Contents

1 Supplementary table 1

Table 1

	G>C A>T	**G>C A=T**	**G>C A<T**	**G=C A>T**	**G=C A=T**	**G=C A<T**	**G<C A>T**	**G<C A=T**	**G<C A<T**
All Bacteria	33	73	205	1	33	13	1	1	0
Acidobacteria	0	0	0	0	1	0	0	0	0
Actinobacteria	0	2	12	1	2	3	1	1	0
Aquificales	0	0	0	0	1	0	0	0	0
Bacteroidetes	0	2	4	0	0	0	0	0	0
Chlorobi	0	0	3	0	0	0	0	0	0
Chlamydiae	1	2	8	0	0	0	0	0	0
Chloroflexi	0	0	2	0	0	0	0	0	0
Cyanobacteria	0	0	9	0	7	1	0	0	0
Deinococcus Thermus	0	0	1	0	1	3	0	0	0
Firmicutes Bacilli	27	27	4	0	0	0	0	0	0
Firmicutes Clostridia	3	2	2	0	0	0	0	0	0
Firmicutes Mollicutes	0	3	1	0	10	2	0	0	0
Fusobacteria	1	0	0	0	0	0	0	0	0
Nitrospirae	0	0	0	0	0	0	0	0	0
Planctomycetes	0	0	1	0	0	0	0	0	0
α Proteobacteria	0	6	42	0	5	2	0	0	0
β Proteobacteria	0	1	36	0	0	0	0	0	0
δ Proteobacteria	0	1	10	0	0	0	0	0	0
ϵ Proteobacteria	0	3	6	0	0	0	0	0	0
γ Proteobacteria	1	22	57	0	6	2	0	0	0
Spirochaetes	0	1	7	0	0	0	0	0	0
Thermotogae	0	1	0	0	0	0	0	0	0
All Archaea	0	4	6	0	11	6	0	1	1
Crenarchaeota Thermoprotei	0	0	0	0	5	0	0	0	0
Euryarchaeota Archaeoglobi	0	0	0	0	1	0	0	0	0
Euryarchaeota Halobacteria	0	0	0	0	2	1	0	1	1
Euryarchaeota Methanobacteria	0	1	0	0	1	0	0	0	0
Euryarchaeota Methanomicrobia	0	0	3	0	0	2	0	0	0

Table 1 continued

Euryarchaeota Methanococci	0	1	1	0	0	0	0	0	0
Euryarchaeota Methanopyri	0	0	0	0	0	1	0	0	0
Euryarchaeota Thermoplasmata	0	1	1	0	1	0	0	0	0
Euryarchaeota Thermococci	0	1	1	0	0	2	0	0	0
Nanoarchaeota Nanoarchaeum	0	0	0	0	1	0	0	0	0

Table 1: Contingency table for the distribution of replication-related effects on the GC-skew and AT-skew in Bacteria and Archaea. The columns of the table indicate the sign of the nucleotide skews on the leading strand, induced by the replication mechanism. For instance, $\mathbf{G > C}$ means that the leading strand is enriched in G over C, thus the sign of the GC-skew on the leading strand is positive, while $\mathbf{G = C}$ means that no significant effect of replication on the GC-skew could be detected. The cells of the table contain the number of chromosomes that we found to present the respective GC-skew and AT-skew signs on the leading strand.

2 Supplementary table 2

	species	accession	AT	T&C, 2000	L&S, 2002	GC	T&C, 2000	L& S, 2002
1	A. bacterium El	NC_008009	0	1	1	0	1	1
2	A. sp ADP1	NC_005966	0	1	1	1	1	1
3	A. pernix	NC_000854	0	NA	NA	0	NA	NA
4	A. tumefaciens	NC_003062	1	1	1	1	1	1
5	A. tumefaciens	NC_003063	1	1	1	1	1	1
6	A. variabilis A	NC_007413	0	0	0	0	0	0
7	A. dehalogenans	NC_007760	0	0	0	1	0	1
8	A. marginale St	NC_004842	1	1	1	1	1	1
9	A. aeolicus	NC_000918	0	0	0	0	0	0
10	A. fulgidus	NC_000917	0	NA	NA	0	NA	NA
11	A. yellows witc	NC_007716	1	1	1	1	1	1
12	A. sp EbN1	NC_006513	1	1	1	1	1	1
13	B. anthracis Am	NC_003997	1	1	1	1	1	1
14	B. fragilis NCT	NC_003228	1	1	1	1	1	1
15	B. henselae Hou	NC_005956	1	1	1	1	1	1
16	B. cicadellinic	NC_007984	0	NA	NA	0	NA	NA
17	B. bacteriovoru	NC_005363	1	1	1	1	1	1
18	B. longum	NC_004307	0	1	1	0	1	1
19	B. bronchisepti	NC_002927	1	1	1	1	1	1
20	B. burgdorferi	NC_001318	1	1	1	1	1	1
21	B. japonicum	NC_004463	1	1	1	1	1	1
22	B. abortus 9-94	NC_006932	1	1	1	1	1	1
23	B. abortus 9-94	NC_006933	1	1	1	1	1	1
24	B. aphidicola	NC_004545	1	1	1	1	1	1
25	B. 383	NC_007509	1	1	1	1	1	1
26	B. 383	NC_007510	1	1	1	1	1	1
27	B. 383	NC_007511	1	1	1	1	1	1
28	C. jejuni	NC_002163	1	1	1	1	1	1
29	C. Blochmannia	NC_005061	1	1	1	1	1	1
30	C. hydrogenofor	NC_007503	0	0	0	1	0	1
31	C. crescentus	NC_002696	1	1	1	1	1	1
32	C. muridarum	NC_002620	1	1	1	1	1	1
33	C. abortus S26	NC_004552	1	1	1	1	1	1
34	C. chlorochroma	NC_007514	1	1	1	1	1	1
35	C. violaceum	NC_005085	1	1	1	1	1	1
36	C. salexigens D	NC_007963	1	1	1	1	1	1
37	C. acetobutylic	NC_003030	1	1	1	1	1	1
38	C. psychrerythr	NC_003910	1	1	1	1	1	1
39	C. diphtheriae	NC_002935	1	1	1	1	1	1
40	C. burnetii	NC_002971	0	1	1	1	1	1
41	C. bacterium Ye	NC_007775	0	0	0	0	0	0
42	D. aromatica RC	NC_007298	1	1	1	1	1	1
43	D. CBDB1	NC_007356	1	1	1	1	1	1
44	D. geothermalis	NC_008025	1	1	1	1	1	1
45	D. hafniense Y5	NC_007907	0	0	0	1	0	1
46	D. psychrophila	NC_006138	1	1	1	1	1	1
47	D. desulfurican	NC_007519	1	1	1	1	1	1
48	E. canis Jake	NC_007354	1	1	1	1	1	1

49	E. faecalis V58	NC_004668	1	1	1	1	1	1
50	E. carotovora a	NC_004547	1	1	1	1	1	1
51	E. litoralis HT	NC_007722	1	1	1	1	1	1
52	E. coli 536	NC_008253	0	1	1	1	1	1
53	F. tularensis h	NC_007880	1	1	1	1	1	1
54	F. CcI3	NC_007777	1	1	1	1	1	1
55	F. nucleatum	NC_003454	1	1	1	1	1	1
56	G. kaustophilus	NC_006510	1	1	1	1	1	1
57	G. metallireduc	NC_007517	1	1	1	1	1	1
58	G. violaceus	NC_005125	0	NA	NA	0	NA	NA
59	G. oxydans 621H	NC_006677	1	1	1	1	1	1
60	H. ducreyi 3500	NC_002940	1	1	1	1	1	1
61	H. chejuensis K	NC_007645	1	1	1	1	1	1
62	H. marismortui	NC_006396	1	1	1	0	1	1
63	H. marismortui	NC_006397	0	NA	NA	0	NA	NA
64	H. sp	NC_002607	0	NA	NA	1	NA	NA
65	H. walsbyi	NC_008212	0	NA	NA	0	NA	NA
66	H. acinonychis	NC_008229	0	0	1	1	0	1
67	I. loihiensis L	NC_006512	0	1	1	1	1	1
68	J. CCS1	NC_007802	1	1	1	1	1	1
69	L. acidophilus	NC_006814	0	0	0	1	0	1
70	C. hutchinsonii	NC_008255	0	1	0	1	1	1
71	L. lactis	NC_002662	1	1	1	1	1	1
72	L. intracellula	NC_008011	1	1	1	1	1	1
73	L. pneumophila	NC_006369	1	1	1	1	1	1
74	L. xyli xyli CT	NC_006087	1	1	1	1	1	1
75	L. interrogans	NC_005823	1	1	1	1	1	1
76	L. interrogans	NC_005824	0	1	1	1	1	1
77	L. innocua	NC_003212	1	1	1	1	1	1
78	M. magneticum A	NC_007626	1	1	1	1	1	1
79	M. succinicipro	NC_006300	1	1	1	1	1	1
80	M. florum L1	NC_006055	0	1	1	0	1	0
81	M. BNC1	NC_008254	1	1	1	0	1	1
82	M. thermoautotr	NC_000916	0	1	1	0	1	1
83	M. burtonii DSM	NC_007955	1	1	1	1	1	1
84	M. jannaschii	NC_000909	0	0	0	1	0	0
85	M. kandleri	NC_003551	1	1	1	0	1	0
86	M. acetivorans	NC_003552	1	1	1	1	1	1
87	M. stadtmanae	NC_007681	0	0	1	1	0	1
88	M. hungatei JF-	NC_007796	1	1	1	1	1	1
89	M. flagellatus	NC_007947	1	1	1	1	1	1
90	M. capsulatus B	NC_002977	1	1	1	1	1	1
91	M. thermoacetic	NC_007644	1	0	1	1	0	1
92	M. MCS	NC_008146	1	1	1	1	1	1
93	M. capricolum A	NC_007633	0	0	0	0	0	1
94	M. xanthus DK 1	NC_008095	1	1	1	1	1	1
95	N. equitans	NC_005213	0	NA	NA	0	NA	NA
96	N. pharaonis	NC_007426	1	1	1	1	1	1
97	N. gonorrhoeae	NC_002946	1	1	1	1	1	1
98	N. sennetsu Miy	NC_007798	1	1	1	1	1	1
99	N. hamburgensis	NC_007964	1	1	1	1	1	1

