231.04	0	0	3 600 000	0	+-	A		\(3)
6182	Hha1	59	ttc	228.933	230	229.24	228.79	228.77	447.21	129.35	155.22	-=	\ (-)		\(3)
6183	Hha1	33	agc	110.905	111	110.83	110.98	0	12 700 000	12 900 000	0	=-	\		\(3)
6184	Hha1	12	agt	174.913	174	174.81	174.85	175.08	3 231.64	4 123.87	3 601.1	==	-		\(3)
6185	Hha1	26	ctg	229.185	230	229.14	0	229.23	14 300 000	0	3 300 000	-=(-)	\		\(3)
6186	Hha1	26	ctg	230.06	230	230.11	230.01	0	8 300 000	3 300 000	0	-=	\		\(3)
6187	Hha1	26	ctg	231.04	230	0	231.04	0	0	3 600 000	0	+-	A		\(3)
6188	Hha1	59	ttc	228.933	230	229.24	228.79	228.77	447.21	129.35	155.22	-=	\ (-)		\(3)
6189	Hha1	33	agc	110.905	111	110.83	110.98	0	12 700 000	12 900 000	0	=-	\		\(3)
6190	Hha1	12	agt	174.913	174	174.81	174.85	175.08	3 231.64	4 123.87	3 601.1	==	-		\(3)
6191	Hha1	26	ctg	229.185	230	229.14	0	229.23	14 300 000	0	3 300 000	-=(-)	\		\(3)
6192	Hha1	26	ctg	230.06	230	230.11	230.01	0	8 300 000	3 300 000	0	-=	\		\(3)
6193	Hha1	26	ctg	231.04	230	0	231.04	0	0	3 600 000	0	+-	A		\(3)
6194	Hha1	59	ttc	228.933	230	229.24	228.79	228.77	447.21	129.35	155.22	-=	\ (-)		\(3)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
6152	RATNIAA.PE1	neurexin I-alp	neurexin I-alpha		gct	tgt	increased
6153	RATNIAA.PE1	neurexin I-alp	neurexin I-alpha		gct	tgt	increased
6154	RATNIAA.PE1	neurexin I-alp	neurexin I-alpha		caa	ctc	increased
6155	RATNIAA.PE1	neurexin I-alp	neurexin I-alpha		caa	ctc	increased
6156	RATNIAA.PE1	neurexin I-alp	neurexin I-alpha		caa	ctc	increased
6157	RATNIAA.PE1	neurexin I-alp	neurexin I-alpha		caa	ctc	increased
6158	RATNIIBA.PE1	nc	neurexin II-beta-a		tgg	agg	decreased
6159	RATNIIBA.PE1	nc	neurexin II-beta-a		ccc	tcc	decreased
6160	RATNIIBA.PE1	nc	neurexin II-beta-a		ccc	tcc	decreased
6161	RATNIIBA.PE1	nc	neurexin II-beta-a		ttc	tcg	decreased
6162	RATNIIBA.PE1	nc	neurexin II-beta-a		ttc	tcg	decreased
6163	RATNIIBA.PE1	nc	neurexin II-beta-a		ttc	tcg	decreased
6164	RATNIIBA.PE1	nc	neurexin II-beta-a		agt	cca	decreased
6165	RATNIIBA.PE1	nc	neurexin II-beta-a		agt	cca	decreased
6166	RATNIIBA.PE1	nc	neurexin II-beta-a		agt	cca	decreased
6167	RATNIIBA.PE1	nc	neurexin II-beta-a		gac	agg	decreased
6168	RATNIIBA.PE1	nc	neurexin II-beta-a		gac	agg	decreased
6169	RATNIIBA.PE1	nc	neurexin II-beta-a		ctg	cag	decreased
6170	RATNIIBA.PE1	nc	neurexin II-beta-a		ctg	cag	decreased
6171	RATNIIIA.PE1	nc	neurexin III-alpha		agc	tca	increased
6172	RATNIIIA.PE1	nc	neurexin III-alpha		agt	agt	increased
6173	RATNIIIA.PE1	nc	neurexin III-alpha		ttc	ctg	increased
6174	RATNIIIA.PE1	nc	neurexin III-alpha		ttc	ctg	increased
6175	RATNIIIA.PE1	nc	neurexin III-alpha		ttc	ctg	increased
6176	RATNIIIA.PE1	nc	neurexin III-alpha		ttc	ctg	increased
6177	RATNIIIA.PE2	nc	neurexin III-alpha		agc	tca	increased
6178	RATNIIIA.PE2	nc	neurexin III-alpha		agt	agt	increased
6179	RATNIIIA.PE2	nc	neurexin III-alpha		ttc	ctg	increased
6180	RATNIIIA.PE2	nc	neurexin III-alpha		ttc	ctg	increased
6181	RATNIIIA.PE2	nc	neurexin III-alpha		ttc	ctg	increased
6182	RATNIIIA.PE2	nc	neurexin III-alpha		ttc	ctg	increased
6183	RATNIIIA.PE3	nc	neurexin III-alpha		agc	tca	increased
6184	RATNIIIA.PE3	nc	neurexin III-alpha		agt	agt	increased
6185	RATNIIIA.PE3	nc	neurexin III-alpha		ttc	ctg	increased
6186	RATNIIIA.PE3	nc	neurexin III-alpha		ttc	ctg	increased
6187	RATNIIIA.PE3	nc	neurexin III-alpha		ttc	ctg	increased
6188	RATNIIIA.PE3	nc	neurexin III-alpha		ttc	ctg	increased
6189	RATNIIIA.PE4	nc	neurexin III-alpha		agc	tca	increased
6190	RATNIIIA.PE4	nc	neurexin III-alpha		agt	agt	increased
6191	RATNIIIA.PE4	nc	neurexin III-alpha		ttc	ctg	increased
6192	RATNIIIA.PE4	nc	neurexin III-alpha		ttc	ctg	increased
6193	RATNIIIA.PE4	nc	neurexin III-alpha		ttc	ctg	increased
6194	RATNIIIA.PE4	nc	neurexin III-alpha		ttc	ctg	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
6195	Hha1	33	agc	110.905	111	110.83	110.98	0	12 700 000	12 900 000	0	=-	\		\(3)
6196	Hha1	12	agt	174.913	174	174.81	174.85	175.08	3 231.64	4 123.87	3 601.1	==	-		\(3)
6197	Hha1	26	ctg	229.185	230	229.14	0	229.23	14 300 000	0	3 300 000	-=(-)	\		\(3)
6198	Hha1	26	ctg	230.06	230	230.11	230.01	0	8 300 000	3 300 000	0	-=	\		\(3)
6199	Hha1	26	ctg	231.04	230	0	231.04	0	0	3 600 000	0	+-	A		\(3)
6200	Hha1	59	ttc	228.933	230	229.24	228.79	228.77	447.21	129.35	155.22	-=	\ (-)		\(3)
6201	Hha1	33	agc	110.905	111	110.83	110.98	0	12 700 000	12 900 000	0	=-	\		\(3)
6202	Hha1	12	agt	174.913	174	174.81	174.85	175.08	3 231.64	4 123.87	3 601.1	==	-		\(3)
6203	Hha1	26	ctg	229.185	230	229.14	0	229.23	14 300 000	0	3 300 000	-=(-)	\		\(3)
6204	Hha1	26	ctg	230.06	230	230.11	230.01	0	8 300 000	3 300 000	0	-=	\		\(3)
6205	Hha1	26	ctg	231.04	230	0	231.04	0	0	3 600 000	0	+-	A		\(3)
6206	Hha1	59	ttc	228.933	230	229.24	228.79	228.77	447.21	129.35	155.22	-=	\ (-)		\(3)
6207	Hha1	39	agg	76.73	77	76.8	76.51	76.88	549.85	1 540.39	329.58	+-	A		A(3)
6208	Hha1	27	acg	123.15	123	0	123.15	0	0	3 600 000	0	+-	A		A(3)
6209	Hha1	40	tgg	122.55	123	0	122.55	0	0	3 900 000	0	+-	A		A(3)
6210	Hha1	40	tgg	123.29	123	0	123.13	123.45	0	6 200 000	4 300 000	+=	/		A(3)
6211	Taq1	45	gcc	256.03	257	256.06	256	0	3 900 000	4 800 000	0	=-	\		A(3)
6212	Taq1	45	gcc	257.05	257	257.05	0	0	3 400 000	0	0	-=	\		A(3)
6213	Taq1	45	gcc	257.86	257	0	0	257.86	0	0	3 200 000	=+	/		A(3)
6214	Hha1	27	acg	60.24	60	0	0	60.24	0	0	5 700 000	=+	/		/(2)
6215	Hha1	33	agc	64.945	65	0	65.19	64.7	0	4 100 000	31 500 000	=+	/		/(2)
6216	Hha1	27	acg	60.24	60	0	0	60.24	0	0	5 700 000	=+	/		/(2)
6217	Hha1	33	agc	64.945	65	0	65.19	64.7	0	4 100 000	31 500 000	=+	/		/(2)
6218	Hha1	27	acg	60.24	60	0	0	60.24	0	0	5 700 000	=+	/		/(2)
6219	Hha1	33	agc	64.945	65	0	65.19	64.7	0	4 100 000	31 500 000	=+	/		/(2)
6220	Taq1	14	gat	175.757	175	175.7	175.7	175.87	7 200 000	7 200 000	4 900 000	==	-	-	
6221	Taq1	63	ctt	175.553	175	175.54	175.49	175.63	3 000 000	3 300 000	3 200 000	==	-	-	
6222	Hha1	61	tct	189.98	190	190.02	189.96	189.96	4 700 000	4 900 000	3 900 000	==	-	(-)	
6223	Hha1	49	aaa	189.967	191	189.91	189.98	190.01	22 700 000	39 700 000	5 300 000	=-	\ (-)	(-)	
6224	Hha1	20	ctc	135.12	135	135.12	0	0	406.33	0	0	-=	\	(\)	
6225	Hha1	39	agg	134.885	135	134.82	0	134.95	454.54	0	227.86	-+(-)	V (\)	(\)	
6226	Hha1	59	ttc	72.683	73	72.76	72.64	72.65	925.63	675.52	8 573.72	=+	/ (-)		-2
6227	Hha1	27	acg	86.307	86	86.3	86.35	86.27	21 200 000	3 600 000	3 400 000	-=	\ (-)		-2
6228	Hha1	20	ctc	75.97	76	75.87	0	76.07	571.62	0	632.15	-+(=)	V		V(2)
6229	Hha1	44	cgg	81.375	81	81.44	0	81.31	4 500 000	0	4 700 000	-+(=)	V		V(2)
6230	Hha1	41	ccc	94.935	95	94.75	0	95.12	4 700 000	0	3 000 000	-+(=)	V		V(2)
6231	Hha1	41	ccc	95.465	95	95.52	95.41	0	68 600 000	8 000 000	0	-=	\		V(2)
6232	Hha1	27	acg	95.46	96	95.48	0	95.44	3 400 000	0	3 400 000	-+(=)	V		V(2)
6233	Hha1	27	acg	96.293	96	96.26	96.34	96.28	16 200 000	6 700 000	15 600 000	-+	V		V(2)
6234	Hha1	40	tgg	115.65	116	115.65	0	0	3 000 000	0	0	-=	\		\(12)
6235	Hha1	40	tgg	116.43	116	116.43	0	0	8 900 000	0	0	-=	\		\(12)
6236	Taq1	8	gaa	121.827	122	122.07	121.68	121.73	9 600 000	3 000 000	3 800 000	-=	\ (-)		\(12)
6237	Hha1	8	gaa	122.317	122	122.3	122.31	122.34	20 200 000	8 200 000	14 600 000	-=	\ (-)		\(12)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
6195	RATNIIIA.PE5	nc	neurexin III-alpha		agc	tca	increased
6196	RATNIIIA.PE5	nc	neurexin III-alpha		agt	agt	increased
6197	RATNIIIA.PE5	nc	neurexin III-alpha		ttc	ctg	increased
6198	RATNIIIA.PE5	nc	neurexin III-alpha		ttc	ctg	increased
6199	RATNIIIA.PE5	nc	neurexin III-alpha		ttc	ctg	increased
6200	RATNIIIA.PE5	nc	neurexin III-alpha		ttc	ctg	increased
6201	RATNIIIA.PE6	nc	neurexin III-alpha		agc	tca	increased
6202	RATNIIIA.PE6	nc	neurexin III-alpha		agt	agt	increased
6203	RATNIIIA.PE6	nc	neurexin III-alpha		ttc	ctg	increased
6204	RATNIIIA.PE6	nc	neurexin III-alpha		ttc	ctg	increased
6205	RATNIIIA.PE6	nc	neurexin III-alpha		ttc	ctg	increased
6206	RATNIIIA.PE6	nc	neurexin III-alpha		ttc	ctg	increased
6207	RATNCAN.PE1	nc	neurocan		aca	agg	increased by mild
6208	RATNCAN.PE1	nc	neurocan		tgg	acg	increased by mild
6209	RATNCAN.PE1	nc	neurocan		tgg	acg	increased by mild
6210	RATNCAN.PE1	nc	neurocan		tgg	acg	increased by mild
6211	RATNCAN.PE1	nc	neurocan		gcc	ttt	increased by mild
6212	RATNCAN.PE1	nc	neurocan		gcc	ttt	increased by mild
6213	RATNCAN.PE1	nc	neurocan		gcc	ttt	increased by mild
6214	AF105254.PE1	nc	neuroendocrine secretory protein 55		cga	acg	decreased
6215	AF105254.PE1	nc	neuroendocrine secretory protein 55		agc	tct	decreased
6216	AF107844.PE1	XLalphas	neuroendocrine-specific Golgi protein p55	*	cga	acg	decreased
6217	AF107844.PE1	XLalphas	neuroendocrine-specific Golgi protein p55	*	agc	tct	decreased
6218	AF107845.PE1	XLalphas	neuroendocrine-specific Golgi protein p55	*	cga	acg	decreased
6219	AF107845.PE1	XLalphas	neuroendocrine-specific Golgi protein p55	*	agc	tct	decreased
6220	RNNFMMR.PE1	nc	Neurofilament protein middle (NF-M)		gat	ctt	No change
6221	RNNFMMR.PE1	nc	Neurofilament protein middle (NF-M)		gat	ctt	No change
6222	RNNFMMR.PE1	nc	Neurofilament protein middle (NF-M)		aaa	tct	No change
6223	RNNFMMR.PE1	nc	Neurofilament protein middle (NF-M)		aaa	tct	No change
6224	RNU67777.PE1	nc	neurogenin		ctc	agg	increased
6225	RNU67777.PE1	nc	neurogenin		ctc	agg	increased
6226	RNU41662.PE1	nc	neuroligin 2		ttc	act	No change
6227	RNU41662.PE1	nc	neuroligin 2		ccg	acg	No change
6228	RNU41663.PE1	nc	neuroligin 3		ctc	cgc	decreased by mild
6229	RNU41663.PE1	nc	neuroligin 3		ccg	cgg	decreased by mild
6230	AF155959.PE1	nc	neuronal migration protein doublecortin		ccc	acg	decreased by mild
6231	AF155959.PE1	nc	neuronal migration protein doublecortin		ccc	acg	decreased by mild
6232	AF155959.PE1	nc	neuronal migration protein doublecortin		ccc	acg	decreased by mild
6233	AF155959.PE1	nc	neuronal migration protein doublecortin		ccc	acg	decreased by mild
6234	RNU67309.PE1	nc	neuronal nitric oxide synthase		cct	tgg	increased
6235	RNU67309.PE1	nc	neuronal nitric oxide synthase		cct	tgg	increased
6236	RNU67309.PE1	nc	neuronal nitric oxide synthase		tca	gaa	increased
6237	RNU67309.PE1	nc	neuronal nitric oxide synthase		tca	gaa	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
6238	Taq1	8	gaa	122.65	122	0	122.62	122.68	0	3 300 000	6 800 000	++	/		\(12)
6239	Taq1	55	tca	121.44	122	0	121.44	0	0	21 900 000	0	+-	A		\(12)
6240	Taq1	55	tca	122.14	122	0	122.14	0	0	26 800 000	0	+-	A		\(12)
6241	Taq1	11	act	138.63	139	0	0	138.63	0	0	21 400 000	=+	/		\(12)
6242	Hha1	11	act	138.875	139	138.89	138.86	0	13 800 000	15 700 000	0	=-	\		\(12)
6243	Hha1	11	act	139.37	139	0	0	139.37	0	0	7 200 000	=+	/		\(12)
6244	Taq1	11	act	139.06	139	139.11	139.01	0	16 300 000	76 300 000	0	+-	A		\(12)
6245	Taq1	11	act	139.68	139	0	0	139.68	0	0	6 400 000	=+	/		\(12)
6246	Hha1	11	act	139.72	139	139.72	0	0	6 400 000	0	0	-=	\		\(12)
6247	Taq1	30	cgt	139.31	139	139.31	0	0	3 600 000	0	0	-=	\		\(12)
6248	Hha1	8	gaa	172.563	173	172.45	172.65	172.59	5 800 000	6 900 000	3 100 000	=-	\ (-)		\(12)
6249	Taq1	8	gaa	173.14	173	173.14	0	0	3 000 000	0	0	-=	\		\(12)
6250	Taq1	8	gaa	174	173	0	0	174	0	0	3 100 000	=+	/		\(12)
6251	Hha1	8	gaa	173.603	173	173.72	173.58	173.51	11 600 000	9 300 000	3 000 000	=-	\ (-)	(-)	\(12)
6252	Taq1	29	gca	172.643	173	172.69	172.62	172.62	15 100 000	11 200 000	5 400 000	==	-		\(12)
6253	Taq1	29	gca	173.67	173	173.73	173.62	173.66	6 400 000	4 400 000	6 500 000	==	-	(-)	\(12)
6254	Hha1	3	aac	174.78	175	174.78	0	0	4 000 000	0	0	-=	\		\(12)
6255	Hha1	3	aac	176.03	175	175.89	175.88	176.32	3 200 000	4 800 000	3 300 000	==	-	-	\(12)
6256	Taq1	19	cac	174.867	175	174.82	174.87	174.91	10 500 000	7 500 000	4 300 000	==	-		\(12)
6257	Taq1	19	cac	175.857	175	175.77	175.82	175.98	7 900 000	10 400 000	6 900 000	==	-	-	\(12)
6258	Taq1	17	cca	190.26	191	0	190.26	0	0	425.47	0	+-	A		\(12)
6259	Taq1	17	cca	191.373	191	191.43	191.21	191.48	157.89	279.21	571.34	=+	/ (-)		\(12)
6260	Taq1	26	ctg	190.3	191	0	0	190.3	0	0	7 800 000	=+	/		\(12)
6261	Taq1	26	ctg	190.87	191	0	190.87	0	0	3 500 000	0	+-	A		\(12)
6262	Taq1	57	ctg	190.315	191	190.34	190.29	0	3 700 000	3 700 000	0	=-	\		\(12)
6263	Taq1	57	ctg	191.06	191	191.06	0	0	3 000 000	0	0	-=	\		\(12)
6264	Taq1	57	ctg	191.22	191	191.22	0	0	3 100 000	0	0	-=	\		\(12)
6265	Taq1	45	gcc	320.855	320	320.79	320.92	0	4 200 000	5 200 000	0	=-	\		\(12)
6266	Taq1	45	gcc	321.905	320	321.9	321.91	0	7 800 000	9 200 000	0	=-	\		\(12)
6267	Hha1	33	agc	76.7	77	76.7	0	0	3 200 000	0	0	-=	\		/(2)
6268	Hha1	33	agc	85.25	85	0	0	85.25	0	0	13 400 000	=+	/		/(2)
6269	Hha1	39	agg	190.03	191	0	0	190.03	0	0	146.48	=+	/		/(2)
6270	Hha1	39	agg	190.715	191	0	190.77	190.66	0	197.02	146.48	+=	/		/(2)
6271	Hha1	39	agg	191.23	191	0	0	191.23	0	0	183.1	=+	/		/(2)
6272	Hha1	59	ttc	79.593	80	79.5	79.64	79.64	4 362.97	2 230.65	2 129.2	-=	\ (-)		-4
6273	Hha1	59	ttc	80.225	80	80.31	0	80.14	2 028.08	0	1 836.85	-+(=)	V		-4
6274	Hha1	33	agc	88.273	88	88.16	88.2	88.46	57 000 000	40 900 000	16 400 000	==	-		-4
6275	Hha1	33	agc	91.3	91	91.16	91.44	0	3 500 000	4 000 000	0	=-	\		-4
6276	Hha1	26	ctg	108.8	109	108.86	108.8	108.74	5 700 000	5 700 000	4 900 000	==	-	-	-4
6277	Hha1	33	agc	108.77	109	108.83	108.8	108.68	11 600 000	9 300 000	8 800 000	==	-	-	-4
6278	Taq1	7	caa	151.545	152	151.59	151.5	0	3 200 000	5 000 000	0	=-	\		\(4)
6279	Hha1	7	caa	152.167	152	151.98	152.29	152.23	8 400 000	9 900 000	3 600 000	=-	\ (-)		\(4)
6280	Taq1	7	caa	152.59	152	152.59	0	0	3 200 000	0	0	-=	\		\(4)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
6238	RNU67309.PE1	nc	neuronal nitric oxide synthase		tca	gaa	increased
6239	RNU67309.PE1	nc	neuronal nitric oxide synthase		tca	gaa	increased
6240	RNU67309.PE1	nc	neuronal nitric oxide synthase		tca	gaa	increased
6241	RNU67309.PE1	nc	neuronal nitric oxide synthase		cgt	act	increased
6242	RNU67309.PE1	nc	neuronal nitric oxide synthase		cgt	act	increased
6243	RNU67309.PE1	nc	neuronal nitric oxide synthase		cgt	act	increased
6244	RNU67309.PE1	nc	neuronal nitric oxide synthase		cgt	act	increased
6245	RNU67309.PE1	nc	neuronal nitric oxide synthase		cgt	act	increased
6246	RNU67309.PE1	nc	neuronal nitric oxide synthase		cgt	act	increased
6247	RNU67309.PE1	nc	neuronal nitric oxide synthase		cgt	act	increased
6248	RNU67309.PE1	nc	neuronal nitric oxide synthase		gaa	gca	increased
6249	RNU67309.PE1	nc	neuronal nitric oxide synthase		gaa	gca	increased
6250	RNU67309.PE1	nc	neuronal nitric oxide synthase		gaa	gca	increased
6251	RNU67309.PE1	nc	neuronal nitric oxide synthase		gaa	gca	No change
6252	RNU67309.PE1	nc	neuronal nitric oxide synthase		gaa	gca	increased
6253	RNU67309.PE1	nc	neuronal nitric oxide synthase		gaa	gca	No change
6254	RNU67309.PE1	nc	neuronal nitric oxide synthase		aac	cac	increased
6255	RNU67309.PE1	nc	neuronal nitric oxide synthase		aac	cac	No change
6256	RNU67309.PE1	nc	neuronal nitric oxide synthase		aac	cac	increased
6257	RNU67309.PE1	nc	neuronal nitric oxide synthase		aac	cac	No change
6258	RNU67309.PE1	nc	neuronal nitric oxide synthase		cca	gag	increased
6259	RNU67309.PE1	nc	neuronal nitric oxide synthase		cca	gag	increased
6260	RNU67309.PE1	nc	neuronal nitric oxide synthase		ctg	gag	increased
6261	RNU67309.PE1	nc	neuronal nitric oxide synthase		ctg	gag	increased
6262	RNU67309.PE1	nc	neuronal nitric oxide synthase		ctg	gag	increased
6263	RNU67309.PE1	nc	neuronal nitric oxide synthase		ctg	gag	increased
6264	RNU67309.PE1	nc	neuronal nitric oxide synthase		ctg	gag	increased
6265	RNU67309.PE1	nc	neuronal nitric oxide synthase		tgg	gcc	increased
6266	RNU67309.PE1	nc	neuronal nitric oxide synthase		tgg	gcc	increased
6267	AF005099.PE1	nc	neuronal pentraxin receptor		gga	agc	decreased
6268	AF005099.PE1	nc	neuronal pentraxin receptor		aag	agc	decreased
6269	AF005099.PE1	nc	neuronal pentraxin receptor		agg	tcg	decreased
6270	AF005099.PE1	nc	neuronal pentraxin receptor		agg	tcg	decreased
6271	AF005099.PE1	nc	neuronal pentraxin receptor		agg	tcg	decreased
6272	RNRNALRBF.NOR.2	NOR.2	neuron-derived orphan receptor		ttc	ggg	No change
6273	RNRNALRBF.NOR.2	NOR.2	neuron-derived orphan receptor		ttc	ggg	No change
6274	RNRNALRBF.NOR.2	NOR.2	neuron-derived orphan receptor		tca	agc	No change
6275	RNRNALRBF.NOR.2	NOR.2	neuron-derived orphan receptor		cca	agc	No change
6276	RNRNALRBF.NOR.2	NOR.2	neuron-derived orphan receptor		ctg	agc	No change
6277	RNRNALRBF.NOR.2	NOR.2	neuron-derived orphan receptor		ctg	agc	No change
6278	AF459021.PE1	nc	neuron-specific class III beta-tubulin		caa	agg	increased
6279	AF459021.PE1	nc	neuron-specific class III beta-tubulin		caa	agg	increased
6280	AF459021.PE1	nc	neuron-specific class III beta-tubulin		caa	agg	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
6281	Taq1	39	agg	151.215	152	151.33	151.1	0	14 900 000	38 500 000	0	+-	A		\(4)
6282	Taq1	39	agg	152.155	152	152.37	151.94	0	20 800 000	30 900 000	0	=-	\		\(4)
6283	Taq1	39	agg	151.33	152	151.33	0	0	553.32	0	0	-=	\		\(4)
6284	Taq1	39	agg	152.52	152	152.37	152.63	152.56	772.43	25 800 000	20 700 000	+=	/ (-)		\(4)
6285	Taq1	39	agg	151.1	152	0	151.1	0	0	386.93	0	+-	A		\(4)
6286	Taq1	39	agg	151.94	152	0	151.94	0	0	310.55	0	+-	A		\(4)
6287	Taq1	39	agg	152.595	152	0	152.63	152.56	0	259.29	609.72	=+	/		\(4)
6288	Hha1	60	ttg	217.55	217	0	0	217.55	0	0	5 900 000	=+	/		\(4)
6289	Hha1	21	acc	106.475	107	0	106.29	106.66	0	5 200 000	9 700 000	++	/	(/)	/(6)
6290	Hha1	21	acc	106.58	107	0	106.58	0	0	3 900 000	0	+-	A		/(6)
6291	Taq1	21	acc	106.53	107	106.49	0	106.57	18 200 000	0	37 000 000	-+(+)	V (/)	(/)	/(6)
6292	Taq1	21	acc	107.02	107	0	107.02	0	0	10 000 000	0	+-	A		/(6)
6293	Hha1	6	aga	143.277	143	143.37	143.3	143.16	10 800 000	5 000 000	3 900 000	-=	\ (-)		/(6)
6294	Hha1	11	act	142.36	143	0	0	142.36	0	0	5 600 000	=+	/		/(6)
6295	Taq1	11	act	142.53	143	142.43	0	142.63	3 000 000	0	42 500 000	=+(+)	/		/(6)
6296	Hha1	11	act	143.3	143	143.29	143.26	143.35	7 600 000	5 700 000	14 500 000	=+	/ (-)		/(6)
6297	Taq1	11	act	143.46	143	143.38	143.28	143.72	5 200 000	3 900 000	13 300 000	=+	/ (-)		/(6)
6298	Taq1	55	tca	82.173	82	82.13	82.3	82.09	3 300 000	6 500 000	5 200 000	+=	/ (-)		/(2)
6299	Taq1	26	ctg	235.85	235	0	0	235.85	0	0	4 000 000	=+	/		/(2)
6300	Hha1	44	cgg	64.027	64	64.08	63.99	64.01	41 800 000	46 500 000	111 400 000	=+	/ (-)		-2
6301	Hha1	44	cgg	71.307	71	71.21	71.39	71.32	26 500 000	4 100 000	9 300 000	-=	\ (-)		-2
6302	Hha1	44	cgg	64.027	64	64.08	63.99	64.01	41 800 000	46 500 000	111 400 000	=+	/ (-)		-2
6303	Hha1	44	cgg	71.307	71	71.21	71.39	71.32	26 500 000	4 100 000	9 300 000	-=	\ (-)		-2
6304	Taq1	22	tcc	211.705	211	211.67	211.74	0	3 400 000	4 100 000	0	=-	\	\	
6305	Hha1	22	tcc	211.76	211	211.76	0	0	8 500 000	0	0	-=	\	\	
6306	Taq1	22	tcc	211.705	211	211.67	211.74	0	3 400 000	4 100 000	0	=-	\	\	
6307	Hha1	22	tcc	211.76	211	211.76	0	0	8 500 000	0	0	-=	\	\	
6308	Hha1	31	gac	87.46	87	87.42	87.56	87.4	9 500 000	4 500 000	16 100 000	=+	/ (-)		\(4)
6309	Hha1	20	ctc	88.21	88	0	0	88.21	0	0	620.22	=+	/		\(4)
6310	Taq1	17	cca	186.01	187	185.78	186.24	0	260.06	465.36	0	=-	\		\(4)
6311	Taq1	17	cca	187.32	187	187.3	187.34	0	185.76	285.86	0	=-	\		\(4)
6312	Taq1	17	cca	187.57	187	187.57	0	0	148.6	0	0	-=	\		\(4)
6313	Taq1	40	tgg	186.34	187	186.34	0	0	3 900 000	0	0	-=	\		\(4)
6314	Taq1	18	cct	188.187	189	188.32	188.23	188.01	4 800 000	7 400 000	4 200 000	==	-		\(4)
6315	Taq1	18	cct	189.14	189	189.15	189.13	0	9 100 000	9 100 000	0	=-	\		\(4)
6316	Taq1	36	ggt	188.07	189	188.07	0	0	3 000 000	0	0	-=	\		\(4)
6317	Taq1	36	ggt	189.88	189	189.88	0	0	3 100 000	0	0	-=	\		\(4)
6318	Hha1	31	gac	87.46	87	87.42	87.56	87.4	9 500 000	4 500 000	16 100 000	=+	/ (-)		\(4)
6319	Hha1	20	ctc	88.21	88	0	0	88.21	0	0	620.22	=+	/		\(4)
6320	Taq1	17	cca	186.01	187	185.78	186.24	0	260.06	465.36	0	=-	\		\(4)
6321	Taq1	17	cca	187.32	187	187.3	187.34	0	185.76	285.86	0	=-	\		\(4)
6322	Taq1	17	cca	187.57	187	187.57	0	0	148.6	0	0	-=	\		\(4)
6323	Taq1	40	tgg	186.34	187	186.34	0	0	3 900 000	0	0	-=	\		\(4)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
6281	AF459021.PE1	nc	neuron-specific class III beta-tubulin		caa	agg	increased
6282	AF459021.PE1	nc	neuron-specific class III beta-tubulin		caa	agg	increased
6283	AF459021.PE1	nc	neuron-specific class III beta-tubulin		caa	agg	increased
6284	AF459021.PE1	nc	neuron-specific class III beta-tubulin		caa	agg	increased
6285	AF459021.PE1	nc	neuron-specific class III beta-tubulin		caa	agg	increased
6286	AF459021.PE1	nc	neuron-specific class III beta-tubulin		caa	agg	increased
6287	AF459021.PE1	nc	neuron-specific class III beta-tubulin		caa	agg	increased
6288	AF459021.PE1	nc	neuron-specific class III beta-tubulin		atg	ttg	increased
6289	AY089719.PE1	nc	neuron-specific epidermal growth factor-like		acc	taa	decreased
6290	AY089719.PE1	nc	neuron-specific epidermal growth factor-like		acc	taa	decreased
6291	AY089719.PE1	nc	neuron-specific epidermal growth factor-like		acc	taa	decreased
6292	AY089719.PE1	nc	neuron-specific epidermal growth factor-like		acc	taa	decreased
6293	AY089719.PE1	nc	neuron-specific epidermal growth factor-like		aga	act	decreased
6294	AY089719.PE1	nc	neuron-specific epidermal growth factor-like		aga	act	decreased
6295	AY089719.PE1	nc	neuron-specific epidermal growth factor-like		aga	act	decreased
6296	AY089719.PE1	nc	neuron-specific epidermal growth factor-like		aga	act	decreased
6297	AY089719.PE1	nc	neuron-specific epidermal growth factor-like		aga	act	decreased
6298	AF016296.PE1	nc	neuropilin		ttt	tca	decreased
6299	AF016296.PE1	nc	neuropilin		ttt	ctg	decreased
6300	RNO294475.GFRA4	Gfra4	neurotrophic factor receptor		cgc	cgg	No change
6301	RNO294475.GFRA4	Gfra4	neurotrophic factor receptor		cct	cgg	No change
6302	RNO294476.GFRA4	Gfra4	neurotrophic factor receptor		cgc	cgg	No change
6303	RNO294476.GFRA4	Gfra4	neurotrophic factor receptor		cct	cgg	No change
6304	RATNT4P.NT-4	NT-4	neurotrophin-4		gac	tcc	increased
6305	RATNT4P.NT-4	NT-4	neurotrophin-4		gac	tcc	increased
6306	S69323.PE1	nc	neurotrophin-5		gac	tcc	increased
6307	S69323.PE1	nc	neurotrophin-5		gac	tcc	increased
6308	AF547392.NCF1	Ncf1	neutrophil cytosolic factor 1	*	gac	gga	increased
6309	AF547392.NCF1	Ncf1	neutrophil cytosolic factor 1	*	ctc	tgc	increased
6310	AF547392.NCF1	Ncf1	neutrophil cytosolic factor 1	*	cca	tgg	increased
6311	AF547392.NCF1	Ncf1	neutrophil cytosolic factor 1	*	cca	tgg	increased
6312	AF547392.NCF1	Ncf1	neutrophil cytosolic factor 1	*	cca	tgg	increased
6313	AF547392.NCF1	Ncf1	neutrophil cytosolic factor 1	*	cca	tgg	increased
6314	AF547392.NCF1	Ncf1	neutrophil cytosolic factor 1	*	ggt	cct	increased
6315	AF547392.NCF1	Ncf1	neutrophil cytosolic factor 1	*	ggt	cct	increased
6316	AF547392.NCF1	Ncf1	neutrophil cytosolic factor 1	*	ggt	cct	increased
6317	AF547392.NCF1	Ncf1	neutrophil cytosolic factor 1	*	ggt	cct	increased
6318	AF547393.NCF1	Ncf1	neutrophil cytosolic factor 1		gac	gga	increased
6319	AF547393.NCF1	Ncf1	neutrophil cytosolic factor 1		ctc	tgc	increased
6320	AF547393.NCF1	Ncf1	neutrophil cytosolic factor 1		cca	tgg	increased
6321	AF547393.NCF1	Ncf1	neutrophil cytosolic factor 1		cca	tgg	increased
6322	AF547393.NCF1	Ncf1	neutrophil cytosolic factor 1		cca	tgg	increased
6323	AF547393.NCF1	Ncf1	neutrophil cytosolic factor 1		cca	tgg	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
6324	Taq1	18	cct	188.187	189	188.32	188.23	188.01	4 800 000	7 400 000	4 200 000	==	-		\(4)
6325	Taq1	18	cct	189.14	189	189.15	189.13	0	9 100 000	9 100 000	0	=-	\		\(4)
6326	Taq1	36	ggt	188.07	189	188.07	0	0	3 000 000	0	0	-=	\		\(4)
6327	Taq1	36	ggt	189.88	189	189.88	0	0	3 100 000	0	0	-=	\		\(4)
6328	Hha1	33	agc	112.82	113	112.83	112.81	0	17 300 000	12 900 000	0	=-	\		\(3)
6329	Hha1	39	agg	159.2	160	159.37	159.03	0	271.26	310.46	0	=-	\		\(3)
6330	Hha1	39	agg	160.39	160	160.39	0	0	278.59	0	0	-=	\	\	\(3)
6331	Hha1	49	aaa	160.525	161	160.71	160.34	0	12 400 000	3 400 000	0	-=	\	\	\(3)
6332	Hha1	49	aaa	161.79	161	161.67	161.91	0	5 600 000	6 400 000	0	=-	\		\(3)
6333	Hha1	41	ccc	187.17	187	187.17	0	0	4 100 000	0	0	-=	\		\(2)
6334	Hha1	54	ttt	192.6	192	192.81	192.34	192.65	10 800 000	5 700 000	3 000 000	-=	\ (-)		\(2)
6335	Taq1	12	agt	171.43	172	171.43	171.35	171.51	8 900 000	7 500 000	12 400 000	==	-	-	-3
6336	Taq1	12	agt	172.507	172	172.52	172.44	172.56	4 100 000	3 300 000	3 600 000	==	-	-	-3
6337	Taq1	29	gca	171.597	172	171.57	171.61	171.61	11 800 000	7 900 000	5 400 000	==	-	-	-3
6338	Taq1	29	gca	172.643	172	172.69	172.62	172.62	15 100 000	11 200 000	5 400 000	==	-	-	-3
6339	Hha1	26	ctg	222.855	223	222.86	222.85	0	5 200 000	4 600 000	0	=-	\	\	-3
6340	Hha1	26	ctg	223.743	223	223.77	223.71	223.75	5 400 000	3 100 000	9 800 000	=+	/ (-)		-3
6341	Hha1	40	tgg	222.635	223	222.71	222.56	0	4 400 000	4 800 000	0	=-	\	\	-3
6342	Taq1	45	gcc	138.683	139	138.69	138.86	138.5	4 900 000	4 800 000	13 500 000	=+	/ (-)		A(4)
6343	Taq1	45	gcc	139.21	139	0	139.21	0	0	4 500 000	0	+-	A		A(4)
6344	Taq1	8	gaa	140.055	140	140.11	140	0	6 200 000	4 200 000	0	=-	\		A(4)
6345	Hha1	8	gaa	140.44	140	0	140.44	0	0	3 900 000	0	+-	A		A(4)
6346	Taq1	8	gaa	140.58	140	0	140.58	0	0	5 400 000	0	+-	A		A(4)
6347	Hha1	59	ttc	190.04	191	190.04	0	0	327.61	0	0	-=	\		A(4)
6348	Hha1	59	ttc	191.82	191	0	191.82	0	0	89.11	0	+-	A		A(4)
6349	Hha1	7	caa	106.513	106	106.47	106.53	106.54	6 100 000	7 600 000	3 700 000	=-	\ (-)		\(5)
6350	Taq1	18	cct	105.52	106	0	0	105.52	0	0	8 300 000	=+	/		\(5)
6351	Taq1	18	cct	106.62	106	106.68	106.73	106.45	20 900 000	15 800 000	36 700 000	=+	/ (-)		\(5)
6352	Taq1	18	cct	117.557	118	117.47	117.46	117.74	4 600 000	6 200 000	24 000 000	=+	/ (-)		\(5)
6353	Taq1	18	cct	118.45	118	118.41	0	118.49	5 500 000	0	6 200 000	-+(=)	V		\(5)
6354	Taq1	31	gac	118.135	118	0	118.06	118.21	0	10 700 000	19 400 000	+=	/		\(5)
6355	Taq1	31	gac	118.57	118	118.57	0	0	8 200 000	0	0	-=	\		\(5)
6356	Taq1	56	tga	141.003	141	140.94	140.91	141.16	71 400 000	66 700 000	3 800 000	=-	\ (-)		\(5)
6357	Taq1	49	aaa	177.99	178	178.1	177.88	0	3 800 000	4 800 000	0	=-	\		\(5)
6358	Taq1	49	aaa	178.53	178	0	178.53	0	0	4 600 000	0	+-	A		\(5)
6359	Taq1	39	agg	198.005	199	198.21	0	197.8	10 400 000	0	4 200 000	-=(-)	\		\(5)
6360	Taq1	39	agg	198.78	199	198.92	198.64	0	9 700 000	16 300 000	0	=-	\		\(5)
6361	Taq1	39	agg	199.37	199	0	199.37	0	0	18 600 000	0	+-	A		\(5)
6362	Taq1	39	agg	200.01	199	200.01	0	0	10 800 000	0	0	-=	\		\(5)
6363	Taq1	39	agg	198.21	199	198.21	0	0	386.21	0	0	-=	\		\(5)
6364	Taq1	39	agg	198.92	199	198.92	0	0	360.21	0	0	-=	\		\(5)
6365	Taq1	39	agg	200.01	199	200.01	0	0	401.06	0	0	-=	\		\(5)
6366	Taq1	39	agg	198.64	199	0	198.64	0	0	163.82	0	+-	A		\(5)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
6324	AF547393.NCF1	Ncf1	neutrophil cytosolic factor 1		ggt	cct	increased
6325	AF547393.NCF1	Ncf1	neutrophil cytosolic factor 1		ggt	cct	increased
6326	AF547393.NCF1	Ncf1	neutrophil cytosolic factor 1		ggt	cct	increased
6327	AF547393.NCF1	Ncf1	neutrophil cytosolic factor 1		ggt	cct	increased
6328	AB012235.NF1-X	NF1-X	NF1-X1		agt	agc	increased
6329	AB012235.NF1-X	NF1-X	NF1-X1		aaa	agg	increased
6330	AB012235.NF1-X	NF1-X	NF1-X1		aaa	agg	increased
6331	AB012235.NF1-X	NF1-X	NF1-X1		aaa	agg	increased
6332	AB012235.NF1-X	NF1-X	NF1-X1		aaa	agg	increased
6333	D86041.PE1	nc	N-G,N-G-dimethylarginine dimethylaminohydrolase		cag	ccc	increased
6334	D86041.PE1	nc	N-G,N-G-dimethylarginine dimethylaminohydrolase		aga	ttt	increased
6335	RNNG2.PE1	nc	NG2 proteoglycan		gca	agt	No change
6336	RNNG2.PE1	nc	NG2 proteoglycan		gca	agt	No change
6337	RNNG2.PE1	nc	NG2 proteoglycan		gca	agt	No change
6338	RNNG2.PE1	nc	NG2 proteoglycan		gca	agt	No change
6339	RNNG2.PE1	nc	NG2 proteoglycan		ctg	tgg	increased
6340	RNNG2.PE1	nc	NG2 proteoglycan		ctg	tgg	No change
6341	RNNG2.PE1	nc	NG2 proteoglycan		ctg	tgg	increased
6342	RATNHEPSUL.PE1	nc	N-heparan sulfate sulfotransferase		gcc	gaa	increased by mild
6343	RATNHEPSUL.PE1	nc	N-heparan sulfate sulfotransferase		gcc	gaa	increased by mild
6344	RATNHEPSUL.PE1	nc	N-heparan sulfate sulfotransferase		gcc	gaa	increased by mild
6345	RATNHEPSUL.PE1	nc	N-heparan sulfate sulfotransferase		gcc	gaa	increased by mild
6346	RATNHEPSUL.PE1	nc	N-heparan sulfate sulfotransferase		gcc	gaa	increased by mild
6347	RATNHEPSUL.PE1	nc	N-heparan sulfate sulfotransferase		aga	ttc	increased by mild
6348	RATNHEPSUL.PE1	nc	N-heparan sulfate sulfotransferase		aga	ttc	increased by mild
6349	RATNARA6S.PE1	nc	nicotinic acetylcholine receptor alpha 6		cct	caa	increased
6350	RATNARA6S.PE1	nc	nicotinic acetylcholine receptor alpha 6		cct	caa	increased
6351	RATNARA6S.PE1	nc	nicotinic acetylcholine receptor alpha 6		cct	caa	increased
6352	RATNARA6S.PE1	nc	nicotinic acetylcholine receptor alpha 6		gac	cct	increased
6353	RATNARA6S.PE1	nc	nicotinic acetylcholine receptor alpha 6		gac	cct	increased
6354	RATNARA6S.PE1	nc	nicotinic acetylcholine receptor alpha 6		gac	cct	increased
6355	RATNARA6S.PE1	nc	nicotinic acetylcholine receptor alpha 6		gac	cct	increased
6356	RATNARA6S.PE1	nc	nicotinic acetylcholine receptor alpha 6		ttc	tga	increased
6357	RATNARA6S.PE1	nc	nicotinic acetylcholine receptor alpha 6		aaa	tca	increased
6358	RATNARA6S.PE1	nc	nicotinic acetylcholine receptor alpha 6		aaa	tca	increased
6359	RATNARA6S.PE1	nc	nicotinic acetylcholine receptor alpha 6		agg	ttt	increased
6360	RATNARA6S.PE1	nc	nicotinic acetylcholine receptor alpha 6		agg	ttt	increased
6361	RATNARA6S.PE1	nc	nicotinic acetylcholine receptor alpha 6		agg	ttt	increased
6362	RATNARA6S.PE1	nc	nicotinic acetylcholine receptor alpha 6		agg	ttt	increased
6363	RATNARA6S.PE1	nc	nicotinic acetylcholine receptor alpha 6		agg	ttt	increased
6364	RATNARA6S.PE1	nc	nicotinic acetylcholine receptor alpha 6		agg	ttt	increased
6365	RATNARA6S.PE1	nc	nicotinic acetylcholine receptor alpha 6		agg	ttt	increased
6366	RATNARA6S.PE1	nc	nicotinic acetylcholine receptor alpha 6		agg	ttt	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
6367	Taq1	39	agg	199.37	199	0	199.37	0	0	186.93	0	+-	A		\(5)
6368	Hha1	41	ccc	151.12	152	151.08	151.08	151.2	6 400 000	3 200 000	3 700 000	-=	\ (-)		-2
6369	Hha1	41	ccc	151.955	152	151.96	151.95	0	14 300 000	4 500 000	0	-=	\		-2
6370	Hha1	54	ttt	153.43	154	153.5	153.41	153.38	25 700 000	17 100 000	9 600 000	==	-		-2
6371	Hha1	54	ttt	154.653	154	154.69	154.6	154.67	13 800 000	8 200 000	7 000 000	==	-		-2
6372	Taq1	24	cgt	141.467	142	141.42	141.39	141.59	15 900 000	18 300 000	6 900 000	=-	\ (-)	(-)	
6373	Taq1	24	cgt	142.49	142	142.48	142.44	142.55	11 700 000	15 800 000	10 100 000	==	-	-	
6374	Taq1	25	cat	141.587	142	141.72	141.65	141.39	232.01	903.88	1 543.12	==	-	(-)	
6375	Taq1	25	cat	142.583	142	142.77	142.7	142.28	750.64	980.26	1 267.56	==	-	-	
6376	Hha1	8	gaa	234.315	235	0	234.45	234.18	0	4 000 000	5 300 000	+=	/		\(3)
6377	Hha1	8	gaa	235.04	235	235.04	0	0	4 300 000	0	0	-=	\		\(3)
6378	Taq1	8	gaa	235.63	235	235.63	0	0	3 800 000	0	0	-=	\		\(3)
6379	Hha1	8	gaa	236.3	235	236.33	236.27	0	3 900 000	3 100 000	0	=-	\		\(3)
6380	Taq1	17	cca	165.57	166	0	165.54	165.6	0	438.77	541.27	+=	/	/	
6381	Taq1	17	cca	166.77	166	0	0	166.77	0	0	466.09	=+	/	/	
6382	Taq1	27	acg	165.77	166	165.75	165.74	165.82	5 500 000	3 500 000	9 900 000	=+	/ (-)	/	
6383	Taq1	27	acg	166.76	166	0	0	166.76	0	0	4 700 000	=+	/	/	
6384	Taq1	17	cca	165.57	166	0	165.54	165.6	0	438.77	541.27	+=	/	/	
6385	Taq1	17	cca	166.77	166	0	0	166.77	0	0	466.09	=+	/	/	
6386	Taq1	27	acg	165.77	166	165.75	165.74	165.82	5 500 000	3 500 000	9 900 000	=+	/ (-)	/	
6387	Taq1	27	acg	166.76	166	0	0	166.76	0	0	4 700 000	=+	/	/	
6388	Taq1	17	cca	165.57	166	0	165.54	165.6	0	438.77	541.27	+=	/	/	
6389	Taq1	17	cca	166.77	166	0	0	166.77	0	0	466.09	=+	/	/	
6390	Taq1	27	acg	165.77	166	165.75	165.74	165.82	5 500 000	3 500 000	9 900 000	=+	/ (-)	/	
6391	Taq1	27	acg	166.76	166	0	0	166.76	0	0	4 700 000	=+	/	/	
6392	Taq1	17	cca	165.57	166	0	165.54	165.6	0	438.77	541.27	+=	/	/	
6393	Taq1	17	cca	166.77	166	0	0	166.77	0	0	466.09	=+	/	/	
6394	Taq1	27	acg	165.77	166	165.75	165.74	165.82	5 500 000	3 500 000	9 900 000	=+	/ (-)	/	
6395	Taq1	27	acg	166.76	166	0	0	166.76	0	0	4 700 000	=+	/	/	
6396	Taq1	18	cct	156.12	157	156.1	156.14	0	15 200 000	16 300 000	0	=-	\	\	
6397	Taq1	39	agg	156.06	157	156.06	0	0	185.68	0	0	-=	\	\	
6398	Hha1	27	acg	112.86	113	112.72	112.78	113.08	5 900 000	3 000 000	3 900 000	-=	\ (-)	\	
6399	Hha1	33	agc	112.82	113	112.83	112.81	0	17 300 000	12 900 000	0	=-	\	\	
6400	Hha1	27	acg	112.86	113	112.72	112.78	113.08	5 900 000	3 000 000	3 900 000	-=	\ (-)	\	
6401	Hha1	33	agc	112.82	113	112.83	112.81	0	17 300 000	12 900 000	0	=-	\	\	
6402	Hha1	60	ttg	101.403	101	101.3	101.63	101.28	7 000 000	5 100 000	5 600 000	==	-		-2
6403	Hha1	44	cgg	103.53	104	0	0	103.53	0	0	5 200 000	=+	/		-2
6404	Hha1	44	cgg	104.397	104	104.37	104.38	104.44	3 500 000	11 100 000	12 300 000	+=	/ (-)		-2
6405	Hha1	39	agg	116	116	0	0	116	0	0	174.96	=+	/		/(3)
6406	Hha1	39	agg	116.65	116	0	0	116.65	0	0	150.55	=+	/		/(3)
6407	Hha1	33	agc	185.35	185	0	185.35	0	0	4 700 000	0	+-	A		/(3)
6408	Hha1	61	tct	187.957	189	188.05	187.91	187.91	6 000 000	11 300 000	11 700 000	+=	/ (-)		/(3)
6409	Hha1	61	tct	188.58	189	188.58	0	0	4 300 000	0	0	-=	\		/(3)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
6367	RATNARA6S.PE1	nc	nicotinic acetylcholine receptor alpha 6		agg	ttt	increased
6368	RATNARB.PE1	nc	nicotinic acetylcholine receptor beta 2 subunit		ttt	ccc	No change
6369	RATNARB.PE1	nc	nicotinic acetylcholine receptor beta 2 subunit		ttt	ccc	No change
6370	RATNARB.PE1	nc	nicotinic acetylcholine receptor beta 2 subunit		ttt	ccc	No change
6371	RATNARB.PE1	nc	nicotinic acetylcholine receptor beta 2 subunit		ttt	ccc	No change
6372	RATNACHRR.PE1	nAChR-relate	nicotinic acetylcholine receptor-related protein		cgt	cat	No change
6373	RATNACHRR.PE1	nAChR-relate	nicotinic acetylcholine receptor-related protein		cgt	cat	No change
6374	RATNACHRR.PE1	nAChR-relate	nicotinic acetylcholine receptor-related protein		cgt	cat	No change
6375	RATNACHRR.PE1	nAChR-relate	nicotinic acetylcholine receptor-related protein		cgt	cat	No change
6376	AY334013.PE1	nc	NIMA-related expressed kinase 6		gaa	tga	increased
6377	AY334013.PE1	nc	NIMA-related expressed kinase 6		gaa	tga	increased
6378	AY334013.PE1	nc	NIMA-related expressed kinase 6		gaa	tga	increased
6379	AY334013.PE1	nc	NIMA-related expressed kinase 6		gaa	tga	increased
6380	RATNOS.PE1	nc	nitric oxide synthase		cca	acg	decreased
6381	RATNOS.PE1	nc	nitric oxide synthase		cca	acg	decreased
6382	RATNOS.PE1	nc	nitric oxide synthase		cca	acg	decreased
6383	RATNOS.PE1	nc	nitric oxide synthase		cca	acg	decreased
6384	RATNOSI.PE1	nc	nitric oxide synthase		cca	acg	decreased
6385	RATNOSI.PE1	nc	nitric oxide synthase		cca	acg	decreased
6386	RATNOSI.PE1	nc	nitric oxide synthase		cca	acg	decreased
6387	RATNOSI.PE1	nc	nitric oxide synthase		cca	acg	decreased
6388	RATVSMNOS.PE1	nc	nitric oxide synthase		cca	acg	decreased
6389	RATVSMNOS.PE1	nc	nitric oxide synthase		cca	acg	decreased
6390	RATVSMNOS.PE1	nc	nitric oxide synthase		cca	acg	decreased
6391	RATVSMNOS.PE1	nc	nitric oxide synthase		cca	acg	decreased
6392	RNU03699.NOS	nc	nitric oxide synthase		cca	acg	decreased
6393	RNU03699.NOS	nc	nitric oxide synthase		cca	acg	decreased
6394	RNU03699.NOS	nc	nitric oxide synthase		cca	acg	decreased
6395	RNU03699.NOS	nc	nitric oxide synthase		cca	acg	decreased
6396	RATNMCA2C.PE1	nc	NMDA receptor subtype 2C		agg	cct	increased
6397	RATNMCA2C.PE1	nc	NMDA receptor subtype 2C		agg	cct	increased
6398	RATNR2DA.PE1	nc	NMDA receptor subunit NR2D		agc	acg	increased
6399	RATNR2DA.PE1	nc	NMDA receptor subunit NR2D		agc	acg	increased
6400	RATNR2DB.PE1	nc	NMDA receptor subunit NR2D		agc	acg	increased
6401	RATNR2DB.PE1	nc	NMDA receptor subunit NR2D		agc	acg	increased
6402	RNU29873.PE1	nc	NMDAR-L		act	ttg	No change
6403	RNU29873.PE1	nc	NMDAR-L		tca	cgg	No change
6404	RNU29873.PE1	nc	NMDAR-L		tca	cgg	No change
6405	RNU08265.NMDAR1	NMDAR1	N-methyl-D-aspartate receptor NMDAR1-3a subunit		agc	agg	decreased
6406	RNU08265.NMDAR1	NMDAR1	N-methyl-D-aspartate receptor NMDAR1-3a subunit		agc	agg	decreased
6407	RNU08265.NMDAR1	NMDAR1	N-methyl-D-aspartate receptor NMDAR1-3a subunit		agc	atg	decreased
6408	RNU08265.NMDAR1	NMDAR1	N-methyl-D-aspartate receptor NMDAR1-3a subunit		atc	tct	decreased
6409	RNU08265.NMDAR1	NMDAR1	N-methyl-D-aspartate receptor NMDAR1-3a subunit		atc	tct	decreased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
6410	Hha1	61	tct	189.98	189	190.02	189.96	189.96	4 700 000	4 900 000	3 900 000	==	-		/(3)
6411	Hha1	60	ttg	201.167	201	201.18	201.11	201.21	6 200 000	4 700 000	14 100 000	=+	/ (-)		/(3)
6412	Hha1	39	agg	116	116	0	0	116	0	0	174.96	=+	/		/(3)
6413	Hha1	39	agg	116.65	116	0	0	116.65	0	0	150.55	=+	/		/(3)
6414	Hha1	60	ttg	123.78	124	123.63	123.93	0	9 700 000	4 500 000	0	--	\		/(3)
6415	Hha1	60	ttg	124.64	124	0	124.88	124.4	0	4 200 000	3 300 000	+=	/		/(3)
6416	Hha1	33	agc	185.35	185	0	185.35	0	0	4 700 000	0	+-	A		/(3)
6417	Hha1	61	tct	187.957	189	188.05	187.91	187.91	6 000 000	11 300 000	11 700 000	+=	/ (-)		/(3)
6418	Hha1	61	tct	188.58	189	188.58	0	0	4 300 000	0	0	-=	\		/(3)
6419	Hha1	61	tct	189.98	189	190.02	189.96	189.96	4 700 000	4 900 000	3 900 000	==	-		/(3)
6420	Hha1	39	agg	116	116	0	0	116	0	0	174.96	=+	/		/(3)
6421	Hha1	39	agg	116.65	116	0	0	116.65	0	0	150.55	=+	/		/(3)
6422	Hha1	33	agc	185.35	185	0	185.35	0	0	4 700 000	0	+-	A		/(3)
6423	Hha1	61	tct	187.957	189	188.05	187.91	187.91	6 000 000	11 300 000	11 700 000	+=	/ (-)		/(3)
6424	Hha1	61	tct	188.58	189	188.58	0	0	4 300 000	0	0	-=	\		/(3)
6425	Hha1	61	tct	189.98	189	190.02	189.96	189.96	4 700 000	4 900 000	3 900 000	==	-		/(3)
6426	Hha1	60	ttg	201.167	201	201.18	201.11	201.21	6 200 000	4 700 000	14 100 000	=+	/ (-)		/(3)
6427	Hha1	39	agg	116	116	0	0	116	0	0	174.96	=+	/		/(3)
6428	Hha1	39	agg	116.65	116	0	0	116.65	0	0	150.55	=+	/		/(3)
6429	Hha1	60	ttg	123.78	124	123.63	123.93	0	9 700 000	4 500 000	0	--	\		/(3)
6430	Hha1	60	ttg	124.64	124	0	124.88	124.4	0	4 200 000	3 300 000	+=	/		/(3)
6431	Hha1	33	agc	185.35	185	0	185.35	0	0	4 700 000	0	+-	A		/(3)
6432	Hha1	61	tct	187.957	189	188.05	187.91	187.91	6 000 000	11 300 000	11 700 000	+=	/ (-)		/(3)
6433	Hha1	61	tct	188.58	189	188.58	0	0	4 300 000	0	0	-=	\		/(3)
6434	Hha1	61	tct	189.98	189	190.02	189.96	189.96	4 700 000	4 900 000	3 900 000	==	-		/(3)
6435	Taq1	18	cct	156.12	157	156.1	156.14	0	15 200 000	16 300 000	0	=-	\	\	
6436	Taq1	39	agg	156.06	157	156.06	0	0	185.68	0	0	-=	\	\	
6437	Hha1	27	acg	112.86	113	112.72	112.78	113.08	5 900 000	3 000 000	3 900 000	-=	\ (-)	\	
6438	Hha1	33	agc	112.82	113	112.83	112.81	0	17 300 000	12 900 000	0	=-	\	\	
6439	Hha1	60	ttg	101.403	101	101.3	101.63	101.28	7 000 000	5 100 000	5 600 000	==	-		-2
6440	Hha1	44	cgg	103.53	104	0	0	103.53	0	0	5 200 000	=+	/		-2
6441	Hha1	44	cgg	104.397	104	104.37	104.38	104.44	3 500 000	11 100 000	12 300 000	+=	/ (-)		-2
6442	Taq1	18	cct	156.12	157	156.1	156.14	0	15 200 000	16 300 000	0	=-	\	\	
6443	Taq1	39	agg	156.06	157	156.06	0	0	185.68	0	0	-=	\	\	
6444	Hha1	27	acg	112.86	113	112.72	112.78	113.08	5 900 000	3 000 000	3 900 000	-=	\ (-)	\	
6445	Hha1	33	agc	112.82	113	112.83	112.81	0	17 300 000	12 900 000	0	=-	\	\	
6446	Taq1	64	gtt	104.68	105	104.69	104.64	104.71	4 800 000	5 600 000	3 000 000	=-	\ (-)		\(2)
6447	Hha1	28	tcg	149.535	150	0	149.55	149.52	0	6 500 000	8 500 000	+=	/		\(2)
6448	Hha1	28	tcg	150.6	150	150.68	0	150.52	7 200 000	0	3 100 000	-=(-)	\		\(2)
6449	Hha1	39	agg	65.37	65	65.38	65.36	0	2 631.96	1 355.3	0	--	\		\(5)
6450	Hha1	33	agc	77.803	78	77.78	77.86	77.77	56 700 000	20 100 000	9 400 000	-=	\ (-)		\(5)
6451	Hha1	31	gac	92.68	93	92.68	0	0	11 500 000	0	0	-=	\		\(5)
6452	Hha1	31	gac	93.357	93	93.35	93.32	93.4	28 700 000	11 500 000	7 200 000	-=	\ (-)		\(5)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
6410	RNU08265.NMDAR1	NMDAR1	N-methyl-D-aspartate receptor NMDAR1-3a subunit		atc	tct	decreased
6411	RNU08265.NMDAR1	NMDAR1	N-methyl-D-aspartate receptor NMDAR1-3a subunit		ttg	ggt	decreased
6412	RNU08266.NMDAR1	NMDAR1	N-methyl-D-aspartate receptor NMDAR1-3b subunit		agc	agg	decreased
6413	RNU08266.NMDAR1	NMDAR1	N-methyl-D-aspartate receptor NMDAR1-3b subunit		agc	agg	decreased
6414	RNU08266.NMDAR1	NMDAR1	N-methyl-D-aspartate receptor NMDAR1-3b subunit		ttg	ttg	decreased
6415	RNU08266.NMDAR1	NMDAR1	N-methyl-D-aspartate receptor NMDAR1-3b subunit		ttg	ttg	decreased
6416	RNU08266.NMDAR1	NMDAR1	N-methyl-D-aspartate receptor NMDAR1-3b subunit		agc	atg	decreased
6417	RNU08266.NMDAR1	NMDAR1	N-methyl-D-aspartate receptor NMDAR1-3b subunit		atc	tct	decreased
6418	RNU08266.NMDAR1	NMDAR1	N-methyl-D-aspartate receptor NMDAR1-3b subunit		atc	tct	decreased
6419	RNU08266.NMDAR1	NMDAR1	N-methyl-D-aspartate receptor NMDAR1-3b subunit		atc	tct	decreased
6420	RNU08267.NMDAR1	NMDAR1	N-methyl-D-aspartate receptor NMDAR1-4a subunit		agc	agg	decreased
6421	RNU08267.NMDAR1	NMDAR1	N-methyl-D-aspartate receptor NMDAR1-4a subunit		agc	agg	decreased
6422	RNU08267.NMDAR1	NMDAR1	N-methyl-D-aspartate receptor NMDAR1-4a subunit		agc	atg	decreased
6423	RNU08267.NMDAR1	NMDAR1	N-methyl-D-aspartate receptor NMDAR1-4a subunit		atc	tct	decreased
6424	RNU08267.NMDAR1	NMDAR1	N-methyl-D-aspartate receptor NMDAR1-4a subunit		atc	tct	decreased
6425	RNU08267.NMDAR1	NMDAR1	N-methyl-D-aspartate receptor NMDAR1-4a subunit		atc	tct	decreased
6426	RNU08267.NMDAR1	NMDAR1	N-methyl-D-aspartate receptor NMDAR1-4a subunit		ttg	ggt	decreased
6427	RNU08268.NMDAR1	NMDAR1	N-methyl-D-aspartate receptor NMDAR1-4b subunit		agc	agg	decreased
6428	RNU08268.NMDAR1	NMDAR1	N-methyl-D-aspartate receptor NMDAR1-4b subunit		agc	agg	decreased
6429	RNU08268.NMDAR1	NMDAR1	N-methyl-D-aspartate receptor NMDAR1-4b subunit		ttg	ttg	decreased
6430	RNU08268.NMDAR1	NMDAR1	N-methyl-D-aspartate receptor NMDAR1-4b subunit		ttg	ttg	decreased
6431	RNU08268.NMDAR1	NMDAR1	N-methyl-D-aspartate receptor NMDAR1-4b subunit		agc	atg	decreased
6432	RNU08268.NMDAR1	NMDAR1	N-methyl-D-aspartate receptor NMDAR1-4b subunit		atc	tct	decreased
6433	RNU08268.NMDAR1	NMDAR1	N-methyl-D-aspartate receptor NMDAR1-4b subunit		atc	tct	decreased
6434	RNU08268.NMDAR1	NMDAR1	N-methyl-D-aspartate receptor NMDAR1-4b subunit		atc	tct	decreased
6435	RNU08259.PE1	nc	N-methyl-D-aspartate receptor NMDAR2C subunit		agg	cct	increased
6436	RNU08259.PE1	nc	N-methyl-D-aspartate receptor NMDAR2C subunit		agg	cct	increased
6437	RNU08260.PE1	nc	N-methyl-D-aspartate receptor NMDAR2D subunit		agc	acg	increased
6438	RNU08260.PE1	nc	N-methyl-D-aspartate receptor NMDAR2D subunit		agc	acg	increased
6439	AF073379.NR3A	NR3A	N-methyl-D-aspartate receptor splice variant		act	ttg	No change
6440	AF073379.NR3A	NR3A	N-methyl-D-aspartate receptor splice variant		tca	cgg	No change
6441	AF073379.NR3A	NR3A	N-methyl-D-aspartate receptor splice variant		tca	cgg	No change
6442	RATNMDARC.PE1	nc	N-methyl-D-aspartate receptor subunit		agg	cct	increased
6443	RATNMDARC.PE1	nc	N-methyl-D-aspartate receptor subunit		agg	cct	increased
6444	RATNMDARD1.PE1	nc	N-methyl-D-aspartate receptor subunit		agc	acg	increased
6445	RATNMDARD1.PE1	nc	N-methyl-D-aspartate receptor subunit		agc	acg	increased
6446	RNNMYC.N-MYC	N-myc	N-myc protein		gtt	gtc	increased
6447	RNNMYC.N-MYC	N-myc	N-myc protein		cac	tcg	increased
6448	RNNMYC.N-MYC	N-myc	N-myc protein		cac	tcg	increased
6449	AF532860.NGRH1	Ngrh1	Nogo-66 receptor homolog-1		ggg	agg	increased
6450	AF532860.NGRH1	Ngrh1	Nogo-66 receptor homolog-1		ccg	agc	increased
6451	AF532860.NGRH1	Ngrh1	Nogo-66 receptor homolog-1		gac	ggc	increased
6452	AF532860.NGRH1	Ngrh1	Nogo-66 receptor homolog-1		gac	ggc	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
6453	Hha1	20	ctc	113.32	114	113.32	0	0	1 721.76	0	0	-=	\		\(5)
6454	Hha1	20	ctc	114.24	114	0	0	114.24	0	0	500.95	=+	/		\(5)
6455	Hha1	32	gtc	113.725	114	0	113.77	113.68	0	2 034.58	3 549.93	+=	/		\(5)
6456	Hha1	33	agc	113.725	114	113.86	113.59	0	6 500 000	9 600 000	0	=-	\		\(5)
6457	Hha1	26	ctg	120.87	121	0	120.81	120.93	0	8 500 000	4 900 000	+=	/		\(5)
6458	Hha1	33	agc	76.7	77	76.7	0	0	3 200 000	0	0	-=	\		\(2)
6459	Taq1	49	aaa	161.04	162	0	161.04	0	0	3 800 000	0	+-	A		\(2)
6460	Taq1	49	aaa	161.65	162	0	161.65	0	0	11 200 000	0	+-	A		\(2)
6461	Taq1	49	aaa	162.35	162	162.33	0	162.37	61 600 000	0	3 700 000	-=(-)	\		\(2)
6462	Taq1	39	agg	61.033	61	61.09	61.22	60.79	83 000 000	79 000 000	10 400 000	=-	\ (-)		/(5)
6463	Taq1	39	agg	61.273	61	61.09	61.22	61.51	3 082.29	793.97	8 400 000	=+	/ (-)		/(5)
6464	Taq1	39	agg	60.79	61	0	0	60.79	0	0	306.33	=+	/		/(5)
6465	Hha1	33	agc	64.945	65	0	65.19	64.7	0	4 100 000	31 500 000	=+	/		/(5)
6466	Taq1	29	gca	135.507	136	135.56	135.44	135.52	24 600 000	19 200 000	8 000 000	=-	\ (-)		/(5)
6467	Taq1	29	gca	136.547	136	136.54	136.49	136.61	6 000 000	3 900 000	8 100 000	=+	/ (-)		/(5)
6468	Hha1	26	ctg	140.475	140	140.32	0	140.63	3 700 000	0	3 100 000	-+(=)	V		/(5)
6469	Hha1	60	ttg	183.685	183	0	183.89	183.48	0	5 300 000	4 500 000	+=	/		/(5)
6470	Hha1	33	agc	196.56	196	0	0	196.56	0	0	5 200 000	=+	/		/(5)
6471	Hha1	20	ctc	73.83	74	73.76	73.99	73.74	392.56	655.65	369.75	==	-		-5
6472	Hha1	20	ctc	74.44	74	0	74.49	74.39	0	773.66	763.35	+=	/		-5
6473	Hha1	28	tcg	109.673	110	109.63	109.74	109.65	22 900 000	11 800 000	28 300 000	=+	/ (-)	(-)	-5
6474	Hha1	33	agc	109.83	110	109.86	109.86	109.77	6 400 000	4 300 000	6 200 000	==	-	(-)	-5
6475	Taq1	61	tct	132.773	133	132.74	132.72	132.86	4 100 000	3 200 000	7 600 000	=+	/ (-)		-5
6476	Taq1	61	tct	133.13	133	0	133.13	0	0	4 300 000	0	+-	A		-5
6477	Taq1	61	tct	133.775	133	133.64	0	133.91	3 400 000	0	7 100 000	-+(+)	V (/)		-5
6478	Hha1	33	agc	149.31	150	149.36	149.36	149.21	10 900 000	13 300 000	3 500 000	=-	\ (-)		-5
6479	Hha1	33	agc	150.42	150	150.39	150.45	0	5 500 000	5 500 000	0	=-	\		-5
6480	Taq1	18	cct	252.35	252	0	252.35	0	0	3 300 000	0	+-	A		-5
6481	Hha1	59	ttc	79.593	80	79.5	79.64	79.64	4 362.97	2 230.65	2 129.2	-=	\ (-)		-5
6482	Hha1	59	ttc	80.225	80	80.31	0	80.14	2 028.08	0	1 836.85	-+(=)	V		-5
6483	Hha1	33	agc	88.273	88	88.16	88.2	88.46	57 000 000	40 900 000	16 400 000	==	-		-5
6484	Hha1	33	agc	91.3	91	91.16	91.44	0	3 500 000	4 000 000	0	=-	\		-5
6485	Hha1	26	ctg	108.8	109	108.86	108.8	108.74	5 700 000	5 700 000	4 900 000	==	-	-	-5
6486	Hha1	33	agc	108.77	109	108.83	108.8	108.68	11 600 000	9 300 000	8 800 000	==	-	-	-5
6487	Taq1	45	gcc	242.277	243	242.16	242.17	242.5	21 600 000	15 100 000	3 800 000	=-	\ (-)		-5
6488	Taq1	45	gcc	243.12	243	243.11	243.13	0	8 400 000	12 000 000	0	=-	\		-5
6489	Taq1	45	gcc	244.105	243	243.98	244.23	0	4 700 000	4 000 000	0	=-	\		-5
6490	Taq1	55	tca	106.22	106	0	106.24	106.2	0	8 300 000	9 500 000	+=	/	/	
6491	Taq1	62	tgt	106.45	106	106.33	106.57	106.45	3 300 000	5 400 000	34 300 000	=+	/ (-)	/	
6492	Hha1	25	cag	115.48	115	115.48	0	0	9 000 000	0	0	-=	\	\	
6493	Taq1	31	gac	115.32	115	115.32	0	0	34 600 000	0	0	-=	\	\	
6494	Hha1	7	caa	192.13	193	192.24	192.02	0	6 100 000	3 000 000	0	--	\	\	
6495	Hha1	7	caa	193.13	193	0	193.13	0	0	3 500 000	0	+-	A	A	

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
6453	AF532860.NGRH1	Ngrh1	Nogo-66 receptor homolog-1		agc	ctc	increased
6454	AF532860.NGRH1	Ngrh1	Nogo-66 receptor homolog-1		agc	ctc	increased
6455	AF532860.NGRH1	Ngrh1	Nogo-66 receptor homolog-1		tcc	gtc	increased
6456	AF532860.NGRH1	Ngrh1	Nogo-66 receptor homolog-1		agc	ctc	increased
6457	AF532860.NGRH1	Ngrh1	Nogo-66 receptor homolog-1		cca	ctg	increased
6458	RNU18419.PE1	nc	nonmuscle caldesmon		ccc	agc	increased
6459	RNU18419.PE1	nc	nonmuscle caldesmon		aaa	tca	increased
6460	RNU18419.PE1	nc	nonmuscle caldesmon		aaa	tca	increased
6461	RNU18419.PE1	nc	nonmuscle caldesmon		aaa	tca	increased
6462	RNU31463.PE1	nc	nonmuscle myosin heavy chain-A		gat	agg	decreased
6463	RNU31463.PE1	nc	nonmuscle myosin heavy chain-A		gat	agg	decreased
6464	RNU31463.PE1	nc	nonmuscle myosin heavy chain-A		gat	agg	decreased
6465	RNU31463.PE1	nc	nonmuscle myosin heavy chain-A		agc	att	decreased
6466	RNU31463.PE1	nc	nonmuscle myosin heavy chain-A		gca	tgc	decreased
6467	RNU31463.PE1	nc	nonmuscle myosin heavy chain-A		gca	tgc	decreased
6468	RNU31463.PE1	nc	nonmuscle myosin heavy chain-A		ctt	ctg	decreased
6469	RNU31463.PE1	nc	nonmuscle myosin heavy chain-A		tgg	ttg	decreased
6470	RNU31463.PE1	nc	nonmuscle myosin heavy chain-A		agc	aga	decreased
6471	AF139055.PE1	nc	nonmuscle myosin heavy chain-B		ctc	cgc	No change
6472	AF139055.PE1	nc	nonmuscle myosin heavy chain-B		ctc	cgc	No change
6473	AF139055.PE1	nc	nonmuscle myosin heavy chain-B		agc	tcg	No change
6474	AF139055.PE1	nc	nonmuscle myosin heavy chain-B		agc	tcg	No change
6475	AF139055.PE1	nc	nonmuscle myosin heavy chain-B		ggc	tct	No change
6476	AF139055.PE1	nc	nonmuscle myosin heavy chain-B		ggc	tct	No change
6477	AF139055.PE1	nc	nonmuscle myosin heavy chain-B		ggc	tct	No change
6478	AF139055.PE1	nc	nonmuscle myosin heavy chain-B		agc	tcc	No change
6479	AF139055.PE1	nc	nonmuscle myosin heavy chain-B		agc	tcc	No change
6480	AF139055.PE1	nc	nonmuscle myosin heavy chain-B		att	cct	No change
6481	RATNOR1.PE1	nc	NOR-1		ttc	ggg	No change
6482	RATNOR1.PE1	nc	NOR-1		ttc	ggg	No change
6483	RATNOR1.PE1	nc	NOR-1		tca	agc	No change
6484	RATNOR1.PE1	nc	NOR-1		cca	agc	No change
6485	RATNOR1.PE1	nc	NOR-1		ctg	agc	No change
6486	RATNOR1.PE1	nc	NOR-1		ctg	agc	No change
6487	RATNOR1.PE1	nc	NOR-1		cgt	gcc	No change
6488	RATNOR1.PE1	nc	NOR-1		cgt	gcc	No change
6489	RATNOR1.PE1	nc	NOR-1		cgt	gcc	No change
6490	RATNOTCHX.PE1	nc	NOTCH2		tca	tgt	decreased
6491	RATNOTCHX.PE1	nc	NOTCH2		tca	tgt	decreased
6492	RATNOTCHX.PE1	nc	NOTCH2		gac	cag	increased
6493	RATNOTCHX.PE1	nc	NOTCH2		gac	cag	increased
6494	RATNOTCHX.PE1	nc	NOTCH2		caa	tgc	increased
6495	RATNOTCHX.PE1	nc	NOTCH2		caa	tgc	increased by mild

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
6496	Taq1	7	caa	192.28	193	192.28	0	0	3 300 000	0	0	-=	\	\	
6497	Taq1	7	caa	193.16	193	0	193.16	0	0	3 900 000	0	+-	A	A	
6498	Hha1	43	cgc	134.06	134	134.09	134.03	0	5 900 000	3 900 000	0	=-	\		-3
6499	Hha1	43	cgc	134.75	134	134.85	134.79	134.61	7 700 000	6 300 000	3 100 000	==	-		-3
6500	Hha1	54	ttt	135.313	136	135.32	135.36	135.26	14 400 000	10 900 000	10 200 000	==	-		-3
6501	Hha1	54	ttt	135.85	136	0	0	135.85	0	0	7 900 000	=+	/		-3
6502	Hha1	54	ttt	136.483	136	136.55	136.4	136.5	15 300 000	13 400 000	7 200 000	==	-		-3
6503	Hha1	27	acg	153.45	153	153.42	0	153.48	9 500 000	0	3 900 000	-=(-)	\		-3
6504	Hha1	61	tct	153.043	153	152.96	153.02	153.15	12 000 000	20 800 000	21 800 000	==	-		-3
6505	Hha1	8	gaa	165.633	165	165.68	165.59	165.63	4 100 000	5 700 000	3 200 000	==	-	-	
6506	Hha1	25	cag	165.743	165	165.75	165.82	165.66	5 000 000	4 200 000	6 200 000	==	-	-	
6507	Hha1	31	gac	124.24	124	0	0	124.24	0	0	4 800 000	=+	/		/(3)
6508	Hha1	56	tga	142.217	143	142.21	142.37	142.07	1 009.27	198.15	1 241.16	-+	V		/(3)
6509	Hha1	56	tga	143.065	143	143.21	0	142.92	294.2	0	2 309.94	=+(+)	/	/	/(3)
6510	Hha1	62	tgt	142.86	143	0	0	142.86	0	0	4 700 000	=+	/	/	/(3)
6511	Hha1	31	gac	124.24	124	0	0	124.24	0	0	4 800 000	=+	/		/(3)
6512	Hha1	56	tga	142.217	143	142.21	142.37	142.07	1 009.27	198.15	1 241.16	-+	V		/(3)
6513	Hha1	56	tga	143.065	143	143.21	0	142.92	294.2	0	2 309.94	=+(+)	/	/	/(3)
6514	Hha1	62	tgt	142.86	143	0	0	142.86	0	0	4 700 000	=+	/	/	/(3)
6515	Hha1	26	ctg	108.8	109	108.86	108.8	108.74	5 700 000	5 700 000	4 900 000	==	-	-	-2
6516	Hha1	33	agc	108.77	109	108.83	108.8	108.68	11 600 000	9 300 000	8 800 000	==	-	-	-2
6517	Taq1	61	tct	205.395	206	205.46	205.33	0	5 900 000	16 400 000	0	+-	A		-2
6518	Taq1	61	tct	206.36	206	0	206.36	0	0	5 200 000	0	+-	A		-2
6519	Hha1	20	ctc	67.16	67	67.27	0	67.05	282.36	0	536.73	-+(+)	V (/)		V(2)
6520	Hha1	61	tct	128.763	129	128.69	128.75	128.85	13 000 000	21 700 000	16 000 000	==	-		V(2)
6521	Hha1	40	tgg	252.785	253	252.6	0	252.97	6 600 000	0	5 200 000	-+(=)	V		V(2)
6522	Hha1	40	tgg	253.49	253	253.49	0	0	7 300 000	0	0	-=	\		V(2)
6523	Hha1	40	tgg	254.44	253	254.41	254.47	0	3 900 000	6 300 000	0	=-	\		V(2)
6524	Hha1	59	ttc	97.02	97	0	97.18	96.86	0	114.98	385.48	=+	/		/(2)
6525	Taq1	40	tgg	141.19	142	141.39	0	140.99	7 000 000	0	9 300 000	-+(=)	V		/(2)
6526	Taq1	40	tgg	142.03	142	0	0	142.03	0	0	10 400 000	=+	/		/(2)
6527	Taq1	14	gat	171.67	172	171.61	171.61	171.79	4 200 000	4 200 000	5 900 000	==	-	-	-2
6528	Taq1	14	gat	172.67	172	172.64	172.64	172.73	3 600 000	3 600 000	4 300 000	==	-	-	-2
6529	Taq1	29	gca	171.597	172	171.57	171.61	171.61	11 800 000	7 900 000	5 400 000	==	-	-	-2
6530	Taq1	29	gca	172.643	172	172.69	172.62	172.62	15 100 000	11 200 000	5 400 000	==	-	-	-2
6531	Taq1	52	att	96.72	97	0	0	96.72	0	0	4 800 000	=+	/		\(2)
6532	Taq1	39	agg	109.455	110	109.31	109.6	0	12 800 000	59 600 000	0	+-	A		\(2)
6533	Taq1	39	agg	110.24	110	110.01	0	110.47	13 800 000	0	8 600 000	-+(=)	V		\(2)
6534	Taq1	39	agg	109.455	110	109.31	109.6	0	475.34	599	0	=-	\		\(2)
6535	Taq1	39	agg	110.01	110	110.01	0	0	512.47	0	0	-=	\		\(2)
6536	Taq1	51	ata	110.7	111	110.7	0	0	3 700 000	0	0	-=	\		\(2)
6537	Taq1	51	ata	111.57	111	111.57	0	0	9 100 000	0	0	-=	\		\(2)
6538	Hha1	31	gac	60.15	60	0	60.15	0	0	4 700 000	0	+-	A		-(2) A(2)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
6496	RATNOTCHX.PE1	nc	NOTCH2		caa	tgc	increased
6497	RATNOTCHX.PE1	nc	NOTCH2		caa	tgc	increased by mild
6498	RNNTR2REC.PE1	nc	NTR2 receptor		cgc	ttt	No change
6499	RNNTR2REC.PE1	nc	NTR2 receptor		cgc	ttt	No change
6500	RNNTR2REC.PE1	nc	NTR2 receptor		cgc	ttt	No change
6501	RNNTR2REC.PE1	nc	NTR2 receptor		cgc	ttt	No change
6502	RNNTR2REC.PE1	nc	NTR2 receptor		cgc	ttt	No change
6503	RNNTR2REC.PE1	nc	NTR2 receptor		tct	acg	No change
6504	RNNTR2REC.PE1	nc	NTR2 receptor		tct	acg	No change
6505	RNU95160.PE1	nc	nuclear protein E3-3 orf1		cag	gaa	No change
6506	RNU95160.PE1	nc	nuclear protein E3-3 orf1		cag	gaa	No change
6507	AB104736.CAR	CAR	nuclear receptor		tca	gac	decreased
6508	AB104736.CAR	CAR	nuclear receptor		tga	tgt	decreased
6509	AB104736.CAR	CAR	nuclear receptor		tga	tgt	decreased
6510	AB104736.CAR	CAR	nuclear receptor		tga	tgt	decreased
6511	AB105071.CAR	CAR	nuclear receptor		tca	gac	decreased
6512	AB105071.CAR	CAR	nuclear receptor		tga	tgt	decreased
6513	AB105071.CAR	CAR	nuclear receptor		tga	tgt	decreased
6514	AB105071.CAR	CAR	nuclear receptor		tga	tgt	decreased
6515	AF322224.PE1	nc	nuclear receptor coactivator AIB1		agc	ctg	No change
6516	AF322224.PE1	nc	nuclear receptor coactivator AIB1		agc	ctg	No change
6517	AF322224.PE1	nc	nuclear receptor coactivator AIB1		tgg	tct	No change
6518	AF322224.PE1	nc	nuclear receptor coactivator AIB1		tgg	tct	No change
6519	AF336828.PE1	nc	nucleobindin	*	ctc	ccc	decreased by mild
6520	AF336828.PE1	nc	nucleobindin	*	tcc	tct	decreased by mild
6521	AF336828.PE1	nc	nucleobindin	*	atg	tgg	decreased by mild
6522	AF336828.PE1	nc	nucleobindin	*	atg	tgg	decreased by mild
6523	AF336828.PE1	nc	nucleobindin	*	atg	tgg	decreased by mild
6524	AB072798.GPX4	GPx4	nucleolar phospholipid hydroperoxide glutathione		ggc	ttc	decreased
6525	AB072798.GPX4	GPx4	nucleolar phospholipid hydroperoxide glutathione		tgg	cta	decreased
6526	AB072798.GPX4	GPx4	nucleolar phospholipid hydroperoxide glutathione		tgg	cta	decreased
6527	RATGUABIND.PE1	nc	nucleotide binding protein ARD 1		gat	gca	No change
6528	RATGUABIND.PE1	nc	nucleotide binding protein ARD 1		gat	gca	No change
6529	RATGUABIND.PE1	nc	nucleotide binding protein ARD 1		gat	gca	No change
6530	RATGUABIND.PE1	nc	nucleotide binding protein ARD 1		gat	gca	No change
6531	RNU76557.OGT	OGT	O-GlcNAc transferase, p110 subunit		att	taa	increased
6532	RNU76557.OGT	OGT	O-GlcNAc transferase, p110 subunit		agg	ata	increased
6533	RNU76557.OGT	OGT	O-GlcNAc transferase, p110 subunit		agg	ata	increased
6534	RNU76557.OGT	OGT	O-GlcNAc transferase, p110 subunit		agg	ata	increased
6535	RNU76557.OGT	OGT	O-GlcNAc transferase, p110 subunit		agg	ata	increased
6536	RNU76557.OGT	OGT	O-GlcNAc transferase, p110 subunit		agg	ata	increased
6537	RNU76557.OGT	OGT	O-GlcNAc transferase, p110 subunit		agg	ata	increased
6538	RATRORA.ROR-A	ROR-A	opioid receptor A	*	tgc	gac	No change