100	N. oceani ATCC	NC_007484	1	1	1	1	1	1
101	N. europaea	NC_004757	1	1	1	1	1	1
102	N. multiformis	NC_007614	1	1	1	1	1	1
103	N. farcinica IF	NC_006361	0	NA	NA	0	NA	NA
104	N. sp	NC_003272	0	0	0	0	0	0
105	N. aromaticivor	NC_007794	1	1	1	1	1	1
106	O. iheyensis	NC_004193	1	1	1	1	1	1
107	O. yellows phyt	NC_005303	1	1	1	0	1	1
108	P. sp UWE25	NC_005861	1	1	1	1	1	1
109	P. multocida	NC_002663	1	1	1	1	1	1
110	P. carbinolicus	NC_007498	1	1	1	1	1	1
111	P. luteolum DSM	NC_007512	1	1	1	1	1	1
112	P. profundum SS	NC_006370	1	1	1	1	1	1
113	P. profundum SS	NC_006371	1	1	1	1	1	1
114	P. luminescens	NC_005126	1	1	1	1	1	1
115	P. torridus DSM	NC_005877	0	NA	NA	0	NA	NA
116	P. sp	NC_005027	1	1	1	1	1	1
117	P. JS666	NC_007948	1	1	1	1	1	1
118	P. gingivalis W	NC_002950	1	1	1	1	1	1
119	P. marinus CCMP	NC_005042	1	1	1	1	1	1
120	P. acnes KPA171	NC_006085	1	1	1	1	1	1
121	P. atlantica T6	NC_008228	1	1	1	1	1	1
122	P. aeruginosa	NC_002516	1	1	1	1	1	1
123	P. arcticum 273	NC_007204	0	0	1	1	0	1
124	P. aerophilum	NC_003364	0	NA	NA	0	NA	NA
125	P. abyssi	NC_000868	1	1	1	1	1	1
126	R. eutropha JMP	NC_007347	1	1	1	1	1	1
127	R. eutropha JMP	NC_007348	1	1	1	1	1	1
128	R. etli CFN 42	NC_007761	0	NA	NA	0	NA	NA
129	R. sphaeroides	NC_007493	0	1	1	1	1	1
130	R. sphaeroides	NC_007494	0	NA	NA	0	NA	NA
131	R. ferrireducen	NC_007908	1	1	1	1	1	1
132	R. palustris Bi	NC_007925	1	1	1	1	1	1
133	R. rubrum ATCC	NC_007643	1	1	1	1	1	1
134	R. bellii RML36	NC_007940	0	1	0	1	1	1
135	R. denitrifican	NC_008209	1	1	1	1	1	1
136	R. xylanophilus	NC_008148	1	1	1	1	1	1
137	S. degradans 2-	NC_007912	1	1	1	1	1	1
138	S. ruber DSM 13	NC_007677	0	0	1	1	0	1
139	S. enterica Cho	NC_006905	0	1	1	1	1	1
140	S. denitrifican	NC_007954	1	1	1	1	1	1
141	S. boydii Sb227	NC_007613	0	1	0	0	1	1
142	S. TM1040	NC_008044	1	1	1	1	1	1
143	S. meliloti	NC_003047	1	1	1	1	1	1
144	S. glossinidius	NC_007712	1	1	1	1	1	1
145	S. alaskensis R	NC_008048	1	1	1	1	1	1
146	S. aureus COL	NC_002951	1	1	1	1	1	1
147	S. agalactiae 2	NC_004116	0	0	0	1	0	1
148	S. avermitilis	NC_003155	1	1	0	0	1	1
149	S. acidocaldari	NC_007181	0	NA	NA	0	NA	NA
150	S. thermophilum	NC_006177	1	1	1	1	1	1

151	S. CC9605	NC_007516	1	1	1	1	1	1
152	S. PCC6803	NC_000911	0	0	0	0	0	0
153	S. aciditrophic	NC_007759	1	1	1	1	1	1
154	T. tengcongensi	NC_003869	1	1	1	1	1	1
155	T. fusca YX	NC_007333	1	1	1	1	1	1
156	T. kodakaraensi	NC_006624	1	1	1	0	1	0
157	T. acidophilum	NC_002578	0	1	1	1	1	1
158	T. elongatus	NC_004113	0	0	0	0	0	1
159	T. maritima	NC_000853	0	1	1	1	1	1
160	T. thermophilus	NC_005835	1	1	1	0	1	1
161	T. denitrifican	NC_007404	1	1	1	1	1	1
162	T. crunogena XC	NC_007520	1	1	1	1	1	1
163	T. denticola AT	NC_002967	1	1	1	1	1	1
164	T. whipplei TW0	NC_004551	1	1	1	0	1	0
165	U. urealyticum	NC_002162	0	0	0	1	0	1
166	V. cholerae	NC_002505	1	1	1	1	1	1
167	V. cholerae	NC_002506	1	1	1	1	1	1
168	W. brevipalpis	NC_004344	0	NA	NA	0	NA	NA
169	W. endosymbiont	NC_006833	0	NA	NA	0	NA	NA
170	W. succinogenes	NC_005090	1	1	1	1	1	1
171	X. campestris	NC_003902	1	1	1	1	1	1
172	X. fastidiosa	NC_002488	1	1	1	1	1	1
173	Y. pestis Antiq	NC_008150	1	1	1	1	1	1
174	Z. mobilis ZM4	NC_006526	0	1	1	0	1	1

Table 2: Comparison between our approach and the methods proposed by Tillier and Collins, 2000 and Lobry and Sueoka, 2002, for 173 chromosomes for which we have performed significance computations. Cases where the p-values are not available for these two methods correspond to chromosomes where the origin and terminus could not be determined with certainty.

3 Supplementary figure 1

Figure 1:

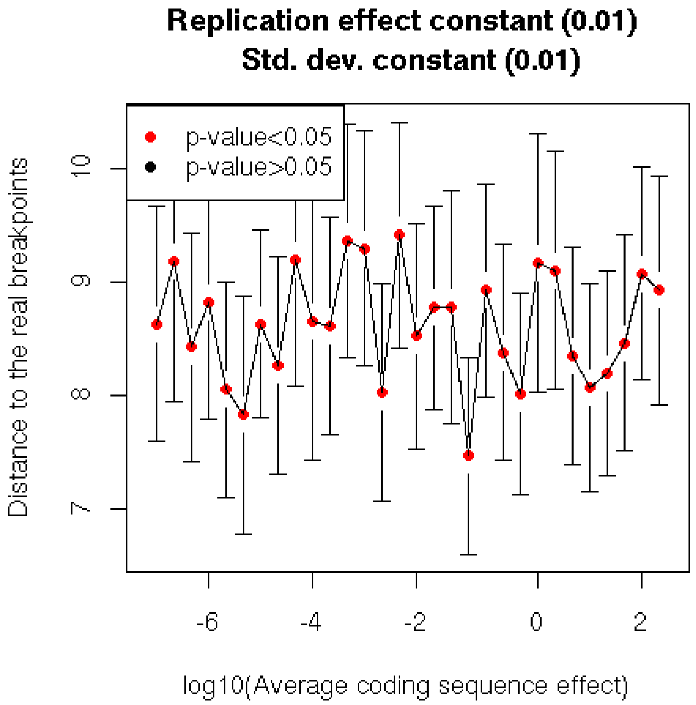


Figure 1: Results from simulations where the effect of replication is constant (r=0.1), the standard variation of the nucleotide skews is constant for both groups of genes (sd=0.01), the breakpoint location is constant (fr=0.25), and the coding sequence related effects (m) vary. The y-axis represents the distance between the real and the estimated breakpoints.

4 Supplementary figure 2

Figure 2:

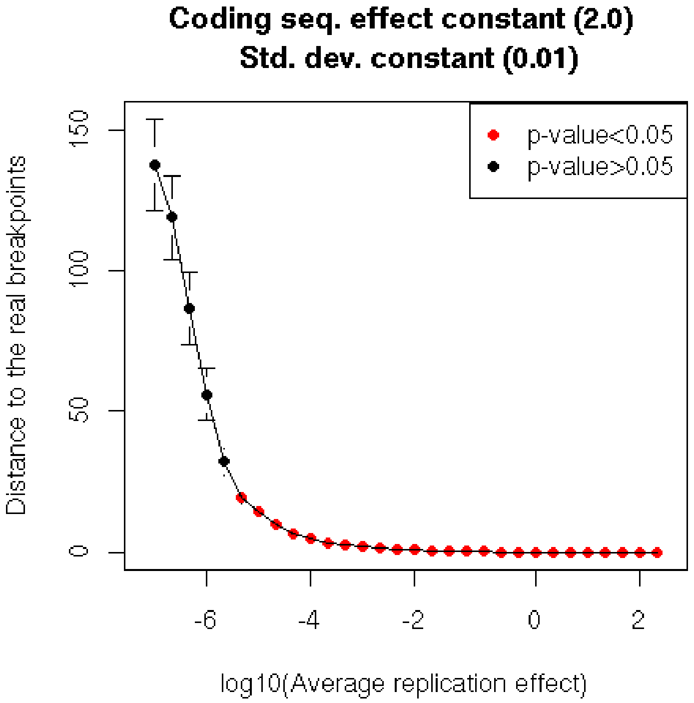


Figure 2: Results from simulations where the coding-sequence related effect is constant (m=0.1), the standard variation of the nucleotide skews is constant for both groups of genes (sd=0.01), the breakpoint location is constant (fr=0.25), and the replication effect (r) varies. The y-axis represents the distance between the real and the estimated breakpoints.

5 Supplementary figure 3

Figure 3:

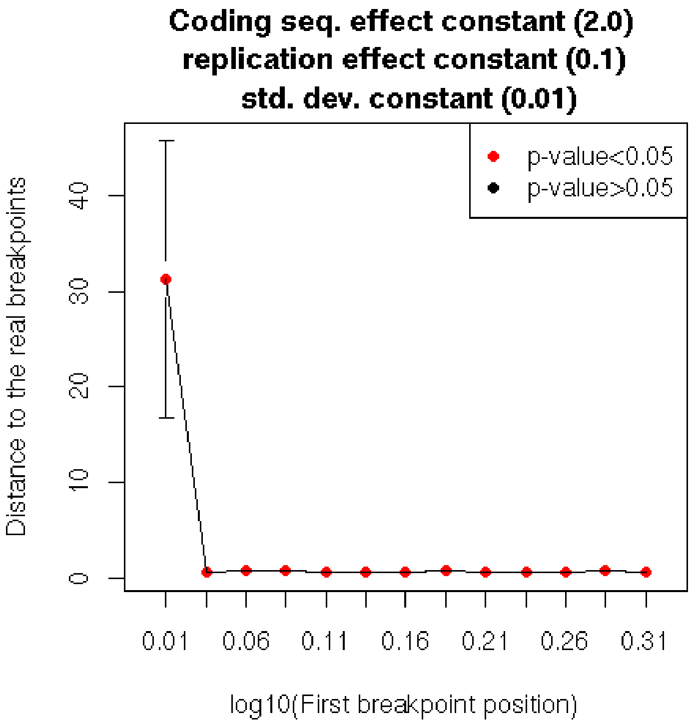


Figure 3: Results from simulations where the replication and the coding-sequence related effects are constant (m=2.0 and r=0.1), the standard variation of the nucleotide skews is constant for both groups of genes (sd=0.01), but the position of the breakpoint (fr) varies. The y-axis represents the distance between the real and the estimated breakpoints.

6 Supplementary figure 4

Figure 4:

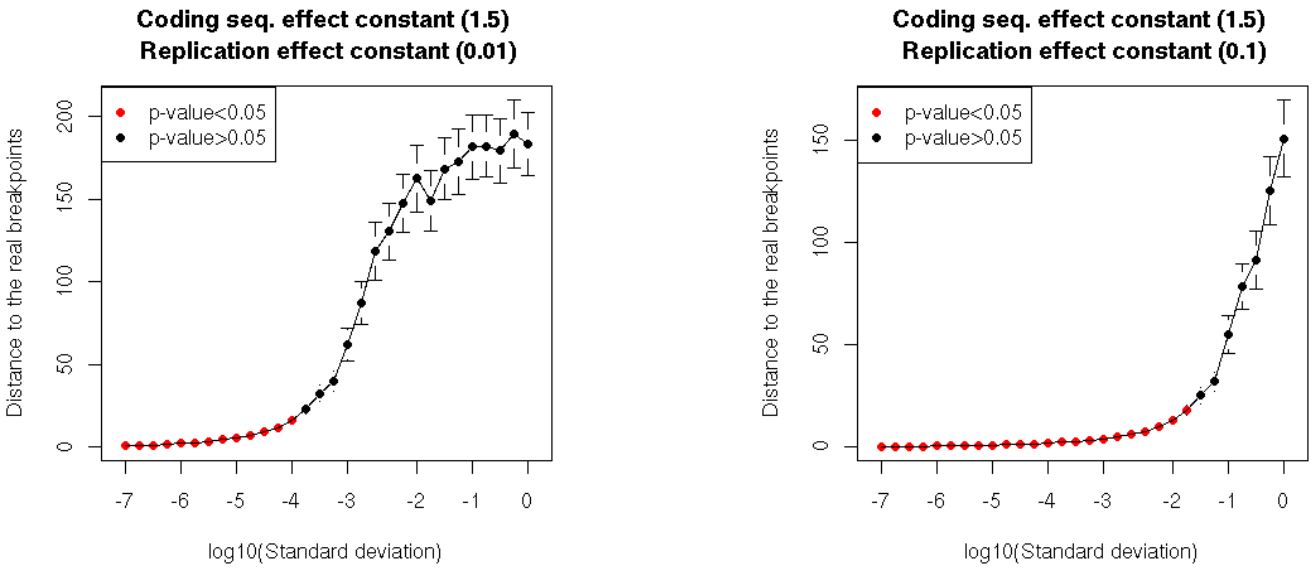


Figure 4: Results from simulations where the effect of replication is constant (r=0.01 for the first graph and r=0.1 for the second graph), the coding sequence related effect is constant (m=2.0), the breakpoint location is constant (fr=0.25) and the standard variation of the nucleotide skews varies. The y-axis represents the distance between the real and the estimated breakpoints.

7 Results for 389 prokaryotic chromosomes

This supplementary material contains, for each chromosome we analyzed, the following information:

- the taxonomic position;
- the NCBI RefSeq accession number;
- the chromosome size in base pairs (bp);
- the number of protein-coding genes found on the chromosome;
- the Oriloc predictions for the origin and the terminus of replication;
- the predictions for the origin and terminus of replication provided by Worning *et al.*, 2006, taken from `http://www.cbs.dtu.dk/services/GenomeAtlas/`;
- a graphics representing the cumulative nucleotide skews (computed on the third codon positions of the protein coding genes) and the cumulative CDS-skew, on the original chromosome (before rearrangement);
- a graphics representing the cumulative nucleotide skews (computed on the third codon positions of the protein coding genes) and the CDS-skew, on the artificially rearranged chromosome;
- a table giving the position of the breakpoints found on the rearranged skew, the p-value associated to each breakpoint (when available), and the corresponding coordinate on the original chromosome;
- a table giving some information on the segments delimited by the breakpoints on the rearranged nucleotide skews - the beginning and the end position for each segment (in gene index on the rearranged chromosome and in kb on the original chromosome), the strand (leading, lagging or NA), and the slope of the rearranged nucleotide skew on that segment;
- if a clear pattern could be discerned (see below), the direction of the nucleotide skews on the leading strand is given.

Oriloc predictions for the origin and terminus of replication

We used Oriloc to predict the origin and the terminus of replication in the following manner: we computed the positions of the minimum and the maximum of the composite cumulative skew. To decide which of these positions corresponds to the origin and which to the terminus of replication, we assumed that most protein-coding genes are encoded on the leading strand. Under this assumption, the slope of the cumulative CDS-skew is positive between the origin and the terminus of replication. This allowed us distinguish the origin from the terminus, without making any *a priori* assumptions on the direction of the nucleotide skews. When this procedure did not provide any clear-cut results, we referred to the litterature, or we used the positions given by Worning *et al.*, 2006.

Strand characterization for the segments

To determine the direction of the nucleotide skews on the leading strand for replication, we first needed to characterize the segments delimited by the breakpoints in the rearranged skews, into leading or lagging. To do so, we assumed that a segment is placed on the leading strand, if at least 85%

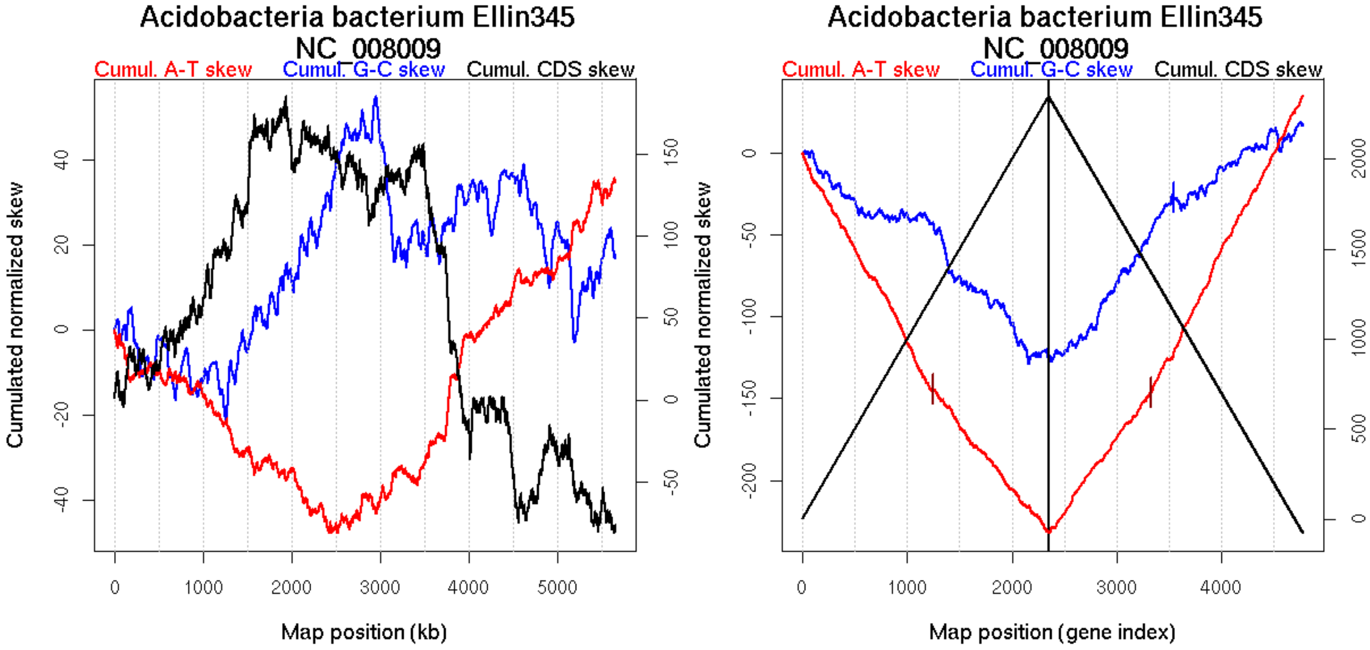
of the length of the segment is found in the 3' region of the origin and the 5' region of the terminus of replication. We assumed that a segment is placed on the lagging strand if this proportion was lower than 15%. In other cases, no characterization was given for the segment.