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
6539	Hha1	40	tgg	101.637	102	101.34	101.84	101.73	16 300 000	13 700 000	17 400 000	==	-	-	-(2) A(2)
6540	Hha1	40	tgg	102.35	102	0	102.35	0	0	10 700 000	0	+-	A		-(2) A(2)
6541	Hha1	60	ttg	101.403	102	101.3	101.63	101.28	7 000 000	5 100 000	5 600 000	==	-	-	-(2) A(2)
6542	Taq1	39	agg	207.22	208	207.11	207.33	0	9 300 000	12 600 000	0	=-	\		A(2)
6543	Taq1	39	agg	207.975	208	207.91	208.04	0	12 200 000	36 700 000	0	+-	A		A(2)
6544	Taq1	39	agg	207.33	208	0	207.33	0	0	126.63	0	+-	A		A(2)
6545	Taq1	39	agg	208.04	208	0	208.04	0	0	368.84	0	+-	A		A(2)
6546	Taq1	39	agg	208.98	208	208.98	0	0	5 100 000	0	0	-=	\		A(2)
6547	Taq1	39	agg	207.11	208	207.11	0	0	345.36	0	0	-=	\		A(2)
6548	Taq1	39	agg	207.91	208	207.91	0	0	453.06	0	0	-=	\		A(2)
6549	Taq1	39	agg	208.98	208	208.98	0	0	189.39	0	0	-=	\		A(2)
6550	Hha1	49	aaa	284.51	284	0	284.51	0	0	4 000 000	0	+-	A		A(2)
6551	Hha1	6	aga	177.05	178	0	0	177.05	0	0	9 400 000	=+	/		\(3)
6552	Hha1	6	aga	177.935	178	177.81	0	178.06	3 900 000	0	10 900 000	=+(+)	/	/	\(3)
6553	Hha1	6	aga	178.07	178	178.07	0	0	4 000 000	0	0	-=	\		\(3)
6554	Taq1	61	tct	177.88	178	0	0	177.88	0	0	10 000 000	=+	/	/	\(3)
6555	Taq1	61	tct	178.87	178	0	0	178.87	0	0	10 100 000	=+	/		\(3)
6556	Hha1	8	gaa	238.66	239	238.83	238.49	0	4 500 000	3 100 000	0	=-	\		\(3)
6557	Taq1	50	aat	240.36	240	240.36	0	0	3 800 000	0	0	-=	\		\(3)
6558	Hha1	39	agg	72.68	73	72.69	72.5	72.85	5 711.14	2 561.34	12 300.61	=+	/ (-)	/	-1
6559	Hha1	59	ttc	72.683	73	72.76	72.64	72.65	925.63	675.52	8 573.72	=+	/ (-)	/	-1
6560	Hha1	39	agg	72.68	73	72.69	72.5	72.85	5 711.14	2 561.34	12 300.61	=+	/ (-)	/	-1
6561	Hha1	59	ttc	72.683	73	72.76	72.64	72.65	925.63	675.52	8 573.72	=+	/ (-)	/	-1
6562	Hha1	43	cgc	94.177	94	94.16	94.19	94.18	79 000 000	101 100 000	31 200 000	=-	\ (-)		\(2)
6563	Hha1	20	ctc	128.19	128	0	128.34	128.04	0	511.4	477.09	+=	/		\(2)
6564	Hha1	20	ctc	128.15	128	0	0	128.15	0	0	477.09	=+	/		\(2)
6565	Taq1	39	agg	228.995	229	228.85	229.14	0	15 000 000	29 200 000	0	+-	A		\(2)
6566	Taq1	39	agg	228.995	229	228.85	229.14	0	557.04	293.47	0	--	\		\(2)
6567	Hha1	40	tgg	106.01	106	106.04	105.8	106.19	81 800 000	135 500 000	216 000 000	==	-		-2
6568	Hha1	27	acg	134.077	134	134.21	133.96	134.06	9 700 000	3 700 000	5 700 000	-=	\ (-)		-2
6569	Hha1	39	agg	188.97	190	0	0	188.97	0	0	166.82	=+	/		-2
6570	Hha1	39	agg	189.565	190	0	189.7	189.43	0	238.82	195.31	+=	/		-2
6571	Hha1	39	agg	190.03	190	0	0	190.03	0	0	146.48	=+	/		-2
6572	Hha1	39	agg	190.715	190	0	190.77	190.66	0	197.02	146.48	+=	/		-2
6573	Hha1	59	ttc	154.15	154	0	154.15	0	0	146.6	0	+-	A		A(2)
6574	Hha1	59	ttc	154.915	154	155	0	154.83	166.4	0	225.07	-+(=)	V		A(2)
6575	Taq1	39	agg	204.01	205	204.03	203.99	0	8 600 000	59 700 000	0	+-	A		A(2)
6576	Taq1	39	agg	204.42	205	0	204.42	0	0	52 400 000	0	+-	A		A(2)
6577	Taq1	39	agg	205.345	205	205.13	205.56	0	14 600 000	98 100 000	0	+-	A		A(2)
6578	Taq1	39	agg	203.99	205	0	203.99	0	0	600	0	+-	A		A(2)
6579	Taq1	39	agg	204.42	205	0	204.42	0	0	526.63	0	+-	A		A(2)
6580	Taq1	39	agg	205.56	205	0	205.56	0	0	985.93	0	+-	A		A(2)
6581	Taq1	39	agg	204.03	205	204.03	0	0	319.37	0	0	-=	\		A(2)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
6539	RATRORA.ROR-A	ROR-A	opioid receptor A	*	tgg	ttg	No change
6540	RATRORA.ROR-A	ROR-A	opioid receptor A	*	tgg	ttg	No change
6541	RATRORA.ROR-A	ROR-A	opioid receptor A	*	tgg	ttg	No change
6542	AB105378.RATORC1	ratOrc1	origin recognition complex subunit 1		tca	agg	increased by mild
6543	AB105378.RATORC1	ratOrc1	origin recognition complex subunit 1		tca	agg	increased by mild
6544	AB105378.RATORC1	ratOrc1	origin recognition complex subunit 1		tca	agg	increased by mild
6545	AB105378.RATORC1	ratOrc1	origin recognition complex subunit 1		tca	agg	increased by mild
6546	AB105378.RATORC1	ratOrc1	origin recognition complex subunit 1		tca	agg	increased by mild
6547	AB105378.RATORC1	ratOrc1	origin recognition complex subunit 1		tca	agg	increased by mild
6548	AB105378.RATORC1	ratOrc1	origin recognition complex subunit 1		tca	agg	increased by mild
6549	AB105378.RATORC1	ratOrc1	origin recognition complex subunit 1		tca	agg	increased by mild
6550	AB105378.RATORC1	ratOrc1	origin recognition complex subunit 1		gag	aaa	increased by mild
6551	RRU15660.HZF-2	HZF-2	orphan nuclear receptor HZF-2		tct	aga	increased
6552	RRU15660.HZF-2	HZF-2	orphan nuclear receptor HZF-2		tct	aga	decreased
6553	RRU15660.HZF-2	HZF-2	orphan nuclear receptor HZF-2		tct	aga	increased
6554	RRU15660.HZF-2	HZF-2	orphan nuclear receptor HZF-2		tct	aga	decreased
6555	RRU15660.HZF-2	HZF-2	orphan nuclear receptor HZF-2		tct	aga	increased
6556	RRU15660.HZF-2	HZF-2	orphan nuclear receptor HZF-2		gaa	aat	increased
6557	RRU15660.HZF-2	HZF-2	orphan nuclear receptor HZF-2		gaa	aat	increased
6558	RNU20389.PE1	nc	orphan nuclear receptor OR-1		ttc	agg	decreased
6559	RNU20389.PE1	nc	orphan nuclear receptor OR-1		ttc	agg	decreased
6560	RNU14533.PE1	nc	orphan receptor		ttc	agg	decreased
6561	RNU14533.PE1	nc	orphan receptor		ttc	agg	decreased
6562	AB023065.PRSMG1	Prsmg1/Gcpl1	O-sialoglycoprotease		caa	cgc	increased
6563	AB023065.PRSMG1	Prsmg1/Gcpl1	O-sialoglycoprotease		aca	ctc	increased
6564	AB023065.PRSMG1	Prsmg1/Gcpl1	O-sialoglycoprotease		aca	ctc	increased
6565	AB023065.PRSMG1	Prsmg1/Gcpl1	O-sialoglycoprotease		agg	tgt	increased
6566	AB023065.PRSMG1	Prsmg1/Gcpl1	O-sialoglycoprotease		agg	tgt	increased
6567	D88450.PE1	nc	osteoclast-derived zinc finger (OCZF) protein		cag	tgg	No change
6568	D88450.PE1	nc	osteoclast-derived zinc finger (OCZF) protein		ggc	acg	No change
6569	D88450.PE1	nc	osteoclast-derived zinc finger (OCZF) protein		agg	cgc	No change
6570	D88450.PE1	nc	osteoclast-derived zinc finger (OCZF) protein		agg	cgc	No change
6571	D88450.PE1	nc	osteoclast-derived zinc finger (OCZF) protein		agg	cgc	No change
6572	D88450.PE1	nc	osteoclast-derived zinc finger (OCZF) protein		agg	cgc	No change
6573	RNOSTEONE.PE1	nc	osteonectin		atg	ttc	increased by mild
6574	RNOSTEONE.PE1	nc	osteonectin		atg	ttc	increased by mild
6575	RNOSTEONE.PE1	nc	osteonectin		gga	agg	increased by mild
6576	RNOSTEONE.PE1	nc	osteonectin		gga	agg	increased by mild
6577	RNOSTEONE.PE1	nc	osteonectin		gga	agg	increased by mild
6578	RNOSTEONE.PE1	nc	osteonectin		gga	agg	increased by mild
6579	RNOSTEONE.PE1	nc	osteonectin		gga	agg	increased by mild
6580	RNOSTEONE.PE1	nc	osteonectin		gga	agg	increased by mild
6581	RNOSTEONE.PE1	nc	osteonectin		gga	agg	increased by mild

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
6582	Taq1	39	agg	205.13	205	205.13	0	0	542.18	0	0	-=	\		A(2)
6583	Taq1	39	agg	206.22	205	206.22	0	0	393.64	0	0	-=	\		A(2)
6584	Hha1	31	gac	89.2	89	89.43	89.14	89.03	4 200 000	7 100 000	26 600 000	=+	/ (-)		A(4)
6585	Hha1	56	tga	119.6	120	119.85	119.35	0	9 704.57	225.67	0	-=	\		A(4)
6586	Hha1	56	tga	119.71	120	0	119.71	0	0	297.22	0	+-	A		A(4)
6587	Hha1	59	ttc	119.5	120	119.76	119.46	119.28	410.81	376.56	250.95	==	-		A(4)
6588	Hha1	59	ttc	120.06	120	0	120.06	0	0	218.46	0	+-	A		A(4)
6589	Hha1	59	ttc	120.7	120	120.7	0	0	956.83	0	0	-=	\		A(4)
6590	Taq1	40	tgg	148.97	149	148.83	0	149.11	3 900 000	0	6 600 000	-+(=)	V		A(4)
6591	Taq1	40	tgg	149.38	149	0	149.38	0	0	5 000 000	0	+-	A		A(4)
6592	Taq1	8	gaa	330.55	331	0	330.55	0	0	6 400 000	0	+-	A		A(4)
6593	Taq1	8	gaa	332.005	331	0	332	332.01	0	3 400 000	11 900 000	=+	/		A(4)
6594	Hha1	28	tcg	147.46	148	0	147.35	147.57	0	4 500 000	3 700 000	+=	/		/(2)
6595	Hha1	54	ttt	148.59	149	0	0	148.59	0	0	3 600 000	=+	/		/(2)
6596	Hha1	28	tcg	147.46	148	0	147.35	147.57	0	4 500 000	3 700 000	+=	/		/(2)
6597	Hha1	54	ttt	148.59	149	0	0	148.59	0	0	3 600 000	=+	/		/(2)
6598	Hha1	56	tga	133.09	133	133.09	133.24	132.94	1 356.59	363.27	1 361.83	-+	V		A(2)
6599	Hha1	59	ttc	132.867	133	132.98	132.83	132.79	358.81	592.15	328.56	==	-		A(2)
6600	Hha1	59	ttc	133.55	133	0	133.55	0	0	238.58	0	+-	A		A(2)
6601	Hha1	40	tgg	193.56	194	0	193.56	0	0	5 600 000	0	+-	A		A(2)
6602	Hha1	40	tgg	193.88	194	0	193.88	0	0	3 900 000	0	+-	A		A(2)
6603	Hha1	40	tgg	194.63	194	0	194.63	0	0	3 300 000	0	+-	A		A(2)
6604	Hha1	33	agc	62.84	63	62.76	62.92	62.84	4 400 000	18 500 000	17 900 000	+=	/ (-)		-(2) /(2) \(2)
6605	Hha1	20	ctc	74.577	75	74.85	74.49	74.39	3 567.49	773.66	763.35	-=	\ (-)		-(2) /(2) \(2)
6606	Hha1	20	ctc	74.93	75	0	75.01	74.85	0	1 363.75	894.56	+=	/		-(2) /(2) \(2)
6607	Hha1	33	agc	110.905	111	110.83	110.98	0	12 700 000	12 900 000	0	=-	\		-(2) /(2) \(2)
6608	Hha1	33	agc	62.84	63	62.76	62.92	62.84	4 400 000	18 500 000	17 900 000	+=	/ (-)		-(2) /(2) \(2)
6609	Hha1	20	ctc	74.577	75	74.85	74.49	74.39	3 567.49	773.66	763.35	-=	\ (-)		-(2) /(2) \(2)
6610	Hha1	20	ctc	74.93	75	0	75.01	74.85	0	1 363.75	894.56	+=	/		-(2) /(2) \(2)
6611	Hha1	33	agc	110.905	111	110.83	110.98	0	12 700 000	12 900 000	0	=-	\		-(2) /(2) \(2)
6612	Hha1	33	agc	123.97	124	123.91	124.03	0	3 500 000	4 200 000	0	=-	\		\(2)
6613	Hha1	6	aga	187.02	187	187.02	0	0	4 800 000	0	0	-=	\		\(2)
6614	Hha1	6	aga	188.12	187	188.12	0	0	10 100 000	0	0	-=	\		\(2)
6615	Hha1	33	agc	123.97	124	123.91	124.03	0	3 500 000	4 200 000	0	=-	\		\(2)
6616	Hha1	6	aga	187.02	187	187.02	0	0	4 800 000	0	0	-=	\		\(2)
6617	Hha1	6	aga	188.12	187	188.12	0	0	10 100 000	0	0	-=	\		\(2)
6618	Hha1	33	agc	123.97	124	123.91	124.03	0	3 500 000	4 200 000	0	=-	\		\(2)
6619	Hha1	6	aga	187.02	187	187.02	0	0	4 800 000	0	0	-=	\		\(2)
6620	Hha1	6	aga	188.12	187	188.12	0	0	10 100 000	0	0	-=	\		\(2)
6621	Hha1	33	agc	62.84	63	62.76	62.92	62.84	4 400 000	18 500 000	17 900 000	+=	/ (-)		-(2) /(2) \(2)
6622	Hha1	20	ctc	74.577	75	74.85	74.49	74.39	3 567.49	773.66	763.35	-=	\ (-)		-(2) /(2) \(2)
6623	Hha1	20	ctc	74.93	75	0	75.01	74.85	0	1 363.75	894.56	+=	/		-(2) /(2) \(2)
6624	Hha1	33	agc	110.905	111	110.83	110.98	0	12 700 000	12 900 000	0	=-	\		-(2) /(2) \(2)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
6582	RNOSTEONE.PE1	nc	osteonectin		gga	agg	increased by mild
6583	RNOSTEONE.PE1	nc	osteonectin		gga	agg	increased by mild
6584	AF003944.PE1	nc	ovalbumin upstream promoter beta nuclear		gac	ctg	increased by mild
6585	AF003944.PE1	nc	ovalbumin upstream promoter beta nuclear		ttc	tga	increased by mild
6586	AF003944.PE1	nc	ovalbumin upstream promoter beta nuclear		ttc	tga	increased by mild
6587	AF003944.PE1	nc	ovalbumin upstream promoter beta nuclear		ttc	tga	increased by mild
6588	AF003944.PE1	nc	ovalbumin upstream promoter beta nuclear		ttc	tga	increased by mild
6589	AF003944.PE1	nc	ovalbumin upstream promoter beta nuclear		ttc	tga	increased by mild
6590	AF003944.PE1	nc	ovalbumin upstream promoter beta nuclear		gcg	tgg	increased by mild
6591	AF003944.PE1	nc	ovalbumin upstream promoter beta nuclear		gcg	tgg	increased by mild
6592	AF003944.PE1	nc	ovalbumin upstream promoter beta nuclear		gaa	cgt	increased by mild
6593	AF003944.PE1	nc	ovalbumin upstream promoter beta nuclear		gaa	cgt	increased by mild
6594	AY071925.PE1	nc	oxidoreductase ERO1		ttt	tcg	decreased
6595	AY071925.PE1	nc	oxidoreductase ERO1		ttt	tcg	decreased
6596	AY071924.PE1	nc	oxidoreductase ERO1-L		ttt	tcg	decreased
6597	AY071924.PE1	nc	oxidoreductase ERO1-L		ttt	tcg	decreased
6598	AB089316.PE1	nc	oxysterol-binding protein		tga	ttc	increased by mild
6599	AB089316.PE1	nc	oxysterol-binding protein		tga	ttc	increased by mild
6600	AB089316.PE1	nc	oxysterol-binding protein		tga	ttc	increased by mild
6601	AB089316.PE1	nc	oxysterol-binding protein		tgg	gtg	increased by mild
6602	AB089316.PE1	nc	oxysterol-binding protein		tgg	gtg	increased by mild
6603	AB089316.PE1	nc	oxysterol-binding protein		tgg	gtg	increased by mild
6604	RNOXY.PE1	nc	oxytocin	*	tgc	agc	No change
6605	RNOXY.PE1	nc	oxytocin	*	gga	ctc	No change
6606	RNOXY.PE1	nc	oxytocin	*	gga	ctc	No change
6607	RNOXY.PE1	nc	oxytocin	*	tgc	agc	No change
6608	RNVAOXY.PE1	nc	oxytocin	*	tgc	agc	No change
6609	RNVAOXY.PE1	nc	oxytocin	*	gga	ctc	No change
6610	RNVAOXY.PE1	nc	oxytocin	*	gga	ctc	No change
6611	RNVAOXY.PE1	nc	oxytocin	*	tgc	agc	No change
6612	AF257237.PE1	nc	oxytocin receptor		cgc	agc	increased
6613	AF257237.PE1	nc	oxytocin receptor		ccg	aga	increased
6614	AF257237.PE1	nc	oxytocin receptor		ccg	aga	increased
6615	L81169.PE1	nc	oxytocin receptor		cgc	agc	increased
6616	L81169.PE1	nc	oxytocin receptor		ccg	aga	increased
6617	L81169.PE1	nc	oxytocin receptor		ccg	aga	increased
6618	RNOTR2.OTR	OTR	oxytocin receptor		cgc	agc	increased
6619	RNOTR2.OTR	OTR	oxytocin receptor		ccg	aga	increased
6620	RNOTR2.OTR	OTR	oxytocin receptor		ccg	aga	increased
6621	RATOXTNP.OXT	Oxt	oxytocin/neurophysin	*	tgc	agc	No change
6622	RATOXTNP.OXT	Oxt	oxytocin/neurophysin	*	gga	ctc	No change
6623	RATOXTNP.OXT	Oxt	oxytocin/neurophysin	*	gga	ctc	No change
6624	RATOXTNP.OXT	Oxt	oxytocin/neurophysin	*	tgc	agc	No change

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
6625	Taq1	8	gaa	102.51	103	0	0	102.51	0	0	10 400 000	=+	/		/(6)
6626	Hha1	8	gaa	102.99	103	0	102.99	0	0	3 400 000	0	+-	A		/(6)
6627	Taq1	8	gaa	103.32	103	0	0	103.32	0	0	19 700 000	=+	/	/	/(6)
6628	Taq1	31	gac	102.457	103	102.55	102.37	102.45	8 400 000	3 300 000	87 800 000	=+	/ (-)		/(6)
6629	Taq1	31	gac	103.36	103	0	0	103.36	0	0	17 800 000	=+	/	/	/(6)
6630	Taq1	23	cga	126.45	127	0	0	126.45	0	0	9 800 000	=+	/		/(6)
6631	Taq1	23	cga	127.71	127	0	0	127.71	0	0	4 100 000	=+	/		/(6)
6632	Hha1	28	tcg	147.46	148	0	147.35	147.57	0	4 500 000	3 700 000	+=	/		/(6)
6633	Hha1	33	agc	162.513	163	162.57	162.48	162.49	4 300 000	4 100 000	3 700 000	==	-		/(6)
6634	Hha1	33	agc	163.62	163	163.55	163.69	0	3 600 000	3 100 000	0	=-	\		/(6)
6635	Hha1	6	aga	164.44	165	0	0	164.44	0	0	3 000 000	=+	/		/(6)
6636	Hha1	6	aga	165.59	165	165.63	165.53	165.61	7 400 000	4 900 000	5 400 000	==	-		/(6)
6637	Hha1	11	act	173.71	173	173.62	173.62	173.89	10 000 000	8 900 000	5 100 000	==	-	-	
6638	Taq1	11	act	173.763	173	173.78	173.76	173.75	8 400 000	13 500 000	16 100 000	==	-	-	
6639	Hha1	26	ctg	95.663	96	95.63	95.62	95.74	10 700 000	24 800 000	16 000 000	+=	/ (-)		-1
6640	Hha1	60	ttg	108.59	109	108.56	108.62	0	12 100 000	12 400 000	0	=-	\		-1
6641	Hha1	60	ttg	109.273	109	109.15	109.55	109.12	8 900 000	6 200 000	12 000 000	=+	/ (-)		-1
6642	Hha1	60	ttg	108.59	109	108.56	108.62	0	12 100 000	12 400 000	0	=-	\		-1
6643	Hha1	60	ttg	109.273	109	109.15	109.55	109.12	8 900 000	6 200 000	12 000 000	=+	/ (-)		-1
6644	Taq1	26	ctg	151.67	152	0	151.67	0	0	3 500 000	0	+-	A		-2
6645	Taq1	26	ctg	152.673	152	152.54	152.61	152.87	3 100 000	5 600 000	6 900 000	==	-		-2
6646	Taq1	57	ctg	151.277	152	151.29	151.32	151.22	5 900 000	4 100 000	4 900 000	==	-		-2
6647	Taq1	57	ctg	152.233	152	152.25	152.09	152.36	4 800 000	7 600 000	7 500 000	==	-		-2
6648	Hha1	56	tga	110.023	110	110.19	110.02	109.86	155.27	1 111.84	1 206.68	+=	/ (-)		-1
6649	Hha1	26	ctg	136.21	137	0	0	136.21	0	0	3 600 000	=+	/		-1
6650	Hha1	26	ctg	137.165	137	0	137.17	137.16	0	4 000 000	3 300 000	+=	/		-1
6651	Hha1	59	ttc	165.58	165	165.44	165.5	165.8	166.4	135.1	85.37	==	-		-1
6652	Hha1	31	gac	87.46	87	87.42	87.56	87.4	9 500 000	4 500 000	16 100 000	=+	/ (-)		\(4)
6653	Hha1	20	ctc	88.21	88	0	0	88.21	0	0	620.22	=+	/		\(4)
6654	Taq1	17	cca	186.01	187	185.78	186.24	0	260.06	465.36	0	=-	\		\(4)
6655	Taq1	17	cca	187.32	187	187.3	187.34	0	185.76	285.86	0	=-	\		\(4)
6656	Taq1	17	cca	187.57	187	187.57	0	0	148.6	0	0	-=	\		\(4)
6657	Taq1	40	tgg	186.34	187	186.34	0	0	3 900 000	0	0	-=	\		\(4)
6658	Taq1	18	cct	188.187	189	188.32	188.23	188.01	4 800 000	7 400 000	4 200 000	==	-		\(4)
6659	Taq1	18	cct	189.14	189	189.15	189.13	0	9 100 000	9 100 000	0	=-	\		\(4)
6660	Taq1	36	ggt	188.07	189	188.07	0	0	3 000 000	0	0	-=	\		\(4)
6661	Taq1	36	ggt	189.88	189	189.88	0	0	3 100 000	0	0	-=	\		\(4)
6662	Hha1	33	agc	60.667	61	60.61	60.65	60.74	8 100 000	13 200 000	3 900 000	=-	\ (-)		-(4) \(4)
6663	Hha1	2	tta	96.563	97	96.68	96.45	96.56	172 600 000	85 700 000	50 000 000	-=	\ (-)		-(4) \(4)
6664	Hha1	2	tta	97.21	97	97.31	97.11	0	93 200 000	89 300 000	0	=-	\		-(4) \(4)
6665	Hha1	43	cgc	107.583	108	107.51	107.56	107.68	10 100 000	13 700 000	4 700 000	=-	\ (-)		-(4) \(4)
6666	Hha1	28	tcg	108.88	109	108.89	108.86	108.89	24 900 000	32 000 000	44 800 000	==	-		-(4) \(4)
6667	Hha1	54	ttt	110.195	110	110.24	0	110.15	4 700 000	0	5 200 000	-+(=)	V		-(4) \(4)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
6625	RNU83883.PE1	nc	p105 coactivator		gaa	gac	decreased
6626	RNU83883.PE1	nc	p105 coactivator		gaa	gac	decreased
6627	RNU83883.PE1	nc	p105 coactivator		gaa	gac	decreased
6628	RNU83883.PE1	nc	p105 coactivator		gaa	gac	decreased
6629	RNU83883.PE1	nc	p105 coactivator		gaa	gac	decreased
6630	RNU83883.PE1	nc	p105 coactivator		gac	cga	decreased
6631	RNU83883.PE1	nc	p105 coactivator		gac	cga	decreased
6632	RNU83883.PE1	nc	p105 coactivator		tcg	atg	decreased
6633	RNU83883.PE1	nc	p105 coactivator		agc	tcc	decreased
6634	RNU83883.PE1	nc	p105 coactivator		agc	tcc	decreased
6635	RNU83883.PE1	nc	p105 coactivator		aga	aca	decreased
6636	RNU83883.PE1	nc	p105 coactivator		aga	aca	decreased
6637	L81167.PE1	nc	p16 protein P16INK4a	*	act	gcg	No change
6638	L81167.PE1	nc	p16 protein P16INK4a	*	act	gcg	No change
6639	AF020758.P2X2	P2X2	P2X2-5 receptor		ctg	acc	No change
6640	AF020758.P2X2	P2X2	P2X2-5 receptor		ttg	cga	No change
6641	AF020758.P2X2	P2X2	P2X2-5 receptor		ttg	cga	No change
6642	AF020758.P2X2	P2X2	P2X2-5 receptor		ttg	cga	No change
6643	AF020758.P2X2	P2X2	P2X2-5 receptor		ttg	cga	No change
6644	AF083269.PE1	nc	p41-Arc		ctg	tta	No change
6645	AF083269.PE1	nc	p41-Arc		ctg	tta	No change
6646	AF083269.PE1	nc	p41-Arc		ctg	tta	No change
6647	AF083269.PE1	nc	p41-Arc		ctg	tta	No change
6648	RATP45OC.CYP27	CYP27	P-450c27/25		tga	tag	No change
6649	RATP45OC.CYP27	CYP27	P-450c27/25		ctg	ctg	No change
6650	RATP45OC.CYP27	CYP27	P-450c27/25		ctg	ctg	No change
6651	RATP45OC.CYP27	CYP27	P-450c27/25		ttc	ggt	No change
6652	AY029167.PE1	nc	p47 phox	*	gac	gga	increased
6653	AY029167.PE1	nc	p47 phox	*	ctc	tgc	increased
6654	AY029167.PE1	nc	p47 phox	*	cca	tgg	increased
6655	AY029167.PE1	nc	p47 phox	*	cca	tgg	increased
6656	AY029167.PE1	nc	p47 phox	*	cca	tgg	increased
6657	AY029167.PE1	nc	p47 phox	*	cca	tgg	increased
6658	AY029167.PE1	nc	p47 phox	*	ggt	cct	increased
6659	AY029167.PE1	nc	p47 phox	*	ggt	cct	increased
6660	AY029167.PE1	nc	p47 phox	*	ggt	cct	increased
6661	AY029167.PE1	nc	p47 phox	*	ggt	cct	increased
6662	RNPTF1P48.PE1	PTF1 p48	p48 DNA-binding subunit of transcription factor	*	ctc	agc	No change
6663	RNPTF1P48.PE1	PTF1 p48	p48 DNA-binding subunit of transcription factor	*	tta	agt	No change
6664	RNPTF1P48.PE1	PTF1 p48	p48 DNA-binding subunit of transcription factor	*	tta	agt	No change
6665	RNPTF1P48.PE1	PTF1 p48	p48 DNA-binding subunit of transcription factor	*	cgc	ttt	No change
6666	RNPTF1P48.PE1	PTF1 p48	p48 DNA-binding subunit of transcription factor	*	tcg	ccc	No change
6667	RNPTF1P48.PE1	PTF1 p48	p48 DNA-binding subunit of transcription factor	*	cgc	ttt	No change

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
6668	Hha1	20	ctc	188.13	189	188.13	0	0	309.91	0	0	-=	\		-(4) \(4)
6669	Hha1	20	ctc	189.2	189	189.2	0	0	337.46	0	0	-=	\		-(4) \(4)
6670	Hha1	49	aaa	102.43	103	0	0	102.43	0	0	6 800 000	=+	/		\(2)
6671	Hha1	49	aaa	103.07	103	103.19	102.95	0	10 700 000	15 200 000	0	=-	\		\(2)
6672	Hha1	49	aaa	103.595	103	103.59	0	103.6	7 700 000	0	4 600 000	-+(=)	V		\(2)
6673	Hha1	44	cgg	114.53	115	0	114.53	0	0	6 900 000	0	+-	A		\(2)
6674	Hha1	44	cgg	115.615	115	115.44	115.79	0	4 400 000	7 700 000	0	=-	\		\(2)
6675	Taq1	8	gaa	82.635	83	82.54	82.73	0	7 300 000	5 600 000	0	=-	\		\(2)
6676	Taq1	8	gaa	83.06	83	83.06	0	0	6 700 000	0	0	-=	\		\(2)
6677	Hha1	44	cgg	104.397	105	104.37	104.38	104.44	3 500 000	11 100 000	12 300 000	+=	/ (-)		\(2)
6678	Taq1	39	agg	201.075	202	201.22	200.93	0	11 500 000	11 100 000	0	=-	\		\(2)
6679	Taq1	39	agg	201.935	202	201.96	201.91	0	8 700 000	38 600 000	0	+-	A		\(2)
6680	Taq1	39	agg	202.85	202	202.85	0	0	8 800 000	0	0	-=	\		\(2)
6681	Taq1	39	agg	201.075	202	201.22	200.93	0	427.06	111.55	0	-=	\		\(2)
6682	Taq1	39	agg	201.935	202	201.96	201.91	0	323.08	387.94	0	=-	\		\(2)
6683	Taq1	39	agg	202.85	202	202.85	0	0	326.79	0	0	-=	\		\(2)
6684	Hha1	20	ctc	120.853	121	120.78	120.99	120.79	2 561.98	1 114.6	512.88	-=	\ (-)	(-)	
6685	Hha1	39	agg	121.03	121	121.19	121.17	120.73	373.9	268.67	297.03	==	-	(-)	
6686	Hha1	20	ctc	120.853	121	120.78	120.99	120.79	2 561.98	1 114.6	512.88	-=	\ (-)	(-)	
6687	Hha1	39	agg	121.03	121	121.19	121.17	120.73	373.9	268.67	297.03	==	-	(-)	
6688	Taq1	29	gca	94.33	94	94.4	94.33	94.26	154 300 000	149 200 000	8 300 000	=-	\ (-)		-(2) \(2)
6689	Taq1	45	gcc	205.715	206	205.61	205.82	0	4 400 000	3 100 000	0	=-	\		-(2) \(2)
6690	Taq1	45	gcc	205.85	206	205.85	0	0	4 200 000	0	0	-=	\		-(2) \(2)
6691	Taq1	45	gcc	206.677	206	206.83	206.38	206.82	5 700 000	3 200 000	5 400 000	==	-		-(2) \(2)
6692	Taq1	45	gcc	206.98	206	0	206.98	0	0	5 500 000	0	+-	A		-(2) \(2)
6693	Hha1	21	acc	106.475	107	0	106.29	106.66	0	5 200 000	9 700 000	++	/	(/)	
6694	Taq1	21	acc	106.53	107	106.49	0	106.57	18 200 000	0	37 000 000	-+(+)	V (/)	(/)	
6695	Taq1	23	cga	126.45	127	0	0	126.45	0	0	9 800 000	=+	/	/	/(2)
6696	Taq1	23	cga	127.71	127	0	0	127.71	0	0	4 100 000	=+	/	/	/(2)
6697	Taq1	62	tgt	126.573	127	126.54	126.64	126.54	5 600 000	10 400 000	6 400 000	+=	/ (-)	/	/(2)
6698	Taq1	62	tgt	127.55	127	0	127.74	127.36	0	5 000 000	8 700 000	+=	/	/	/(2)
6699	Hha1	58	gta	128.243	129	128.27	128.25	128.21	15 800 000	12 100 000	17 300 000	==	-		\(6) A(5)
6700	Hha1	58	gta	129.233	129	129.24	129.25	129.21	6 600 000	40 500 000	10 200 000	+-	A		\(6) A(5)
6701	Taq1	48	ggg	132.387	133	132.18	132.66	132.32	2 212.38	408.26	2 071.32	-+	V		\(6) A(5)
6702	Taq1	48	ggg	133.415	133	133.19	133.64	0	1 011.37	1 795.14	0	=-	\	\	\(6) A(5)
6703	Taq1	30	cgt	133.28	134	133.24	133.32	0	4 400 000	4 400 000	0	=-	\	\	\(6) A(5)
6704	Taq1	22	tcc	152.11	153	152.09	152.06	152.18	7 400 000	4 700 000	6 400 000	==	-		\(6) A(5)
6705	Taq1	22	tcc	152.57	153	0	152.57	0	0	3 000 000	0	+-	A		\(6) A(5)
6706	Taq1	22	tcc	153.17	153	0	0	153.17	0	0	9 900 000	=+	/		\(6) A(5)
6707	Hha1	22	tcc	153.445	153	0	153.65	153.24	0	6 200 000	3 100 000	+-	A		\(6) A(5)
6708	Taq1	22	tcc	153.625	153	153.61	153.64	0	22 200 000	18 200 000	0	=-	\		\(6) A(5)
6709	Taq1	39	agg	186.487	187	186.76	186.39	186.31	11 500 000	7 700 000	3 900 000	==	-		\(6) A(5)
6710	Taq1	39	agg	186.31	187	0	0	186.31	0	0	114.87	=+	/		\(6) A(5)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
6668	RNPTF1P48.PE1	PTF1 p48	p48 DNA-binding subunit of transcription factor	*	ctc	acg	No change
6669	RNPTF1P48.PE1	PTF1 p48	p48 DNA-binding subunit of transcription factor	*	ctc	acg	No change
6670	RRU05341.PE1	nc	p55CDC		aaa	tgt	increased
6671	RRU05341.PE1	nc	p55CDC		aaa	tgt	increased
6672	RRU05341.PE1	nc	p55CDC		aaa	tgt	increased
6673	RRU05341.PE1	nc	p55CDC		cgg	tca	increased
6674	RRU05341.PE1	nc	p55CDC		cgg	tca	increased
6675	RNU44129.PE1	nc	p58		gaa	cct	increased
6676	RNU44129.PE1	nc	p58		gaa	cct	increased
6677	RNU44129.PE1	nc	p58		cct	cgg	increased
6678	RNU44129.PE1	nc	p58		gta	agg	increased
6679	RNU44129.PE1	nc	p58		gta	agg	increased
6680	RNU44129.PE1	nc	p58		gta	agg	increased
6681	RNU44129.PE1	nc	p58		gta	agg	increased
6682	RNU44129.PE1	nc	p58		gta	agg	increased
6683	RNU44129.PE1	nc	p58		gta	agg	increased
6684	AF192493.PE1	nc	p62 dynactin subunit		ctc	agg	No change
6685	AF192493.PE1	nc	p62 dynactin subunit		ctc	agg	No change
6686	AF192494.PE1	nc	p62 dynactin subunit isoform 2		ctc	agg	No change
6687	AF192494.PE1	nc	p62 dynactin subunit isoform 2		ctc	agg	No change
6688	RNAJ2424.P65	p65	p65 protein		gca	ggt	No change
6689	RNAJ2424.P65	p65	p65 protein		gcc	tgt	No change
6690	RNAJ2424.P65	p65	p65 protein		gcc	tgt	No change
6691	RNAJ2424.P65	p65	p65 protein		gcc	tgt	No change
6692	RNAJ2424.P65	p65	p65 protein		gcc	tgt	No change
6693	AF289091.PE1	nc	p97/VCP-binding protein p135		tgc	acc	decreased
6694	AF289091.PE1	nc	p97/VCP-binding protein p135		tgc	acc	decreased
6695	AF056208.PCIP1	PCIP1	PAM COOH-terminal interactor protein 1		tgt	cga	decreased
6696	AF056208.PCIP1	PCIP1	PAM COOH-terminal interactor protein 1		tgt	cga	decreased
6697	AF056208.PCIP1	PCIP1	PAM COOH-terminal interactor protein 1		tgt	cga	decreased
6698	AF056208.PCIP1	PCIP1	PAM COOH-terminal interactor protein 1		tgt	cga	decreased
6699	RNAF000114.PE1	nc	paranodin		gta	tgc	increased
6700	RNAF000114.PE1	nc	paranodin		gta	tgc	increased
6701	RNAF000114.PE1	nc	paranodin		ggg	cgt	increased
6702	RNAF000114.PE1	nc	paranodin		ggg	cgt	increased
6703	RNAF000114.PE1	nc	paranodin		ggg	cgt	increased
6704	RNAF000114.PE1	nc	paranodin		gtg	tcc	increased
6705	RNAF000114.PE1	nc	paranodin		gtg	tcc	increased
6706	RNAF000114.PE1	nc	paranodin		gtg	tcc	increased
6707	RNAF000114.PE1	nc	paranodin		gtg	tcc	increased
6708	RNAF000114.PE1	nc	paranodin		gtg	tcc	increased
6709	RNAF000114.PE1	nc	paranodin		aaa	agg	increased
6710	RNAF000114.PE1	nc	paranodin		aaa	agg	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
6711	Taq1	39	agg	187.38	187	187.52	187.24	0	6 200 000	40 100 000	0	+-	A		\(6) A(5)
6712	Taq1	39	agg	186.76	187	186.76	0	0	427.06	0	0	-=	\		\(6) A(5)
6713	Taq1	39	agg	187.52	187	187.52	0	0	230.24	0	0	-=	\	\	\(6) A(5)
6714	Taq1	39	agg	186.39	187	0	186.39	0	0	77.38	0	+-	A		\(6) A(5)
6715	Taq1	39	agg	187.24	187	0	187.24	0	0	403.01	0	+-	A		\(6) A(5)
6716	Taq1	49	aaa	187.55	188	187.55	0	0	14 100 000	0	0	-=	\	\	\(6) A(5)
6717	Taq1	49	aaa	188.285	188	188.37	188.2	0	41 600 000	18 100 000	0	-=	\		\(6) A(5)
6718	Hha1	40	tgg	201.08	202	0	201.08	0	0	6 200 000	0	+-	A		\(6) A(5)
6719	Hha1	40	tgg	202.96	202	202.96	0	0	4 200 000	0	0	-=	\		\(6) A(5)
6720	Hha1	20	ctc	90.57	91	0	90.64	90.5	0	537.63	357.82	+=	/		\(3)
6721	Hha1	20	ctc	91.11	91	0	0	91.11	0	0	584.44	=+	/		\(3)
6722	Hha1	20	ctc	91.505	91	0	91.62	91.39	0	904.79	584.44	+=	/		\(3)
6723	Hha1	33	agc	114.89	115	114.89	0	0	3 800 000	0	0	-=	\		\(3)
6724	Hha1	59	ttc	114.603	115	114.73	114.55	114.53	218.4	526.04	488.96	+=	/ (-)		\(3)
6725	Hha1	59	ttc	115.51	115	0	115.28	115.74	0	201.21	152.64	+=	/		\(3)
6726	Taq1	45	gcc	219.4	219	219.42	219.38	0	4 400 000	5 900 000	0	=-	\		\(3)
6727	Taq1	34	tgc	218.93	220	218.93	0	0	3 000 000	0	0	-=	\		\(3)
6728	Hha1	20	ctc	68	68	68	0	0	426.99	0	0	-=	\		\(6)
6729	Hha1	33	agc	78.69	79	78.69	0	0	4 200 000	0	0	-=	\		\(6)
6730	Hha1	43	cgc	99.97	100	99.92	100.02	0	25 600 000	8 600 000	0	-=	\		\(6)
6731	Hha1	28	tcg	101.17	101	0	101.17	0	0	4 100 000	0	+-	A		\(6)
6732	Hha1	26	ctg	102.86	103	0	0	102.86	0	0	5 200 000	=+	/		\(6)
6733	Hha1	40	tgg	102.66	103	102.77	102.55	0	17 300 000	10 800 000	0	=-	\		\(6)
6734	Hha1	26	ctg	206.33	207	206.33	0	0	3 000 000	0	0	-=	\		\(6)
6735	Hha1	26	ctg	207.46	207	0	207.46	0	0	3 500 000	0	+-	A		\(6)
6736	Hha1	49	aaa	313.15	315	313.15	0	0	7 300 000	0	0	-=	\		\(6)
6737	Hha1	49	aaa	313.85	315	0	313.85	0	0	7 000 000	0	+-	A		\(6)
6738	Hha1	49	aaa	315.17	315	315.19	315.15	0	43 200 000	6 300 000	0	-=	\		\(6)
6739	Hha1	49	aaa	315.78	315	0	315.78	0	0	6 200 000	0	+-	A		\(6)
6740	Taq1	26	ctg	190.3	190	0	0	190.3	0	0	7 800 000	=+	/		/(2) \(2) A(2)
6741	Taq1	26	ctg	190.87	190	0	190.87	0	0	3 500 000	0	+-	A		/(2) \(2) A(2)
6742	Taq1	57	ctg	189.34	190	0	0	189.34	0	0	3 300 000	=+	/		/(2) \(2) A(2)
6743	Taq1	57	ctg	190.315	190	190.34	190.29	0	3 700 000	3 700 000	0	=-	\		/(2) \(2) A(2)
6744	Taq1	57	ctg	191.06	190	191.06	0	0	3 000 000	0	0	-=	\		/(2) \(2) A(2)
6745	Taq1	61	tct	189.22	190	189.22	0	0	4 700 000	0	0	-=	\		/(2) \(2) A(2)
6746	Taq1	61	tct	190.11	190	190.21	189.87	190.25	7 700 000	3 100 000	3 700 000	-=	\ (-)		/(2) \(2) A(2)
6747	Taq1	61	tct	190.42	190	0	190.42	0	0	4 800 000	0	+-	A		/(2) \(2) A(2)
6748	Hha1	20	ctc	68	68	68	0	0	426.99	0	0	-=	\		\(6)
6749	Hha1	33	agc	78.69	79	78.69	0	0	4 200 000	0	0	-=	\		\(6)
6750	Hha1	43	cgc	99.97	100	99.92	100.02	0	25 600 000	8 600 000	0	-=	\		\(6)
6751	Hha1	28	tcg	101.17	101	0	101.17	0	0	4 100 000	0	+-	A		\(6)
6752	Hha1	26	ctg	102.86	103	0	0	102.86	0	0	5 200 000	=+	/		\(6)
6753	Hha1	40	tgg	102.66	103	102.77	102.55	0	17 300 000	10 800 000	0	=-	\		\(6)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
6711	RNAF000114.PE1	nc	paranodin		aaa	agg	increased
6712	RNAF000114.PE1	nc	paranodin		aaa	agg	increased
6713	RNAF000114.PE1	nc	paranodin		aaa	agg	increased
6714	RNAF000114.PE1	nc	paranodin		aaa	agg	increased
6715	RNAF000114.PE1	nc	paranodin		aaa	agg	increased
6716	RNAF000114.PE1	nc	paranodin		aaa	agg	increased
6717	RNAF000114.PE1	nc	paranodin		aaa	agg	increased
6718	RNAF000114.PE1	nc	paranodin		tgg	cca	increased
6719	RNAF000114.PE1	nc	paranodin		tgg	cca	increased
6720	AY278739.SPG7	Spg7	paraplegin		tgg	ctc	increased
6721	AY278739.SPG7	Spg7	paraplegin		tgg	ctc	increased
6722	AY278739.SPG7	Spg7	paraplegin		tgg	ctc	increased
6723	AY278739.SPG7	Spg7	paraplegin		agc	ttc	increased
6724	AY278739.SPG7	Spg7	paraplegin		agc	ttc	increased
6725	AY278739.SPG7	Spg7	paraplegin		agc	ttc	increased
6726	AY278739.SPG7	Spg7	paraplegin		tgc	gcc	increased
6727	AY278739.SPG7	Spg7	paraplegin		tgc	gcc	increased
6728	RATPATHYR.PE1	nc	parathyroid hormone receptor	*	ctc	gat	increased
6729	RATPATHYR.PE1	nc	parathyroid hormone receptor	*	aac	agc	increased
6730	RATPATHYR.PE1	nc	parathyroid hormone receptor	*	cgc	tcg	increased
6731	RATPATHYR.PE1	nc	parathyroid hormone receptor	*	cgc	tcg	increased
6732	RATPATHYR.PE1	nc	parathyroid hormone receptor	*	tgg	ctg	increased
6733	RATPATHYR.PE1	nc	parathyroid hormone receptor	*	tgg	ctg	increased
6734	RATPATHYR.PE1	nc	parathyroid hormone receptor	*	aat	ctg	increased
6735	RATPATHYR.PE1	nc	parathyroid hormone receptor	*	aat	ctg	increased
6736	RATPATHYR.PE1	nc	parathyroid hormone receptor	*	aaa	aga	increased
6737	RATPATHYR.PE1	nc	parathyroid hormone receptor	*	aaa	aga	increased
6738	RATPATHYR.PE1	nc	parathyroid hormone receptor	*	aaa	aga	increased
6739	RATPATHYR.PE1	nc	parathyroid hormone receptor	*	aaa	aga	increased
6740	RNU55836.PE1	nc	parathyroid hormone receptor PTH2		ctg	tct	decreased
6741	RNU55836.PE1	nc	parathyroid hormone receptor PTH2		ctg	tct	decreased
6742	RNU55836.PE1	nc	parathyroid hormone receptor PTH2		ctg	tct	decreased
6743	RNU55836.PE1	nc	parathyroid hormone receptor PTH2		ctg	tct	decreased
6744	RNU55836.PE1	nc	parathyroid hormone receptor PTH2		ctg	tct	decreased
6745	RNU55836.PE1	nc	parathyroid hormone receptor PTH2		ctg	tct	decreased
6746	RNU55836.PE1	nc	parathyroid hormone receptor PTH2		ctg	tct	decreased
6747	RNU55836.PE1	nc	parathyroid hormone receptor PTH2		ctg	tct	decreased
6748	RATPTHR.PE1	nc	parathyroid hormone/parathyroid hormone	*	ctc	gat	increased
6749	RATPTHR.PE1	nc	parathyroid hormone/parathyroid hormone	*	aac	agc	increased
6750	RATPTHR.PE1	nc	parathyroid hormone/parathyroid hormone	*	cgc	tcg	increased
6751	RATPTHR.PE1	nc	parathyroid hormone/parathyroid hormone	*	cgc	tcg	increased
6752	RATPTHR.PE1	nc	parathyroid hormone/parathyroid hormone	*	tgg	ctg	increased
6753	RATPTHR.PE1	nc	parathyroid hormone/parathyroid hormone	*	tgg	ctg	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
6754	Hha1	26	ctg	206.33	207	206.33	0	0	3 000 000	0	0	-=	\		\(6)
6755	Hha1	26	ctg	207.46	207	0	207.46	0	0	3 500 000	0	+-	A		\(6)
6756	Hha1	49	aaa	313.15	315	313.15	0	0	7 300 000	0	0	-=	\		\(6)
6757	Hha1	49	aaa	313.85	315	0	313.85	0	0	7 000 000	0	+-	A		\(6)
6758	Hha1	49	aaa	315.17	315	315.19	315.15	0	43 200 000	6 300 000	0	-=	\		\(6)
6759	Hha1	49	aaa	313.15	315	313.15	0	0	7 300 000	0	0	-=	\		\(6)
6760	Hha1	49	aaa	315.19	315	315.19	0	0	43 200 000	0	0	-=	\		\(6)
6761	Hha1	49	aaa	315.78	315	0	315.78	0	0	6 200 000	0	+-	A		\(6)
6762	Hha1	49	aaa	313.85	315	0	313.85	0	0	7 000 000	0	+-	A		\(6)
6763	Hha1	49	aaa	315.15	315	0	315.15	0	0	6 300 000	0	+-	A		\(6)
6764	Hha1	49	aaa	315.78	315	0	315.78	0	0	6 200 000	0	+-	A		\(6)
6765	Taq1	22	tcc	170.13	171	170.36	0	169.9	7 700 000	0	4 400 000	-+(=)	V		/(2)
6766	Taq1	22	tcc	170.79	171	0	170.67	170.91	0	4 500 000	5 200 000	+=	/		/(2)
6767	Taq1	22	tcc	171.84	171	0	0	171.84	0	0	5 800 000	=+	/		/(2)
6768	Taq1	40	tgg	171.46	171	0	0	171.46	0	0	6 800 000	=+	/		/(2)
6769	Taq1	48	ggg	113.04	113	112.86	0	113.22	1 833.12	0	768.73	-=(-)	\		\(5)
6770	Taq1	48	ggg	113.37	113	0	113.37	0	0	2 563.64	0	+-	A		\(5)
6771	Taq1	18	cct	113.567	114	113.4	113.59	113.71	10 100 000	9 800 000	6 400 000	==	-		\(5)
6772	Taq1	18	cct	114.52	114	114.5	114.54	114.52	21 700 000	29 300 000	7 500 000	=-	\ (-)		\(5)
6773	Hha1	54	ttt	159.56	160	159.54	159.58	0	4 400 000	6 100 000	0	=-	\		\(5)
6774	Hha1	54	ttt	160.59	160	160.59	0	0	3 000 000	0	0	-=	\		\(5)
6775	Hha1	61	tct	223.88	225	223.85	223.91	0	10 500 000	7 000 000	0	=-	\		\(5)
6776	Hha1	61	tct	225.16	225	225.29	0	225.03	5 900 000	0	5 600 000	-+(=)	V		\(5)
6777	Hha1	61	tct	225.05	225	225.05	0	0	6 200 000	0	0	-=	\		\(5)
6778	Hha1	61	tct	225.68	225	0	0	225.68	0	0	3 300 000	=+	/		\(5)
6779	Taq1	17	cca	285.64	287	285.64	0	0	143.96	0	0	-=	\		\(5)
6780	Taq1	17	cca	286.62	287	286.62	0	0	301.86	0	0	-=	\		\(5)
6781	Taq1	17	cca	287.85	287	287.85	0	0	153.25	0	0	-=	\		\(5)
6782	Taq1	48	ggg	113.04	113	112.86	0	113.22	1 833.12	0	768.73	-=(-)	\		\(5)
6783	Taq1	48	ggg	113.37	113	0	113.37	0	0	2 563.64	0	+-	A		\(5)
6784	Taq1	18	cct	113.567	114	113.4	113.59	113.71	10 100 000	9 800 000	6 400 000	==	-		\(5)
6785	Taq1	18	cct	114.52	114	114.5	114.54	114.52	21 700 000	29 300 000	7 500 000	=-	\ (-)		\(5)
6786	Hha1	54	ttt	159.56	160	159.54	159.58	0	4 400 000	6 100 000	0	=-	\		\(5)
6787	Hha1	54	ttt	160.59	160	160.59	0	0	3 000 000	0	0	-=	\		\(5)
6788	Hha1	61	tct	223.88	225	223.85	223.91	0	10 500 000	7 000 000	0	=-	\		\(5)
6789	Hha1	61	tct	225.16	225	225.29	0	225.03	5 900 000	0	5 600 000	-+(=)	V		\(5)
6790	Hha1	61	tct	225.05	225	225.05	0	0	6 200 000	0	0	-=	\		\(5)
6791	Hha1	61	tct	225.68	225	0	0	225.68	0	0	3 300 000	=+	/		\(5)
6792	Taq1	17	cca	285.64	287	285.64	0	0	143.96	0	0	-=	\		\(5)
6793	Taq1	17	cca	286.62	287	286.62	0	0	301.86	0	0	-=	\		\(5)
6794	Taq1	17	cca	287.85	287	287.85	0	0	153.25	0	0	-=	\		\(5)
6795	Hha1	6	aga	228.03	229	228.03	0	0	4 100 000	0	0	-=	\		\(2)
6796	Hha1	6	aga	228.935	229	228.92	228.95	0	74 800 000	6 100 000	0	-=	\		\(2)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
6754	RATPTHR.PE1	nc	parathyroid hormone/parathyroid hormone	*	aat	ctg	increased
6755	RATPTHR.PE1	nc	parathyroid hormone/parathyroid hormone	*	aat	ctg	increased
6756	RATPTHR.PE1	nc	parathyroid hormone/parathyroid hormone	*	aaa	aga	increased
6757	RATPTHR.PE1	nc	parathyroid hormone/parathyroid hormone	*	aaa	aga	increased
6758	RATPTHR.PE1	nc	parathyroid hormone/parathyroid hormone	*	aaa	aga	increased
6759	RATPTHR.PE1	nc	parathyroid hormone/parathyroid hormone	*	aaa	aga	increased
6760	RATPTHR.PE1	nc	parathyroid hormone/parathyroid hormone	*	aaa	aga	increased
6761	RATPTHR.PE1	nc	parathyroid hormone/parathyroid hormone	*	aaa	aga	increased
6762	RATPTHR.PE1	nc	parathyroid hormone/parathyroid hormone	*	aaa	aga	increased
6763	RATPTHR.PE1	nc	parathyroid hormone/parathyroid hormone	*	aaa	aga	increased
6764	RATPTHR.PE1	nc	parathyroid hormone/parathyroid hormone	*	aaa	aga	increased
6765	RATPC3A.PC3	PC3	PC3 NGF-inducible anti-proliferative putative		tcc	tgg	decreased
6766	RATPC3A.PC3	PC3	PC3 NGF-inducible anti-proliferative putative		tcc	tgg	decreased
6767	RATPC3A.PC3	PC3	PC3 NGF-inducible anti-proliferative putative		tcc	tgg	decreased
6768	RATPC3A.PC3	PC3	PC3 NGF-inducible anti-proliferative putative		tcc	tgg	decreased
6769	AB027155.PDE10A	PDE10A	PDE10A2		ggg	cct	increased
6770	AB027155.PDE10A	PDE10A	PDE10A2		ggg	cct	increased
6771	AB027155.PDE10A	PDE10A	PDE10A2		ggg	cct	increased
6772	AB027155.PDE10A	PDE10A	PDE10A2		ggg	cct	increased
6773	AB027155.PDE10A	PDE10A	PDE10A2		ttt	tgc	increased
6774	AB027155.PDE10A	PDE10A	PDE10A2		ttt	tgc	increased
6775	AB027155.PDE10A	PDE10A	PDE10A2		tct	ggg	increased
6776	AB027155.PDE10A	PDE10A	PDE10A2		tct	ggg	increased
6777	AB027155.PDE10A	PDE10A	PDE10A2		tct	ggg	increased
6778	AB027155.PDE10A	PDE10A	PDE10A2		tct	ggg	increased
6779	AB027155.PDE10A	PDE10A	PDE10A2		cca	tgg	increased
6780	AB027155.PDE10A	PDE10A	PDE10A2		cca	tgg	increased
6781	AB027155.PDE10A	PDE10A	PDE10A2		cca	tgg	increased
6782	AB027156.PDE10A	PDE10A	PDE10A3		ggg	cct	increased
6783	AB027156.PDE10A	PDE10A	PDE10A3		ggg	cct	increased
6784	AB027156.PDE10A	PDE10A	PDE10A3		ggg	cct	increased
6785	AB027156.PDE10A	PDE10A	PDE10A3		ggg	cct	increased
6786	AB027156.PDE10A	PDE10A	PDE10A3		ttt	tgc	increased
6787	AB027156.PDE10A	PDE10A	PDE10A3		ttt	tgc	increased
6788	AB027156.PDE10A	PDE10A	PDE10A3		tct	ggg	increased
6789	AB027156.PDE10A	PDE10A	PDE10A3		tct	ggg	increased
6790	AB027156.PDE10A	PDE10A	PDE10A3		tct	ggg	increased
6791	AB027156.PDE10A	PDE10A	PDE10A3		tct	ggg	increased
6792	AB027156.PDE10A	PDE10A	PDE10A3		cca	tgg	increased
6793	AB027156.PDE10A	PDE10A	PDE10A3		cca	tgg	increased
6794	AB027156.PDE10A	PDE10A	PDE10A3		cca	tgg	increased
6795	AY305029.PE1	nc	PDIP1		gct	aga	increased
6796	AY305029.PE1	nc	PDIP1		gct	aga	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
6797	Hha1	39	agg	242.315	243	242.2	242.43	0	975.07	388.08	0	-=	\		\(2)
6798	Hha1	39	agg	243.143	243	243.16	243.32	242.95	945.74	1 397.09	1 110.83	==	-		\(2)
6799	Hha1	39	agg	244.015	243	244.13	0	243.9	263.92	0	122.07	-+(-)	V (\)		\(2)
6800	Hha1	44	cgg	79.327	79	79.34	79.27	79.37	37 600 000	23 400 000	20 600 000	==	-		-2
6801	Hha1	27	acg	79.843	80	79.84	79.89	79.8	180 200 000	39 500 000	96 500 000	-=	\ (-)		-2
6802	Hha1	58	gta	130.967	131	131	130.93	130.97	29 200 000	202 800 000	80 200 000	+-	A		-2
6803	Hha1	44	cgg	79.327	79	79.34	79.27	79.37	37 600 000	23 400 000	20 600 000	==	-		-2
6804	Hha1	27	acg	79.843	80	79.84	79.89	79.8	180 200 000	39 500 000	96 500 000	-=	\ (-)		-2
6805	Hha1	58	gta	130.967	131	131	130.93	130.97	29 200 000	202 800 000	80 200 000	+-	A		-2
6806	Hha1	39	agg	62.237	62	62.19	62.23	62.29	1 187.68	4 901.78	655.11	+-	A		/(2)
6807	Taq1	31	gac	124.28	125	0	0	124.28	0	0	8 400 000	=+	/	/	/(2)
6808	Taq1	31	gac	125.22	125	0	0	125.22	0	0	3 300 000	=+	/		/(2)
6809	Taq1	40	tgg	124.435	125	0	124.28	124.59	0	5 600 000	39 000 000	=+	/	/	/(2)
6810	Taq1	40	tgg	125.63	125	0	0	125.63	0	0	13 400 000	=+	/		/(2)
6811	Hha1	31	gac	71.965	72	71.97	71.96	0	4 400 000	3 500 000	0	=-	\		\(3)
6812	Hha1	61	tct	95.43	96	0	95.46	95.4	0	5 600 000	4 300 000	+=	/		\(3)
6813	Hha1	61	tct	96.277	96	96.28	96.35	96.2	12 800 000	6 000 000	3 200 000	-=	\ (-)		\(3)
6814	Hha1	64	gtt	159.11	160	159.29	0	158.93	7 600 000	0	3 800 000	-+(-)	V (\)		\(3)
6815	Hha1	60	ttg	221.88	222	0	221.88	0	0	3 200 000	0	+-	A		\(3)
6816	Hha1	60	ttg	222.82	222	0	0	222.82	0	0	4 600 000	=+	/		\(3)
6817	Hha1	32	gtc	114.705	115	0	114.75	114.66	0	5 228.89	6 931.4	+=	/	/	/(2)
6818	Hha1	39	agg	114.915	115	0	115.09	114.74	0	322.4	435.38	+=	/	/	/(2)
6819	Hha1	43	cgc	134.06	134	134.09	134.03	0	5 900 000	3 900 000	0	=-	\		/(2)
6820	Hha1	43	cgc	134.75	134	134.85	134.79	134.61	7 700 000	6 300 000	3 100 000	==	-		/(2)
6821	Taq1	26	ctg	117.175	117	117.21	117.14	0	6 000 000	5 500 000	0	=-	\		\(3)
6822	Taq1	57	ctg	117.11	117	0	0	117.11	0	0	4 900 000	=+	/		\(3)
6823	Hha1	6	aga	124.12	124	124.12	0	0	4 500 000	0	0	-=	\		\(3)
6824	Taq1	34	tgc	144.205	145	144.22	144.19	0	5 700 000	3 200 000	0	=-	\		\(3)
6825	Taq1	40	tgg	144.835	145	144.73	0	144.94	3 200 000	0	25 000 000	=+(+)	/		\(3)
6826	Hha1	3	aac	295.39	296	295.39	0	0	4 100 000	0	0	-=	\		\(2)
6827	Taq1	17	cca	297.01	296	297.01	0	0	171.82	0	0	-=	\		\(2)
6828	Hha1	3	aac	295.39	296	295.39	0	0	4 100 000	0	0	-=	\		\(2)
6829	Taq1	17	cca	297.01	296	297.01	0	0	171.82	0	0	-=	\		\(2)
6830	Hha1	3	aac	295.39	296	295.39	0	0	4 100 000	0	0	-=	\		\(2)
6831	Taq1	17	cca	297.01	296	297.01	0	0	171.82	0	0	-=	\		\(2)
6832	Hha1	3	aac	295.39	296	295.39	0	0	4 100 000	0	0	-=	\		\(2)
6833	Taq1	17	cca	297.01	296	297.01	0	0	171.82	0	0	-=	\		\(2)
6834	Hha1	3	aac	295.39	296	295.39	0	0	4 100 000	0	0	-=	\		\(2)
6835	Taq1	17	cca	297.01	296	297.01	0	0	171.82	0	0	-=	\		\(2)
6836	Hha1	59	ttc	139.577	140	139.65	139.64	139.44	442.01	534.66	879.62	==	-		\(2)
6837	Hha1	59	ttc	140.02	140	140.02	0	0	452.41	0	0	-=	\		\(2)
6838	Hha1	59	ttc	158.69	159	0	158.66	158.72	0	169.59	150.05	+=	/		\(2)
6839	Hha1	59	ttc	159.255	159	159.3	159.21	0	161.2	166.72	0	=-	\		\(2)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
6797	AY305029.PE1	nc	PDIP1		tgc	agg	increased
6798	AY305029.PE1	nc	PDIP1		tgc	agg	increased
6799	AY305029.PE1	nc	PDIP1		tgc	agg	increased
6800	AB010245.MRT1	mrt1	PDZ protein Mrt1a		cgg	acg	No change
6801	AB010245.MRT1	mrt1	PDZ protein Mrt1a		cgg	acg	No change
6802	AB010245.MRT1	mrt1	PDZ protein Mrt1a		att	gta	No change
6803	AB051816.MRT1	mrt1	PDZ protein Mrt1b		cgg	acg	No change
6804	AB051816.MRT1	mrt1	PDZ protein Mrt1b		cgg	acg	No change
6805	AB051816.MRT1	mrt1	PDZ protein Mrt1b		att	gta	No change
6806	AF167412.PDS	Pds	pendrin		agg	cag	decreased
6807	AF167412.PDS	Pds	pendrin		tgg	gac	decreased
6808	AF167412.PDS	Pds	pendrin		tgg	gac	decreased
6809	AF167412.PDS	Pds	pendrin		tgg	gac	decreased
6810	AF167412.PDS	Pds	pendrin		tgg	gac	decreased
6811	AB026665.RPHT2	rPHT2	peptide histidine transporter 1 homolog rPHT2		gac	caa	increased
6812	AB026665.RPHT2	rPHT2	peptide histidine transporter 1 homolog rPHT2		tgg	tct	increased
6813	AB026665.RPHT2	rPHT2	peptide histidine transporter 1 homolog rPHT2		tgg	tct	increased
6814	AB026665.RPHT2	rPHT2	peptide histidine transporter 1 homolog rPHT2		cga	gtt	increased
6815	AB026665.RPHT2	rPHT2	peptide histidine transporter 1 homolog rPHT2		ttg	cct	increased
6816	AB026665.RPHT2	rPHT2	peptide histidine transporter 1 homolog rPHT2		ttg	cct	increased
6817	AB000280.PHT1	PHT1	peptide/histidine transporter		agg	gtc	decreased
6818	AB000280.PHT1	PHT1	peptide/histidine transporter		agg	gtc	decreased
6819	AB000280.PHT1	PHT1	peptide/histidine transporter		cgc	tcc	decreased
6820	AB000280.PHT1	PHT1	peptide/histidine transporter		cgc	tcc	decreased
6821	AY043169.PCSCL	Pcscl	peroxisomal Ca-dependent solute carrier-like		ctg	gtg	increased
6822	AY043169.PCSCL	Pcscl	peroxisomal Ca-dependent solute carrier-like		ctg	gtg	increased
6823	AY043169.PCSCL	Pcscl	peroxisomal Ca-dependent solute carrier-like		aga	ttc	increased
6824	AY043169.PCSCL	Pcscl	peroxisomal Ca-dependent solute carrier-like		tgc	tgg	increased
6825	AY043169.PCSCL	Pcscl	peroxisomal Ca-dependent solute carrier-like		tgc	tgg	increased
6826	RNPPARGM2.PE1	nc	peroxisome proliferator activated receptor		cca	aac	increased
6827	RNPPARGM2.PE1	nc	peroxisome proliferator activated receptor		cca	aac	increased
6828	AF246457.PE1	nc	peroxisome proliferator-activated receptor	*	cca	aac	increased
6829	AF246457.PE1	nc	peroxisome proliferator-activated receptor	*	cca	aac	increased
6830	AF246458.PE1	nc	peroxisome proliferator-activated receptor	*	cca	aac	increased
6831	AF246458.PE1	nc	peroxisome proliferator-activated receptor	*	cca	aac	increased
6832	AF156665.PE1	PPARgamma1	peroxisome proliferator-activated receptor gamma	*	cca	aac	increased
6833	AF156665.PE1	PPARgamma1	peroxisome proliferator-activated receptor gamma	*	cca	aac	increased
6834	AF156666.PE1	PPARgamma2	peroxisome proliferator-activated receptor gamma		cca	aac	increased
6835	AF156666.PE1	PPARgamma2	peroxisome proliferator-activated receptor gamma		cca	aac	increased
6836	AY188951.PE1	nc	peroxisome proliferator-activated receptor gamma		ccg	ttc	increased
6837	AY188951.PE1	nc	peroxisome proliferator-activated receptor gamma		ccg	ttc	increased
6838	AY188951.PE1	nc	peroxisome proliferator-activated receptor gamma		ttc	cgt	increased
6839	AY188951.PE1	nc	peroxisome proliferator-activated receptor gamma		ttc	cgt	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
6840	Hha1	35	gga	114.66	114	114.53	114.85	114.6	3 798.19	3 634.95	5 767.01	==	-	(-)	
6841	Hha1	59	ttc	114.603	114	114.73	114.55	114.53	218.4	526.04	488.96	+=	/ (-)	(-)	
6842	Taq1	29	gca	111.443	112	111.45	111.52	111.36	31 900 000	22 900 000	12 100 000	==	-	-	-2
6843	Taq1	29	gca	112.417	112	112.41	112.41	112.43	98 300 000	83 200 000	8 800 000	=-	\ (-)	(-)	-2
6844	Taq1	36	ggt	111.507	112	111.35	111.52	111.65	3 000 000	5 000 000	3 500 000	==	-	-	-2
6845	Taq1	36	ggt	112.537	112	112.59	112.56	112.46	5 000 000	8 200 000	5 100 000	==	-	(-)	-2
6846	Hha1	10	atg	106.79	107	106.79	0	0	4 800 000	0	0	-=	\	\	
6847	Taq1	10	atg	106.69	107	106.69	0	0	8 900 000	0	0	-=	\	\	
6848	Hha1	6	aga	187.02	188	187.02	0	0	4 800 000	0	0	-=	\		\(2)
6849	Hha1	6	aga	188.12	188	188.12	0	0	10 100 000	0	0	-=	\		\(2)
6850	Taq1	25	cat	187.575	188	187.73	187.42	0	791.59	509.22	0	=-	\		\(2)
6851	Taq1	25	cat	188.605	188	188.8	188.41	0	1 296.57	1 654.99	0	=-	\		\(2)
6852	Hha1	26	ctg	153.167	154	153.14	153.14	153.22	17 400 000	5 700 000	7 400 000	-=	\ (-)	(-)	-(2) \(2)
6853	Hha1	26	ctg	154.083	154	154.07	154.1	154.08	55 500 000	17 300 000	45 300 000	-+	V		-(2) \(2)
6854	Hha1	32	gtc	153.09	154	153.08	153.11	153.08	4 046.13	2 583.92	3 140.79	==	-	(-)	-(2) \(2)
6855	Hha1	32	gtc	154.103	154	154.18	154.17	153.96	1 318.19	915.56	806.25	==	-		-(2) \(2)
6856	Hha1	6	aga	289.61	289	289.61	0	0	3 000 000	0	0	-=	\		-(2) \(2)
6857	Taq1	49	aaa	174.62	175	174.62	0	0	25 700 000	0	0	-=	\		\(2)
6858	Taq1	49	aaa	175.89	175	175.69	176.09	0	20 900 000	13 900 000	0	=-	\		\(2)
6859	Taq1	51	ata	254.21	255	254.21	0	0	3 400 000	0	0	-=	\		\(2)
6860	Taq1	51	ata	256.15	255	256.15	0	0	6 400 000	0	0	-=	\		\(2)
6861	Hha1	59	ttc	85.28	85	85.4	85.16	0	962.03	94.86	0	-=	\		\(2)
6862	Taq1	39	agg	272.64	274	0	272.64	0	0	79 800 000	0	+-	A		\(2)
6863	Taq1	39	agg	275.01	274	274.96	275.06	0	3 000 000	38 800 000	0	+-	A		\(2)
6864	Taq1	39	agg	274.96	274	274.96	0	0	111.4	0	0	-=	\		\(2)
6865	Taq1	39	agg	272.64	274	0	272.64	0	0	802.01	0	+-	A		\(2)
6866	Taq1	39	agg	275.06	274	0	275.06	0	0	389.95	0	+-	A		\(2)
6867	Taq1	45	gcc	74.013	74	74.04	74.1	73.9	59 800 000	21 500 000	13 700 000	-=	\ (-)		-2
6868	Hha1	9	atc	255.81	255	255.63	255.83	255.97	4 900 000	4 100 000	6 300 000	==	-		-2
6869	Taq1	45	gcc	74.013	74	74.04	74.1	73.9	59 800 000	21 500 000	13 700 000	-=	\ (-)		-2
6870	Hha1	9	atc	255.81	255	255.63	255.83	255.97	4 900 000	4 100 000	6 300 000	==	-		-2
6871	Hha1	59	ttc	124.75	125	124.75	124.75	0	223.6	370.81	0	=-	\		\(2)
6872	Hha1	59	ttc	125.685	125	125.59	125.78	0	213.2	218.46	0	=-	\		\(2)
6873	Hha1	40	tgg	141.62	142	0	141.62	0	0	5 100 000	0	+-	A		\(2)
6874	Hha1	40	tgg	141.81	142	0	141.81	0	0	5 300 000	0	+-	A		\(2)
6875	Hha1	40	tgg	142.665	142	0	142.82	142.51	0	3 200 000	3 800 000	+=	/		\(2)
6876	Hha1	60	ttg	141.94	142	141.94	0	0	4 200 000	0	0	-=	\		\(2)
6877	Hha1	27	acg	112.86	113	112.72	112.78	113.08	5 900 000	3 000 000	3 900 000	-=	\ (-)		/(3) \(3)
6878	Hha1	39	agg	134.885	135	134.82	0	134.95	454.54	0	227.86	-+(-)	V (\)	(\)	/(3) \(3)
6879	Hha1	39	agg	135.25	135	0	0	135.25	0	0	236	=+	/		/(3) \(3)
6880	Hha1	60	ttg	134.34	135	134.17	134.45	134.4	3 500 000	4 200 000	19 300 000	=+	/ (-)		/(3) \(3)
6881	Hha1	60	ttg	134.675	135	134.55	134.8	0	3 800 000	5 000 000	0	=-	\	(\)	/(3) \(3)
6882	Hha1	60	ttg	135.66	135	0	135.66	0	0	11 100 000	0	+-	A		/(3) \(3)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
6840	AF286167.MDR1A	Mdr1a	P-glycoprotein		ttc	gga	No change
6841	AF286167.MDR1A	Mdr1a	P-glycoprotein		ttc	gga	No change
6842	RATPGLYCO.PE1	nc	P-glycoprotein		ggt	gca	No change
6843	RATPGLYCO.PE1	nc	P-glycoprotein		ggt	gca	No change
6844	RATPGLYCO.PE1	nc	P-glycoprotein		ggt	gca	No change
6845	RATPGLYCO.PE1	nc	P-glycoprotein		ggt	gca	No change
6846	AF010597.SPGP	spgp	P-glycoprotein sister		atc	atg	increased
6847	AF010597.SPGP	spgp	P-glycoprotein sister		atc	atg	increased
6848	RNU36899.PE1	nc	pheromone receptor VN2		cat	aga	increased
6849	RNU36899.PE1	nc	pheromone receptor VN2		cat	aga	increased
6850	RNU36899.PE1	nc	pheromone receptor VN2		cat	aga	increased
6851	RNU36899.PE1	nc	pheromone receptor VN2		cat	aga	increased
6852	RNPEX.PHEX	PHEX	PHEX protein		gtc	ctg	No change
6853	RNPEX.PHEX	PHEX	PHEX protein		gtc	ctg	No change
6854	RNPEX.PHEX	PHEX	PHEX protein		gtc	ctg	No change
6855	RNPEX.PHEX	PHEX	PHEX protein		gtc	ctg	No change
6856	RNPEX.PHEX	PHEX	PHEX protein		tct	aga	No change
6857	RATPHDUCIN.PE1	nc	phosducin		aaa	agc	increased
6858	RATPHDUCIN.PE1	nc	phosducin		aaa	agc	increased
6859	RATPHDUCIN.PE1	nc	phosducin		ata	tat	increased
6860	RATPHDUCIN.PE1	nc	phosducin		ata	tat	increased
6861	RNO6710.VPS34	vps34	phosphatidylinositol 3-kinase		ttc	atg	increased
6862	RNO6710.VPS34	vps34	phosphatidylinositol 3-kinase		agg	tca	increased
6863	RNO6710.VPS34	vps34	phosphatidylinositol 3-kinase		agg	tca	increased
6864	RNO6710.VPS34	vps34	phosphatidylinositol 3-kinase		agg	tca	increased
6865	RNO6710.VPS34	vps34	phosphatidylinositol 3-kinase		agg	tca	increased
6866	RNO6710.VPS34	vps34	phosphatidylinositol 3-kinase		agg	tca	increased
6867	AB022890.PIS1	PIS1	phosphatidylinositol synthase	*	gcc	gca	No change
6868	AB022890.PIS1	PIS1	phosphatidylinositol synthase	*	atc	ggg	No change
6869	D82928.PE1	nc	phosphatidylinositol synthase	*	gcc	gca	No change
6870	D82928.PE1	nc	phosphatidylinositol synthase	*	atc	ggg	No change
6871	RATPHOSA.PE1	nc	phosphodiesterase		cgc	ttc	increased
6872	RATPHOSA.PE1	nc	phosphodiesterase		cgc	ttc	increased
6873	RATPHOSA.PE1	nc	phosphodiesterase		ttg	tgg	increased
6874	RATPHOSA.PE1	nc	phosphodiesterase		ttg	tgg	increased
6875	RATPHOSA.PE1	nc	phosphodiesterase		ttg	tgg	increased
6876	RATPHOSA.PE1	nc	phosphodiesterase		ttg	tgg	increased
6877	RATPHOSE.PE1	nc	phosphodiesterase		acg	acg	decreased
6878	RATPHOSE.PE1	nc	phosphodiesterase		agg	ttg	increased
6879	RATPHOSE.PE1	nc	phosphodiesterase		agg	ttg	decreased
6880	RATPHOSE.PE1	nc	phosphodiesterase		agg	ttg	decreased
6881	RATPHOSE.PE1	nc	phosphodiesterase		agg	ttg	increased
6882	RATPHOSE.PE1	nc	phosphodiesterase		agg	ttg	decreased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
6883	Taq1	62	tgt	171.29	172	171.22	171.39	171.26	4 900 000	9 300 000	3 100 000	+-	A		/(3) \(3)
6884	Taq1	62	tgt	172.215	172	0	172.35	172.08	0	3 200 000	3 400 000	+=	/		/(3) \(3)
6885	Taq1	7	caa	162.62	163	0	0	162.62	0	0	3 300 000	=+	/	/	
6886	Hha1	7	caa	162.727	163	162.94	162.57	162.67	3 500 000	12 300 000	12 600 000	+=	/ (-)	/	
6887	Taq1	7	caa	162.62	163	0	0	162.62	0	0	3 300 000	=+	/	/	
6888	Hha1	7	caa	162.727	163	162.94	162.57	162.67	3 500 000	12 300 000	12 600 000	+=	/ (-)	/	
6889	Taq1	45	gcc	200.335	200	200.34	200.33	0	5 800 000	3 800 000	0	=-	\		\(3)
6890	Taq1	45	gcc	201.17	200	201.17	0	0	4 400 000	0	0	-=	\	\	\(3)
6891	Taq1	17	cca	199.84	201	199.84	0	0	250.77	0	0	-=	\		\(3)
6892	Taq1	17	cca	200.38	201	0	200.38	0	0	226.03	0	+-	A		\(3)
6893	Taq1	17	cca	201.29	201	201.29	0	0	283.28	0	0	-=	\	\	\(3)
6894	Taq1	50	aat	211.18	211	211.13	0	211.23	12 000 000	0	7 200 000	-+(=)	V		\(3)
6895	Taq1	52	att	211.475	211	211.56	211.39	0	6 400 000	4 500 000	0	=-	\		\(3)
6896	Taq1	36	ggt	149.03	149	0	0	149.03	0	0	4 400 000	=+	/		/(3)
6897	Taq1	49	aaa	149.53	150	0	149.51	149.55	0	16 700 000	5 000 000	+-	A		/(3)
6898	Taq1	49	aaa	150.427	150	150.37	150.5	150.41	51 400 000	26 100 000	112 600 000	=+	/ (-)		/(3)
6899	Taq1	40	tgg	175.59	175	0	0	175.59	0	0	7 000 000	=+	/		/(3)
6900	Hha1	6	aga	151.84	151	0	151.84	0	0	5 700 000	0	+-	A	A	
6901	Taq1	26	ctg	151.67	151	0	151.67	0	0	3 500 000	0	+-	A	A	
6902	Taq1	56	tga	68.4	68	68.65	68.15	0	9 700 000	5 800 000	0	=-	\		\(3)
6903	Taq1	39	agg	84.68	85	84.72	0	84.64	32 600 000	0	8 100 000	-=(-)	\		\(3)
6904	Taq1	39	agg	84.72	85	84.72	0	0	1 210.63	0	0	-=	\		\(3)
6905	Taq1	39	agg	84.64	85	0	0	84.64	0	0	238.58	=+	/		\(3)
6906	Taq1	22	tcc	170.13	171	170.36	0	169.9	7 700 000	0	4 400 000	-+(=)	V		\(3)
6907	Taq1	22	tcc	170.79	171	0	170.67	170.91	0	4 500 000	5 200 000	+=	/		\(3)
6908	Taq1	22	tcc	171.84	171	0	0	171.84	0	0	5 800 000	=+	/		\(3)
6909	Hha1	25	cag	305.22	306	305.22	0	0	3 100 000	0	0	-=	\		\(3)
6910	Hha1	25	cag	305.89	306	305.89	0	0	3 400 000	0	0	-=	\		\(3)
6911	Hha1	25	cag	139.67	139	139.66	139.67	139.68	42 600 000	27 300 000	54 600 000	=+	/ (-)	/	
6912	Taq1	31	gac	139.81	139	139.93	0	139.69	3 000 000	0	32 800 000	=+(+)	/	/	
6913	Taq1	17	cca	250.98	250	250.98	0	0	213.62	0	0	-=	\	\	
6914	Taq1	19	cac	251.21	250	251.21	0	0	3 000 000	0	0	-=	\	\	
6915	Taq1	40	tgg	113.38	114	0	0	113.38	0	0	4 800 000	=+	/		/(3) -(2)
6916	Taq1	40	tgg	114.37	114	0	0	114.37	0	0	17 700 000	=+	/	/	/(3) -(2)
6917	Taq1	52	att	114.585	115	0	114.42	114.75	0	3 100 000	3 800 000	+=	/	/	/(3) -(2)
6918	Taq1	52	att	115.27	115	115.4	115.37	115.04	4 400 000	3 300 000	5 200 000	==	-		/(3) -(2)
6919	Taq1	19	cac	229.923	231	229.85	229.91	230.01	4 800 000	3 400 000	3 300 000	==	-		/(3) -(2)
6920	Taq1	19	cac	230.897	231	230.83	230.92	230.94	3 800 000	4 400 000	3 600 000	==	-		/(3) -(2)
6921	Taq1	19	cac	231.985	231	0	231.98	231.99	0	4 000 000	3 200 000	+=	/		/(3) -(2)
6922	Taq1	40	tgg	113.38	114	0	0	113.38	0	0	4 800 000	=+	/		/(3) -(2)
6923	Taq1	40	tgg	114.37	114	0	0	114.37	0	0	17 700 000	=+	/	/	/(3) -(2)
6924	Taq1	52	att	114.585	115	0	114.42	114.75	0	3 100 000	3 800 000	+=	/	/	/(3) -(2)
6925	Taq1	52	att	115.27	115	115.4	115.37	115.04	4 400 000	3 300 000	5 200 000	==	-		/(3) -(2)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
6883	RATPHOSE.PE1	nc	phosphodiesterase		tgt	ggg	decreased
6884	RATPHOSE.PE1	nc	phosphodiesterase		tgt	ggg	decreased
6885	AF327836.PE1	nc	phosphodiesterase 1A		aga	caa	decreased
6886	AF327836.PE1	nc	phosphodiesterase 1A		aga	caa	decreased
6887	AF327838.PE1	nc	phosphodiesterase 1A		aga	caa	decreased
6888	AF327838.PE1	nc	phosphodiesterase 1A		aga	caa	decreased
6889	RATNPHIII.PE1	NPH-type III	phosphodiesterase I		gcc	cca	increased
6890	RATNPHIII.PE1	NPH-type III	phosphodiesterase I		gcc	cca	increased
6891	RATNPHIII.PE1	NPH-type III	phosphodiesterase I		gcc	cca	increased
6892	RATNPHIII.PE1	NPH-type III	phosphodiesterase I		gcc	cca	increased
6893	RATNPHIII.PE1	NPH-type III	phosphodiesterase I		gcc	cca	increased
6894	RATNPHIII.PE1	NPH-type III	phosphodiesterase I		att	aat	increased
6895	RATNPHIII.PE1	NPH-type III	phosphodiesterase I		att	aat	increased
6896	AY145898.PE1	nc	phosphodiesterase type 9		aaa	ggt	decreased
6897	AY145898.PE1	nc	phosphodiesterase type 9		aaa	ggt	decreased
6898	AY145898.PE1	nc	phosphodiesterase type 9		aaa	ggt	decreased
6899	AY145898.PE1	nc	phosphodiesterase type 9		tgg	tgg	decreased
6900	RATPHOSPHZ.PE1	nc	phosphoglucomutase		aga	ctg	increased by mild
6901	RATPHOSPHZ.PE1	nc	phosphoglucomutase		aga	ctg	increased by mild
6902	AB009636.PE1	nc	phosphoinositide 3-kinase		aag	tga	increased
6903	AB009636.PE1	nc	phosphoinositide 3-kinase		ggt	agg	increased
6904	AB009636.PE1	nc	phosphoinositide 3-kinase		ggt	agg	increased
6905	AB009636.PE1	nc	phosphoinositide 3-kinase		ggt	agg	increased
6906	AB009636.PE1	nc	phosphoinositide 3-kinase		tcc	tca	increased
6907	AB009636.PE1	nc	phosphoinositide 3-kinase		tcc	tca	increased
6908	AB009636.PE1	nc	phosphoinositide 3-kinase		tcc	tca	increased
6909	AB009636.PE1	nc	phosphoinositide 3-kinase		gca	cag	increased
6910	AB009636.PE1	nc	phosphoinositide 3-kinase		gca	cag	increased
6911	AF323615.PE1	nc	phosphoinositide-specific phospholipase C		gac	cag	decreased
6912	AF323615.PE1	nc	phosphoinositide-specific phospholipase C		gac	cag	decreased
6913	AB000778.PE1	nc	phospholipase D		cca	cac	increased
6914	AB000778.PE1	nc	phospholipase D		cca	cac	increased
6915	AF017251.PLDS	PLDs	phospholipase D		att	tgg	decreased
6916	AF017251.PLDS	PLDs	phospholipase D		att	tgg	decreased
6917	AF017251.PLDS	PLDs	phospholipase D		att	tgg	decreased
6918	AF017251.PLDS	PLDs	phospholipase D		att	tgg	decreased
6919	AF017251.PLDS	PLDs	phospholipase D		cac	cgt	decreased
6920	AF017251.PLDS	PLDs	phospholipase D		cac	cgt	decreased
6921	AF017251.PLDS	PLDs	phospholipase D		cac	cgt	decreased
6922	RNU88986.PE1	nc	phospholipase D 1		att	tgg	decreased
6923	RNU88986.PE1	nc	phospholipase D 1		att	tgg	decreased
6924	RNU88986.PE1	nc	phospholipase D 1		att	tgg	decreased
6925	RNU88986.PE1	nc	phospholipase D 1		att	tgg	decreased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
6926	Taq1	19	cac	229.923	231	229.85	229.91	230.01	4 800 000	3 400 000	3 300 000	==	-		/(3) -(2)
6927	Taq1	19	cac	230.897	231	230.83	230.92	230.94	3 800 000	4 400 000	3 600 000	==	-		/(3) -(2)
6928	Taq1	19	cac	231.985	231	0	231.98	231.99	0	4 000 000	3 200 000	+=	/		/(3) -(2)
6929	Taq1	9	atc	71.895	72	71.9	71.89	0	6 900 000	8 000 000	0	=-	\		/(7)
6930	Hha1	54	ttt	82.98	83	0	0	82.98	0	0	9 300 000	=+	/		/(7)
6931	Taq1	40	tgg	113.38	114	0	0	113.38	0	0	4 800 000	=+	/		/(7)
6932	Taq1	40	tgg	114.37	114	0	0	114.37	0	0	17 700 000	=+	/	/	/(7)
6933	Taq1	52	att	114.585	115	0	114.42	114.75	0	3 100 000	3 800 000	+=	/	/	/(7)
6934	Taq1	52	att	115.27	115	115.4	115.37	115.04	4 400 000	3 300 000	5 200 000	==	-		/(7)
6935	Hha1	40	tgg	118.51	119	0	118.44	118.58	0	7 000 000	7 000 000	+=	/		/(7)
6936	Hha1	40	tgg	119.34	119	0	119.59	119.09	0	10 300 000	4 300 000	+-	A		/(7)
6937	Hha1	62	tgt	118.66	119	118.69	0	118.63	6 500 000	0	6 400 000	-+(=)	V		/(7)
6938	Hha1	59	ttc	134.335	135	134.37	134.3	0	166.4	103.48	0	=-	\		/(7)
6939	Hha1	59	ttc	135	135	0	135.19	134.81	0	120.73	77.61	+=	/		/(7)
6940	Hha1	59	ttc	135.777	135	135.9	135.93	135.5	317.21	86.23	77.61	-=	\ (-)		/(7)
6941	Taq1	23	cga	154.13	154	0	0	154.13	0	0	5 700 000	=+	/		/(7)
6942	Taq1	19	cac	229.923	231	229.85	229.91	230.01	4 800 000	3 400 000	3 300 000	==	-		/(7)
6943	Taq1	19	cac	230.897	231	230.83	230.92	230.94	3 800 000	4 400 000	3 600 000	==	-		/(7)
6944	Taq1	19	cac	231.985	231	0	231.98	231.99	0	4 000 000	3 200 000	+=	/		/(7)
6945	Taq1	17	cca	248.62	250	248.62	0	0	218.26	0	0	-=	\		/(7)
6946	Taq1	17	cca	249.7	250	249.7	0	0	204.33	0	0	-=	\		/(7)
6947	Taq1	17	cca	250.98	250	250.98	0	0	213.62	0	0	-=	\	\	/(7)
6948	Taq1	19	cac	249.26	250	249.15	249.32	249.31	3 000 000	3 400 000	3 200 000	==	-		/(7)
6949	Taq1	19	cac	251.21	250	251.21	0	0	3 000 000	0	0	-=	\	\	/(7)
6950	Taq1	40	tgg	114.37	114	0	0	114.37	0	0	17 700 000	=+	/	/	
6951	Taq1	52	att	114.585	115	0	114.42	114.75	0	3 100 000	3 800 000	+=	/	/	
6952	Taq1	17	cca	250.98	250	250.98	0	0	213.62	0	0	-=	\	\	
6953	Taq1	19	cac	251.21	250	251.21	0	0	3 000 000	0	0	-=	\	\	
6954	Taq1	45	gcc	265.96	265	0	265.96	0	0	3 300 000	0	+-	A	A	
6955	Hha1	25	cag	266.15	266	0	266.15	0	0	3 000 000	0	+-	A	A	
6956	Hha1	59	ttc	97.02	97	0	97.18	96.86	0	114.98	385.48	=+	/		/(2)
6957	Taq1	40	tgg	141.19	142	141.39	0	140.99	7 000 000	0	9 300 000	-+(=)	V		/(2)
6958	Taq1	40	tgg	142.03	142	0	0	142.03	0	0	10 400 000	=+	/		/(2)
6959	Taq1	40	tgg	141.19	142	141.39	0	140.99	7 000 000	0	9 300 000	-+(=)	V		/(2)
6960	Taq1	40	tgg	142.03	142	0	0	142.03	0	0	10 400 000	=+	/		/(2)
6961	Taq1	40	tgg	141.19	142	141.39	0	140.99	7 000 000	0	9 300 000	-+(=)	V		/(2)
6962	Taq1	40	tgg	142.03	142	0	0	142.03	0	0	10 400 000	=+	/		/(2)
6963	Taq1	48	ggg	95.96	96	95.96	0	0	2 939.31	0	0	-=	\		\(3)
6964	Taq1	16	tag	138.41	139	138.28	0	138.54	3 400 000	0	4 100 000	-+(=)	V		\(3)
6965	Taq1	16	tag	139.29	139	139.29	0	0	4 900 000	0	0	-=	\		\(3)
6966	Hha1	16	tag	139.375	139	139.57	0	139.18	3 100 000	0	9 900 000	=+(+)	/		\(3)
6967	Taq1	64	gtt	138.69	139	138.67	138.71	0	7 000 000	9 900 000	0	=-	\		\(3)
6968	Taq1	64	gtt	139.803	139	139.84	139.75	139.82	4 800 000	5 500 000	4 800 000	==	-		\(3)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
6926	RNU88986.PE1	nc	phospholipase D 1		cac	cgt	decreased
6927	RNU88986.PE1	nc	phospholipase D 1		cac	cgt	decreased
6928	RNU88986.PE1	nc	phospholipase D 1		cac	cgt	decreased
6929	AB003170.PE1	nc	phospholipase D1a		gtg	atc	decreased
6930	AB003170.PE1	nc	phospholipase D1a		atg	ttt	decreased
6931	AB003170.PE1	nc	phospholipase D1a		att	tgg	decreased
6932	AB003170.PE1	nc	phospholipase D1a		att	tgg	decreased
6933	AB003170.PE1	nc	phospholipase D1a		att	tgg	decreased
6934	AB003170.PE1	nc	phospholipase D1a		att	tgg	decreased
6935	AB003170.PE1	nc	phospholipase D1a		tgg	tgt	decreased
6936	AB003170.PE1	nc	phospholipase D1a		tgg	tgt	decreased
6937	AB003170.PE1	nc	phospholipase D1a		tgg	tgt	decreased
6938	AB003170.PE1	nc	phospholipase D1a		agt	ttc	decreased
6939	AB003170.PE1	nc	phospholipase D1a		agt	ttc	decreased
6940	AB003170.PE1	nc	phospholipase D1a		agt	ttc	decreased
6941	AB003170.PE1	nc	phospholipase D1a		cga	cgc	decreased
6942	AB003170.PE1	nc	phospholipase D1a		cac	cgt	decreased
6943	AB003170.PE1	nc	phospholipase D1a		cac	cgt	decreased
6944	AB003170.PE1	nc	phospholipase D1a		cac	cgt	decreased
6945	AB003170.PE1	nc	phospholipase D1a		cca	cac	decreased
6946	AB003170.PE1	nc	phospholipase D1a		cca	cac	decreased
6947	AB003170.PE1	nc	phospholipase D1a		cca	cac	increased
6948	AB003170.PE1	nc	phospholipase D1a		cca	cac	decreased
6949	AB003170.PE1	nc	phospholipase D1a		cca	cac	increased
6950	AB003171.PE1	nc	phospholipase D1b		att	tgg	decreased
6951	AB003171.PE1	nc	phospholipase D1b		att	tgg	decreased
6952	AB003171.PE1	nc	phospholipase D1b		cca	cac	increased
6953	AB003171.PE1	nc	phospholipase D1b		cca	cac	increased
6954	AB003171.PE1	nc	phospholipase D1b		cag	gcc	increased by mild
6955	AB003171.PE1	nc	phospholipase D1b		cag	gcc	increased by mild
6956	RNO537598.PE3	gpx-4	phospholipid hydroperoxide glutathione		ggc	ttc	decreased
6957	RNO537598.PE3	gpx-4	phospholipid hydroperoxide glutathione		tgg	cta	decreased
6958	RNO537598.PE3	gpx-4	phospholipid hydroperoxide glutathione		tgg	cta	decreased
6959	RNO537598.PE3	gpx-4	phospholipid hydroperoxide glutathione		tgg	cta	decreased
6960	RNO537598.PE3	gpx-4	phospholipid hydroperoxide glutathione		tgg	cta	decreased
6961	RNO537598.PE3	gpx-4	phospholipid hydroperoxide glutathione		tgg	cta	decreased
6962	RNO537598.PE3	gpx-4	phospholipid hydroperoxide glutathione		tgg	cta	decreased
6963	RNU12203.PE1	nc	phosphoprotein phosphatase		ggg	aca	increased
6964	RNU12203.PE1	nc	phosphoprotein phosphatase		gtt	tag	increased
6965	RNU12203.PE1	nc	phosphoprotein phosphatase		gtt	tag	increased
6966	RNU12203.PE1	nc	phosphoprotein phosphatase		gtt	tag	increased
6967	RNU12203.PE1	nc	phosphoprotein phosphatase		gtt	tag	increased
6968	RNU12203.PE1	nc	phosphoprotein phosphatase		gtt	tag	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
6969	Hha1	39	agg	81.873	82	81.97	81.6	82.05	1 392.96	2 161.32	789.38	=-	\ (-)		\(3)
6970	Taq1	47	ggc	140.863	141	140.76	140.89	140.94	3 446.15	1 973.26	2 159.82	==	-		\(3)
6971	Taq1	39	agg	141.93	142	141.93	0	0	10 900 000	0	0	-=	\		\(3)
6972	Taq1	39	agg	141.93	142	141.93	0	0	404.78	0	0	-=	\		\(3)
6973	Taq1	49	aaa	327.79	329	327.79	0	0	20 500 000	0	0	-=	\		\(3)
6974	Taq1	49	aaa	330.16	329	330.16	0	0	9 300 000	0	0	-=	\		\(3)
6975	Hha1	3	aac	148.287	149	148.24	148.3	148.32	25 200 000	12 300 000	7 400 000	-=	\ (-)	\	\(2)
6976	Hha1	3	aac	149.38	149	149.38	149.35	149.41	10 000 000	4 600 000	5 900 000	-=	\ (-)		\(2)
6977	Taq1	39	agg	148.14	149	148.24	148.04	0	11 300 000	15 600 000	0	=-	\	\	\(2)
6978	Taq1	39	agg	149.417	149	149.28	149.27	149.7	5 300 000	107 400 000	3 000 000	+-	A		\(2)
6979	Taq1	39	agg	148.14	149	148.24	148.04	0	419.63	156.78	0	-=	\	\	\(2)
6980	Taq1	39	agg	149.275	149	149.28	149.27	0	196.82	1 079.4	0	+-	A		\(2)
6981	Taq1	39	agg	149.7	149	0	0	149.7	0	0	88.36	=+	/		\(2)
6982	Hha1	39	agg	71.64	72	71.65	71.55	71.72	13 563.04	1 176.18	2 046.71	-=	\ (-)		-2
6983	Hha1	54	ttt	73.23	73	73.16	73.25	73.28	57 300 000	58 000 000	79 100 000	==	-		-2
6984	Taq1	44	cgg	98.92	99	98.69	0	99.15	249.97	0	1 300.15	=+(+)	/		/(2)
6985	Taq1	44	cgg	99.495	99	99.59	99.4	0	1 086.69	3 007.68	0	+-	A		/(2)
6986	Taq1	62	tgt	99.61	100	0	0	99.61	0	0	22 600 000	=+	/		/(2)
6987	Taq1	10	atg	269.56	270	269.56	0	0	3 400 000	0	0	-=	\		\(2)
6988	Taq1	10	atg	270.29	270	270.29	0	0	4 100 000	0	0	-=	\		\(2)
6989	Taq1	10	atg	271.23	270	271.23	0	0	7 000 000	0	0	-=	\		\(2)
6990	Taq1	52	att	269.97	271	269.97	0	0	3 100 000	0	0	-=	\		\(2)
6991	Taq1	52	att	271.23	271	0	0	271.23	0	0	8 300 000	=+	/		\(2)
6992	Taq1	49	aaa	431.27	431	0	431.27	0	0	3 100 000	0	+-	A		\(2)
6993	Hha1	39	agg	118.747	119	118.62	119	118.62	241.93	555.25	512.69	+=	/ (-)		A(2)
6994	Hha1	39	agg	119.115	119	118.93	0	119.3	234.6	0	146.48	-+(=)	V		A(2)
6995	Hha1	39	agg	119.21	119	119.01	0	119.41	234.6	0	130.2	-+(=)	V		A(2)
6996	Hha1	39	agg	119.58	119	0	119.61	119.55	0	274.64	146.48	+-	A		A(2)
6997	Taq1	39	agg	290.45	291	0	290.45	0	0	20 900 000	0	+-	A		A(2)
6998	Taq1	39	agg	290.45	291	0	290.45	0	0	210.05	0	+-	A		A(2)
6999	Hha1	39	agg	118.747	119	118.62	119	118.62	241.93	555.25	512.69	+=	/ (-)		A(2)
7000	Hha1	39	agg	119.115	119	118.93	0	119.3	234.6	0	146.48	-+(=)	V		A(2)
7001	Hha1	39	agg	119.21	119	119.01	0	119.41	234.6	0	130.2	-+(=)	V		A(2)
7002	Hha1	39	agg	119.58	119	0	119.61	119.55	0	274.64	146.48	+-	A		A(2)
7003	Taq1	39	agg	290.45	291	0	290.45	0	0	20 900 000	0	+-	A		A(2)
7004	Taq1	39	agg	290.45	291	0	290.45	0	0	210.05	0	+-	A		A(2)
7005	Taq1	31	gac	96.42	97	96.37	96.33	96.56	55 000 000	43 400 000	3 100 000	=-	\ (-)	(-)	A(3)
7006	Taq1	31	gac	97.437	97	97.4	97.32	97.59	62 800 000	57 200 000	11 100 000	=-	\ (-)	\	A(3)
7007	Taq1	62	tgt	96.507	97	96.37	96.38	96.77	6 900 000	9 300 000	15 900 000	==	-	(-)	A(3)
7008	Taq1	62	tgt	97.33	97	97.16	97.5	0	5 900 000	12 100 000	0	+-	A		A(3)
7009	Taq1	62	tgt	97.34	97	97.34	0	0	5 600 000	0	0	-=	\	\	A(3)
7010	Taq1	31	gac	110.557	111	110.36	110.6	110.71	16 700 000	37 900 000	3 100 000	+-	A		A(3)
7011	Taq1	31	gac	111.515	111	111.36	111.67	0	4 100 000	28 000 000	0	+-	A		A(3)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
6969	AY094093.PE1	nc	pincher		tcg	agg	increased
6970	AY094093.PE1	nc	pincher		ggc	agg	increased
6971	AY094093.PE1	nc	pincher		ggc	agg	increased
6972	AY094093.PE1	nc	pincher		ggc	agg	increased
6973	AY094093.PE1	nc	pincher		aaa	tga	increased
6974	AY094093.PE1	nc	pincher		aaa	tga	increased
6975	RNU73030.PTTG	PTTG	pituitary tumor transforming gene protein		aac	agg	increased
6976	RNU73030.PTTG	PTTG	pituitary tumor transforming gene protein		aac	agg	increased
6977	RNU73030.PTTG	PTTG	pituitary tumor transforming gene protein		aac	agg	increased
6978	RNU73030.PTTG	PTTG	pituitary tumor transforming gene protein		aac	agg	increased
6979	RNU73030.PTTG	PTTG	pituitary tumor transforming gene protein		aac	agg	increased
6980	RNU73030.PTTG	PTTG	pituitary tumor transforming gene protein		aac	agg	increased
6981	RNU73030.PTTG	PTTG	pituitary tumor transforming gene protein		aac	agg	increased
6982	AB015723.PE1	nc	PiUS		ttt	agg	No change
6983	AB015723.PE1	nc	PiUS		ttt	agg	No change
6984	AY050673.CPI	Cpi	PKC-potentiated PP1 inhibitory protein	*	cgg	tgt	decreased
6985	AY050673.CPI	Cpi	PKC-potentiated PP1 inhibitory protein	*	cgg	tgt	decreased
6986	AY050673.CPI	Cpi	PKC-potentiated PP1 inhibitory protein	*	cgg	tgt	decreased
6987	RATPATISS.T-PA	t-PA	plasminogen activator		att	atg	increased
6988	RATPATISS.T-PA	t-PA	plasminogen activator		att	atg	increased
6989	RATPATISS.T-PA	t-PA	plasminogen activator		att	atg	increased
6990	RATPATISS.T-PA	t-PA	plasminogen activator		att	atg	increased
6991	RATPATISS.T-PA	t-PA	plasminogen activator		att	atg	increased
6992	RATPATISS.T-PA	t-PA	plasminogen activator		aaa	tca	increased
6993	AY147866.PE1	nc	plasticity-related protein PRG-2	*	tcc	agg	increased by mild
6994	AY147866.PE1	nc	plasticity-related protein PRG-2	*	tcc	agg	increased by mild
6995	AY147866.PE1	nc	plasticity-related protein PRG-2	*	tcc	agg	increased by mild
6996	AY147866.PE1	nc	plasticity-related protein PRG-2	*	tcc	agg	increased by mild
6997	AY147866.PE1	nc	plasticity-related protein PRG-2	*	tgt	agg	increased by mild
6998	AY147866.PE1	nc	plasticity-related protein PRG-2	*	tgt	agg	increased by mild
6999	AY300027.PE1	nc	plasticity-related protein PRG-2	*	tcc	agg	increased by mild
7000	AY300027.PE1	nc	plasticity-related protein PRG-2	*	tcc	agg	increased by mild
7001	AY300027.PE1	nc	plasticity-related protein PRG-2	*	tcc	agg	increased by mild
7002	AY300027.PE1	nc	plasticity-related protein PRG-2	*	tcc	agg	increased by mild
7003	AY300027.PE1	nc	plasticity-related protein PRG-2	*	tgt	agg	increased by mild
7004	AY300027.PE1	nc	plasticity-related protein PRG-2	*	tgt	agg	increased by mild
7005	RATAPDGFR.PDGF-A	PDGF A	platelet-derived growth factor A chain		gac	tgt	No change
7006	RATAPDGFR.PDGF-A	PDGF A	platelet-derived growth factor A chain		gac	tgt	increased
7007	RATAPDGFR.PDGF-A	PDGF A	platelet-derived growth factor A chain		gac	tgt	No change
7008	RATAPDGFR.PDGF-A	PDGF A	platelet-derived growth factor A chain		gac	tgt	increased by mild
7009	RATAPDGFR.PDGF-A	PDGF A	platelet-derived growth factor A chain		gac	tgt	increased
7010	RATAPDGFR.PDGF-A	PDGF A	platelet-derived growth factor A chain		gtg	gac	increased by mild
7011	RATAPDGFR.PDGF-A	PDGF A	platelet-derived growth factor A chain		gtg	gac	increased by mild