Skew direction on the leading strand

If all the segments delimited by the breakpoints could be assigned to either leading or lagging strand, we compared the slopes of the two types of segments, for both forward and reverse encoded groups of genes. If more than one segment could be characterized as “leading” or “lagging” for one group of genes, we considered the slope of the largest segment. If the slope of the GC-skew was higher on the leading strand than on the lagging strand, we conclude that the leading strand contains more G than C, *idem* for the AT-skew. If the segments that couldn't be clearly characterized as “leading” or “lagging” totalized more than 25% of the total size of one group of genes, we did not analyze the skew direction for that group of genes.

8 Acidobacteria bacterium Ellin345

Bacteria; Acidobacteria; Acidobacteriales; Acidobacteriaceae.
Accession number: NC_008009; **Genome size (bp)**: 5650368.
Number of genes: 4777.
Oriloc predictions: Origin NA Terminus NA
Worning et al., 2006: Origin 930 kb Terminus 2625 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1264.387 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.73 kb, 4005.22 kb
Consensus predictions: Origin 1264 kb Terminus 2944 kb



Significant breakpoints (p-value <0.05):

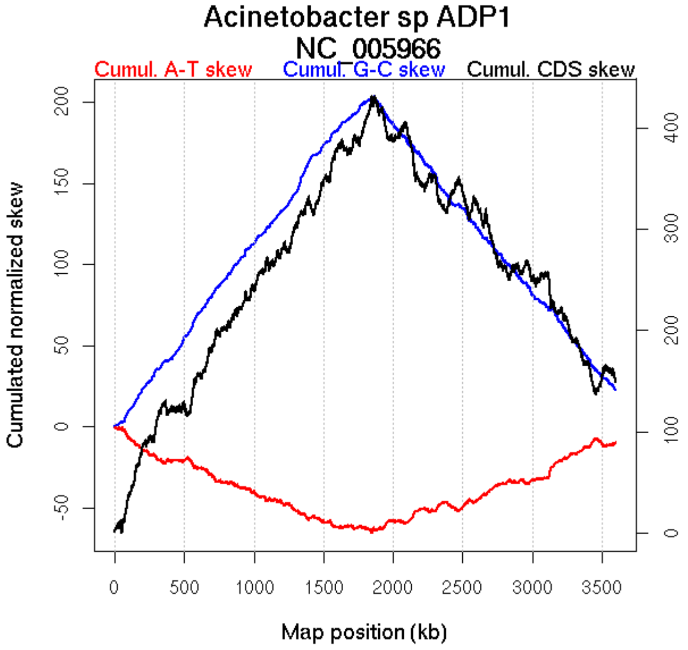
	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew reverse	3542	0.02	2969
AT-skew forward	1248	0.02667	2800
AT-skew reverse	3330	0.01333	2525

Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew reverse	2350 (0 kb)	3542 (2969.2575 kb)	NA	0.09
	3543(2973.28 kb)	4777 (5649.92 kb)	lagging	0.042
AT-skew forward	1 (0 kb)	1248 (2799.932 kb)	NA	-0.114
	1249(2801.269 kb)	2349 (5649.92 kb)	lagging	-0.079
AT-skew reverse	2350 (0 kb)	3330 (2525.4965 kb)	NA	0.088
	3331(2527.5545 kb)	4777(5649.92 kb)	lagging	0.125

9 Acinetobacter sp ADP1

Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Moraxellaceae; Acinetobacter.
Accession number: NC_005966; **Genome size (bp)**: 3598621.
Number of genes: 3325.
Oriloc predictions: Origin 0 kb Terminus 1847 kb
Worning et al., 2006: Origin 0 kb Terminus 1870 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 397.895 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 2585.74 kb
Consensus predictions: Origin 0 kb Terminus 1847 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1035	0	1816
GC-skew reverse	2376	0	1855
AT-skew forward	666	0.01333	1164
AT-skew reverse	2640	0.00667	2316

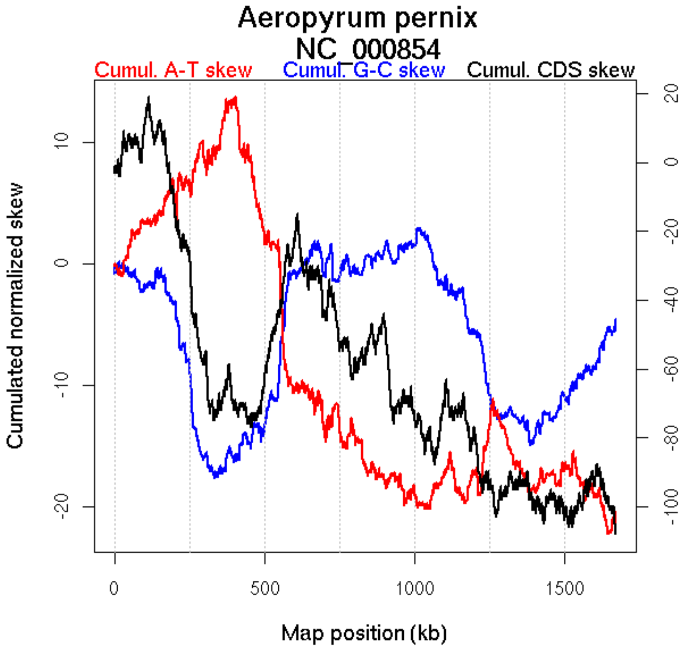
Segments:

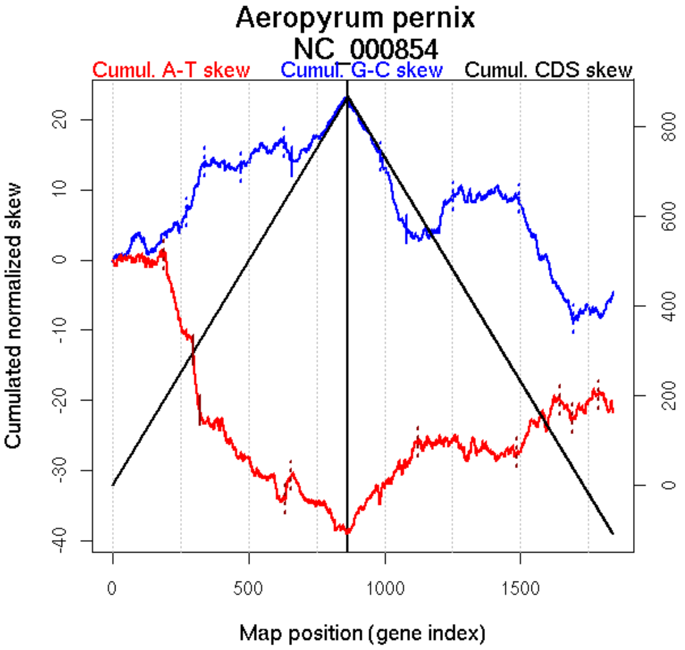
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1035 (1816.092 kb)	leading	0.193
	1036(1817.195 kb)	1737 (3598.157 kb)	lagging	-0.025
GC-skew reverse	1738 (0 kb)	2376 (1855.2675 kb)	leading	0.016
	2377(1855.7825 kb)	3325 (3598.157 kb)	lagging	-0.171
AT-skew forward	1 (0 kb)	666 (1164.267 kb)	leading	-0.151
	667(1164.8115 kb)	1737 (3598.157 kb)	NA	-0.125
AT-skew reverse	1738 (0 kb)	2640 (2315.994 kb)	NA	0.135
	2641(2316.677 kb)	3325(3598.157 kb)	lagging	0.159

More G than C on the leading strand for replication.

10 Aeropyrum pernix

Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales; Desulfurococcaceae; Aeropyrum.
Accession number: NC_000854; **Genome size (bp)**: 1669695.
Number of genes: 1840.
Oriloc predictions: Origin NA Terminus NA
Worning et al., 2006: Origin 445 kb Terminus 966 kb
Position(s) of the ORC/Cdc6 gene(s): 112.73 kb, 332.04 kb, 870.73 kb, 1574.25 kb
Consensus predictions: Origin NA Terminus NA





Significant breakpoints (p-value <0.05):

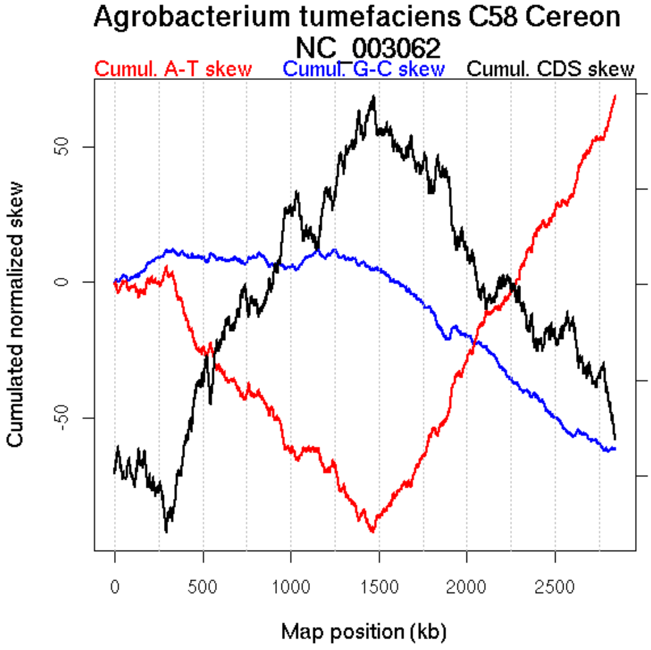
	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	271	0.09867	515
	338	0.05333	598
	472	0.82533	856
	631	0.05333	1192
	661	0.03067	1257
GC-skew reverse	986	0.39467	207
	1081	0.02533	323
	1251	0.70133	630
	1493	0.192	1033
	1693	0.11733	1392
AT-skew forward	188	0.12133	386
	296	0.032	551
	323	0.008	574
	635	0.05067	1197
	657	0.05333	1251
AT-skew reverse	1124	0.64667	393
	1487	0.624	1024
	1646	0.24	1301
	1691	0.26667	1386
	1787	0.28667	1577

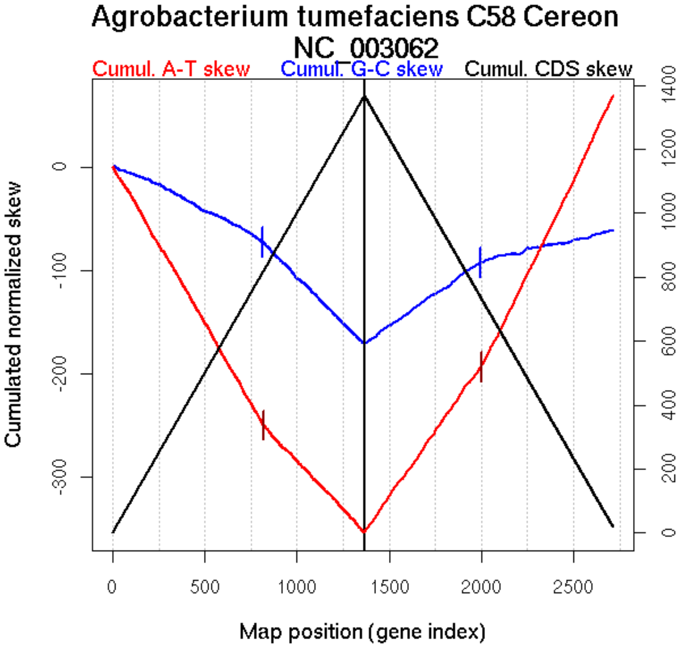
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	271 (515.1065 kb)	NA	0.019
	272(516.651 kb)	338 (598.023 kb)	NA	0.119
	339(598.466 kb)	472 (856.3625 kb)	NA	-0.006
	473(858.149 kb)	631 (1191.713 kb)	NA	0.021
	632(1193.231 kb)	661 (1257.254 kb)	NA	-0.105
	662(1258.8705 kb)	866 (1669.432 kb)	NA	0.047
GC-skew reverse	867 (0 kb)	986 (207.237 kb)	NA	-0.064
	987(207.7095 kb)	1081 (322.6145 kb)	NA	-0.12
	1082(325.004 kb)	1251 (629.52 kb)	NA	0.033
	1252(632.3795 kb)	1493 (1033.4525 kb)	NA	-0.002
	1494(1033.8865 kb)	1693 (1391.517 kb)	NA	-0.08
	1694(1392.4365 kb)	1840 (1669.432 kb)	NA	0.014
AT-skew forward	1 (0 kb)	188 (386.293 kb)	NA	0.001
	189(391.2955 kb)	296 (551.4345 kb)	NA	-0.124
	297(551.801 kb)	323 (574.282 kb)	NA	-0.315
	324(574.789 kb)	635 (1197.3135 kb)	NA	-0.04
	636(1199.401 kb)	657 (1251.204 kb)	NA	0.122
	658(1253.4705 kb)	866 (1669.432 kb)	NA	-0.037
AT-skew reverse	867 (0 kb)	1124 (392.544 kb)	NA	0.044
	1125(394.6545 kb)	1487(1023.9315 kb)	NA	-0.005
	1488(1024.9055 kb)	1646(1301.088 kb)	NA	0.046
	1647(1302.835 kb)	1691(1386.0495 kb)	NA	-0.058
	1692(1388.383 kb)	1787(1576.641 kb)	NA	0.039
	1788(1578.856 kb)	1840(1669.432 kb)	NA	-0.055

11 Agrobacterium tumefaciens C58 Cereon

Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Rhizobium/Agroba group; Agrobacterium.
Accession number: NC_003062; **Genome size (bp)**: 2841581.
Number of genes: 2715.
Oriloc predictions: Origin 0 kb Terminus 1463 kb
Worning et al., 2006: Origin 0 kb Terminus 1479 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 2841.493 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 318.11 kb
Consensus predictions: Origin 0 kb Terminus 1463 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	812	0	1465
GC-skew reverse	1997	0	1478
AT-skew forward	820	0	1473
AT-skew reverse	2000	0	1481

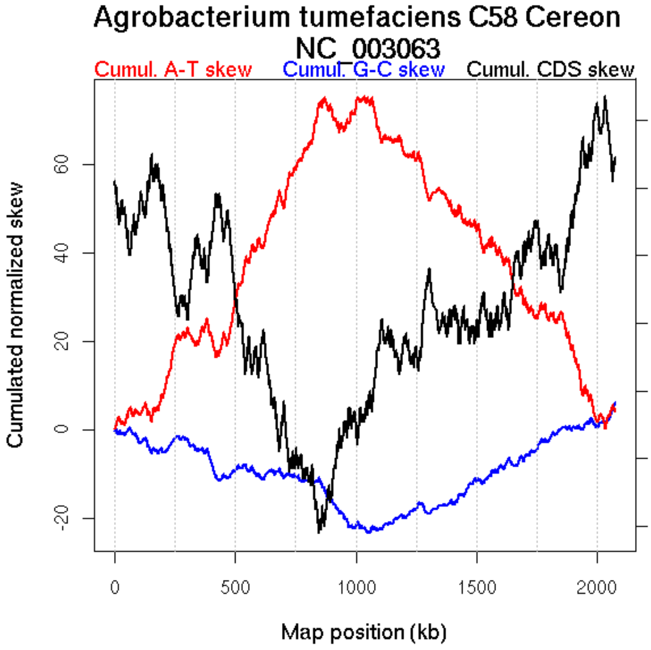
Segments:

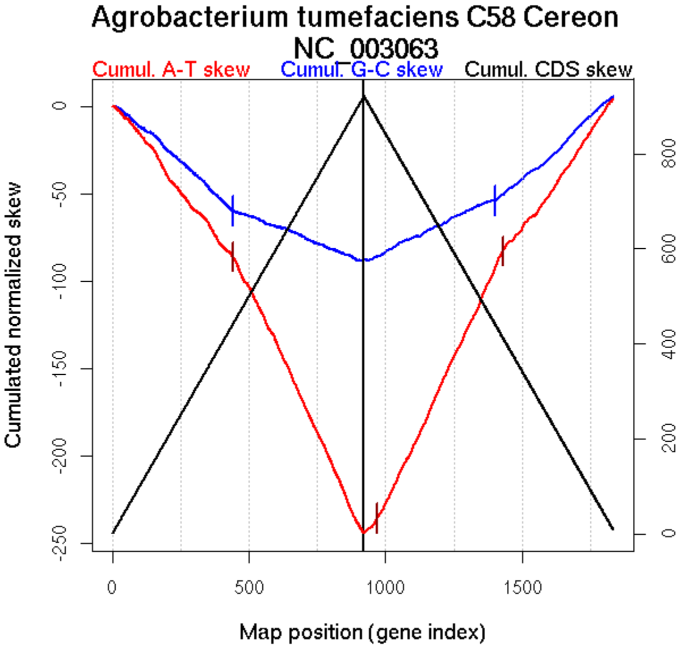
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	812 (1464.6615 kb)	leading	-0.09
	813(1465.4655 kb)	1367 (2841.173 kb)	lagging	-0.179
GC-skew reverse	1368 (0 kb)	1997 (1478.482 kb)	leading	0.125
	1998(1479.264 kb)	2715 (2841.173 kb)	lagging	0.04
AT-skew forward	1 (0 kb)	820 (1473.1535 kb)	leading	-0.307
	821(1482.158 kb)	1367 (2841.173 kb)	lagging	-0.186
AT-skew reverse	1368 (0 kb)	2000 (1480.5975 kb)	leading	0.254
	2001(1482.1665 kb)	2715(2841.173 kb)	lagging	0.367