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
7012	Hha1	61	tct	142.125	142	0	142.12	142.13	0	8 500 000	3 000 000	+-	A		A(3)
7013	Taq1	47	ggc	155.29	156	155.27	155.31	0	2 215.38	1 273.07	0	=-	\		\(2) V(2)
7014	Taq1	47	ggc	156.325	156	0	156.37	156.28	0	2 450.66	2 105.83	+=	/		\(2) V(2)
7015	Taq1	50	aat	157.055	158	157.08	0	157.03	3 900 000	0	3 900 000	-+(=)	V		\(2) V(2)
7016	Taq1	50	aat	157.95	158	157.95	0	0	6 200 000	0	0	-=	\		\(2) V(2)
7017	Taq1	29	gca	207.385	207	207.37	0	207.4	3 800 000	0	3 000 000	-+(=)	V		\(2) V(2)
7018	Hha1	2	tta	137.345	138	137.31	0	137.38	20 100 000	0	9 100 000	-+(-)	V (\)		\(5)
7019	Hha1	2	tta	138.15	138	138.33	137.97	0	17 400 000	25 000 000	0	=-	\		\(5)
7020	Hha1	33	agc	153.6	154	153.57	153.63	0	4 100 000	4 700 000	0	=-	\		\(5)
7021	Hha1	56	tga	153.09	154	153.09	0	0	261.51	0	0	-=	\		\(5)
7022	Hha1	56	tga	153.95	154	153.7	0	154.2	731.41	0	603.34	-+(=)	V		\(5)
7023	Hha1	49	aaa	196.655	197	196.41	196.9	0	3 000 000	9 700 000	0	+-	A		\(5)
7024	Hha1	49	aaa	197.42	197	197.42	0	0	16 900 000	0	0	-=	\		\(5)
7025	Hha1	49	aaa	197.97	197	197.97	0	0	5 900 000	0	0	-=	\		\(5)
7026	Taq1	17	cca	314.59	316	314.59	0	0	139.32	0	0	-=	\		\(5)
7027	Hha1	10	atg	206.4	207	206.27	206.53	0	3 000 000	3 000 000	0	=-	\		\(2)
7028	Taq1	10	atg	207.79	207	207.78	207.8	0	8 100 000	5 300 000	0	=-	\		\(2)
7029	Hha1	33	agc	98.18	98	98.15	98.21	0	3 100 000	3 100 000	0	=-	\		\(3)
7030	Taq1	12	agt	186.95	188	186.95	186.95	186.95	8 900 000	5 800 000	4 200 000	==	-		\(3)
7031	Taq1	12	agt	187.95	188	187.94	187.94	187.97	8 900 000	12 200 000	5 900 000	=-	\ (-)		\(3)
7032	Taq1	12	agt	188.985	188	188.96	189.01	0	5 200 000	4 900 000	0	=-	\		\(3)
7033	Hha1	26	ctg	217.95	218	217.95	0	0	4 400 000	0	0	-=	\		\(3)
7034	Hha1	8	gaa	263.67	265	263.67	0	0	7 000 000	0	0	-=	\		\(2)
7035	Hha1	8	gaa	263.67	265	263.67	0	0	7 000 000	0	0	-=	\		\(2)
7036	Hha1	8	gaa	263.67	265	263.67	0	0	7 000 000	0	0	-=	\		\(2)
7037	Hha1	8	gaa	264.4	265	0	264.4	0	0	3 700 000	0	+-	A		\(2)
7038	Hha1	8	gaa	264.4	265	0	264.4	0	0	3 700 000	0	+-	A		\(2)
7039	Hha1	8	gaa	264.4	265	0	264.4	0	0	3 700 000	0	+-	A		\(2)
7040	Taq1	8	gaa	264.34	265	0	0	264.34	0	0	3 500 000	=+	/		\(2)
7041	Taq1	8	gaa	264.34	265	0	0	264.34	0	0	3 500 000	=+	/		\(2)
7042	Taq1	8	gaa	264.34	265	0	0	264.34	0	0	3 500 000	=+	/		\(2)
7043	Taq1	8	gaa	264.92	265	264.92	264.92	0	11 000 000	10 100 000	0	=-	\		\(2)
7044	Taq1	8	gaa	264.92	265	264.92	264.92	0	11 000 000	10 100 000	0	=-	\		\(2)
7045	Taq1	8	gaa	264.92	265	264.92	264.92	0	11 000 000	10 100 000	0	=-	\		\(2)
7046	Taq1	44	cgg	139.79	139	139.74	0	139.84	277.74	0	986.32	=+(+)	/	/	
7047	Taq1	29	gca	139.62	140	0	0	139.62	0	0	5 300 000	=+	/	/	
7048	Hha1	54	ttt	62.977	63	62.96	63.05	62.92	4 600 000	5 700 000	10 700 000	=+	/ (-)		\(3)
7049	Taq1	55	tca	86.67	87	86.82	86.35	86.84	5 500 000	8 100 000	4 100 000	=-	\ (-)		\(3)
7050	Taq1	55	tca	87.34	87	0	87.34	0	0	14 400 000	0	+-	A		\(3)
7051	Hha1	39	agg	97.8	98	0	97.94	97.66	0	531.37	508.62	+=	/		\(3)
7052	Hha1	39	agg	98.28	98	98.28	0	0	329.91	0	0	-=	\		\(3)
7053	Hha1	44	cgg	109.855	110	109.99	109.72	0	6 800 000	7 400 000	0	=-	\		\(3)
7054	Taq1	9	atc	80.145	80	80.03	0	80.26	5 900 000	0	17 600 000	=+(+)	/		/(2)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
7012	RATAPDGFR.PDGF-A	PDGF A	platelet-derived growth factor A chain		aga	tct	increased by mild
7013	RNU10188.PLK	plk	polo like kinase		aat	ggc	increased
7014	RNU10188.PLK	plk	polo like kinase		aat	ggc	increased
7015	RNU10188.PLK	plk	polo like kinase		aat	ggc	increased
7016	RNU10188.PLK	plk	polo like kinase		aat	ggc	increased
7017	RNU10188.PLK	plk	polo like kinase		gca	agc	increased
7018	RNO298278.PABP1	pabp1	poly(A) binding protein		aga	tta	increased
7019	RNO298278.PABP1	pabp1	poly(A) binding protein		aga	tta	increased
7020	RNO298278.PABP1	pabp1	poly(A) binding protein		agc	tga	increased
7021	RNO298278.PABP1	pabp1	poly(A) binding protein		agc	tga	increased
7022	RNO298278.PABP1	pabp1	poly(A) binding protein		agc	tga	increased
7023	RNO298278.PABP1	pabp1	poly(A) binding protein		aaa	cca	increased
7024	RNO298278.PABP1	pabp1	poly(A) binding protein		aaa	cca	increased
7025	RNO298278.PABP1	pabp1	poly(A) binding protein		aaa	cca	increased
7026	RNO298278.PABP1	pabp1	poly(A) binding protein		ttt	cca	increased
7027	RNU35890.PE1	nc	polypeptide GalNAc transferase		atg	tga	increased
7028	RNU35890.PE1	nc	polypeptide GalNAc transferase		atg	tga	increased
7029	RNTBFII.TBFII	TBFII	polypyrimidine tract binding protein		cca	agc	increased
7030	RNTBFII.TBFII	TBFII	polypyrimidine tract binding protein		agt	tgc	increased
7031	RNTBFII.TBFII	TBFII	polypyrimidine tract binding protein		agt	tgc	increased
7032	RNTBFII.TBFII	TBFII	polypyrimidine tract binding protein		agt	tgc	increased
7033	RNTBFII.TBFII	TBFII	polypyrimidine tract binding protein		ccg	ctg	increased
7034	RATPOLYU.PE1	nc	polyubiquitin		gaa	tgg	increased
7035	RATPOLYU.PE1	nc	polyubiquitin		gaa	tgg	increased
7036	RATPOLYU.PE1	nc	polyubiquitin		gaa	tgg	increased
7037	RATPOLYU.PE1	nc	polyubiquitin		gaa	tgg	increased
7038	RATPOLYU.PE1	nc	polyubiquitin		gaa	tgg	increased
7039	RATPOLYU.PE1	nc	polyubiquitin		gaa	tgg	increased
7040	RATPOLYU.PE1	nc	polyubiquitin		gaa	tgg	increased
7041	RATPOLYU.PE1	nc	polyubiquitin		gaa	tgg	increased
7042	RATPOLYU.PE1	nc	polyubiquitin		gaa	tgg	increased
7043	RATPOLYU.PE1	nc	polyubiquitin		gaa	tgg	increased
7044	RATPOLYU.PE1	nc	polyubiquitin		gaa	tgg	increased
7045	RATPOLYU.PE1	nc	polyubiquitin		gaa	tgg	increased
7046	AF061957.ELK1	elk1	potassium channel		cgg	gca	decreased
7047	AF061957.ELK1	elk1	potassium channel		cgg	gca	decreased
7048	AF087453.KCNQ2	KCNQ2	potassium channel		ggg	ttt	increased
7049	AF087453.KCNQ2	KCNQ2	potassium channel		ggc	tca	increased
7050	AF087453.KCNQ2	KCNQ2	potassium channel		ggc	tca	increased
7051	AF087453.KCNQ2	KCNQ2	potassium channel		cac	agg	increased
7052	AF087453.KCNQ2	KCNQ2	potassium channel		cac	agg	increased
7053	AF087453.KCNQ2	KCNQ2	potassium channel		aac	cgg	increased
7054	RATCDRK.KV2.2	Kv2.2	potassium channel		atc	gtg	decreased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
7055	Hha1	62	tgt	151.16	152	0	151.16	0	0	3 500 000	0	+-	A		/(2)
7056	Hha1	62	tgt	152.74	152	0	0	152.74	0	0	3 500 000	=+	/		/(2)
7057	Hha1	31	gac	68.817	69	68.74	68.86	68.85	14 900 000	8 700 000	12 900 000	==	-		-(2) \(2)
7058	Taq1	45	gcc	87.54	88	87.68	87.4	0	7 400 000	6 000 000	0	=-	\		-(2) \(2)
7059	Taq1	45	gcc	88.357	88	88.36	88.4	88.31	27 200 000	28 500 000	3 500 000	=-	\ (-)		-(2) \(2)
7060	Taq1	50	aat	347.5	349	0	0	347.5	0	0	3 700 000	=+	/		-(2) \(2)
7061	Taq1	50	aat	350.81	349	350.81	0	0	3 400 000	0	0	-=	\		-(2) \(2)
7062	Taq1	48	ggg	113.37	114	0	113.37	0	0	2 563.64	0	+-	A		A(4)
7063	Taq1	48	ggg	114.2	114	114.2	114.2	0	1 485.46	1 464.93	0	=-	\		A(4)
7064	Hha1	6	aga	114.53	115	0	114.53	0	0	11 200 000	0	+-	A		A(4)
7065	Hha1	6	aga	114.53	115	0	114.53	0	0	11 200 000	0	+-	A		A(4)
7066	Hha1	6	aga	115.065	115	115.05	0	115.08	16 900 000	0	4 400 000	-=(-)	\		A(4)
7067	Hha1	6	aga	115.065	115	115.05	0	115.08	16 900 000	0	4 400 000	-=(-)	\		A(4)
7068	Hha1	6	aga	115.65	115	115.64	115.66	0	9 500 000	3 500 000	0	-=	\		A(4)
7069	Hha1	6	aga	115.65	115	115.64	115.66	0	9 500 000	3 500 000	0	-=	\		A(4)
7070	Hha1	6	aga	126.475	127	126.51	0	126.44	89 200 000	0	7 100 000	-=(-)	\		A(4)
7071	Hha1	6	aga	127.097	127	127.18	127.06	127.05	30 600 000	3 500 000	5 400 000	-=	\ (-)		A(4)
7072	Hha1	6	aga	127.6	127	0	127.54	127.66	0	3 100 000	6 300 000	++	/		A(4)
7073	Hha1	20	ctc	166.875	167	166.87	166.88	0	268.59	747.44	0	+-	A		A(4)
7074	Hha1	20	ctc	167.745	167	0	167.76	167.73	0	524.52	489.02	+=	/		A(4)
7075	Hha1	59	ttc	167.38	167	0	167.38	167.38	0	215.59	2 054.17	=+	/		A(4)
7076	Taq1	8	gaa	259.31	259	0	259.31	0	0	3 100 000	0	+-	A		A(4)
7077	Hha1	59	ttc	108.493	109	108.38	108.48	108.62	244.4	393.81	238.01	==	-		/(5)
7078	Hha1	59	ttc	109.09	109	109.09	0	0	280.81	0	0	-=	\		/(5)
7079	Hha1	41	ccc	125.767	126	125.78	125.72	125.8	9 000 000	9 400 000	46 200 000	=+	/ (-)		/(5)
7080	Hha1	39	agg	153.21	154	153.21	0	0	322.58	0	0	-=	\		/(5)
7081	Hha1	39	agg	153.74	154	153.63	0	153.85	535.19	0	142.41	-=(-)	\		/(5)
7082	Hha1	39	agg	154.16	154	0	0	154.16	0	0	142.41	=+	/		/(5)
7083	Hha1	39	agg	154.535	154	0	154.74	154.33	0	232.84	126.13	+-	A		/(5)
7084	Taq1	31	gac	159.96	160	0	0	159.96	0	0	13 000 000	=+	/		/(5)
7085	Taq1	31	gac	160.94	160	0	0	160.94	0	0	13 800 000	=+	/		/(5)
7086	Taq1	56	tga	192.29	193	0	0	192.29	0	0	6 500 000	=+	/		/(5)
7087	Taq1	56	tga	194.08	193	0	194.08	0	0	3 500 000	0	+-	A		/(5)
7088	Taq1	34	tgc	384.57	385	0	0	384.57	0	0	6 100 000	=+	/		/(5)
7089	Hha1	20	ctc	95.33	95	95.33	0	0	475.2	0	0	-=	\		\(4)
7090	Taq1	18	cct	177.895	178	0	177.91	177.88	0	3 000 000	3 400 000	+=	/		\(4)
7091	Taq1	18	cct	178.855	178	178.85	178.86	0	8 200 000	4 700 000	0	=-	\		\(4)
7092	Hha1	49	aaa	205.12	206	0	205.12	0	0	9 300 000	0	+-	A		\(4)
7093	Hha1	49	aaa	206.04	206	206.05	206.03	0	12 600 000	5 700 000	0	--	\		\(4)
7094	Hha1	49	aaa	206.43	206	206.43	0	0	13 100 000	0	0	-=	\		\(4)
7095	Hha1	49	aaa	207.17	206	207.17	0	0	13 400 000	0	0	-=	\		\(4)
7096	Taq1	29	gca	208.325	209	208.3	208.35	0	3 900 000	3 200 000	0	=-	\		\(4)
7097	Taq1	29	gca	209.41	209	209.46	209.43	209.34	4 900 000	5 000 000	3 100 000	==	-		\(4)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
7055	RATCDRK.KV2.2	Kv2.2	potassium channel		tgt	tca	decreased
7056	RATCDRK.KV2.2	Kv2.2	potassium channel		tgt	tca	decreased
7057	RNKCP.PE1	nc	potassium channel		gat	gac	No change
7058	RNKCP.PE1	nc	potassium channel		gcc	ggt	No change
7059	RNKCP.PE1	nc	potassium channel		gcc	ggt	No change
7060	RNKCP.PE1	nc	potassium channel		aat	aga	No change
7061	RNKCP.PE1	nc	potassium channel		aat	aga	No change
7062	RATPCKV32B.PE1	nc	potassium channel Kv3.2b	*	ggg	aga	increased by mild
7063	RATPCKV32B.PE1	nc	potassium channel Kv3.2b	*	ggg	aga	increased by mild
7064	RATPCKV32B.PE1	nc	potassium channel Kv3.2b	*	ggg	aga	increased by mild
7065	RATPCKV32B.PE1	nc	potassium channel Kv3.2b	*	ggg	aga	increased by mild
7066	RATPCKV32B.PE1	nc	potassium channel Kv3.2b	*	ggg	aga	increased by mild
7067	RATPCKV32B.PE1	nc	potassium channel Kv3.2b	*	ggg	aga	increased by mild
7068	RATPCKV32B.PE1	nc	potassium channel Kv3.2b	*	ggg	aga	increased by mild
7069	RATPCKV32B.PE1	nc	potassium channel Kv3.2b	*	ggg	aga	increased by mild
7070	RATPCKV32B.PE1	nc	potassium channel Kv3.2b	*	tcg	aga	increased by mild
7071	RATPCKV32B.PE1	nc	potassium channel Kv3.2b	*	tcg	aga	increased by mild
7072	RATPCKV32B.PE1	nc	potassium channel Kv3.2b	*	tcg	aga	increased by mild
7073	RATPCKV32B.PE1	nc	potassium channel Kv3.2b	*	ttc	ctc	increased by mild
7074	RATPCKV32B.PE1	nc	potassium channel Kv3.2b	*	ttc	ctc	increased by mild
7075	RATPCKV32B.PE1	nc	potassium channel Kv3.2b	*	ttc	ctc	increased by mild
7076	RATPCKV32B.PE1	nc	potassium channel Kv3.2b	*	gaa	agc	increased by mild
7077	RATPTP.PE1	potassium cha	potassium channel protein		ttc	atg	decreased
7078	RATPTP.PE1	potassium cha	potassium channel protein		ttc	atg	decreased
7079	RATPTP.PE1	potassium cha	potassium channel protein		tac	ccc	decreased
7080	RATPTP.PE1	potassium cha	potassium channel protein		agg	tcc	decreased
7081	RATPTP.PE1	potassium cha	potassium channel protein		agg	tcc	decreased
7082	RATPTP.PE1	potassium cha	potassium channel protein		agg	tcc	decreased
7083	RATPTP.PE1	potassium cha	potassium channel protein		agg	tcc	decreased
7084	RATPTP.PE1	potassium cha	potassium channel protein		gac	agc	decreased
7085	RATPTP.PE1	potassium cha	potassium channel protein		gac	agc	decreased
7086	RATPTP.PE1	potassium cha	potassium channel protein		taa	tga	decreased
7087	RATPTP.PE1	potassium cha	potassium channel protein		taa	tga	decreased
7088	RATPTP.PE1	potassium cha	potassium channel protein		tgc	tgc	decreased
7089	RNPTCHS.PE1	nc	potassium channel subunit		ctg	ctc	increased
7090	RNPTCHS.PE1	nc	potassium channel subunit		cct	tat	increased
7091	RNPTCHS.PE1	nc	potassium channel subunit		cct	tat	increased
7092	RNPTCHS.PE1	nc	potassium channel subunit		aaa	agg	increased
7093	RNPTCHS.PE1	nc	potassium channel subunit		aaa	agg	increased
7094	RNPTCHS.PE1	nc	potassium channel subunit		aaa	agg	increased
7095	RNPTCHS.PE1	nc	potassium channel subunit		aaa	agg	increased
7096	RNPTCHS.PE1	nc	potassium channel subunit		aat	gca	increased
7097	RNPTCHS.PE1	nc	potassium channel subunit		aat	gca	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
7098	Taq1	50	aat	209.09	210	209.28	208.9	0	3 100 000	5 900 000	0	+-	A		\(4)
7099	Taq1	50	aat	211.18	210	211.13	0	211.23	12 000 000	0	7 200 000	-+(=)	V		\(4)
7100	Hha1	8	gaa	262.35	262	0	262.35	0	0	3 200 000	0	+-	A		\(4)
7101	Hha1	39	agg	66.61	67	0	66.57	66.65	0	1 629.94	2 937.82	+=	/		/(4)
7102	Hha1	33	agc	82.077	82	81.92	82	82.31	23 000 000	20 100 000	4 600 000	=-	\ (-)		/(4)
7103	Hha1	31	gac	88.09	88	88.11	87.84	88.32	15 300 000	5 000 000	8 800 000	-=	\ (-)		/(4)
7104	Hha1	31	gac	88.52	88	0	88.52	0	0	6 700 000	0	+-	A		/(4)
7105	Hha1	26	ctg	94.26	94	0	0	94.26	0	0	3 300 000	=+	/		/(4)
7106	Hha1	44	cgg	112.525	113	0	112.65	112.4	0	3 300 000	4 600 000	+=	/		/(4)
7107	Hha1	26	ctg	117.02	117	0	0	117.02	0	0	3 100 000	=+	/		/(4)
7108	Hha1	4	aag	96.66	97	96.66	0	0	19 600 000	0	0	-=	\		\(3)
7109	Hha1	4	aag	97.52	97	97.52	0	0	4 000 000	0	0	-=	\		\(3)
7110	Taq1	54	ttt	97.627	98	97.63	97.38	97.87	2 723.96	1 705.28	2 655.24	==	-		\(3)
7111	Taq1	54	ttt	98.3	98	98.21	98.39	0	1 638.74	1 340.7	0	=-	\		\(3)
7112	Taq1	39	agg	172.98	173	173.19	172.77	0	7 500 000	35 200 000	0	+-	A		\(3)
7113	Taq1	39	agg	173.29	173	0	173.29	0	0	57 600 000	0	+-	A		\(3)
7114	Taq1	39	agg	172.98	173	173.19	172.77	0	278.52	353.77	0	=-	\		\(3)
7115	Taq1	39	agg	173.29	173	0	173.29	0	0	578.9	0	+-	A		\(3)
7116	Hha1	26	ctg	97.47	98	0	97.47	0	0	4 100 000	0	+-	A		\(2)
7117	Hha1	26	ctg	98.155	98	98.13	98.18	0	5 200 000	3 900 000	0	=-	\		\(2)
7118	Hha1	26	ctg	132.96	133	132.96	132.96	0	15 400 000	13 700 000	0	=-	\		\(2)
7119	Hha1	3	aac	295.39	296	295.39	0	0	4 100 000	0	0	-=	\		\(2)
7120	Taq1	17	cca	297.01	296	297.01	0	0	171.82	0	0	-=	\		\(2)
7121	Taq1	7	caa	176.98	178	176.98	0	0	5 400 000	0	0	-=	\		\(5)
7122	Hha1	7	caa	177.59	178	177.59	0	0	8 400 000	0	0	-=	\		\(5)
7123	Hha1	7	caa	178.37	178	178.37	0	0	3 700 000	0	0	-=	\		\(5)
7124	Taq1	7	caa	178.64	178	178.64	0	0	3 200 000	0	0	-=	\		\(5)
7125	Taq1	19	cac	177.955	178	177.92	0	177.99	5 100 000	0	9 400 000	-+(+)	V (/)		\(5)
7126	Taq1	19	cac	178.937	178	178.91	178.89	179.01	5 800 000	3 000 000	4 200 000	-=	\ (-)		\(5)
7127	Taq1	18	cct	215.54	216	215.53	215.55	0	3 100 000	5 300 000	0	=-	\		\(5)
7128	Taq1	18	cct	216.67	216	0	0	216.67	0	0	3 700 000	=+	/		\(5)
7129	Hha1	21	acc	102.6	103	102.73	102.62	102.45	23 900 000	3 100 000	10 100 000	-=	\ (-)	\	
7130	Taq1	21	acc	102.665	103	102.55	102.78	0	21 100 000	3 000 000	0	-=	\	\	
7131	Hha1	21	acc	103.33	103	0	103.33	103.33	0	3 900 000	16 800 000	=+	/	/	
7132	Taq1	21	acc	103.5	103	0	0	103.5	0	0	3 500 000	=+	/	/	
7133	Taq1	48	ggg	95.96	96	95.96	0	0	2 939.31	0	0	-=	\		\(2)
7134	Taq1	44	cgg	175.42	176	175.42	0	0	249.97	0	0	-=	\		\(2)
7135	Taq1	44	cgg	176.09	176	176.21	175.97	0	270.8	1 457.18	0	+-	A		\(2)
7136	Taq1	40	tgg	177.575	177	177.51	0	177.64	4 400 000	0	5 200 000	-+(=)	V		\(2)
7137	Hha1	26	ctg	172.8	172	172.68	0	172.92	3 000 000	0	8 400 000	=+(+)	/	/	
7138	Hha1	39	agg	172.59	172	0	0	172.59	0	0	231.93	=+	/	/	
7139	Taq1	12	agt	100.297	100	100.31	100.28	100.3	8 100 000	5 300 000	13 800 000	=+	/ (-)	/	
7140	Taq1	35	gga	100.28	100	0	0	100.28	0	0	4 000 000	=+	/	/	

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
7098	RNPTCHS.PE1	nc	potassium channel subunit		aat	gca	increased
7099	RNPTCHS.PE1	nc	potassium channel subunit		aat	gca	increased
7100	RNPTCHS.PE1	nc	potassium channel subunit		gaa	tgc	increased
7101	RNO17606.KV9.1	Kv9.1	potassium channel, alpha subunit		tat	agg	decreased
7102	RNO17606.KV9.1	Kv9.1	potassium channel, alpha subunit		atc	agc	decreased
7103	RNO17606.KV9.1	Kv9.1	potassium channel, alpha subunit		cgc	gac	decreased
7104	RNO17606.KV9.1	Kv9.1	potassium channel, alpha subunit		cgc	gac	decreased
7105	RNO17606.KV9.1	Kv9.1	potassium channel, alpha subunit		gat	ctg	decreased
7106	RNO17606.KV9.1	Kv9.1	potassium channel, alpha subunit		aac	cgg	decreased
7107	RNO17606.KV9.1	Kv9.1	potassium channel, alpha subunit		ctg	cag	decreased
7108	AY009158.SLC24A3	SLC24A3	potassium-dependent sodium-calcium exchanger		aag	ttt	increased
7109	AY009158.SLC24A3	SLC24A3	potassium-dependent sodium-calcium exchanger		aag	ttt	increased
7110	AY009158.SLC24A3	SLC24A3	potassium-dependent sodium-calcium exchanger		aag	ttt	increased
7111	AY009158.SLC24A3	SLC24A3	potassium-dependent sodium-calcium exchanger		aag	ttt	increased
7112	AY009158.SLC24A3	SLC24A3	potassium-dependent sodium-calcium exchanger		tga	agg	increased
7113	AY009158.SLC24A3	SLC24A3	potassium-dependent sodium-calcium exchanger		tga	agg	increased
7114	AY009158.SLC24A3	SLC24A3	potassium-dependent sodium-calcium exchanger		tga	agg	increased
7115	AY009158.SLC24A3	SLC24A3	potassium-dependent sodium-calcium exchanger		tga	agg	increased
7116	AF055286.OCT3	oct-03	potential-sensitive polyspecific organic cation		ctg	tca	increased
7117	AF055286.OCT3	oct-03	potential-sensitive polyspecific organic cation		ctg	tca	increased
7118	AF055286.OCT3	oct-03	potential-sensitive polyspecific organic cation		ctg	tca	increased
7119	AB011365.PE1	nc	PPAR-gamma protein	*	cca	aac	increased
7120	AB011365.PE1	nc	PPAR-gamma protein	*	cca	aac	increased
7121	AB081730.PE1	nc	pre-B-cell colony-enhancing factor		cac	caa	increased
7122	AB081730.PE1	nc	pre-B-cell colony-enhancing factor		cac	caa	increased
7123	AB081730.PE1	nc	pre-B-cell colony-enhancing factor		cac	caa	increased
7124	AB081730.PE1	nc	pre-B-cell colony-enhancing factor		cac	caa	increased
7125	AB081730.PE1	nc	pre-B-cell colony-enhancing factor		cac	caa	increased
7126	AB081730.PE1	nc	pre-B-cell colony-enhancing factor		cac	caa	increased
7127	AB081730.PE1	nc	pre-B-cell colony-enhancing factor		ggg	cct	increased
7128	AB081730.PE1	nc	pre-B-cell colony-enhancing factor		ggg	cct	increased
7129	RNCALRET.PE1	nc	precursor (AA -17 to 399)	*	acc	tat	increased
7130	RNCALRET.PE1	nc	precursor (AA -17 to 399)	*	acc	tat	increased
7131	RNCALRET.PE1	nc	precursor (AA -17 to 399)	*	acc	tat	decreased
7132	RNCALRET.PE1	nc	precursor (AA -17 to 399)	*	acc	tat	decreased
7133	D63761.PE1	nc	precursor for adrenodoxin reductase		ggg	gct	increased
7134	D63761.PE1	nc	precursor for adrenodoxin reductase		cgg	tgg	increased
7135	D63761.PE1	nc	precursor for adrenodoxin reductase		cgg	tgg	increased
7136	D63761.PE1	nc	precursor for adrenodoxin reductase		cgg	tgg	increased
7137	RNFIBRON.PE1	nc	precursor polypeptide (AA -32 to 2445)		ctg	agg	decreased
7138	RNFIBRON.PE1	nc	precursor polypeptide (AA -32 to 2445)		ctg	agg	decreased
7139	RNPROC.PE1	nc	precursor protein C		gga	agt	decreased
7140	RNPROC.PE1	nc	precursor protein C		gga	agt	decreased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
7141	Hha1	49	aaa	69.087	69	68.93	69.38	68.95	15 400 000	17 900 000	3 500 000	=-	\ (-)		-(4) \(4)
7142	Hha1	26	ctg	130.91	131	130.91	0	0	7 800 000	0	0	-=	\		-(4) \(4)
7143	Hha1	3	aac	133.207	134	133.21	133.02	133.39	5 800 000	3 800 000	3 700 000	==	-		-(4) \(4)
7144	Hha1	3	aac	134.06	134	134.06	0	0	5 500 000	0	0	-=	\		-(4) \(4)
7145	Taq1	31	gac	155.917	156	156.15	155.73	155.87	9 200 000	3 700 000	7 000 000	-=	\ (-)		-(4) \(4)
7146	Hha1	55	tca	155.483	156	155.56	155.46	155.43	4 400 000	3 100 000	3 000 000	==	-		-(4) \(4)
7147	Hha1	26	ctg	109.847	110	109.83	109.83	109.88	4 200 000	6 200 000	4 100 000	==	-	-	-2
7148	Hha1	33	agc	109.83	110	109.86	109.86	109.77	6 400 000	4 300 000	6 200 000	==	-	-	-2
7149	Hha1	40	tgg	142.665	143	0	142.82	142.51	0	3 200 000	3 800 000	+=	/		-2
7150	Hha1	40	tgg	143.785	143	0	143.72	143.85	0	5 200 000	3 000 000	+=	/		-2
7151	Hha1	4	aag	153.23	154	153.47	153.13	153.09	3 800 000	5 300 000	7 000 000	==	-		-2
7152	Hha1	4	aag	154.33	154	154.33	0	0	15 800 000	0	0	-=	\		-2
7153	Taq1	12	agt	153.727	154	153.72	153.64	153.82	3 700 000	4 400 000	3 000 000	==	-		-2
7154	Taq1	12	agt	154.81	154	154.79	154.75	154.89	8 600 000	12 600 000	9 000 000	==	-		-2
7155	Taq1	45	gcc	219.4	219	219.42	219.38	0	4 400 000	5 900 000	0	=-	\		\(2)
7156	Taq1	17	cca	219.81	220	219.81	0	0	441.18	0	0	-=	\		\(2)
7157	Taq1	17	cca	221.24	220	221.24	0	0	218.26	0	0	-=	\		\(2)
7158	Hha1	26	ctg	138.603	139	138.45	138.77	138.59	8 200 000	3 300 000	3 900 000	-=	\ (-)	\	-(2) \(2)
7159	Hha1	26	ctg	139.08	139	139.08	0	0	3 600 000	0	0	-=	\		-(2) \(2)
7160	Hha1	61	tct	138.613	139	138.54	138.59	138.71	62 000 000	9 200 000	22 400 000	-=	\ (-)	\	-(2) \(2)
7161	Hha1	61	tct	139.377	139	139.61	139.14	139.38	8 000 000	6 200 000	3 900 000	==	-		-(2) \(2)
7162	Taq1	8	gaa	96.89	97	96.89	0	0	3 100 000	0	0	-=	\		\(9)
7163	Hha1	8	gaa	97.105	97	0	96.98	97.23	0	5 600 000	4 200 000	+=	/		\(9)
7164	Taq1	8	gaa	97.5	97	97.58	97.42	0	6 400 000	4 500 000	0	=-	\		\(9)
7165	Hha1	25	cag	154.14	155	0	154.14	0	0	6 500 000	0	+-	A		\(9)
7166	Hha1	25	cag	155.29	155	155.2	155.38	0	6 300 000	5 500 000	0	=-	\		\(9)
7167	Taq1	34	tgc	161.27	162	161.27	0	0	7 600 000	0	0	-=	\		\(9)
7168	Taq1	34	tgc	162.33	162	162.33	0	0	7 000 000	0	0	-=	\		\(9)
7169	Hha1	6	aga	171.6	172	171.6	0	0	11 000 000	0	0	-=	\		\(9)
7170	Hha1	6	aga	172.825	172	172.66	0	172.99	6 800 000	0	5 700 000	-+(=)	V		\(9)
7171	Hha1	8	gaa	186.175	187	186	186.35	0	5 000 000	3 000 000	0	=-	\		\(9)
7172	Taq1	8	gaa	186.59	187	0	186.59	0	0	4 300 000	0	+-	A		\(9)
7173	Hha1	8	gaa	187.115	187	187.09	0	187.14	3 100 000	0	4 100 000	-+(=)	V		\(9)
7174	Taq1	25	cat	186.75	187	186.75	0	0	416.26	0	0	-=	\		\(9)
7175	Taq1	25	cat	187.575	187	187.73	187.42	0	791.59	509.22	0	=-	\		\(9)
7176	Hha1	10	atg	215.46	215	215.46	0	0	3 800 000	0	0	-=	\	\	\(9)
7177	Taq1	10	atg	215.46	215	215.46	0	0	3 400 000	0	0	-=	\	\	\(9)
7178	Taq1	10	atg	215.99	215	0	215.99	0	0	5 900 000	0	+-	A		\(9)
7179	Taq1	8	gaa	96.89	97	96.89	0	0	3 100 000	0	0	-=	\		\(9)
7180	Hha1	8	gaa	97.105	97	0	96.98	97.23	0	5 600 000	4 200 000	+=	/		\(9)
7181	Taq1	8	gaa	97.5	97	97.58	97.42	0	6 400 000	4 500 000	0	=-	\		\(9)
7182	Hha1	25	cag	154.14	155	0	154.14	0	0	6 500 000	0	+-	A		\(9)
7183	Hha1	25	cag	155.29	155	155.2	155.38	0	6 300 000	5 500 000	0	=-	\		\(9)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
7141	RNAPOAI.PE1	nc	preproapolipoprotein A-I		aaa	atc	No change
7142	RNAPOAI.PE1	nc	preproapolipoprotein A-I		ctg	ggg	No change
7143	RNAPOAI.PE1	nc	preproapolipoprotein A-I		ggc	aac	No change
7144	RNAPOAI.PE1	nc	preproapolipoprotein A-I		ggc	aac	No change
7145	RNAPOAI.PE1	nc	preproapolipoprotein A-I		gac	tca	No change
7146	RNAPOAI.PE1	nc	preproapolipoprotein A-I		gac	tca	No change
7147	AB084278.PE1	prepro-NPW	prepro-Neuropeptide W polypeptide		ctg	agc	No change
7148	AB084278.PE1	prepro-NPW	prepro-Neuropeptide W polypeptide		ctg	agc	No change
7149	AB084278.PE1	prepro-NPW	prepro-Neuropeptide W polypeptide		tgg	tgg	No change
7150	AB084278.PE1	prepro-NPW	prepro-Neuropeptide W polypeptide		tgg	tgg	No change
7151	AY240029.PE2	nc	preprorelaxin		agt	aag	No change
7152	AY240029.PE2	nc	preprorelaxin		agt	aag	No change
7153	AY240029.PE2	nc	preprorelaxin		agt	aag	No change
7154	AY240029.PE2	nc	preprorelaxin		agt	aag	No change
7155	RATPROHIB.PHB	phb	prohibitin		cca	gcc	increased
7156	RATPROHIB.PHB	phb	prohibitin		cca	gcc	increased
7157	RATPROHIB.PHB	phb	prohibitin		cca	gcc	increased
7158	AF226608.PE1	nc	prolactin-like protein M		ctg	tct	increased
7159	AF226608.PE1	nc	prolactin-like protein M		ctg	tct	No change
7160	AF226608.PE1	nc	prolactin-like protein M		ctg	tct	increased
7161	AF226608.PE1	nc	prolactin-like protein M		ctg	tct	No change
7162	AF386758.PE1	nc	prominin		ttc	gaa	increased
7163	AF386758.PE1	nc	prominin		ttc	gaa	increased
7164	AF386758.PE1	nc	prominin		ttc	gaa	increased
7165	AF386758.PE1	nc	prominin		ttg	cag	increased
7166	AF386758.PE1	nc	prominin		ttg	cag	increased
7167	AF386758.PE1	nc	prominin		gga	tgc	increased
7168	AF386758.PE1	nc	prominin		gga	tgc	increased
7169	AF386758.PE1	nc	prominin		aga	tgc	increased
7170	AF386758.PE1	nc	prominin		aga	tgc	increased
7171	AF386758.PE1	nc	prominin		gaa	cat	increased
7172	AF386758.PE1	nc	prominin		gaa	cat	increased
7173	AF386758.PE1	nc	prominin		gaa	cat	increased
7174	AF386758.PE1	nc	prominin		gaa	cat	increased
7175	AF386758.PE1	nc	prominin		gaa	cat	increased
7176	AF386758.PE1	nc	prominin		gga	atg	increased
7177	AF386758.PE1	nc	prominin		gga	atg	increased
7178	AF386758.PE1	nc	prominin		gga	atg	increased
7179	AY262731.PROM1	Prom1	prominin-1 splice variant		ttc	gaa	increased
7180	AY262731.PROM1	Prom1	prominin-1 splice variant		ttc	gaa	increased
7181	AY262731.PROM1	Prom1	prominin-1 splice variant		ttc	gaa	increased
7182	AY262731.PROM1	Prom1	prominin-1 splice variant		ttg	cag	increased
7183	AY262731.PROM1	Prom1	prominin-1 splice variant		ttg	cag	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
7184	Taq1	34	tgc	161.27	162	161.27	0	0	7 600 000	0	0	-=	\		\(9)
7185	Taq1	34	tgc	162.33	162	162.33	0	0	7 000 000	0	0	-=	\		\(9)
7186	Hha1	6	aga	171.6	172	171.6	0	0	11 000 000	0	0	-=	\		\(9)
7187	Hha1	6	aga	172.825	172	172.66	0	172.99	6 800 000	0	5 700 000	-+(=)	V		\(9)
7188	Hha1	8	gaa	186.175	187	186	186.35	0	5 000 000	3 000 000	0	=-	\		\(9)
7189	Taq1	8	gaa	186.59	187	0	186.59	0	0	4 300 000	0	+-	A		\(9)
7190	Hha1	8	gaa	187.115	187	187.09	0	187.14	3 100 000	0	4 100 000	-+(=)	V		\(9)
7191	Taq1	25	cat	186.75	187	186.75	0	0	416.26	0	0	-=	\		\(9)
7192	Taq1	25	cat	187.575	187	187.73	187.42	0	791.59	509.22	0	=-	\		\(9)
7193	Hha1	10	atg	215.46	215	215.46	0	0	3 800 000	0	0	-=	\	\	\(9)
7194	Taq1	10	atg	215.46	215	215.46	0	0	3 400 000	0	0	-=	\	\	\(9)
7195	Taq1	10	atg	215.99	215	0	215.99	0	0	5 900 000	0	+-	A		\(9)
7196	Hha1	33	agc	84.25	84	0	0	84.25	0	0	8 900 000	=+	/	/	
7197	Hha1	39	agg	84.255	84	0	84.39	84.12	0	877.66	655.11	+=	/	/	
7198	Hha1	33	agc	120.02	120	119.88	120.11	120.07	7 500 000	6 500 000	11 300 000	==	-		-2
7199	Hha1	54	ttt	121.03	121	121.1	121.03	120.96	10 700 000	12 400 000	3 000 000	=-	\ (-)		-2
7200	Hha1	26	ctg	104.535	105	104.54	104.53	0	10 900 000	3 300 000	0	-=	\		/(3)
7201	Hha1	26	ctg	105.54	105	105.54	0	0	3 100 000	0	0	-=	\		/(3)
7202	Hha1	59	ttc	116.49	117	0	116.49	0	0	117.85	0	+-	A		/(3)
7203	Hha1	59	ttc	117.215	117	0	117.03	117.4	0	143.72	1 360.82	=+	/		/(3)
7204	Hha1	58	gta	174.98	175	0	0	174.98	0	0	3 900 000	=+	/		/(3)
7205	Hha1	58	gta	175.76	175	0	175.74	175.78	0	8 500 000	6 900 000	+=	/		/(3)
7206	Hha1	49	aaa	232.39	233	232.41	232.38	232.38	4 100 000	41 000 000	22 900 000	+=	/ (-)		/(3)
7207	Hha1	49	aaa	233.615	233	233.71	233.52	0	5 000 000	13 300 000	0	+-	A		/(3)
7208	Hha1	44	cgg	72.173	72	72.07	72.24	72.21	157 200 000	31 700 000	60 300 000	-=	\ (-)		-2
7209	Hha1	43	cgc	138.53	138	138.52	138.57	138.5	5 500 000	4 700 000	3 800 000	==	-		-2
7210	Hha1	44	cgg	72.173	72	72.07	72.24	72.21	157 200 000	31 700 000	60 300 000	-=	\ (-)		-2
7211	Hha1	43	cgc	138.53	138	138.52	138.57	138.5	5 500 000	4 700 000	3 800 000	==	-		-2
7212	Hha1	6	aga	126.475	127	126.51	0	126.44	89 200 000	0	7 100 000	-=(-)	\		/(3)
7213	Hha1	6	aga	127.097	127	127.18	127.06	127.05	30 600 000	3 500 000	5 400 000	-=	\ (-)		/(3)
7214	Hha1	6	aga	127.6	127	0	127.54	127.66	0	3 100 000	6 300 000	++	/		/(3)
7215	Hha1	9	atc	126.45	127	0	0	126.45	0	0	4 400 000	=+	/		/(3)
7216	Taq1	9	atc	127.09	127	0	0	127.09	0	0	12 500 000	=+	/		/(3)
7217	Hha1	9	atc	127.14	127	127.14	0	0	6 500 000	0	0	-=	\		/(3)
7218	Hha1	6	aga	126.475	127	126.51	0	126.44	89 200 000	0	7 100 000	-=(-)	\		/(3)
7219	Hha1	6	aga	127.097	127	127.18	127.06	127.05	30 600 000	3 500 000	5 400 000	-=	\ (-)		/(3)
7220	Hha1	6	aga	127.6	127	0	127.54	127.66	0	3 100 000	6 300 000	++	/		/(3)
7221	Hha1	9	atc	126.45	127	0	0	126.45	0	0	4 400 000	=+	/		/(3)
7222	Taq1	9	atc	127.09	127	0	0	127.09	0	0	12 500 000	=+	/		/(3)
7223	Hha1	9	atc	127.14	127	127.14	0	0	6 500 000	0	0	-=	\		/(3)
7224	Hha1	39	agg	152.55	153	152.55	0	0	469.2	0	0	-=	\		-2
7225	Hha1	39	agg	153.06	153	153.06	0	0	359.23	0	0	-=	\		-2
7226	Hha1	39	agg	153.21	153	153.21	0	0	322.58	0	0	-=	\		-2

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
7184	AY262731.PROM1	Prom1	prominin-1 splice variant		gga	tgc	increased
7185	AY262731.PROM1	Prom1	prominin-1 splice variant		gga	tgc	increased
7186	AY262731.PROM1	Prom1	prominin-1 splice variant		aga	tgc	increased
7187	AY262731.PROM1	Prom1	prominin-1 splice variant		aga	tgc	increased
7188	AY262731.PROM1	Prom1	prominin-1 splice variant		gaa	cat	increased
7189	AY262731.PROM1	Prom1	prominin-1 splice variant		gaa	cat	increased
7190	AY262731.PROM1	Prom1	prominin-1 splice variant		gaa	cat	increased
7191	AY262731.PROM1	Prom1	prominin-1 splice variant		gaa	cat	increased
7192	AY262731.PROM1	Prom1	prominin-1 splice variant		gaa	cat	increased
7193	AY262731.PROM1	Prom1	prominin-1 splice variant		gga	atg	increased
7194	AY262731.PROM1	Prom1	prominin-1 splice variant		gga	atg	increased
7195	AY262731.PROM1	Prom1	prominin-1 splice variant		gga	atg	increased
7196	AF181561.PE1	nc	proSAAS		agg	agc	decreased
7197	AF181561.PE1	nc	proSAAS		agg	agc	decreased
7198	RNO278800.PE1	proSAPiP2	ProSAPiP2 protein		ttt	agc	No change
7199	RNO278800.PE1	proSAPiP2	ProSAPiP2 protein		ttt	agc	No change
7200	RNU92289.PE1	nc	prostaglandin D2 receptor		tgc	ctg	decreased
7201	RNU92289.PE1	nc	prostaglandin D2 receptor		tgc	ctg	decreased
7202	RNU92289.PE1	nc	prostaglandin D2 receptor		tcc	ttc	decreased
7203	RNU92289.PE1	nc	prostaglandin D2 receptor		tcc	ttc	decreased
7204	RNU92289.PE1	nc	prostaglandin D2 receptor		gat	gta	decreased
7205	RNU92289.PE1	nc	prostaglandin D2 receptor		gat	gta	decreased
7206	RNU92289.PE1	nc	prostaglandin D2 receptor		aaa	cac	decreased
7207	RNU92289.PE1	nc	prostaglandin D2 receptor		aaa	cac	decreased
7208	RATPEREP2S.PE1	nc	prostaglandin E receptor EP4 subtype		ctc	cgg	No change
7209	RATPEREP2S.PE1	nc	prostaglandin E receptor EP4 subtype		cgc	tgc	No change
7210	AY266421.PTGER	Ptger	prostaglandin E2 receptor type 4		ctc	cgg	No change
7211	AY266421.PTGER	Ptger	prostaglandin E2 receptor type 4		cgc	tgc	No change
7212	RATP22KGA.PE1	prostatic 22-k	prostatic 22-kD glycoprotein		aga	atc	decreased
7213	RATP22KGA.PE1	prostatic 22-k	prostatic 22-kD glycoprotein		aga	atc	decreased
7214	RATP22KGA.PE1	prostatic 22-k	prostatic 22-kD glycoprotein		aga	atc	decreased
7215	RATP22KGA.PE1	prostatic 22-k	prostatic 22-kD glycoprotein		aga	atc	decreased
7216	RATP22KGA.PE1	prostatic 22-k	prostatic 22-kD glycoprotein		aga	atc	decreased
7217	RATP22KGA.PE1	prostatic 22-k	prostatic 22-kD glycoprotein		aga	atc	decreased
7218	RNPROST22.PE1	nc	prostatic 22kDa glycoprotein	*	aga	atc	decreased
7219	RNPROST22.PE1	nc	prostatic 22kDa glycoprotein	*	aga	atc	decreased
7220	RNPROST22.PE1	nc	prostatic 22kDa glycoprotein	*	aga	atc	decreased
7221	RNPROST22.PE1	nc	prostatic 22kDa glycoprotein	*	aga	atc	decreased
7222	RNPROST22.PE1	nc	prostatic 22kDa glycoprotein	*	aga	atc	decreased
7223	RNPROST22.PE1	nc	prostatic 22kDa glycoprotein	*	aga	atc	decreased
7224	RATTBP7B.PE1	nc	proteasomal ATPase (Tat-binding protein7)		agg	aca	No change
7225	RATTBP7B.PE1	nc	proteasomal ATPase (Tat-binding protein7)		agg	aca	No change
7226	RATTBP7B.PE1	nc	proteasomal ATPase (Tat-binding protein7)		agg	aca	No change

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
7227	Hha1	39	agg	153.74	153	153.63	0	153.85	535.19	0	142.41	-=(-)	\		-2
7228	Taq1	12	agt	160.007	160	160.08	159.88	160.06	3 800 000	5 800 000	3 500 000	==	-	-	-2
7229	Taq1	18	cct	159.18	160	0	0	159.18	0	0	5 500 000	=+	/		-2
7230	Taq1	18	cct	160.18	160	160.12	160.21	160.21	6 200 000	3 800 000	4 200 000	==	-	-	-2
7231	Hha1	6	aga	114.095	114	114.18	0	114.01	3 200 000	0	13 400 000	=+(+)	/		/(2)
7232	Hha1	6	aga	114.53	114	0	114.53	0	0	11 200 000	0	+-	A		/(2)
7233	Taq1	20	ctc	113.383	114	113.37	113.27	113.51	5 700 000	4 400 000	37 800 000	=+	/ (-)		/(2)
7234	Taq1	20	ctc	114.437	114	114.43	114.38	114.5	3 300 000	5 500 000	8 900 000	==	-		/(2)
7235	Hha1	15	tac	179.05	178	0	0	179.05	0	0	3 900 000	=+	/		/(2)
7236	Hha1	39	agg	176.94	178	0	177.1	176.78	0	310.46	236	+=	/		/(2)
7237	Hha1	39	agg	178.22	178	0	178.4	178.04	0	220.9	183.1	+=	/		/(2)
7238	Hha1	2	tta	169.97	169	0	0	169.97	0	0	3 000 000	=+	/		/(2)
7239	Hha1	54	ttt	169.61	170	0	0	169.61	0	0	3 800 000	=+	/		/(2)
7240	Hha1	54	ttt	170.915	170	170.89	170.94	0	3 800 000	4 400 000	0	=-	\		/(2)
7241	Hha1	33	agc	60.14	60	0	60.14	0	0	4 600 000	0	+-	A		A(2)
7242	Hha1	44	cgg	107.93	108	0	107.93	0	0	3 700 000	0	+-	A		A(2)
7243	Hha1	44	cgg	108.59	108	108.6	108.58	0	3 200 000	5 000 000	0	=-	\		A(2)
7244	Hha1	21	acc	106.475	107	0	106.29	106.66	0	5 200 000	9 700 000	++	/	(/)	/(6)
7245	Hha1	21	acc	106.58	107	0	106.58	0	0	3 900 000	0	+-	A		/(6)
7246	Taq1	21	acc	106.53	107	106.49	0	106.57	18 200 000	0	37 000 000	-+(+)	V (/)	(/)	/(6)
7247	Taq1	21	acc	107.02	107	0	107.02	0	0	10 000 000	0	+-	A		/(6)
7248	Hha1	6	aga	143.277	143	143.37	143.3	143.16	10 800 000	5 000 000	3 900 000	-=	\ (-)		/(6)
7249	Hha1	11	act	142.36	143	0	0	142.36	0	0	5 600 000	=+	/		/(6)
7250	Taq1	11	act	142.53	143	142.43	0	142.63	3 000 000	0	42 500 000	=+(+)	/		/(6)
7251	Hha1	11	act	143.3	143	143.29	143.26	143.35	7 600 000	5 700 000	14 500 000	=+	/ (-)		/(6)
7252	Taq1	11	act	143.46	143	143.38	143.28	143.72	5 200 000	3 900 000	13 300 000	=+	/ (-)		/(6)
7253	Taq1	56	tga	131.19	131	0	0	131.19	0	0	4 700 000	=+	/	/	
7254	Taq1	63	ctt	131.04	131	0	0	131.04	0	0	3 300 000	=+	/	/	
7255	Taq1	41	ccc	121.91	122	0	121.91	0	0	14 800 000	0	+-	A		A(4)
7256	Taq1	41	ccc	194.21	195	0	194.21	0	0	4 900 000	0	+-	A		A(4)
7257	Taq1	41	ccc	195	195	0	195	0	0	5 900 000	0	+-	A		A(4)
7258	Taq1	41	ccc	196.04	195	0	196.04	0	0	3 800 000	0	+-	A		A(4)
7259	Taq1	61	tct	195.46	196	195.46	0	0	3 000 000	0	0	-=	\		A(4)
7260	Taq1	61	tct	196.3	196	0	0	196.3	0	0	5 900 000	=+	/		A(4)
7261	Hha1	40	tgg	206.36	207	0	0	206.36	0	0	3 500 000	=+	/		A(4)
7262	Hha1	59	ttc	206.05	207	0	0	206.05	0	0	204.38	=+	/		A(4)
7263	Hha1	59	ttc	207.49	207	207.5	207.3	207.67	166.4	399.56	124.18	+-	A		A(4)
7264	Taq1	39	agg	256.83	258	0	256.83	0	0	11 900 000	0	+-	A		A(4)
7265	Taq1	39	agg	257.89	258	258.11	257.67	0	7 900 000	3 400 000	0	-=	\		A(4)
7266	Taq1	39	agg	258.69	258	258.77	258.61	0	8 200 000	29 000 000	0	+-	A		A(4)
7267	Taq1	39	agg	256.83	258	0	256.83	0	0	119.59	0	+-	A		A(4)
7268	Taq1	39	agg	257.67	258	0	257.67	0	0	34.17	0	+-	A		A(4)
7269	Taq1	39	agg	258.61	258	0	258.61	0	0	291.46	0	+-	A		A(4)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
7227	RATTBP7B.PE1	nc	proteasomal ATPase (Tat-binding protein7)		agg	aca	No change
7228	RATTBP7B.PE1	nc	proteasomal ATPase (Tat-binding protein7)		cct	agt	No change
7229	RATTBP7B.PE1	nc	proteasomal ATPase (Tat-binding protein7)		cct	agt	No change
7230	RATTBP7B.PE1	nc	proteasomal ATPase (Tat-binding protein7)		cct	agt	No change
7231	AF059530.PRMT3	PRMT3	protein arginine N-methyltransferase 3		aga	ctc	decreased
7232	AF059530.PRMT3	PRMT3	protein arginine N-methyltransferase 3		aga	ctc	decreased
7233	AF059530.PRMT3	PRMT3	protein arginine N-methyltransferase 3		aga	ctc	decreased
7234	AF059530.PRMT3	PRMT3	protein arginine N-methyltransferase 3		aga	ctc	decreased
7235	RNPEPPRES.RT1.AG	RT1.Ag	protein involved in peptide presentation		tac	agg	decreased
7236	RNPEPPRES.RT1.AG	RT1.Ag	protein involved in peptide presentation		tac	agg	decreased
7237	RNPEPPRES.RT1.AG	RT1.Ag	protein involved in peptide presentation		tac	agg	decreased
7238	AB003357.SK2	SK2	protein kinase		ttt	tta	decreased
7239	AB003357.SK2	SK2	protein kinase		ttt	tta	decreased
7240	AB003357.SK2	SK2	protein kinase		ttt	tta	decreased
7241	D85435.SRBC	SRBC	protein kinase C delta-bindig protein		agc	tcc	increased by mild
7242	D85435.SRBC	SRBC	protein kinase C delta-bindig protein		cgg	ctc	increased by mild
7243	D85435.SRBC	SRBC	protein kinase C delta-bindig protein		cgg	ctc	increased by mild
7244	RNU48245.PE1	nc	protein kinase C-binding protein NELL2		acc	taa	decreased
7245	RNU48245.PE1	nc	protein kinase C-binding protein NELL2		acc	taa	decreased
7246	RNU48245.PE1	nc	protein kinase C-binding protein NELL2		acc	taa	decreased
7247	RNU48245.PE1	nc	protein kinase C-binding protein NELL2		acc	taa	decreased
7248	RNU48245.PE1	nc	protein kinase C-binding protein NELL2		aga	act	decreased
7249	RNU48245.PE1	nc	protein kinase C-binding protein NELL2		aga	act	decreased
7250	RNU48245.PE1	nc	protein kinase C-binding protein NELL2		aga	act	decreased
7251	RNU48245.PE1	nc	protein kinase C-binding protein NELL2		aga	act	decreased
7252	RNU48245.PE1	nc	protein kinase C-binding protein NELL2		aga	act	decreased
7253	AF057026.KID1	Kid1	protein kinase KID-1		ctt	tga	decreased
7254	AF057026.KID1	Kid1	protein kinase KID-1		ctt	tga	decreased
7255	AF136583.SNK	Snk	protein kinase SNK		ggg	ccc	increased by mild
7256	AF136583.SNK	Snk	protein kinase SNK		ccc	tct	increased by mild
7257	AF136583.SNK	Snk	protein kinase SNK		ccc	tct	increased by mild
7258	AF136583.SNK	Snk	protein kinase SNK		ccc	tct	increased by mild
7259	AF136583.SNK	Snk	protein kinase SNK		ccc	tct	increased by mild
7260	AF136583.SNK	Snk	protein kinase SNK		ccc	tct	increased by mild
7261	AF136583.SNK	Snk	protein kinase SNK		tgg	ttc	increased by mild
7262	AF136583.SNK	Snk	protein kinase SNK		tgg	ttc	increased by mild
7263	AF136583.SNK	Snk	protein kinase SNK		tgg	ttc	increased by mild
7264	AF136583.SNK	Snk	protein kinase SNK		taa	agg	increased by mild
7265	AF136583.SNK	Snk	protein kinase SNK		taa	agg	increased by mild
7266	AF136583.SNK	Snk	protein kinase SNK		taa	agg	increased by mild
7267	AF136583.SNK	Snk	protein kinase SNK		taa	agg	increased by mild
7268	AF136583.SNK	Snk	protein kinase SNK		taa	agg	increased by mild
7269	AF136583.SNK	Snk	protein kinase SNK		taa	agg	increased by mild