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

12 Agrobacterium tumefaciens C58 Cereon

Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Rhizobium/Agroba group; Agrobacterium.
Accession number: NC_003063; **Genome size (bp)**: 2074782.
Number of genes: 1833.
Oriloc predictions: Origin 1047 kb Terminus 0 kb
Worning et al., 2006: Origin NA kb Terminus NA kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 569.322 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): NA
Consensus predictions: Origin 1047 kb Terminus 0 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	441	0.00667	1046
GC-skew reverse	1400	0	973
AT-skew forward	441	0	1046
AT-skew reverse	969	0.00667	78
	1430	0.01667	1057

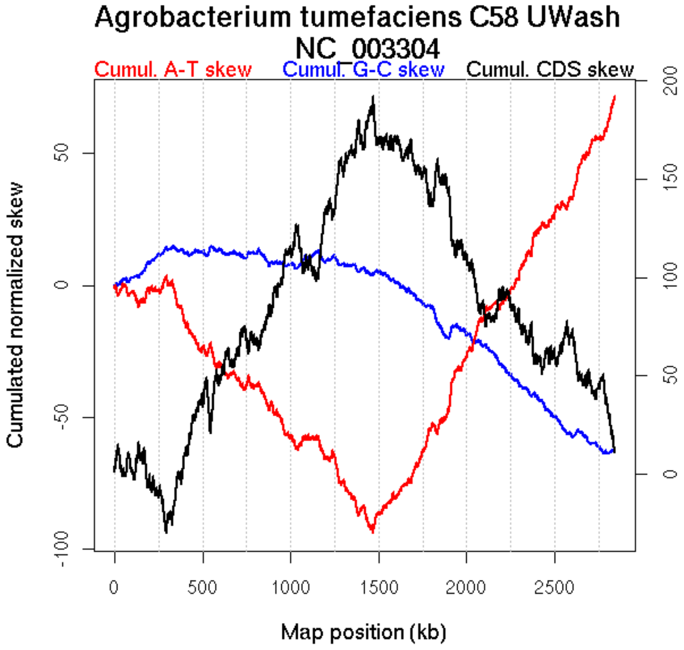
Segments:

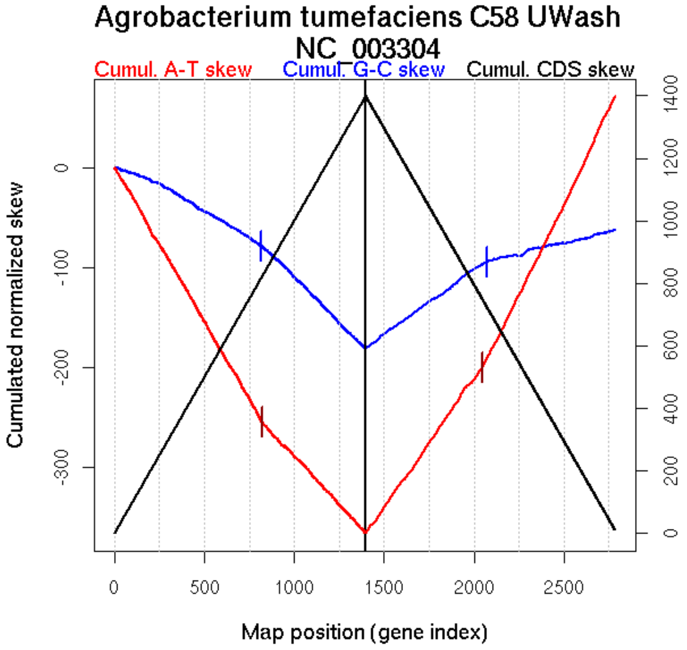
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	441 (1045.5915 kb)	lagging	-0.14
	442(1049.4 kb)	921 (2073.818 kb)	leading	-0.062
GC-skew reverse	922 (0 kb)	1400 (972.503 kb)	lagging	0.076
	1401(975.064 kb)	1833 (2073.818 kb)	leading	0.141
AT-skew forward	1 (0 kb)	441 (1045.5915 kb)	lagging	-0.205
	442(1049.4 kb)	921 (2073.818 kb)	leading	-0.336
AT-skew reverse	922 (0 kb)	969 (78.2705 kb)	lagging	0.155
	970(81.562 kb)	1430(1057.083 kb)	lagging	0.336
	1431(1060.181 kb)	1833(2073.818 kb)	leading	0.22

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

13 Agrobacterium tumefaciens C58 UWash

Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Rhizobium/Agroba group; Agrobacterium.
Accession number: NC_003304; **Genome size (bp)**: 2841490.
Number of genes: 2785.
Oriloc predictions: Origin 0 kb Terminus 1469 kb
Worning et al., 2006: Origin 0 kb Terminus 1479 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 0.114 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 318.33 kb
Consensus predictions: Origin 0 kb Terminus 1469 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	818	NA	1467
GC-skew reverse	2069	NA	1526
AT-skew forward	822	NA	1492
AT-skew reverse	2046	NA	1484

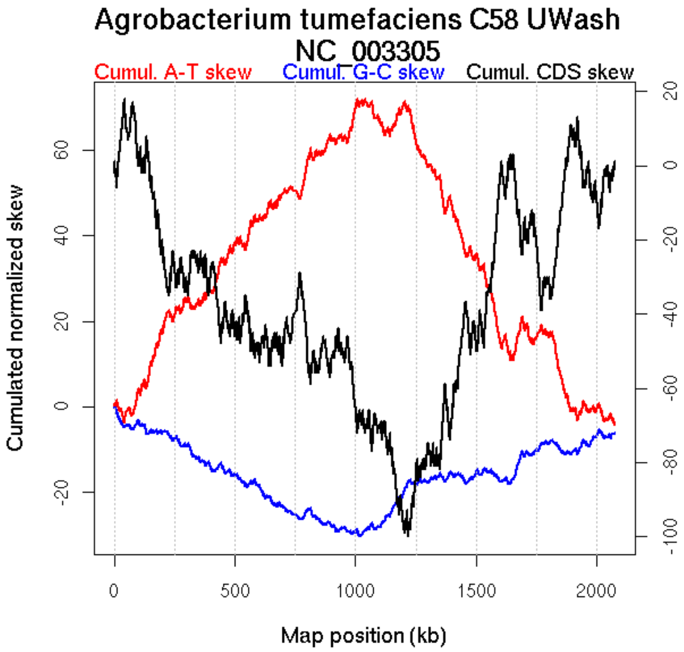
Segments:

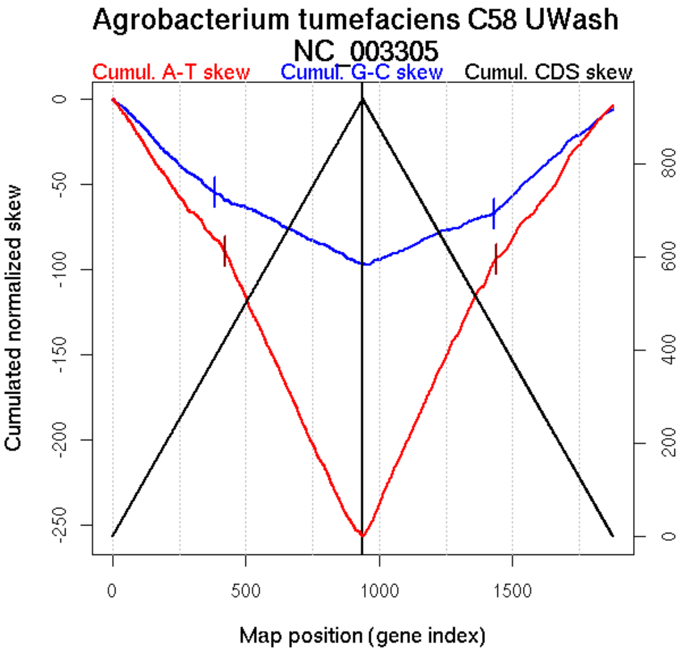
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	818 (1467.27 kb)	leading	-0.099
	819(1468.11 kb)	1398 (2841.284 kb)	lagging	-0.181
GC-skew reverse	1399 (0 kb)	2069 (1526.3505 kb)	leading	0.129
	2070(1527.2945 kb)	2785 (2841.284 kb)	lagging	0.043
AT-skew forward	1 (0 kb)	822 (1492.1715 kb)	leading	-0.31
	823(1493.571 kb)	1398 (2841.284 kb)	lagging	-0.191
AT-skew reverse	1399 (0 kb)	2046 (1484.304 kb)	leading	0.259
	2047(1485.498 kb)	2785(2841.284 kb)	lagging	0.368

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

14 Agrobacterium tumefaciens C58 UWash

Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Rhizobium/Agroba group; Agrobacterium.
Accession number: NC_003305; **Genome size (bp)**: 2075560.
Number of genes: 1876.
Oriloc predictions: Origin 1025 kb Terminus 0 kb
Worning et al., 2006: Origin NA kb Terminus NA kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1505.434 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): NA
Consensus predictions: Origin 1025 kb Terminus 0 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	382	NA	917
GC-skew reverse	1429	NA	1024
AT-skew forward	421	NA	1021
AT-skew reverse	1437	NA	1041

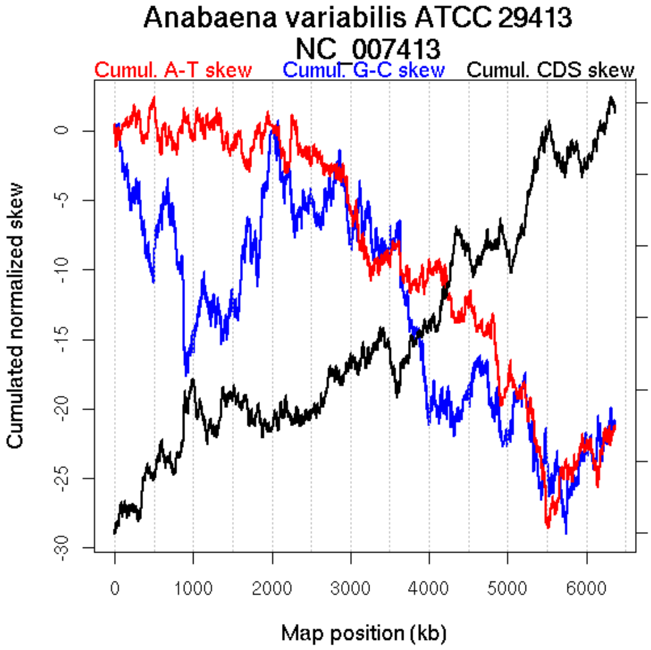
Segments:

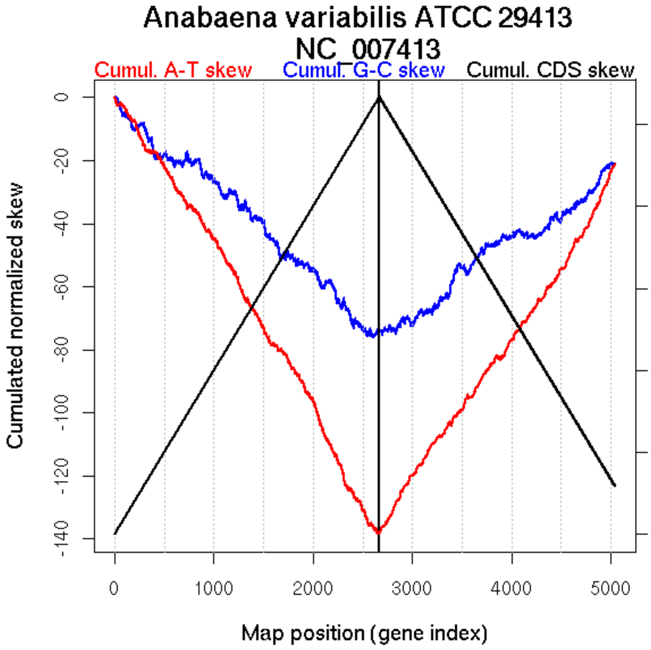
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	382 (916.798 kb)	lagging	-0.149
	383(917.7785 kb)	938 (2075.102 kb)	leading	-0.076
GC-skew reverse	939 (0 kb)	1429 (1024.1195 kb)	lagging	0.064
	1430(1025.4565 kb)	1876 (2075.102 kb)	leading	0.139
AT-skew forward	1 (0 kb)	421 (1021.4475 kb)	lagging	-0.216
	422(1022.5515 kb)	938 (2075.102 kb)	leading	-0.335
AT-skew reverse	939 (0 kb)	1437 (1041.2255 kb)	lagging	0.333
	1438(1047.2975 kb)	1876(2075.102 kb)	leading	0.215

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

15 Anabaena variabilis ATCC 29413

Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
Accession number: NC_007413; **Genome size (bp)**: 6365727.
Number of genes: 5043.
Oriloc predictions: Origin NA Terminus NA
Worning et al., 2006: Origin 416 kb Terminus 4350 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1.686 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.81 kb
Consensus predictions: Origin 0 kb Terminus 3250 kb

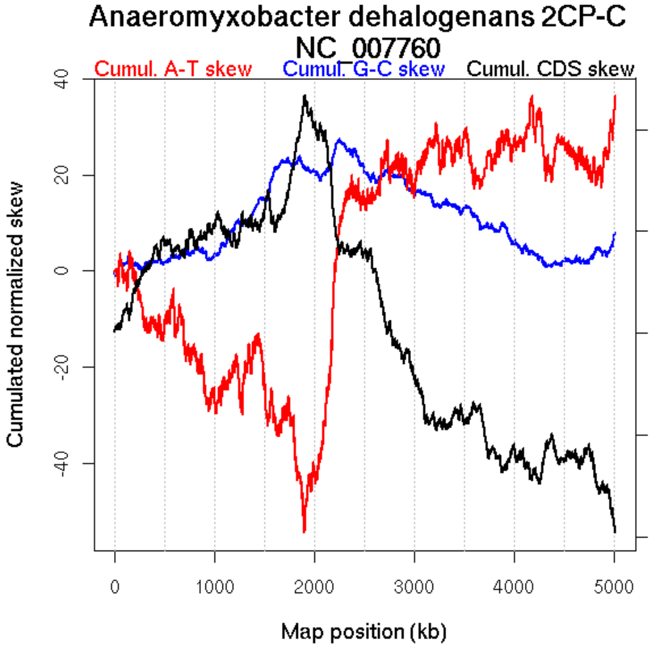


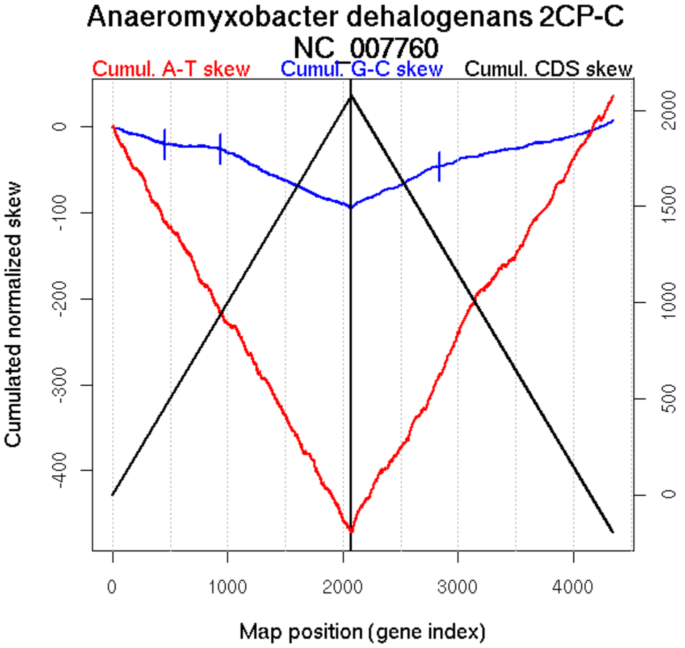


No significant breakpoints.

16 Anaeromyxobacter dehalogenans 2CP-C

Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales; Cystobacterineae; Myxococcaceae; Anaeromyxobacter.
Accession number: NC_007760; **Genome size (bp)**: 5013479.
Number of genes: 4346.
Oriloc predictions: Origin NA Terminus NA
Worning et al., 2006: Origin 3425 kb Terminus 1901 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 4753.998 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.71 kb
Consensus predictions: Origin 0 kb Terminus 2249 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	455	0.04667	934
	935	0.01333	1895
GC-skew reverse	2843	0	2004

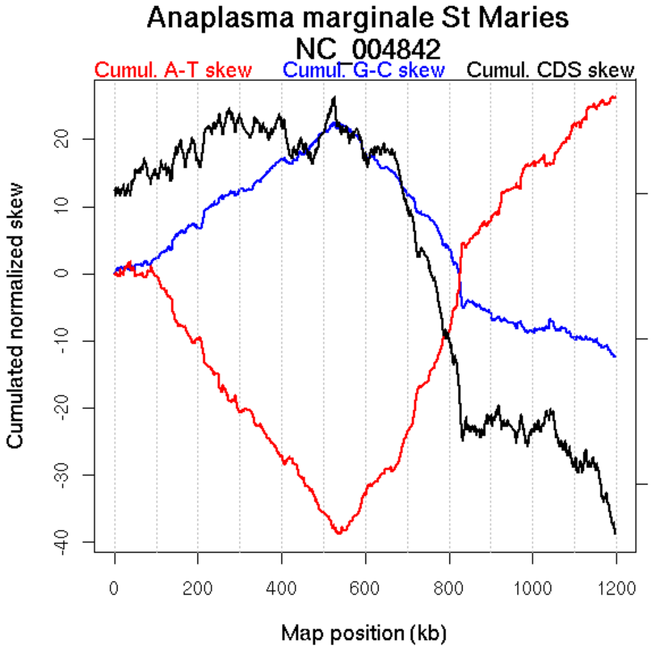
Segments:

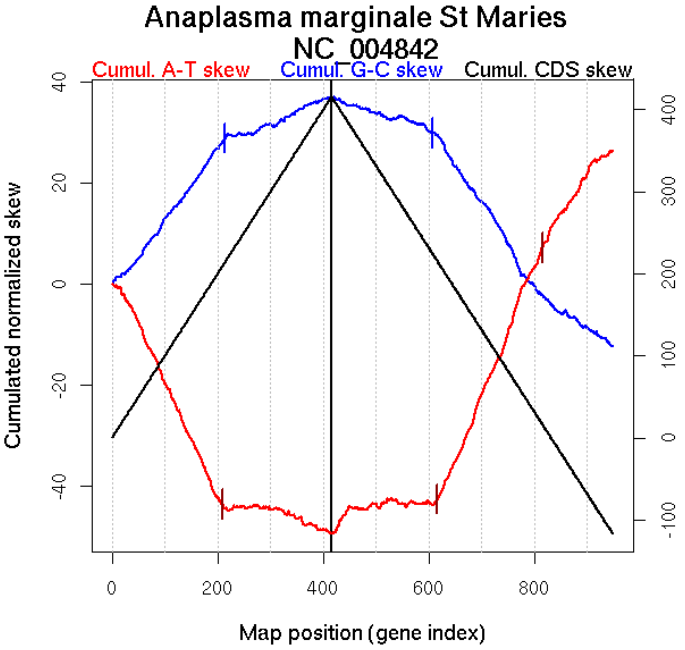
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	455 (933.5755 kb)	leading	-0.041
	456(934.6805 kb)	935 (1894.901 kb)	leading	-0.009
	936(1895.6405 kb)	2075 (5013.21 kb)	lagging	-0.061
GC-skew reverse	2076 (0 kb)	2843 (2003.79 kb)	leading	0.062
	2844(2004.3765 kb)	4346 (5013.21 kb)	lagging	0.031

More G than C on the leading strand for replication.