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
7270	Taq1	39	agg	258.11	258	258.11	0	0	293.37	0	0	-=	\		A(4)
7271	Taq1	39	agg	258.77	258	258.77	0	0	304.51	0	0	-=	\		A(4)
7272	Hha1	6	aga	263.63	265	263.63	0	0	3 900 000	0	0	-=	\		A(4)
7273	Hha1	6	aga	265.59	265	265.59	0	0	3 200 000	0	0	-=	\		A(4)
7274	Hha1	6	aga	99.99	100	0	99.99	0	0	8 000 000	0	+-	A		/(6)
7275	Hha1	6	aga	100.575	100	100.64	0	100.51	5 900 000	0	4 400 000	-+(=)	V		/(6)
7276	Hha1	6	aga	99.96	100	99.96	0	0	6 400 000	0	0	-=	\		/(6)
7277	Taq1	62	tgt	99.61	100	0	0	99.61	0	0	22 600 000	=+	/		/(6)
7278	Hha1	4	aag	117.37	118	117.34	0	117.4	69 600 000	0	6 700 000	-=(-)	\		/(6)
7279	Hha1	4	aag	118.01	118	0	0	118.01	0	0	5 700 000	=+	/		/(6)
7280	Taq1	22	tcc	124.525	125	0	124.63	124.42	0	10 400 000	54 800 000	=+	/		/(6)
7281	Hha1	22	tcc	124.863	125	124.69	125.12	124.78	32 500 000	3 200 000	3 600 000	-=	\ (-)		/(6)
7282	Taq1	22	tcc	125.597	125	125.44	125.82	125.53	5 300 000	4 700 000	13 300 000	=+	/ (-)		/(6)
7283	Taq1	50	aat	125.33	126	125.56	125.15	125.28	8 800 000	14 300 000	13 600 000	==	-		/(6)
7284	Taq1	50	aat	126.193	126	126.13	126.35	126.1	16 700 000	7 800 000	44 200 000	=+	/ (-)		/(6)
7285	Hha1	21	acc	139.53	140	0	0	139.53	0	0	10 800 000	=+	/		/(6)
7286	Taq1	21	acc	139.66	140	139.51	0	139.81	10 400 000	0	8 400 000	-+(=)	V		/(6)
7287	Hha1	21	acc	140.62	140	140.62	0	0	4 500 000	0	0	-=	\		/(6)
7288	Hha1	41	ccc	94.935	95	94.75	0	95.12	4 700 000	0	3 000 000	-+(=)	V		\(2) V(2)
7289	Hha1	41	ccc	95.465	95	95.52	95.41	0	68 600 000	8 000 000	0	-=	\		\(2) V(2)
7290	Hha1	60	ttg	96.59	97	96.81	96.37	0	3 700 000	6 600 000	0	=-	\		\(2) V(2)
7291	Hha1	60	ttg	97.01	97	0	0	97.01	0	0	5 800 000	=+	/		\(2) V(2)
7292	Hha1	60	ttg	96.91	97	96.81	0	97.01	3 700 000	0	5 800 000	-+(=)	V		\(2) V(2)
7293	Taq1	23	cga	183.04	184	0	183.04	0	0	5 600 000	0	+-	A		/(2)
7294	Taq1	23	cga	184.9	184	0	184.72	185.08	0	3 100 000	4 000 000	+=	/		/(2)
7295	Taq1	57	ctg	183.445	184	183.63	0	183.26	4 000 000	0	4 500 000	-+(=)	V		/(2)
7296	Taq1	57	ctg	184.32	184	0	0	184.32	0	0	7 900 000	=+	/		/(2)
7297	Taq1	48	ggg	95.96	96	95.96	0	0	2 939.31	0	0	-=	\		\(3)
7298	Taq1	16	tag	138.41	139	138.28	0	138.54	3 400 000	0	4 100 000	-+(=)	V		\(3)
7299	Taq1	16	tag	139.29	139	139.29	0	0	4 900 000	0	0	-=	\		\(3)
7300	Hha1	16	tag	139.375	139	139.57	0	139.18	3 100 000	0	9 900 000	=+(+)	/		\(3)
7301	Taq1	64	gtt	138.69	139	138.67	138.71	0	7 000 000	9 900 000	0	=-	\		\(3)
7302	Taq1	64	gtt	139.803	139	139.84	139.75	139.82	4 800 000	5 500 000	4 800 000	==	-		\(3)
7303	Taq1	19	cac	153.06	153	153.06	153.02	153.1	8 400 000	16 800 000	13 500 000	+=	/ (-)		/(4)
7304	Taq1	29	gca	227.715	229	227.65	227.78	0	3 000 000	3 100 000	0	=-	\		/(4)
7305	Taq1	29	gca	228.87	229	0	0	228.87	0	0	3 100 000	=+	/		/(4)
7306	Taq1	29	gca	229.87	229	229.87	0	0	3 000 000	0	0	-=	\		/(4)
7307	Taq1	61	tct	229.27	229	0	229.27	0	0	3 400 000	0	+-	A		/(4)
7308	Taq1	8	gaa	254.69	256	0	0	254.69	0	0	12 000 000	=+	/		/(4)
7309	Hha1	8	gaa	256.06	256	0	0	256.06	0	0	3 200 000	=+	/		/(4)
7310	Hha1	59	ttc	68.59	69	0	68.61	68.57	0	12 182.36	2 196.46	+-	A		-1
7311	Hha1	64	gtt	114.39	115	114.41	114.41	114.35	4 600 000	4 200 000	6 400 000	==	-		-1
7312	Hha1	64	gtt	115.33	115	0	0	115.33	0	0	4 300 000	=+	/		-1

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
7270	AF136583.SNK	Snk	protein kinase SNK		taa	agg	increased by mild
7271	AF136583.SNK	Snk	protein kinase SNK		taa	agg	increased by mild
7272	AF136583.SNK	Snk	protein kinase SNK		aga	tgt	increased by mild
7273	AF136583.SNK	Snk	protein kinase SNK		aga	tgt	increased by mild
7274	AF227741.WNK1	WNK1	protein kinase WNK1		aga	tgt	decreased
7275	AF227741.WNK1	WNK1	protein kinase WNK1		aga	tgt	decreased
7276	AF227741.WNK1	WNK1	protein kinase WNK1		aga	tgt	decreased
7277	AF227741.WNK1	WNK1	protein kinase WNK1		aga	tgt	decreased
7278	AF227741.WNK1	WNK1	protein kinase WNK1		aag	aca	decreased
7279	AF227741.WNK1	WNK1	protein kinase WNK1		aag	aca	decreased
7280	AF227741.WNK1	WNK1	protein kinase WNK1		aat	tcc	decreased
7281	AF227741.WNK1	WNK1	protein kinase WNK1		aat	tcc	decreased
7282	AF227741.WNK1	WNK1	protein kinase WNK1		aat	tcc	decreased
7283	AF227741.WNK1	WNK1	protein kinase WNK1		aat	tcc	decreased
7284	AF227741.WNK1	WNK1	protein kinase WNK1		aat	tcc	decreased
7285	AF227741.WNK1	WNK1	protein kinase WNK1		gtc	acc	decreased
7286	AF227741.WNK1	WNK1	protein kinase WNK1		gtc	acc	decreased
7287	AF227741.WNK1	WNK1	protein kinase WNK1		gtc	acc	decreased
7288	RNO271837.PPM1B1	ppm1b1	protein phosphatase 1B1 43 kDa isoform		aat	ccc	increased
7289	RNO271837.PPM1B1	ppm1b1	protein phosphatase 1B1 43 kDa isoform		aat	ccc	increased
7290	RNO271837.PPM1B1	ppm1b1	protein phosphatase 1B1 43 kDa isoform		att	ttg	increased
7291	RNO271837.PPM1B1	ppm1b1	protein phosphatase 1B1 43 kDa isoform		att	ttg	increased
7292	RNO271837.PPM1B1	ppm1b1	protein phosphatase 1B1 43 kDa isoform		att	ttg	increased
7293	AY128641S2.PE1	Gadd34	protein phosphatase regulatory subunit 15A		ctg	cga	decreased
7294	AY128641S2.PE1	Gadd34	protein phosphatase regulatory subunit 15A		ctg	cga	decreased
7295	AY128641S2.PE1	Gadd34	protein phosphatase regulatory subunit 15A		ctg	cga	decreased
7296	AY128641S2.PE1	Gadd34	protein phosphatase regulatory subunit 15A		ctg	cga	decreased
7297	RNPPT.PE1	nc	protein phosphatase T (PPT)		ggg	aca	increased
7298	RNPPT.PE1	nc	protein phosphatase T (PPT)		gtt	tag	increased
7299	RNPPT.PE1	nc	protein phosphatase T (PPT)		gtt	tag	increased
7300	RNPPT.PE1	nc	protein phosphatase T (PPT)		gtt	tag	increased
7301	RNPPT.PE1	nc	protein phosphatase T (PPT)		gtt	tag	increased
7302	RNPPT.PE1	nc	protein phosphatase T (PPT)		gtt	tag	increased
7303	RNEIF2BDS.PE1	nc	protein synthesis initiation factor eIF-2B delta		tcg	cac	decreased
7304	RNEIF2BDS.PE1	nc	protein synthesis initiation factor eIF-2B delta		gca	tct	decreased
7305	RNEIF2BDS.PE1	nc	protein synthesis initiation factor eIF-2B delta		gca	tct	decreased
7306	RNEIF2BDS.PE1	nc	protein synthesis initiation factor eIF-2B delta		gca	tct	decreased
7307	RNEIF2BDS.PE1	nc	protein synthesis initiation factor eIF-2B delta		gca	tct	decreased
7308	RNEIF2BDS.PE1	nc	protein synthesis initiation factor eIF-2B delta		gaa	cat	decreased
7309	RNEIF2BDS.PE1	nc	protein synthesis initiation factor eIF-2B delta		gaa	cat	decreased
7310	RNU69673.PE1	nc	protein tyrosine phosphatase 20		ttc	ccg	No change
7311	RNU69673.PE1	nc	protein tyrosine phosphatase 20		cca	gtt	No change
7312	RNU69673.PE1	nc	protein tyrosine phosphatase 20		cca	gtt	No change

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
7313	Hha1	39	agg	121.03	121	121.19	121.17	120.73	373.9	268.67	297.03	==	-		-1
7314	Hha1	39	agg	121.6	121	0	0	121.6	0	0	337.72	=+	/		-1
7315	Hha1	54	ttt	98.527	99	98.56	98.49	98.53	43 400 000	26 600 000	11 400 000	==	-		-3
7316	Hha1	33	agc	108.77	109	108.83	108.8	108.68	11 600 000	9 300 000	8 800 000	==	-		-3
7317	Hha1	61	tct	108.5	109	108.43	108.77	108.3	13 700 000	3 100 000	4 300 000	-=	\ (-)		-3
7318	Hha1	61	tct	109.345	109	109.11	0	109.58	7 200 000	0	6 100 000	-+(=)	V		-3
7319	Hha1	61	tct	109.65	109	109.66	109.64	0	10 200 000	7 100 000	0	=-	\		-3
7320	Taq1	50	aat	95.223	95	95.19	95.24	95.24	68 800 000	12 500 000	27 000 000	-=	\ (-)		A(2) \(2)
7321	Taq1	54	ttt	94.85	95	0	94.99	94.71	0	2 622.6	1 241.97	+-	A		A(2) \(2)
7322	Taq1	10	atg	260.52	262	260.52	0	0	10 000 000	0	0	-=	\		A(2) \(2)
7323	Taq1	10	atg	261.3	262	261.3	0	0	5 700 000	0	0	-=	\		A(2) \(2)
7324	Taq1	10	atg	263.17	262	0	263.17	0	0	3 900 000	0	+-	A		A(2) \(2)
7325	Hha1	40	tgg	157.975	158	157.8	158.15	0	7 600 000	10 900 000	0	=-	\		\(2)
7326	Hha1	40	tgg	158.805	158	159.02	0	158.59	4 200 000	0	4 000 000	-+(=)	V		\(2)
7327	Hha1	62	tgt	157.33	158	157.33	0	0	3 500 000	0	0	-=	\		\(2)
7328	Hha1	39	agg	78.64	79	78.87	78.41	0	2 023.46	728.4	0	-=	\		/(3) -(2)
7329	Hha1	39	agg	78.96	79	0	0	78.96	0	0	960.28	=+	/		/(3) -(2)
7330	Taq1	45	gcc	135.293	136	135.33	135.33	135.22	5 900 000	4 700 000	6 200 000	==	-		/(3) -(2)
7331	Taq1	45	gcc	136.317	136	136.21	136.62	136.12	7 500 000	4 100 000	8 100 000	=+	/ (-)	/	/(3) -(2)
7332	Taq1	56	tga	136.38	137	0	0	136.38	0	0	27 700 000	=+	/	/	/(3) -(2)
7333	Taq1	56	tga	137.043	137	137.02	136.95	137.16	3 500 000	3 900 000	8 500 000	=+	/ (-)		/(3) -(2)
7334	Hha1	25	cag	112.047	112	112.2	111.86	112.08	64 500 000	11 300 000	21 100 000	-=	\ (-)	(-)	
7335	Taq1	61	tct	111.877	112	111.69	112.15	111.79	7 800 000	8 900 000	25 800 000	=+	/ (-)	(-)	
7336	Taq1	56	tga	87.863	88	87.7	87.87	88.02	6 500 000	7 900 000	15 400 000	=+	/ (-)		-(3) \(3)
7337	Hha1	6	aga	162.405	163	162.45	0	162.36	4 500 000	0	5 900 000	-+(=)	V		-(3) \(3)
7338	Hha1	6	aga	163.67	163	163.92	163.51	163.58	15 700 000	3 600 000	3 000 000	-=	\ (-)	(-)	-(3) \(3)
7339	Taq1	17	cca	162.45	163	162.45	0	0	218.26	0	0	-=	\		-(3) \(3)
7340	Taq1	17	cca	163.46	163	163.15	163.63	163.6	190.4	339.05	586.37	==	-	(-)	-(3) \(3)
7341	Taq1	39	agg	262.855	264	262.78	262.93	0	6 000 000	87 800 000	0	+-	A		-(3) \(3)
7342	Taq1	39	agg	263.915	264	263.88	263.95	0	10 600 000	5 000 000	0	--	\		-(3) \(3)
7343	Taq1	39	agg	262.78	264	262.78	0	0	222.81	0	0	-=	\		-(3) \(3)
7344	Taq1	39	agg	263.88	264	263.88	0	0	393.64	0	0	-=	\		-(3) \(3)
7345	Taq1	39	agg	265.03	264	0	265.03	0	0	67 300 000	0	+-	A		-(3) \(3)
7346	Taq1	39	agg	262.93	264	0	262.93	0	0	882.42	0	+-	A		-(3) \(3)
7347	Taq1	39	agg	263.95	264	0	263.95	0	0	50.25	0	+-	A		-(3) \(3)
7348	Taq1	39	agg	265.03	264	0	265.03	0	0	676.38	0	+-	A		-(3) \(3)
7349	Hha1	33	agc	77.803	78	77.78	77.86	77.77	56 700 000	20 100 000	9 400 000	-=	\ (-)		-3
7350	Hha1	31	gac	147.24	148	0	0	147.24	0	0	4 100 000	=+	/		-3
7351	Hha1	31	gac	148.343	148	148.4	148.37	148.26	7 300 000	4 900 000	5 100 000	==	-		-3
7352	Hha1	33	agc	159.603	160	159.63	159.66	159.52	4 200 000	6 000 000	31 200 000	=+	/ (-)		-3
7353	Hha1	33	agc	160.593	160	160.67	160.58	160.53	4 200 000	6 100 000	26 700 000	=+	/ (-)		-3
7354	Hha1	62	tgt	159.265	160	159.3	0	159.23	4 800 000	0	3 700 000	-+(=)	V		-3
7355	Hha1	20	ctc	129.17	129	0	129.32	129.02	0	406.5	584.44	+=	/		/(6)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
7313	RNU69673.PE1	nc	protein tyrosine phosphatase 20		agg	tcc	No change
7314	RNU69673.PE1	nc	protein tyrosine phosphatase 20		agg	tcc	No change
7315	AF077000.PE1	PTP-TD14	protein tyrosine phosphatase TD14		tgc	ttt	No change
7316	AF077000.PE1	PTP-TD14	protein tyrosine phosphatase TD14		tct	agc	No change
7317	AF077000.PE1	PTP-TD14	protein tyrosine phosphatase TD14		tct	agc	No change
7318	AF077000.PE1	PTP-TD14	protein tyrosine phosphatase TD14		tct	agc	No change
7319	AF077000.PE1	PTP-TD14	protein tyrosine phosphatase TD14		tct	agc	No change
7320	RNPTPS.PTP-S	PTP-S	protein-tyrosine phosphatase		aat	ttt	increased by mild
7321	RNPTPS.PTP-S	PTP-S	protein-tyrosine phosphatase		aat	ttt	increased by mild
7322	RNPTPS.PTP-S	PTP-S	protein-tyrosine phosphatase		atg	atg	increased by mild
7323	RNPTPS.PTP-S	PTP-S	protein-tyrosine phosphatase		atg	atg	increased by mild
7324	RNPTPS.PTP-S	PTP-S	protein-tyrosine phosphatase		atg	atg	increased by mild
7325	RNU77038.SHP-1	SHP-1	protein-tyrosine phosphatase		tgg	tgt	increased
7326	RNU77038.SHP-1	SHP-1	protein-tyrosine phosphatase		tgg	tgt	increased
7327	RNU77038.SHP-1	SHP-1	protein-tyrosine phosphatase		tgg	tgt	increased
7328	RATPTPXA.PE1	nc	protein-tyrosine-phospatase	*	agg	agt	decreased
7329	RATPTPXA.PE1	nc	protein-tyrosine-phospatase	*	agg	agt	decreased
7330	RATPTPXA.PE1	nc	protein-tyrosine-phospatase	*	tga	gcc	decreased
7331	RATPTPXA.PE1	nc	protein-tyrosine-phospatase	*	tga	gcc	decreased
7332	RATPTPXA.PE1	nc	protein-tyrosine-phospatase	*	tga	gcc	decreased
7333	RATPTPXA.PE1	nc	protein-tyrosine-phospatase	*	tga	gcc	decreased
7334	AF100960.FAT	Fat	protocadherin		cag	tct	No change
7335	AF100960.FAT	Fat	protocadherin		cag	tct	No change
7336	RNU94403.PE1	nc	proton gated cation channel ASIC1		agc	tga	No change
7337	RNU94403.PE1	nc	proton gated cation channel ASIC1		cca	aga	No change
7338	RNU94403.PE1	nc	proton gated cation channel ASIC1		cca	aga	No change
7339	RNU94403.PE1	nc	proton gated cation channel ASIC1		cca	aga	No change
7340	RNU94403.PE1	nc	proton gated cation channel ASIC1		cca	aga	No change
7341	RNU94403.PE1	nc	proton gated cation channel ASIC1		gac	agg	No change
7342	RNU94403.PE1	nc	proton gated cation channel ASIC1		gac	agg	No change
7343	RNU94403.PE1	nc	proton gated cation channel ASIC1		gac	agg	No change
7344	RNU94403.PE1	nc	proton gated cation channel ASIC1		gac	agg	No change
7345	RNU94403.PE1	nc	proton gated cation channel ASIC1		gac	agg	No change
7346	RNU94403.PE1	nc	proton gated cation channel ASIC1		gac	agg	No change
7347	RNU94403.PE1	nc	proton gated cation channel ASIC1		gac	agg	No change
7348	RNU94403.PE1	nc	proton gated cation channel ASIC1		gac	agg	No change
7349	RNO315643.HMIT	Hmit	proton myo-inositol transporter		agc	cct	No change
7350	RNO315643.HMIT	Hmit	proton myo-inositol transporter		gac	cgc	No change
7351	RNO315643.HMIT	Hmit	proton myo-inositol transporter		gac	cgc	No change
7352	RNO315643.HMIT	Hmit	proton myo-inositol transporter		agc	tgt	No change
7353	RNO315643.HMIT	Hmit	proton myo-inositol transporter		agc	tgt	No change
7354	RNO315643.HMIT	Hmit	proton myo-inositol transporter		agc	tgt	No change
7355	RATPRPU.PE1	nc	proton pump polypeptide		aaa	ctc	decreased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
7356	Hha1	49	aaa	129.23	130	129.19	129.38	129.12	48 400 000	55 900 000	6 200 000	=-	\ (-)		/(6)
7357	Hha1	49	aaa	129.907	130	129.8	129.97	129.95	10 300 000	30 100 000	9 800 000	+-	A		/(6)
7358	Hha1	49	aaa	130.74	130	130.88	0	130.6	8 200 000	0	5 600 000	-+(=)	V		/(6)
7359	Hha1	55	tca	134.21	135	134.21	0	134.21	4 300 000	0	6 300 000	-+(=)	V		/(6)
7360	Hha1	55	tca	135.215	135	135.28	135.15	0	5 800 000	4 600 000	0	=-	\		/(6)
7361	Taq1	55	tca	135.1	135	0	134.95	135.25	0	4 800 000	3 400 000	+=	/		/(6)
7362	Taq1	55	tca	135.55	135	135.55	0	0	4 000 000	0	0	-=	\		/(6)
7363	Taq1	49	aaa	135.23	136	0	135.23	0	0	3 100 000	0	+-	A		/(6)
7364	Taq1	49	aaa	135.845	136	135.85	135.84	0	5 800 000	10 800 000	0	+-	A		/(6)
7365	Taq1	49	aaa	136.687	136	136.54	136.82	136.7	8 200 000	6 300 000	36 500 000	=+	/ (-)		/(6)
7366	Taq1	49	aaa	142.64	143	142.87	0	142.41	9 400 000	0	102 000 000	=+(+)	/		/(6)
7367	Taq1	49	aaa	143.11	143	0	143.11	0	0	15 900 000	0	+-	A		/(6)
7368	Taq1	49	aaa	143.74	143	143.68	143.8	0	45 300 000	36 700 000	0	=-	\		/(6)
7369	Taq1	23	cga	177.927	178	177.97	177.91	177.9	14 500 000	9 600 000	4 600 000	==	-		/(6)
7370	Taq1	23	cga	178.95	178	178.89	178.95	179.01	5 000 000	3 500 000	4 100 000	==	-		/(6)
7371	Taq1	62	tgt	177.45	178	0	177.55	177.35	0	3 100 000	6 100 000	++	/		/(6)
7372	Taq1	62	tgt	178.47	178	0	178.65	178.29	0	3 000 000	9 300 000	=+	/		/(6)
7373	Taq1	49	aaa	225.82	227	0	225.79	225.85	0	4 100 000	3 200 000	+=	/		/(6)
7374	Taq1	49	aaa	227.96	227	227.96	0	0	11 800 000	0	0	-=	\		/(6)
7375	Taq1	56	tga	87.863	88	87.7	87.87	88.02	6 500 000	7 900 000	15 400 000	=+	/ (-)		-(3) \(2)
7376	Hha1	6	aga	162.405	163	162.45	0	162.36	4 500 000	0	5 900 000	-+(=)	V		-(3) \(2)
7377	Hha1	6	aga	163.67	163	163.92	163.51	163.58	15 700 000	3 600 000	3 000 000	-=	\ (-)	(-)	-(3) \(2)
7378	Taq1	17	cca	162.45	163	162.45	0	0	218.26	0	0	-=	\		-(3) \(2)
7379	Taq1	17	cca	163.46	163	163.15	163.63	163.6	190.4	339.05	586.37	==	-	(-)	-(3) \(2)
7380	Taq1	62	tgt	126.573	127	126.54	126.64	126.54	5 600 000	10 400 000	6 400 000	+=	/ (-)		/(2)
7381	Taq1	62	tgt	127.55	127	0	127.74	127.36	0	5 000 000	8 700 000	+=	/		/(2)
7382	Taq1	63	ctt	126.98	127	0	0	126.98	0	0	3 100 000	=+	/		/(2)
7383	Hha1	8	gaa	286.61	288	286.61	0	0	3 100 000	0	0	-=	\		/(2)
7384	Taq1	52	att	127.365	128	0	127.49	127.24	0	5 500 000	4 200 000	+=	/		\(2)
7385	Taq1	52	att	127.39	128	0	0	127.39	0	0	4 200 000	=+	/		\(2)
7386	Taq1	52	att	128.03	128	0	0	128.03	0	0	7 200 000	=+	/		\(2)
7387	Hha1	6	aga	161.59	162	161.71	0	161.47	8 900 000	0	4 000 000	-=(-)	\		\(2)
7388	Hha1	6	aga	162.405	162	162.45	0	162.36	4 500 000	0	5 900 000	-+(=)	V		\(2)
7389	Taq1	50	aat	224.05	224	224.05	0	0	4 000 000	0	0	-=	\		\(2)
7390	Taq1	50	aat	224.97	224	224.97	0	0	3 600 000	0	0	-=	\		\(2)
7391	Hha1	20	ctc	68.973	69	68.95	69.09	68.88	550.96	485.18	1 145.03	=+	/ (-)		-7
7392	Hha1	39	agg	68.607	69	68.64	68.57	68.61	828.44	603.02	406.9	==	-		-7
7393	Hha1	33	agc	72.64	73	0	0	72.64	0	0	33 300 000	=+	/		-7
7394	Hha1	64	gtt	130.69	131	130.82	130.55	130.7	11 500 000	3 900 000	10 500 000	-+	V		-7
7395	Hha1	64	gtt	131.643	131	131.71	131.6	131.62	10 800 000	3 100 000	3 900 000	-=	\ (-)		-7
7396	Taq1	9	atc	150.35	151	150.31	150.39	0	4 000 000	3 900 000	0	=-	\		-7
7397	Hha1	9	atc	150.377	151	150.25	150.5	150.38	3 500 000	4 700 000	3 800 000	==	-		-7
7398	Taq1	9	atc	151.4	151	151.36	151.44	0	4 200 000	7 600 000	0	=-	\		-7

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
7356	RATPRPU.PE1	nc	proton pump polypeptide		aaa	ctc	decreased
7357	RATPRPU.PE1	nc	proton pump polypeptide		aaa	ctc	decreased
7358	RATPRPU.PE1	nc	proton pump polypeptide		aaa	ctc	decreased
7359	RATPRPU.PE1	nc	proton pump polypeptide		aaa	tca	decreased
7360	RATPRPU.PE1	nc	proton pump polypeptide		aaa	tca	decreased
7361	RATPRPU.PE1	nc	proton pump polypeptide		aaa	tca	decreased
7362	RATPRPU.PE1	nc	proton pump polypeptide		aaa	tca	decreased
7363	RATPRPU.PE1	nc	proton pump polypeptide		aaa	tca	decreased
7364	RATPRPU.PE1	nc	proton pump polypeptide		aaa	tca	decreased
7365	RATPRPU.PE1	nc	proton pump polypeptide		aaa	tca	decreased
7366	RATPRPU.PE1	nc	proton pump polypeptide		aaa	aaa	decreased
7367	RATPRPU.PE1	nc	proton pump polypeptide		aaa	aaa	decreased
7368	RATPRPU.PE1	nc	proton pump polypeptide		aaa	aaa	decreased
7369	RATPRPU.PE1	nc	proton pump polypeptide		cga	tgt	decreased
7370	RATPRPU.PE1	nc	proton pump polypeptide		cga	tgt	decreased
7371	RATPRPU.PE1	nc	proton pump polypeptide		cga	tgt	decreased
7372	RATPRPU.PE1	nc	proton pump polypeptide		cga	tgt	decreased
7373	RATPRPU.PE1	nc	proton pump polypeptide		aaa	tcc	decreased
7374	RATPRPU.PE1	nc	proton pump polypeptide		aaa	tcc	decreased
7375	AB049451.PE1	ASIC-beta2	proton-gated cation channel subunit ASIC-beta2		agc	tga	No change
7376	AB049451.PE1	ASIC-beta2	proton-gated cation channel subunit ASIC-beta2		cca	aga	No change
7377	AB049451.PE1	ASIC-beta2	proton-gated cation channel subunit ASIC-beta2		cca	aga	No change
7378	AB049451.PE1	ASIC-beta2	proton-gated cation channel subunit ASIC-beta2		cca	aga	No change
7379	AB049451.PE1	ASIC-beta2	proton-gated cation channel subunit ASIC-beta2		cca	aga	No change
7380	RNU35365.P59FYN	p59fyn	proto-oncogene FYN		ctt	tgt	decreased
7381	RNU35365.P59FYN	p59fyn	proto-oncogene FYN		ctt	tgt	decreased
7382	RNU35365.P59FYN	p59fyn	proto-oncogene FYN		ctt	tgt	decreased
7383	RNU35365.P59FYN	p59fyn	proto-oncogene FYN		gaa	gca	decreased
7384	AF106945.PRX-IV	PRx IV	PRx IV		att	ggg	increased
7385	AF106945.PRX-IV	PRx IV	PRx IV		att	ggg	increased
7386	AF106945.PRX-IV	PRx IV	PRx IV		att	ggg	increased
7387	AF106945.PRX-IV	PRx IV	PRx IV		aga	taa	increased
7388	AF106945.PRX-IV	PRx IV	PRx IV		aga	taa	increased
7389	AF106945.PRX-IV	PRx IV	PRx IV		tga	aat	increased
7390	AF106945.PRX-IV	PRx IV	PRx IV		tga	aat	increased
7391	AB003594.PE1	nc	PSD-95 binding protein		cga	ctc	No change
7392	AB003594.PE1	nc	PSD-95 binding protein		agg	tgg	No change
7393	AB003594.PE1	nc	PSD-95 binding protein		agc	tct	No change
7394	AB003594.PE1	nc	PSD-95 binding protein		ggg	gtt	No change
7395	AB003594.PE1	nc	PSD-95 binding protein		ggg	gtt	No change
7396	AB003594.PE1	nc	PSD-95 binding protein		atc	tag	No change
7397	AB003594.PE1	nc	PSD-95 binding protein		atc	tag	No change
7398	AB003594.PE1	nc	PSD-95 binding protein		atc	tag	No change

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
7399	Hha1	9	atc	151.423	151	151.24	151.55	151.48	12 100 000	8 400 000	3 700 000	==	-		-7
7400	Taq1	16	tag	150.747	151	150.7	150.69	150.85	4 400 000	4 500 000	10 700 000	=+	/ (-)		-7
7401	Hha1	16	tag	151.153	151	151.41	150.99	151.06	3 600 000	5 700 000	4 800 000	==	-		-7
7402	Taq1	16	tag	151.86	151	0	0	151.86	0	0	8 400 000	=+	/		-7
7403	Taq1	9	atc	103.42	104	103.37	0	103.47	4 500 000	0	8 500 000	-+(+)	V (/)		\(3)
7404	Hha1	9	atc	103.88	104	103.63	0	104.13	5 100 000	0	3 000 000	-+(=)	V		\(3)
7405	Hha1	9	atc	104.35	104	104.35	0	0	24 300 000	0	0	-=	\		\(3)
7406	Taq1	9	atc	104.5	104	104.51	104.54	104.45	20 600 000	3 100 000	11 400 000	-=	\ (-)	\	\(3)
7407	Taq1	39	agg	104.227	104	104.06	104.44	104.18	14 000 000	87 600 000	14 900 000	+-	A		\(3)
7408	Taq1	39	agg	104.37	104	104.49	104.44	104.18	16 800 000	880.41	438.88	-=	\ (-)	\	\(3)
7409	Taq1	39	agg	103.47	104	103.47	0	0	583.03	0	0	-=	\		\(3)
7410	Taq1	39	agg	104.06	104	104.06	0	0	519.9	0	0	-=	\		\(3)
7411	Taq1	39	agg	104.49	104	104.49	0	0	623.88	0	0	-=	\	\	\(3)
7412	Hha1	59	ttc	73.915	74	0	73.97	73.86	0	1 069.33	721.8	+=	/		\(2)
7413	Hha1	31	gac	176.7	177	176.7	0	0	3 700 000	0	0	-=	\	\	\(2)
7414	Hha1	31	gac	177.61	177	0	177.61	0	0	3 900 000	0	+-	A		\(2)
7415	Hha1	60	ttg	176.86	177	176.86	0	0	4 600 000	0	0	-=	\	\	\(2)
7416	Hha1	60	ttg	177.81	177	177.85	177.67	177.91	7 300 000	5 600 000	6 800 000	==	-		\(2)
7417	Taq1	31	gac	121.415	121	121.62	0	121.21	3 500 000	0	70 000 000	=+(+)	/	/	
7418	Taq1	52	att	121.445	122	0	121.5	121.39	0	3 000 000	3 300 000	+=	/	/	
7419	Hha1	44	cgg	180.213	181	179.96	180.37	180.31	3 700 000	4 100 000	4 700 000	==	-		-2
7420	Hha1	44	cgg	180.86	181	0	180.86	0	0	5 200 000	0	+-	A		-2
7421	Hha1	26	ctg	241.467	242	241.43	241.52	241.45	18 500 000	4 400 000	8 000 000	-=	\ (-)		-2
7422	Hha1	26	ctg	242.62	242	242.69	242.58	242.59	20 900 000	6 100 000	23 900 000	-+	V		-2
7423	Hha1	26	ctg	243.22	242	243.26	243.21	243.19	20 300 000	4 100 000	22 300 000	-+	V		-2
7424	Hha1	27	acg	114.9	115	114.91	114.76	115.03	32 300 000	12 000 000	19 700 000	-=	\ (-)		\(2)
7425	Hha1	33	agc	151.405	152	151.45	151.36	0	7 400 000	7 400 000	0	=-	\		\(2)
7426	Hha1	33	agc	152.495	152	152.42	152.57	0	4 000 000	3 100 000	0	=-	\		\(2)
7427	Hha1	26	ctg	121.91	122	0	121.95	121.87	0	8 100 000	10 200 000	+=	/		/(2)
7428	Hha1	33	agc	197.52	198	0	0	197.52	0	0	5 600 000	=+	/		/(2)
7429	Hha1	33	agc	198.51	198	0	0	198.51	0	0	6 500 000	=+	/		/(2)
7430	Taq1	20	ctc	144.705	145	144.69	144.72	0	6 000 000	5 600 000	0	=-	\		\(2)
7431	Taq1	20	ctc	145.755	145	145.7	145.81	0	19 600 000	5 700 000	0	-=	\		\(2)
7432	Taq1	54	ttt	145.64	146	0	0	145.64	0	0	2 462.52	=+	/		\(2)
7433	Taq1	54	ttt	146.45	146	146.52	146.38	0	2 104.87	811.47	0	-=	\		\(2)
7434	Taq1	62	tgt	167.14	168	167.21	167.3	166.91	5 600 000	9 000 000	3 500 000	=-	\ (-)		\(2)
7435	Taq1	62	tgt	167.75	168	0	0	167.75	0	0	4 500 000	=+	/		\(2)
7436	Taq1	62	tgt	168.27	168	0	168.27	0	0	4 900 000	0	+-	A		\(2)
7437	Hha1	40	tgg	218.38	219	218.38	0	0	3 300 000	0	0	-=	\		\(2)
7438	Hha1	44	cgg	63.01	63	62.97	0	63.05	19 800 000	0	23 500 000	-+(=)	V		\(2)
7439	Hha1	43	cgc	107.03	107	106.98	107.08	0	6 700 000	8 500 000	0	=-	\		\(2)
7440	Hha1	43	cgc	107.583	107	107.51	107.56	107.68	10 100 000	13 700 000	4 700 000	=-	\ (-)		\(2)
7441	Hha1	49	aaa	180.93	181	180.93	0	0	68 500 000	0	0	-=	\		\(2)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
7399	AB003594.PE1	nc	PSD-95 binding protein		atc	tag	No change
7400	AB003594.PE1	nc	PSD-95 binding protein		atc	tag	No change
7401	AB003594.PE1	nc	PSD-95 binding protein		atc	tag	No change
7402	AB003594.PE1	nc	PSD-95 binding protein		atc	tag	No change
7403	RNU67138.PE1	nc	PSD-95/SAP90-associated protein-2		atc	agg	increased
7404	RNU67138.PE1	nc	PSD-95/SAP90-associated protein-2		atc	agg	increased
7405	RNU67138.PE1	nc	PSD-95/SAP90-associated protein-2		atc	agg	increased
7406	RNU67138.PE1	nc	PSD-95/SAP90-associated protein-2		atc	agg	increased
7407	RNU67138.PE1	nc	PSD-95/SAP90-associated protein-2		atc	agg	increased
7408	RNU67138.PE1	nc	PSD-95/SAP90-associated protein-2		atc	agg	increased
7409	RNU67138.PE1	nc	PSD-95/SAP90-associated protein-2		atc	agg	increased
7410	RNU67138.PE1	nc	PSD-95/SAP90-associated protein-2		atc	agg	increased
7411	RNU67138.PE1	nc	PSD-95/SAP90-associated protein-2		atc	agg	increased
7412	RNU67139.PE1	nc	PSD-95/SAP90-associated protein-3		tcc	ttc	increased
7413	RNU67139.PE1	nc	PSD-95/SAP90-associated protein-3		gac	ttg	increased
7414	RNU67139.PE1	nc	PSD-95/SAP90-associated protein-3		gac	ttg	increased
7415	RNU67139.PE1	nc	PSD-95/SAP90-associated protein-3		gac	ttg	increased
7416	RNU67139.PE1	nc	PSD-95/SAP90-associated protein-3		gac	ttg	increased
7417	RATPSELECT.PE1	nc	P-selectin		gac	att	decreased
7418	RATPSELECT.PE1	nc	P-selectin		gac	att	decreased
7419	AB047298.PTX1	ptx1	Ptx1 homeodomain protein		aag	cgg	No change
7420	AB047298.PTX1	ptx1	Ptx1 homeodomain protein		aag	cgg	No change
7421	AB047298.PTX1	ptx1	Ptx1 homeodomain protein		cgc	ctg	No change
7422	AB047298.PTX1	ptx1	Ptx1 homeodomain protein		cgc	ctg	No change
7423	AB047298.PTX1	ptx1	Ptx1 homeodomain protein		cgc	ctg	No change
7424	RNO011005.PTX3	ptx3	Ptx3 protein		acg	gtg	increased
7425	RNO011005.PTX3	ptx3	Ptx3 protein		agc	ctt	increased
7426	RNO011005.PTX3	ptx3	Ptx3 protein		agc	ctt	increased
7427	RNAMHR.PE1	nc	put. anti-mullerian hormone receptor		ctg	tgc	decreased
7428	RNAMHR.PE1	nc	put. anti-mullerian hormone receptor		agc	agc	decreased
7429	RNAMHR.PE1	nc	put. anti-mullerian hormone receptor		agc	agc	decreased
7430	RNO271642.ASIC4	asic4	putative acid-sensing ion channel		ctc	ttt	increased
7431	RNO271642.ASIC4	asic4	putative acid-sensing ion channel		ctc	ttt	increased
7432	RNO271642.ASIC4	asic4	putative acid-sensing ion channel		ctc	ttt	increased
7433	RNO271642.ASIC4	asic4	putative acid-sensing ion channel		ctc	ttt	increased
7434	RNO302031.PE1	nc	putative alpha 1B-glycoprotein		tgt	ttg	increased
7435	RNO302031.PE1	nc	putative alpha 1B-glycoprotein		tgt	ttg	increased
7436	RNO302031.PE1	nc	putative alpha 1B-glycoprotein		tgt	ttg	increased
7437	RNO302031.PE1	nc	putative alpha 1B-glycoprotein		agt	tgg	increased
7438	RNO535753.FUT11	fut11	putative alpha3-fucosyltransferase		cgg	tcc	increased
7439	RNO535753.FUT11	fut11	putative alpha3-fucosyltransferase		cgc	atg	increased
7440	RNO535753.FUT11	fut11	putative alpha3-fucosyltransferase		cgc	atg	increased
7441	RNO535753.FUT11	fut11	putative alpha3-fucosyltransferase		tcc	aaa	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
7442	Hha1	61	tct	99.33	99	0	0	99.33	0	0	6 200 000	=+	/		/(2)
7443	Hha1	56	tga	121.79	122	0	0	121.79	0	0	930.87	=+	/		/(2)
7444	Hha1	43	cgc	107.03	107	106.98	107.08	0	6 700 000	8 500 000	0	=-	\		-1
7445	Hha1	43	cgc	107.583	107	107.51	107.56	107.68	10 100 000	13 700 000	4 700 000	=-	\ (-)		-1
7446	Hha1	62	tgt	108.04	108	0	0	108.04	0	0	26 500 000	=+	/		-1
7447	Hha1	41	ccc	109.51	110	109.75	109.29	109.49	11 900 000	3 000 000	5 900 000	-=	\ (-)		-1
7448	Hha1	41	ccc	110.295	110	0	110.09	110.5	0	4 800 000	16 400 000	=+	/		-1
7449	Hha1	28	tcg	110.803	111	110.66	110.9	110.85	4 200 000	8 900 000	17 200 000	=+	/ (-)		-1
7450	Hha1	31	gac	178.83	179	0	178.8	178.86	0	3 300 000	8 100 000	=+	/		/(2)
7451	Hha1	39	agg	178.22	179	0	178.4	178.04	0	220.9	183.1	+=	/		/(2)
7452	Taq1	10	atg	258.65	260	0	258.65	0	0	3 600 000	0	+-	A		/(2)
7453	Taq1	10	atg	260.52	260	260.52	0	0	10 000 000	0	0	-=	\		/(2)
7454	Taq1	10	atg	261.3	260	261.3	0	0	5 700 000	0	0	-=	\		/(2)
7455	Taq1	25	cat	139.41	140	0	139.63	139.19	0	1 234.88	992	+=	/		/(2) \(2)
7456	Taq1	25	cat	139.7	140	139.7	0	0	1 344.34	0	0	-=	\		/(2) \(2)
7457	Taq1	25	cat	140.385	140	140.17	140.6	0	1 637.77	1 718.65	0	=-	\		/(2) \(2)
7458	Taq1	25	cat	140.79	140	140.79	0	0	1 446.7	0	0	-=	\	(\)	/(2) \(2)
7459	Taq1	40	tgg	139.98	140	0	0	139.98	0	0	3 300 000	=+	/		/(2) \(2)
7460	Taq1	40	tgg	140.815	140	140.64	0	140.99	18 700 000	0	9 300 000	-+(-)	V (\)	(\)	/(2) \(2)
7461	Hha1	22	tcc	129.3	130	0	0	129.3	0	0	3 700 000	=+	/		/(8)
7462	Hha1	22	tcc	129.85	130	129.85	0	0	3 300 000	0	0	-=	\		/(8)
7463	Taq1	22	tcc	129.68	130	0	0	129.68	0	0	14 500 000	=+	/		/(8)
7464	Taq1	22	tcc	130.72	130	0	0	130.72	0	0	10 200 000	=+	/		/(8)
7465	Hha1	25	cag	130.167	130	130.17	130.17	130.16	10 700 000	10 200 000	7 800 000	==	-		/(8)
7466	Taq1	11	act	163.557	164	163.63	163.71	163.33	5 000 000	3 600 000	22 300 000	=+	/ (-)	/	/(8)
7467	Hha1	11	act	163.677	164	163.77	163.57	163.69	9 000 000	5 300 000	13 200 000	=+	/ (-)	/	/(8)
7468	Taq1	11	act	164.44	164	0	0	164.44	0	0	6 200 000	=+	/	/	/(8)
7469	Hha1	11	act	164.59	164	0	0	164.59	0	0	3 900 000	=+	/	/	/(8)
7470	Taq1	19	cac	163.57	164	0	0	163.57	0	0	20 000 000	=+	/		/(8)
7471	Taq1	19	cac	164.475	164	164.43	0	164.52	3 500 000	0	9 000 000	=+(+)	/		/(8)
7472	Taq1	20	ctc	226.77	228	0	226.77	0	0	3 300 000	0	+-	A		/(8)
7473	Taq1	39	agg	237.885	239	237.68	0	238.09	3 900 000	0	4 500 000	-+(=)	V		/(8)
7474	Taq1	39	agg	238.24	239	0	238.24	0	0	100 400 000	0	+-	A		/(8)
7475	Taq1	39	agg	238.24	239	0	238.24	0	0	1 009.05	0	+-	A		/(8)
7476	Taq1	39	agg	239.18	239	239.24	0	239.12	9 400 000	0	46 900 000	=+(+)	/		/(8)
7477	Taq1	39	agg	237.885	239	237.68	0	238.09	144.83	0	132.54	-+(=)	V		/(8)
7478	Taq1	39	agg	239.18	239	239.24	0	239.12	349.07	0	1 381.44	=+(+)	/		/(8)
7479	Taq1	18	cct	122.39	123	0	0	122.39	0	0	9 400 000	=+	/		/(3)
7480	Taq1	18	cct	123.28	123	123.14	0	123.42	3 300 000	0	5 700 000	-+(=)	V		/(3)
7481	Taq1	22	tcc	124.525	125	0	124.63	124.42	0	10 400 000	54 800 000	=+	/		/(3)
7482	Hha1	22	tcc	124.863	125	124.69	125.12	124.78	32 500 000	3 200 000	3 600 000	-=	\ (-)		/(3)
7483	Taq1	22	tcc	125.597	125	125.44	125.82	125.53	5 300 000	4 700 000	13 300 000	=+	/ (-)		/(3)
7484	Hha1	8	gaa	106.345	106	0	106.18	106.51	0	5 600 000	6 200 000	+=	/	/	

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
7442	AF296762.PE1	nc	putative blood group A transferase T2	*	tct	tca	decreased
7443	AF296762.PE1	nc	putative blood group A transferase T2	*	ttt	tga	decreased
7444	RNO494720.FADS3	fads3	putative fatty acid desaturase		cgc	tgt	No change
7445	RNO494720.FADS3	fads3	putative fatty acid desaturase		cgc	tgt	No change
7446	RNO494720.FADS3	fads3	putative fatty acid desaturase		cgc	tgt	No change
7447	RNO494720.FADS3	fads3	putative fatty acid desaturase		ccc	tcg	No change
7448	RNO494720.FADS3	fads3	putative fatty acid desaturase		ccc	tcg	No change
7449	RNO494720.FADS3	fads3	putative fatty acid desaturase		ccc	tcg	No change
7450	RNGPROCR.PE1	nc	putative G-protein coupled receptor		agg	gac	decreased
7451	RNGPROCR.PE1	nc	putative G-protein coupled receptor		agg	gac	decreased
7452	RNGPROCR.PE1	nc	putative G-protein coupled receptor		atg	ccg	decreased
7453	RNGPROCR.PE1	nc	putative G-protein coupled receptor		atg	ccg	decreased
7454	RNGPROCR.PE1	nc	putative G-protein coupled receptor		atg	ccg	decreased
7455	AF053987.PE1	nc	putative pheromone receptor V2R1		tgg	cat	decreased
7456	AF053987.PE1	nc	putative pheromone receptor V2R1		tgg	cat	decreased
7457	AF053987.PE1	nc	putative pheromone receptor V2R1		tgg	cat	decreased
7458	AF053987.PE1	nc	putative pheromone receptor V2R1		tgg	cat	increased
7459	AF053987.PE1	nc	putative pheromone receptor V2R1		tgg	cat	decreased
7460	AF053987.PE1	nc	putative pheromone receptor V2R1		tgg	cat	increased
7461	AF332004.PE1	nc	putative protein serine/threonine phosphatase		cag	tcc	decreased
7462	AF332004.PE1	nc	putative protein serine/threonine phosphatase		cag	tcc	decreased
7463	AF332004.PE1	nc	putative protein serine/threonine phosphatase		cag	tcc	decreased
7464	AF332004.PE1	nc	putative protein serine/threonine phosphatase		cag	tcc	decreased
7465	AF332004.PE1	nc	putative protein serine/threonine phosphatase		cag	tcc	decreased
7466	AF332004.PE1	nc	putative protein serine/threonine phosphatase		cac	act	decreased
7467	AF332004.PE1	nc	putative protein serine/threonine phosphatase		cac	act	decreased
7468	AF332004.PE1	nc	putative protein serine/threonine phosphatase		cac	act	decreased
7469	AF332004.PE1	nc	putative protein serine/threonine phosphatase		cac	act	decreased
7470	AF332004.PE1	nc	putative protein serine/threonine phosphatase		cac	act	decreased
7471	AF332004.PE1	nc	putative protein serine/threonine phosphatase		cac	act	decreased
7472	AF332004.PE1	nc	putative protein serine/threonine phosphatase		gct	ctc	decreased
7473	AF332004.PE1	nc	putative protein serine/threonine phosphatase		gct	agg	decreased
7474	AF332004.PE1	nc	putative protein serine/threonine phosphatase		gct	agg	decreased
7475	AF332004.PE1	nc	putative protein serine/threonine phosphatase		gct	agg	decreased
7476	AF332004.PE1	nc	putative protein serine/threonine phosphatase		gct	agg	decreased
7477	AF332004.PE1	nc	putative protein serine/threonine phosphatase		gct	agg	decreased
7478	AF332004.PE1	nc	putative protein serine/threonine phosphatase		gct	agg	decreased
7479	AF484685.ATP2C2	Atp2C2	putative secretory pathway Ca-ATPase SPCA2		cct	gta	decreased
7480	AF484685.ATP2C2	Atp2C2	putative secretory pathway Ca-ATPase SPCA2		cct	gta	decreased
7481	AF484685.ATP2C2	Atp2C2	putative secretory pathway Ca-ATPase SPCA2		tcc	gcg	decreased
7482	AF484685.ATP2C2	Atp2C2	putative secretory pathway Ca-ATPase SPCA2		tcc	gcg	decreased
7483	AF484685.ATP2C2	Atp2C2	putative secretory pathway Ca-ATPase SPCA2		tcc	gcg	decreased
7484	AF069511.NBC	NBC	putative sodium bicarbonate cotransporter		gaa	acg	decreased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
7485	Taq1	8	gaa	106.5	106	0	0	106.5	0	0	30 800 000	=+	/	/	
7486	Taq1	8	gaa	99.785	100	100.02	99.55	0	7 200 000	4 400 000	0	=-	\	\	
7487	Hha1	8	gaa	99.967	100	99.94	100.01	99.95	27 900 000	11 900 000	20 600 000	-=	\ (-)	\	
7488	Taq1	51	ata	142.45	143	0	0	142.45	0	0	4 100 000	=+	/		A(3)
7489	Taq1	51	ata	143.11	143	0	143.14	143.08	0	23 500 000	5 000 000	+-	A		A(3)
7490	Taq1	36	ggt	171.453	172	171.36	171.53	171.47	5 800 000	6 900 000	3 200 000	=-	\ (-)		A(3)
7491	Taq1	36	ggt	172.45	172	172.42	172.48	0	4 200 000	8 800 000	0	+-	A	A	A(3)
7492	Taq1	61	tct	171.605	172	171.53	0	171.68	5 100 000	0	5 000 000	-+(=)	V		A(3)
7493	Taq1	61	tct	172.575	172	0	172.51	172.64	0	9 000 000	4 400 000	+-	A	A	A(3)
7494	Hha1	39	agg	70.653	71	70.61	70.7	70.65	13 936.95	471.66	406.9	-=	\ (-)		\(2)
7495	Hha1	43	cgc	156.85	157	0	156.85	0	0	6 300 000	0	+-	A		\(2)
7496	Hha1	43	cgc	157.54	157	157.54	0	0	4 400 000	0	0	-=	\		\(2)
7497	Hha1	33	agc	98.18	98	98.15	98.21	0	3 100 000	3 100 000	0	=-	\		\(2)
7498	Taq1	12	agt	186.95	188	186.95	186.95	186.95	8 900 000	5 800 000	4 200 000	==	-		\(2)
7499	Taq1	12	agt	187.95	188	187.94	187.94	187.97	8 900 000	12 200 000	5 900 000	=-	\ (-)		\(2)
7500	Taq1	12	agt	188.985	188	188.96	189.01	0	5 200 000	4 900 000	0	=-	\		\(2)
7501	Hha1	33	agc	98.18	98	98.15	98.21	0	3 100 000	3 100 000	0	=-	\		\(3)
7502	Hha1	26	ctg	147.13	148	147.09	147.06	147.24	7 700 000	4 900 000	4 100 000	==	-		\(3)
7503	Hha1	26	ctg	148.08	148	0	0	148.08	0	0	3 900 000	=+	/		\(3)
7504	Hha1	39	agg	147.545	148	147.33	0	147.76	256.59	0	264.48	-+(=)	V		\(3)
7505	Hha1	39	agg	148.44	148	148.38	148.5	0	373.9	262.7	0	=-	\		\(3)
7506	Taq1	12	agt	186.95	188	186.95	186.95	186.95	8 900 000	5 800 000	4 200 000	==	-		\(3)
7507	Taq1	12	agt	187.95	188	187.94	187.94	187.97	8 900 000	12 200 000	5 900 000	=-	\ (-)		\(3)
7508	Taq1	12	agt	188.985	188	188.96	189.01	0	5 200 000	4 900 000	0	=-	\		\(3)
7509	Hha1	59	ttc	159.255	160	159.3	159.21	0	161.2	166.72	0	=-	\		\(2)
7510	Hha1	59	ttc	160.1	160	0	160.1	0	0	120.73	0	+-	A		\(2)
7511	Hha1	59	ttc	160.46	160	0	160.31	160.61	0	89.11	85.37	+=	/		\(2)
7512	Hha1	49	aaa	160.525	161	160.71	160.34	0	12 400 000	3 400 000	0	-=	\		\(2)
7513	Hha1	49	aaa	161.79	161	161.67	161.91	0	5 600 000	6 400 000	0	=-	\		\(2)
7514	Taq1	31	gac	137.613	138	137.71	137.51	137.62	10 400 000	5 200 000	17 800 000	=+	/ (-)		-2
7515	Taq1	31	gac	138.627	138	138.72	138.52	138.64	5 100 000	4 700 000	30 400 000	=+	/ (-)		-2
7516	Taq1	61	tct	137.773	138	137.63	137.76	137.93	3 500 000	9 900 000	3 400 000	+-	A		-2
7517	Taq1	61	tct	137.86	138	137.86	0	0	4 000 000	0	0	-=	\		-2
7518	Taq1	12	agt	172.507	173	172.52	172.44	172.56	4 100 000	3 300 000	3 600 000	==	-		-2
7519	Taq1	12	agt	173.553	173	173.55	173.48	173.63	7 100 000	7 700 000	8 100 000	==	-		-2
7520	Taq1	14	gat	173.683	174	173.61	173.61	173.83	5 300 000	5 300 000	6 100 000	==	-	-	
7521	Taq1	22	tcc	173.843	174	173.58	174.03	173.92	5 200 000	6 900 000	8 700 000	==	-	-	
7522	Taq1	9	atc	92.44	92	92.34	92.54	0	8 200 000	5 500 000	0	=-	\		A(5) \(4)
7523	Taq1	56	tga	92.175	92	92.33	0	92.02	3 000 000	0	5 100 000	-+(=)	V		A(5) \(4)
7524	Taq1	56	tga	124.81	125	0	124.81	0	0	9 100 000	0	+-	A		A(5) \(4)
7525	Taq1	49	aaa	140.155	141	139.95	140.36	0	47 800 000	11 900 000	0	-=	\		A(5) \(4)
7526	Taq1	49	aaa	140.69	141	140.75	0	140.63	55 100 000	0	61 000 000	-+(=)	V		A(5) \(4)
7527	Taq1	49	aaa	141.17	141	0	141.17	0	0	14 100 000	0	+-	A		A(5) \(4)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
7485	AF069511.NBC	NBC	putative sodium bicarbonate cotransporter		gaa	acg	decreased
7486	AF144731.YT521	YT521	putative splicing factor YT521-B		gaa	taa	increased
7487	AF144731.YT521	YT521	putative splicing factor YT521-B		gaa	taa	increased
7488	AF181259.LUZP	Luzp	putative transcription factor LUZP		ata	gtg	increased by mild
7489	AF181259.LUZP	Luzp	putative transcription factor LUZP		ata	gtg	increased by mild
7490	AF181259.LUZP	Luzp	putative transcription factor LUZP		ggt	tct	increased by mild
7491	AF181259.LUZP	Luzp	putative transcription factor LUZP		ggt	tct	increased by mild
7492	AF181259.LUZP	Luzp	putative transcription factor LUZP		ggt	tct	increased by mild
7493	AF181259.LUZP	Luzp	putative transcription factor LUZP		ggt	tct	increased by mild
7494	AF154831.PE1	nc	PV-1		agg	act	increased
7495	AF154831.PE1	nc	PV-1		cga	cgc	increased
7496	AF154831.PE1	nc	PV-1		cga	cgc	increased
7497	RNPYB1.PYBP1	PYBP1	pyrimidine binding protein 1		cca	agc	increased
7498	RNPYB1.PYBP1	PYBP1	pyrimidine binding protein 1		agt	tgc	increased
7499	RNPYB1.PYBP1	PYBP1	pyrimidine binding protein 1		agt	tgc	increased
7500	RNPYB1.PYBP1	PYBP1	pyrimidine binding protein 1		agt	tgc	increased
7501	RNPYB2.PYBP2	PYBP2	pyrimidine binding protein 2		cca	agc	increased
7502	RNPYB2.PYBP2	PYBP2	pyrimidine binding protein 2		agg	ctg	increased
7503	RNPYB2.PYBP2	PYBP2	pyrimidine binding protein 2		agg	ctg	increased
7504	RNPYB2.PYBP2	PYBP2	pyrimidine binding protein 2		agg	ctg	increased
7505	RNPYB2.PYBP2	PYBP2	pyrimidine binding protein 2		agg	ctg	increased
7506	RNPYB2.PYBP2	PYBP2	pyrimidine binding protein 2		agt	tgc	increased
7507	RNPYB2.PYBP2	PYBP2	pyrimidine binding protein 2		agt	tgc	increased
7508	RNPYB2.PYBP2	PYBP2	pyrimidine binding protein 2		agt	tgc	increased
7509	AF143410.MEFV	Mefv	pyrin		ttc	aaa	increased
7510	AF143410.MEFV	Mefv	pyrin		ttc	aaa	increased
7511	AF143410.MEFV	Mefv	pyrin		ttc	aaa	increased
7512	AF143410.MEFV	Mefv	pyrin		ttc	aaa	increased
7513	AF143410.MEFV	Mefv	pyrin		ttc	aaa	increased
7514	AF149284.PE1	nc	R8f DNA-binding protein		tct	gac	No change
7515	AF149284.PE1	nc	R8f DNA-binding protein		tct	gac	No change
7516	AF149284.PE1	nc	R8f DNA-binding protein		tct	gac	No change
7517	AF149284.PE1	nc	R8f DNA-binding protein		tct	gac	No change
7518	AF149284.PE1	nc	R8f DNA-binding protein		agt	agc	No change
7519	AF149284.PE1	nc	R8f DNA-binding protein		agt	agc	No change
7520	RNU49058.PE2	nc	rA4		gat	tcc	No change
7521	RNU49058.PE2	nc	rA4		gat	tcc	No change
7522	RNU49055.PE1	nc	rA8		atc	tga	increased by mild
7523	RNU49055.PE1	nc	rA8		atc	tga	increased by mild
7524	RNU49055.PE1	nc	rA8		tga	taa	increased by mild
7525	RNU49055.PE1	nc	rA8		aaa	ttt	increased by mild
7526	RNU49055.PE1	nc	rA8		aaa	ttt	increased by mild
7527	RNU49055.PE1	nc	rA8		aaa	ttt	increased by mild

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
7528	Taq1	49	aaa	141.68	141	141.68	0	0	25 400 000	0	0	-=	\		A(5) \(4)
7529	Taq1	54	ttt	140.24	141	140.26	140.15	140.31	1 383.83	1 622.95	4 004.28	=+	/ (-)		A(5) \(4)
7530	Taq1	54	ttt	140.88	141	140.77	140.99	0	1 128.91	2 128.66	0	+-	A		A(5) \(4)
7531	Taq1	54	ttt	141.39	141	141.28	0	141.5	713.76	0	5 160.59	=+(+)	/		A(5) \(4)
7532	Taq1	61	tct	223.245	224	223.09	223.4	0	3 900 000	4 500 000	0	=-	\		A(5) \(4)
7533	Taq1	61	tct	224.52	224	0	224.52	0	0	7 300 000	0	+-	A		A(5) \(4)
7534	Taq1	50	aat	249.1	250	249.1	0	0	7 800 000	0	0	-=	\		A(5) \(4)
7535	Taq1	50	aat	249.26	250	249.26	0	0	7 400 000	0	0	-=	\		A(5) \(4)
7536	Taq1	50	aat	250.39	250	0	250.39	0	0	3 500 000	0	+-	A		A(5) \(4)
7537	Taq1	50	aat	250.9	250	250.9	0	0	4 700 000	0	0	-=	\		A(5) \(4)
7538	Hha1	8	gaa	166.71	167	166.79	166.67	166.67	5 900 000	11 600 000	8 600 000	+=	/ (-)	/	
7539	Taq1	8	gaa	166.82	167	0	0	166.82	0	0	3 900 000	=+	/	/	
7540	Taq1	39	agg	195.24	196	195.24	0	0	5 700 000	0	0	-=	\		/(2)
7541	Taq1	39	agg	196.265	196	0	196.04	196.49	0	54 300 000	29 200 000	+-	A		/(2)
7542	Taq1	39	agg	195.24	196	195.24	0	0	211.67	0	0	-=	\		/(2)
7543	Taq1	39	agg	196.04	196	0	196.04	0	0	545.73	0	+-	A		/(2)
7544	Taq1	39	agg	196.49	196	0	0	196.49	0	0	860.08	=+	/		/(2)
7545	Taq1	63	ctt	195.14	196	0	0	195.14	0	0	3 300 000	=+	/		/(2)
7546	Taq1	63	ctt	197.17	196	0	0	197.17	0	0	3 100 000	=+	/		/(2)
7547	Taq1	36	ggt	123.405	124	123.33	0	123.48	3 000 000	0	6 900 000	=+(+)	/	/	-1
7548	Taq1	36	ggt	124.65	124	0	0	124.65	0	0	6 100 000	=+	/	/	-1
7549	Taq1	39	agg	123.357	124	123.5	123.11	123.46	16 600 000	48 400 000	30 400 000	+=	/ (-)	/	-1
7550	Taq1	39	agg	123.55	124	0	123.55	0	0	39 600 000	0	+-	A		-1
7551	Taq1	39	agg	124.58	124	124.64	124.48	124.62	11 500 000	33 000 000	92 300 000	=+	/ (-)	/	-1
7552	Taq1	39	agg	123.357	124	123.5	123.11	123.46	616.45	486.43	895.43	=+	/ (-)	/	-1
7553	Taq1	39	agg	123.55	124	0	123.55	0	0	397.99	0	+-	A		-1
7554	Taq1	39	agg	124.58	124	124.64	124.48	124.62	427.06	331.66	2 718.7	=+	/ (-)	/	-1
7555	Hha1	26	ctg	144.19	145	0	0	144.19	0	0	48 200 000	=+	/		-1
7556	Hha1	26	ctg	145.12	145	145.08	145.05	145.23	7 300 000	10 100 000	6 000 000	==	-		-1
7557	Hha1	25	cag	240.613	241	240.57	240.6	240.67	9 700 000	5 800 000	3 200 000	==	-		-1
7558	Hha1	25	cag	241.73	241	241.71	241.75	0	23 300 000	7 200 000	0	-=	\		-1
7559	Hha1	20	ctc	78.76	79	78.76	0	0	557.85	0	0	-=	\	\	\(3)
7560	Hha1	39	agg	78.64	79	78.87	78.41	0	2 023.46	728.4	0	-=	\	\	\(3)
7561	Hha1	39	agg	78.96	79	0	0	78.96	0	0	960.28	=+	/		\(3)
7562	Hha1	39	agg	216.617	217	216.63	216.72	216.5	461.87	220.9	236	-=	\ (-)		\(3)
7563	Hha1	26	ctg	152.34	153	152.25	152.28	152.49	13 300 000	4 100 000	4 700 000	-=	\ (-)		\(3)
7564	Hha1	26	ctg	153.167	153	153.14	153.14	153.22	17 400 000	5 700 000	7 400 000	-=	\ (-)		\(3)
7565	Hha1	28	tcg	152.68	153	152.68	0	0	11 200 000	0	0	-=	\		\(3)
7566	Hha1	28	tcg	153.265	153	0	153.25	153.28	0	13 000 000	7 200 000	+=	/		\(3)
7567	Taq1	12	agt	222.61	223	222.65	222.57	0	3 400 000	4 300 000	0	=-	\		\(3)
7568	Taq1	12	agt	223.58	223	0	223.58	0	0	3 600 000	0	+-	A		\(3)
7569	Hha1	27	acg	94.437	95	94.45	94.44	94.42	22 300 000	8 700 000	10 700 000	-=	\ (-)		\(2)
7570	Hha1	27	acg	95.46	95	95.48	0	95.44	3 400 000	0	3 400 000	-+(=)	V		\(2)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
7528	RNU49055.PE1	nc	rA8		aaa	ttt	increased by mild
7529	RNU49055.PE1	nc	rA8		aaa	ttt	increased by mild
7530	RNU49055.PE1	nc	rA8		aaa	ttt	increased by mild
7531	RNU49055.PE1	nc	rA8		aaa	ttt	increased by mild
7532	RNU49055.PE1	nc	rA8		tca	tct	increased by mild
7533	RNU49055.PE1	nc	rA8		tca	tct	increased by mild
7534	RNU49055.PE1	nc	rA8		ttt	aat	increased by mild
7535	RNU49055.PE1	nc	rA8		ttt	aat	increased by mild
7536	RNU49055.PE1	nc	rA8		ttt	aat	increased by mild
7537	RNU49055.PE1	nc	rA8		ttt	aat	increased by mild
7538	RNU49057.PE1	nc	rA9		gct	gaa	decreased
7539	RNU49057.PE1	nc	rA9		gct	gaa	decreased
7540	RNU18771.PE1	nc	Rab26		ctt	agg	decreased
7541	RNU18771.PE1	nc	Rab26		ctt	agg	decreased
7542	RNU18771.PE1	nc	Rab26		ctt	agg	decreased
7543	RNU18771.PE1	nc	Rab26		ctt	agg	decreased
7544	RNU18771.PE1	nc	Rab26		ctt	agg	decreased
7545	RNU18771.PE1	nc	Rab26		ctt	agg	decreased
7546	RNU18771.PE1	nc	Rab26		ctt	agg	decreased
7547	RNU72995.PE1	nc	Rab3 GDP/GTP exchange protein		ggt	agg	decreased
7548	RNU72995.PE1	nc	Rab3 GDP/GTP exchange protein		ggt	agg	decreased
7549	RNU72995.PE1	nc	Rab3 GDP/GTP exchange protein		ggt	agg	decreased
7550	RNU72995.PE1	nc	Rab3 GDP/GTP exchange protein		ggt	agg	No change
7551	RNU72995.PE1	nc	Rab3 GDP/GTP exchange protein		ggt	agg	decreased
7552	RNU72995.PE1	nc	Rab3 GDP/GTP exchange protein		ggt	agg	decreased
7553	RNU72995.PE1	nc	Rab3 GDP/GTP exchange protein		ggt	agg	No change
7554	RNU72995.PE1	nc	Rab3 GDP/GTP exchange protein		ggt	agg	decreased
7555	RNU72995.PE1	nc	Rab3 GDP/GTP exchange protein		ctg	cgt	No change
7556	RNU72995.PE1	nc	Rab3 GDP/GTP exchange protein		ctg	cgt	No change
7557	RNU72995.PE1	nc	Rab3 GDP/GTP exchange protein		cag	gca	No change
7558	RNU72995.PE1	nc	Rab3 GDP/GTP exchange protein		cag	gca	No change
7559	RNU70777.PE1	nc	rabaptin		agg	ctc	increased
7560	RNU70777.PE1	nc	rabaptin		agg	ctc	increased
7561	RNU70777.PE1	nc	rabaptin		agg	ctc	increased
7562	RNU70777.PE1	nc	rabaptin		agg	tcg	increased
7563	RATRPKBB.PE1	nc	RAC protein kinase beta		ctg	tcg	increased
7564	RATRPKBB.PE1	nc	RAC protein kinase beta		ctg	tcg	increased
7565	RATRPKBB.PE1	nc	RAC protein kinase beta		ctg	tcg	increased
7566	RATRPKBB.PE1	nc	RAC protein kinase beta		ctg	tcg	increased
7567	RATRPKBB.PE1	nc	RAC protein kinase beta		ctc	agt	increased
7568	RATRPKBB.PE1	nc	RAC protein kinase beta		ctc	agt	increased
7569	RNU12187.RAD	rad	Rad		acg	aca	increased
7570	RNU12187.RAD	rad	Rad		acg	aca	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
7571	Hha1	39	agg	133.55	134	0	133.55	0	0	208.96	0	+-	A		\(2)
7572	Hha1	41	ccc	182.45	183	182.45	0	0	4 300 000	0	0	-=	\		\(2)
7573	Hha1	62	tgt	150.41	151	0	150.2	150.62	0	3 300 000	3 900 000	+=	/		\(2) A(2)
7574	Hha1	62	tgt	151.16	151	0	151.16	0	0	3 500 000	0	+-	A		\(2) A(2)
7575	Taq1	62	tgt	189.04	190	0	189.04	0	0	4 100 000	0	+-	A		\(2) A(2)
7576	Taq1	62	tgt	189.87	190	189.87	0	0	3 900 000	0	0	-=	\		\(2) A(2)
7577	Taq1	49	aaa	434.9	434	434.9	0	0	3 900 000	0	0	-=	\		\(2) A(2)
7578	Hha1	4	aag	184.14	185	0	184.18	184.1	0	3 700 000	5 200 000	+=	/	/	/(2)
7579	Hha1	4	aag	185.06	185	0	185.06	0	0	3 000 000	0	+-	A		/(2)
7580	Hha1	4	aag	186.1	185	0	186.14	186.06	0	4 500 000	4 700 000	+=	/		/(2)
7581	Taq1	14	gat	184.14	185	0	0	184.14	0	0	4 100 000	=+	/	/	/(2)
7582	Taq1	14	gat	185.15	185	0	0	185.15	0	0	3 000 000	=+	/		/(2)
7583	Hha1	39	agg	114.915	115	0	115.09	114.74	0	322.4	435.38	+=	/		/(4)
7584	Hha1	40	tgg	150.935	151	150.78	151.09	0	3 200 000	6 300 000	0	+-	A		/(4)
7585	Hha1	40	tgg	151.76	151	151.76	0	0	7 700 000	0	0	-=	\		/(4)
7586	Hha1	4	aag	176.01	177	176.06	0	175.96	18 400 000	0	8 200 000	-=(-)	\		/(4)
7587	Hha1	4	aag	177.077	177	176.99	177.25	176.99	13 100 000	5 600 000	6 300 000	-=	\ (-)		/(4)
7588	Taq1	62	tgt	177.45	177	0	177.55	177.35	0	3 100 000	6 100 000	++	/		/(4)
7589	Hha1	39	agg	183.51	184	0	183.67	183.35	0	220.9	142.41	+=	/		/(4)
7590	Hha1	59	ttc	183.483	184	183.53	183.45	183.47	18 627.141	12 282.97	7 932.11	==	-		/(4)
7591	Taq1	17	cca	210.41	211	210.17	210.65	0	190.4	312.45	0	=-	\		/(4)
7592	Taq1	17	cca	211.557	211	211.33	211.53	211.81	255.42	245.97	511.2	=+	/ (-)		/(4)
7593	Hha1	39	agg	114.915	115	0	115.09	114.74	0	322.4	435.38	+=	/		/(4)
7594	Hha1	40	tgg	150.935	151	150.78	151.09	0	3 200 000	6 300 000	0	+-	A		/(4)
7595	Hha1	40	tgg	151.76	151	151.76	0	0	7 700 000	0	0	-=	\		/(4)
7596	Hha1	4	aag	176.01	177	176.06	0	175.96	18 400 000	0	8 200 000	-=(-)	\		/(4)
7597	Hha1	4	aag	177.077	177	176.99	177.25	176.99	13 100 000	5 600 000	6 300 000	-=	\ (-)		/(4)
7598	Taq1	62	tgt	177.45	177	0	177.55	177.35	0	3 100 000	6 100 000	++	/		/(4)
7599	Hha1	39	agg	183.51	184	0	183.67	183.35	0	220.9	142.41	+=	/		/(4)
7600	Hha1	59	ttc	183.483	184	183.53	183.45	183.47	18 627.141	12 282.97	7 932.11	==	-		/(4)
7601	Taq1	17	cca	210.41	211	210.17	210.65	0	190.4	312.45	0	=-	\		/(4)
7602	Taq1	17	cca	211.557	211	211.33	211.53	211.81	255.42	245.97	511.2	=+	/ (-)		/(4)
7603	Taq1	11	act	186.21	187	186.27	186.2	186.16	4 400 000	4 700 000	10 300 000	=+	/ (-)	(-)	
7604	Hha1	11	act	186.25	187	186.23	186.32	186.2	4 300 000	5 100 000	5 400 000	==	-	(-)	
7605	Taq1	11	act	186.21	187	186.27	186.2	186.16	4 400 000	4 700 000	10 300 000	=+	/ (-)	(-)	
7606	Hha1	11	act	186.25	187	186.23	186.32	186.2	4 300 000	5 100 000	5 400 000	==	-	(-)	
7607	Taq1	56	tga	76.38	76	76.42	0	76.34	25 100 000	0	25 800 000	-+(=)	V		V(2)
7608	Taq1	63	ctt	113.95	114	113.92	0	113.98	3 200 000	0	3 400 000	-+(=)	V		V(2)
7609	Hha1	20	ctc	78.76	79	78.76	0	0	557.85	0	0	-=	\	\	\(3)
7610	Hha1	39	agg	78.64	79	78.87	78.41	0	2 023.46	728.4	0	-=	\	\	\(3)
7611	Hha1	39	agg	78.96	79	0	0	78.96	0	0	960.28	=+	/		\(3)
7612	Hha1	39	agg	216.617	217	216.63	216.72	216.5	461.87	220.9	236	-=	\ (-)		\(3)
7613	Hha1	20	ctc	86.7	87	86.7	0	0	950.41	0	0	-=	\		-2

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
7571	RNU12187.RAD	rad	Rad		aga	agg	increased
7572	RNU12187.RAD	rad	Rad		taa	ccc	increased
7573	AF218576.PE1	nc	Rad50		cgt	tgt	increased
7574	AF218576.PE1	nc	Rad50		cgt	tgt	increased
7575	AF218576.PE1	nc	Rad50		gtc	tgt	increased
7576	AF218576.PE1	nc	Rad50		gtc	tgt	increased
7577	AF218576.PE1	nc	Rad50		aaa	ttt	increased
7578	RNU28830.PE1	nc	RalBP1		gat	aag	decreased
7579	RNU28830.PE1	nc	RalBP1		gat	aag	decreased
7580	RNU28830.PE1	nc	RalBP1		gat	aag	decreased
7581	RNU28830.PE1	nc	RalBP1		gat	aag	decreased
7582	RNU28830.PE1	nc	RalBP1		gat	aag	decreased
7583	RNU11681.RRAFT1	rRAFT1	rapamycin and FKBP12 target-1 protein	*	ggg	agg	decreased
7584	RNU11681.RRAFT1	rRAFT1	rapamycin and FKBP12 target-1 protein	*	tcc	tgg	decreased
7585	RNU11681.RRAFT1	rRAFT1	rapamycin and FKBP12 target-1 protein	*	tcc	tgg	decreased
7586	RNU11681.RRAFT1	rRAFT1	rapamycin and FKBP12 target-1 protein	*	aag	tgt	decreased
7587	RNU11681.RRAFT1	rRAFT1	rapamycin and FKBP12 target-1 protein	*	aag	tgt	decreased
7588	RNU11681.RRAFT1	rRAFT1	rapamycin and FKBP12 target-1 protein	*	aag	tgt	decreased
7589	RNU11681.RRAFT1	rRAFT1	rapamycin and FKBP12 target-1 protein	*	ttc	agg	decreased
7590	RNU11681.RRAFT1	rRAFT1	rapamycin and FKBP12 target-1 protein	*	ttc	agg	decreased
7591	RNU11681.RRAFT1	rRAFT1	rapamycin and FKBP12 target-1 protein	*	gta	cca	decreased
7592	RNU11681.RRAFT1	rRAFT1	rapamycin and FKBP12 target-1 protein	*	gta	cca	decreased
7593	RATRATA.PE1	nc	rapamycin target	*	ggg	agg	decreased
7594	RATRATA.PE1	nc	rapamycin target	*	tcc	tgg	decreased
7595	RATRATA.PE1	nc	rapamycin target	*	tcc	tgg	decreased
7596	RATRATA.PE1	nc	rapamycin target	*	aag	tgt	decreased
7597	RATRATA.PE1	nc	rapamycin target	*	aag	tgt	decreased
7598	RATRATA.PE1	nc	rapamycin target	*	aag	tgt	decreased
7599	RATRATA.PE1	nc	rapamycin target	*	ttc	agg	decreased
7600	RATRATA.PE1	nc	rapamycin target	*	ttc	agg	decreased
7601	RATRATA.PE1	nc	rapamycin target	*	gta	cca	decreased
7602	RATRATA.PE1	nc	rapamycin target	*	gta	cca	decreased
7603	AB019257.PE1	nc	rat brain 4.1(L)		tat	act	No change
7604	AB019257.PE1	nc	rat brain 4.1(L)		tat	act	No change
7605	AB019256.PE1	nc	rat brain 4.1(S)		tat	act	No change
7606	AB019256.PE1	nc	rat brain 4.1(S)		tat	act	No change
7607	RATGCP60.PE1	nc	rat GCP360		gac	tga	decreased by mild
7608	RATGCP60.PE1	nc	rat GCP360		gat	ctt	decreased by mild
7609	D85844.PE1	nc	rat rabaptin-5		agg	ctc	increased
7610	D85844.PE1	nc	rat rabaptin-5		agg	ctc	increased
7611	D85844.PE1	nc	rat rabaptin-5		agg	ctc	increased
7612	D85844.PE1	nc	rat rabaptin-5		agg	tcg	increased
7613	RNRPL36.PE1	nc	rat ribosomal protein L36		ctc	aca	No change

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
7614	Hha1	20	ctc	87.47	87	87.43	87.49	87.49	654.26	970.36	1 514.79	==	-		-2
7615	Hha1	35	gga	130.74	131	130.53	131.02	130.67	4 047.57	2 784.22	2 860.43	==	-		-2
7616	Hha1	35	gga	131.777	131	131.66	132.03	131.64	1 361.97	2 397.52	2 099.19	==	-		-2
7617	Hha1	59	ttc	85.28	85	85.4	85.16	0	962.03	94.86	0	-=	\		\(4)
7618	Hha1	62	tgt	118.66	118	118.69	0	118.63	6 500 000	0	6 400 000	-+(=)	V		\(4)
7619	Hha1	44	cgg	123.83	124	123.83	0	0	13 600 000	0	0	-=	\		\(4)
7620	Hha1	31	gac	125.437	125	125.48	125.45	125.38	8 400 000	4 400 000	4 200 000	-=	\ (-)		\(4)
7621	Hha1	26	ctg	163.42	164	163.39	163.45	0	3 300 000	5 000 000	0	=-	\		\(4)
7622	Taq1	45	gcc	81.755	82	81.62	0	81.89	14 000 000	0	7 400 000	-+(-)	V (\)		\(4)
7623	Taq1	45	gcc	82.24	82	82.18	82.3	0	5 200 000	4 300 000	0	=-	\		\(4)
7624	Hha1	59	ttc	115.51	116	0	115.28	115.74	0	201.21	152.64	+=	/		\(4)
7625	Hha1	59	ttc	116.287	116	116.49	116	116.37	447.21	580.65	155.22	=-	\ (-)		\(4)
7626	Hha1	59	ttc	116.49	116	0	116.49	0	0	117.85	0	+-	A		\(4)
7627	Taq1	34	tgc	144.205	145	144.22	144.19	0	5 700 000	3 200 000	0	=-	\		\(4)
7628	Taq1	40	tgg	144.835	145	144.73	0	144.94	3 200 000	0	25 000 000	=+(+)	/		\(4)
7629	Hha1	8	gaa	286.61	288	286.61	0	0	3 100 000	0	0	-=	\		\(4)
7630	Taq1	45	gcc	81.755	82	81.62	0	81.89	14 000 000	0	7 400 000	-+(-)	V (\)		\(4)
7631	Taq1	45	gcc	82.24	82	82.18	82.3	0	5 200 000	4 300 000	0	=-	\		\(4)
7632	Hha1	59	ttc	115.51	116	0	115.28	115.74	0	201.21	152.64	+=	/		\(4)
7633	Hha1	59	ttc	116.287	116	116.49	116	116.37	447.21	580.65	155.22	=-	\ (-)		\(4)
7634	Hha1	59	ttc	116.49	116	0	116.49	0	0	117.85	0	+-	A		\(4)
7635	Taq1	34	tgc	144.205	145	144.22	144.19	0	5 700 000	3 200 000	0	=-	\		\(4)
7636	Taq1	40	tgg	144.835	145	144.73	0	144.94	3 200 000	0	25 000 000	=+(+)	/		\(4)
7637	Hha1	8	gaa	286.61	288	286.61	0	0	3 100 000	0	0	-=	\		\(4)
7638	Taq1	45	gcc	81.755	82	81.62	0	81.89	14 000 000	0	7 400 000	-+(-)	V (\)		\(4)
7639	Taq1	45	gcc	82.24	82	82.18	82.3	0	5 200 000	4 300 000	0	=-	\		\(4)
7640	Hha1	59	ttc	115.51	116	0	115.28	115.74	0	201.21	152.64	+=	/		\(4)
7641	Hha1	59	ttc	116.287	116	116.49	116	116.37	447.21	580.65	155.22	=-	\ (-)		\(4)
7642	Hha1	59	ttc	116.49	116	0	116.49	0	0	117.85	0	+-	A		\(4)
7643	Taq1	34	tgc	144.205	145	144.22	144.19	0	5 700 000	3 200 000	0	=-	\		\(4)
7644	Taq1	40	tgg	144.835	145	144.73	0	144.94	3 200 000	0	25 000 000	=+(+)	/		\(4)
7645	Hha1	8	gaa	286.61	288	286.61	0	0	3 100 000	0	0	-=	\		\(4)
7646	Hha1	20	ctc	78.76	79	78.76	0	0	557.85	0	0	-=	\		\(5)
7647	Taq1	9	atc	180.007	181	179.95	180.01	180.06	5 900 000	8 600 000	3 200 000	=-	\ (-)		\(5)
7648	Hha1	9	atc	180.32	181	0	180.32	0	0	5 200 000	0	+-	A		\(5)
7649	Hha1	9	atc	180.92	181	180.92	0	0	11 700 000	0	0	-=	\		\(5)
7650	Taq1	29	gca	180.85	181	0	0	180.85	0	0	4 800 000	=+	/		\(5)
7651	Taq1	29	gca	181.89	181	0	0	181.89	0	0	4 100 000	=+	/		\(5)
7652	Hha1	40	tgg	202.96	203	202.96	0	0	4 200 000	0	0	-=	\		\(5)
7653	Taq1	19	cac	249.26	250	249.15	249.32	249.31	3 000 000	3 400 000	3 200 000	==	-		\(5)
7654	Taq1	19	cac	251.21	250	251.21	0	0	3 000 000	0	0	-=	\		\(5)
7655	Taq1	26	ctg	249.92	250	0	0	249.92	0	0	4 600 000	=+	/		\(5)
7656	Hha1	20	ctc	78.76	79	78.76	0	0	557.85	0	0	-=	\		\(5)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
7614	RNRPL36.PE1	nc	rat ribosomal protein L36		ctc	aca	No change
7615	RNRPL36.PE1	nc	rat ribosomal protein L36		cct	gga	No change
7616	RNRPL36.PE1	nc	rat ribosomal protein L36		cct	gga	No change
7617	RATTA2R.PE1	nc	rat thromboxane A2 receptor		ttc	gac	increased
7618	RATTA2R.PE1	nc	rat thromboxane A2 receptor		tgt	cca	increased
7619	RATTA2R.PE1	nc	rat thromboxane A2 receptor		gac	cgg	increased
7620	RATTA2R.PE1	nc	rat thromboxane A2 receptor		gac	cgg	increased
7621	RATTA2R.PE1	nc	rat thromboxane A2 receptor		ctg	tcc	increased
7622	AF041838.ERBB4	ERBB4	receptor tyrosine kinase		gcc	agt	increased
7623	AF041838.ERBB4	ERBB4	receptor tyrosine kinase		gcc	agt	increased
7624	AF041838.ERBB4	ERBB4	receptor tyrosine kinase		ttc	aag	increased
7625	AF041838.ERBB4	ERBB4	receptor tyrosine kinase		ttc	aag	increased
7626	AF041838.ERBB4	ERBB4	receptor tyrosine kinase		ttc	aag	increased
7627	AF041838.ERBB4	ERBB4	receptor tyrosine kinase		tgc	tgg	increased
7628	AF041838.ERBB4	ERBB4	receptor tyrosine kinase		tgc	tgg	increased
7629	AF041838.ERBB4	ERBB4	receptor tyrosine kinase		gaa	ctt	increased
7630	AY375306.ERBB4	Erbb4	receptor tyrosine kinase isoform JMa cyt1		gcc	agt	increased
7631	AY375306.ERBB4	Erbb4	receptor tyrosine kinase isoform JMa cyt1		gcc	agt	increased
7632	AY375306.ERBB4	Erbb4	receptor tyrosine kinase isoform JMa cyt1		ttc	aag	increased
7633	AY375306.ERBB4	Erbb4	receptor tyrosine kinase isoform JMa cyt1		ttc	aag	increased
7634	AY375306.ERBB4	Erbb4	receptor tyrosine kinase isoform JMa cyt1		ttc	aag	increased
7635	AY375306.ERBB4	Erbb4	receptor tyrosine kinase isoform JMa cyt1		tgc	tgg	increased
7636	AY375306.ERBB4	Erbb4	receptor tyrosine kinase isoform JMa cyt1		tgc	tgg	increased
7637	AY375306.ERBB4	Erbb4	receptor tyrosine kinase isoform JMa cyt1		gaa	ctt	increased
7638	AY375307.ERBB4	Erbb4	receptor tyrosine kinase isoform JMa cyt2		gcc	agt	increased
7639	AY375307.ERBB4	Erbb4	receptor tyrosine kinase isoform JMa cyt2		gcc	agt	increased
7640	AY375307.ERBB4	Erbb4	receptor tyrosine kinase isoform JMa cyt2		ttc	aag	increased
7641	AY375307.ERBB4	Erbb4	receptor tyrosine kinase isoform JMa cyt2		ttc	aag	increased
7642	AY375307.ERBB4	Erbb4	receptor tyrosine kinase isoform JMa cyt2		ttc	aag	increased
7643	AY375307.ERBB4	Erbb4	receptor tyrosine kinase isoform JMa cyt2		tgc	tgg	increased
7644	AY375307.ERBB4	Erbb4	receptor tyrosine kinase isoform JMa cyt2		tgc	tgg	increased
7645	AY375307.ERBB4	Erbb4	receptor tyrosine kinase isoform JMa cyt2		gaa	ctt	increased
7646	AF402785.VEGFR3	Vegfr3	receptor tyrosine kinase VEGFR-3		ctc	aga	increased
7647	AF402785.VEGFR3	Vegfr3	receptor tyrosine kinase VEGFR-3		atc	gca	increased
7648	AF402785.VEGFR3	Vegfr3	receptor tyrosine kinase VEGFR-3		atc	gca	increased
7649	AF402785.VEGFR3	Vegfr3	receptor tyrosine kinase VEGFR-3		atc	gca	increased
7650	AF402785.VEGFR3	Vegfr3	receptor tyrosine kinase VEGFR-3		atc	gca	increased
7651	AF402785.VEGFR3	Vegfr3	receptor tyrosine kinase VEGFR-3		atc	gca	increased
7652	AF402785.VEGFR3	Vegfr3	receptor tyrosine kinase VEGFR-3		tgg	cac	increased
7653	AF402785.VEGFR3	Vegfr3	receptor tyrosine kinase VEGFR-3		ctg	cac	increased
7654	AF402785.VEGFR3	Vegfr3	receptor tyrosine kinase VEGFR-3		ctg	cac	increased
7655	AF402785.VEGFR3	Vegfr3	receptor tyrosine kinase VEGFR-3		ctg	cac	increased
7656	AF402786.VEGFR3	Vegfr3	receptor tyrosine kinase VEGFR-3kt		ctc	aga	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
7657	Taq1	9	atc	180.007	181	179.95	180.01	180.06	5 900 000	8 600 000	3 200 000	=-	\ (-)		\(5)
7658	Hha1	9	atc	180.32	181	0	180.32	0	0	5 200 000	0	+-	A		\(5)
7659	Hha1	9	atc	180.92	181	180.92	0	0	11 700 000	0	0	-=	\		\(5)
7660	Taq1	29	gca	180.85	181	0	0	180.85	0	0	4 800 000	=+	/		\(5)
7661	Taq1	29	gca	181.89	181	0	0	181.89	0	0	4 100 000	=+	/		\(5)
7662	Hha1	40	tgg	202.96	203	202.96	0	0	4 200 000	0	0	-=	\		\(5)
7663	Taq1	19	cac	249.26	250	249.15	249.32	249.31	3 000 000	3 400 000	3 200 000	==	-		\(5)
7664	Taq1	19	cac	251.21	250	251.21	0	0	3 000 000	0	0	-=	\		\(5)
7665	Taq1	26	ctg	249.92	250	0	0	249.92	0	0	4 600 000	=+	/		\(5)
7666	Hha1	9	atc	141.147	141	140.98	141.22	141.24	34 400 000	9 400 000	4 400 000	-=	\ (-)	(-)	
7667	Taq1	9	atc	141.32	141	141.34	141.25	141.37	6 600 000	5 100 000	6 500 000	==	-	(-)	
7668	Hha1	9	atc	141.147	141	140.98	141.22	141.24	34 400 000	9 400 000	4 400 000	-=	\ (-)	(-)	
7669	Taq1	9	atc	141.32	141	141.34	141.25	141.37	6 600 000	5 100 000	6 500 000	==	-	(-)	
7670	Hha1	33	agc	61.923	62	61.88	61.97	61.92	37 200 000	64 600 000	37 900 000	==	-		-2
7671	Hha1	27	acg	93.515	94	93.45	0	93.58	5 600 000	0	3 700 000	-+(=)	V		-2
7672	Hha1	27	acg	94.437	94	94.45	94.44	94.42	22 300 000	8 700 000	10 700 000	-=	\ (-)		-2
7673	Hha1	9	atc	122.9	123	122.82	122.98	0	55 200 000	16 800 000	0	-=	\	\	
7674	Taq1	9	atc	123.077	123	123.34	122.9	122.99	11 000 000	5 900 000	10 700 000	-=	\ (-)	\	
7675	Hha1	11	act	142.36	143	0	0	142.36	0	0	5 600 000	=+	/	/	
7676	Taq1	11	act	142.53	143	142.43	0	142.63	3 000 000	0	42 500 000	=+(+)	/	/	
7677	Hha1	11	act	143.3	143	143.29	143.26	143.35	7 600 000	5 700 000	14 500 000	=+	/ (-)	/	
7678	Taq1	11	act	143.46	143	143.38	143.28	143.72	5 200 000	3 900 000	13 300 000	=+	/ (-)	/	
7679	Hha1	9	atc	122.9	123	122.82	122.98	0	55 200 000	16 800 000	0	-=	\	\	
7680	Taq1	9	atc	123.077	123	123.34	122.9	122.99	11 000 000	5 900 000	10 700 000	-=	\ (-)	\	
7681	Hha1	11	act	142.36	143	0	0	142.36	0	0	5 600 000	=+	/	/	
7682	Taq1	11	act	142.53	143	142.43	0	142.63	3 000 000	0	42 500 000	=+(+)	/	/	
7683	Hha1	11	act	143.3	143	143.29	143.26	143.35	7 600 000	5 700 000	14 500 000	=+	/ (-)	/	
7684	Taq1	11	act	143.46	143	143.38	143.28	143.72	5 200 000	3 900 000	13 300 000	=+	/ (-)	/	
7685	Hha1	4	aag	135.755	136	135.78	0	135.73	44 900 000	0	3 500 000	-=(-)	\	\	/(2) \(2)
7686	Taq1	29	gca	135.507	136	135.56	135.44	135.52	24 600 000	19 200 000	8 000 000	=-	\ (-)	\	/(2) \(2)
7687	Taq1	29	gca	136.547	136	136.54	136.49	136.61	6 000 000	3 900 000	8 100 000	=+	/ (-)		/(2) \(2)
7688	Taq1	62	tgt	177.45	178	0	177.55	177.35	0	3 100 000	6 100 000	++	/		/(2) \(2)
7689	Taq1	62	tgt	178.47	178	0	178.65	178.29	0	3 000 000	9 300 000	=+	/		/(2) \(2)
7690	Taq1	45	gcc	170.59	171	170.59	0	0	4 500 000	0	0	-=	\		\(2)
7691	Taq1	45	gcc	171.75	171	171.59	0	171.91	3 200 000	0	7 100 000	-+(+)	V (/)		\(2)
7692	Taq1	39	agg	171.09	172	171.09	0	0	14 500 000	0	0	-=	\		\(2)
7693	Taq1	39	agg	171.44	172	171.44	0	0	12 200 000	0	0	-=	\		\(2)
7694	Taq1	39	agg	172.98	172	173.19	172.77	0	7 500 000	35 200 000	0	+-	A		\(2)
7695	Taq1	39	agg	171.09	172	171.09	0	0	538.47	0	0	-=	\		\(2)
7696	Taq1	39	agg	171.44	172	171.44	0	0	453.06	0	0	-=	\		\(2)
7697	Taq1	39	agg	172.77	172	0	172.77	0	0	353.77	0	+-	A		\(2)
7698	Hha1	8	gaa	238.66	239	238.83	238.49	0	4 500 000	3 100 000	0	=-	\		\(2)
7699	Taq1	50	aat	240.36	240	240.36	0	0	3 800 000	0	0	-=	\		\(2)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
7657	AF402786.VEGFR3	Vegfr3	receptor tyrosine kinase VEGFR-3kt		atc	gca	increased
7658	AF402786.VEGFR3	Vegfr3	receptor tyrosine kinase VEGFR-3kt		atc	gca	increased
7659	AF402786.VEGFR3	Vegfr3	receptor tyrosine kinase VEGFR-3kt		atc	gca	increased
7660	AF402786.VEGFR3	Vegfr3	receptor tyrosine kinase VEGFR-3kt		atc	gca	increased
7661	AF402786.VEGFR3	Vegfr3	receptor tyrosine kinase VEGFR-3kt		atc	gca	increased
7662	AF402786.VEGFR3	Vegfr3	receptor tyrosine kinase VEGFR-3kt		tgg	cac	increased
7663	AF402786.VEGFR3	Vegfr3	receptor tyrosine kinase VEGFR-3kt		ctg	cac	increased
7664	AF402786.VEGFR3	Vegfr3	receptor tyrosine kinase VEGFR-3kt		ctg	cac	increased
7665	AF402786.VEGFR3	Vegfr3	receptor tyrosine kinase VEGFR-3kt		ctg	cac	increased
7666	AB049473.RELN	Reln	reelin		ctt	atc	No change
7667	AB049473.RELN	Reln	reelin		ctt	atc	No change
7668	AB062680.RELN	Reln	reelin		ctt	atc	No change
7669	AB062680.RELN	Reln	reelin		ctt	atc	No change
7670	AF318578.RBP1	Rbp1	reg I binding protein I		cga	agc	No change
7671	AF318578.RBP1	Rbp1	reg I binding protein I		tgt	acg	No change
7672	AF318578.RBP1	Rbp1	reg I binding protein I		tgt	acg	No change
7673	AF320224S2.PE1	nc	retinal homeobox transcription factor Rx/rax		agc	atc	increased
7674	AF320224S2.PE1	nc	retinal homeobox transcription factor Rx/rax		agc	atc	increased
7675	AF320224S2.PE1	nc	retinal homeobox transcription factor Rx/rax		agg	act	decreased
7676	AF320224S2.PE1	nc	retinal homeobox transcription factor Rx/rax		agg	act	decreased
7677	AF320224S2.PE1	nc	retinal homeobox transcription factor Rx/rax		agg	act	decreased
7678	AF320224S2.PE1	nc	retinal homeobox transcription factor Rx/rax		agg	act	decreased
7679	AF320224S2.PE2	nc	retinal homeobox transcription factor Rx/rax		agc	atc	increased
7680	AF320224S2.PE2	nc	retinal homeobox transcription factor Rx/rax		agc	atc	increased
7681	AF320224S2.PE2	nc	retinal homeobox transcription factor Rx/rax		agg	act	decreased
7682	AF320224S2.PE2	nc	retinal homeobox transcription factor Rx/rax		agg	act	decreased
7683	AF320224S2.PE2	nc	retinal homeobox transcription factor Rx/rax		agg	act	decreased
7684	AF320224S2.PE2	nc	retinal homeobox transcription factor Rx/rax		agg	act	decreased
7685	AF035673.RPE65	Rpe65	retinal pigment epithelium-specific protein		gca	aag	increased
7686	AF035673.RPE65	Rpe65	retinal pigment epithelium-specific protein		gca	aag	increased
7687	AF035673.RPE65	Rpe65	retinal pigment epithelium-specific protein		gca	aag	decreased
7688	AF035673.RPE65	Rpe65	retinal pigment epithelium-specific protein		tgt	aca	decreased
7689	AF035673.RPE65	Rpe65	retinal pigment epithelium-specific protein		tgt	aca	decreased
7690	AY178865.PE1	nc	retinol dehydrogenase 10		gcc	agg	increased
7691	AY178865.PE1	nc	retinol dehydrogenase 10		gcc	agg	increased
7692	AY178865.PE1	nc	retinol dehydrogenase 10		gcc	agg	increased
7693	AY178865.PE1	nc	retinol dehydrogenase 10		gcc	agg	increased
7694	AY178865.PE1	nc	retinol dehydrogenase 10		gcc	agg	increased
7695	AY178865.PE1	nc	retinol dehydrogenase 10		gcc	agg	increased
7696	AY178865.PE1	nc	retinol dehydrogenase 10		gcc	agg	increased
7697	AY178865.PE1	nc	retinol dehydrogenase 10		gcc	agg	increased
7698	RNSDEAR4.PE1	Rev-erb-Beta	Rev-erb-Beta2		gaa	aat	increased
7699	RNSDEAR4.PE1	Rev-erb-Beta	Rev-erb-Beta2		gaa	aat	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
7700	Hha1	3	aac	196.405	196	196.4	196.41	0	5 900 000	3 100 000	0	--	\		\(2)
7701	Taq1	12	agt	194.985	196	195.06	194.91	0	3 200 000	4 300 000	0	=-	\		\(2)
7702	Taq1	12	agt	196.133	196	196.14	196.06	196.2	5 600 000	5 800 000	3 800 000	==	-		\(2)
7703	Taq1	12	agt	197.037	196	197.09	197.06	196.96	4 200 000	4 900 000	3 300 000	==	-		\(2)
7704	Taq1	26	ctg	116.05	116	116.04	116	116.11	3 700 000	5 800 000	5 200 000	==	-	-	-2
7705	Taq1	57	ctg	115.863	116	115.82	115.82	115.95	23 100 000	20 800 000	33 000 000	==	-	-	-2
7706	Taq1	45	gcc	86.003	86	85.99	85.93	86.09	14 600 000	21 500 000	4 600 000	=-	\ (-)		\(2)
7707	Taq1	45	gcc	86.44	86	86.44	0	0	12 700 000	0	0	-=	\		\(2)
7708	Hha1	6	aga	242.38	241	242.38	0	0	5 800 000	0	0	-=	\		\(2)
7709	Hha1	20	ctc	222.675	224	222.7	222.65	0	323.69	1 193.28	0	+-	A		-2
7710	Hha1	20	ctc	223.71	224	223.67	223.76	223.7	1 887.05	2 045.63	2 242.36	==	-		-2
7711	Hha1	20	ctc	224.77	224	0	0	224.77	0	0	441.31	=+	/		-2
7712	Hha1	61	tct	222.903	224	222.89	222.92	222.9	145 900 000	74 900 000	90 600 000	-=	\ (-)		-2
7713	Hha1	61	tct	223.88	224	223.85	223.91	0	10 500 000	7 000 000	0	=-	\		-2
7714	Hha1	61	tct	225.16	224	225.29	0	225.03	5 900 000	0	5 600 000	-+(=)	V		-2
7715	Hha1	61	tct	225.05	224	225.05	0	0	6 200 000	0	0	-=	\		-2
7716	Taq1	9	atc	139.227	140	139.17	139.12	139.39	17 300 000	17 800 000	3 300 000	=-	\ (-)	\	
7717	Hha1	9	atc	139.297	140	139.19	139.37	139.33	17 200 000	20 700 000	9 300 000	=-	\ (-)	\	
7718	Hha1	20	ctc	79.795	80	79.87	0	79.72	365.01	0	417.46	-+(=)	V		V(3)
7719	Hha1	59	ttc	79.593	80	79.5	79.64	79.64	4 362.97	2 230.65	2 129.2	-=	\ (-)		V(3)
7720	Hha1	59	ttc	80.225	80	80.31	0	80.14	2 028.08	0	1 836.85	-+(=)	V		V(3)
7721	Taq1	8	gaa	87.73	88	87.91	87.49	87.79	5 300 000	38 700 000	32 000 000	+=	/ (-)		V(3)
7722	Hha1	27	acg	92.385	92	92.23	0	92.54	8 600 000	0	4 700 000	-+(-)	V (\)		V(3)
7723	Hha1	11	act	143.3	144	143.29	143.26	143.35	7 600 000	5 700 000	14 500 000	=+	/ (-)	/	/(3)
7724	Taq1	11	act	143.46	144	143.38	143.28	143.72	5 200 000	3 900 000	13 300 000	=+	/ (-)	/	/(3)
7725	Taq1	11	act	144.575	144	144.5	0	144.65	5 900 000	0	32 000 000	=+(+)	/		/(3)
7726	Taq1	63	ctt	143.15	144	0	0	143.15	0	0	3 000 000	=+	/		/(3)
7727	Taq1	63	ctt	144.2	144	0	0	144.2	0	0	5 100 000	=+	/		/(3)
7728	Taq1	10	atg	275.11	275	275.11	0	0	3 400 000	0	0	-=	\		/(3)
7729	Taq1	10	atg	276.09	275	276.09	0	0	3 900 000	0	0	-=	\		/(3)
7730	Hha1	44	cgg	242.14	243	242.19	242.08	242.15	38 600 000	5 400 000	22 100 000	-=	\ (-)		\(2)
7731	Hha1	44	cgg	243.22	243	0	0	243.22	0	0	5 400 000	=+	/		\(2)
7732	Hha1	54	ttt	244.455	245	244.49	0	244.42	30 800 000	0	11 200 000	-=(-)	\		\(2)
7733	Hha1	54	ttt	245.35	245	245.35	0	0	4 900 000	0	0	-=	\		\(2)
7734	Taq1	45	gcc	162.66	162	0	162.66	0	0	6 800 000	0	+-	A		A(2)
7735	Taq1	12	agt	177.703	178	177.74	177.55	177.82	7 000 000	12 900 000	6 800 000	+-	A		A(2)
7736	Taq1	12	agt	178.63	178	178.69	178.63	178.57	4 400 000	7 600 000	3 800 000	=-	\ (-)		A(2)
7737	Taq1	29	gca	177.79	178	0	0	177.79	0	0	4 000 000	=+	/		A(2)
7738	Taq1	29	gca	178.75	178	178.78	0	178.72	3 100 000	0	3 800 000	-+(=)	V		A(2)
7739	Hha1	26	ctg	97.47	97	0	97.47	0	0	4 100 000	0	+-	A		/(2)
7740	Hha1	59	ttc	97.02	97	0	97.18	96.86	0	114.98	385.48	=+	/		/(2)
7741	Hha1	59	ttc	188.09	189	188.19	188.04	188.04	1 180.44	741.63	388.06	==	-		/(2)
7742	Hha1	59	ttc	189.127	189	189.18	189.08	189.12	509.62	129.35	183.68	-=	\ (-)		/(2)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
7700	AB060653.RGPR	RGPR	RGPR-p117		agt	aac	increased
7701	AB060653.RGPR	RGPR	RGPR-p117		agt	aac	increased
7702	AB060653.RGPR	RGPR	RGPR-p117		agt	aac	increased
7703	AB060653.RGPR	RGPR	RGPR-p117		agt	aac	increased
7704	AB006013.PE1	nc	RGS8		ctg	tat	No change
7705	AB006013.PE1	nc	RGS8		ctg	tat	No change
7706	RNU61266.PE1	nc	Rho-associated kinase beta		ctc	gcc	increased
7707	RNU61266.PE1	nc	Rho-associated kinase beta		ctc	gcc	increased
7708	RNU61266.PE1	nc	Rho-associated kinase beta		aga	gga	increased
7709	AY348868.PE1	nc	rhotekin isoform 2		tct	ctc	No change
7710	AY348868.PE1	nc	rhotekin isoform 2		tct	ctc	No change
7711	AY348868.PE1	nc	rhotekin isoform 2		tct	ctc	No change
7712	AY348868.PE1	nc	rhotekin isoform 2		tct	ctc	No change
7713	AY348868.PE1	nc	rhotekin isoform 2		tct	ctc	No change
7714	AY348868.PE1	nc	rhotekin isoform 2		tct	ctc	No change
7715	AY348868.PE1	nc	rhotekin isoform 2		tct	ctc	No change
7716	AF222712.PE1	nc	ribeye		atc	atc	increased
7717	AF222712.PE1	nc	ribeye		atc	atc	increased
7718	RNRIBI.PE1	nc	ribophorin I		ctc	ttc	decreased by mild
7719	RNRIBI.PE1	nc	ribophorin I		ctc	ttc	decreased by mild
7720	RNRIBI.PE1	nc	ribophorin I		ctc	ttc	decreased by mild
7721	RNRIBI.PE1	nc	ribophorin I		gaa	tct	decreased by mild
7722	RNRIBI.PE1	nc	ribophorin I		acg	cag	decreased by mild
7723	RRRIBOII.PE1	ribophorin II	ribophorin II		ctt	act	decreased
7724	RRRIBOII.PE1	ribophorin II	ribophorin II		ctt	act	decreased
7725	RRRIBOII.PE1	ribophorin II	ribophorin II		ctt	act	decreased
7726	RRRIBOII.PE1	ribophorin II	ribophorin II		ctt	act	decreased
7727	RRRIBOII.PE1	ribophorin II	ribophorin II		ctt	act	decreased
7728	RRRIBOII.PE1	ribophorin II	ribophorin II		atg	tct	decreased
7729	RRRIBOII.PE1	ribophorin II	ribophorin II		atg	tct	decreased
7730	RNL19RP.RPL19	RPL19	ribosomal protein L19	*	cgg	ttt	increased
7731	RNL19RP.RPL19	RPL19	ribosomal protein L19	*	cgg	ttt	increased
7732	RNL19RP.RPL19	RPL19	ribosomal protein L19	*	cgg	ttt	increased
7733	RNL19RP.RPL19	RPL19	ribosomal protein L19	*	cgg	ttt	increased
7734	RNL4.PE1	nc	ribosomal protein L4		ccg	gcc	increased by mild
7735	RNL4.PE1	nc	ribosomal protein L4		gca	agt	increased by mild
7736	RNL4.PE1	nc	ribosomal protein L4		gca	agt	increased by mild
7737	RNL4.PE1	nc	ribosomal protein L4		gca	agt	increased by mild
7738	RNL4.PE1	nc	ribosomal protein L4		gca	agt	increased by mild
7739	BC058149.PE1	nc	ribosomal protein S6		ctg	ttc	decreased
7740	BC058149.PE1	nc	ribosomal protein S6		ctg	ttc	decreased
7741	BC058149.PE1	nc	ribosomal protein S6		cca	ttc	decreased
7742	BC058149.PE1	nc	ribosomal protein S6		cca	ttc	decreased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
7743	Hha1	59	ttc	189.69	189	0	189.52	189.86	0	152.35	1 249.57	=+	/		/(2)
7744	Hha1	59	ttc	190.04	189	190.04	0	0	327.61	0	0	-=	\		/(2)
7745	Hha1	26	ctg	98.71	99	0	0	98.71	0	0	4 900 000	=+	/		A(2) \(2)
7746	Hha1	26	ctg	99.44	99	99.53	99.35	0	10 500 000	4 000 000	0	-=	\		A(2) \(2)
7747	Taq1	54	ttt	106.78	107	106.7	106.86	0	480.69	1 070.21	0	+-	A		A(2) \(2)
7748	Taq1	54	ttt	107.32	107	107.43	107.21	0	473.41	1 011.4	0	+-	A		A(2) \(2)
7749	Taq1	49	aaa	381.8	382	0	381.8	0	0	9 100 000	0	+-	A		A(2) \(2)
7750	Taq1	49	aaa	383.05	382	383.05	0	0	30 700 000	0	0	-=	\		A(2) \(2)
7751	Taq1	8	gaa	300.225	299	300.21	300.24	0	3 900 000	3 000 000	0	=-	\		\(2)
7752	Taq1	39	agg	299.4	300	299.45	299.35	0	330.51	177.89	0	--	\		\(2)
7753	Taq1	39	agg	299.91	300	299.91	0	0	334.22	0	0	-=	\		\(2)
7754	Taq1	8	gaa	79.77	80	79.63	0	79.91	8 400 000	0	7 400 000	-+(=)	V		\(2)
7755	Taq1	8	gaa	80.205	80	80.18	80.23	0	4 500 000	6 200 000	0	=-	\		\(2)
7756	Hha1	6	aga	151.28	152	151.28	0	0	25 900 000	0	0	-=	\		\(2)
7757	Hha1	6	aga	151.84	152	0	151.84	0	0	5 700 000	0	+-	A		\(2)
7758	Hha1	56	tga	184.103	185	183.99	184.19	184.13	388.18	187.14	1 310.11	=+	/ (-)		\(2)
7759	Hha1	56	tga	185.11	185	0	185.2	185.02	0	181.63	999.82	=+	/		\(2)
7760	Hha1	56	tga	186	185	185.91	186.09	186	424.95	176.13	982.58	=+	/ (-)		\(2)
7761	Hha1	8	gaa	114.817	115	114.81	114.79	114.85	13 300 000	15 500 000	8 300 000	=-	\ (-)		\(7)
7762	Taq1	8	gaa	115.33	115	0	115.33	0	0	3 100 000	0	+-	A		\(7)
7763	Taq1	40	tgg	114.37	115	0	0	114.37	0	0	17 700 000	=+	/		\(7)
7764	Taq1	40	tgg	115.43	115	0	0	115.43	0	0	7 900 000	=+	/		\(7)
7765	Hha1	27	acg	129.31	129	129.32	129.25	129.36	18 400 000	7 000 000	12 600 000	-=	\ (-)		\(7)
7766	Taq1	44	cgg	131.987	132	131.84	132.23	131.89	996.42	1 823.27	941.49	+-	A		\(7)
7767	Taq1	44	cgg	132.4	132	132.4	0	0	864.49	0	0	-=	\		\(7)
7768	Hha1	57	cta	175.613	176	175.58	175.66	175.6	2 609.44	928.91	377.84	-=	\ (-)		\(7)
7769	Hha1	57	cta	176.53	176	176.58	176.48	0	1 466.46	565.42	0	-=	\		\(7)
7770	Hha1	25	cag	220.41	220	0	220.52	220.3	0	11 700 000	5 200 000	+-	A		\(7)
7771	Hha1	25	cag	220.96	220	220.96	0	0	18 600 000	0	0	-=	\		\(7)
7772	Taq1	39	agg	219.085	220	218.98	219.19	0	23 800 000	61 600 000	0	+-	A		\(7)
7773	Taq1	39	agg	219.965	220	219.91	220.02	0	6 900 000	66 700 000	0	+-	A		\(7)
7774	Taq1	39	agg	220.56	220	220.56	0	0	6 900 000	0	0	-=	\		\(7)
7775	Taq1	39	agg	218.98	220	218.98	0	0	883.83	0	0	-=	\		\(7)
7776	Taq1	39	agg	219.91	220	219.91	0	0	256.23	0	0	-=	\		\(7)
7777	Taq1	39	agg	220.56	220	220.56	0	0	256.23	0	0	-=	\		\(7)
7778	Taq1	39	agg	221.2	220	0	221.2	0	0	228 600 000	0	+-	A		\(7)
7779	Taq1	39	agg	219.19	220	0	219.19	0	0	619.1	0	+-	A		\(7)
7780	Taq1	39	agg	220.02	220	0	220.02	0	0	670.35	0	+-	A		\(7)
7781	Taq1	39	agg	221.2	220	0	221.2	0	0	2 297.51	0	+-	A		\(7)
7782	Hha1	6	aga	242.38	241	242.38	0	0	5 800 000	0	0	-=	\		\(7)
7783	Taq1	8	gaa	99.785	100	100.02	99.55	0	7 200 000	4 400 000	0	=-	\	\	
7784	Hha1	8	gaa	99.967	100	99.94	100.01	99.95	27 900 000	11 900 000	20 600 000	-=	\ (-)	\	
7785	Taq1	39	agg	210.71	211	0	210.71	0	0	9 200 000	0	+-	A		A(2) \(2)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
7743	BC058149.PE1	nc	ribosomal protein S6		cca	ttc	decreased
7744	BC058149.PE1	nc	ribosomal protein S6		cca	ttc	decreased
7745	RNRPS8MR.PE1	nc	ribosomal protein S8		caa	ctg	increased by mild
7746	RNRPS8MR.PE1	nc	ribosomal protein S8		caa	ctg	increased by mild
7747	RNRPS8MR.PE1	nc	ribosomal protein S8		gct	ttt	increased by mild
7748	RNRPS8MR.PE1	nc	ribosomal protein S8		gct	ttt	increased by mild
7749	RNRPS8MR.PE1	nc	ribosomal protein S8		aaa	cct	increased by mild
7750	RNRPS8MR.PE1	nc	ribosomal protein S8		aaa	cct	increased by mild
7751	RATRA301.PE1	nc	RNA binding protein (transformer-2-like)		ttt	gaa	increased
7752	RATRA301.PE1	nc	RNA binding protein (transformer-2-like)		agg	ccc	increased
7753	RATRA301.PE1	nc	RNA binding protein (transformer-2-like)		agg	ccc	increased
7754	RNU25746.PE1	nc	RNA helicase		gaa	aaa	increased
7755	RNU25746.PE1	nc	RNA helicase		gaa	aaa	increased
7756	RNU25746.PE1	nc	RNA helicase		aga	tca	increased
7757	RNU25746.PE1	nc	RNA helicase		aga	tca	increased
7758	RNU25746.PE1	nc	RNA helicase		tga	atg	increased
7759	RNU25746.PE1	nc	RNA helicase		tga	atg	increased
7760	RNU25746.PE1	nc	RNA helicase		tga	atg	increased
7761	AF025424.PE1	nc	RNA polymerase I 127 kDa subunit		gaa	tgg	increased
7762	AF025424.PE1	nc	RNA polymerase I 127 kDa subunit		gaa	tgg	increased
7763	AF025424.PE1	nc	RNA polymerase I 127 kDa subunit		gaa	tgg	increased
7764	AF025424.PE1	nc	RNA polymerase I 127 kDa subunit		gaa	tgg	increased
7765	AF025424.PE1	nc	RNA polymerase I 127 kDa subunit		acg	tca	increased
7766	AF025424.PE1	nc	RNA polymerase I 127 kDa subunit		ccg	cgg	increased
7767	AF025424.PE1	nc	RNA polymerase I 127 kDa subunit		ccg	cgg	increased
7768	AF025424.PE1	nc	RNA polymerase I 127 kDa subunit		cta	caa	increased
7769	AF025424.PE1	nc	RNA polymerase I 127 kDa subunit		cta	caa	increased
7770	AF025424.PE1	nc	RNA polymerase I 127 kDa subunit		cag	agg	increased
7771	AF025424.PE1	nc	RNA polymerase I 127 kDa subunit		cag	agg	increased
7772	AF025424.PE1	nc	RNA polymerase I 127 kDa subunit		cag	agg	increased
7773	AF025424.PE1	nc	RNA polymerase I 127 kDa subunit		cag	agg	increased
7774	AF025424.PE1	nc	RNA polymerase I 127 kDa subunit		cag	agg	increased
7775	AF025424.PE1	nc	RNA polymerase I 127 kDa subunit		cag	agg	increased
7776	AF025424.PE1	nc	RNA polymerase I 127 kDa subunit		cag	agg	increased
7777	AF025424.PE1	nc	RNA polymerase I 127 kDa subunit		cag	agg	increased
7778	AF025424.PE1	nc	RNA polymerase I 127 kDa subunit		cag	agg	increased
7779	AF025424.PE1	nc	RNA polymerase I 127 kDa subunit		cag	agg	increased
7780	AF025424.PE1	nc	RNA polymerase I 127 kDa subunit		cag	agg	increased
7781	AF025424.PE1	nc	RNA polymerase I 127 kDa subunit		cag	agg	increased
7782	AF025424.PE1	nc	RNA polymerase I 127 kDa subunit		ttt	aga	increased
7783	D78303.YT521	YT521	RNA splicing-related protein		gaa	taa	increased
7784	D78303.YT521	YT521	RNA splicing-related protein		gaa	taa	increased
7785	AB023966.ROD1	ROD1	Rod1		aaa	agg	increased by mild

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
7786	Taq1	39	agg	211.56	211	211.56	0	0	9 900 000	0	0	-=	\		A(2) \(2)
7787	Taq1	39	agg	211.56	211	211.56	0	0	367.64	0	0	-=	\		A(2) \(2)
7788	Taq1	39	agg	210.71	211	0	210.71	0	0	92.46	0	+-	A		A(2) \(2)
7789	Taq1	49	aaa	211.115	212	211.05	211.18	0	14 200 000	25 500 000	0	=-	\		A(2) \(2)
7790	Taq1	49	aaa	211.827	212	211.97	211.89	211.62	3 400 000	18 000 000	3 900 000	+-	A		A(2) \(2)
7791	Taq1	49	aaa	213.1	212	0	213.1	0	0	6 800 000	0	+-	A		A(2) \(2)
7792	Hha1	20	ctc	62.935	63	0	63.07	62.8	0	1 101.49	1 300.09	+=	/		\(2)
7793	Taq1	49	aaa	211.115	212	211.05	211.18	0	14 200 000	25 500 000	0	=-	\		\(2)
7794	Taq1	49	aaa	211.827	212	211.97	211.89	211.62	3 400 000	18 000 000	3 900 000	+-	A		\(2)
7795	Taq1	49	aaa	213.1	212	0	213.1	0	0	6 800 000	0	+-	A		\(2)
7796	Taq1	52	att	211.475	212	211.56	211.39	0	6 400 000	4 500 000	0	=-	\		\(2)
7797	Taq1	35	gga	123.8	124	0	0	123.8	0	0	3 500 000	=+	/		/(2)
7798	Taq1	35	gga	124.71	124	0	0	124.71	0	0	3 600 000	=+	/		/(2)
7799	Hha1	4	aag	129.81	130	0	129.83	129.79	0	6 200 000	3 800 000	+=	/		/(2)
7800	Taq1	31	gac	129.22	130	0	129.22	0	0	9 500 000	0	+-	A		/(2)
7801	Taq1	31	gac	130.415	130	130.52	130.31	0	7 400 000	6 800 000	0	=-	\		/(2)
7802	Hha1	43	cgc	129.77	129	0	0	129.77	0	0	14 400 000	=+	/		\(2)
7803	Hha1	41	ccc	182.45	183	182.45	0	0	4 300 000	0	0	-=	\		\(2)
7804	Hha1	44	cgg	239.245	238	239.27	0	239.22	10 700 000	0	4 900 000	-+(-)	V (\)		\(2)
7805	Taq1	22	tcc	216.755	217	0	216.82	216.69	0	3 200 000	3 100 000	+=	/		\(3)
7806	Taq1	22	tcc	217.46	217	0	217.46	0	0	5 700 000	0	+-	A		\(3)
7807	Taq1	22	tcc	218.27	217	218.11	218.43	0	9 300 000	3 800 000	0	-=	\		\(3)
7808	Hha1	25	cag	216.557	217	216.61	216.33	216.73	64 000 000	9 800 000	18 200 000	-=	\ (-)		\(3)
7809	Taq1	17	cca	314.59	314	314.59	0	0	139.32	0	0	-=	\		\(3)
7810	Hha1	39	agg	73.733	74	73.74	73.57	73.89	4 428.15	12 096.24	4 785.15	+-	A		/(2)
7811	Hha1	56	tga	166.463	167	166.5	166.68	166.21	130.75	203.65	1 086.01	=+	/ (-)		/(2)
7812	Hha1	56	tga	167.52	167	167.48	167.56	0	371.83	374.28	0	=-	\		/(2)
7813	Hha1	59	ttc	167.38	167	0	167.38	167.38	0	215.59	2 054.17	=+	/		/(2)
7814	Hha1	33	agc	84.25	84	0	0	84.25	0	0	8 900 000	=+	/		\(2)
7815	Hha1	39	agg	88.14	88	88.14	0	0	755.13	0	0	-=	\		\(2)
7816	Hha1	26	ctg	217.95	219	217.95	0	0	4 400 000	0	0	-=	\		\(2)
7817	Hha1	7	caa	192.13	192	192.24	192.02	0	6 100 000	3 000 000	0	--	\	\	
7818	Taq1	7	caa	192.28	192	192.28	0	0	3 300 000	0	0	-=	\	\	
7819	Hha1	39	agg	169.657	170	169.84	169.79	169.34	2 126.09	555.25	524.9	-=	\ (-)		\(2)
7820	Taq1	29	gca	227.715	227	227.65	227.78	0	3 000 000	3 100 000	0	=-	\		\(2)
7821	Hha1	39	agg	169.657	170	169.84	169.79	169.34	2 126.09	555.25	524.9	-=	\ (-)		\(2)
7822	Taq1	29	gca	227.715	227	227.65	227.78	0	3 000 000	3 100 000	0	=-	\		\(2)
7823	Hha1	20	ctc	81.21	81	0	81.21	0	0	1 337.52	0	+-	A		\(4)
7824	Hha1	64	gtt	80.81	81	80.81	0	0	3 100 000	0	0	-=	\		\(4)
7825	Taq1	12	agt	185.92	187	185.96	185.84	185.96	10 800 000	9 700 000	8 600 000	==	-		\(4)
7826	Taq1	12	agt	186.95	187	186.95	186.95	186.95	8 900 000	5 800 000	4 200 000	==	-		\(4)
7827	Taq1	12	agt	187.95	187	187.94	187.94	187.97	8 900 000	12 200 000	5 900 000	=-	\ (-)		\(4)
7828	Taq1	17	cca	186.01	187	185.78	186.24	0	260.06	465.36	0	=-	\		\(4)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
7786	AB023966.ROD1	ROD1	Rod1		aaa	agg	increased by mild
7787	AB023966.ROD1	ROD1	Rod1		aaa	agg	increased by mild
7788	AB023966.ROD1	ROD1	Rod1		aaa	agg	increased by mild
7789	AB023966.ROD1	ROD1	Rod1		aaa	agg	increased by mild
7790	AB023966.ROD1	ROD1	Rod1		aaa	agg	increased by mild
7791	AB023966.ROD1	ROD1	Rod1		aaa	agg	increased by mild
7792	RNU38481.PE1	nc	ROK-alpha		ggg	ctc	increased
7793	RNU38481.PE1	nc	ROK-alpha		aaa	att	increased
7794	RNU38481.PE1	nc	ROK-alpha		aaa	att	increased
7795	RNU38481.PE1	nc	ROK-alpha		aaa	att	increased
7796	RNU38481.PE1	nc	ROK-alpha		aaa	att	increased
7797	AB016532.RPER2	rPer2	rPER2		gga	gtc	decreased
7798	AB016532.RPER2	rPer2	rPER2		gga	gtc	decreased
7799	AB016532.RPER2	rPer2	rPER2		gac	aag	decreased
7800	AB016532.RPER2	rPer2	rPER2		gac	aag	decreased
7801	AB016532.RPER2	rPer2	rPER2		gac	aag	decreased
7802	RNU77931.PE1	nc	rRNA promoter binding protein		cct	cgc	increased
7803	RNU77931.PE1	nc	rRNA promoter binding protein		ccc	cgg	increased
7804	RNU77931.PE1	nc	rRNA promoter binding protein		cgg	ggg	increased
7805	AF032666.PE1	nc	rsec5		tcc	cag	increased
7806	AF032666.PE1	nc	rsec5		tcc	cag	increased
7807	AF032666.PE1	nc	rsec5		tcc	cag	increased
7808	AF032666.PE1	nc	rsec5		tcc	cag	increased
7809	AF032666.PE1	nc	rsec5		gac	cca	increased
7810	AB019576.PE1	nc	rTIM		agg	cag	decreased
7811	AB019576.PE1	nc	rTIM		ttc	tga	decreased
7812	AB019576.PE1	nc	rTIM		ttc	tga	decreased
7813	AB019576.PE1	nc	rTIM		ttc	tga	decreased
7814	AF334162.PE1	nc	RTP801		tcc	agc	increased
7815	AF334162.PE1	nc	RTP801		ctg	agg	increased
7816	AF334162.PE1	nc	RTP801		gag	ctg	increased
7817	AB006914.PE1	nc	salt-tolerant protein		caa	gtc	increased
7818	AB006914.PE1	nc	salt-tolerant protein		caa	gtc	increased
7819	RATSANTI.PE1	nc	S-antigen		ctt	agg	increased
7820	RATSANTI.PE1	nc	S-antigen		tcg	gca	increased
7821	RNSAGMR.S-AG	S-Ag	S-antigen		ctt	agg	increased
7822	RNSAGMR.S-AG	S-Ag	S-antigen		tcg	gca	increased
7823	RNU27562.PE1	nc	SC1 protein		ctc	gtt	increased
7824	RNU27562.PE1	nc	SC1 protein		ctc	gtt	increased
7825	RNU27562.PE1	nc	SC1 protein		cca	agt	increased
7826	RNU27562.PE1	nc	SC1 protein		cca	agt	increased
7827	RNU27562.PE1	nc	SC1 protein		cca	agt	increased
7828	RNU27562.PE1	nc	SC1 protein		cca	agt	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
7829	Taq1	17	cca	187.32	187	187.3	187.34	0	185.76	285.86	0	=-	\		\(4)
7830	Taq1	17	cca	187.57	187	187.57	0	0	148.6	0	0	-=	\		\(4)
7831	Taq1	50	aat	263.305	264	263.07	263.54	0	7 400 000	4 900 000	0	=-	\		\(4)
7832	Taq1	50	aat	264.4	264	264.29	264.51	0	3 300 000	4 800 000	0	=-	\		\(4)
7833	Hha1	33	agc	60.14	60	0	60.14	0	0	4 600 000	0	+-	A		V(2)
7834	Hha1	31	gac	79.737	80	79.73	79.76	79.72	86 200 000	16 800 000	89 400 000	-+	V		V(2)
7835	Hha1	31	gac	146.27	146	146.34	0	146.2	3 700 000	0	4 900 000	-+(=)	V		V(2)
7836	Hha1	20	ctc	120.853	121	120.78	120.99	120.79	2 561.98	1 114.6	512.88	-=	\ (-)		-2
7837	Hha1	40	tgg	120.58	121	0	120.52	120.64	0	5 500 000	6 800 000	+=	/		-2
7838	Hha1	40	tgg	121.487	121	121.74	121.29	121.43	8 400 000	4 900 000	4 000 000	==	-		-2
7839	Hha1	33	agc	67.933	68	67.9	68.03	67.87	4 300 000	8 100 000	32 400 000	=+	/ (-)		-1
7840	Hha1	20	ctc	91.505	92	0	91.62	91.39	0	904.79	584.44	+=	/		-1
7841	Hha1	20	ctc	92.38	92	92.45	92.39	92.3	2 031.68	1 507.99	1 312.02	==	-		-1
7842	Hha1	7	caa	255.95	256	255.95	0	0	6 600 000	0	0	-=	\		\(2)
7843	Taq1	7	caa	256.42	256	0	256.42	0	0	3 700 000	0	+-	A		\(2)
7844	Hha1	7	caa	257.12	256	257.12	0	0	8 200 000	0	0	-=	\		\(2)
7845	Taq1	21	acc	151.12	152	0	151.03	151.21	0	5 700 000	5 900 000	+=	/	/	
7846	Hha1	21	acc	151.31	152	0	151.34	151.28	0	7 400 000	4 900 000	+=	/	/	
7847	Taq1	56	tga	131.19	131	0	0	131.19	0	0	4 700 000	=+	/	/	
7848	Taq1	63	ctt	131.04	131	0	0	131.04	0	0	3 300 000	=+	/	/	
7849	Hha1	33	agc	66.89	67	66.93	66.98	66.76	12 300 000	23 100 000	248 400 000	=+	/ (-)		-1
7850	Taq1	31	gac	136.6	137	136.69	136.54	136.57	9 200 000	8 100 000	6 800 000	==	-		-1
7851	Taq1	31	gac	137.613	137	137.71	137.51	137.62	10 400 000	5 200 000	17 800 000	=+	/ (-)		-1
7852	Hha1	27	acg	77.433	77	77.42	77.47	77.41	37 200 000	27 700 000	98 400 000	=+	/ (-)		\(4)
7853	Hha1	39	agg	76.73	77	76.8	76.51	76.88	549.85	1 540.39	329.58	+-	A		\(4)
7854	Hha1	40	tgg	124.83	125	124.6	125.06	0	7 700 000	7 300 000	0	=-	\		\(4)
7855	Hha1	40	tgg	125.75	125	125.75	0	0	42 700 000	0	0	-=	\		\(4)
7856	Hha1	40	tgg	130.81	131	130.81	0	0	4 400 000	0	0	-=	\		\(4)
7857	Hha1	6	aga	177.05	178	0	0	177.05	0	0	9 400 000	=+	/		\(4)
7858	Hha1	6	aga	177.935	178	177.81	0	178.06	3 900 000	0	10 900 000	=+(+)	/	/	\(4)
7859	Hha1	6	aga	178.07	178	178.07	0	0	4 000 000	0	0	-=	\		\(4)
7860	Taq1	18	cct	177.895	178	0	177.91	177.88	0	3 000 000	3 400 000	+=	/	/	\(4)
7861	Taq1	18	cct	178.855	178	178.85	178.86	0	8 200 000	4 700 000	0	=-	\		\(4)
7862	Taq1	31	gac	120.267	120	120.41	120.16	120.23	7 500 000	4 100 000	71 600 000	=+	/ (-)		-2
7863	Taq1	62	tgt	119.57	120	119.52	119.61	119.58	5 300 000	3 900 000	6 800 000	==	-		-2
7864	Taq1	62	tgt	120.55	120	120.53	120.61	120.51	4 300 000	8 300 000	9 100 000	==	-		-2
7865	Taq1	1	tat	118.535	119	118.61	118.46	0	5 400 000	5 600 000	0	=-	\		-(4) \(4)
7866	Taq1	1	tat	119.56	119	0	119.56	0	0	5 300 000	0	+-	A		-(4) \(4)
7867	Hha1	3	aac	120.607	121	120.55	120.7	120.57	7 100 000	8 300 000	3 700 000	=-	\ (-)		-(4) \(4)
7868	Hha1	3	aac	121.393	121	121.39	121.42	121.37	33 500 000	37 100 000	6 600 000	=-	\ (-)		-(4) \(4)
7869	Hha1	6	aga	121.083	121	121.14	121.23	120.88	15 100 000	6 600 000	6 200 000	-=	\ (-)		-(4) \(4)
7870	Taq1	29	gca	146.79	147	0	0	146.79	0	0	7 500 000	=+	/		-(4) \(4)
7871	Taq1	29	gca	147.773	147	147.75	147.76	147.81	5 600 000	4 700 000	6 600 000	==	-		-(4) \(4)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
7829	RNU27562.PE1	nc	SC1 protein		cca	agt	increased
7830	RNU27562.PE1	nc	SC1 protein		cca	agt	increased
7831	RNU27562.PE1	nc	SC1 protein		tga	aat	increased
7832	RNU27562.PE1	nc	SC1 protein		tga	aat	increased
7833	RNSC65MR.PE1	nc	Sc65 synaptonemal complex protein		tgc	agc	decreased by mild
7834	RNSC65MR.PE1	nc	Sc65 synaptonemal complex protein		gac	gta	decreased by mild
7835	RNSC65MR.PE1	nc	Sc65 synaptonemal complex protein		gac	cca	decreased by mild
7836	AY004290.PE1	nc	scg10-like-protein		tgg	ctc	No change
7837	AY004290.PE1	nc	scg10-like-protein		tgg	ctc	No change
7838	AY004290.PE1	nc	scg10-like-protein		tgg	ctc	No change
7839	AF326741.PE1	nc	sclerostin		agc	cgc	No change
7840	AF326741.PE1	nc	sclerostin		ctc	ggt	No change
7841	AF326741.PE1	nc	sclerostin		ctc	ggt	No change
7842	RNRNASCP3.SCP3	SCP3	SCP3 protein		caa	aca	increased
7843	RNRNASCP3.SCP3	SCP3	SCP3 protein		caa	aca	increased
7844	RNRNASCP3.SCP3	SCP3	SCP3 protein		caa	aca	increased
7845	AF226993.PE1	nc	selective LIM binding factor		aga	acc	decreased
7846	AF226993.PE1	nc	selective LIM binding factor		aga	acc	decreased
7847	AF086624.PIM-3	pim-3	serine threonine kinase		ctt	tga	decreased
7848	AF086624.PIM-3	pim-3	serine threonine kinase		ctt	tga	decreased
7849	RNMARK2.MARK2	mark2	serine/threonine kinase		agc	cgc	No change
7850	RNMARK2.MARK2	mark2	serine/threonine kinase		gac	gct	No change
7851	RNMARK2.MARK2	mark2	serine/threonine kinase		gac	gct	No change
7852	AB010154.SBK	sbk	serine/threonine protein kinase		acg	agg	increased
7853	AB010154.SBK	sbk	serine/threonine protein kinase		acg	agg	increased
7854	AB010154.SBK	sbk	serine/threonine protein kinase		tgg	cag	increased
7855	AB010154.SBK	sbk	serine/threonine protein kinase		tgg	cag	increased
7856	AB010154.SBK	sbk	serine/threonine protein kinase		tgg	ggt	increased
7857	AB010154.SBK	sbk	serine/threonine protein kinase		cct	aga	increased
7858	AB010154.SBK	sbk	serine/threonine protein kinase		cct	aga	decreased
7859	AB010154.SBK	sbk	serine/threonine protein kinase		cct	aga	increased
7860	AB010154.SBK	sbk	serine/threonine protein kinase		cct	aga	decreased
7861	AB010154.SBK	sbk	serine/threonine protein kinase		cct	aga	increased
7862	RATSGPK.PE1	nc	serine/threonine protein kinase		gac	tgt	No change
7863	RATSGPK.PE1	nc	serine/threonine protein kinase		gac	tgt	No change
7864	RATSGPK.PE1	nc	serine/threonine protein kinase		gac	tgt	No change
7865	AF084205.PE1	nc	serine/threonine protein kinase TAO1		gag	tat	No change
7866	AF084205.PE1	nc	serine/threonine protein kinase TAO1		gag	tat	No change
7867	AF084205.PE1	nc	serine/threonine protein kinase TAO1		aac	aga	No change
7868	AF084205.PE1	nc	serine/threonine protein kinase TAO1		aac	aga	No change
7869	AF084205.PE1	nc	serine/threonine protein kinase TAO1		aac	aga	No change
7870	AF084205.PE1	nc	serine/threonine protein kinase TAO1		gag	gca	No change
7871	AF084205.PE1	nc	serine/threonine protein kinase TAO1		gag	gca	No change

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
7872	Hha1	6	aga	165.59	166	165.63	165.53	165.61	7 400 000	4 900 000	5 400 000	==	-		-(4) \(4)
7873	Hha1	6	aga	166.585	166	166.62	0	166.55	6 200 000	0	4 300 000	-+(=)	V		-(4) \(4)
7874	Taq1	49	aaa	166.595	167	166.65	166.54	0	31 700 000	13 800 000	0	-=	\		-(4) \(4)
7875	Taq1	49	aaa	167.645	167	167.55	167.74	0	7 100 000	12 700 000	0	=-	\		-(4) \(4)
7876	Taq1	20	ctc	166.32	166	0	166.32	0	0	3 700 000	0	+-	A	A	A(3)
7877	Taq1	63	ctt	166.23	166	0	166.23	0	0	3 000 000	0	+-	A	A	A(3)
7878	Hha1	40	tgg	191.925	193	191.73	192.12	0	3 900 000	4 200 000	0	=-	\		A(3)
7879	Hha1	40	tgg	193.56	193	0	193.56	0	0	5 600 000	0	+-	A		A(3)
7880	Hha1	40	tgg	193.88	193	0	193.88	0	0	3 900 000	0	+-	A		A(3)
7881	Hha1	10	atg	201.445	202	201.33	201.56	0	9 200 000	3 400 000	0	-=	\		\(4)
7882	Taq1	10	atg	201.73	202	201.73	0	0	3 700 000	0	0	-=	\		\(4)
7883	Hha1	10	atg	202.34	202	202.34	0	0	3 200 000	0	0	-=	\		\(4)
7884	Taq1	39	agg	201.075	202	201.22	200.93	0	11 500 000	11 100 000	0	=-	\		\(4)
7885	Taq1	39	agg	201.935	202	201.96	201.91	0	8 700 000	38 600 000	0	+-	A		\(4)
7886	Taq1	39	agg	202.85	202	202.85	0	0	8 800 000	0	0	-=	\		\(4)
7887	Taq1	39	agg	201.075	202	201.22	200.93	0	427.06	111.55	0	-=	\		\(4)
7888	Taq1	39	agg	201.935	202	201.96	201.91	0	323.08	387.94	0	=-	\		\(4)
7889	Taq1	39	agg	202.85	202	202.85	0	0	326.79	0	0	-=	\		\(4)
7890	Taq1	18	cct	113.567	114	113.4	113.59	113.71	10 100 000	9 800 000	6 400 000	==	-	(-)	-2
7891	Taq1	18	cct	114.52	114	114.5	114.54	114.52	21 700 000	29 300 000	7 500 000	=-	\ (-)	(-)	-2
7892	Taq1	20	ctc	113.383	114	113.37	113.27	113.51	5 700 000	4 400 000	37 800 000	=+	/ (-)	(-)	-2
7893	Taq1	20	ctc	114.437	114	114.43	114.38	114.5	3 300 000	5 500 000	8 900 000	==	-	(-)	-2
7894	Hha1	20	ctc	78.76	79	78.76	0	0	557.85	0	0	-=	\		\(2)
7895	Hha1	20	ctc	148.52	149	148.52	0	0	268.59	0	0	-=	\		\(2)
7896	Hha1	20	ctc	78.76	79	78.76	0	0	557.85	0	0	-=	\		\(2)
7897	Hha1	20	ctc	148.52	149	148.52	0	0	268.59	0	0	-=	\		\(2)
7898	Hha1	40	tgg	157.975	158	157.8	158.15	0	7 600 000	10 900 000	0	=-	\		\(2)
7899	Hha1	40	tgg	158.805	158	159.02	0	158.59	4 200 000	0	4 000 000	-+(=)	V		\(2)
7900	Hha1	62	tgt	157.33	158	157.33	0	0	3 500 000	0	0	-=	\		\(2)
7901	Taq1	47	ggc	119.735	120	119.73	119.74	0	2 215.38	1 750.47	0	=-	\		\(2)
7902	Taq1	47	ggc	120.71	120	120.68	120.74	0	2 830.76	1 241.24	0	-=	\		\(2)
7903	Hha1	60	ttg	144.88	145	144.91	144.85	0	8 300 000	9 000 000	0	=-	\		\(2)
7904	Hha1	60	ttg	145.557	145	145.4	145.86	145.41	5 100 000	7 700 000	4 100 000	=-	\ (-)		\(2)
7905	Taq1	56	tga	78.733	79	78.58	79.04	78.58	23 900 000	5 500 000	3 400 000	-=	\ (-)		-(4) /(3) \(3)
7906	Taq1	12	agt	121.123	121	121.11	121.1	121.16	4 100 000	4 200 000	4 800 000	==	-		-(4) /(3) \(3)
7907	Taq1	40	tgg	120.38	121	120.22	120.32	120.6	5 900 000	107 000 000	9 700 000	+-	A		-(4) /(3) \(3)
7908	Taq1	40	tgg	120.94	121	120.79	121.09	0	22 800 000	13 300 000	0	=-	\		-(4) /(3) \(3)
7909	Taq1	40	tgg	121.58	121	0	0	121.58	0	0	8 700 000	=+	/		-(4) /(3) \(3)
7910	Taq1	62	tgt	120.55	121	120.53	120.61	120.51	4 300 000	8 300 000	9 100 000	==	-		-(4) /(3) \(3)
7911	Taq1	62	tgt	121.485	121	121.49	0	121.48	3 400 000	0	10 100 000	=+(+)	/		-(4) /(3) \(3)
7912	Taq1	49	aaa	170.027	171	169.83	170.12	170.13	9 600 000	4 900 000	3 400 000	-=	\ (-)		-(4) /(3) \(3)
7913	Taq1	49	aaa	171.005	171	0	170.94	171.07	0	12 900 000	58 400 000	=+	/		-(4) /(3) \(3)
7914	Taq1	49	aaa	171.86	171	172	171.76	171.82	64 500 000	9 700 000	4 200 000	-=	\ (-)		-(4) /(3) \(3)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
7872	AF084205.PE1	nc	serine/threonine protein kinase TAO1		aaa	aga	No change
7873	AF084205.PE1	nc	serine/threonine protein kinase TAO1		aaa	aga	No change
7874	AF084205.PE1	nc	serine/threonine protein kinase TAO1		aaa	aga	No change
7875	AF084205.PE1	nc	serine/threonine protein kinase TAO1		aaa	aga	No change
7876	AF140556.TAO2	tao2	serine/threonine protein kinase TAO2		ctc	ctt	increased by mild
7877	AF140556.TAO2	tao2	serine/threonine protein kinase TAO2		ctc	ctt	increased by mild
7878	AF140556.TAO2	tao2	serine/threonine protein kinase TAO2		aag	tgg	increased by mild
7879	AF140556.TAO2	tao2	serine/threonine protein kinase TAO2		aag	tgg	increased by mild
7880	AF140556.TAO2	tao2	serine/threonine protein kinase TAO2		aag	tgg	increased by mild
7881	RNCALCA.PE1	calcineurin A (	serine/threonine specific protein phosphatase		atg	agg	increased
7882	RNCALCA.PE1	calcineurin A (	serine/threonine specific protein phosphatase		atg	agg	increased
7883	RNCALCA.PE1	calcineurin A (	serine/threonine specific protein phosphatase		atg	agg	increased
7884	RNCALCA.PE1	calcineurin A (	serine/threonine specific protein phosphatase		atg	agg	increased
7885	RNCALCA.PE1	calcineurin A (	serine/threonine specific protein phosphatase		atg	agg	increased
7886	RNCALCA.PE1	calcineurin A (	serine/threonine specific protein phosphatase		atg	agg	increased
7887	RNCALCA.PE1	calcineurin A (	serine/threonine specific protein phosphatase		atg	agg	increased
7888	RNCALCA.PE1	calcineurin A (	serine/threonine specific protein phosphatase		atg	agg	increased
7889	RNCALCA.PE1	calcineurin A (	serine/threonine specific protein phosphatase		atg	agg	increased
7890	RAT5HT1D.PE1	nc	serotonin receptor		cct	ctc	No change
7891	RAT5HT1D.PE1	nc	serotonin receptor		cct	ctc	No change
7892	RAT5HT1D.PE1	nc	serotonin receptor		cct	ctc	No change
7893	RAT5HT1D.PE1	nc	serotonin receptor		cct	ctc	No change
7894	AF274872.SRY1	Sry1	sex-determining region Y protein	*	ccc	ctc	increased
7895	AF274872.SRY1	Sry1	sex-determining region Y protein	*	aag	ctc	increased
7896	AF275682.SRY3	Sry3	sex-determining region Y protein	*	ccc	ctc	increased
7897	AF275682.SRY3	Sry3	sex-determining region Y protein	*	aag	ctc	increased
7898	AF468653.PE1	nc	SH2 phosphatase 1		tgg	tgt	increased
7899	AF468653.PE1	nc	SH2 phosphatase 1		tgg	tgt	increased
7900	AF468653.PE1	nc	SH2 phosphatase 1		tgg	tgt	increased
7901	AB025794.PE1	nc	SH2-containing inositol phosphatase 2 (SHIP2)		ggc	agc	increased
7902	AB025794.PE1	nc	SH2-containing inositol phosphatase 2 (SHIP2)		ggc	agc	increased
7903	AB025794.PE1	nc	SH2-containing inositol phosphatase 2 (SHIP2)		tat	ttg	increased
7904	AB025794.PE1	nc	SH2-containing inositol phosphatase 2 (SHIP2)		tat	ttg	increased
7905	AF131867.SETA	Seta	SH3 domain-containing adapter protein		gga	tga	No change
7906	AF131867.SETA	Seta	SH3 domain-containing adapter protein		tgt	agt	No change
7907	AF131867.SETA	Seta	SH3 domain-containing adapter protein		ttg	tgg	No change
7908	AF131867.SETA	Seta	SH3 domain-containing adapter protein		ttg	tgg	No change
7909	AF131867.SETA	Seta	SH3 domain-containing adapter protein		ttg	tgg	No change
7910	AF131867.SETA	Seta	SH3 domain-containing adapter protein		tgt	agt	No change
7911	AF131867.SETA	Seta	SH3 domain-containing adapter protein		tgt	agt	No change
7912	AF131867.SETA	Seta	SH3 domain-containing adapter protein		aaa	tgc	No change
7913	AF131867.SETA	Seta	SH3 domain-containing adapter protein		aaa	tgc	No change
7914	AF131867.SETA	Seta	SH3 domain-containing adapter protein		aaa	tgc	No change

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
7915	Taq1	12	agt	121.123	121	121.11	121.1	121.16	4 100 000	4 200 000	4 800 000	==	-		-1
7916	Taq1	40	tgg	120.38	121	120.22	120.32	120.6	5 900 000	107 000 000	9 700 000	+-	A		-1
7917	Taq1	40	tgg	120.94	121	120.79	121.09	0	22 800 000	13 300 000	0	=-	\		-1
7918	Taq1	40	tgg	121.58	121	0	0	121.58	0	0	8 700 000	=+	/		-1
7919	Taq1	62	tgt	120.55	121	120.53	120.61	120.51	4 300 000	8 300 000	9 100 000	==	-		-1
7920	Taq1	62	tgt	121.485	121	121.49	0	121.48	3 400 000	0	10 100 000	=+(+)	/		-1
7921	Taq1	49	aaa	170.027	171	169.83	170.12	170.13	9 600 000	4 900 000	3 400 000	-=	\ (-)		-1
7922	Taq1	49	aaa	171.005	171	0	170.94	171.07	0	12 900 000	58 400 000	=+	/		-1
7923	Taq1	49	aaa	171.86	171	172	171.76	171.82	64 500 000	9 700 000	4 200 000	-=	\ (-)		-1
7924	Taq1	56	tga	78.733	79	78.58	79.04	78.58	23 900 000	5 500 000	3 400 000	-=	\ (-)		-(4) /(3) \(3)
7925	Taq1	12	agt	121.123	121	121.11	121.1	121.16	4 100 000	4 200 000	4 800 000	==	-		-(4) /(3) \(3)
7926	Taq1	40	tgg	120.38	121	120.22	120.32	120.6	5 900 000	107 000 000	9 700 000	+-	A		-(4) /(3) \(3)
7927	Taq1	40	tgg	120.94	121	120.79	121.09	0	22 800 000	13 300 000	0	=-	\		-(4) /(3) \(3)
7928	Taq1	40	tgg	121.58	121	0	0	121.58	0	0	8 700 000	=+	/		-(4) /(3) \(3)
7929	Taq1	62	tgt	120.55	121	120.53	120.61	120.51	4 300 000	8 300 000	9 100 000	==	-		-(4) /(3) \(3)
7930	Taq1	62	tgt	121.485	121	121.49	0	121.48	3 400 000	0	10 100 000	=+(+)	/		-(4) /(3) \(3)
7931	Taq1	49	aaa	170.027	171	169.83	170.12	170.13	9 600 000	4 900 000	3 400 000	-=	\ (-)		-(4) /(3) \(3)
7932	Taq1	49	aaa	171.005	171	0	170.94	171.07	0	12 900 000	58 400 000	=+	/		-(4) /(3) \(3)
7933	Taq1	49	aaa	171.86	171	172	171.76	171.82	64 500 000	9 700 000	4 200 000	-=	\ (-)		-(4) /(3) \(3)
7934	Taq1	27	acg	105.725	106	105.69	105.76	0	3 000 000	3 400 000	0	=-	\		-(3) /(3) \(3)
7935	Taq1	27	acg	106.547	106	106.58	106.57	106.49	8 100 000	3 800 000	12 600 000	=+	/ (-)	(/)	-(3) /(3) \(3)
7936	Taq1	50	aat	106.475	107	106.5	0	106.45	11 500 000	0	21 700 000	-+(+)	V (/)	(/)	-(3) /(3) \(3)
7937	Taq1	50	aat	107.43	107	0	107.44	107.42	0	21 200 000	4 000 000	+-	A		-(3) /(3) \(3)
7938	Taq1	30	cgt	132.237	133	132.2	132.28	132.23	3 400 000	3 300 000	4 600 000	==	-		-(3) /(3) \(3)
7939	Taq1	30	cgt	133.28	133	133.24	133.32	0	4 400 000	4 400 000	0	=-	\		-(3) /(3) \(3)
7940	Taq1	36	ggt	132.707	133	132.69	132.69	132.74	26 200 000	38 000 000	7 200 000	=-	\ (-)		-(3) /(3) \(3)
7941	Taq1	17	cca	160.5	161	160.51	0	160.49	190.4	0	451.05	=+(+)	/		-(3) /(3) \(3)
7942	Taq1	17	cca	161.493	161	161.51	161.44	161.53	636.23	212.73	872.04	-+	V		-(3) /(3) \(3)
7943	Taq1	39	agg	67.183	67	67.29	67.21	67.05	3 900 000	74 300 000	6 900 000	+-	A		\(5)
7944	Taq1	39	agg	67.183	67	67.29	67.21	67.05	144.83	746.74	203.24	+-	A		\(5)
7945	Taq1	45	gcc	74.013	74	74.04	74.1	73.9	59 800 000	21 500 000	13 700 000	-=	\ (-)		\(5)
7946	Hha1	44	cgg	81.375	81	81.44	0	81.31	4 500 000	0	4 700 000	-+(=)	V		\(5)
7947	Hha1	33	agc	90.39	90	90.34	90.44	0	13 700 000	18 700 000	0	=-	\		\(5)
7948	Taq1	56	tga	100.495	100	100.4	100.59	0	5 100 000	9 000 000	0	=-	\		\(5)
7949	Taq1	56	tga	99.73	100	0	99.73	0	0	4 600 000	0	+-	A		\(5)
7950	Taq1	40	tgg	153.42	154	0	153.42	0	0	314 800 000	0	+-	A		\(5)
7951	Taq1	40	tgg	154.225	154	0	154.28	154.17	0	65 000 000	11 300 000	+-	A		\(5)
7952	Hha1	33	agc	164.63	165	0	0	164.63	0	0	3 300 000	=+	/		\(5)
7953	Hha1	33	agc	165.545	165	165.57	0	165.52	3 600 000	0	4 000 000	-+(=)	V		\(5)
7954	Taq1	64	gtt	167.207	168	167.27	167.13	167.22	6 300 000	7 500 000	3 900 000	=-	\ (-)		\(5)
7955	Taq1	64	gtt	168.247	168	168.28	168.23	168.23	5 000 000	6 100 000	10 900 000	==	-		\(5)
7956	Hha1	44	cgg	219.64	219	219.64	0	0	5 700 000	0	0	-=	\		\(5)
7957	Taq1	10	atg	75.825	76	75.88	75.77	0	4 400 000	3 800 000	0	=-	\		\(3)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
7915	AF230519.SETA	SETA	SH3 domain-containing adapter protein isoform		tgt	agt	No change
7916	AF230519.SETA	SETA	SH3 domain-containing adapter protein isoform		ttg	tgg	No change
7917	AF230519.SETA	SETA	SH3 domain-containing adapter protein isoform		ttg	tgg	No change
7918	AF230519.SETA	SETA	SH3 domain-containing adapter protein isoform		ttg	tgg	No change
7919	AF230519.SETA	SETA	SH3 domain-containing adapter protein isoform		tgt	agt	No change
7920	AF230519.SETA	SETA	SH3 domain-containing adapter protein isoform		tgt	agt	No change
7921	AF230519.SETA	SETA	SH3 domain-containing adapter protein isoform		aaa	tgc	No change
7922	AF230519.SETA	SETA	SH3 domain-containing adapter protein isoform		aaa	tgc	No change
7923	AF230519.SETA	SETA	SH3 domain-containing adapter protein isoform		aaa	tgc	No change
7924	AF230520.SETA	SETA	SH3 domain-containing adapter protein isoform		gga	tga	No change
7925	AF230520.SETA	SETA	SH3 domain-containing adapter protein isoform		tgt	agt	No change
7926	AF230520.SETA	SETA	SH3 domain-containing adapter protein isoform		ttg	tgg	No change
7927	AF230520.SETA	SETA	SH3 domain-containing adapter protein isoform		ttg	tgg	No change
7928	AF230520.SETA	SETA	SH3 domain-containing adapter protein isoform		ttg	tgg	No change
7929	AF230520.SETA	SETA	SH3 domain-containing adapter protein isoform		tgt	agt	No change
7930	AF230520.SETA	SETA	SH3 domain-containing adapter protein isoform		tgt	agt	No change
7931	AF230520.SETA	SETA	SH3 domain-containing adapter protein isoform		aaa	tgc	No change
7932	AF230520.SETA	SETA	SH3 domain-containing adapter protein isoform		aaa	tgc	No change
7933	AF230520.SETA	SETA	SH3 domain-containing adapter protein isoform		aaa	tgc	No change
7934	AF026505.PE1	nc	SH3-containing protein p4015		aat	acg	No change
7935	AF026505.PE1	nc	SH3-containing protein p4015		aat	acg	decreased
7936	AF026505.PE1	nc	SH3-containing protein p4015		aat	acg	decreased
7937	AF026505.PE1	nc	SH3-containing protein p4015		aat	acg	No change
7938	AF026505.PE1	nc	SH3-containing protein p4015		ggt	cgt	No change
7939	AF026505.PE1	nc	SH3-containing protein p4015		ggt	cgt	No change
7940	AF026505.PE1	nc	SH3-containing protein p4015		ggt	cgt	No change
7941	AF026505.PE1	nc	SH3-containing protein p4015		cca	gtg	No change
7942	AF026505.PE1	nc	SH3-containing protein p4015		cca	gtg	No change
7943	AF131951.PE1	nc	Shank1a		ttg	agg	increased
7944	AF131951.PE1	nc	Shank1a		ttg	agg	increased
7945	AF131951.PE1	nc	Shank1a		cat	gcc	increased
7946	AF131951.PE1	nc	Shank1a		aga	cgg	increased
7947	AF131951.PE1	nc	Shank1a		agc	gtg	increased
7948	AF131951.PE1	nc	Shank1a		gtc	tga	increased
7949	AF131951.PE1	nc	Shank1a		gtc	tga	increased
7950	AF131951.PE1	nc	Shank1a		tgg	tgg	increased
7951	AF131951.PE1	nc	Shank1a		tgg	tgg	increased
7952	AF131951.PE1	nc	Shank1a		gga	agc	increased
7953	AF131951.PE1	nc	Shank1a		gga	agc	increased
7954	AF131951.PE1	nc	Shank1a		gtt	agc	increased
7955	AF131951.PE1	nc	Shank1a		gtt	agc	increased
7956	AF131951.PE1	nc	Shank1a		cgg	cag	increased
7957	AY298755.SHANK2	Shank2	Shank2E		gtg	atg	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
7958	Taq1	18	cct	127.63	128	127.59	127.67	0	4 100 000	4 100 000	0	=-	\		\(3)
7959	Taq1	18	cct	128.64	128	128.63	128.69	128.6	32 900 000	52 700 000	4 000 000	=-	\ (-)		\(3)
7960	Taq1	63	ctt	127.92	128	127.92	0	0	3 300 000	0	0	-=	\		\(3)
7961	Taq1	41	ccc	152.86	153	0	152.86	0	0	13 800 000	0	+-	A		\(3)
7962	Taq1	41	ccc	153.793	153	153.81	153.8	153.77	3 900 000	25 100 000	3 300 000	+-	A		\(3)
7963	Taq1	62	tgt	153.833	154	153.93	153.86	153.71	3 300 000	4 400 000	4 700 000	==	-		\(3)
7964	Taq1	62	tgt	154.92	154	155.02	154.85	154.89	4 200 000	6 200 000	4 900 000	==	-		\(3)
7965	Taq1	22	tcc	125.597	125	125.44	125.82	125.53	5 300 000	4 700 000	13 300 000	=+	/ (-)	/	
7966	Taq1	23	cga	125.45	125	125.33	0	125.57	3 500 000	0	13 700 000	=+(+)	/	/	
7967	Taq1	21	acc	123.68	124	0	0	123.68	0	0	6 600 000	=+	/		/(4)
7968	Hha1	21	acc	124.025	124	124.13	0	123.92	145 600 000	0	3 200 000	-=(-)	\		/(4)
7969	Hha1	21	acc	124.57	124	0	0	124.57	0	0	4 500 000	=+	/	/	/(4)
7970	Taq1	35	gga	123.8	124	0	0	123.8	0	0	3 500 000	=+	/		/(4)
7971	Taq1	35	gga	124.71	124	0	0	124.71	0	0	3 600 000	=+	/	/	/(4)
7972	Hha1	26	ctg	171.777	172	171.59	171.8	171.94	8 700 000	6 900 000	47 500 000	=+	/ (-)		/(4)
7973	Hha1	26	ctg	172.8	172	172.68	0	172.92	3 000 000	0	8 400 000	=+(+)	/		/(4)
7974	Hha1	6	aga	99.99	100	0	99.99	0	0	8 000 000	0	+-	A		/(2)
7975	Hha1	6	aga	100.575	100	100.64	0	100.51	5 900 000	0	4 400 000	-+(=)	V		/(2)
7976	Hha1	6	aga	99.96	100	99.96	0	0	6 400 000	0	0	-=	\		/(2)
7977	Taq1	35	gga	100.28	100	0	0	100.28	0	0	4 000 000	=+	/		/(2)
7978	Taq1	61	tct	125.835	126	0	125.82	125.85	0	6 500 000	8 700 000	+=	/		/(2)
7979	Hha1	26	ctg	111.957	112	112.11	111.77	111.99	20 800 000	12 300 000	11 700 000	==	-		-2
7980	Hha1	33	agc	111.683	112	111.66	111.72	111.67	5 800 000	3 100 000	5 100 000	-=	\ (-)		-2
7981	Hha1	26	ctg	147.13	148	147.09	147.06	147.24	7 700 000	4 900 000	4 100 000	==	-		/(3)
7982	Hha1	26	ctg	148.08	148	0	0	148.08	0	0	3 900 000	=+	/		/(3)
7983	Hha1	28	tcg	147.46	148	0	147.35	147.57	0	4 500 000	3 700 000	+=	/		/(3)
7984	Taq1	34	tgc	384.57	385	0	0	384.57	0	0	6 100 000	=+	/		/(3)
7985	Hha1	26	ctg	147.13	148	147.09	147.06	147.24	7 700 000	4 900 000	4 100 000	==	-		/(2)
7986	Hha1	26	ctg	148.08	148	0	0	148.08	0	0	3 900 000	=+	/		/(2)
7987	Hha1	28	tcg	147.46	148	0	147.35	147.57	0	4 500 000	3 700 000	+=	/		/(2)
7988	Hha1	26	ctg	147.13	148	147.09	147.06	147.24	7 700 000	4 900 000	4 100 000	==	-		/(2)
7989	Hha1	26	ctg	148.08	148	0	0	148.08	0	0	3 900 000	=+	/		/(2)
7990	Hha1	28	tcg	147.46	148	0	147.35	147.57	0	4 500 000	3 700 000	+=	/		/(2)
7991	Taq1	39	agg	258.69	260	258.77	258.61	0	8 200 000	29 000 000	0	+-	A		/(2)
7992	Taq1	39	agg	259.76	260	259.76	0	0	21 600 000	0	0	-=	\		/(2)
7993	Taq1	39	agg	260.48	260	260.48	0	0	6 700 000	0	0	-=	\		/(2)
7994	Taq1	39	agg	258.69	260	258.77	258.61	0	304.51	291.46	0	=-	\		/(2)
7995	Taq1	39	agg	259.76	260	259.76	0	0	802.13	0	0	-=	\		/(2)
7996	Taq1	39	agg	260.48	260	260.48	0	0	248.81	0	0	-=	\		/(2)
7997	Hha1	12	agt	104.783	105	104.76	104.56	105.03	2 171.66	2 037.48	2 862.41	==	-		\(3)
7998	Hha1	20	ctc	105.28	105	0	105.28	0	0	603.19	0	+-	A		\(3)
7999	Taq1	39	agg	151.215	152	151.33	151.1	0	14 900 000	38 500 000	0	+-	A		\(3)
8000	Taq1	39	agg	152.155	152	152.37	151.94	0	20 800 000	30 900 000	0	=-	\		\(3)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
7958	AY298755.SHANK2	Shank2	Shank2E		cct	ctt	increased
7959	AY298755.SHANK2	Shank2	Shank2E		cct	ctt	increased
7960	AY298755.SHANK2	Shank2	Shank2E		cct	ctt	increased
7961	AY298755.SHANK2	Shank2	Shank2E		ccc	tgt	increased
7962	AY298755.SHANK2	Shank2	Shank2E		ccc	tgt	increased
7963	AY298755.SHANK2	Shank2	Shank2E		ccc	tgt	increased
7964	AY298755.SHANK2	Shank2	Shank2E		ccc	tgt	increased
7965	RATSTPBCB.PE1	nc	short type PB-cadherin		cga	tcc	decreased
7966	RATSTPBCB.PE1	nc	short type PB-cadherin		cga	tcc	decreased
7967	RNU24175.STAT5A1	STAT5a1	signal transducer and regulator of transcription		gga	acc	decreased
7968	RNU24175.STAT5A1	STAT5a1	signal transducer and regulator of transcription		gga	acc	decreased
7969	RNU24175.STAT5A1	STAT5a1	signal transducer and regulator of transcription		gga	acc	decreased
7970	RNU24175.STAT5A1	STAT5a1	signal transducer and regulator of transcription		gga	acc	decreased
7971	RNU24175.STAT5A1	STAT5a1	signal transducer and regulator of transcription		gga	acc	decreased
7972	RNU24175.STAT5A1	STAT5a1	signal transducer and regulator of transcription		ctg	tcc	decreased
7973	RNU24175.STAT5A1	STAT5a1	signal transducer and regulator of transcription		ctg	tcc	decreased
7974	AY191521.SMUG1	Smug1	single-strand selective monofunctional		aga	gga	decreased
7975	AY191521.SMUG1	Smug1	single-strand selective monofunctional		aga	gga	decreased
7976	AY191521.SMUG1	Smug1	single-strand selective monofunctional		aga	gga	decreased
7977	AY191521.SMUG1	Smug1	single-strand selective monofunctional		aga	gga	decreased
7978	AY191521.SMUG1	Smug1	single-strand selective monofunctional		tct	gct	decreased
7979	AF450248.ACTN3	Actn3	skeletal muscle-specific alpha-actinin 3		ctg	agc	No change
7980	AF450248.ACTN3	Actn3	skeletal muscle-specific alpha-actinin 3		ctg	agc	No change
7981	AF133730.PE1	nc	Slit1		ctg	tcg	decreased
7982	AF133730.PE1	nc	Slit1		ctg	tcg	decreased
7983	AF133730.PE1	nc	Slit1		ctg	tcg	decreased
7984	AF133730.PE1	nc	Slit1		tgc	agg	decreased
7985	AB073215.SLIT1	SLIT1	SLIT1-La splicing product		ctg	tcg	decreased
7986	AB073215.SLIT1	SLIT1	SLIT1-La splicing product		ctg	tcg	decreased
7987	AB073215.SLIT1	SLIT1	SLIT1-La splicing product		ctg	tcg	decreased
7988	AB073214.SLIT1	SLIT1	SLIT1-Sb splicing product		ctg	tcg	decreased
7989	AB073214.SLIT1	SLIT1	SLIT1-Sb splicing product		ctg	tcg	decreased
7990	AB073214.SLIT1	SLIT1	SLIT1-Sb splicing product		ctg	tcg	decreased
7991	AB073214.SLIT1	SLIT1	SLIT1-Sb splicing product		tgc	agg	decreased
7992	AB073214.SLIT1	SLIT1	SLIT1-Sb splicing product		tgc	agg	decreased
7993	AB073214.SLIT1	SLIT1	SLIT1-Sb splicing product		tgc	agg	decreased
7994	AB073214.SLIT1	SLIT1	SLIT1-Sb splicing product		tgc	agg	decreased
7995	AB073214.SLIT1	SLIT1	SLIT1-Sb splicing product		tgc	agg	decreased
7996	AB073214.SLIT1	SLIT1	SLIT1-Sb splicing product		tgc	agg	decreased
7997	AF141386.PE1	nc	SLIT-2		ctc	agt	increased
7998	AF141386.PE1	nc	SLIT-2		ctc	agt	increased
7999	AF141386.PE1	nc	SLIT-2		agg	tta	increased
8000	AF141386.PE1	nc	SLIT-2		agg	tta	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
8001	Taq1	39	agg	151.33	152	151.33	0	0	553.32	0	0	-=	\		\(3)
8002	Taq1	39	agg	152.52	152	152.37	152.63	152.56	772.43	25 800 000	20 700 000	+=	/ (-)		\(3)
8003	Taq1	39	agg	151.1	152	0	151.1	0	0	386.93	0	+-	A		\(3)
8004	Taq1	39	agg	151.94	152	0	151.94	0	0	310.55	0	+-	A		\(3)
8005	Taq1	39	agg	152.595	152	0	152.63	152.56	0	259.29	609.72	=+	/		\(3)
8006	Taq1	51	ata	256.15	257	256.15	0	0	6 400 000	0	0	-=	\		\(3)
8007	Taq1	51	ata	257.03	257	257.03	0	0	3 500 000	0	0	-=	\		\(3)
8008	Taq1	50	aat	367.715	369	367.73	367.7	0	5 000 000	3 200 000	0	=-	\		\(3)
8009	Taq1	50	aat	369.405	369	369.16	0	369.65	3 600 000	0	3 900 000	-+(=)	V		\(3)
8010	Taq1	47	ggc	95.27	95	0	95.15	95.39	0	4 646.72	4 103.67	+=	/		/(3)
8011	Taq1	20	ctc	138.68	139	138.66	138.51	138.87	4 900 000	30 000 000	23 900 000	+=	/ (-)		/(3)
8012	Taq1	20	ctc	139.657	139	139.66	139.55	139.76	4 400 000	10 700 000	5 100 000	+-	A		/(3)
8013	Taq1	39	agg	186.487	187	186.76	186.39	186.31	11 500 000	7 700 000	3 900 000	==	-		/(3)
8014	Taq1	39	agg	186.31	187	0	0	186.31	0	0	114.87	=+	/		/(3)
8015	Taq1	39	agg	187.38	187	187.52	187.24	0	6 200 000	40 100 000	0	+-	A		/(3)
8016	Taq1	39	agg	186.76	187	186.76	0	0	427.06	0	0	-=	\		/(3)
8017	Taq1	39	agg	187.52	187	187.52	0	0	230.24	0	0	-=	\		/(3)
8018	Taq1	39	agg	186.39	187	0	186.39	0	0	77.38	0	+-	A		/(3)
8019	Taq1	39	agg	187.24	187	0	187.24	0	0	403.01	0	+-	A		/(3)
8020	Hha1	39	agg	77.763	78	77.79	77.55	77.95	1 092.37	519.43	476.07	-=	\ (-)		/(2) \(2)
8021	Hha1	39	agg	78.41	78	0	78.41	0	0	728.4	0	+-	A		/(2) \(2)
8022	Hha1	26	ctg	117.02	117	0	0	117.02	0	0	3 100 000	=+	/		/(2) \(2)
8023	Taq1	50	aat	218.655	219	218.44	218.87	0	6 000 000	4 400 000	0	=-	\		/(2) \(2)
8024	Taq1	50	aat	219.49	219	0	0	219.49	0	0	4 100 000	=+	/		/(2) \(2)
8025	Taq1	48	ggg	102.757	103	102.58	102.67	103.02	3 318.58	3 608.3	982.27	=-	\ (-)		-(2) \(2)
8026	Taq1	48	ggg	103.12	103	103.12	0	0	2 149.17	0	0	-=	\		-(2) \(2)
8027	Taq1	39	agg	104.227	104	104.06	104.44	104.18	14 000 000	87 600 000	14 900 000	+-	A		-(2) \(2)
8028	Taq1	39	agg	104.37	104	104.49	104.44	104.18	16 800 000	880.41	438.88	-=	\ (-)		-(2) \(2)
8029	Taq1	39	agg	103.47	104	103.47	0	0	583.03	0	0	-=	\		-(2) \(2)
8030	Taq1	39	agg	104.06	104	104.06	0	0	519.9	0	0	-=	\		-(2) \(2)
8031	Taq1	39	agg	104.49	104	104.49	0	0	623.88	0	0	-=	\		-(2) \(2)
8032	Taq1	48	ggg	102.757	103	102.58	102.67	103.02	3 318.58	3 608.3	982.27	=-	\ (-)		-(2) \(2)
8033	Taq1	48	ggg	103.12	103	103.12	0	0	2 149.17	0	0	-=	\		-(2) \(2)
8034	Taq1	39	agg	104.227	104	104.06	104.44	104.18	14 000 000	87 600 000	14 900 000	+-	A		-(2) \(2)
8035	Taq1	39	agg	104.37	104	104.49	104.44	104.18	16 800 000	880.41	438.88	-=	\ (-)		-(2) \(2)
8036	Taq1	39	agg	103.47	104	103.47	0	0	583.03	0	0	-=	\		-(2) \(2)
8037	Taq1	39	agg	104.06	104	104.06	0	0	519.9	0	0	-=	\		-(2) \(2)
8038	Taq1	39	agg	104.49	104	104.49	0	0	623.88	0	0	-=	\		-(2) \(2)
8039	Hha1	62	tgt	152.74	153	0	0	152.74	0	0	3 500 000	=+	/		\(3)
8040	Taq1	45	gcc	172.617	173	172.42	172.54	172.89	4 200 000	7 300 000	8 400 000	==	-		\(3)
8041	Taq1	45	gcc	173.42	173	173.37	173.47	0	5 000 000	4 900 000	0	=-	\		\(3)
8042	Hha1	44	cgg	207.37	207	207.37	0	0	4 700 000	0	0	-=	\	\	\(3)
8043	Hha1	60	ttg	207.21	208	207.19	207.23	0	4 400 000	3 000 000	0	=-	\	\	\(3)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
8001	AF141386.PE1	nc	SLIT-2		agg	tta	increased
8002	AF141386.PE1	nc	SLIT-2		agg	tta	increased
8003	AF141386.PE1	nc	SLIT-2		agg	tta	increased
8004	AF141386.PE1	nc	SLIT-2		agg	tta	increased
8005	AF141386.PE1	nc	SLIT-2		agg	tta	increased
8006	AF141386.PE1	nc	SLIT-2		ata	gga	increased
8007	AF141386.PE1	nc	SLIT-2		ata	gga	increased
8008	AF141386.PE1	nc	SLIT-2		gag	aat	increased
8009	AF141386.PE1	nc	SLIT-2		gag	aat	increased
8010	AF203374.HSPB3	Hspb3	small heat shock protein B3		ggc	tgg	decreased
8011	AF203374.HSPB3	Hspb3	small heat shock protein B3		ggg	ctc	decreased
8012	AF203374.HSPB3	Hspb3	small heat shock protein B3		ggg	ctc	decreased
8013	AF203374.HSPB3	Hspb3	small heat shock protein B3		gga	agg	decreased
8014	AF203374.HSPB3	Hspb3	small heat shock protein B3		gga	agg	decreased
8015	AF203374.HSPB3	Hspb3	small heat shock protein B3		gga	agg	decreased
8016	AF203374.HSPB3	Hspb3	small heat shock protein B3		gga	agg	decreased
8017	AF203374.HSPB3	Hspb3	small heat shock protein B3		gga	agg	decreased
8018	AF203374.HSPB3	Hspb3	small heat shock protein B3		gga	agg	decreased
8019	AF203374.HSPB3	Hspb3	small heat shock protein B3		gga	agg	decreased
8020	AF327513.SMHS2	Smhs2	SMHS2		agg	ggc	decreased
8021	AF327513.SMHS2	Smhs2	SMHS2		agg	ggc	decreased
8022	AF327513.SMHS2	Smhs2	SMHS2		ggg	ctg	decreased
8023	AF327513.SMHS2	Smhs2	SMHS2		gag	aat	decreased
8024	AF327513.SMHS2	Smhs2	SMHS2		gag	aat	decreased
8025	AF262221.PE1	nc	SNARE Vti1a protein		agg	ggg	No change
8026	AF262221.PE1	nc	SNARE Vti1a protein		agg	ggg	No change
8027	AF262221.PE1	nc	SNARE Vti1a protein		agg	ggg	No change
8028	AF262221.PE1	nc	SNARE Vti1a protein		agg	ggg	No change
8029	AF262221.PE1	nc	SNARE Vti1a protein		agg	ggg	No change
8030	AF262221.PE1	nc	SNARE Vti1a protein		agg	ggg	No change
8031	AF262221.PE1	nc	SNARE Vti1a protein		agg	ggg	No change
8032	AF262222.PE1	nc	SNARE Vti1a-beta protein		agg	ggg	No change
8033	AF262222.PE1	nc	SNARE Vti1a-beta protein		agg	ggg	No change
8034	AF262222.PE1	nc	SNARE Vti1a-beta protein		agg	ggg	No change
8035	AF262222.PE1	nc	SNARE Vti1a-beta protein		agg	ggg	No change
8036	AF262222.PE1	nc	SNARE Vti1a-beta protein		agg	ggg	No change
8037	AF262222.PE1	nc	SNARE Vti1a-beta protein		agg	ggg	No change
8038	AF262222.PE1	nc	SNARE Vti1a-beta protein		agg	ggg	No change
8039	RNSNF1KIN.SNRK	snrk	SNF1-related kinase		tgt	cat	increased
8040	RNSNF1KIN.SNRK	snrk	SNF1-related kinase		gga	gcc	increased
8041	RNSNF1KIN.SNRK	snrk	SNF1-related kinase		gga	gcc	increased
8042	RNSNF1KIN.SNRK	snrk	SNF1-related kinase		cgg	ttg	increased
8043	RNSNF1KIN.SNRK	snrk	SNF1-related kinase		cgg	ttg	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
8044	Hha1	60	ttg	208.11	208	208.14	208.06	208.13	12 000 000	6 700 000	8 300 000	==	-		\(3)
8045	Hha1	60	ttg	209.15	208	0	209.15	0	0	4 000 000	0	+-	A		\(3)
8046	Taq1	39	agg	75.62	76	75.37	0	75.87	45 000 000	0	6 000 000	-=(-)	\		/(2) \(2)
8047	Taq1	39	agg	76.37	76	76.57	76.17	0	26 000 000	27 000 000	0	=-	\		/(2) \(2)
8048	Taq1	39	agg	76.02	76	0	76.17	75.87	0	271.35	176.73	+=	/		/(2) \(2)
8049	Taq1	50	aat	136.855	137	136.88	0	136.83	8 000 000	0	5 200 000	-+(=)	V		/(2) \(2)
8050	Taq1	50	aat	137.5	137	137.5	0	0	6 900 000	0	0	-=	\		/(2) \(2)
8051	Taq1	52	att	260.91	262	0	0	260.91	0	0	5 500 000	=+	/		/(2) \(2)
8052	Taq1	45	gcc	74.013	74	74.04	74.1	73.9	59 800 000	21 500 000	13 700 000	-=	\ (-)		-2
8053	Taq1	63	ctt	94.36	94	94.29	94.37	94.42	8 300 000	4 700 000	6 500 000	==	-		-2
8054	Taq1	54	ttt	94.85	95	0	94.99	94.71	0	2 622.6	1 241.97	+-	A		-2
8055	Hha1	28	tcg	109.673	110	109.63	109.74	109.65	22 900 000	11 800 000	28 300 000	=+	/ (-)	/	
8056	Hha1	39	agg	109.507	110	109.65	109.55	109.32	1 092.37	2 173.26	1 485.18	+=	/ (-)	/	
8057	Taq1	12	agt	119.103	119	119.06	119.05	119.2	5 100 000	7 000 000	3 800 000	=-	\ (-)	\	
8058	Taq1	23	cga	119.32	119	119.32	0	0	4 800 000	0	0	-=	\	\	
8059	Taq1	8	gaa	132.82	133	132.71	132.93	0	4 400 000	6 100 000	0	=-	\	\	
8060	Hha1	8	gaa	133.017	133	133.08	133.07	132.9	34 400 000	25 100 000	9 200 000	=-	\ (-)	\	
8061	Taq1	25	cat	154.03	154	154	153.89	154.2	5 056.63	4 468.49	6 640.94	==	-	-	
8062	Taq1	62	tgt	153.833	154	153.93	153.86	153.71	3 300 000	4 400 000	4 700 000	==	-	-	
8063	Hha1	61	tct	147.073	147	147.05	147.04	147.13	8 600 000	27 600 000	17 800 000	+=	/ (-)		-2
8064	Hha1	40	tgg	156.92	156	156.76	156.92	157.08	5 700 000	6 000 000	3 800 000	==	-		-2
8065	Taq1	45	gcc	126.075	126	0	126.14	126.01	0	4 400 000	3 400 000	+=	/		-2
8066	Taq1	45	gcc	126.66	126	126.66	0	0	6 400 000	0	0	-=	\		-2
8067	Taq1	29	gca	126.473	127	126.52	126.46	126.44	6 300 000	5 600 000	9 500 000	==	-		-2
8068	Taq1	29	gca	127.51	127	127.52	127.49	127.52	5 600 000	3 400 000	5 300 000	==	-		-2
8069	Hha1	61	tct	200.247	200	200.01	200.35	200.38	3 300 000	4 500 000	4 700 000	==	-		-2
8070	Hha1	11	act	171.62	171	171.62	171.65	171.59	7 800 000	8 400 000	3 900 000	=-	\ (-)	(-)	
8071	Taq1	11	act	171.703	171	171.76	171.63	171.72	10 500 000	18 200 000	19 700 000	==	-	(-)	
8072	Hha1	26	ctg	107.74	108	0	107.74	0	0	4 200 000	0	+-	A		-(2) A(2)
8073	Hha1	20	ctc	126.45	126	126.46	126.33	126.56	557.85	498.29	1 514.79	=+	/ (-)		-(2) A(2)
8074	Hha1	20	ctc	126.57	126	0	126.57	0	0	576.97	0	+-	A		-(2) A(2)
8075	Hha1	54	ttt	150.39	151	150.39	0	0	4 800 000	0	0	-=	\		-(2) A(2)
8076	Hha1	54	ttt	151.537	151	151.52	151.59	151.5	5 700 000	4 700 000	4 100 000	==	-		-(2) A(2)
8077	Taq1	12	agt	103.24	103	0	0	103.24	0	0	3 200 000	=+	/		\(6)
8078	Taq1	23	cga	141.553	142	141.55	141.5	141.61	15 300 000	17 600 000	6 400 000	=-	\ (-)		\(6)
8079	Taq1	23	cga	142.713	142	142.69	142.67	142.78	31 500 000	41 600 000	5 400 000	=-	\ (-)	\	\(6)
8080	Taq1	64	gtt	141.837	142	141.83	141.83	141.85	6 400 000	4 700 000	4 300 000	==	-		\(6)
8081	Taq1	64	gtt	142.795	142	142.82	142.77	0	5 400 000	7 900 000	0	=-	\	\	\(6)
8082	Taq1	54	ttt	145.64	146	0	0	145.64	0	0	2 462.52	=+	/		\(6)
8083	Taq1	54	ttt	146.45	146	146.52	146.38	0	2 104.87	811.47	0	-=	\		\(6)
8084	Taq1	64	gtt	223.8	225	223.74	223.86	0	3 400 000	3 700 000	0	=-	\		\(6)
8085	Taq1	64	gtt	224.97	225	224.97	0	0	3 700 000	0	0	-=	\		\(6)
8086	Taq1	64	gtt	225.9	225	225.83	225.97	0	3 100 000	3 600 000	0	=-	\		\(6)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
8044	RNSNF1KIN.SNRK	snrk	SNF1-related kinase		cgg	ttg	increased
8045	RNSNF1KIN.SNRK	snrk	SNF1-related kinase		cgg	ttg	increased
8046	RNY09164.SCL-11	SCL-11	sodium channel		gag	agg	decreased
8047	RNY09164.SCL-11	SCL-11	sodium channel		gag	agg	decreased
8048	RNY09164.SCL-11	SCL-11	sodium channel		gag	agg	decreased
8049	RNY09164.SCL-11	SCL-11	sodium channel		aat	aca	decreased
8050	RNY09164.SCL-11	SCL-11	sodium channel		aat	aca	decreased
8051	RNY09164.SCL-11	SCL-11	sodium channel		ttg	att	decreased
8052	AF421190.PE1	nc	sodium channel associated protein 1A		gcc	gtt	No change
8053	AF421190.PE1	nc	sodium channel associated protein 1A		ctt	ttt	No change
8054	AF421190.PE1	nc	sodium channel associated protein 1A		ctt	ttt	No change
8055	RNU53833.PE1	nc	sodium channel PN3		agg	tcg	decreased
8056	RNU53833.PE1	nc	sodium channel PN3		agg	tcg	decreased
8057	RNU53833.PE1	nc	sodium channel PN3		cga	agt	increased
8058	RNU53833.PE1	nc	sodium channel PN3		cga	agt	increased
8059	RATSCP6A.SCP6	SCP6	sodium channel protein 6		gaa	tgg	increased
8060	RATSCP6A.SCP6	SCP6	sodium channel protein 6		gaa	tgg	increased
8061	RATSCP6A.SCP6	SCP6	sodium channel protein 6		cat	tgt	No change
8062	RATSCP6A.SCP6	SCP6	sodium channel protein 6		cat	tgt	No change
8063	RNSMIT.PE1	nc	sodium myo-inositol transporter		tct	cca	No change
8064	RNSMIT.PE1	nc	sodium myo-inositol transporter		tgg	ccg	No change
8065	RNATPAR.ATP1A1	atp1a1	sodium/potassium-transporting ATPase alpha-1		gca	gcc	No change
8066	RNATPAR.ATP1A1	atp1a1	sodium/potassium-transporting ATPase alpha-1		gca	gcc	No change
8067	RNATPAR.ATP1A1	atp1a1	sodium/potassium-transporting ATPase alpha-1		gca	gcc	No change
8068	RNATPAR.ATP1A1	atp1a1	sodium/potassium-transporting ATPase alpha-1		gca	gcc	No change
8069	RNATPAR.ATP1A1	atp1a1	sodium/potassium-transporting ATPase alpha-1		tct	cct	No change
8070	AF080452.PE1	nc	sodium-coupled ascorbic acid transporter SVCT1		act	tga	No change
8071	AF080452.PE1	nc	sodium-coupled ascorbic acid transporter SVCT1		act	tga	No change
8072	RNO132846.ASCT2	asct2	sodium-dependent neutral amino acid transporter,		ctg	tag	No change
8073	RNO132846.ASCT2	asct2	sodium-dependent neutral amino acid transporter,		caa	ctc	No change
8074	RNO132846.ASCT2	asct2	sodium-dependent neutral amino acid transporter,		caa	ctc	No change
8075	RNO132846.ASCT2	asct2	sodium-dependent neutral amino acid transporter,		ttt	tag	No change
8076	RNO132846.ASCT2	asct2	sodium-dependent neutral amino acid transporter,		ttt	tag	No change
8077	AF081941.SAC	SAC	soluble adenylyl cyclase		gag	agt	increased
8078	AF081941.SAC	SAC	soluble adenylyl cyclase		cga	gtt	increased
8079	AF081941.SAC	SAC	soluble adenylyl cyclase		cga	gtt	increased
8080	AF081941.SAC	SAC	soluble adenylyl cyclase		cga	gtt	increased
8081	AF081941.SAC	SAC	soluble adenylyl cyclase		cga	gtt	increased
8082	AF081941.SAC	SAC	soluble adenylyl cyclase		cta	ttt	increased
8083	AF081941.SAC	SAC	soluble adenylyl cyclase		cta	ttt	increased
8084	AF081941.SAC	SAC	soluble adenylyl cyclase		gtt	ttt	increased
8085	AF081941.SAC	SAC	soluble adenylyl cyclase		gtt	ttt	increased
8086	AF081941.SAC	SAC	soluble adenylyl cyclase		gtt	ttt	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
8087	Taq1	51	ata	322.68	324	322.68	0	0	4 100 000	0	0	-=	\		\(6)
8088	Taq1	51	ata	365.68	365	365.68	0	0	3 700 000	0	0	-=	\		\(6)
8089	Hha1	3	aac	188.41	188	188.41	0	0	3 100 000	0	0	-=	\		\(5)
8090	Hha1	3	aac	189.12	188	189.13	189.21	189.02	6 300 000	4 500 000	5 200 000	==	-		\(5)
8091	Hha1	10	atg	187.15	188	187.15	0	0	4 000 000	0	0	-=	\		\(5)
8092	Hha1	10	atg	188.085	188	188.04	188.13	0	8 000 000	3 900 000	0	--	\		\(5)
8093	Taq1	10	atg	188.83	188	188.73	188.93	0	4 900 000	9 900 000	0	+-	A		\(5)
8094	Hha1	10	atg	189.1	188	189.1	0	0	4 400 000	0	0	-=	\		\(5)
8095	Taq1	44	cgg	251.5	253	0	251.59	251.41	0	660.39	672.49	+=	/		\(5)
8096	Taq1	44	cgg	251.97	253	251.97	0	0	184	0	0	-=	\	\	\(5)
8097	Taq1	45	gcc	251.93	253	251.75	252.11	0	158 600 000	3 100 000	0	-=	\	\	\(5)
8098	Taq1	45	gcc	252.22	253	252.22	0	0	5 200 000	0	0	-=	\	\	\(5)
8099	Taq1	45	gcc	254.26	253	0	254.26	0	0	3 700 000	0	+-	A		\(5)
8100	Hha1	44	cgg	63.01	63	62.97	0	63.05	19 800 000	0	23 500 000	-+(=)	V		A(5)
8101	Hha1	33	agc	65.985	66	66.22	0	65.75	32 900 000	0	35 500 000	-+(=)	V		A(5)
8102	Hha1	33	agc	66.3	66	0	66.3	0	0	76 700 000	0	+-	A		A(5)
8103	Hha1	49	aaa	75.565	76	75.53	75.6	0	7 900 000	25 100 000	0	+-	A		A(5)
8104	Hha1	49	aaa	76.317	76	76.35	76.29	76.31	16 000 000	27 700 000	16 400 000	==	-		A(5)
8105	Hha1	20	ctc	82.09	82	0	82.09	0	0	472.06	0	+-	A		A(5)
8106	Hha1	39	agg	157.13	157	0	0	157.13	0	0	325.52	=+	/		A(5)
8107	Hha1	39	agg	157.67	157	0	157.67	0	0	316.43	0	+-	A		A(5)
8108	Hha1	28	tcg	173.593	174	173.58	173.61	173.59	7 000 000	6 400 000	7 000 000	==	-		A(5)
8109	Hha1	40	tgg	173.72	174	0	0	173.72	0	0	4 200 000	=+	/		A(5)
8110	Taq1	12	agt	177.703	178	177.74	177.55	177.82	7 000 000	12 900 000	6 800 000	+-	A		A(5)
8111	Taq1	12	agt	178.63	178	178.69	178.63	178.57	4 400 000	7 600 000	3 800 000	=-	\ (-)	\	A(5)
8112	Taq1	18	cct	177.895	178	0	177.91	177.88	0	3 000 000	3 400 000	+=	/		A(5)
8113	Taq1	18	cct	178.855	178	178.85	178.86	0	8 200 000	4 700 000	0	=-	\	\	A(5)
8114	Taq1	39	agg	67.183	67	67.29	67.21	67.05	3 900 000	74 300 000	6 900 000	+-	A		\(5)
8115	Taq1	39	agg	67.183	67	67.29	67.21	67.05	144.83	746.74	203.24	+-	A		\(5)
8116	Taq1	45	gcc	74.013	74	74.04	74.1	73.9	59 800 000	21 500 000	13 700 000	-=	\ (-)		\(5)
8117	Hha1	44	cgg	81.375	81	81.44	0	81.31	4 500 000	0	4 700 000	-+(=)	V		\(5)
8118	Hha1	33	agc	90.39	90	90.34	90.44	0	13 700 000	18 700 000	0	=-	\		\(5)
8119	Taq1	56	tga	100.495	100	100.4	100.59	0	5 100 000	9 000 000	0	=-	\		\(5)
8120	Taq1	56	tga	99.73	100	0	99.73	0	0	4 600 000	0	+-	A		\(5)
8121	Taq1	40	tgg	153.42	154	0	153.42	0	0	314 800 000	0	+-	A		\(5)
8122	Taq1	40	tgg	154.225	154	0	154.28	154.17	0	65 000 000	11 300 000	+-	A		\(5)
8123	Hha1	33	agc	164.63	165	0	0	164.63	0	0	3 300 000	=+	/		\(5)
8124	Hha1	33	agc	165.545	165	165.57	0	165.52	3 600 000	0	4 000 000	-+(=)	V		\(5)
8125	Taq1	64	gtt	167.207	168	167.27	167.13	167.22	6 300 000	7 500 000	3 900 000	=-	\ (-)		\(5)
8126	Taq1	64	gtt	168.247	168	168.28	168.23	168.23	5 000 000	6 100 000	10 900 000	==	-		\(5)
8127	Hha1	44	cgg	219.64	219	219.64	0	0	5 700 000	0	0	-=	\		\(5)
8128	Taq1	20	ctc	144.705	145	144.69	144.72	0	6 000 000	5 600 000	0	=-	\		\(2)
8129	Taq1	20	ctc	145.755	145	145.7	145.81	0	19 600 000	5 700 000	0	-=	\		\(2)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
8087	AF081941.SAC	SAC	soluble adenylyl cyclase		tat	ata	increased
8088	AF081941.SAC	SAC	soluble adenylyl cyclase		gtt	ata	increased
8089	RNSD.PE1	nc	sorbitol dehydrogenase		atg	aac	increased
8090	RNSD.PE1	nc	sorbitol dehydrogenase		atg	aac	increased
8091	RNSD.PE1	nc	sorbitol dehydrogenase		atg	aac	increased
8092	RNSD.PE1	nc	sorbitol dehydrogenase		atg	aac	increased
8093	RNSD.PE1	nc	sorbitol dehydrogenase		atg	aac	increased
8094	RNSD.PE1	nc	sorbitol dehydrogenase		atg	aac	increased
8095	RNSD.PE1	nc	sorbitol dehydrogenase		gcc	cgg	increased
8096	RNSD.PE1	nc	sorbitol dehydrogenase		gcc	cgg	increased
8097	RNSD.PE1	nc	sorbitol dehydrogenase		gcc	cgg	increased
8098	RNSD.PE1	nc	sorbitol dehydrogenase		gcc	cgg	increased
8099	RNSD.PE1	nc	sorbitol dehydrogenase		gcc	cgg	increased
8100	RNAJ4858.SOX11	Sox11	Sox11 protein		act	cgg	increased by mild
8101	RNAJ4858.SOX11	Sox11	Sox11 protein		agc	ctc	increased by mild
8102	RNAJ4858.SOX11	Sox11	Sox11 protein		agc	ctc	increased by mild
8103	RNAJ4858.SOX11	Sox11	Sox11 protein		aaa	tgg	increased by mild
8104	RNAJ4858.SOX11	Sox11	Sox11 protein		aaa	tgg	increased by mild
8105	RNAJ4858.SOX11	Sox11	Sox11 protein		ctc	ggc	increased by mild
8106	RNAJ4858.SOX11	Sox11	Sox11 protein		agg	tcc	increased by mild
8107	RNAJ4858.SOX11	Sox11	Sox11 protein		agg	tcc	increased by mild
8108	RNAJ4858.SOX11	Sox11	Sox11 protein		tgg	tcg	increased by mild
8109	RNAJ4858.SOX11	Sox11	Sox11 protein		tgg	tcg	increased by mild
8110	RNAJ4858.SOX11	Sox11	Sox11 protein		cct	agt	increased by mild
8111	RNAJ4858.SOX11	Sox11	Sox11 protein		cct	agt	increased
8112	RNAJ4858.SOX11	Sox11	Sox11 protein		cct	agt	increased by mild
8113	RNAJ4858.SOX11	Sox11	Sox11 protein		cct	agt	increased
8114	AF159046.PE1	nc	SPANK-1		ttg	agg	increased
8115	AF159046.PE1	nc	SPANK-1		ttg	agg	increased
8116	AF159046.PE1	nc	SPANK-1		cat	gcc	increased
8117	AF159046.PE1	nc	SPANK-1		aga	cgg	increased
8118	AF159046.PE1	nc	SPANK-1		agc	gtg	increased
8119	AF159046.PE1	nc	SPANK-1		gtc	tga	increased
8120	AF159046.PE1	nc	SPANK-1		gtc	tga	increased
8121	AF159046.PE1	nc	SPANK-1		tgg	tgg	increased
8122	AF159046.PE1	nc	SPANK-1		tgg	tgg	increased
8123	AF159046.PE1	nc	SPANK-1		gga	agc	increased
8124	AF159046.PE1	nc	SPANK-1		gga	agc	increased
8125	AF159046.PE1	nc	SPANK-1		gtt	agc	increased
8126	AF159046.PE1	nc	SPANK-1		gtt	agc	increased
8127	AF159046.PE1	nc	SPANK-1		cgg	cag	increased
8128	RNO242554.SPASIC	spasic	SPASIC protein		ctc	ttt	increased
8129	RNO242554.SPASIC	spasic	SPASIC protein		ctc	ttt	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
8130	Taq1	54	ttt	145.64	146	0	0	145.64	0	0	2 462.52	=+	/		\(2)
8131	Taq1	54	ttt	146.45	146	146.52	146.38	0	2 104.87	811.47	0	-=	\		\(2)
8132	Hha1	27	acg	132.99	133	132.98	132.95	133.04	22 200 000	6 000 000	10 000 000	-=	\ (-)	(-)	
8133	Hha1	40	tgg	133.193	133	133.22	133.26	133.1	3 800 000	8 000 000	6 900 000	+=	/ (-)	(-)	
8134	Hha1	20	ctc	70.987	71	70.8	71.18	70.98	977.96	786.78	918.41	==	-		-2
8135	Hha1	44	cgg	168.743	169	168.78	168.66	168.79	70 900 000	4 500 000	4 100 000	-=	\ (-)		-2
8136	Hha1	44	cgg	169.29	169	0	169.29	169.29	0	3 000 000	3 900 000	+=	/		-2
8137	Hha1	44	cgg	169.4	169	0	169.4	0	0	3 200 000	0	+-	A		-2
8138	Taq1	35	gga	100.28	100	0	0	100.28	0	0	4 000 000	=+	/	/	
8139	Taq1	64	gtt	100.51	100	100.52	100.49	100.52	5 300 000	5 600 000	14 800 000	=+	/ (-)	/	
8140	Taq1	62	tgt	186.89	187	0	186.89	0	0	3 200 000	0	+-	A		/(2) A(2) \(2)
8141	Taq1	62	tgt	187.98	187	187.94	188.02	0	3 000 000	4 500 000	0	=-	\		/(2) A(2) \(2)
8142	Hha1	40	tgg	195.975	196	0	195.9	196.05	0	7 800 000	3 800 000	+-	A		/(2) A(2) \(2)
8143	Hha1	40	tgg	196.87	196	0	196.71	197.03	0	4 900 000	4 600 000	+=	/		/(2) A(2) \(2)
8144	Hha1	26	ctg	205.22	206	0	0	205.22	0	0	3 200 000	=+	/		/(2) A(2) \(2)
8145	Hha1	26	ctg	206.33	206	206.33	0	0	3 000 000	0	0	-=	\		/(2) A(2) \(2)
8146	Taq1	40	tgg	123.5	124	0	0	123.5	0	0	18 400 000	=+	/	/	/(2)
8147	Taq1	40	tgg	124.435	124	0	124.28	124.59	0	5 600 000	39 000 000	=+	/	/	/(2)
8148	Taq1	62	tgt	123.497	124	123.62	123.49	123.38	3 000 000	4 200 000	29 100 000	=+	/ (-)	/	/(2)
8149	Taq1	62	tgt	124.54	124	124.59	124.62	124.41	5 100 000	7 400 000	69 100 000	=+	/ (-)	/	/(2)
8150	Taq1	16	tag	171.64	171	0	171.6	171.68	0	4 300 000	9 200 000	++	/	/	
8151	Hha1	16	tag	171.8	171	171.8	171.8	171.8	7 700 000	17 000 000	19 600 000	+=	/ (-)	/	
8152	Taq1	16	tag	171.64	171	0	171.6	171.68	0	4 300 000	9 200 000	++	/	/	
8153	Hha1	16	tag	171.8	171	171.8	171.8	171.8	7 700 000	17 000 000	19 600 000	+=	/ (-)	/	
8154	Taq1	16	tag	171.64	171	0	171.6	171.68	0	4 300 000	9 200 000	++	/	/	
8155	Hha1	16	tag	171.8	171	171.8	171.8	171.8	7 700 000	17 000 000	19 600 000	+=	/ (-)	/	
8156	Taq1	40	tgg	142.91	143	142.81	0	143.01	11 800 000	0	19 600 000	-+(=)	V		\(2)
8157	Taq1	56	tga	142.833	143	142.99	142.94	142.57	27 400 000	33 000 000	9 400 000	=-	\ (-)		\(2)
8158	Hha1	49	aaa	273.86	274	0	273.86	0	0	5 200 000	0	+-	A		\(2)
8159	Hha1	49	aaa	274.57	274	0	274.57	0	0	8 600 000	0	+-	A		\(2)
8160	Hha1	49	aaa	273.86	274	0	273.86	0	0	5 200 000	0	+-	A		\(2)
8161	Hha1	49	aaa	274.57	274	0	274.57	0	0	8 600 000	0	+-	A		\(2)
8162	Hha1	49	aaa	273.86	274	0	273.86	0	0	5 200 000	0	+-	A		\(2)
8163	Hha1	49	aaa	274.57	274	0	274.57	0	0	8 600 000	0	+-	A		\(2)
8164	Hha1	49	aaa	275.36	274	275.36	0	0	3 600 000	0	0	-=	\		\(2)
8165	Hha1	49	aaa	275.36	274	275.36	0	0	3 600 000	0	0	-=	\		\(2)
8166	Hha1	49	aaa	275.36	274	275.36	0	0	3 600 000	0	0	-=	\		\(2)
8167	Hha1	39	agg	66.61	67	0	66.57	66.65	0	1 629.94	2 937.82	+=	/		/(4)
8168	Hha1	20	ctc	86.105	86	0	86.13	86.08	0	1 180.17	1 693.7	+=	/		/(4)
8169	Taq1	41	ccc	125.43	126	0	125.43	0	0	5 600 000	0	+-	A		/(4)
8170	Taq1	41	ccc	125.95	126	0	0	125.95	0	0	3 900 000	=+	/		/(4)
8171	Taq1	41	ccc	126.62	126	0	126.62	0	0	4 300 000	0	+-	A		/(4)
8172	Hha1	6	aga	126.475	127	126.51	0	126.44	89 200 000	0	7 100 000	-=(-)	\		/(4)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
8130	RNO242554.SPASIC	spasic	SPASIC protein		ctc	ttt	increased
8131	RNO242554.SPASIC	spasic	SPASIC protein		ctc	ttt	increased
8132	AF225960.PE1	nc	spectrin-like protein GTRAP41		acg	tgg	No change
8133	AF225960.PE1	nc	spectrin-like protein GTRAP41		acg	tgg	No change
8134	AF043345.SPAG4	SPAG4	sperm antigen 4		ctc	cac	No change
8135	AF043345.SPAG4	SPAG4	sperm antigen 4		cgg	cag	No change
8136	AF043345.SPAG4	SPAG4	sperm antigen 4		cgg	cag	No change
8137	AF043345.SPAG4	SPAG4	sperm antigen 4		cgg	cag	No change
8138	AF016252.PE1	nc	Spinophilin		gga	gtt	decreased
8139	AF016252.PE1	nc	Spinophilin		gga	gtt	decreased
8140	AF350422.PE1	nc	Spring		tgt	gga	decreased
8141	AF350422.PE1	nc	Spring		tgt	gga	decreased
8142	AF350422.PE1	nc	Spring		ccg	tgg	decreased
8143	AF350422.PE1	nc	Spring		ccg	tgg	decreased
8144	AF350422.PE1	nc	Spring		aag	ctg	decreased
8145	AF350422.PE1	nc	Spring		aag	ctg	decreased
8146	RNU46957.PE1	nc	SRC-CD44s	*	tgg	tgt	decreased
8147	RNU46957.PE1	nc	SRC-CD44s	*	tgg	tgt	decreased
8148	RNU46957.PE1	nc	SRC-CD44s	*	tgg	tgt	decreased
8149	RNU46957.PE1	nc	SRC-CD44s	*	tgg	tgt	decreased
8150	AF026528.PE1	nc	stathmin-like-protein RB3		gac	tag	decreased
8151	AF026528.PE1	nc	stathmin-like-protein RB3		gac	tag	decreased
8152	AF026529.PE1	nc	stathmin-like-protein splice variant RB3'		gac	tag	decreased
8153	AF026529.PE1	nc	stathmin-like-protein splice variant RB3'		gac	tag	decreased
8154	AF026530.PE1	nc	stathmin-like-protein splice variant RB3''		gac	tag	decreased
8155	AF026530.PE1	nc	stathmin-like-protein splice variant RB3''		gac	tag	decreased
8156	AB032243.SCD2	Scd2	stearoyl-CoA desaturase 2		tgg	tga	increased
8157	AB032243.SCD2	Scd2	stearoyl-CoA desaturase 2		tgg	tga	increased
8158	AB032243.SCD2	Scd2	stearoyl-CoA desaturase 2		aaa	tgt	increased
8159	AB032243.SCD2	Scd2	stearoyl-CoA desaturase 2		aaa	tgt	increased
8160	AB032243.SCD2	Scd2	stearoyl-CoA desaturase 2		aaa	tgt	increased
8161	AB032243.SCD2	Scd2	stearoyl-CoA desaturase 2		aaa	tgt	increased
8162	AB032243.SCD2	Scd2	stearoyl-CoA desaturase 2		aaa	tgt	increased
8163	AB032243.SCD2	Scd2	stearoyl-CoA desaturase 2		aaa	tgt	increased
8164	AB032243.SCD2	Scd2	stearoyl-CoA desaturase 2		aaa	tgt	increased
8165	AB032243.SCD2	Scd2	stearoyl-CoA desaturase 2		aaa	tgt	increased
8166	AB032243.SCD2	Scd2	stearoyl-CoA desaturase 2		aaa	tgt	increased
8167	RNU37138.STS	Sts	steroid sulfatase		ctg	agg	decreased
8168	RNU37138.STS	Sts	steroid sulfatase		aac	ctc	decreased
8169	RNU37138.STS	Sts	steroid sulfatase		ccc	aga	decreased
8170	RNU37138.STS	Sts	steroid sulfatase		ccc	aga	decreased
8171	RNU37138.STS	Sts	steroid sulfatase		ccc	aga	decreased
8172	RNU37138.STS	Sts	steroid sulfatase		ccc	aga	decreased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
8173	Hha1	6	aga	127.097	127	127.18	127.06	127.05	30 600 000	3 500 000	5 400 000	-=	\ (-)		/(4)
8174	Hha1	6	aga	127.6	127	0	127.54	127.66	0	3 100 000	6 300 000	++	/		/(4)
8175	Hha1	40	tgg	242.15	243	241.94	0	242.36	11 200 000	0	5 600 000	-+(-)	V (\)		/(4)
8176	Hha1	40	tgg	242.917	243	242.9	242.91	242.94	33 800 000	14 700 000	13 400 000	-=	\ (-)		/(4)
8177	Hha1	40	tgg	243.765	243	243.61	243.92	0	7 100 000	5 000 000	0	=-	\		/(4)
8178	Hha1	39	agg	253.2	252	253.21	253.28	253.11	315.24	334.34	378.41	==	-		/(4)
8179	Taq1	8	gaa	72.803	73	72.97	72.82	72.62	3 000 000	22 500 000	17 300 000	+=	/ (-)		-2
8180	Taq1	55	tca	86.67	87	86.82	86.35	86.84	5 500 000	8 100 000	4 100 000	=-	\ (-)		-2
8181	Taq1	55	tca	87.34	87	0	87.34	0	0	14 400 000	0	+-	A		-2
8182	Taq1	36	ggt	117.5	118	117.47	117.49	117.54	7 000 000	17 400 000	3 900 000	+-	A		\(3)
8183	Taq1	36	ggt	118.645	118	0	118.78	118.51	0	6 200 000	6 200 000	+=	/		\(3)
8184	Hha1	21	acc	189.33	190	189.33	0	0	4 700 000	0	0	-=	\	\	\(3)
8185	Taq1	21	acc	189.49	190	189.49	0	0	5 200 000	0	0	-=	\	\	\(3)
8186	Taq1	21	acc	190.48	190	0	190.55	190.41	0	6 400 000	3 100 000	+-	A		\(3)
8187	Hha1	21	acc	191.02	190	191.02	0	0	39 700 000	0	0	-=	\		\(3)
8188	Hha1	26	ctg	160.49	161	0	0	160.49	0	0	9 400 000	=+	/		/(3) \(3)
8189	Hha1	26	ctg	161.59	161	161.59	0	0	3 000 000	0	0	-=	\		/(3) \(3)
8190	Hha1	61	tct	160.49	161	160.65	160.33	0	3 300 000	3 600 000	0	=-	\		/(3) \(3)
8191	Hha1	61	tct	161.41	161	0	161.41	0	0	13 200 000	0	+-	A		/(3) \(3)
8192	Hha1	32	gtc	164.93	165	164.93	0	0	750.64	0	0	-=	\		/(3) \(3)
8193	Hha1	32	gtc	165.45	165	0	0	165.45	0	0	469.31	=+	/		/(3) \(3)
8194	Hha1	41	ccc	181.43	181	0	0	181.43	0	0	3 400 000	=+	/		/(3) \(3)
8195	Hha1	17	cca	182.767	182	182.67	182.81	182.82	4 592.77	7 157.46	12 053.35	==	-		/(3) \(3)
8196	Hha1	59	ttc	82.87	83	0	82.87	0	0	339.19	0	+-	A		\(2)
8197	Hha1	59	ttc	83.34	83	83.5	83.18	0	421.21	494.42	0	=-	\		\(2)
8198	Taq1	49	aaa	376.8	378	376.8	0	0	13 100 000	0	0	-=	\		\(2)
8199	Taq1	49	aaa	379.575	378	379.37	379.78	0	4 900 000	7 100 000	0	=-	\		\(2)
8200	Hha1	59	ttc	82.87	83	0	82.87	0	0	339.19	0	+-	A		\(2)
8201	Hha1	59	ttc	83.34	83	83.5	83.18	0	421.21	494.42	0	=-	\		\(2)
8202	Taq1	49	aaa	376.8	378	376.8	0	0	13 100 000	0	0	-=	\		\(2)
8203	Taq1	49	aaa	379.575	378	379.37	379.78	0	4 900 000	7 100 000	0	=-	\		\(2)
8204	Hha1	26	ctg	126.61	127	126.75	126.75	126.33	29 700 000	8 000 000	5 600 000	-=	\ (-)		\(2)
8205	Hha1	26	ctg	127.69	127	127.69	0	0	3 600 000	0	0	-=	\		\(2)
8206	Hha1	33	agc	126.97	127	127.07	0	126.87	3 000 000	0	9 600 000	=+(+)	/		\(2)
8207	Hha1	40	tgg	238.06	239	0	238.06	0	0	3 900 000	0	+-	A		\(2)
8208	Hha1	40	tgg	238.845	239	238.71	238.98	0	3 900 000	3 200 000	0	=-	\		\(2)
8209	Hha1	40	tgg	239.97	239	239.97	0	0	4 500 000	0	0	-=	\		\(2)
8210	Taq1	62	tgt	96.507	97	96.37	96.38	96.77	6 900 000	9 300 000	15 900 000	==	-		-(2) \(2)
8211	Taq1	62	tgt	97.33	97	97.16	97.5	0	5 900 000	12 100 000	0	+-	A		-(2) \(2)
8212	Taq1	62	tgt	97.34	97	97.34	0	0	5 600 000	0	0	-=	\	\	-(2) \(2)
8213	Taq1	63	ctt	97.273	97	97.3	97.2	97.32	6 400 000	3 500 000	6 100 000	-=	\ (-)	\	-(2) \(2)
8214	Hha1	16	tag	173.457	174	173.39	173.53	173.45	9 200 000	7 300 000	3 200 000	==	-	(-)	
8215	Taq1	16	tag	173.657	174	173.67	173.57	173.73	3 200 000	3 900 000	12 800 000	=+	/ (-)	(-)	

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
8173	RNU37138.STS	Sts	steroid sulfatase		ccc	aga	decreased
8174	RNU37138.STS	Sts	steroid sulfatase		ccc	aga	decreased
8175	RNU37138.STS	Sts	steroid sulfatase		tgg	tga	decreased
8176	RNU37138.STS	Sts	steroid sulfatase		tgg	tga	decreased
8177	RNU37138.STS	Sts	steroid sulfatase		tgg	tga	decreased
8178	RNU37138.STS	Sts	steroid sulfatase		agg	cat	decreased
8179	AF071501.RSI	RSI	sterol delta 8-isomerase		ggg	gaa	No change
8180	AF071501.RSI	RSI	sterol delta 8-isomerase		ctg	tca	No change
8181	AF071501.RSI	RSI	sterol delta 8-isomerase		ctg	tca	No change
8182	AY300793.PE1	nc	stonin		gag	ggt	increased
8183	AY300793.PE1	nc	stonin		gag	ggt	increased
8184	AY300793.PE1	nc	stonin		gct	acc	increased
8185	AY300793.PE1	nc	stonin		gct	acc	increased
8186	AY300793.PE1	nc	stonin		gct	acc	increased
8187	AY300793.PE1	nc	stonin		gct	acc	increased
8188	RNSTOP.PE1	nc	STOP protein		ctg	tct	decreased
8189	RNSTOP.PE1	nc	STOP protein		ctg	tct	decreased
8190	RNSTOP.PE1	nc	STOP protein		ctg	tct	decreased
8191	RNSTOP.PE1	nc	STOP protein		ctg	tct	decreased
8192	RNSTOP.PE1	nc	STOP protein		ggc	gtc	decreased
8193	RNSTOP.PE1	nc	STOP protein		ggc	gtc	decreased
8194	RNSTOP.PE1	nc	STOP protein		ccc	cca	decreased
8195	RNSTOP.PE1	nc	STOP protein		ccc	cca	decreased
8196	RATSAPKA.PE1	nc	stress activated protein kinase		cac	ttc	increased
8197	RATSAPKA.PE1	nc	stress activated protein kinase		cac	ttc	increased
8198	RATSAPKA.PE1	nc	stress activated protein kinase		aaa	gac	increased
8199	RATSAPKA.PE1	nc	stress activated protein kinase		aaa	gac	increased
8200	RATSAPKB.PE1	nc	stress activated protein kinase		cac	ttc	increased
8201	RATSAPKB.PE1	nc	stress activated protein kinase		cac	ttc	increased
8202	RATSAPKB.PE1	nc	stress activated protein kinase		aaa	gac	increased
8203	RATSAPKB.PE1	nc	stress activated protein kinase		aaa	gac	increased
8204	AB029330.RSAC2B	rSAC2b	stretch activated channel 2B		ctg	agc	increased
8205	AB029330.RSAC2B	rSAC2b	stretch activated channel 2B		ctg	agc	increased
8206	AB029330.RSAC2B	rSAC2b	stretch activated channel 2B		ctg	agc	increased
8207	AB029330.RSAC2B	rSAC2b	stretch activated channel 2B		tgg	act	increased
8208	AB029330.RSAC2B	rSAC2b	stretch activated channel 2B		tgg	act	increased
8209	AB029330.RSAC2B	rSAC2b	stretch activated channel 2B		tgg	act	increased
8210	S49400.PE1	striatum enric	striatum enriched phosphatase		ctt	tgt	No change
8211	S49400.PE1	striatum enric	striatum enriched phosphatase		ctt	tgt	No change
8212	S49400.PE1	striatum enric	striatum enriched phosphatase		ctt	tgt	increased
8213	S49400.PE1	striatum enric	striatum enriched phosphatase		ctt	tgt	increased
8214	AF230072.PE1	nc	sulfatase FP		tag	aac	No change
8215	AF230072.PE1	nc	sulfatase FP		tag	aac	No change

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
8216	Hha1	41	ccc	101.51	102	0	0	101.51	0	0	5 200 000	=+	/		\(5)
8217	Hha1	41	ccc	102.115	102	102.1	102.13	0	16 000 000	6 700 000	0	-=	\		\(5)
8218	Taq1	45	gcc	121.295	121	121.4	0	121.19	6 000 000	0	11 700 000	-+(+)	V (/)		\(5)
8219	Taq1	47	ggc	120.71	121	120.68	120.74	0	2 830.76	1 241.24	0	-=	\		\(5)
8220	Taq1	45	gcc	132.71	133	0	132.71	0	0	7 200 000	0	+-	A		\(5)
8221	Taq1	19	cac	133.633	134	133.6	133.63	133.67	35 400 000	22 500 000	5 400 000	=-	\ (-)		\(5)
8222	Taq1	19	cac	134.553	134	134.52	134.55	134.59	7 800 000	23 100 000	15 200 000	+=	/ (-)		\(5)
8223	Hha1	49	aaa	177.075	178	177.01	177.14	0	8 500 000	6 900 000	0	=-	\		\(5)
8224	Hha1	49	aaa	177.64	178	177.64	0	0	13 400 000	0	0	-=	\		\(5)
8225	Hha1	49	aaa	178.21	178	178.08	178.34	0	8 200 000	6 100 000	0	=-	\		\(5)
8226	Hha1	49	aaa	178.905	178	178.97	178.84	0	11 500 000	5 600 000	0	--	\		\(5)
8227	Hha1	16	tag	253.16	254	253.16	0	0	21 900 000	0	0	-=	\		\(5)
8228	Hha1	16	tag	254.97	254	254.89	254.97	255.05	3 600 000	4 100 000	5 800 000	==	-		\(5)
8229	Hha1	2	tta	110.547	110	110.33	110.67	110.64	3 900 000	4 000 000	10 100 000	=+	/ (-)		-2
8230	Hha1	27	acg	109.64	110	109.7	109.62	109.6	73 000 000	17 000 000	49 400 000	-=	\ (-)		-2
8231	Taq1	18	cct	111.553	112	111.49	111.59	111.58	25 800 000	21 800 000	5 300 000	=-	\ (-)	\	
8232	Taq1	18	cct	112.613	112	112.59	112.64	112.61	32 900 000	30 500 000	3 000 000	=-	\ (-)	\	
8233	Taq1	39	agg	112.42	112	112.2	112.43	112.63	10 300 000	4 800 000	8 200 000	-=	\ (-)	\	
8234	Taq1	39	agg	111.6	112	111.6	0	0	360.21	0	0	-=	\	\	
8235	Taq1	64	gtt	216.533	217	216.5	216.51	216.59	4 200 000	4 000 000	3 500 000	==	-		\(2)
8236	Taq1	64	gtt	217.51	217	217.56	217.46	0	4 900 000	4 600 000	0	=-	\		\(2)
8237	Taq1	17	cca	309.28	310	309.28	0	0	199.69	0	0	-=	\		\(2)
8238	Taq1	17	cca	310.96	310	0	310.96	0	0	505.25	0	+-	A		\(2)
8239	Taq1	64	gtt	216.533	217	216.5	216.51	216.59	4 200 000	4 000 000	3 500 000	==	-		\(2)
8240	Taq1	64	gtt	217.51	217	217.56	217.46	0	4 900 000	4 600 000	0	=-	\		\(2)
8241	Taq1	17	cca	309.28	310	309.28	0	0	199.69	0	0	-=	\		\(2)
8242	Taq1	17	cca	310.96	310	0	310.96	0	0	505.25	0	+-	A		\(2)
8243	Taq1	64	gtt	216.533	217	216.5	216.51	216.59	4 200 000	4 000 000	3 500 000	==	-		\(2)
8244	Taq1	64	gtt	217.51	217	217.56	217.46	0	4 900 000	4 600 000	0	=-	\		\(2)
8245	Taq1	17	cca	309.28	310	309.28	0	0	199.69	0	0	-=	\		\(2)
8246	Taq1	17	cca	310.96	310	0	310.96	0	0	505.25	0	+-	A		\(2)
8247	Taq1	50	aat	196.29	197	196.44	196.14	0	7 500 000	5 400 000	0	=-	\		\(3)
8248	Taq1	50	aat	197.2	197	196.99	0	197.41	9 700 000	0	7 200 000	-+(=)	V		\(3)
8249	Taq1	50	aat	198.16	197	0	198.16	0	0	7 200 000	0	+-	A		\(3)
8250	Taq1	52	att	196.04	197	0	0	196.04	0	0	5 900 000	=+	/		\(3)
8251	Taq1	52	att	196.88	197	196.88	0	0	3 100 000	0	0	-=	\		\(3)
8252	Taq1	45	gcc	249.12	250	249.12	0	0	4 600 000	0	0	-=	\		\(3)
8253	Taq1	45	gcc	249.73	250	249.73	0	0	4 300 000	0	0	-=	\		\(3)
8254	Taq1	45	gcc	250.13	250	250.13	0	0	4 000 000	0	0	-=	\		\(3)
8255	Hha1	3	aac	196.405	196	196.4	196.41	0	5 900 000	3 100 000	0	--	\		\(2)
8256	Taq1	52	att	196.04	197	0	0	196.04	0	0	5 900 000	=+	/		\(2)
8257	Taq1	52	att	196.88	197	196.88	0	0	3 100 000	0	0	-=	\		\(2)
8258	Taq1	18	cct	111.553	112	111.49	111.59	111.58	25 800 000	21 800 000	5 300 000	=-	\ (-)	\	

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
8216	RATSAT1A.SAT-1	sat-1	sulfate anion transporter		cat	ccc	increased
8217	RATSAT1A.SAT-1	sat-1	sulfate anion transporter		cat	ccc	increased
8218	RATSAT1A.SAT-1	sat-1	sulfate anion transporter		ggc	gcc	increased
8219	RATSAT1A.SAT-1	sat-1	sulfate anion transporter		ggc	gcc	increased
8220	RATSAT1A.SAT-1	sat-1	sulfate anion transporter		cac	gcc	increased
8221	RATSAT1A.SAT-1	sat-1	sulfate anion transporter		cac	gcc	increased
8222	RATSAT1A.SAT-1	sat-1	sulfate anion transporter		cac	gcc	increased
8223	RATSAT1A.SAT-1	sat-1	sulfate anion transporter		aaa	tgt	increased
8224	RATSAT1A.SAT-1	sat-1	sulfate anion transporter		aaa	tgt	increased
8225	RATSAT1A.SAT-1	sat-1	sulfate anion transporter		aaa	tgt	increased
8226	RATSAT1A.SAT-1	sat-1	sulfate anion transporter		aaa	tgt	increased
8227	RATSAT1A.SAT-1	sat-1	sulfate anion transporter		tgg	tag	increased
8228	RATSAT1A.SAT-1	sat-1	sulfate anion transporter		tgg	tag	increased
8229	AB044285.SOX	SOx	sulfhydryl oxidase		tta	acg	No change
8230	AB044285.SOX	SOx	sulfhydryl oxidase		tta	acg	No change
8231	RATSUR.SUR	SUR	sulfonylurea receptor		cct	agg	increased
8232	RATSUR.SUR	SUR	sulfonylurea receptor		cct	agg	increased
8233	RATSUR.SUR	SUR	sulfonylurea receptor		cct	agg	increased
8234	RATSUR.SUR	SUR	sulfonylurea receptor		cct	agg	increased
8235	RATSURES1.PE1	nc	sulfonylurea receptor		cca	gtt	increased
8236	RATSURES1.PE1	nc	sulfonylurea receptor		cca	gtt	increased
8237	RATSURES1.PE1	nc	sulfonylurea receptor		agt	cca	increased
8238	RATSURES1.PE1	nc	sulfonylurea receptor		agt	cca	increased
8239	AF019628.PE1	nc	sulfonylurea receptor 2B		cca	gtt	increased
8240	AF019628.PE1	nc	sulfonylurea receptor 2B		cca	gtt	increased
8241	AF019628.PE1	nc	sulfonylurea receptor 2B		agt	cca	increased
8242	AF019628.PE1	nc	sulfonylurea receptor 2B		agt	cca	increased
8243	AF087838.SUR2B	SUR2B	sulfonylurea receptor 2B		cca	gtt	increased
8244	AF087838.SUR2B	SUR2B	sulfonylurea receptor 2B		cca	gtt	increased
8245	AF087838.SUR2B	SUR2B	sulfonylurea receptor 2B		agt	cca	increased
8246	AF087838.SUR2B	SUR2B	sulfonylurea receptor 2B		agt	cca	increased
8247	RNO238391.SULTK1	sultK1	sulfotransferase K1		aat	att	increased
8248	RNO238391.SULTK1	sultK1	sulfotransferase K1		aat	att	increased
8249	RNO238391.SULTK1	sultK1	sulfotransferase K1		aat	att	increased
8250	RNO238391.SULTK1	sultK1	sulfotransferase K1		aat	att	increased
8251	RNO238391.SULTK1	sultK1	sulfotransferase K1		aat	att	increased
8252	RNO238391.SULTK1	sultK1	sulfotransferase K1		cat	gcc	increased
8253	RNO238391.SULTK1	sultK1	sulfotransferase K1		cat	gcc	increased
8254	RNO238391.SULTK1	sultK1	sulfotransferase K1		cat	gcc	increased
8255	RNO238392.SULTK2	sultK2	sulfotransferase K2		aac	att	increased
8256	RNO238392.SULTK2	sultK2	sulfotransferase K2		aac	att	increased
8257	RNO238392.SULTK2	sultK2	sulfotransferase K2		aac	att	increased
8258	AB052294.SUR1	SUR1	sulphonylurea receptor 1		cct	agg	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
8259	Taq1	18	cct	112.613	112	112.59	112.64	112.61	32 900 000	30 500 000	3 000 000	=-	\ (-)	\	
8260	Taq1	39	agg	112.42	112	112.2	112.43	112.63	10 300 000	4 800 000	8 200 000	-=	\ (-)	\	
8261	Taq1	39	agg	111.6	112	111.6	0	0	360.21	0	0	-=	\	\	
8262	Taq1	39	agg	194.44	195	0	0	194.44	0	0	3 000 000	=+	/		\(3)
8263	Taq1	39	agg	195.24	195	195.24	0	0	5 700 000	0	0	-=	\		\(3)
8264	Taq1	39	agg	195.24	195	195.24	0	0	211.67	0	0	-=	\		\(3)
8265	Taq1	39	agg	194.44	195	0	0	194.44	0	0	88.36	=+	/		\(3)
8266	Taq1	64	gtt	216.533	217	216.5	216.51	216.59	4 200 000	4 000 000	3 500 000	==	-		\(3)
8267	Taq1	64	gtt	217.51	217	217.56	217.46	0	4 900 000	4 600 000	0	=-	\		\(3)
8268	Taq1	17	cca	309.28	310	309.28	0	0	199.69	0	0	-=	\		\(3)
8269	Taq1	17	cca	310.96	310	0	310.96	0	0	505.25	0	+-	A		\(3)
8270	Hha1	31	gac	68.3	68	0	0	68.3	0	0	13 700 000	=+	/		\(3)
8271	Hha1	27	acg	80.793	81	80.8	80.87	80.71	27 600 000	3 900 000	13 400 000	-=	\ (-)		\(3)
8272	Hha1	44	cgg	122.3	123	122.42	122.18	0	10 500 000	5 700 000	0	--	\		\(3)
8273	Hha1	43	cgc	164.33	165	164.33	0	0	5 300 000	0	0	-=	\		\(3)
8274	Hha1	20	ctc	82.09	82	0	82.09	0	0	472.06	0	+-	A		A(3)
8275	Taq1	17	cca	103.3	103	103.08	0	103.52	682.67	0	586.37	-+(=)	V		A(3)
8276	Taq1	18	cct	131.687	132	131.61	131.67	131.78	7 500 000	10 900 000	3 000 000	=-	\ (-)		A(3)
8277	Taq1	18	cct	132.74	132	132.73	132.74	132.75	29 100 000	32 500 000	4 200 000	=-	\ (-)		A(3)
8278	Taq1	31	gac	131.425	132	131.49	131.36	0	4 800 000	12 200 000	0	+-	A		A(3)
8279	Taq1	31	gac	132.45	132	132.57	132.33	0	14 200 000	8 500 000	0	=-	\		A(3)
8280	Hha1	56	tga	169.467	170	169.38	169.55	169.47	339.14	462.35	930.87	=+	/ (-)		A(3)
8281	Hha1	56	tga	170.2	170	169.96	0	170.44	441.3	0	1 223.92	=+(+)	/		A(3)
8282	Hha1	56	tga	170.645	170	170.74	170.55	0	126.67	242.18	0	+-	A		A(3)
8283	Hha1	39	agg	65.37	65	65.38	65.36	0	2 631.96	1 355.3	0	--	\		-1
8284	Hha1	44	cgg	99.107	99	99.18	99	99.14	15 800 000	7 100 000	8 700 000	-=	\ (-)		-1
8285	Hha1	56	tga	99.62	100	99.59	99.85	99.42	277.85	297.22	1 379.07	=+	/ (-)		-1
8286	Hha1	32	gtc	123.9	124	0	0	123.9	0	0	361.01	=+	/		-1
8287	Hha1	28	tcg	126.443	127	126.26	126.6	126.47	3 200 000	6 200 000	4 600 000	+=	/ (-)		-1
8288	Hha1	28	tcg	127.14	127	0	127.08	127.2	0	11 300 000	8 900 000	+=	/		-1
8289	Hha1	39	agg	65.37	65	65.38	65.36	0	2 631.96	1 355.3	0	--	\		-1
8290	Hha1	44	cgg	99.107	99	99.18	99	99.14	15 800 000	7 100 000	8 700 000	-=	\ (-)		-1
8291	Hha1	56	tga	99.62	100	99.59	99.85	99.42	277.85	297.22	1 379.07	=+	/ (-)		-1
8292	Hha1	32	gtc	123.9	124	0	0	123.9	0	0	361.01	=+	/		-1
8293	Hha1	28	tcg	126.443	127	126.26	126.6	126.47	3 200 000	6 200 000	4 600 000	+=	/ (-)		-1
8294	Hha1	28	tcg	127.14	127	0	127.08	127.2	0	11 300 000	8 900 000	+=	/		-1
8295	Hha1	44	cgg	114.53	114	0	114.53	0	0	6 900 000	0	+-	A		/(4)
8296	Hha1	40	tgg	114.97	115	0	115.21	114.73	0	4 900 000	4 700 000	+=	/		/(4)
8297	Hha1	40	tgg	115.65	115	115.65	0	0	3 000 000	0	0	-=	\		/(4)
8298	Taq1	31	gac	123.23	123	0	0	123.23	0	0	30 100 000	=+	/		/(4)
8299	Hha1	33	agc	144.21	145	144.2	0	144.22	4 000 000	0	3 500 000	-+(=)	V		/(4)
8300	Hha1	33	agc	145.22	145	0	0	145.22	0	0	7 200 000	=+	/		/(4)
8301	Hha1	33	agc	198.51	199	0	0	198.51	0	0	6 500 000	=+	/		/(4)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
8259	AB052294.SUR1	SUR1	sulphonylurea receptor 1		cct	agg	increased
8260	AB052294.SUR1	SUR1	sulphonylurea receptor 1		cct	agg	increased
8261	AB052294.SUR1	SUR1	sulphonylurea receptor 1		cct	agg	increased
8262	AB045281.SUR2B	SUR2b	sulphonylurea receptor 2b		agg	agg	increased
8263	AB045281.SUR2B	SUR2b	sulphonylurea receptor 2b		agg	agg	increased
8264	AB045281.SUR2B	SUR2b	sulphonylurea receptor 2b		agg	agg	increased
8265	AB045281.SUR2B	SUR2b	sulphonylurea receptor 2b		agg	agg	increased
8266	AB045281.SUR2B	SUR2b	sulphonylurea receptor 2b		cca	gtt	increased
8267	AB045281.SUR2B	SUR2b	sulphonylurea receptor 2b		cca	gtt	increased
8268	AB045281.SUR2B	SUR2b	sulphonylurea receptor 2b		agt	cca	increased
8269	AB045281.SUR2B	SUR2b	sulphonylurea receptor 2b		agt	cca	increased
8270	RNO243123.SOCS-1	socs-1	suppressor of cytokine signalling 1		gac	gaa	increased
8271	RNO243123.SOCS-1	socs-1	suppressor of cytokine signalling 1		acg	acc	increased
8272	RNO243123.SOCS-1	socs-1	suppressor of cytokine signalling 1		cgt	cgg	increased
8273	RNO243123.SOCS-1	socs-1	suppressor of cytokine signalling 1		tca	cgc	increased
8274	AF060173.SVOP	SVOP	SV2 related protein		ctc	cac	increased by mild
8275	AF060173.SVOP	SVOP	SV2 related protein		gct	cca	increased by mild
8276	AF060173.SVOP	SVOP	SV2 related protein		gac	cct	increased by mild
8277	AF060173.SVOP	SVOP	SV2 related protein		gac	cct	increased by mild
8278	AF060173.SVOP	SVOP	SV2 related protein		gac	cct	increased by mild
8279	AF060173.SVOP	SVOP	SV2 related protein		gac	cct	increased by mild
8280	AF060173.SVOP	SVOP	SV2 related protein		tgc	tga	increased by mild
8281	AF060173.SVOP	SVOP	SV2 related protein		tgc	tga	increased by mild
8282	AF060173.SVOP	SVOP	SV2 related protein		tgc	tga	increased by mild
8283	RATS2A.PE1	synapsin 2a	synapsin 2a		agg	ggg	No change
8284	RATS2A.PE1	synapsin 2a	synapsin 2a		cgg	tga	No change
8285	RATS2A.PE1	synapsin 2a	synapsin 2a		cgg	tga	No change
8286	RATS2A.PE1	synapsin 2a	synapsin 2a		cga	gtc	No change
8287	RATS2A.PE1	synapsin 2a	synapsin 2a		ccg	tcg	No change
8288	RATS2A.PE1	synapsin 2a	synapsin 2a		ccg	tcg	No change
8289	RATS2B.PE1	synapsin 2b	synapsin 2b		agg	ggg	No change
8290	RATS2B.PE1	synapsin 2b	synapsin 2b		cgg	tga	No change
8291	RATS2B.PE1	synapsin 2b	synapsin 2b		cgg	tga	No change
8292	RATS2B.PE1	synapsin 2b	synapsin 2b		cga	gtc	No change
8293	RATS2B.PE1	synapsin 2b	synapsin 2b		ccg	tcg	No change
8294	RATS2B.PE1	synapsin 2b	synapsin 2b		ccg	tcg	No change
8295	RATSV2AA.SV2	SV2	synaptic vesicle protein		tgg	cgg	decreased
8296	RATSV2AA.SV2	SV2	synaptic vesicle protein		tgg	cgg	decreased
8297	RATSV2AA.SV2	SV2	synaptic vesicle protein		tgg	cgg	decreased
8298	RATSV2AA.SV2	SV2	synaptic vesicle protein		gac	gac	decreased
8299	RATSV2AA.SV2	SV2	synaptic vesicle protein		agc	cag	decreased
8300	RATSV2AA.SV2	SV2	synaptic vesicle protein		agc	cag	decreased
8301	RATSV2AA.SV2	SV2	synaptic vesicle protein		tgg	agc	decreased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
8302	Hha1	33	agc	199.49	199	0	0	199.49	0	0	7 700 000	=+	/		/(4)
8303	Hha1	40	tgg	198.35	199	198.35	0	0	4 300 000	0	0	-=	\		/(4)
8304	Hha1	40	tgg	200.105	199	199.94	200.27	0	4 100 000	4 000 000	0	=-	\		/(4)
8305	Hha1	59	ttc	218.29	219	218.29	0	0	187.2	0	0	-=	\		/(4)
8306	Hha1	26	ctg	161.59	162	161.59	0	0	3 000 000	0	0	-=	\		\(2)
8307	Hha1	59	ttc	161.135	162	161.27	161	0	202.8	301.82	0	=-	\		\(2)
8308	Hha1	59	ttc	161.55	162	0	0	161.55	0	0	426.87	=+	/		\(2)
8309	Hha1	26	ctg	161.59	162	161.59	0	0	3 000 000	0	0	-=	\		\(2)
8310	Hha1	59	ttc	161.135	162	161.27	161	0	202.8	301.82	0	=-	\		\(2)
8311	Hha1	59	ttc	161.55	162	0	0	161.55	0	0	426.87	=+	/		\(2)
8312	Hha1	11	act	201.35	201	0	0	201.35	0	0	3 800 000	=+	/	/	
8313	Taq1	11	act	201.4	201	0	0	201.4	0	0	3 700 000	=+	/	/	
8314	Taq1	45	gcc	186.905	188	186.86	186.95	0	10 000 000	4 500 000	0	--	\		\(2)
8315	Taq1	45	gcc	187.92	188	187.92	0	0	3 100 000	0	0	-=	\		\(2)
8316	Taq1	45	gcc	189.03	188	188.98	189.08	0	7 500 000	5 300 000	0	=-	\		\(2)
8317	Taq1	25	cat	188.605	189	188.8	188.41	0	1 296.57	1 654.99	0	=-	\		\(2)
8318	Taq1	25	cat	189.415	189	189.39	189.44	0	1 351.16	11 063.01	0	+-	A		\(2)
8319	Hha1	11	act	201.35	201	0	0	201.35	0	0	3 800 000	=+	/	/	
8320	Taq1	11	act	201.4	201	0	0	201.4	0	0	3 700 000	=+	/	/	
8321	Taq1	45	gcc	186.905	188	186.86	186.95	0	10 000 000	4 500 000	0	--	\		\(2)
8322	Taq1	45	gcc	187.92	188	187.92	0	0	3 100 000	0	0	-=	\		\(2)
8323	Taq1	45	gcc	189.03	188	188.98	189.08	0	7 500 000	5 300 000	0	=-	\		\(2)
8324	Taq1	25	cat	188.605	189	188.8	188.41	0	1 296.57	1 654.99	0	=-	\		\(2)
8325	Taq1	25	cat	189.415	189	189.39	189.44	0	1 351.16	11 063.01	0	+-	A		\(2)
8326	Hha1	3	aac	215.87	216	215.87	0	0	4 500 000	0	0	-=	\		\(2)
8327	Hha1	6	aga	215.46	216	215.46	0	0	6 800 000	0	0	-=	\		\(2)
8328	Hha1	6	aga	215.98	216	0	0	215.98	0	0	3 100 000	=+	/		\(2)
8329	Hha1	6	aga	216.94	216	216.94	0	0	74 800 000	0	0	-=	\		\(2)
8330	Taq1	22	tcc	159.33	160	0	0	159.33	0	0	9 900 000	=+	/		/(4)
8331	Hha1	22	tcc	159.96	160	0	159.96	0	0	3 900 000	0	+-	A		/(4)
8332	Taq1	22	tcc	160.37	160	0	0	160.37	0	0	4 000 000	=+	/		/(4)
8333	Taq1	54	ttt	160.17	161	160.17	0	0	997.81	0	0	-=	\		/(4)
8334	Taq1	54	ttt	160.8	161	160.71	160.91	160.78	1 988.34	858.52	3 875.8	=+	/ (-)		/(4)
8335	Taq1	54	ttt	161.917	161	161.97	161.87	161.91	2 097.59	1 023.16	3 019.27	=+	/ (-)		/(4)
8336	Hha1	9	atc	207.44	208	207.43	207.47	207.42	16 400 000	19 600 000	37 700 000	=+	/ (-)	(-)	/(4)
8337	Hha1	9	atc	208.77	208	0	208.93	208.61	0	3 300 000	3 900 000	+=	/		/(4)
8338	Taq1	19	cac	207.43	208	207.39	207.47	207.43	6 800 000	4 900 000	3 500 000	==	-	(-)	/(4)
8339	Taq1	19	cac	208.407	208	208.43	208.38	208.41	4 500 000	4 800 000	6 400 000	==	-		/(4)
8340	Hha1	41	ccc	181.43	182	0	0	181.43	0	0	3 400 000	=+	/		\(2)
8341	Hha1	41	ccc	182.45	182	182.45	0	0	4 300 000	0	0	-=	\		\(2)
8342	Hha1	44	cgg	207.37	207	207.37	0	0	4 700 000	0	0	-=	\		\(2)
8343	Hha1	59	ttc	83.91	84	0	83.91	0	0	379.44	0	+-	A		-2
8344	Hha1	59	ttc	84.45	84	84.45	0	0	358.81	0	0	-=	\		-2

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
8302	RATSV2AA.SV2	SV2	synaptic vesicle protein		tgg	agc	decreased
8303	RATSV2AA.SV2	SV2	synaptic vesicle protein		tgg	agc	decreased
8304	RATSV2AA.SV2	SV2	synaptic vesicle protein		tgg	agc	decreased
8305	RATSV2AA.SV2	SV2	synaptic vesicle protein		ttc	ctc	decreased
8306	RNU26402.PE1	nc	synaptotagmin 5	*	ctg	ttc	increased
8307	RNU26402.PE1	nc	synaptotagmin 5	*	ctg	ttc	increased
8308	RNU26402.PE1	nc	synaptotagmin 5	*	ctg	ttc	increased
8309	RNRNASYNV.PE1	nc	synaptotagmin V	*	ctg	ttc	increased
8310	RNRNASYNV.PE1	nc	synaptotagmin V	*	ctg	ttc	increased
8311	RNRNASYNV.PE1	nc	synaptotagmin V	*	ctg	ttc	increased
8312	AF139492.PE1	nc	syndapin IIaa		act	agg	decreased
8313	AF139492.PE1	nc	syndapin IIaa		act	agg	decreased
8314	AF139493.PE1	nc	syndapin IIab		gcc	cat	increased
8315	AF139493.PE1	nc	syndapin IIab		gcc	cat	increased
8316	AF139493.PE1	nc	syndapin IIab		gcc	cat	increased
8317	AF139493.PE1	nc	syndapin IIab		gcc	cat	increased
8318	AF139493.PE1	nc	syndapin IIab		gcc	cat	increased
8319	AF139494.PE1	nc	syndapin IIba		act	agg	decreased
8320	AF139494.PE1	nc	syndapin IIba		act	agg	decreased
8321	AF139495.PE1	nc	syndapin IIbb		gcc	cat	increased
8322	AF139495.PE1	nc	syndapin IIbb		gcc	cat	increased
8323	AF139495.PE1	nc	syndapin IIbb		gcc	cat	increased
8324	AF139495.PE1	nc	syndapin IIbb		gcc	cat	increased
8325	AF139495.PE1	nc	syndapin IIbb		gcc	cat	increased
8326	AF033109.PE1	nc	syntaxin 8		aga	aac	increased
8327	AF033109.PE1	nc	syntaxin 8		aga	aac	increased
8328	AF033109.PE1	nc	syntaxin 8		aga	aac	increased
8329	AF033109.PE1	nc	syntaxin 8		aga	aac	increased
8330	AF173682.SAT2	SAT2	system A transporter isoform 2	*	ttt	tcc	decreased
8331	AF173682.SAT2	SAT2	system A transporter isoform 2	*	ttt	tcc	decreased
8332	AF173682.SAT2	SAT2	system A transporter isoform 2	*	ttt	tcc	decreased
8333	AF173682.SAT2	SAT2	system A transporter isoform 2	*	ttt	tcc	decreased
8334	AF173682.SAT2	SAT2	system A transporter isoform 2	*	ttt	tcc	decreased
8335	AF173682.SAT2	SAT2	system A transporter isoform 2	*	ttt	tcc	decreased
8336	AF173682.SAT2	SAT2	system A transporter isoform 2	*	atc	cac	No change
8337	AF173682.SAT2	SAT2	system A transporter isoform 2	*	atc	cac	decreased
8338	AF173682.SAT2	SAT2	system A transporter isoform 2	*	atc	cac	No change
8339	AF173682.SAT2	SAT2	system A transporter isoform 2	*	atc	cac	decreased
8340	AF203697.CACNA1I	Cacna1i	T calcium channel alpha1I subunit, delta36B		cgc	ccc	increased
8341	AF203697.CACNA1I	Cacna1i	T calcium channel alpha1I subunit, delta36B		cgc	ccc	increased
8342	AF203697.CACNA1I	Cacna1i	T calcium channel alpha1I subunit, delta36B		cag	cgg	increased
8343	AF287301.KCNK13	Kcnk13	tandem pore domain potassium channel THIK-1		ttc	cgc	No change
8344	AF287301.KCNK13	Kcnk13	tandem pore domain potassium channel THIK-1		ttc	cgc	No change

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
8345	Hha1	26	ctg	144.19	145	0	0	144.19	0	0	48 200 000	=+	/		-2
8346	Hha1	26	ctg	145.12	145	145.08	145.05	145.23	7 300 000	10 100 000	6 000 000	==	-		-2
8347	Hha1	27	acg	145.58	145	145.46	145.6	145.68	9 300 000	5 700 000	5 900 000	==	-		-2
8348	Hha1	33	agc	123.97	124	123.91	124.03	0	3 500 000	4 200 000	0	=-	\		\(3)
8349	Hha1	20	ctc	138.81	139	138.81	0	0	426.99	0	0	-=	\		\(3)
8350	Hha1	20	ctc	139.71	139	139.73	0	139.69	550.96	0	477.09	-+(=)	V		\(3)
8351	Hha1	40	tgg	145.52	146	145.53	145.44	145.59	3 100 000	9 400 000	9 100 000	+=	/ (-)		\(3)
8352	Hha1	40	tgg	146.47	146	0	146.34	146.6	0	9 800 000	16 400 000	+=	/		\(3)
8353	Hha1	59	ttc	202.71	203	202.9	202.52	0	228.8	160.97	0	=-	\		\(3)
8354	Hha1	59	ttc	203.25	203	0	203.25	0	0	238.58	0	+-	A		\(3)
8355	Taq1	64	gtt	97.34	97	97.3	97.26	97.46	14 000 000	12 900 000	14 000 000	==	-		-2
8356	Hha1	26	ctg	126.61	127	126.75	126.75	126.33	29 700 000	8 000 000	5 600 000	-=	\ (-)		-2
8357	Hha1	26	ctg	127.69	127	127.69	0	0	3 600 000	0	0	-=	\		-2
8358	Hha1	27	acg	109.64	110	109.7	109.62	109.6	73 000 000	17 000 000	49 400 000	-=	\ (-)		-(3) \(3)
8359	Hha1	40	tgg	109.35	110	0	0	109.35	0	0	21 600 000	=+	/		-(3) \(3)
8360	Hha1	40	tgg	110.207	110	110.02	110.18	110.42	6 400 000	10 400 000	8 000 000	==	-		-(3) \(3)
8361	Hha1	27	acg	114.05	114	114.04	0	114.06	11 200 000	0	8 100 000	-+(=)	V		-(3) \(3)
8362	Hha1	58	gta	142.27	143	142.32	142.22	0	9 100 000	10 200 000	0	=-	\		-(3) \(3)
8363	Hha1	58	gta	143.29	143	143.3	143.26	143.31	34 900 000	80 400 000	17 000 000	+-	A		-(3) \(3)
8364	Hha1	59	ttc	142.43	143	0	142.43	0	0	238.58	0	+-	A		-(3) \(3)
8365	Hha1	59	ttc	143.267	143	143.26	143.18	143.36	343.21	408.18	152.64	=-	\ (-)		-(3) \(3)
8366	Hha1	59	ttc	97.02	97	0	97.18	96.86	0	114.98	385.48	=+	/		/(3) A(2)
8367	Hha1	4	aag	181.09	182	0	181.09	0	0	3 800 000	0	+-	A		/(3) A(2)
8368	Hha1	4	aag	182.08	182	0	182.09	182.07	0	3 200 000	8 700 000	=+	/		/(3) A(2)
8369	Hha1	4	aag	182.81	182	0	0	182.81	0	0	3 100 000	=+	/		/(3) A(2)
8370	Hha1	4	aag	183.04	182	0	0	183.04	0	0	3 200 000	=+	/		/(3) A(2)
8371	Hha1	59	ttc	210.83	212	0	210.83	0	0	209.84	0	+-	A		/(3) A(2)
8372	Hha1	59	ttc	212.235	212	0	212.38	212.09	0	103.48	807.18	=+	/		/(3) A(2)
8373	Hha1	59	ttc	212.83	212	0	0	212.83	0	0	87.96	=+	/		/(3) A(2)
8374	Hha1	39	agg	87.397	87	87.19	87.6	87.4	1 312.31	447.78	545.24	-=	\ (-)		-1
8375	Taq1	19	cac	136.657	137	136.65	136.74	136.58	6 900 000	4 400 000	16 200 000	=+	/ (-)		-1
8376	Taq1	19	cac	137.673	137	137.58	137.63	137.81	10 700 000	7 000 000	3 500 000	==	-		-1
8377	Taq1	36	ggt	136.843	137	136.84	136.95	136.74	4 000 000	22 200 000	6 500 000	+-	A		-1
8378	Taq1	36	ggt	137.72	137	0	0	137.72	0	0	3 500 000	=+	/		-1
8379	Taq1	44	cgg	143.71	144	143.55	143.58	144	708.25	538.36	762.16	==	-		\(4)
8380	Hha1	8	gaa	144.2	145	144.05	144.49	144.06	14 700 000	4 700 000	10 300 000	-=	\ (-)		\(4)
8381	Hha1	8	gaa	144.4	145	0	0	144.4	0	0	10 400 000	=+	/		\(4)
8382	Taq1	8	gaa	145.64	145	145.76	145.52	0	3 700 000	3 600 000	0	=-	\	\	\(4)
8383	Hha1	8	gaa	145.41	145	145.41	0	0	6 400 000	0	0	-=	\	\	\(4)
8384	Taq1	49	aaa	289.78	291	0	289.78	0	0	5 500 000	0	+-	A		\(4)
8385	Taq1	49	aaa	290.615	291	290.39	290.84	0	16 600 000	7 000 000	0	-=	\		\(4)
8386	Hha1	39	agg	64.247	64	64.4	64.03	64.31	3 643.69	1 003.04	1 786.29	-=	\ (-)		\(3)
8387	Hha1	49	aaa	83.23	83	83.34	83.06	83.29	78 500 000	26 300 000	16 900 000	-=	\ (-)		\(3)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
8345	AF287301.KCNK13	Kcnk13	tandem pore domain potassium channel THIK-1		ctg	acg	No change
8346	AF287301.KCNK13	Kcnk13	tandem pore domain potassium channel THIK-1		ctg	acg	No change
8347	AF287301.KCNK13	Kcnk13	tandem pore domain potassium channel THIK-1		ctg	acg	No change
8348	AF467250.PE1	nc	tandem pore potassium channel		agc	tcc	increased
8349	AF467250.PE1	nc	tandem pore potassium channel		act	ctc	increased
8350	AF467250.PE1	nc	tandem pore potassium channel		act	ctc	increased
8351	AF467250.PE1	nc	tandem pore potassium channel		tgc	tgg	increased
8352	AF467250.PE1	nc	tandem pore potassium channel		tgc	tgg	increased
8353	AF467250.PE1	nc	tandem pore potassium channel		ttc	gtt	increased
8354	AF467250.PE1	nc	tandem pore potassium channel		ttc	gtt	increased
8355	AB027520.TAPL	TAPL	TAP-like ABC transporter		gtt	gat	No change
8356	AB027520.TAPL	TAPL	TAP-like ABC transporter		ctg	acc	No change
8357	AB027520.TAPL	TAPL	TAP-like ABC transporter		ctg	acc	No change
8358	AB048823.KCNK3B	KCNK3b	TASK1 splice bvariant (TASK1b)		acg	ccg	No change
8359	AB048823.KCNK3B	KCNK3b	TASK1 splice bvariant (TASK1b)		tgg	cac	No change
8360	AB048823.KCNK3B	KCNK3b	TASK1 splice bvariant (TASK1b)		tgg	cac	No change
8361	AB048823.KCNK3B	KCNK3b	TASK1 splice bvariant (TASK1b)		ctt	acg	No change
8362	AB048823.KCNK3B	KCNK3b	TASK1 splice bvariant (TASK1b)		ttc	gta	No change
8363	AB048823.KCNK3B	KCNK3b	TASK1 splice bvariant (TASK1b)		ttc	gta	No change
8364	AB048823.KCNK3B	KCNK3b	TASK1 splice bvariant (TASK1b)		ttc	gta	No change
8365	AB048823.KCNK3B	KCNK3b	TASK1 splice bvariant (TASK1b)		ttc	gta	No change
8366	BC058463.PE1	nc	TCEB2 protein		cac	ttc	decreased
8367	BC058463.PE1	nc	TCEB2 protein		ggg	aag	decreased
8368	BC058463.PE1	nc	TCEB2 protein		ggg	aag	decreased
8369	BC058463.PE1	nc	TCEB2 protein		ggg	aag	decreased
8370	BC058463.PE1	nc	TCEB2 protein		ggg	aag	decreased
8371	BC058463.PE1	nc	TCEB2 protein		atc	ttc	decreased
8372	BC058463.PE1	nc	TCEB2 protein		atc	ttc	decreased
8373	BC058463.PE1	nc	TCEB2 protein		atc	ttc	decreased
8374	RNO306427.PE1	nc	tektin		tga	agg	No change
8375	RNO306427.PE1	nc	tektin		ggt	cac	No change
8376	RNO306427.PE1	nc	tektin		ggt	cac	No change
8377	RNO306427.PE1	nc	tektin		ggt	cac	No change
8378	RNO306427.PE1	nc	tektin		ggt	cac	No change
8379	AF146738.PE1	nc	testis specific protein		gaa	cgg	increased
8380	AF146738.PE1	nc	testis specific protein		gaa	cgg	increased
8381	AF146738.PE1	nc	testis specific protein		gaa	cgg	increased
8382	AF146738.PE1	nc	testis specific protein		gaa	cgg	increased
8383	AF146738.PE1	nc	testis specific protein		gaa	cgg	increased
8384	AF146738.PE1	nc	testis specific protein		agt	aaa	increased
8385	AF146738.PE1	nc	testis specific protein		agt	aaa	increased
8386	RNTSAKAP.PE1	nc	Testis-specific A-kinase-anchoring-protein		ctt	agg	increased
8387	RNTSAKAP.PE1	nc	Testis-specific A-kinase-anchoring-protein		cag	aaa	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
8388	Taq1	49	aaa	309.47	311	0	309.47	0	0	4 900 000	0	+-	A		\(3)
8389	Taq1	49	aaa	311.91	311	0	311.91	0	0	3 100 000	0	+-	A		\(3)
8390	Taq1	49	aaa	312.61	311	312.61	0	0	6 500 000	0	0	-=	\		\(3)
8391	Taq1	25	cat	114.983	115	115	114.86	115.09	716.52	432.84	2 590.24	=+	/ (-)		\(2)
8392	Taq1	25	cat	115.55	115	115.55	0	0	627.81	0	0	-=	\		\(2)
8393	Taq1	39	agg	243.37	244	0	243.37	0	0	16 700 000	0	+-	A		\(2)
8394	Taq1	39	agg	243.37	244	0	243.37	0	0	167.84	0	+-	A		\(2)
8395	Taq1	39	agg	244.99	244	244.99	0	0	4 200 000	0	0	-=	\		\(2)
8396	Taq1	39	agg	244.99	244	244.99	0	0	155.97	0	0	-=	\		\(2)
8397	Hha1	27	acg	72.105	72	0	72.1	72.11	0	3 400 000	5 600 000	+=	/		/(2)
8398	Hha1	27	acg	116.92	117	116.92	0	0	3 700 000	0	0	-=	\		/(2)
8399	Taq1	56	tga	151.42	151	0	0	151.42	0	0	3 000 000	=+	/		/(2)
8400	Taq1	25	cat	114.983	115	115	114.86	115.09	716.52	432.84	2 590.24	=+	/ (-)		\(2)
8401	Taq1	25	cat	115.55	115	115.55	0	0	627.81	0	0	-=	\		\(2)
8402	Taq1	39	agg	243.37	244	0	243.37	0	0	16 700 000	0	+-	A		\(2)
8403	Taq1	39	agg	243.37	244	0	243.37	0	0	167.84	0	+-	A		\(2)
8404	Taq1	39	agg	244.99	244	244.99	0	0	4 200 000	0	0	-=	\		\(2)
8405	Taq1	39	agg	244.99	244	244.99	0	0	155.97	0	0	-=	\		\(2)
8406	Hha1	26	ctg	186.76	187	0	186.76	0	0	3 000 000	0	+-	A		A(2)
8407	Hha1	26	ctg	188.1	187	188.1	0	0	3 500 000	0	0	-=	\		A(2)
8408	Hha1	61	tct	185.955	187	0	185.97	185.94	0	8 300 000	5 300 000	+=	/		A(2)
8409	Hha1	61	tct	186.79	187	0	0	186.79	0	0	4 200 000	=+	/		A(2)
8410	Hha1	61	tct	187.957	187	188.05	187.91	187.91	6 000 000	11 300 000	11 700 000	+=	/ (-)		A(2)
8411	Hha1	59	ttc	196.9	198	0	196.9	0	0	106.35	0	+-	A		A(2)
8412	Hha1	54	ttt	87.58	88	0	0	87.58	0	0	12 600 000	=+	/		\(3)
8413	Hha1	39	agg	159.2	160	159.37	159.03	0	271.26	310.46	0	=-	\		\(3)
8414	Hha1	39	agg	160.39	160	160.39	0	0	278.59	0	0	-=	\		\(3)
8415	Hha1	3	aac	190.345	191	190.34	190.35	0	4 500 000	4 900 000	0	=-	\	\	\(3)
8416	Hha1	3	aac	191.21	191	191.09	191.33	0	6 500 000	5 200 000	0	=-	\		\(3)
8417	Hha1	6	aga	190.215	191	190.2	0	190.23	10 700 000	0	3 000 000	-=(-)	\	\	\(3)
8418	Hha1	6	aga	190.85	191	190.85	0	0	9 800 000	0	0	-=	\		\(3)
8419	Hha1	6	aga	191.46	191	0	0	191.46	0	0	3 800 000	=+	/		\(3)
8420	Taq1	17	cca	153.253	154	153.4	153.13	153.23	227.55	1 183.35	736.73	+=	/ (-)		/(3) -(2)
8421	Taq1	17	cca	154.253	154	154.31	154.15	154.3	469.04	678.1	1 428.35	=+	/ (-)		/(3) -(2)
8422	Taq1	61	tct	153.125	154	153.08	0	153.17	5 500 000	0	9 100 000	-+(=)	V		/(3) -(2)
8423	Taq1	61	tct	153.99	154	0	153.85	154.13	0	4 700 000	7 000 000	+=	/		/(3) -(2)
8424	Taq1	50	aat	306.507	308	306.54	306.51	306.47	7 100 000	4 500 000	4 800 000	==	-		/(3) -(2)
8425	Taq1	50	aat	306.64	308	0	0	306.64	0	0	4 800 000	=+	/		/(3) -(2)
8426	Taq1	50	aat	308.47	308	308.26	308.68	0	4 400 000	4 900 000	0	=-	\		/(3) -(2)
8427	Taq1	50	aat	309.48	308	0	309.48	0	0	5 800 000	0	+-	A		/(3) -(2)
8428	Hha1	58	gta	119.3	119	0	119.3	0	0	4 500 000	0	+-	A		\(4)
8429	Hha1	59	ttc	118.745	119	118.81	118.68	0	228.8	324.82	0	=-	\		\(4)
8430	Hha1	59	ttc	119.5	119	119.76	119.46	119.28	410.81	376.56	250.95	==	-		\(4)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
8388	RNTSAKAP.PE1	nc	Testis-specific A-kinase-anchoring-protein		aaa	atc	increased
8389	RNTSAKAP.PE1	nc	Testis-specific A-kinase-anchoring-protein		aaa	atc	increased
8390	RNTSAKAP.PE1	nc	Testis-specific A-kinase-anchoring-protein		aaa	atc	increased
8391	AF153013.PE1	TGF-beta2	TGF-beta 2 short form precursor		cat	agc	increased
8392	AF153013.PE1	TGF-beta2	TGF-beta 2 short form precursor		cat	agc	increased
8393	AF153013.PE1	TGF-beta2	TGF-beta 2 short form precursor		tgt	agg	increased
8394	AF153013.PE1	TGF-beta2	TGF-beta 2 short form precursor		tgt	agg	increased
8395	AF153013.PE1	TGF-beta2	TGF-beta 2 short form precursor		tgt	agg	increased
8396	AF153013.PE1	TGF-beta2	TGF-beta 2 short form precursor		tgt	agg	increased
8397	RATTGFB.PE1	TGF-beta mas	TGF-beta masking protein large subunit		acg	acc	decreased
8398	RATTGFB.PE1	TGF-beta mas	TGF-beta masking protein large subunit		cca	acg	decreased
8399	RATTGFB.PE1	TGF-beta mas	TGF-beta masking protein large subunit		tga	ggc	decreased
8400	RNO132718.PE1	tgf-beta2	TGF-beta2 protein		cat	agc	increased
8401	RNO132718.PE1	tgf-beta2	TGF-beta2 protein		cat	agc	increased
8402	RNO132718.PE1	tgf-beta2	TGF-beta2 protein		tgt	agg	increased
8403	RNO132718.PE1	tgf-beta2	TGF-beta2 protein		tgt	agg	increased
8404	RNO132718.PE1	tgf-beta2	TGF-beta2 protein		tgt	agg	increased
8405	RNO132718.PE1	tgf-beta2	TGF-beta2 protein		tgt	agg	increased
8406	RNU10097.PE1	nc	thiazide-sensitive sodium-chloride		tct	ctg	increased by mild
8407	RNU10097.PE1	nc	thiazide-sensitive sodium-chloride		tct	ctg	increased by mild
8408	RNU10097.PE1	nc	thiazide-sensitive sodium-chloride		tct	ctg	increased by mild
8409	RNU10097.PE1	nc	thiazide-sensitive sodium-chloride		tct	ctg	increased by mild
8410	RNU10097.PE1	nc	thiazide-sensitive sodium-chloride		tct	ctg	increased by mild
8411	RNU10097.PE1	nc	thiazide-sensitive sodium-chloride		ttc	tgt	increased by mild
8412	AF022743.PE1	nc	thrombomodulin		ttt	tgg	increased
8413	AF022743.PE1	nc	thrombomodulin		tcc	agg	increased
8414	AF022743.PE1	nc	thrombomodulin		tcc	agg	increased
8415	AF022743.PE1	nc	thrombomodulin		aac	aga	increased
8416	AF022743.PE1	nc	thrombomodulin		aac	aga	increased
8417	AF022743.PE1	nc	thrombomodulin		aac	aga	increased
8418	AF022743.PE1	nc	thrombomodulin		aac	aga	increased
8419	AF022743.PE1	nc	thrombomodulin		aac	aga	increased
8420	RNTSP4.TSP-4	TSP-4	thrombospondin-4		cca	tct	decreased
8421	RNTSP4.TSP-4	TSP-4	thrombospondin-4		cca	tct	decreased
8422	RNTSP4.TSP-4	TSP-4	thrombospondin-4		cca	tct	decreased
8423	RNTSP4.TSP-4	TSP-4	thrombospondin-4		cca	tct	decreased
8424	RNTSP4.TSP-4	TSP-4	thrombospondin-4		aat	gga	decreased
8425	RNTSP4.TSP-4	TSP-4	thrombospondin-4		aat	gga	decreased
8426	RNTSP4.TSP-4	TSP-4	thrombospondin-4		aat	gga	decreased
8427	RNTSP4.TSP-4	TSP-4	thrombospondin-4		aat	gga	decreased
8428	RNU60282.PE1	nc	thyroid sodium/iodide symporter NIS		ttc	gta	increased
8429	RNU60282.PE1	nc	thyroid sodium/iodide symporter NIS		ttc	gta	increased
8430	RNU60282.PE1	nc	thyroid sodium/iodide symporter NIS		ttc	gta	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
8431	Hha1	33	agc	134.21	134	134.21	0	0	3 800 000	0	0	-=	\		\(4)
8432	Hha1	26	ctg	194.26	195	194.26	0	0	3 000 000	0	0	-=	\		\(4)
8433	Hha1	33	agc	194.47	195	0	0	194.47	0	0	3 500 000	=+	/		\(4)
8434	Hha1	26	ctg	239.63	240	239.63	0	0	12 600 000	0	0	-=	\		\(4)
8435	Hha1	26	ctg	240.543	240	240.57	240.52	240.54	103 900 000	16 200 000	45 400 000	-=	\ (-)		\(4)
8436	Hha1	40	tgg	218.38	219	218.38	0	0	3 300 000	0	0	-=	\	\	
8437	Hha1	59	ttc	218.29	219	218.29	0	0	187.2	0	0	-=	\	\	
8438	Taq1	56	tga	118.02	118	0	0	118.02	0	0	3 700 000	=+	/		/(2)
8439	Taq1	61	tct	202.325	203	0	202.16	202.49	0	3 900 000	6 100 000	+=	/		/(2)
8440	Hha1	9	atc	240.57	242	240.57	0	0	6 100 000	0	0	-=	\		\(2)
8441	Taq1	39	agg	241.875	242	242	241.75	0	4 900 000	32 100 000	0	+-	A		\(2)
8442	Taq1	39	agg	242	242	242	0	0	181.96	0	0	-=	\		\(2)
8443	Taq1	39	agg	243.37	242	0	243.37	0	0	16 700 000	0	+-	A		\(2)
8444	Taq1	39	agg	241.75	242	0	241.75	0	0	322.61	0	+-	A		\(2)
8445	Taq1	39	agg	243.37	242	0	243.37	0	0	167.84	0	+-	A		\(2)
8446	Taq1	21	acc	181.01	180	181.01	0	0	4 100 000	0	0	-=	\	\	
8447	Taq1	39	agg	181.01	180	180.86	181.16	0	954.39	640.2	0	=-	\	\	
8448	Hha1	40	tgg	97.03	97	97.14	96.93	97.02	4 100 000	11 500 000	5 300 000	+-	A		\(5)
8449	Taq1	21	acc	179.055	180	178.84	179.27	0	8 600 000	3 200 000	0	-=	\		\(5)
8450	Hha1	21	acc	179.96	180	0	0	179.96	0	0	6 200 000	=+	/		\(5)
8451	Taq1	21	acc	180.16	180	0	0	180.16	0	0	4 400 000	=+	/		\(5)
8452	Taq1	21	acc	181.01	180	181.01	0	0	4 100 000	0	0	-=	\	\	\(5)
8453	Taq1	39	agg	180.27	180	0	180.27	0	0	17 400 000	0	+-	A		\(5)
8454	Taq1	39	agg	181.01	180	180.86	181.16	0	25 700 000	63 700 000	0	+-	A		\(5)
8455	Taq1	39	agg	180.27	180	0	180.27	0	0	174.87	0	+-	A		\(5)
8456	Taq1	39	agg	181.01	180	180.86	181.16	0	954.39	640.2	0	=-	\	\	\(5)
8457	Hha1	2	tta	192.81	193	0	0	192.81	0	0	7 800 000	=+	/		\(5)
8458	Hha1	2	tta	193.68	193	0	0	193.68	0	0	3 700 000	=+	/		\(5)
8459	Taq1	56	tga	215.765	217	215.8	215.73	0	3 300 000	7 600 000	0	+-	A		\(5)
8460	Taq1	56	tga	216.81	217	0	216.81	0	0	9 200 000	0	+-	A		\(5)
8461	Taq1	56	tga	217.8	217	0	217.8	0	0	13 600 000	0	+-	A		\(5)
8462	Hha1	59	ttc	286.47	285	286.47	0	0	234	0	0	-=	\		\(5)
8463	Taq1	39	agg	293.64	295	293.64	0	0	4 700 000	0	0	-=	\		\(5)
8464	Taq1	39	agg	294.57	295	0	294.57	0	0	14 900 000	0	+-	A		\(5)
8465	Taq1	39	agg	296.655	295	296.82	0	296.49	8 000 000	0	10 700 000	-+(=)	V		\(5)
8466	Taq1	39	agg	293.64	295	293.64	0	0	174.53	0	0	-=	\		\(5)
8467	Taq1	39	agg	296.655	295	296.82	0	296.49	297.08	0	315.16	-+(=)	V		\(5)
8468	Taq1	39	agg	294.57	295	0	294.57	0	0	149.75	0	+-	A		\(5)
8469	Taq1	21	acc	181.01	180	181.01	0	0	4 100 000	0	0	-=	\	\	
8470	Taq1	39	agg	181.01	180	180.86	181.16	0	954.39	640.2	0	=-	\	\	
8471	Hha1	22	tcc	114.313	115	114.13	114.38	114.43	8 700 000	9 400 000	12 200 000	==	-	-	-4
8472	Taq1	22	tcc	114.36	115	114.26	114.34	114.48	11 500 000	12 200 000	9 500 000	==	-	-	-4
8473	Hha1	22	tcc	114.98	115	0	114.98	0	0	22 900 000	0	+-	A		-4

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
8431	RNU60282.PE1	nc	thyroid sodium/iodide symporter NIS		ggg	agc	increased
8432	RNU60282.PE1	nc	thyroid sodium/iodide symporter NIS		agc	ctg	increased
8433	RNU60282.PE1	nc	thyroid sodium/iodide symporter NIS		agc	ctg	increased
8434	RNU60282.PE1	nc	thyroid sodium/iodide symporter NIS		ctg	tgc	increased
8435	RNU60282.PE1	nc	thyroid sodium/iodide symporter NIS		ctg	tgc	increased
8436	RATTTF1.TTF-1	TTF-1	thyroid transcription factor-1		ttc	tgg	increased
8437	RATTTF1.TTF-1	TTF-1	thyroid transcription factor-1		ttc	tgg	increased
8438	AF015953.TIC	TIC	TIC		cta	tga	decreased
8439	AF015953.TIC	TIC	TIC		tgc	tct	decreased
8440	D87671.TIP120	tip120	TIP120		atc	agg	increased
8441	D87671.TIP120	tip120	TIP120		atc	agg	increased
8442	D87671.TIP120	tip120	TIP120		atc	agg	increased
8443	D87671.TIP120	tip120	TIP120		atc	agg	increased
8444	D87671.TIP120	tip120	TIP120		atc	agg	increased
8445	D87671.TIP120	tip120	TIP120		atc	agg	increased
8446	AB029324.TIP120B	tip120b	TIP120-family protein TIP120B		acc	agg	increased
8447	AB029324.TIP120B	tip120b	TIP120-family protein TIP120B		acc	agg	increased
8448	AB029341.TIP120B	tip120b	TIP120-family protein TIP120B, alternatiely		tgg	agt	increased
8449	AB029341.TIP120B	tip120b	TIP120-family protein TIP120B, alternatiely		acc	agg	increased
8450	AB029341.TIP120B	tip120b	TIP120-family protein TIP120B, alternatiely		acc	agg	increased
8451	AB029341.TIP120B	tip120b	TIP120-family protein TIP120B, alternatiely		acc	agg	increased
8452	AB029341.TIP120B	tip120b	TIP120-family protein TIP120B, alternatiely		acc	agg	increased
8453	AB029341.TIP120B	tip120b	TIP120-family protein TIP120B, alternatiely		acc	agg	increased
8454	AB029341.TIP120B	tip120b	TIP120-family protein TIP120B, alternatiely		acc	agg	increased
8455	AB029341.TIP120B	tip120b	TIP120-family protein TIP120B, alternatiely		acc	agg	increased
8456	AB029341.TIP120B	tip120b	TIP120-family protein TIP120B, alternatiely		acc	agg	increased
8457	AB029341.TIP120B	tip120b	TIP120-family protein TIP120B, alternatiely		tta	tcg	increased
8458	AB029341.TIP120B	tip120b	TIP120-family protein TIP120B, alternatiely		tta	tcg	increased
8459	AB029341.TIP120B	tip120b	TIP120-family protein TIP120B, alternatiely		gtg	tga	increased
8460	AB029341.TIP120B	tip120b	TIP120-family protein TIP120B, alternatiely		gtg	tga	increased
8461	AB029341.TIP120B	tip120b	TIP120-family protein TIP120B, alternatiely		gtg	tga	increased
8462	AB029341.TIP120B	tip120b	TIP120-family protein TIP120B, alternatiely		ttc	agc	increased
8463	AB029341.TIP120B	tip120b	TIP120-family protein TIP120B, alternatiely		ccc	agg	increased
8464	AB029341.TIP120B	tip120b	TIP120-family protein TIP120B, alternatiely		ccc	agg	increased
8465	AB029341.TIP120B	tip120b	TIP120-family protein TIP120B, alternatiely		ccc	agg	increased
8466	AB029341.TIP120B	tip120b	TIP120-family protein TIP120B, alternatiely		ccc	agg	increased
8467	AB029341.TIP120B	tip120b	TIP120-family protein TIP120B, alternatiely		ccc	agg	increased
8468	AB029341.TIP120B	tip120b	TIP120-family protein TIP120B, alternatiely		ccc	agg	increased
8469	AB029342.TIP120B	tip120b	TIP120-family protein TIP120B, short form		acc	agg	increased
8470	AB029342.TIP120B	tip120b	TIP120-family protein TIP120B, short form		acc	agg	increased
8471	AF349723.PE1	nc	TOB1		gca	tcc	No change
8472	AF349723.PE1	nc	TOB1		gca	tcc	No change
8473	AF349723.PE1	nc	TOB1		gca	tcc	No change

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
8474	Taq1	22	tcc	115.423	115	115.31	115.48	115.48	8 400 000	6 700 000	13 900 000	=+	/ (-)		-4
8475	Taq1	29	gca	114.373	115	114.44	114.4	114.28	28 100 000	22 400 000	13 600 000	==	-		-4
8476	Taq1	29	gca	115.263	115	115.29	115.18	115.32	34 900 000	21 600 000	6 400 000	==	-		-4
8477	Taq1	12	agt	153.727	154	153.72	153.64	153.82	3 700 000	4 400 000	3 000 000	==	-		/(8)
8478	Taq1	12	agt	154.81	154	154.79	154.75	154.89	8 600 000	12 600 000	9 000 000	==	-		/(8)
8479	Taq1	51	ata	154.09	155	0	0	154.09	0	0	4 800 000	=+	/		/(8)
8480	Taq1	51	ata	155.34	155	155.34	0	0	4 800 000	0	0	-=	\		/(8)
8481	Taq1	16	tag	177.887	178	177.92	177.95	177.79	4 200 000	9 800 000	4 800 000	+-	A		/(8)
8482	Hha1	11	act	218.97	220	0	0	218.97	0	0	3 400 000	=+	/		/(8)
8483	Taq1	11	act	219.64	220	0	0	219.64	0	0	3 200 000	=+	/		/(8)
8484	Hha1	11	act	220.01	220	0	0	220.01	0	0	3 300 000	=+	/		/(8)
8485	Hha1	11	act	220.935	220	220.93	220.94	0	3 100 000	5 200 000	0	=-	\		/(8)
8486	Taq1	11	act	220.76	220	0	0	220.76	0	0	3 900 000	=+	/	/	/(8)
8487	Hha1	11	act	220.9	220	0	0	220.9	0	0	3 800 000	=+	/	/	/(8)
8488	Taq1	26	ctg	272.34	271	0	0	272.34	0	0	5 300 000	=+	/		/(8)
8489	Taq1	51	ata	535.57	537	0	535.57	535.57	0	4 100 000	12 500 000	=+	/		/(8)
8490	Hha1	39	agg	68.607	69	68.64	68.57	68.61	828.44	603.02	406.9	==	-		-(2) \(2)
8491	Hha1	20	ctc	151.363	152	151.43	151.51	151.15	344.35	576.97	381.67	==	-		-(2) \(2)
8492	Hha1	20	ctc	152.48	152	152.32	152.64	0	413.22	485.18	0	=-	\	\	-(2) \(2)
8493	Hha1	28	tcg	151.175	152	0	151.08	151.27	0	10 700 000	4 800 000	+-	A		-(2) \(2)
8494	Hha1	28	tcg	152.68	152	152.68	0	0	11 200 000	0	0	-=	\	\	-(2) \(2)
8495	Hha1	8	gaa	122.317	123	122.3	122.31	122.34	20 200 000	8 200 000	14 600 000	-=	\ (-)		/(3)
8496	Taq1	8	gaa	122.65	123	0	122.62	122.68	0	3 300 000	6 800 000	++	/		/(3)
8497	Taq1	8	gaa	123.28	123	0	0	123.28	0	0	22 900 000	=+	/		/(3)
8498	Hha1	8	gaa	123.7	123	0	0	123.7	0	0	3 900 000	=+	/		/(3)
8499	Taq1	40	tgg	122.505	123	122.4	0	122.61	46 900 000	0	13 200 000	-=(-)	\		/(3)
8500	Taq1	40	tgg	123.5	123	0	0	123.5	0	0	18 400 000	=+	/		/(3)
8501	Hha1	39	agg	63.33	63	63.42	63.39	63.18	1 656.89	674.66	1 318.35	-=	\ (-)		\(8)
8502	Taq1	39	agg	92.245	92	92.24	92.25	0	4 700 000	120 800 000	0	+-	A		\(8)
8503	Taq1	39	agg	92.245	92	92.24	92.25	0	174.53	1 214.08	0	+-	A		\(8)
8504	Hha1	54	ttt	148.59	149	0	0	148.59	0	0	3 600 000	=+	/		\(8)
8505	Taq1	47	ggc	154.283	154	154.2	154.31	154.34	5 353.84	2 259.7	1 943.84	-=	\ (-)		\(8)
8506	Taq1	40	tgg	165.26	166	0	0	165.26	0	0	13 300 000	=+	/		\(8)
8507	Hha1	44	cgg	180.213	180	179.96	180.37	180.31	3 700 000	4 100 000	4 700 000	==	-		\(8)
8508	Hha1	44	cgg	180.86	180	0	180.86	0	0	5 200 000	0	+-	A		\(8)
8509	Hha1	7	caa	186.09	187	0	186.06	186.12	0	9 200 000	12 500 000	+=	/		\(8)
8510	Taq1	7	caa	186.42	187	186.42	0	0	3 100 000	0	0	-=	\		\(8)
8511	Hha1	7	caa	187.055	187	0	187.08	187.03	0	4 300 000	6 400 000	+=	/		\(8)
8512	Hha1	7	caa	187.67	187	187.67	0	0	5 200 000	0	0	-=	\		\(8)
8513	Taq1	7	caa	187.39	187	0	187.39	0	0	5 200 000	0	+-	A		\(8)
8514	Taq1	12	agt	185.92	187	185.96	185.84	185.96	10 800 000	9 700 000	8 600 000	==	-		\(8)
8515	Taq1	12	agt	186.95	187	186.95	186.95	186.95	8 900 000	5 800 000	4 200 000	==	-		\(8)
8516	Taq1	12	agt	187.95	187	187.94	187.94	187.97	8 900 000	12 200 000	5 900 000	=-	\ (-)		\(8)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
8474	AF349723.PE1	nc	TOB1		gca	tcc	No change
8475	AF349723.PE1	nc	TOB1		gca	tcc	No change
8476	AF349723.PE1	nc	TOB1		gca	tcc	No change
8477	AB116229.TLR3	Tlr3	toll-like receptor 3		ata	agt	decreased
8478	AB116229.TLR3	Tlr3	toll-like receptor 3		ata	agt	decreased
8479	AB116229.TLR3	Tlr3	toll-like receptor 3		ata	agt	decreased
8480	AB116229.TLR3	Tlr3	toll-like receptor 3		ata	agt	decreased
8481	AB116229.TLR3	Tlr3	toll-like receptor 3		agc	tag	decreased
8482	AB116229.TLR3	Tlr3	toll-like receptor 3		act	acg	decreased
8483	AB116229.TLR3	Tlr3	toll-like receptor 3		act	acg	decreased
8484	AB116229.TLR3	Tlr3	toll-like receptor 3		act	acg	decreased
8485	AB116229.TLR3	Tlr3	toll-like receptor 3		act	acg	decreased
8486	AB116229.TLR3	Tlr3	toll-like receptor 3		act	acg	decreased
8487	AB116229.TLR3	Tlr3	toll-like receptor 3		act	acg	decreased
8488	AB116229.TLR3	Tlr3	toll-like receptor 3		ctg	agt	decreased
8489	AB116229.TLR3	Tlr3	toll-like receptor 3		aga	ata	decreased
8490	AF292116.PE1	nc	TPRA40 protein		gag	agg	No change
8491	AF292116.PE1	nc	TPRA40 protein		ctc	tcg	No change
8492	AF292116.PE1	nc	TPRA40 protein		ctc	tcg	increased
8493	AF292116.PE1	nc	TPRA40 protein		ctc	tcg	No change
8494	AF292116.PE1	nc	TPRA40 protein		ctc	tcg	increased
8495	AF054810.TCII	TCII	transcobalamin II precursor		gaa	tgg	decreased
8496	AF054810.TCII	TCII	transcobalamin II precursor		gaa	tgg	decreased
8497	AF054810.TCII	TCII	transcobalamin II precursor		gaa	tgg	decreased
8498	AF054810.TCII	TCII	transcobalamin II precursor		gaa	tgg	decreased
8499	AF054810.TCII	TCII	transcobalamin II precursor		gaa	tgg	decreased
8500	AF054810.TCII	TCII	transcobalamin II precursor		gaa	tgg	decreased
8501	RNO440711.PE1	smctf-1	transcription factor 1		agg	cac	increased
8502	RNO440711.PE1	smctf-1	transcription factor 1		gca	agg	increased
8503	RNO440711.PE1	smctf-1	transcription factor 1		gca	agg	increased
8504	RNO440711.PE1	smctf-1	transcription factor 1		ttt	cat	increased
8505	RNO440711.PE1	smctf-1	transcription factor 1		ttc	ggc	increased
8506	RNO440711.PE1	smctf-1	transcription factor 1		gag	tgg	increased
8507	RNO440711.PE1	smctf-1	transcription factor 1		cgg	caa	increased
8508	RNO440711.PE1	smctf-1	transcription factor 1		cgg	caa	increased
8509	RNO440711.PE1	smctf-1	transcription factor 1		caa	agt	increased
8510	RNO440711.PE1	smctf-1	transcription factor 1		caa	agt	increased
8511	RNO440711.PE1	smctf-1	transcription factor 1		caa	agt	increased
8512	RNO440711.PE1	smctf-1	transcription factor 1		caa	agt	increased
8513	RNO440711.PE1	smctf-1	transcription factor 1		caa	agt	increased
8514	RNO440711.PE1	smctf-1	transcription factor 1		caa	agt	increased
8515	RNO440711.PE1	smctf-1	transcription factor 1		caa	agt	increased
8516	RNO440711.PE1	smctf-1	transcription factor 1		caa	agt	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
8517	Hha1	26	ctg	215.46	216	215.46	0	0	4 300 000	0	0	-=	\		\(8)
8518	Taq1	12	agt	218.47	219	0	218.47	0	0	3 000 000	0	+-	A		\(8)
8519	Taq1	12	agt	219.45	219	219.47	219.43	0	3 000 000	4 200 000	0	=-	\		\(8)
8520	Taq1	21	acc	305.29	307	305.29	0	0	4 600 000	0	0	-=	\		\(8)
8521	Taq1	21	acc	306.53	307	306.53	0	0	6 400 000	0	0	-=	\		\(8)
8522	Hha1	49	aaa	178.21	179	178.08	178.34	0	8 200 000	6 100 000	0	=-	\	\	\(2)
8523	Hha1	49	aaa	178.905	179	178.97	178.84	0	11 500 000	5 600 000	0	--	\	\	\(2)
8524	Hha1	49	aaa	179.56	179	179.58	179.54	0	4 100 000	16 100 000	0	+-	A		\(2)
8525	Hha1	54	ttt	178.065	179	178.05	178.08	0	9 200 000	3 700 000	0	-=	\	\	\(2)
8526	Hha1	54	ttt	179.07	179	179.07	0	0	8 900 000	0	0	-=	\	\	\(2)
8527	Hha1	17	cca	183.867	184	183.78	183.92	183.9	19 473.359	12 065.43	22 343.971	=+	/ (-)		\(2)
8528	Taq1	45	gcc	71.91	72	72.01	71.95	71.77	69 000 000	19 500 000	4 500 000	-=	\ (-)		\(4)
8529	Hha1	28	tcg	97.11	97	97.11	0	0	32 700 000	0	0	-=	\		\(4)
8530	Hha1	2	tta	135.693	136	135.81	135.62	135.65	51 400 000	31 400 000	42 600 000	==	-		\(4)
8531	Hha1	2	tta	136.553	136	136.32	136.67	136.67	40 700 000	36 100 000	33 800 000	==	-		\(4)
8532	Hha1	59	ttc	156.935	157	0	156.95	156.92	0	135.1	93.13	+=	/		\(4)
8533	Hha1	59	ttc	157.73	157	0	157.73	0	0	261.58	0	+-	A		\(4)
8534	Taq1	44	cgg	221.42	222	221.42	0	0	958.23	0	0	-=	\		\(4)
8535	Taq1	44	cgg	222.785	222	222.72	222.85	0	1 038.08	373.26	0	-=	\		\(4)
8536	Hha1	54	ttt	223.693	224	223.69	223.65	223.74	29 300 000	11 600 000	23 700 000	-=	\ (-)		\(4)
8537	Hha1	54	ttt	224.59	224	224.66	0	224.52	3 400 000	0	4 200 000	-+(=)	V		\(4)
8538	Hha1	33	agc	60.667	61	60.61	60.65	60.74	8 100 000	13 200 000	3 900 000	=-	\ (-)		-(4) \(4)
8539	Hha1	2	tta	96.563	97	96.68	96.45	96.56	172 600 000	85 700 000	50 000 000	-=	\ (-)		-(4) \(4)
8540	Hha1	2	tta	97.21	97	97.31	97.11	0	93 200 000	89 300 000	0	=-	\		-(4) \(4)
8541	Hha1	43	cgc	107.583	108	107.51	107.56	107.68	10 100 000	13 700 000	4 700 000	=-	\ (-)		-(4) \(4)
8542	Hha1	28	tcg	108.88	109	108.89	108.86	108.89	24 900 000	32 000 000	44 800 000	==	-		-(4) \(4)
8543	Hha1	54	ttt	110.195	110	110.24	0	110.15	4 700 000	0	5 200 000	-+(=)	V		-(4) \(4)
8544	Hha1	20	ctc	188.13	189	188.13	0	0	309.91	0	0	-=	\		-(4) \(4)
8545	Hha1	20	ctc	189.2	189	189.2	0	0	337.46	0	0	-=	\		-(4) \(4)
8546	Hha1	49	aaa	72.013	72	71.86	71.97	72.21	18 000 000	75 000 000	4 100 000	+-	A		\(4)
8547	Hha1	49	aaa	72.38	72	72.38	0	0	33 400 000	0	0	-=	\		\(4)
8548	Hha1	41	ccc	144.06	144	144.06	0	0	4 500 000	0	0	-=	\		\(4)
8549	Hha1	41	ccc	144.62	144	0	0	144.62	0	0	3 500 000	=+	/		\(4)
8550	Hha1	43	cgc	167.38	168	167.34	167.42	0	9 700 000	6 000 000	0	=-	\		\(4)
8551	Hha1	43	cgc	168.41	168	0	168.41	0	0	3 000 000	0	+-	A		\(4)
8552	Hha1	40	tgg	168.195	169	168.32	168.07	0	18 800 000	9 000 000	0	--	\		\(4)
8553	Hha1	40	tgg	169.29	169	169.37	169.22	169.28	180 800 000	17 500 000	9 100 000	-=	\ (-)		\(4)
8554	Taq1	10	atg	246.48	247	0	246.48	0	0	5 500 000	0	+-	A	A	A(2)
8555	Taq1	50	aat	246.545	248	246.34	246.75	0	3 200 000	8 300 000	0	+-	A	A	A(2)
8556	Taq1	50	aat	247.46	248	247.45	247.47	0	6 900 000	7 700 000	0	=-	\		A(2)
8557	Taq1	50	aat	248.04	248	248.04	0	0	13 800 000	0	0	-=	\		A(2)
8558	Taq1	50	aat	249.1	248	249.1	0	0	7 800 000	0	0	-=	\		A(2)
8559	Taq1	50	aat	249.26	248	249.26	0	0	7 400 000	0	0	-=	\		A(2)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
8517	RNO440711.PE1	smctf-1	transcription factor 1		aca	ctg	increased
8518	RNO440711.PE1	smctf-1	transcription factor 1		ccg	agt	increased
8519	RNO440711.PE1	smctf-1	transcription factor 1		ccg	agt	increased
8520	RNO440711.PE1	smctf-1	transcription factor 1		acc	gat	increased
8521	RNO440711.PE1	smctf-1	transcription factor 1		acc	gat	increased
8522	AF391798.PE1	nc	transcription factor IIIA		aaa	ttt	increased
8523	AF391798.PE1	nc	transcription factor IIIA		aaa	ttt	increased
8524	AF391798.PE1	nc	transcription factor IIIA		aaa	ttt	increased
8525	AF391798.PE1	nc	transcription factor IIIA		aaa	ttt	increased
8526	AF391798.PE1	nc	transcription factor IIIA		aaa	ttt	increased
8527	AF391798.PE1	nc	transcription factor IIIA		cca	gag	increased
8528	RATRFIIICA.PE1	nc	transcription factor IIIC alpha-subunit		gtc	gcc	increased
8529	RATRFIIICA.PE1	nc	transcription factor IIIC alpha-subunit		tcg	ggg	increased
8530	RATRFIIICA.PE1	nc	transcription factor IIIC alpha-subunit		aac	tta	increased
8531	RATRFIIICA.PE1	nc	transcription factor IIIC alpha-subunit		aac	tta	increased
8532	RATRFIIICA.PE1	nc	transcription factor IIIC alpha-subunit		aag	ttc	increased
8533	RATRFIIICA.PE1	nc	transcription factor IIIC alpha-subunit		aag	ttc	increased
8534	RATRFIIICA.PE1	nc	transcription factor IIIC alpha-subunit		cgg	ttt	increased
8535	RATRFIIICA.PE1	nc	transcription factor IIIC alpha-subunit		cgg	ttt	increased
8536	RATRFIIICA.PE1	nc	transcription factor IIIC alpha-subunit		cta	ttt	increased
8537	RATRFIIICA.PE1	nc	transcription factor IIIC alpha-subunit		cta	ttt	increased
8538	RNP48PTF1.PE1	nc	transcription factor PTF1	*	ctc	agc	No change
8539	RNP48PTF1.PE1	nc	transcription factor PTF1	*	tta	agt	No change
8540	RNP48PTF1.PE1	nc	transcription factor PTF1	*	tta	agt	No change
8541	RNP48PTF1.PE1	nc	transcription factor PTF1	*	cgc	ttt	No change
8542	RNP48PTF1.PE1	nc	transcription factor PTF1	*	tcg	ccc	No change
8543	RNP48PTF1.PE1	nc	transcription factor PTF1	*	cgc	ttt	No change
8544	RNP48PTF1.PE1	nc	transcription factor PTF1	*	ctc	acg	No change
8545	RNP48PTF1.PE1	nc	transcription factor PTF1	*	ctc	acg	No change
8546	RATDBPA.DBP	DBP	transcriptional activator		tca	aaa	increased
8547	RATDBPA.DBP	DBP	transcriptional activator		tca	aaa	increased
8548	RATDBPA.DBP	DBP	transcriptional activator		aag	ccc	increased
8549	RATDBPA.DBP	DBP	transcriptional activator		aag	ccc	increased
8550	RATDBPA.DBP	DBP	transcriptional activator		cgc	tgg	increased
8551	RATDBPA.DBP	DBP	transcriptional activator		cgc	tgg	increased
8552	RATDBPA.DBP	DBP	transcriptional activator		cgc	tgg	increased
8553	RATDBPA.DBP	DBP	transcriptional activator		cgc	tgg	increased
8554	RATTA.PE1	nc	transferrin		aat	atg	increased by mild
8555	RATTA.PE1	nc	transferrin		aat	atg	increased by mild
8556	RATTA.PE1	nc	transferrin		aat	atg	increased by mild
8557	RATTA.PE1	nc	transferrin		aat	atg	increased by mild
8558	RATTA.PE1	nc	transferrin		aat	atg	increased by mild
8559	RATTA.PE1	nc	transferrin		aat	atg	increased by mild

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
8560	Taq1	25	cat	114.983	115	115	114.86	115.09	716.52	432.84	2 590.24	=+	/ (-)		\(2)
8561	Taq1	25	cat	115.55	115	115.55	0	0	627.81	0	0	-=	\		\(2)
8562	Taq1	39	agg	243.37	244	0	243.37	0	0	16 700 000	0	+-	A		\(2)
8563	Taq1	39	agg	243.37	244	0	243.37	0	0	167.84	0	+-	A		\(2)
8564	Taq1	39	agg	244.99	244	244.99	0	0	4 200 000	0	0	-=	\		\(2)
8565	Taq1	39	agg	244.99	244	244.99	0	0	155.97	0	0	-=	\		\(2)
8566	Hha1	15	tac	111.707	112	111.71	111.71	111.7	39 700 000	46 200 000	54 500 000	==	-		\(3) -(2)
8567	Hha1	15	tac	111.84	112	111.84	0	0	7 586.41	0	0	-=	\		\(3) -(2)
8568	Hha1	15	tac	111.705	112	0	111.71	111.7	0	11 898.01	11 852.97	+=	/		\(3) -(2)
8569	Taq1	18	cct	119.417	120	119.32	119.42	119.51	8 400 000	4 000 000	4 500 000	-=	\ (-)		\(3) -(2)
8570	Taq1	18	cct	120.435	120	120.26	0	120.61	4 600 000	0	6 400 000	-+(=)	V		\(3) -(2)
8571	Taq1	39	agg	119.78	120	119.93	119.63	0	19 400 000	32 300 000	0	=-	\		\(3) -(2)
8572	Taq1	39	agg	119.93	120	119.93	0	0	720.43	0	0	-=	\		\(3) -(2)
8573	Taq1	39	agg	119.63	120	0	119.63	0	0	324.62	0	+-	A		\(3) -(2)
8574	Taq1	64	gtt	164.147	165	164.22	164.14	164.08	3 800 000	5 400 000	4 000 000	==	-		-2
8575	Taq1	64	gtt	165.167	165	165.2	165.09	165.21	4 800 000	7 200 000	4 500 000	==	-		-2
8576	Hha1	25	cag	240.613	241	240.57	240.6	240.67	9 700 000	5 800 000	3 200 000	==	-		-2
8577	Hha1	25	cag	241.73	241	241.71	241.75	0	23 300 000	7 200 000	0	-=	\		-2
8578	Hha1	43	cgc	112.583	113	112.63	112.59	112.53	98 500 000	133 800 000	31 700 000	=-	\ (-)		\(3)
8579	Hha1	43	cgc	113.67	113	0	0	113.67	0	0	3 900 000	=+	/		\(3)
8580	Hha1	33	agc	113.725	114	113.86	113.59	0	6 500 000	9 600 000	0	=-	\		\(3)
8581	Hha1	8	gaa	279.89	281	279.89	0	0	3 800 000	0	0	-=	\		\(3)
8582	Taq1	8	gaa	280.27	281	0	280.27	0	0	3 500 000	0	+-	A		\(3)
8583	Hha1	61	tct	185.955	187	0	185.97	185.94	0	8 300 000	5 300 000	+=	/		-(2) \(2)
8584	Hha1	61	tct	186.79	187	0	0	186.79	0	0	4 200 000	=+	/		-(2) \(2)
8585	Hha1	61	tct	187.957	187	188.05	187.91	187.91	6 000 000	11 300 000	11 700 000	+=	/ (-)	(-)	-(2) \(2)
8586	Hha1	64	gtt	185.895	187	186	0	185.79	15 500 000	0	3 200 000	-=(-)	\		-(2) \(2)
8587	Hha1	64	gtt	186	187	186	0	0	6 200 000	0	0	-=	\		-(2) \(2)
8588	Hha1	64	gtt	187.85	187	187.89	187.91	187.75	7 300 000	3 200 000	4 700 000	-=	\ (-)	(-)	-(2) \(2)
8589	Taq1	50	aat	240.36	239	240.36	0	0	3 800 000	0	0	-=	\		-(2) \(2)
8590	Hha1	20	ctc	62	62	0	61.95	62.05	0	694.99	453.24	+=	/		\(3)
8591	Hha1	40	tgg	103.63	104	103.63	0	0	4 300 000	0	0	-=	\		\(3)
8592	Hha1	56	tga	103.59	104	0	103.59	0	0	517.39	0	+-	A		\(3)
8593	Hha1	56	tga	104.497	104	104.32	104.59	104.58	1 090.99	544.91	792.96	-=	\ (-)		\(3)
8594	Hha1	60	ttg	185.79	186	185.79	185.79	0	5 000 000	6 400 000	0	=-	\		\(3)
8595	Taq1	8	gaa	87.73	88	87.91	87.49	87.79	5 300 000	38 700 000	32 000 000	+=	/ (-)		/(3)
8596	Taq1	11	act	118.163	118	118.16	118.03	118.3	3 300 000	4 500 000	29 900 000	=+	/ (-)		/(3)
8597	Taq1	17	cca	117.567	118	117.87	117.43	117.4	167.18	1 070.33	1 984.66	++	/		/(3)
8598	Taq1	17	cca	118.43	118	0	118.37	118.49	0	1 303.01	1 157.72	+=	/		/(3)
8599	Taq1	49	aaa	317.54	317	317.54	0	0	16 600 000	0	0	-=	\		/(3)
8600	Taq1	49	aaa	318.31	317	318.24	318.38	0	23 700 000	4 900 000	0	-=	\		/(3)
8601	Taq1	8	gaa	87.73	88	87.91	87.49	87.79	5 300 000	38 700 000	32 000 000	+=	/ (-)		/(3)
8602	Taq1	11	act	118.163	118	118.16	118.03	118.3	3 300 000	4 500 000	29 900 000	=+	/ (-)		/(3)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
8560	AF135598.PE1	nc	transforming growth factor beta 2 precursor		cat	agc	increased
8561	AF135598.PE1	nc	transforming growth factor beta 2 precursor		cat	agc	increased
8562	AF135598.PE1	nc	transforming growth factor beta 2 precursor		tgt	agg	increased
8563	AF135598.PE1	nc	transforming growth factor beta 2 precursor		tgt	agg	increased
8564	AF135598.PE1	nc	transforming growth factor beta 2 precursor		tgt	agg	increased
8565	AF135598.PE1	nc	transforming growth factor beta 2 precursor		tgt	agg	increased
8566	RRU03491.PE1	nc	transforming growth factor beta-3		tac	aca	increased
8567	RRU03491.PE1	nc	transforming growth factor beta-3		tac	aca	increased
8568	RRU03491.PE1	nc	transforming growth factor beta-3		tac	aca	increased
8569	RRU03491.PE1	nc	transforming growth factor beta-3		cct	agg	increased
8570	RRU03491.PE1	nc	transforming growth factor beta-3		cct	agg	increased
8571	RRU03491.PE1	nc	transforming growth factor beta-3		cct	agg	increased
8572	RRU03491.PE1	nc	transforming growth factor beta-3		cct	agg	increased
8573	RRU03491.PE1	nc	transforming growth factor beta-3		cct	agg	increased
8574	RNTMDCI.PE1	nc	transmembrane protein tMDC I		aca	gtt	No change
8575	RNTMDCI.PE1	nc	transmembrane protein tMDC I		aca	gtt	No change
8576	RNTMDCI.PE1	nc	transmembrane protein tMDC I		gac	cag	No change
8577	RNTMDCI.PE1	nc	transmembrane protein tMDC I		gac	cag	No change
8578	AF276997.PE1	nc	tricarboxylate carrier-like protein		cgc	agc	increased
8579	AF276997.PE1	nc	tricarboxylate carrier-like protein		cgc	agc	increased
8580	AF276997.PE1	nc	tricarboxylate carrier-like protein		cgc	agc	increased
8581	AF276997.PE1	nc	tricarboxylate carrier-like protein		gaa	tgc	increased
8582	AF276997.PE1	nc	tricarboxylate carrier-like protein		gaa	tgc	increased
8583	RATCTP2X.PE1	nc	tricarboxylate transport protein		tct	gtt	No change
8584	RATCTP2X.PE1	nc	tricarboxylate transport protein		tct	gtt	No change
8585	RATCTP2X.PE1	nc	tricarboxylate transport protein		tct	gtt	No change
8586	RATCTP2X.PE1	nc	tricarboxylate transport protein		tct	gtt	No change
8587	RATCTP2X.PE1	nc	tricarboxylate transport protein		tct	gtt	No change
8588	RATCTP2X.PE1	nc	tricarboxylate transport protein		tct	gtt	No change
8589	RATCTP2X.PE1	nc	tricarboxylate transport protein		aat	aca	No change
8590	RATTRKPREC.TRK	trk	trk precursor		ctc	gtg	increased
8591	RATTRKPREC.TRK	trk	trk precursor		tgg	tga	increased
8592	RATTRKPREC.TRK	trk	trk precursor		tgg	tga	increased
8593	RATTRKPREC.TRK	trk	trk precursor		tgg	tga	increased
8594	RATTRKPREC.TRK	trk	trk precursor		cag	ttg	increased
8595	RATCTTG.PE1	nc	troponin T		gaa	tcc	decreased
8596	RATCTTG.PE1	nc	troponin T		cca	act	decreased
8597	RATCTTG.PE1	nc	troponin T		cca	act	decreased
8598	RATCTTG.PE1	nc	troponin T		cca	act	decreased
8599	RATCTTG.PE1	nc	troponin T		aaa	tgg	decreased
8600	RATCTTG.PE1	nc	troponin T		aaa	tgg	decreased
8601	RATTROTA.PE1	nc	troponin T		gaa	tcc	decreased
8602	RATTROTA.PE1	nc	troponin T		cca	act	decreased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
8603	Taq1	17	cca	117.567	118	117.87	117.43	117.4	167.18	1 070.33	1 984.66	++	/		/(3)
8604	Taq1	17	cca	118.43	118	0	118.37	118.49	0	1 303.01	1 157.72	+=	/		/(3)
8605	Taq1	49	aaa	317.54	317	317.54	0	0	16 600 000	0	0	-=	\		/(3)
8606	Taq1	49	aaa	318.31	317	318.24	318.38	0	23 700 000	4 900 000	0	-=	\		/(3)
8607	Hha1	26	ctg	111.957	112	112.11	111.77	111.99	20 800 000	12 300 000	11 700 000	==	-		-2
8608	Hha1	33	agc	111.683	112	111.66	111.72	111.67	5 800 000	3 100 000	5 100 000	-=	\ (-)		-2
8609	Taq1	16	tag	104.21	104	0	0	104.21	0	0	4 700 000	=+	/	/	/(2)
8610	Taq1	29	gca	103.48	104	0	0	103.48	0	0	6 200 000	=+	/		/(2)
8611	Taq1	29	gca	104.42	104	0	0	104.42	0	0	7 100 000	=+	/	/	/(2)
8612	Taq1	47	ggc	139.07	139	139.06	139.08	0	2 953.84	1 623.16	0	--	\		\(2)
8613	Taq1	56	tga	139.383	140	139.51	139.44	139.2	37 300 000	35 400 000	4 700 000	=-	\ (-)		\(2)
8614	Hha1	43	cgc	172.56	172	172.56	0	0	11 600 000	0	0	-=	\	\	
8615	Hha1	27	acg	172.57	173	172.57	0	0	3 700 000	0	0	-=	\	\	
8616	Hha1	44	cgg	71.307	71	71.21	71.39	71.32	26 500 000	4 100 000	9 300 000	-=	\ (-)		\(6)
8617	Hha1	39	agg	144.21	145	0	144.41	144.01	0	191.05	211.58	+=	/		\(6)
8618	Hha1	39	agg	144.63	145	0	0	144.63	0	0	215.65	=+	/		\(6)
8619	Hha1	39	agg	145.82	145	0	146	145.64	0	770.19	797.52	+=	/		\(6)
8620	Taq1	39	agg	147.14	148	0	147.14	0	0	45 500 000	0	+-	A		\(6)
8621	Taq1	39	agg	148.14	148	148.24	148.04	0	11 300 000	15 600 000	0	=-	\		\(6)
8622	Taq1	39	agg	147.14	148	0	147.14	0	0	457.29	0	+-	A		\(6)
8623	Taq1	39	agg	148.14	148	148.24	148.04	0	419.63	156.78	0	-=	\		\(6)
8624	Taq1	44	cgg	177.595	178	177.37	177.82	0	1 024.19	602.97	0	=-	\		\(6)
8625	Taq1	44	cgg	178.5	178	0	178.5	0	0	861.38	0	+-	A		\(6)
8626	Taq1	21	acc	178.015	179	177.93	0	178.1	4 900 000	0	4 000 000	-+(=)	V		\(6)
8627	Taq1	21	acc	179.055	179	178.84	179.27	0	8 600 000	3 200 000	0	-=	\		\(6)
8628	Hha1	21	acc	179.96	179	0	0	179.96	0	0	6 200 000	=+	/		\(6)
8629	Hha1	40	tgg	209.925	210	0	210.06	209.79	0	3 000 000	4 400 000	+=	/		\(6)
8630	Hha1	40	tgg	210.2	210	0	0	210.2	0	0	4 100 000	=+	/		\(6)
8631	Hha1	40	tgg	210.95	210	210.85	211.05	0	5 400 000	7 700 000	0	=-	\		\(6)
8632	Taq1	50	aat	472.41	470	472.41	0	0	3 200 000	0	0	-=	\		\(6)
8633	Hha1	11	act	165.617	165	165.57	165.7	165.58	6 800 000	5 700 000	11 200 000	=+	/ (-)	/	
8634	Taq1	11	act	165.613	165	165.65	165.78	165.41	3 700 000	5 700 000	19 100 000	=+	/ (-)	/	
8635	Hha1	39	agg	107.28	107	0	107.46	107.1	0	656.75	1 257.32	++	/		/(3)
8636	Hha1	33	agc	144.21	145	144.2	0	144.22	4 000 000	0	3 500 000	-+(=)	V		/(3)
8637	Hha1	33	agc	145.22	145	0	0	145.22	0	0	7 200 000	=+	/	/	/(3)
8638	Hha1	59	ttc	144.413	145	144.33	144.48	144.43	280.81	235.71	372.54	==	-		/(3)
8639	Hha1	59	ttc	145.175	145	0	145.08	145.27	0	503.04	3 433.1	=+	/	/	/(3)
8640	Hha1	39	agg	107.28	107	0	107.46	107.1	0	656.75	1 257.32	++	/		/(3)
8641	Hha1	33	agc	144.21	145	144.2	0	144.22	4 000 000	0	3 500 000	-+(=)	V		/(3)
8642	Hha1	33	agc	145.22	145	0	0	145.22	0	0	7 200 000	=+	/	/	/(3)
8643	Hha1	59	ttc	144.413	145	144.33	144.48	144.43	280.81	235.71	372.54	==	-		/(3)
8644	Hha1	59	ttc	145.175	145	0	145.08	145.27	0	503.04	3 433.1	=+	/	/	/(3)
8645	Hha1	39	agg	72.68	73	72.69	72.5	72.85	5 711.14	2 561.34	12 300.61	=+	/ (-)		-1

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
8603	RATTROTA.PE1	nc	troponin T		cca	act	decreased
8604	RATTROTA.PE1	nc	troponin T		cca	act	decreased
8605	RATTROTA.PE1	nc	troponin T		aaa	tgg	decreased
8606	RATTROTA.PE1	nc	troponin T		aaa	tgg	decreased
8607	AY096238.ACTN3	Actn3	truncated alpha-actinin		ctg	agc	No change
8608	AY096238.ACTN3	Actn3	truncated alpha-actinin		ctg	agc	No change
8609	RATPTRY25.TRYPII	trypII	trypsinogen II		tag	gca	decreased
8610	RATPTRY25.TRYPII	trypII	trypsinogen II		tag	gca	decreased
8611	RATPTRY25.TRYPII	trypII	trypsinogen II		tag	gca	decreased
8612	RATT23D.PE1	nc	tryptophan-2,3-dioxygenase		tga	ggc	increased
8613	RATT23D.PE1	nc	tryptophan-2,3-dioxygenase		tga	ggc	increased
8614	RNTTF2PRT.TTF-2	ttf-2	TTF-2 protein		cgc	acg	increased
8615	RNTTF2PRT.TTF-2	ttf-2	TTF-2 protein		cgc	acg	increased
8616	AF125161.PE1	nc	T-type calcium channel isoform		gga	cgg	increased
8617	AF125161.PE1	nc	T-type calcium channel isoform		atc	agg	increased
8618	AF125161.PE1	nc	T-type calcium channel isoform		atc	agg	increased
8619	AF125161.PE1	nc	T-type calcium channel isoform		atc	agg	increased
8620	AF125161.PE1	nc	T-type calcium channel isoform		gcg	agg	increased
8621	AF125161.PE1	nc	T-type calcium channel isoform		gcg	agg	increased
8622	AF125161.PE1	nc	T-type calcium channel isoform		gcg	agg	increased
8623	AF125161.PE1	nc	T-type calcium channel isoform		gcg	agg	increased
8624	AF125161.PE1	nc	T-type calcium channel isoform		cgg	acc	increased
8625	AF125161.PE1	nc	T-type calcium channel isoform		cgg	acc	increased
8626	AF125161.PE1	nc	T-type calcium channel isoform		cgg	acc	increased
8627	AF125161.PE1	nc	T-type calcium channel isoform		cgg	acc	increased
8628	AF125161.PE1	nc	T-type calcium channel isoform		cgg	acc	increased
8629	AF125161.PE1	nc	T-type calcium channel isoform		tag	tgg	increased
8630	AF125161.PE1	nc	T-type calcium channel isoform		tag	tgg	increased
8631	AF125161.PE1	nc	T-type calcium channel isoform		tag	tgg	increased
8632	AF125161.PE1	nc	T-type calcium channel isoform		gta	aat	increased
8633	AF207605.TTL	Ttl	tubulin tyrosine ligase		act	aga	decreased
8634	AF207605.TTL	Ttl	tubulin tyrosine ligase		act	aga	decreased
8635	AF238865.PE1	nc	tumor suppressor pHyde	*	cat	agg	decreased
8636	AF238865.PE1	nc	tumor suppressor pHyde	*	ttc	agc	decreased
8637	AF238865.PE1	nc	tumor suppressor pHyde	*	ttc	agc	decreased
8638	AF238865.PE1	nc	tumor suppressor pHyde	*	ttc	agc	decreased
8639	AF238865.PE1	nc	tumor suppressor pHyde	*	ttc	agc	decreased
8640	AF335281.PE1	nc	tumor suppressor pHyde	*	cat	agg	decreased
8641	AF335281.PE1	nc	tumor suppressor pHyde	*	ttc	agc	decreased
8642	AF335281.PE1	nc	tumor suppressor pHyde	*	ttc	agc	decreased
8643	AF335281.PE1	nc	tumor suppressor pHyde	*	ttc	agc	decreased
8644	AF335281.PE1	nc	tumor suppressor pHyde	*	ttc	agc	decreased
8645	RNO131845.TWIST	twist	twist protein		acc	agg	No change

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**		**size**			**fluorescence**		**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
8646	Hha1	60	ttg	110.32	110	110.48	110.44	110.04	8 800 000	19 300 000	18 200 000	+=	/ (-)		-1
8647	Hha1	39	agg	97.8	98	0	97.94	97.66	0	531.37	508.62	+=	/	/	/(5)
8648	Hha1	39	agg	98.28	98	98.28	0	0	329.91	0	0	-=	\		/(5)
8649	Hha1	40	tgg	97.635	98	97.61	0	97.66	3 500 000	0	9 600 000	=+(+)	/	/	/(5)
8650	Hha1	40	tgg	98.265	98	98.2	98.33	0	4 400 000	9 300 000	0	+-	A		/(5)
8651	Taq1	31	gac	100.507	100	100.59	100.44	100.49	15 800 000	5 300 000	73 500 000	=+	/ (-)		/(5)
8652	Taq1	31	gac	99.487	100	99.54	99.43	99.49	5 700 000	3 000 000	31 500 000	=+	/ (-)		/(5)
8653	Taq1	56	tga	100.495	100	100.4	100.59	0	5 100 000	9 000 000	0	=-	\		/(5)
8654	Taq1	56	tga	99.73	100	0	99.73	0	0	4 600 000	0	+-	A		/(5)
8655	Hha1	6	aga	154.4	155	154.27	0	154.53	14 200 000	0	12 300 000	-+(=)	V		/(5)
8656	Hha1	6	aga	154.99	155	0	154.99	0	0	4 100 000	0	+-	A		/(5)
8657	Hha1	6	aga	155.5	155	0	0	155.5	0	0	17 000 000	=+	/		/(5)
8658	Taq1	23	cga	154.13	155	0	0	154.13	0	0	5 700 000	=+	/		/(5)
8659	Taq1	23	cga	155.117	155	155.13	155.06	155.16	4 300 000	5 600 000	5 900 000	==	-		/(5)
8660	Hha1	56	tga	119.6	120	119.85	119.35	0	9 704.57	225.67	0	-=	\		\(2) A(2)
8661	Hha1	56	tga	119.71	120	0	119.71	0	0	297.22	0	+-	A		\(2) A(2)
8662	Hha1	59	ttc	119.5	120	119.76	119.46	119.28	410.81	376.56	250.95	==	-		\(2) A(2)
8663	Hha1	59	ttc	120.06	120	0	120.06	0	0	218.46	0	+-	A		\(2) A(2)
8664	Hha1	59	ttc	120.7	120	120.7	0	0	956.83	0	0	-=	\		\(2) A(2)
8665	Taq1	9	atc	96.553	97	96.55	96.57	96.54	13 600 000	19 600 000	3 500 000	=-	\ (-)		\(7)
8666	Hha1	9	atc	97.07	97	97.07	0	0	6 600 000	0	0	-=	\		\(7)
8667	Taq1	9	atc	97.555	97	97.48	97.63	0	8 400 000	22 500 000	0	+-	A		\(7)
8668	Taq1	31	gac	96.42	97	96.37	96.33	96.56	55 000 000	43 400 000	3 100 000	=-	\ (-)		\(7)
8669	Taq1	31	gac	97.437	97	97.4	97.32	97.59	62 800 000	57 200 000	11 100 000	=-	\ (-)		\(7)
8670	Taq1	51	ata	132.83	133	132.83	0	0	8 800 000	0	0	-=	\		\(7)
8671	Taq1	52	att	132.26	133	132.26	0	0	5 700 000	0	0	-=	\		\(7)
8672	Taq1	52	att	132.85	133	0	132.89	132.81	0	3 200 000	5 300 000	+=	/		\(7)
8673	Taq1	52	att	133.64	133	0	133.47	133.81	0	3 800 000	8 800 000	=+	/		\(7)
8674	Hha1	20	ctc	154.58	155	154.58	0	0	268.59	0	0	-=	\		\(7)
8675	Hha1	26	ctg	154.083	155	154.07	154.1	154.08	55 500 000	17 300 000	45 300 000	-+	V		\(7)
8676	Hha1	26	ctg	155.007	155	154.99	155.02	155.01	8 900 000	3 900 000	8 500 000	-+	V		\(7)
8677	Hha1	26	ctg	176.465	177	176.41	0	176.52	12 900 000	0	4 600 000	-=(-)	\		\(7)
8678	Hha1	26	ctg	177.995	177	0	177.99	178	0	3 600 000	5 400 000	+=	/		\(7)
8679	Taq1	9	atc	96.553	97	96.55	96.57	96.54	13 600 000	19 600 000	3 500 000	=-	\ (-)		\(7)
8680	Hha1	9	atc	97.07	97	97.07	0	0	6 600 000	0	0	-=	\		\(7)
8681	Taq1	9	atc	97.555	97	97.48	97.63	0	8 400 000	22 500 000	0	+-	A		\(7)
8682	Taq1	31	gac	96.42	97	96.37	96.33	96.56	55 000 000	43 400 000	3 100 000	=-	\ (-)		\(7)
8683	Taq1	31	gac	97.437	97	97.4	97.32	97.59	62 800 000	57 200 000	11 100 000	=-	\ (-)		\(7)
8684	Taq1	51	ata	132.83	133	132.83	0	0	8 800 000	0	0	-=	\		\(7)
8685	Taq1	52	att	132.26	133	132.26	0	0	5 700 000	0	0	-=	\		\(7)
8686	Taq1	52	att	132.85	133	0	132.89	132.81	0	3 200 000	5 300 000	+=	/		\(7)
8687	Taq1	52	att	133.64	133	0	133.47	133.81	0	3 800 000	8 800 000	=+	/		\(7)
8688	Hha1	20	ctc	154.58	155	154.58	0	0	268.59	0	0	-=	\		\(7)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
8646	RNO131845.TWIST	twist	twist protein		ggg	ttg	No change
8647	AF259502.PE1	nc	two pore K+ channel KT4.1		agg	tgg	decreased
8648	AF259502.PE1	nc	two pore K+ channel KT4.1		agg	tgg	decreased
8649	AF259502.PE1	nc	two pore K+ channel KT4.1		agg	tgg	decreased
8650	AF259502.PE1	nc	two pore K+ channel KT4.1		agg	tgg	decreased
8651	AF259502.PE1	nc	two pore K+ channel KT4.1		gac	tga	decreased
8652	AF259502.PE1	nc	two pore K+ channel KT4.1		gac	tga	decreased
8653	AF259502.PE1	nc	two pore K+ channel KT4.1		gac	tga	decreased
8654	AF259502.PE1	nc	two pore K+ channel KT4.1		gac	tga	decreased
8655	AF259502.PE1	nc	two pore K+ channel KT4.1		cga	aga	decreased
8656	AF259502.PE1	nc	two pore K+ channel KT4.1		cga	aga	decreased
8657	AF259502.PE1	nc	two pore K+ channel KT4.1		cga	aga	decreased
8658	AF259502.PE1	nc	two pore K+ channel KT4.1		cga	aga	decreased
8659	AF259502.PE1	nc	two pore K+ channel KT4.1		cga	aga	decreased
8660	AF157005.MYHC	MYHC	type 2X myosin heavy chain		tga	ttc	increased
8661	AF157005.MYHC	MYHC	type 2X myosin heavy chain		tga	ttc	increased
8662	AF157005.MYHC	MYHC	type 2X myosin heavy chain		tga	ttc	increased
8663	AF157005.MYHC	MYHC	type 2X myosin heavy chain		tga	ttc	increased
8664	AF157005.MYHC	MYHC	type 2X myosin heavy chain		tga	ttc	increased
8665	AB032827.PE1	nc	type II brain 4.1		gac	atc	increased
8666	AB032827.PE1	nc	type II brain 4.1		gac	atc	increased
8667	AB032827.PE1	nc	type II brain 4.1		gac	atc	increased
8668	AB032827.PE1	nc	type II brain 4.1		gac	atc	increased
8669	AB032827.PE1	nc	type II brain 4.1		gac	atc	increased
8670	AB032827.PE1	nc	type II brain 4.1		ata	att	increased
8671	AB032827.PE1	nc	type II brain 4.1		ata	att	increased
8672	AB032827.PE1	nc	type II brain 4.1		ata	att	increased
8673	AB032827.PE1	nc	type II brain 4.1		ata	att	increased
8674	AB032827.PE1	nc	type II brain 4.1		ctc	ctg	increased
8675	AB032827.PE1	nc	type II brain 4.1		ctc	ctg	increased
8676	AB032827.PE1	nc	type II brain 4.1		ctc	ctg	increased
8677	AB032827.PE1	nc	type II brain 4.1		cca	ctg	increased
8678	AB032827.PE1	nc	type II brain 4.1		cca	ctg	increased
8679	AB032828.PE1	nc	type II brain 4.1 minor isoform		gac	atc	increased
8680	AB032828.PE1	nc	type II brain 4.1 minor isoform		gac	atc	increased
8681	AB032828.PE1	nc	type II brain 4.1 minor isoform		gac	atc	increased
8682	AB032828.PE1	nc	type II brain 4.1 minor isoform		gac	atc	increased
8683	AB032828.PE1	nc	type II brain 4.1 minor isoform		gac	atc	increased
8684	AB032828.PE1	nc	type II brain 4.1 minor isoform		ata	att	increased
8685	AB032828.PE1	nc	type II brain 4.1 minor isoform		ata	att	increased
8686	AB032828.PE1	nc	type II brain 4.1 minor isoform		ata	att	increased
8687	AB032828.PE1	nc	type II brain 4.1 minor isoform		ata	att	increased
8688	AB032828.PE1	nc	type II brain 4.1 minor isoform		ctc	ctg	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
8689	Hha1	26	ctg	154.083	155	154.07	154.1	154.08	55 500 000	17 300 000	45 300 000	-+	V		\(7)
8690	Hha1	26	ctg	155.007	155	154.99	155.02	155.01	8 900 000	3 900 000	8 500 000	-+	V		\(7)
8691	Hha1	26	ctg	176.465	177	176.41	0	176.52	12 900 000	0	4 600 000	-=(-)	\		\(7)
8692	Hha1	26	ctg	177.995	177	0	177.99	178	0	3 600 000	5 400 000	+=	/		\(7)
8693	Taq1	55	tca	72.935	73	0	73	72.87	0	16 200 000	7 500 000	+-	A		A(3)
8694	Taq1	56	tga	72.6	73	72.48	72.72	0	3 800 000	47 300 000	0	+-	A		A(3)
8695	Hha1	59	ttc	74.587	75	74.58	74.6	74.58	618.82	2 365.75	1 122.81	+-	A		A(3)
8696	Hha1	59	ttc	75.45	75	75.5	75.4	0	2 407.69	991.72	0	-=	\		A(3)
8697	Hha1	33	agc	60.667	61	60.61	60.65	60.74	8 100 000	13 200 000	3 900 000	=-	\ (-)		\(4)
8698	Hha1	39	agg	102.82	103	102.98	102.66	0	447.21	250.76	0	=-	\		\(4)
8699	Hha1	39	agg	103.52	103	0	103.55	103.49	0	179.11	122.07	+=	/		\(4)
8700	Hha1	59	ttc	103.43	103	0	103.43	0	0	937.1	0	+-	A		\(4)
8701	Hha1	20	ctc	114.997	115	115.12	115.1	114.77	530.3	511.4	441.31	==	-		\(4)
8702	Hha1	31	gac	152.12	153	152.17	152.14	152.05	16 300 000	5 800 000	10 000 000	-=	\ (-)		\(4)
8703	Hha1	31	gac	153.287	153	153.26	153.41	153.19	4 300 000	4 800 000	4 300 000	==	-		\(4)
8704	Hha1	56	tga	153.09	153	153.09	0	0	261.51	0	0	-=	\		\(4)
8705	Taq1	62	tgt	174.315	175	0	174.44	174.19	0	4 000 000	3 300 000	+=	/		\(4)
8706	Taq1	62	tgt	175.4	175	0	175.48	175.32	0	6 400 000	3 900 000	+=	/		\(4)
8707	Hha1	8	gaa	263.67	265	263.67	0	0	7 000 000	0	0	-=	\		\(2)
8708	Hha1	8	gaa	264.4	265	0	264.4	0	0	3 700 000	0	+-	A		\(2)
8709	Taq1	8	gaa	264.34	265	0	0	264.34	0	0	3 500 000	=+	/		\(2)
8710	Taq1	8	gaa	264.92	265	264.92	264.92	0	11 000 000	10 100 000	0	=-	\		\(2)
8711	Hha1	8	gaa	235.04	236	235.04	0	0	4 300 000	0	0	-=	\		\(3)
8712	Taq1	8	gaa	235.63	236	235.63	0	0	3 800 000	0	0	-=	\		\(3)
8713	Hha1	8	gaa	236.3	236	236.33	236.27	0	3 900 000	3 100 000	0	=-	\		\(3)
8714	Hha1	27	acg	105.62	106	105.62	0	0	9 100 000	0	0	-=	\	\	-(2) \(2)
8715	Hha1	59	ttc	105.495	106	105.47	105.52	0	452.41	641.02	0	=-	\	\	-(2) \(2)
8716	Hha1	59	ttc	106.19	106	106.48	106.04	106.05	2 142.48	2 489.36	814.94	=-	\ (-)		-(2) \(2)
8717	Hha1	40	tgg	109.003	109	109.05	109.17	108.79	4 200 000	7 400 000	27 300 000	=+	/ (-)		-(2) \(2)
8718	Hha1	40	tgg	109.35	109	0	0	109.35	0	0	21 600 000	=+	/		-(2) \(2)
8719	Hha1	44	cgg	60.04	60	0	0	60.04	0	0	92 100 000	=+	/		/(2)
8720	Hha1	44	cgg	171.37	172	0	0	171.37	0	0	5 000 000	=+	/		/(2)
8721	Hha1	44	cgg	172.38	172	0	0	172.38	0	0	3 500 000	=+	/		/(2)
8722	Hha1	6	aga	128.355	129	128.33	128.38	0	16 000 000	6 100 000	0	-=	\		-3
8723	Hha1	6	aga	128.907	129	128.97	128.86	128.89	35 300 000	4 300 000	9 300 000	-=	\ (-)		-3
8724	Hha1	6	aga	129.19	129	0	129.19	0	0	5 000 000	0	+-	A		-3
8725	Hha1	8	gaa	152.267	153	152.3	152.4	152.1	4 600 000	4 500 000	7 200 000	==	-		-3
8726	Taq1	8	gaa	152.32	153	0	152.38	152.26	0	4 000 000	20 100 000	=+	/		-3
8727	Hha1	8	gaa	153.27	153	153.26	153.27	153.28	33 600 000	19 100 000	9 100 000	==	-		-3
8728	Taq1	50	aat	340.96	342	341.03	340.89	0	4 900 000	3 000 000	0	=-	\		-3
8729	Taq1	50	aat	342.16	342	342.16	0	0	4 800 000	0	0	-=	\		-3
8730	Hha1	41	ccc	123.8	124	123.8	0	0	5 400 000	0	0	-=	\		A(2) \(2)
8731	Taq1	45	gcc	246.65	247	0	246.65	0	0	3 300 000	0	+-	A		A(2) \(2)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
8689	AB032828.PE1	nc	type II brain 4.1 minor isoform		ctc	ctg	increased
8690	AB032828.PE1	nc	type II brain 4.1 minor isoform		ctc	ctg	increased
8691	AB032828.PE1	nc	type II brain 4.1 minor isoform		cca	ctg	increased
8692	AB032828.PE1	nc	type II brain 4.1 minor isoform		cca	ctg	increased
8693	RATRII51.PE1	nc	type II cAMP-dependent protein kinase regulatory		tca	tga	increased by mild
8694	RATRII51.PE1	nc	type II cAMP-dependent protein kinase regulatory		tca	tga	increased by mild
8695	RATRII51.PE1	nc	type II cAMP-dependent protein kinase regulatory		ttc	ccg	increased by mild
8696	RATRII51.PE1	nc	type II cAMP-dependent protein kinase regulatory		ttc	ccg	increased by mild
8697	RNU24282.DIOIII	dioIII	type III iodiothyronine deiodinase		agc	ctt	increased
8698	RNU24282.DIOIII	dioIII	type III iodiothyronine deiodinase		ttc	agg	increased
8699	RNU24282.DIOIII	dioIII	type III iodiothyronine deiodinase		ttc	agg	increased
8700	RNU24282.DIOIII	dioIII	type III iodiothyronine deiodinase		ttc	agg	increased
8701	RNU24282.DIOIII	dioIII	type III iodiothyronine deiodinase		ctc	aac	increased
8702	RNU24282.DIOIII	dioIII	type III iodiothyronine deiodinase		gac	tga	increased
8703	RNU24282.DIOIII	dioIII	type III iodiothyronine deiodinase		gac	tga	increased
8704	RNU24282.DIOIII	dioIII	type III iodiothyronine deiodinase		gac	tga	increased
8705	RNU24282.DIOIII	dioIII	type III iodiothyronine deiodinase		cta	tgt	increased
8706	RNU24282.DIOIII	dioIII	type III iodiothyronine deiodinase		cta	tgt	increased
8707	RATTGFBET.PE1	nc	type III TGF-beta receptor		gaa	gag	increased
8708	RATTGFBET.PE1	nc	type III TGF-beta receptor		gaa	gag	increased
8709	RATTGFBET.PE1	nc	type III TGF-beta receptor		gaa	gag	increased
8710	RATTGFBET.PE1	nc	type III TGF-beta receptor		gaa	gag	increased
8711	RNCOLL.PE1	nc	type IV collagenase		gac	gaa	increased
8712	RNCOLL.PE1	nc	type IV collagenase		gac	gaa	increased
8713	RNCOLL.PE1	nc	type IV collagenase		gac	gaa	increased
8714	RATTOHAB.PE1	nc	tyrosine hydroxylase	*	ttc	acg	increased
8715	RATTOHAB.PE1	nc	tyrosine hydroxylase	*	ttc	acg	increased
8716	RATTOHAB.PE1	nc	tyrosine hydroxylase	*	ttc	acg	No change
8717	RATTOHAB.PE1	nc	tyrosine hydroxylase	*	cca	tgg	No change
8718	RATTOHAB.PE1	nc	tyrosine hydroxylase	*	cca	tgg	No change
8719	RATPTK3D.PTK-3	Ptk-3	tyrosine kinase receptor		cgg	tct	decreased
8720	RATPTK3D.PTK-3	Ptk-3	tyrosine kinase receptor		cgg	aga	decreased
8721	RATPTK3D.PTK-3	Ptk-3	tyrosine kinase receptor		cgg	aga	decreased
8722	AF076167.PE1	nc	UDP-GalNAc:polypeptide		gag	aga	No change
8723	AF076167.PE1	nc	UDP-GalNAc:polypeptide		gag	aga	No change
8724	AF076167.PE1	nc	UDP-GalNAc:polypeptide		gag	aga	No change
8725	AF076167.PE1	nc	UDP-GalNAc:polypeptide		gaa	ggc	No change
8726	AF076167.PE1	nc	UDP-GalNAc:polypeptide		gaa	ggc	No change
8727	AF076167.PE1	nc	UDP-GalNAc:polypeptide		gaa	ggc	No change
8728	AF076167.PE1	nc	UDP-GalNAc:polypeptide		act	aat	No change
8729	AF076167.PE1	nc	UDP-GalNAc:polypeptide		act	aat	No change
8730	AF461737.PE1	nc	UDP-glucuronosyltransferase 1A6		ctc	ccc	increased by mild
8731	AF461737.PE1	nc	UDP-glucuronosyltransferase 1A6		gcc	ccc	increased by mild

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
8732	Taq1	45	gcc	248.04	247	0	248.04	0	0	3 500 000	0	+-	A		A(2) \(2)
8733	Taq1	51	ata	278.34	280	278.34	0	0	3 500 000	0	0	-=	\		A(2) \(2)
8734	Taq1	51	ata	279.41	280	279.41	0	0	38 800 000	0	0	-=	\		A(2) \(2)
8735	Taq1	51	ata	281.25	280	0	281.25	0	0	21 000 000	0	+-	A		A(2) \(2)
8736	Hha1	4	aag	132.925	133	0	132.84	133.01	0	11 300 000	8 400 000	+=	/	/	/(2)
8737	Hha1	4	aag	133.68	133	0	133.68	0	0	3 200 000	0	+-	A		/(2)
8738	Taq1	56	tga	133.07	133	0	0	133.07	0	0	3 200 000	=+	/	/	/(2)
8739	Taq1	55	tca	66.87	67	0	66.87	0	0	12 100 000	0	+-	A		/(4)
8740	Hha1	11	act	100.35	100	100.28	100.42	100.35	14 600 000	3 600 000	4 500 000	-=	\ (-)		/(4)
8741	Taq1	11	act	100.52	100	0	0	100.52	0	0	8 700 000	=+	/		/(4)
8742	Taq1	11	act	99.51	100	0	0	99.51	0	0	10 800 000	=+	/		/(4)
8743	Taq1	18	cct	117.557	118	117.47	117.46	117.74	4 600 000	6 200 000	24 000 000	=+	/ (-)	/	/(4)
8744	Taq1	18	cct	118.45	118	118.41	0	118.49	5 500 000	0	6 200 000	-+(=)	V		/(4)
8745	Taq1	35	gga	117.7	118	0	0	117.7	0	0	3 600 000	=+	/	/	/(4)
8746	Hha1	20	ctc	101.455	101	101.45	0	101.46	523.41	0	381.67	-+(=)	V		-2
8747	Hha1	60	ttg	101.403	101	101.3	101.63	101.28	7 000 000	5 100 000	5 600 000	==	-		-2
8748	Hha1	41	ccc	151.12	151	151.08	151.08	151.2	6 400 000	3 200 000	3 700 000	-=	\ (-)		-2
8749	Hha1	2	tta	115.87	116	115.87	0	0	124 100 000	0	0	-=	\		-2
8750	Hha1	2	tta	116.37	116	116.33	116.39	116.39	77 300 000	108 500 000	119 900 000	==	-		-2
8751	Hha1	32	gtc	149.13	150	149.14	149.17	149.08	1 537.89	1 414.03	3 128.76	=+	/ (-)		-2
8752	Hha1	32	gtc	150.08	150	0	0	150.08	0	0	601.68	=+	/		-2
8753	Hha1	44	cgg	143.815	144	143.9	143.73	0	3 600 000	4 400 000	0	=-	\		/(2) A(2) V(2)
8754	Hha1	44	cgg	144.455	144	144.66	144.25	0	4 900 000	3 900 000	0	=-	\		/(2) A(2) V(2)
8755	Hha1	44	cgg	144.01	144	0	144.01	0	0	3 800 000	0	+-	A		/(2) A(2) V(2)
8756	Hha1	44	cgg	144.72	144	0	144.72	0	0	4 100 000	0	+-	A		/(2) A(2) V(2)
8757	Hha1	33	agc	144.21	145	144.2	0	144.22	4 000 000	0	3 500 000	-+(=)	V		/(2) A(2) V(2)
8758	Hha1	33	agc	145.22	145	0	0	145.22	0	0	7 200 000	=+	/		/(2) A(2) V(2)
8759	Taq1	39	agg	237.885	239	237.68	0	238.09	3 900 000	0	4 500 000	-+(=)	V		/(2) A(2) V(2)
8760	Taq1	39	agg	238.24	239	0	238.24	0	0	100 400 000	0	+-	A		/(2) A(2) V(2)
8761	Taq1	39	agg	238.24	239	0	238.24	0	0	1 009.05	0	+-	A		/(2) A(2) V(2)
8762	Taq1	39	agg	239.18	239	239.24	0	239.12	9 400 000	0	46 900 000	=+(+)	/		/(2) A(2) V(2)
8763	Taq1	39	agg	237.885	239	237.68	0	238.09	144.83	0	132.54	-+(=)	V		/(2) A(2) V(2)
8764	Taq1	39	agg	239.18	239	239.24	0	239.12	349.07	0	1 381.44	=+(+)	/		/(2) A(2) V(2)
8765	Taq1	31	gac	107.61	108	0	107.61	0	0	8 500 000	0	+-	A		V(3)
8766	Taq1	56	tga	108.03	108	108.01	0	108.05	3 800 000	0	6 600 000	-+(=)	V		V(3)
8767	Taq1	45	gcc	164.535	165	164.45	0	164.62	3 800 000	0	4 900 000	-+(=)	V		V(3)
8768	Hha1	6	aga	165.59	166	165.63	165.53	165.61	7 400 000	4 900 000	5 400 000	==	-		V(3)
8769	Hha1	6	aga	166.585	166	166.62	0	166.55	6 200 000	0	4 300 000	-+(=)	V		V(3)
8770	Taq1	18	cct	178.855	179	178.85	178.86	0	8 200 000	4 700 000	0	=-	\		V(3)
8771	Taq1	18	cct	179.893	179	179.93	179.92	179.83	4 000 000	3 400 000	4 000 000	==	-		V(3)
8772	Hha1	27	acg	87.243	87	87.23	87.26	87.24	71 300 000	19 700 000	10 100 000	-=	\ (-)		-2
8773	Hha1	44	cgg	100.577	101	100.63	100.49	100.61	15 800 000	12 600 000	6 200 000	==	-		-2
8774	Hha1	64	gtt	104.47	105	104.47	0	0	4 800 000	0	0	-=	\		\(3)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
8732	AF461737.PE1	nc	UDP-glucuronosyltransferase 1A6		gcc	ccc	increased by mild
8733	AF461737.PE1	nc	UDP-glucuronosyltransferase 1A6		ata	tgg	increased by mild
8734	AF461737.PE1	nc	UDP-glucuronosyltransferase 1A6		ata	tgg	increased by mild
8735	AF461737.PE1	nc	UDP-glucuronosyltransferase 1A6		ata	tgg	increased by mild
8736	RRUGTGENE.UGT2A1	ugt2A1	UDP-glucuronosyltransferase 2A1 precursor		aag	tga	decreased
8737	RRUGTGENE.UGT2A1	ugt2A1	UDP-glucuronosyltransferase 2A1 precursor		aag	tga	decreased
8738	RRUGTGENE.UGT2A1	ugt2A1	UDP-glucuronosyltransferase 2A1 precursor		aag	tga	decreased
8739	RNUDPNAGE.PE1	nc	UDP-N-acetylglucosamine 2-epimerase		cgt	tca	decreased
8740	RNUDPNAGE.PE1	nc	UDP-N-acetylglucosamine 2-epimerase		act	tat	decreased
8741	RNUDPNAGE.PE1	nc	UDP-N-acetylglucosamine 2-epimerase		act	tat	decreased
8742	RNUDPNAGE.PE1	nc	UDP-N-acetylglucosamine 2-epimerase		act	tat	decreased
8743	RNUDPNAGE.PE1	nc	UDP-N-acetylglucosamine 2-epimerase		cct	gga	decreased
8744	RNUDPNAGE.PE1	nc	UDP-N-acetylglucosamine 2-epimerase		cct	gga	decreased
8745	RNUDPNAGE.PE1	nc	UDP-N-acetylglucosamine 2-epimerase		cct	gga	decreased
8746	RNU75903.PE1	nc	UGT1A7		ctc	ttg	No change
8747	RNU75903.PE1	nc	UGT1A7		ctc	ttg	No change
8748	RNU75903.PE1	nc	UGT1A7		atg	ccc	No change
8749	AF093625.PE1	nc	ULF-250 protein		ctt	tta	No change
8750	AF093625.PE1	nc	ULF-250 protein		ctt	tta	No change
8751	AF093625.PE1	nc	ULF-250 protein		gtc	gaa	No change
8752	AF093625.PE1	nc	ULF-250 protein		gtc	gaa	No change
8753	AF095741.MG87	MG87	unknown		cgg	agc	decreased
8754	AF095741.MG87	MG87	unknown		cgg	agc	decreased
8755	AF095741.MG87	MG87	unknown		cgg	agc	decreased
8756	AF095741.MG87	MG87	unknown		cgg	agc	decreased
8757	AF095741.MG87	MG87	unknown		cgg	agc	decreased
8758	AF095741.MG87	MG87	unknown		cgg	agc	decreased
8759	AF095741.MG87	MG87	unknown		agg	gca	decreased
8760	AF095741.MG87	MG87	unknown		agg	gca	decreased
8761	AF095741.MG87	MG87	unknown		agg	gca	decreased
8762	AF095741.MG87	MG87	unknown		agg	gca	decreased
8763	AF095741.MG87	MG87	unknown		agg	gca	decreased
8764	AF095741.MG87	MG87	unknown		agg	gca	decreased
8765	BC058456.PE1	nc	Unknown (protein for MGC:72742)		gac	tga	decreased by mild
8766	BC058456.PE1	nc	Unknown (protein for MGC:72742)		gac	tga	decreased by mild
8767	BC058456.PE1	nc	Unknown (protein for MGC:72742)		gcc	aga	decreased by mild
8768	BC058456.PE1	nc	Unknown (protein for MGC:72742)		gcc	aga	decreased by mild
8769	BC058456.PE1	nc	Unknown (protein for MGC:72742)		gcc	aga	decreased by mild
8770	BC058456.PE1	nc	Unknown (protein for MGC:72742)		cct	gtc	decreased by mild
8771	BC058456.PE1	nc	Unknown (protein for MGC:72742)		cct	gtc	decreased by mild
8772	BC058498.PE1	nc	Unknown (protein for MGC:72957)		ggt	acg	No change
8773	BC058498.PE1	nc	Unknown (protein for MGC:72957)		tat	cgg	No change
8774	RNU81518.UT3	UT3	urea transporter		gtt	caa	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
8775	Hha1	64	gtt	105.31	105	105.19	0	105.43	10 200 000	0	5 200 000	-+(-)	V (\)		\(3)
8776	Hha1	56	tga	136.845	137	136.76	136.93	0	559.8	253.19	0	--	\		\(3)
8777	Hha1	62	tgt	137.11	137	137.11	0	0	4 800 000	0	0	-=	\		\(3)
8778	Hha1	33	agc	76.7	77	76.7	0	0	3 200 000	0	0	-=	\		\(3)
8779	Taq1	18	cct	126.43	127	0	0	126.43	0	0	7 900 000	=+	/		\(3)
8780	Taq1	18	cct	127.63	127	127.59	127.67	0	4 100 000	4 100 000	0	=-	\		\(3)
8781	Hha1	40	tgg	151.76	152	151.76	0	0	7 700 000	0	0	-=	\		\(3)
8782	Hha1	40	tgg	152.725	152	152.8	152.65	0	4 000 000	10 100 000	0	+-	A		\(3)
8783	Taq1	26	ctg	174.47	175	0	0	174.47	0	0	3 100 000	=+	/		/(2)
8784	Taq1	26	ctg	175.52	175	0	175.53	175.51	0	4 300 000	31 000 000	=+	/		/(2)
8785	Taq1	57	ctg	174.9	175	0	0	174.9	0	0	3 800 000	=+	/		/(2)
8786	Taq1	57	ctg	175.94	175	0	0	175.94	0	0	3 400 000	=+	/		/(2)
8787	Taq1	54	ttt	135.905	136	135.89	135.92	0	662.78	893.8	0	=-	\		\(2) A(2)
8788	Taq1	54	ttt	136.7	136	0	136.7	0	0	388.09	0	+-	A		\(2) A(2)
8789	Taq1	50	aat	331.74	333	331.74	0	0	4 800 000	0	0	-=	\		\(2) A(2)
8790	Taq1	50	aat	334.54	333	0	334.54	0	0	3 000 000	0	+-	A		\(2) A(2)
8791	Hha1	33	agc	60.667	61	60.61	60.65	60.74	8 100 000	13 200 000	3 900 000	=-	\ (-)		-(3) \(2)
8792	Hha1	26	ctg	113.7	114	113.66	113.69	113.75	8 500 000	5 900 000	5 200 000	==	-		-(3) \(2)
8793	Hha1	54	ttt	114.987	115	114.99	114.98	114.99	41 900 000	41 900 000	20 100 000	=-	\ (-)		-(3) \(2)
8794	Taq1	36	ggt	148	148	148.02	0	147.98	3 400 000	0	3 200 000	-+(=)	V		/(4) V(4)
8795	Taq1	52	att	148.167	149	148.2	148.23	148.07	4 800 000	5 600 000	4 300 000	==	-		/(4) V(4)
8796	Taq1	22	tcc	171.84	172	0	0	171.84	0	0	5 800 000	=+	/		/(4) V(4)
8797	Taq1	22	tcc	172.875	172	172.79	0	172.96	7 100 000	0	9 800 000	-+(=)	V		/(4) V(4)
8798	Taq1	26	ctg	171.56	172	0	0	171.56	0	0	3 500 000	=+	/		/(4) V(4)
8799	Taq1	26	ctg	172.52	172	0	0	172.52	0	0	12 900 000	=+	/		/(4) V(4)
8800	Taq1	57	ctg	171.73	172	0	0	171.73	0	0	3 100 000	=+	/		/(4) V(4)
8801	Taq1	57	ctg	172.8	172	172.73	0	172.87	3 500 000	0	6 600 000	-+(+)	V (/)		/(4) V(4)
8802	Hha1	39	agg	244.015	245	244.13	0	243.9	263.92	0	122.07	-+(-)	V (\)		/(4) V(4)
8803	Hha1	39	agg	244.99	245	0	0	244.99	0	0	146.48	=+	/		/(4) V(4)
8804	Hha1	39	agg	246.39	245	0	0	246.39	0	0	162.76	=+	/		/(4) V(4)
8805	Hha1	26	ctg	126.61	127	126.75	126.75	126.33	29 700 000	8 000 000	5 600 000	-=	\ (-)		\(2)
8806	Hha1	26	ctg	127.69	127	127.69	0	0	3 600 000	0	0	-=	\		\(2)
8807	Hha1	33	agc	126.97	127	127.07	0	126.87	3 000 000	0	9 600 000	=+(+)	/		\(2)
8808	Hha1	40	tgg	238.06	239	0	238.06	0	0	3 900 000	0	+-	A		\(2)
8809	Hha1	40	tgg	238.845	239	238.71	238.98	0	3 900 000	3 200 000	0	=-	\		\(2)
8810	Hha1	40	tgg	239.97	239	239.97	0	0	4 500 000	0	0	-=	\		\(2)
8811	Hha1	22	tcc	114.313	115	114.13	114.38	114.43	8 700 000	9 400 000	12 200 000	==	-	-	
8812	Taq1	22	tcc	114.36	115	114.26	114.34	114.48	11 500 000	12 200 000	9 500 000	==	-	-	
8813	Taq1	64	gtt	153.943	154	153.94	153.89	154	7 100 000	7 900 000	5 300 000	==	-		-2
8814	Taq1	64	gtt	154.923	154	154.96	154.91	154.9	5 600 000	6 500 000	7 600 000	==	-		-2
8815	Taq1	54	ttt	154.675	155	154.61	154.74	0	1 194.46	1 493.59	0	=-	\		-2
8816	Taq1	54	ttt	155.557	155	155.53	155.56	155.58	8 761.83	11 654.71	1 199.14	=-	\ (-)		-2
8817	Hha1	40	tgg	141.62	142	0	141.62	0	0	5 100 000	0	+-	A		/(2) A(2)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
8775	RNU81518.UT3	UT3	urea transporter		gtt	caa	increased
8776	RNU81518.UT3	UT3	urea transporter		tgt	tga	increased
8777	RNU81518.UT3	UT3	urea transporter		tgt	tga	increased
8778	AF093623.PE1	nc	urocortin precursor	*	tac	agc	increased
8779	AF093623.PE1	nc	urocortin precursor	*	cct	ata	increased
8780	AF093623.PE1	nc	urocortin precursor	*	cct	ata	increased
8781	AF093623.PE1	nc	urocortin precursor	*	ggg	tgg	increased
8782	AF093623.PE1	nc	urocortin precursor	*	ggg	tgg	increased
8783	RNURODR.PE1	nc	uroporphyrinogen decarboxylase		ctg	agc	decreased
8784	RNURODR.PE1	nc	uroporphyrinogen decarboxylase		ctg	agc	decreased
8785	RNURODR.PE1	nc	uroporphyrinogen decarboxylase		ctg	agc	decreased
8786	RNURODR.PE1	nc	uroporphyrinogen decarboxylase		ctg	agc	decreased
8787	AF022147.UO	uo	uterus-ovary specific putative transmembrane		agc	ttt	increased
8788	AF022147.UO	uo	uterus-ovary specific putative transmembrane		agc	ttt	increased
8789	AF022147.UO	uo	uterus-ovary specific putative transmembrane		gat	aat	increased
8790	AF022147.UO	uo	uterus-ovary specific putative transmembrane		gat	aat	increased
8791	RNU35244.PE1	nc	vacuolar protein sorting homolog r-vps33a		gag	agc	No change
8792	RNU35244.PE1	nc	vacuolar protein sorting homolog r-vps33a		ttt	ctg	No change
8793	RNU35244.PE1	nc	vacuolar protein sorting homolog r-vps33a		ttt	ctg	No change
8794	RNU35245.PE1	nc	vacuolar protein sorting homolog r-vps33b		att	ggt	decreased
8795	RNU35245.PE1	nc	vacuolar protein sorting homolog r-vps33b		att	ggt	decreased
8796	RNU35245.PE1	nc	vacuolar protein sorting homolog r-vps33b		ctg	tcc	decreased
8797	RNU35245.PE1	nc	vacuolar protein sorting homolog r-vps33b		ctg	tcc	decreased
8798	RNU35245.PE1	nc	vacuolar protein sorting homolog r-vps33b		ctg	tcc	decreased
8799	RNU35245.PE1	nc	vacuolar protein sorting homolog r-vps33b		ctg	tcc	decreased
8800	RNU35245.PE1	nc	vacuolar protein sorting homolog r-vps33b		ctg	tcc	decreased
8801	RNU35245.PE1	nc	vacuolar protein sorting homolog r-vps33b		ctg	tcc	decreased
8802	RNU35245.PE1	nc	vacuolar protein sorting homolog r-vps33b		cta	agg	decreased
8803	RNU35245.PE1	nc	vacuolar protein sorting homolog r-vps33b		cta	agg	decreased
8804	RNU35245.PE1	nc	vacuolar protein sorting homolog r-vps33b		cta	agg	decreased
8805	AF129113.VRL-1	VRL-1	vanilloid receptor-like protein 1		ctg	agc	increased
8806	AF129113.VRL-1	VRL-1	vanilloid receptor-like protein 1		ctg	agc	increased
8807	AF129113.VRL-1	VRL-1	vanilloid receptor-like protein 1		ctg	agc	increased
8808	AF129113.VRL-1	VRL-1	vanilloid receptor-like protein 1		tgg	act	increased
8809	AF129113.VRL-1	VRL-1	vanilloid receptor-like protein 1		tgg	act	increased
8810	AF129113.VRL-1	VRL-1	vanilloid receptor-like protein 1		tgg	act	increased
8811	AF263521.VROAC	Vroac	vanilloid receptor-related osmotically activated		tgg	tcc	No change
8812	AF263521.VROAC	Vroac	vanilloid receptor-related osmotically activated		tgg	tcc	No change
8813	AB027561.VESP11	VESP11	vascular endothelial cell specific protein 11		gtt	ttt	No change
8814	AB027561.VESP11	VESP11	vascular endothelial cell specific protein 11		gtt	ttt	No change
8815	AB027561.VESP11	VESP11	vascular endothelial cell specific protein 11		gtt	ttt	No change
8816	AB027561.VESP11	VESP11	vascular endothelial cell specific protein 11		gtt	ttt	No change
8817	AB031088.VESP14	VESP14	vascular endothelial cell specific protein 14		tgg	ttc	decreased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
8818	Hha1	40	tgg	141.81	142	0	141.81	0	0	5 300 000	0	+-	A		/(2) A(2)
8819	Hha1	40	tgg	142.665	142	0	142.82	142.51	0	3 200 000	3 800 000	+=	/		/(2) A(2)
8820	Hha1	59	ttc	141.54	142	0	0	141.54	0	0	106.07	=+	/		/(2) A(2)
8821	Hha1	59	ttc	142.43	142	0	142.43	0	0	238.58	0	+-	A		/(2) A(2)
8822	Taq1	10	atg	64.65	65	64.51	64.55	64.89	11 600 000	12 000 000	6 100 000	=-	\ (-)		\(2)
8823	Taq1	10	atg	269.56	268	269.56	0	0	3 400 000	0	0	-=	\		\(2)
8824	Taq1	47	ggc	142.09	142	142.09	0	0	1 969.23	0	0	-=	\		\(2)
8825	Hha1	6	aga	143.277	143	143.37	143.3	143.16	10 800 000	5 000 000	3 900 000	-=	\ (-)		\(2)
8826	Hha1	33	agc	62.84	63	62.76	62.92	62.84	4 400 000	18 500 000	17 900 000	+=	/ (-)		-(2) /(2) \(2)
8827	Hha1	20	ctc	74.577	75	74.85	74.49	74.39	3 567.49	773.66	763.35	-=	\ (-)		-(2) /(2) \(2)
8828	Hha1	20	ctc	74.93	75	0	75.01	74.85	0	1 363.75	894.56	+=	/		-(2) /(2) \(2)
8829	Hha1	33	agc	110.905	111	110.83	110.98	0	12 700 000	12 900 000	0	=-	\		-(2) /(2) \(2)
8830	Hha1	33	agc	62.84	63	62.76	62.92	62.84	4 400 000	18 500 000	17 900 000	+=	/ (-)		-(2) /(2) \(2)
8831	Hha1	20	ctc	74.577	75	74.85	74.49	74.39	3 567.49	773.66	763.35	-=	\ (-)		-(2) /(2) \(2)
8832	Hha1	20	ctc	74.93	75	0	75.01	74.85	0	1 363.75	894.56	+=	/		-(2) /(2) \(2)
8833	Hha1	33	agc	110.905	111	110.83	110.98	0	12 700 000	12 900 000	0	=-	\		-(2) /(2) \(2)
8834	Hha1	21	acc	106.475	107	0	106.29	106.66	0	5 200 000	9 700 000	++	/	(/)	
8835	Taq1	21	acc	106.53	107	106.49	0	106.57	18 200 000	0	37 000 000	-+(+)	V (/)	(/)	
8836	Taq1	40	tgg	131.82	132	0	0	131.82	0	0	4 300 000	=+	/		/(2)
8837	Hha1	61	tct	147.073	147	147.05	147.04	147.13	8 600 000	27 600 000	17 800 000	+=	/ (-)		/(2)
8838	Hha1	26	ctg	231.04	232	0	231.04	0	0	3 600 000	0	+-	A		/(2)
8839	Hha1	3	aac	94.513	94	94.54	94.4	94.6	20 700 000	11 000 000	10 800 000	-=	\ (-)		\(2)
8840	Taq1	17	cca	309.28	310	309.28	0	0	199.69	0	0	-=	\		\(2)
8841	Taq1	17	cca	310.96	310	0	310.96	0	0	505.25	0	+-	A		\(2)
8842	Hha1	6	aga	126.475	127	126.51	0	126.44	89 200 000	0	7 100 000	-=(-)	\		/(3)
8843	Hha1	6	aga	127.097	127	127.18	127.06	127.05	30 600 000	3 500 000	5 400 000	-=	\ (-)		/(3)
8844	Hha1	6	aga	127.6	127	0	127.54	127.66	0	3 100 000	6 300 000	++	/		/(3)
8845	Hha1	9	atc	126.45	127	0	0	126.45	0	0	4 400 000	=+	/		/(3)
8846	Taq1	9	atc	127.09	127	0	0	127.09	0	0	12 500 000	=+	/		/(3)
8847	Hha1	9	atc	127.14	127	127.14	0	0	6 500 000	0	0	-=	\		/(3)
8848	Hha1	10	atg	167.46	168	167.52	167.4	0	7 500 000	3 900 000	0	--	\		\(5)
8849	Taq1	10	atg	167.35	168	167.35	0	0	4 400 000	0	0	-=	\		\(5)
8850	Taq1	10	atg	167.88	168	0	167.88	0	0	3 600 000	0	+-	A		\(5)
8851	Taq1	10	atg	168.41	168	168.41	0	0	4 100 000	0	0	-=	\	\	\(5)
8852	Hha1	10	atg	168.52	168	168.52	0	0	4 700 000	0	0	-=	\	\	\(5)
8853	Taq1	39	agg	167.01	168	166.81	167.21	0	8 900 000	7 800 000	0	=-	\		\(5)
8854	Taq1	39	agg	167.16	168	167.16	0	0	8 200 000	0	0	-=	\		\(5)
8855	Taq1	39	agg	167.815	168	0	167.69	167.94	0	12 700 000	4 700 000	+-	A		\(5)
8856	Taq1	39	agg	168.1	168	0	168.26	167.94	0	43 800 000	138.43	+-	A		\(5)
8857	Taq1	39	agg	168.975	168	169.12	168.83	0	9 200 000	19 400 000	0	+-	A		\(5)
8858	Taq1	39	agg	167.01	168	166.81	167.21	0	330.51	78.39	0	-=	\		\(5)
8859	Taq1	39	agg	167.16	168	167.16	0	0	304.51	0	0	-=	\		\(5)
8860	Taq1	39	agg	167.69	168	0	167.69	0	0	127.63	0	+-	A		\(5)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
8818	AB031088.VESP14	VESP14	vascular endothelial cell specific protein 14		tgg	ttc	decreased
8819	AB031088.VESP14	VESP14	vascular endothelial cell specific protein 14		tgg	ttc	decreased
8820	AB031088.VESP14	VESP14	vascular endothelial cell specific protein 14		tgg	ttc	decreased
8821	AB031088.VESP14	VESP14	vascular endothelial cell specific protein 14		tgg	ttc	decreased
8822	RNU40790.PE1	nc	vascular protein tyrosine phosphatase 1		gtc	atg	increased
8823	RNU40790.PE1	nc	vascular protein tyrosine phosphatase 1		atg	gtc	increased
8824	RATVASREC.PE1	nc	vasoactive intestinal polypeptide receptor		ggc	aga	increased
8825	RATVASREC.PE1	nc	vasoactive intestinal polypeptide receptor		ggc	aga	increased
8826	RNVAOXY.PE2	nc	vasopressin	*	tgc	agc	No change
8827	RNVAOXY.PE2	nc	vasopressin	*	gga	ctc	No change
8828	RNVAOXY.PE2	nc	vasopressin	*	gga	ctc	No change
8829	RNVAOXY.PE2	nc	vasopressin	*	tgc	agc	No change
8830	RNVN03.PE1	nc	vasopressin precursor	*	tgc	agc	No change
8831	RNVN03.PE1	nc	vasopressin precursor	*	gga	ctc	No change
8832	RNVN03.PE1	nc	vasopressin precursor	*	gga	ctc	No change
8833	RNVN03.PE1	nc	vasopressin precursor	*	tgc	agc	No change
8834	AB045378.VCIP135	VCIP135	VCP(p97)/p47-interacting protein		tgc	acc	decreased
8835	AB045378.VCIP135	VCIP135	VCP(p97)/p47-interacting protein		tgc	acc	decreased
8836	AB001992.PE1	nc	VD3 1a hydroxylase	*	tgg	gct	decreased
8837	AB001992.PE1	nc	VD3 1a hydroxylase	*	ggt	tct	decreased
8838	AB001992.PE1	nc	VD3 1a hydroxylase	*	ctg	tgc	decreased
8839	AY032729.PE1	nc	VEGF-C		gtc	aac	increased
8840	AY032729.PE1	nc	VEGF-C		cca	ttt	increased
8841	AY032729.PE1	nc	VEGF-C		cca	ttt	increased
8842	RATVPSP.PE1	nc	ventral prostate-specific protein		aga	atc	decreased
8843	RATVPSP.PE1	nc	ventral prostate-specific protein		aga	atc	decreased
8844	RATVPSP.PE1	nc	ventral prostate-specific protein		aga	atc	decreased
8845	RATVPSP.PE1	nc	ventral prostate-specific protein		aga	atc	decreased
8846	RATVPSP.PE1	nc	ventral prostate-specific protein		aga	atc	decreased
8847	RATVPSP.PE1	nc	ventral prostate-specific protein		aga	atc	decreased
8848	AF062402.PE1	nc	versican V0 isoform		atg	agg	increased
8849	AF062402.PE1	nc	versican V0 isoform		atg	agg	increased
8850	AF062402.PE1	nc	versican V0 isoform		atg	agg	increased
8851	AF062402.PE1	nc	versican V0 isoform		atg	agg	increased
8852	AF062402.PE1	nc	versican V0 isoform		atg	agg	increased
8853	AF062402.PE1	nc	versican V0 isoform		atg	agg	increased
8854	AF062402.PE1	nc	versican V0 isoform		atg	agg	increased
8855	AF062402.PE1	nc	versican V0 isoform		atg	agg	increased
8856	AF062402.PE1	nc	versican V0 isoform		atg	agg	increased
8857	AF062402.PE1	nc	versican V0 isoform		atg	agg	increased
8858	AF062402.PE1	nc	versican V0 isoform		atg	agg	increased
8859	AF062402.PE1	nc	versican V0 isoform		atg	agg	increased
8860	AF062402.PE1	nc	versican V0 isoform		atg	agg	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
8861	Taq1	39	agg	168.26	168	0	168.26	0	0	440.2	0	+-	A		\(5)
8862	Taq1	39	agg	168.975	168	169.12	168.83	0	341.65	194.97	0	=-	\		\(5)
8863	Taq1	63	ctt	215.53	215	215.53	0	0	3 000 000	0	0	-=	\		\(5)
8864	Hha1	64	gtt	68.403	68	68.48	68.31	68.42	72 300 000	13 000 000	31 700 000	-=	\ (-)		\(6)
8865	Hha1	27	acg	72.105	72	0	72.1	72.11	0	3 400 000	5 600 000	+=	/		\(6)
8866	Hha1	61	tct	99.33	99	0	0	99.33	0	0	6 200 000	=+	/		\(6)
8867	Hha1	44	cgg	108.59	109	108.6	108.58	0	3 200 000	5 000 000	0	=-	\		\(6)
8868	Hha1	44	cgg	109.155	109	108.95	0	109.36	3 400 000	0	5 000 000	-+(=)	V		\(6)
8869	Hha1	12	agt	121.207	121	121.14	121.19	121.29	17 993.789	11 018.74	7 571.56	==	-		\(6)
8870	Hha1	32	gtc	120.58	121	120.53	120.63	0	1 501.28	579.85	0	-=	\		\(6)
8871	Hha1	26	ctg	132.96	133	132.96	132.96	0	15 400 000	13 700 000	0	=-	\		\(6)
8872	Hha1	28	tcg	146.545	147	0	146.53	146.56	0	3 800 000	3 500 000	+=	/		\(6)
8873	Hha1	28	tcg	147.46	147	0	147.35	147.57	0	4 500 000	3 700 000	+=	/		\(6)
8874	Hha1	49	aaa	147.52	148	0	147.44	147.6	0	15 300 000	3 000 000	+-	A		\(6)
8875	Hha1	49	aaa	147.77	148	0	147.77	0	0	12 800 000	0	+-	A		\(6)
8876	Hha1	49	aaa	148.61	148	148.47	148.75	0	10 300 000	6 900 000	0	=-	\		\(6)
8877	Hha1	49	aaa	148.37	148	0	148.37	0	0	6 200 000	0	+-	A		\(6)
8878	Hha1	27	acg	185.83	186	185.83	0	0	3 000 000	0	0	-=	\		\(6)
8879	Hha1	27	acg	185.94	186	185.94	0	0	3 100 000	0	0	-=	\		\(6)
8880	Hha1	27	acg	186.673	186	186.62	186.62	186.78	6 100 000	3 400 000	4 600 000	==	-		\(6)
8881	Hha1	64	gtt	68.403	68	68.48	68.31	68.42	72 300 000	13 000 000	31 700 000	-=	\ (-)		\(6)
8882	Hha1	27	acg	72.105	72	0	72.1	72.11	0	3 400 000	5 600 000	+=	/		\(6)
8883	Hha1	61	tct	99.33	99	0	0	99.33	0	0	6 200 000	=+	/		\(6)
8884	Hha1	44	cgg	108.59	109	108.6	108.58	0	3 200 000	5 000 000	0	=-	\		\(6)
8885	Hha1	44	cgg	109.155	109	108.95	0	109.36	3 400 000	0	5 000 000	-+(=)	V		\(6)
8886	Hha1	12	agt	121.207	121	121.14	121.19	121.29	17 993.789	11 018.74	7 571.56	==	-		\(6)
8887	Hha1	32	gtc	120.58	121	120.53	120.63	0	1 501.28	579.85	0	-=	\		\(6)
8888	Hha1	26	ctg	132.96	133	132.96	132.96	0	15 400 000	13 700 000	0	=-	\		\(6)
8889	Hha1	28	tcg	146.545	147	0	146.53	146.56	0	3 800 000	3 500 000	+=	/		\(6)
8890	Hha1	28	tcg	147.46	147	0	147.35	147.57	0	4 500 000	3 700 000	+=	/		\(6)
8891	Hha1	49	aaa	147.52	148	0	147.44	147.6	0	15 300 000	3 000 000	+-	A		\(6)
8892	Hha1	49	aaa	147.77	148	0	147.77	0	0	12 800 000	0	+-	A		\(6)
8893	Hha1	49	aaa	148.61	148	148.47	148.75	0	10 300 000	6 900 000	0	=-	\		\(6)
8894	Hha1	49	aaa	148.37	148	0	148.37	0	0	6 200 000	0	+-	A		\(6)
8895	Hha1	27	acg	185.83	186	185.83	0	0	3 000 000	0	0	-=	\		\(6)
8896	Hha1	27	acg	185.94	186	185.94	0	0	3 100 000	0	0	-=	\		\(6)
8897	Hha1	27	acg	186.673	186	186.62	186.62	186.78	6 100 000	3 400 000	4 600 000	==	-		\(6)
8898	Hha1	33	agc	77.803	78	77.78	77.86	77.77	56 700 000	20 100 000	9 400 000	-=	\ (-)		\(8) -(6)
8899	Taq1	56	tga	83.9	84	0	0	83.9	0	0	10 500 000	=+	/		\(8) -(6)
8900	Taq1	62	tgt	96.507	97	96.37	96.38	96.77	6 900 000	9 300 000	15 900 000	==	-		\(8) -(6)
8901	Taq1	62	tgt	97.33	97	97.16	97.5	0	5 900 000	12 100 000	0	+-	A		\(8) -(6)
8902	Taq1	62	tgt	97.34	97	97.34	0	0	5 600 000	0	0	-=	\		\(8) -(6)
8903	Hha1	28	tcg	109.673	110	109.63	109.74	109.65	22 900 000	11 800 000	28 300 000	=+	/ (-)		\(8) -(6)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
8861	AF062402.PE1	nc	versican V0 isoform		atg	agg	increased
8862	AF062402.PE1	nc	versican V0 isoform		atg	agg	increased
8863	AF062402.PE1	nc	versican V0 isoform		ctt	tgg	increased
8864	RNU09211.PE1	nc	vesicular acetylcholine transporter		gtt	cgt	increased
8865	RNU09211.PE1	nc	vesicular acetylcholine transporter		tcc	acg	increased
8866	RNU09211.PE1	nc	vesicular acetylcholine transporter		tct	gaa	increased
8867	RNU09211.PE1	nc	vesicular acetylcholine transporter		gag	cgg	increased
8868	RNU09211.PE1	nc	vesicular acetylcholine transporter		gag	cgg	increased
8869	RNU09211.PE1	nc	vesicular acetylcholine transporter		agt	tca	increased
8870	RNU09211.PE1	nc	vesicular acetylcholine transporter		cac	gtc	increased
8871	RNU09211.PE1	nc	vesicular acetylcholine transporter		ctg	atg	increased
8872	RNU09211.PE1	nc	vesicular acetylcholine transporter		tcg	aaa	increased
8873	RNU09211.PE1	nc	vesicular acetylcholine transporter		tcg	aaa	increased
8874	RNU09211.PE1	nc	vesicular acetylcholine transporter		tcg	aaa	increased
8875	RNU09211.PE1	nc	vesicular acetylcholine transporter		tcg	aaa	increased
8876	RNU09211.PE1	nc	vesicular acetylcholine transporter		tcg	aaa	increased
8877	RNU09211.PE1	nc	vesicular acetylcholine transporter		tcg	aaa	increased
8878	RNU09211.PE1	nc	vesicular acetylcholine transporter		tca	acg	increased
8879	RNU09211.PE1	nc	vesicular acetylcholine transporter		tca	acg	increased
8880	RNU09211.PE1	nc	vesicular acetylcholine transporter		tca	acg	increased
8881	RNU09838.RVACHT	rVAChT	vesicular acetylcholine transporter		gtt	cgt	increased
8882	RNU09838.RVACHT	rVAChT	vesicular acetylcholine transporter		tcc	acg	increased
8883	RNU09838.RVACHT	rVAChT	vesicular acetylcholine transporter		tct	gaa	increased
8884	RNU09838.RVACHT	rVAChT	vesicular acetylcholine transporter		gag	cgg	increased
8885	RNU09838.RVACHT	rVAChT	vesicular acetylcholine transporter		gag	cgg	increased
8886	RNU09838.RVACHT	rVAChT	vesicular acetylcholine transporter		agt	tca	increased
8887	RNU09838.RVACHT	rVAChT	vesicular acetylcholine transporter		cac	gtc	increased
8888	RNU09838.RVACHT	rVAChT	vesicular acetylcholine transporter		ctg	atg	increased
8889	RNU09838.RVACHT	rVAChT	vesicular acetylcholine transporter		tcg	aaa	increased
8890	RNU09838.RVACHT	rVAChT	vesicular acetylcholine transporter		tcg	aaa	increased
8891	RNU09838.RVACHT	rVAChT	vesicular acetylcholine transporter		tcg	aaa	increased
8892	RNU09838.RVACHT	rVAChT	vesicular acetylcholine transporter		tcg	aaa	increased
8893	RNU09838.RVACHT	rVAChT	vesicular acetylcholine transporter		tcg	aaa	increased
8894	RNU09838.RVACHT	rVAChT	vesicular acetylcholine transporter		tcg	aaa	increased
8895	RNU09838.RVACHT	rVAChT	vesicular acetylcholine transporter		tca	acg	increased
8896	RNU09838.RVACHT	rVAChT	vesicular acetylcholine transporter		tca	acg	increased
8897	RNU09838.RVACHT	rVAChT	vesicular acetylcholine transporter		tca	acg	increased
8898	AF030253.VGAT	VGAT	vesicular GABA transporter		gtg	agc	increased
8899	AF030253.VGAT	VGAT	vesicular GABA transporter		ttc	tga	increased
8900	AF030253.VGAT	VGAT	vesicular GABA transporter		tgt	gtg	increased
8901	AF030253.VGAT	VGAT	vesicular GABA transporter		tgt	gtg	increased
8902	AF030253.VGAT	VGAT	vesicular GABA transporter		tgt	gtg	increased
8903	AF030253.VGAT	VGAT	vesicular GABA transporter		tcg	gga	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
8904	Taq1	30	cgt	112.253	112	112.29	112.27	112.2	3 300 000	5 700 000	3 100 000	=-	\ (-)		\(8) -(6)
8905	Taq1	44	cgg	122.525	123	0	122.3	122.75	0	488.12	694.91	+=	/		\(8) -(6)
8906	Taq1	44	cgg	123.1	123	123.1	0	0	1 649.13	0	0	-=	\		\(8) -(6)
8907	Taq1	44	cgg	123.72	123	0	123.72	123.72	0	882.92	806.99	+=	/		\(8) -(6)
8908	Taq1	63	ctt	123.76	124	123.71	123.81	0	3 700 000	3 500 000	0	=-	\		\(8) -(6)
8909	Hha1	39	agg	216.617	217	216.63	216.72	216.5	461.87	220.9	236	-=	\ (-)		\(8) -(6)
8910	Taq1	39	agg	263.915	265	263.88	263.95	0	10 600 000	5 000 000	0	--	\		\(8) -(6)
8911	Taq1	39	agg	263.88	265	263.88	0	0	393.64	0	0	-=	\		\(8) -(6)
8912	Taq1	39	agg	265.03	265	0	265.03	0	0	67 300 000	0	+-	A		\(8) -(6)
8913	Taq1	39	agg	266.05	265	0	266.05	0	0	49 500 000	0	+-	A		\(8) -(6)
8914	Taq1	39	agg	263.95	265	0	263.95	0	0	50.25	0	+-	A		\(8) -(6)
8915	Taq1	39	agg	265.03	265	0	265.03	0	0	676.38	0	+-	A		\(8) -(6)
8916	Taq1	39	agg	266.05	265	0	266.05	0	0	497.49	0	+-	A		\(8) -(6)
8917	Hha1	6	aga	306.42	307	306.42	0	0	5 300 000	0	0	-=	\		\(8) -(6)
8918	Hha1	6	aga	307.27	307	307.37	307.18	307.26	21 400 000	12 000 000	5 200 000	==	-		\(8) -(6)
8919	Hha1	6	aga	308.39	307	0	308.32	308.46	0	10 000 000	8 800 000	+=	/		\(8) -(6)
8920	Taq1	35	gga	112.57	112	0	112.57	0	0	3 700 000	0	+-	A		A(2)
8921	Taq1	61	tct	111.877	112	111.69	112.15	111.79	7 800 000	8 900 000	25 800 000	=+	/ (-)		A(2)
8922	Taq1	61	tct	229.27	229	0	229.27	0	0	3 400 000	0	+-	A		A(2)
8923	Taq1	35	gga	112.57	112	0	112.57	0	0	3 700 000	0	+-	A		/(2)
8924	Taq1	61	tct	111.877	112	111.69	112.15	111.79	7 800 000	8 900 000	25 800 000	=+	/ (-)		/(2)
8925	Taq1	61	tct	195.46	196	195.46	0	0	3 000 000	0	0	-=	\		/(2)
8926	Taq1	61	tct	196.3	196	0	0	196.3	0	0	5 900 000	=+	/		/(2)
8927	Hha1	33	agc	62.84	63	62.76	62.92	62.84	4 400 000	18 500 000	17 900 000	+=	/ (-)		-3
8928	Hha1	33	agc	77.803	78	77.78	77.86	77.77	56 700 000	20 100 000	9 400 000	-=	\ (-)		-3
8929	Hha1	20	ctc	161.05	161	161.26	160.95	160.94	213.49	458.95	596.37	==	-		-3
8930	Hha1	20	ctc	161.51	161	0	0	161.51	0	0	417.46	=+	/		-3
8931	Hha1	27	acg	160.07	161	160.07	0	0	5 400 000	0	0	-=	\		-3
8932	Hha1	31	gac	106.087	106	106.11	106.09	106.06	8 300 000	4 400 000	19 200 000	=+	/ (-)	(-)	-1
8933	Hha1	59	ttc	105.495	106	105.47	105.52	0	452.41	641.02	0	=-	\		-1
8934	Hha1	59	ttc	106.19	106	106.48	106.04	106.05	2 142.48	2 489.36	814.94	=-	\ (-)	(-)	-1
8935	Taq1	19	cac	144.87	145	144.89	144.86	144.86	4 100 000	3 500 000	25 300 000	=+	/ (-)	/	-1
8936	Taq1	29	gca	144.72	145	144.71	0	144.73	3 200 000	0	8 300 000	=+(+)	/	/	-1
8937	Taq1	29	gca	145.72	145	0	0	145.72	0	0	5 900 000	=+	/		-1
8938	Taq1	62	tgt	143.705	144	0	143.78	143.63	0	5 000 000	12 200 000	=+	/		-(2) /(2) \(2)
8939	Taq1	62	tgt	144.817	144	144.88	144.87	144.7	5 900 000	12 100 000	20 800 000	==	-		-(2) /(2) \(2)
8940	Taq1	12	agt	221.54	222	0	221.56	221.52	0	4 000 000	3 200 000	+=	/		-(2) /(2) \(2)
8941	Taq1	12	agt	222.61	222	222.65	222.57	0	3 400 000	4 300 000	0	=-	\	\	-(2) /(2) \(2)
8942	Hha1	25	cag	220.96	222	220.96	0	0	18 600 000	0	0	-=	\		-(2) /(2) \(2)
8943	Hha1	25	cag	222	222	0	222	0	0	3 100 000	0	+-	A		-(2) /(2) \(2)
8944	Hha1	25	cag	222.81	222	222.89	222.76	222.78	19 200 000	9 400 000	10 600 000	-=	\ (-)	\	-(2) /(2) \(2)
8945	Hha1	56	tga	110.023	110	110.19	110.02	109.86	155.27	1 111.84	1 206.68	+=	/ (-)		-1
8946	Hha1	26	ctg	136.21	137	0	0	136.21	0	0	3 600 000	=+	/		-1

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
8904	AF030253.VGAT	VGAT	vesicular GABA transporter		cgt	gcg	increased
8905	AF030253.VGAT	VGAT	vesicular GABA transporter		ctt	cgg	increased
8906	AF030253.VGAT	VGAT	vesicular GABA transporter		ctt	cgg	increased
8907	AF030253.VGAT	VGAT	vesicular GABA transporter		ctt	cgg	increased
8908	AF030253.VGAT	VGAT	vesicular GABA transporter		ctt	cgg	increased
8909	AF030253.VGAT	VGAT	vesicular GABA transporter		tcc	agg	increased
8910	AF030253.VGAT	VGAT	vesicular GABA transporter		agg	cgg	increased
8911	AF030253.VGAT	VGAT	vesicular GABA transporter		agg	cgg	increased
8912	AF030253.VGAT	VGAT	vesicular GABA transporter		agg	cgg	increased
8913	AF030253.VGAT	VGAT	vesicular GABA transporter		agg	cgg	increased
8914	AF030253.VGAT	VGAT	vesicular GABA transporter		agg	cgg	increased
8915	AF030253.VGAT	VGAT	vesicular GABA transporter		agg	cgg	increased
8916	AF030253.VGAT	VGAT	vesicular GABA transporter		agg	cgg	increased
8917	AF030253.VGAT	VGAT	vesicular GABA transporter		agt	aga	increased
8918	AF030253.VGAT	VGAT	vesicular GABA transporter		agt	aga	increased
8919	AF030253.VGAT	VGAT	vesicular GABA transporter		agt	aga	increased
8920	AB007689.VESL-2	vesl-2	Vesl-2		gga	tct	increased by mild
8921	AB007689.VESL-2	vesl-2	Vesl-2		gga	tct	increased by mild
8922	AB007689.VESL-2	vesl-2	Vesl-2		gac	tct	increased by mild
8923	AB007690.PE1	vesl-2(delta 1	Vesl-2(delta 11)		gga	tct	decreased
8924	AB007690.PE1	vesl-2(delta 1	Vesl-2(delta 11)		gga	tct	decreased
8925	AB007690.PE1	vesl-2(delta 1	Vesl-2(delta 11)		gac	tct	decreased
8926	AB007690.PE1	vesl-2(delta 1	Vesl-2(delta 11)		gac	tct	decreased
8927	AB020879.VESL-3	vesl-3	Vesl-3		acg	agc	No change
8928	AB020879.VESL-3	vesl-3	Vesl-3		agc	agc	No change
8929	AB020879.VESL-3	vesl-3	Vesl-3		acg	ctc	No change
8930	AB020879.VESL-3	vesl-3	Vesl-3		acg	ctc	No change
8931	AB020879.VESL-3	vesl-3	Vesl-3		acg	ctc	No change
8932	RNVIM.PE1	nc	vimentin		ttc	gac	No change
8933	RNVIM.PE1	nc	vimentin		ttc	gac	No change
8934	RNVIM.PE1	nc	vimentin		ttc	gac	No change
8935	RNVIM.PE1	nc	vimentin		gca	cac	decreased
8936	RNVIM.PE1	nc	vimentin		gca	cac	decreased
8937	RNVIM.PE1	nc	vimentin		gca	cac	No change
8938	AF439378.PE1	nc	vinexin alpha		gcg	tgt	No change
8939	AF439378.PE1	nc	vinexin alpha		gcg	tgt	No change
8940	AF439378.PE1	nc	vinexin alpha		cag	agt	No change
8941	AF439378.PE1	nc	vinexin alpha		cag	agt	increased
8942	AF439378.PE1	nc	vinexin alpha		cag	agt	No change
8943	AF439378.PE1	nc	vinexin alpha		cag	agt	No change
8944	AF439378.PE1	nc	vinexin alpha		cag	agt	increased
8945	RNCYP27.CYP27	CYP27	vitamin D(3) 25-hydroxylase precursor		tga	tag	No change
8946	RNCYP27.CYP27	CYP27	vitamin D(3) 25-hydroxylase precursor		ctg	ctg	No change

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
8947	Hha1	26	ctg	137.165	137	0	137.17	137.16	0	4 000 000	3 300 000	+=	/		-1
8948	Hha1	59	ttc	165.58	165	165.44	165.5	165.8	166.4	135.1	85.37	==	-		-1
8949	Hha1	44	cgg	221.7	222	221.7	0	0	3 600 000	0	0	-=	\		\(2)
8950	Hha1	44	cgg	222.513	222	222.51	222.5	222.53	9 900 000	5 800 000	5 900 000	==	-		\(2)
8951	Hha1	40	tgg	222.635	223	222.71	222.56	0	4 400 000	4 800 000	0	=-	\		\(2)
8952	Hha1	33	agc	62.84	63	62.76	62.92	62.84	4 400 000	18 500 000	17 900 000	+=	/ (-)		-(2) /(2) \(2)
8953	Hha1	20	ctc	74.577	75	74.85	74.49	74.39	3 567.49	773.66	763.35	-=	\ (-)		-(2) /(2) \(2)
8954	Hha1	20	ctc	74.93	75	0	75.01	74.85	0	1 363.75	894.56	+=	/		-(2) /(2) \(2)
8955	Hha1	33	agc	110.905	111	110.83	110.98	0	12 700 000	12 900 000	0	=-	\		-(2) /(2) \(2)
8956	Hha1	28	tcg	109.673	110	109.63	109.74	109.65	22 900 000	11 800 000	28 300 000	=+	/ (-)	/	
8957	Hha1	39	agg	109.507	110	109.65	109.55	109.32	1 092.37	2 173.26	1 485.18	+=	/ (-)	/	
8958	Taq1	12	agt	119.103	119	119.06	119.05	119.2	5 100 000	7 000 000	3 800 000	=-	\ (-)	\	
8959	Taq1	23	cga	119.32	119	119.32	0	0	4 800 000	0	0	-=	\	\	
8960	Taq1	8	gaa	85.95	86	85.95	0	0	48 300 000	0	0	-=	\		/(3)
8961	Taq1	56	tga	85.71	86	0	85.71	0	0	4 000 000	0	+-	A		/(3)
8962	Taq1	19	cac	98.49	99	0	98.48	98.5	0	14 700 000	10 900 000	+=	/		/(3)
8963	Taq1	19	cac	99.56	99	99.56	0	0	7 300 000	0	0	-=	\		/(3)
8964	Hha1	39	agg	144.21	145	0	144.41	144.01	0	191.05	211.58	+=	/		/(3)
8965	Hha1	39	agg	144.63	145	0	0	144.63	0	0	215.65	=+	/		/(3)
8966	Hha1	39	agg	145.82	145	0	146	145.64	0	770.19	797.52	+=	/		/(3)
8967	Hha1	40	tgg	145.52	145	145.53	145.44	145.59	3 100 000	9 400 000	9 100 000	+=	/ (-)		/(3)
8968	Hha1	12	agt	123.24	123	123.19	123.2	123.33	10 263.7	8 101.05	7 479.22	==	-		-1,5
8969	Hha1	4	aag	128.23	128	128.33	128.15	128.21	3 000 000	10 700 000	6 300 000	+=	/ (-)		-1,5
8970	Taq1	62	tgt	127.55	128	0	127.74	127.36	0	5 000 000	8 700 000	+=	/		-1,5
8971	Taq1	62	tgt	128.573	128	128.58	128.64	128.5	5 900 000	8 500 000	7 100 000	==	-		-1,5
8972	Taq1	8	gaa	132.82	133	132.71	132.93	0	4 400 000	6 100 000	0	=-	\	\	
8973	Hha1	8	gaa	133.017	133	133.08	133.07	132.9	34 400 000	25 100 000	9 200 000	=-	\ (-)	\	
8974	Taq1	25	cat	154.03	154	154	153.89	154.2	5 056.63	4 468.49	6 640.94	==	-	-	
8975	Taq1	62	tgt	153.833	154	153.93	153.86	153.71	3 300 000	4 400 000	4 700 000	==	-	-	
8976	Taq1	8	gaa	132.82	133	132.71	132.93	0	4 400 000	6 100 000	0	=-	\	\	
8977	Hha1	8	gaa	133.017	133	133.08	133.07	132.9	34 400 000	25 100 000	9 200 000	=-	\ (-)	\	
8978	Taq1	25	cat	154.03	154	154	153.89	154.2	5 056.63	4 468.49	6 640.94	==	-	-	
8979	Taq1	62	tgt	153.833	154	153.93	153.86	153.71	3 300 000	4 400 000	4 700 000	==	-	-	
8980	Taq1	45	gcc	66.68	67	66.86	66.68	66.5	33 500 000	13 000 000	7 900 000	-=	\ (-)		\(2)
8981	Taq1	8	gaa	67.66	68	67.66	0	0	5 400 000	0	0	-=	\		\(2)
8982	Taq1	8	gaa	68.05	68	68.05	0	0	7 200 000	0	0	-=	\		\(2)
8983	Hha1	44	cgg	72.173	72	72.07	72.24	72.21	157 200 000	31 700 000	60 300 000	-=	\ (-)		\(4)
8984	Hha1	20	ctc	138.81	139	138.81	0	0	426.99	0	0	-=	\		\(4)
8985	Hha1	20	ctc	139.71	139	139.73	0	139.69	550.96	0	477.09	-+(=)	V		\(4)
8986	Hha1	39	agg	148.44	149	148.38	148.5	0	373.9	262.7	0	=-	\		\(4)
8987	Hha1	56	tga	149.153	149	149.09	149.2	149.17	277.85	710.03	1 516.97	=+	/ (-)		\(4)
8988	Hha1	56	tga	159.665	160	159.43	159.9	0	502.59	1 210.92	0	+-	A		\(4)
8989	Hha1	56	tga	159.87	160	159.87	0	0	380.01	0	0	-=	\		\(4)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
8947	RNCYP27.CYP27	CYP27	vitamin D(3) 25-hydroxylase precursor		ctg	ctg	No change
8948	RNCYP27.CYP27	CYP27	vitamin D(3) 25-hydroxylase precursor		ttc	ggt	No change
8949	AF065387.PE1	nc	vitamin K-dependent gamma-glutamyl carboxylase		tgg	cgg	increased
8950	AF065387.PE1	nc	vitamin K-dependent gamma-glutamyl carboxylase		tgg	cgg	increased
8951	AF065387.PE1	nc	vitamin K-dependent gamma-glutamyl carboxylase		tgg	cgg	increased
8952	RNVN02.PE1	nc	VN-precursor		tgc	agc	No change
8953	RNVN02.PE1	nc	VN-precursor		gga	ctc	No change
8954	RNVN02.PE1	nc	VN-precursor		gga	ctc	No change
8955	RNVN02.PE1	nc	VN-precursor		tgc	agc	No change
8956	RNSNS.SNS	SNS	volatage-gated sodium channel	*	agg	tcg	decreased
8957	RNSNS.SNS	SNS	volatage-gated sodium channel	*	agg	tcg	decreased
8958	RNSNS.SNS	SNS	volatage-gated sodium channel	*	cga	agt	increased
8959	RNSNS.SNS	SNS	volatage-gated sodium channel	*	cga	agt	increased
8960	AB018253.PE1	nc	voltage-gated ca channel		gaa	tga	decreased
8961	AB018253.PE1	nc	voltage-gated ca channel		gaa	tga	decreased
8962	AB018253.PE1	nc	voltage-gated ca channel		cac	ttg	decreased
8963	AB018253.PE1	nc	voltage-gated ca channel		cac	ttg	decreased
8964	AB018253.PE1	nc	voltage-gated ca channel		tgg	agg	decreased
8965	AB018253.PE1	nc	voltage-gated ca channel		tgg	agg	decreased
8966	AB018253.PE1	nc	voltage-gated ca channel		tgg	agg	decreased
8967	AB018253.PE1	nc	voltage-gated ca channel		tgg	agg	decreased
8968	RATCK5A.RK5	RK5	voltage-gated potassium channel protein		agt	cac	No change
8969	RATCK5A.RK5	RK5	voltage-gated potassium channel protein		tgt	aag	No change
8970	RATCK5A.RK5	RK5	voltage-gated potassium channel protein		tgt	aag	No change
8971	RATCK5A.RK5	RK5	voltage-gated potassium channel protein		tgt	aag	No change
8972	AF049239.PE1	nc	voltage-gated sodium channel rPN4		gaa	tgg	increased
8973	AF049239.PE1	nc	voltage-gated sodium channel rPN4		gaa	tgg	increased
8974	AF049239.PE1	nc	voltage-gated sodium channel rPN4		cat	tgt	No change
8975	AF049239.PE1	nc	voltage-gated sodium channel rPN4		cat	tgt	No change
8976	AF049240.PE1	nc	voltage-gated sodium channel variant rPN4a		gaa	tgg	increased
8977	AF049240.PE1	nc	voltage-gated sodium channel variant rPN4a		gaa	tgg	increased
8978	AF049240.PE1	nc	voltage-gated sodium channel variant rPN4a		cat	tgt	No change
8979	AF049240.PE1	nc	voltage-gated sodium channel variant rPN4a		cat	tgt	No change
8980	RATCHIP28A.PE1	CHIP28	water channel		gaa	gcc	increased
8981	RATCHIP28A.PE1	CHIP28	water channel		gaa	gcc	increased
8982	RATCHIP28A.PE1	CHIP28	water channel		gaa	gcc	increased
8983	AY136827.WRNIP	Wrnip	Werner syndrome-interacting protein-like		tgg	cgg	increased
8984	AY136827.WRNIP	Wrnip	Werner syndrome-interacting protein-like		ctc	ggg	increased
8985	AY136827.WRNIP	Wrnip	Werner syndrome-interacting protein-like		ctc	ggg	increased
8986	AY136827.WRNIP	Wrnip	Werner syndrome-interacting protein-like		agg	tga	increased
8987	AY136827.WRNIP	Wrnip	Werner syndrome-interacting protein-like		agg	tga	increased
8988	AY136827.WRNIP	Wrnip	Werner syndrome-interacting protein-like		tga	acc	increased
8989	AY136827.WRNIP	Wrnip	Werner syndrome-interacting protein-like		tga	acc	increased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
8990	Hha1	20	ctc	77.79	78	77.74	77.87	77.76	1 859.5	813	2 850.66	=+	/ (-)	(-)	-1
8991	Hha1	33	agc	77.803	78	77.78	77.86	77.77	56 700 000	20 100 000	9 400 000	-=	\ (-)	(-)	-1
8992	Taq1	39	agg	84.68	85	84.72	0	84.64	32 600 000	0	8 100 000	-=(-)	\		-1
8993	Taq1	39	agg	84.72	85	84.72	0	0	1 210.63	0	0	-=	\		-1
8994	Taq1	39	agg	84.64	85	0	0	84.64	0	0	238.58	=+	/		-1
8995	Taq1	61	tct	106.01	106	0	106.17	105.85	0	5 800 000	13 800 000	=+	/		-1
8996	Hha1	41	ccc	147.425	148	0	147.36	147.49	0	6 700 000	7 000 000	+=	/		-1
8997	Hha1	41	ccc	148.19	148	147.96	148.26	148.35	6 200 000	12 000 000	22 900 000	=+	/ (-)		-1
8998	Hha1	41	ccc	148.78	148	148.78	0	0	4 400 000	0	0	-=	\		-1
8999	Taq1	63	ctt	174.473	175	174.5	174.34	174.58	4 300 000	3 200 000	3 200 000	==	-		-1
9000	Taq1	63	ctt	175.553	175	175.54	175.49	175.63	3 000 000	3 300 000	3 200 000	==	-		-1
9001	Hha1	11	act	145.28	146	0	0	145.28	0	0	9 000 000	=+	/		/(6)
9002	Taq1	11	act	145.563	146	145.42	145.4	145.87	3 800 000	3 800 000	8 400 000	=+	/ (-)		/(6)
9003	Hha1	11	act	146.17	146	0	0	146.17	0	0	4 400 000	=+	/		/(6)
9004	Taq1	11	act	146.62	146	146.51	0	146.73	3 000 000	0	20 200 000	=+(+)	/		/(6)
9005	Taq1	64	gtt	145.913	146	145.85	145.9	145.99	5 400 000	4 900 000	8 900 000	==	-		/(6)
9006	Taq1	64	gtt	146.82	146	146.88	146.82	146.76	6 400 000	7 700 000	5 400 000	==	-		/(6)
9007	Hha1	40	tgg	186.515	187	186.31	186.72	0	3 900 000	4 100 000	0	=-	\		/(6)
9008	Hha1	40	tgg	186.89	187	0	186.89	0	0	3 800 000	0	+-	A		/(6)
9009	Hha1	40	tgg	187.92	187	0	187.92	0	0	3 100 000	0	+-	A		/(6)
9010	Hha1	60	ttg	187.99	187	187.97	188.02	187.98	6 400 000	4 500 000	3 700 000	==	-		/(6)
9011	Hha1	6	aga	192.98	194	192.98	0	0	17 300 000	0	0	-=	\		/(6)
9012	Hha1	6	aga	193.55	194	0	0	193.55	0	0	3 600 000	=+	/		/(6)
9013	Hha1	6	aga	194.62	194	0	0	194.62	0	0	5 100 000	=+	/		/(6)
9014	Taq1	50	aat	194.07	195	194.08	194.06	0	6 000 000	3 300 000	0	--	\		/(6)
9015	Taq1	50	aat	195.115	195	194.98	195.25	0	8 200 000	6 800 000	0	=-	\		/(6)
9016	Taq1	50	aat	195.6	195	0	0	195.6	0	0	7 000 000	=+	/		/(6)
9017	Hha1	64	gtt	73.58	74	73.65	73.39	73.7	17 200 000	3 200 000	4 400 000	-=	\ (-)		\(3)
9018	Hha1	64	gtt	74.403	74	74.47	74.32	74.42	28 600 000	30 000 000	72 400 000	=+	/ (-)		\(3)
9019	Hha1	44	cgg	82.355	82	0	82.34	82.37	0	11 200 000	14 300 000	+=	/		\(3)
9020	Hha1	33	agc	137.335	137	137.26	137.41	0	3 400 000	4 500 000	0	=-	\	\	\(3)
9021	Hha1	62	tgt	137.11	137	137.11	0	0	4 800 000	0	0	-=	\	\	\(3)
9022	Hha1	33	agc	151.405	152	151.45	151.36	0	7 400 000	7 400 000	0	=-	\		\(2)
9023	Hha1	33	agc	152.495	152	152.42	152.57	0	4 000 000	3 100 000	0	=-	\		\(2)
9024	Hha1	41	ccc	169.47	170	169.47	0	0	4 700 000	0	0	-=	\		\(2)
9025	Hha1	41	ccc	170.505	170	170.54	170.47	0	11 400 000	8 000 000	0	=-	\		\(2)
9026	Hha1	61	tct	170.42	171	0	0	170.42	0	0	3 500 000	=+	/		\(2)
9027	Hha1	61	tct	171.42	171	171.41	171.38	171.47	6 600 000	13 300 000	9 000 000	+=	/ (-)		\(2)
9028	Hha1	59	ttc	69.62	70	69.62	0	0	930.83	0	0	-=	\		A(4)
9029	Hha1	49	aaa	70.745	71	0	70.56	70.93	0	31 500 000	3 400 000	+-	A		A(4)
9030	Hha1	49	aaa	71.09	71	71.09	0	0	54 300 000	0	0	-=	\		A(4)
9031	Hha1	33	agc	72.64	73	0	0	72.64	0	0	33 300 000	=+	/		A(4)
9032	Taq1	26	ctg	186.63	187	0	0	186.63	0	0	4 800 000	=+	/	/	A(4)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
8990	AF136378.WFS1	Wfs1	WFS1		agc	ctc	No change
8991	AF136378.WFS1	Wfs1	WFS1		agc	ctc	No change
8992	AF136378.WFS1	Wfs1	WFS1		aca	agg	No change
8993	AF136378.WFS1	Wfs1	WFS1		aca	agg	No change
8994	AF136378.WFS1	Wfs1	WFS1		aca	agg	No change
8995	AF136378.WFS1	Wfs1	WFS1		gct	tct	No change
8996	AF136378.WFS1	Wfs1	WFS1		aag	ccc	No change
8997	AF136378.WFS1	Wfs1	WFS1		aag	ccc	No change
8998	AF136378.WFS1	Wfs1	WFS1		aag	ccc	No change
8999	AF136378.WFS1	Wfs1	WFS1		ctt	agc	No change
9000	AF136378.WFS1	Wfs1	WFS1		ctt	agc	No change
9001	AY192567.PE1	nc	WNK4 Ser/Thr kinase		gtt	act	decreased
9002	AY192567.PE1	nc	WNK4 Ser/Thr kinase		gtt	act	decreased
9003	AY192567.PE1	nc	WNK4 Ser/Thr kinase		gtt	act	decreased
9004	AY192567.PE1	nc	WNK4 Ser/Thr kinase		gtt	act	decreased
9005	AY192567.PE1	nc	WNK4 Ser/Thr kinase		gtt	act	decreased
9006	AY192567.PE1	nc	WNK4 Ser/Thr kinase		gtt	act	decreased
9007	AY192567.PE1	nc	WNK4 Ser/Thr kinase		tgg	ttg	decreased
9008	AY192567.PE1	nc	WNK4 Ser/Thr kinase		tgg	ttg	decreased
9009	AY192567.PE1	nc	WNK4 Ser/Thr kinase		tgg	ttg	decreased
9010	AY192567.PE1	nc	WNK4 Ser/Thr kinase		tgg	ttg	decreased
9011	AY192567.PE1	nc	WNK4 Ser/Thr kinase		aat	aga	decreased
9012	AY192567.PE1	nc	WNK4 Ser/Thr kinase		aat	aga	decreased
9013	AY192567.PE1	nc	WNK4 Ser/Thr kinase		aat	aga	decreased
9014	AY192567.PE1	nc	WNK4 Ser/Thr kinase		aat	aga	decreased
9015	AY192567.PE1	nc	WNK4 Ser/Thr kinase		aat	aga	decreased
9016	AY192567.PE1	nc	WNK4 Ser/Thr kinase		aat	aga	decreased
9017	AF188608.WNT-4	wnt-4	Wnt-4		gta	gtt	increased
9018	AF188608.WNT-4	wnt-4	Wnt-4		gta	gtt	increased
9019	AF188608.WNT-4	wnt-4	Wnt-4		cca	cgg	increased
9020	AF188608.WNT-4	wnt-4	Wnt-4		agc	tgt	increased
9021	AF188608.WNT-4	wnt-4	Wnt-4		agc	tgt	increased
9022	AF188333.WNT-5A	Wnt-5a	Wnt-5a		agc	aca	increased
9023	AF188333.WNT-5A	Wnt-5a	Wnt-5a		agc	aca	increased
9024	AF188333.WNT-5A	Wnt-5a	Wnt-5a		ccc	tct	increased
9025	AF188333.WNT-5A	Wnt-5a	Wnt-5a		ccc	tct	increased
9026	AF188333.WNT-5A	Wnt-5a	Wnt-5a		ccc	tct	increased
9027	AF188333.WNT-5A	Wnt-5a	Wnt-5a		ccc	tct	increased
9028	RSXLAS.XLAS	XLas	XLalphas protein		aaa	ttc	increased by mild
9029	RSXLAS.XLAS	XLas	XLalphas protein		aaa	ttc	increased by mild
9030	RSXLAS.XLAS	XLas	XLalphas protein		aaa	ttc	increased by mild
9031	RSXLAS.XLAS	XLas	XLalphas protein		agc	ggg	increased by mild
9032	RSXLAS.XLAS	XLas	XLalphas protein		ctg	aca	decreased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
9033	Taq1	26	ctg	187.66	187	0	187.66	0	0	3 000 000	0	+-	A	A	A(4)
9034	Taq1	57	ctg	186.41	187	0	0	186.41	0	0	6 500 000	=+	/	/	A(4)
9035	Taq1	57	ctg	187.215	187	0	187.02	187.41	0	3 300 000	5 400 000	+=	/		A(4)
9036	Taq1	57	ctg	187.45	187	0	187.45	0	0	4 800 000	0	+-	A	A	A(4)
9037	Hha1	40	tgg	225.115	226	225.12	225.11	0	4 000 000	3 800 000	0	=-	\		A(4)
9038	Hha1	40	tgg	225.76	226	0	225.76	0	0	6 500 000	0	+-	A		A(4)
9039	Hha1	59	ttc	69.62	70	69.62	0	0	930.83	0	0	-=	\		\(2)
9040	Hha1	49	aaa	70.745	71	0	70.56	70.93	0	31 500 000	3 400 000	+-	A		\(2)
9041	Hha1	49	aaa	71.09	71	71.09	0	0	54 300 000	0	0	-=	\		\(2)
9042	Hha1	33	agc	72.64	73	0	0	72.64	0	0	33 300 000	=+	/		\(2)
9043	Hha1	40	tgg	139.54	140	139.54	0	0	5 600 000	0	0	-=	\		/(4)
9044	Hha1	40	tgg	140.665	140	140.67	140.66	0	13 800 000	9 700 000	0	=-	\		/(4)
9045	Taq1	20	ctc	158.115	159	0	158.1	158.13	0	7 900 000	4 900 000	+=	/		/(4)
9046	Taq1	20	ctc	159.143	159	159.02	159.09	159.32	3 000 000	7 800 000	4 400 000	+=	/ (-)		/(4)
9047	Hha1	6	aga	174.96	176	0	0	174.96	0	0	5 400 000	=+	/		/(4)
9048	Hha1	6	aga	175.995	176	175.96	0	176.03	4 500 000	0	9 800 000	-+(+)	V (/)		/(4)
9049	Hha1	6	aga	177.05	176	0	0	177.05	0	0	9 400 000	=+	/		/(4)
9050	Taq1	40	tgg	175.59	176	0	0	175.59	0	0	7 000 000	=+	/		/(4)
9051	Hha1	32	gtc	208.75	210	0	0	208.75	0	0	385.07	=+	/		/(4)
9052	Hha1	59	ttc	149.18	150	0	149.21	149.15	0	97.73	124.18	+=	/		\(2)
9053	Hha1	59	ttc	149.72	150	149.72	0	0	223.6	0	0	-=	\		\(2)
9054	Hha1	40	tgg	242.917	244	242.9	242.91	242.94	33 800 000	14 700 000	13 400 000	-=	\ (-)		\(2)
9055	Hha1	40	tgg	243.765	244	243.61	243.92	0	7 100 000	5 000 000	0	=-	\		\(2)
9056	Taq1	50	aat	100.32	100	0	100.1	100.54	0	6 400 000	19 200 000	=+	/		/(3)
9057	Taq1	50	aat	99.82	100	0	99.99	99.65	0	5 900 000	44 700 000	=+	/		/(3)
9058	Taq1	21	acc	178.015	179	177.93	0	178.1	4 900 000	0	4 000 000	-+(=)	V		/(3)
9059	Taq1	21	acc	179.055	179	178.84	179.27	0	8 600 000	3 200 000	0	-=	\		/(3)
9060	Hha1	21	acc	179.96	179	0	0	179.96	0	0	6 200 000	=+	/		/(3)
9061	Hha1	6	aga	211.18	212	211.4	0	210.96	16 400 000	0	4 500 000	-=(-)	\		/(3)
9062	Hha1	6	aga	212	212	0	0	212	0	0	3 300 000	=+	/		/(3)
9063	Hha1	6	aga	212.985	212	213.04	0	212.93	13 800 000	0	3 900 000	-=(-)	\		/(3)
9064	Taq1	50	aat	100.32	100	0	100.1	100.54	0	6 400 000	19 200 000	=+	/		/(3)
9065	Taq1	50	aat	99.82	100	0	99.99	99.65	0	5 900 000	44 700 000	=+	/		/(3)
9066	Taq1	21	acc	178.015	179	177.93	0	178.1	4 900 000	0	4 000 000	-+(=)	V		/(3)
9067	Taq1	21	acc	179.055	179	178.84	179.27	0	8 600 000	3 200 000	0	-=	\		/(3)
9068	Hha1	21	acc	179.96	179	0	0	179.96	0	0	6 200 000	=+	/		/(3)
9069	Hha1	6	aga	211.18	212	211.4	0	210.96	16 400 000	0	4 500 000	-=(-)	\		/(3)
9070	Hha1	6	aga	212	212	0	0	212	0	0	3 300 000	=+	/		/(3)
9071	Hha1	6	aga	212.985	212	213.04	0	212.93	13 800 000	0	3 900 000	-=(-)	\		/(3)
9072	Taq1	50	aat	100.32	100	0	100.1	100.54	0	6 400 000	19 200 000	=+	/		/(3)
9073	Taq1	50	aat	99.82	100	0	99.99	99.65	0	5 900 000	44 700 000	=+	/		/(3)
9074	Taq1	21	acc	178.015	179	177.93	0	178.1	4 900 000	0	4 000 000	-+(=)	V		/(3)
9075	Taq1	21	acc	179.055	179	178.84	179.27	0	8 600 000	3 200 000	0	-=	\		/(3)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
9033	RSXLAS.XLAS	XLas	XLalphas protein		ctg	aca	increased by mild
9034	RSXLAS.XLAS	XLas	XLalphas protein		ctg	aca	decreased
9035	RSXLAS.XLAS	XLas	XLalphas protein		ctg	aca	increased by mild
9036	RSXLAS.XLAS	XLas	XLalphas protein		ctg	aca	increased by mild
9037	RSXLAS.XLAS	XLas	XLalphas protein		tcc	tgg	increased by mild
9038	RSXLAS.XLAS	XLas	XLalphas protein		tcc	tgg	increased by mild
9039	AF093569.XLAS	XLas	XLas protein		aaa	ttc	increased
9040	AF093569.XLAS	XLas	XLas protein		aaa	ttc	increased
9041	AF093569.XLAS	XLas	XLas protein		aaa	ttc	increased
9042	AF093569.XLAS	XLas	XLas protein		agc	ggg	increased
9043	AF091457.PE1	nc	zinc finger protein RIN ZF		tgg	tgc	decreased
9044	AF091457.PE1	nc	zinc finger protein RIN ZF		tgg	tgc	decreased
9045	AF091457.PE1	nc	zinc finger protein RIN ZF		cgc	ctc	decreased
9046	AF091457.PE1	nc	zinc finger protein RIN ZF		cgc	ctc	decreased
9047	AF091457.PE1	nc	zinc finger protein RIN ZF		tgg	aga	decreased
9048	AF091457.PE1	nc	zinc finger protein RIN ZF		tgg	aga	decreased
9049	AF091457.PE1	nc	zinc finger protein RIN ZF		tgg	aga	decreased
9050	AF091457.PE1	nc	zinc finger protein RIN ZF		tgg	aga	decreased
9051	AF091457.PE1	nc	zinc finger protein RIN ZF		ggg	gtc	decreased
9052	RNU78875.CPG20	cpg20	zinc finger transcription factor homolog CPG20		ttc	ttc	increased
9053	RNU78875.CPG20	cpg20	zinc finger transcription factor homolog CPG20		ttc	ttc	increased
9054	RNU78875.CPG20	cpg20	zinc finger transcription factor homolog CPG20		tca	tgg	increased
9055	RNU78875.CPG20	cpg20	zinc finger transcription factor homolog CPG20		tca	tgg	increased
9056	AF013965.PE1	nc	Zis	*	aat	gta	decreased
9057	AF013965.PE1	nc	Zis	*	aat	gta	decreased
9058	AF013965.PE1	nc	Zis	*	tcg	acc	decreased
9059	AF013965.PE1	nc	Zis	*	tcg	acc	decreased
9060	AF013965.PE1	nc	Zis	*	tcg	acc	decreased
9061	AF013965.PE1	nc	Zis	*	aga	gac	decreased
9062	AF013965.PE1	nc	Zis	*	aga	gac	decreased
9063	AF013965.PE1	nc	Zis	*	aga	gac	decreased
9064	AF013966.PE1	nc	Zis	*	aat	gta	decreased
9065	AF013966.PE1	nc	Zis	*	aat	gta	decreased
9066	AF013966.PE1	nc	Zis	*	tcg	acc	decreased
9067	AF013966.PE1	nc	Zis	*	tcg	acc	decreased
9068	AF013966.PE1	nc	Zis	*	tcg	acc	decreased
9069	AF013966.PE1	nc	Zis	*	aga	gac	decreased
9070	AF013966.PE1	nc	Zis	*	aga	gac	decreased
9071	AF013966.PE1	nc	Zis	*	aga	gac	decreased
9072	AF013967.PE1	nc	Zis	*	aat	gta	decreased
9073	AF013967.PE1	nc	Zis	*	aat	gta	decreased
9074	AF013967.PE1	nc	Zis	*	tcg	acc	decreased
9075	AF013967.PE1	nc	Zis	*	tcg	acc	decreased

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O
3	**enzyme**	**PCR**	**triplet**	**mean**	**predicted**	**size**			**fluorescence**			**bichar**	**profile of**	**two**	**majority**
4		**n°**		**size**	**size**	**severe**	**mild**	**normoxia**	**severe**	**mild**	**normoxia**		**response**	**ends**	
9076	Hha1	21	acc	179.96	179	0	0	179.96	0	0	6 200 000	=+	/		/(3)
9077	Hha1	6	aga	211.18	212	211.4	0	210.96	16 400 000	0	4 500 000	-=(-)	\		/(3)
9078	Hha1	6	aga	212	212	0	0	212	0	0	3 300 000	=+	/		/(3)
9079	Hha1	6	aga	212.985	212	213.04	0	212.93	13 800 000	0	3 900 000	-=(-)	\		/(3)
9080	Hha1	26	ctg	110.77	111	110.8	110.74	0	10 600 000	5 600 000	0	--	\		\(3)
9081	Hha1	61	tct	110.7	111	110.72	110.76	110.62	4 500 000	3 400 000	7 000 000	=+	/ (-)		\(3)
9082	Hha1	61	tct	111.587	111	111.58	111.6	111.58	20 300 000	4 100 000	12 100 000	-=	\ (-)		\(3)
9083	Hha1	33	agc	113.725	114	113.86	113.59	0	6 500 000	9 600 000	0	=-	\		\(3)

	P	Q	R	S	T	U	V
3	**n∞GeneBank**	**gene**	**product**	**redondant**	**triplet**		**response to**
4					**5'**	**3'**	**hypoxia**
9076	AF013967.PE1	nc	Zis	*	tcg	acc	decreased
9077	AF013967.PE1	nc	Zis	*	aga	gac	decreased
9078	AF013967.PE1	nc	Zis	*	aga	gac	decreased
9079	AF013967.PE1	nc	Zis	*	aga	gac	decreased
9080	AY283175.ZAR1	Zar1	zygote arrest 1		ctg	tct	increased
9081	AY283175.ZAR1	Zar1	zygote arrest 1		ctg	tct	increased
9082	AY283175.ZAR1	Zar1	zygote arrest 1		ctg	tct	increased
9083	AY283175.ZAR1	Zar1	zygote arrest 1		agc	ggg	increased