17 Anaplasma marginale St Maries

Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales; Anaplasmataceae; Anaplasma.
Accession number: NC_004842; **Genome size (bp)**: 1197687.
Number of genes: 949.
Oriloc predictions: Origin 0 kb Terminus 546 kb
Worning et al., 2006: Origin 1140 kb Terminus 532 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 392.565 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 390.23 kb
Consensus predictions: Origin 0 kb Terminus 546 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	214	0.00667	537
GC-skew reverse	607	0	538
AT-skew forward	209	0	522
AT-skew reverse	616	0	557
	815	0.04667	931

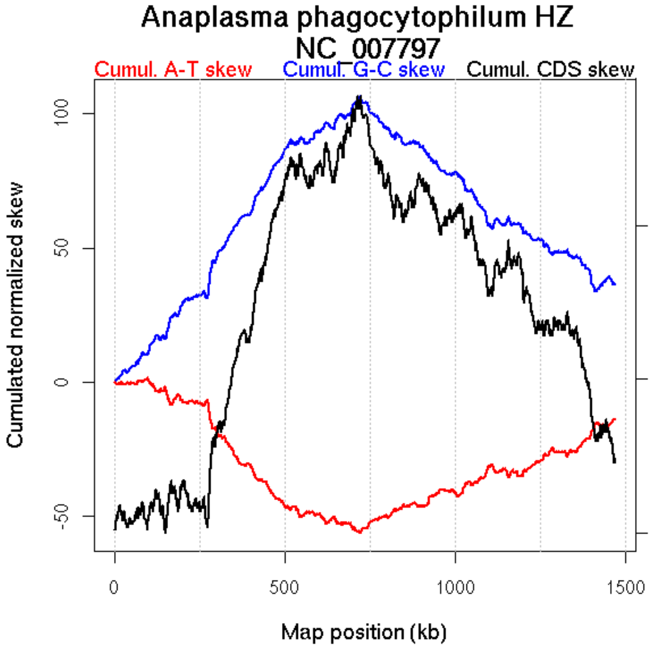
Segments:

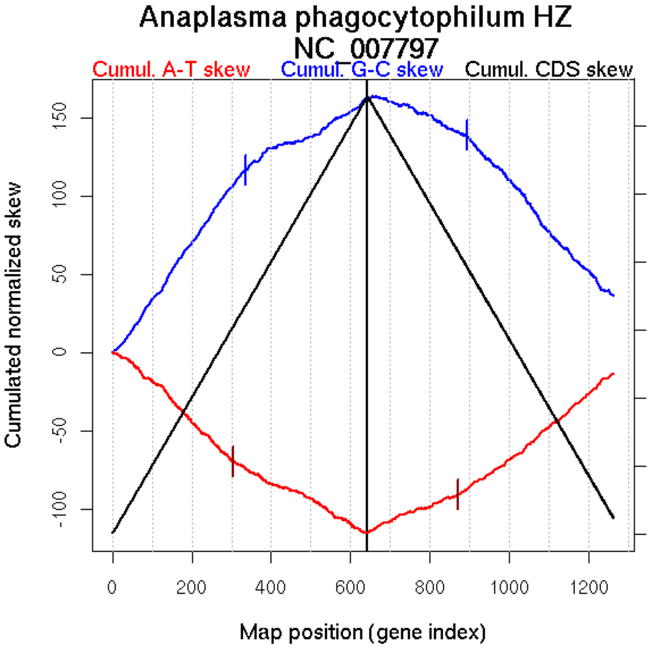
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	214 (536.705 kb)	leading	0.139
	215(539.844 kb)	416 (1197.306 kb)	lagging	0.044
GC-skew reverse	417 (0 kb)	607 (537.612 kb)	leading	-0.031
	608(539.3305 kb)	949 (1197.306 kb)	lagging	-0.13
AT-skew forward	1 (0 kb)	209 (522.2575 kb)	leading	-0.223
	210(523.7105 kb)	416 (1197.306 kb)	lagging	-0.026
AT-skew reverse	417 (0 kb)	616 (557.142 kb)	leading	0.019
	617(558.1065 kb)	815(930.8425 kb)	lagging	0.257
	816(932.4595 kb)	949(1197.306 kb)	lagging	0.148

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

18 Anaplasma phagocytophilum HZ

Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales; Anaplasmataceae; Anaplasma; phagocytophilum group.
Accession number: NC_007797; **Genome size (bp)**: 1471282.
Number of genes: 1263.
Oriloc predictions: Origin 0 kb Terminus 724 kb
Worning et al., 2006: Origin 1468 kb Terminus 724 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 20.704 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 502.5 kb
Consensus predictions: Origin 0 kb Terminus 724 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	335	NA	620
GC-skew reverse	893	NA	722
AT-skew forward	303	NA	548
AT-skew reverse	870	NA	652

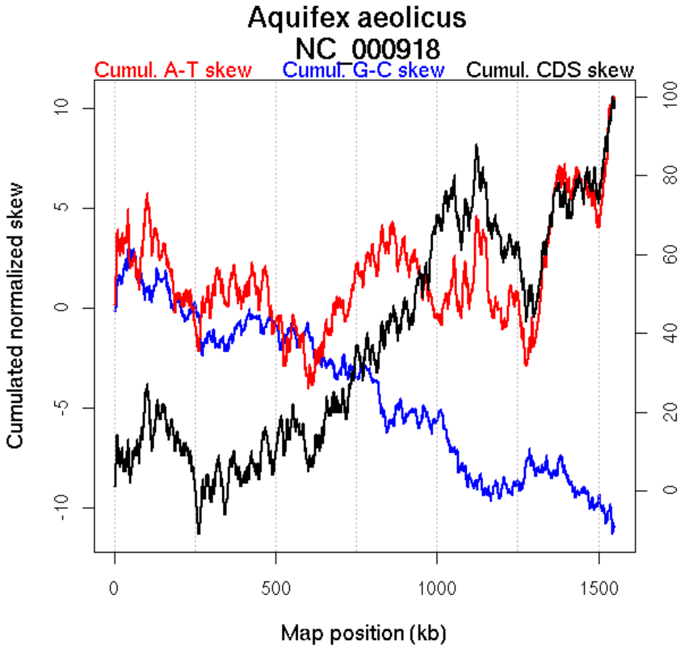
Segments:

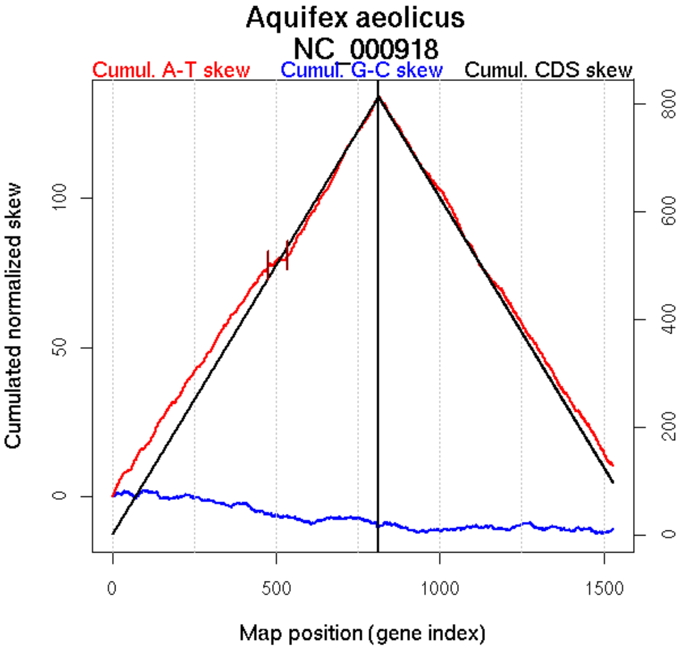
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	335 (619.997 kb)	leading	0.363
	336(620.393 kb)	643 (1471.214 kb)	NA	0.13
GC-skew reverse	644 (0 kb)	893 (722.036 kb)	leading	-0.108
	894(725.158 kb)	1263 (1471.214 kb)	lagging	-0.288
AT-skew forward	1 (0 kb)	303 (548.4695 kb)	leading	-0.242
	304(555.334 kb)	643 (1471.214 kb)	NA	-0.132
AT-skew reverse	644 (0 kb)	870 (651.706 kb)	leading	0.102
	871(656.675 kb)	1263(1471.214 kb)	lagging	0.202

More T than A on the leading strand for replication - for reverse encoded genes.
More G than C on the leading strand for replication - for reverse encoded genes.

19 Aquifex aeolicus

Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
Accession number: NC_000918; **Genome size (bp)**: 1551335.
Number of genes: 1529.
Oriloc predictions: Origin NA Terminus NA
Worning et al., 2006: Origin 620 kb Terminus 135 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 167.138 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 209.24 kb
Consensus predictions: Origin 167 kb Terminus 827 kb





Significant breakpoints (p-value <0.05):

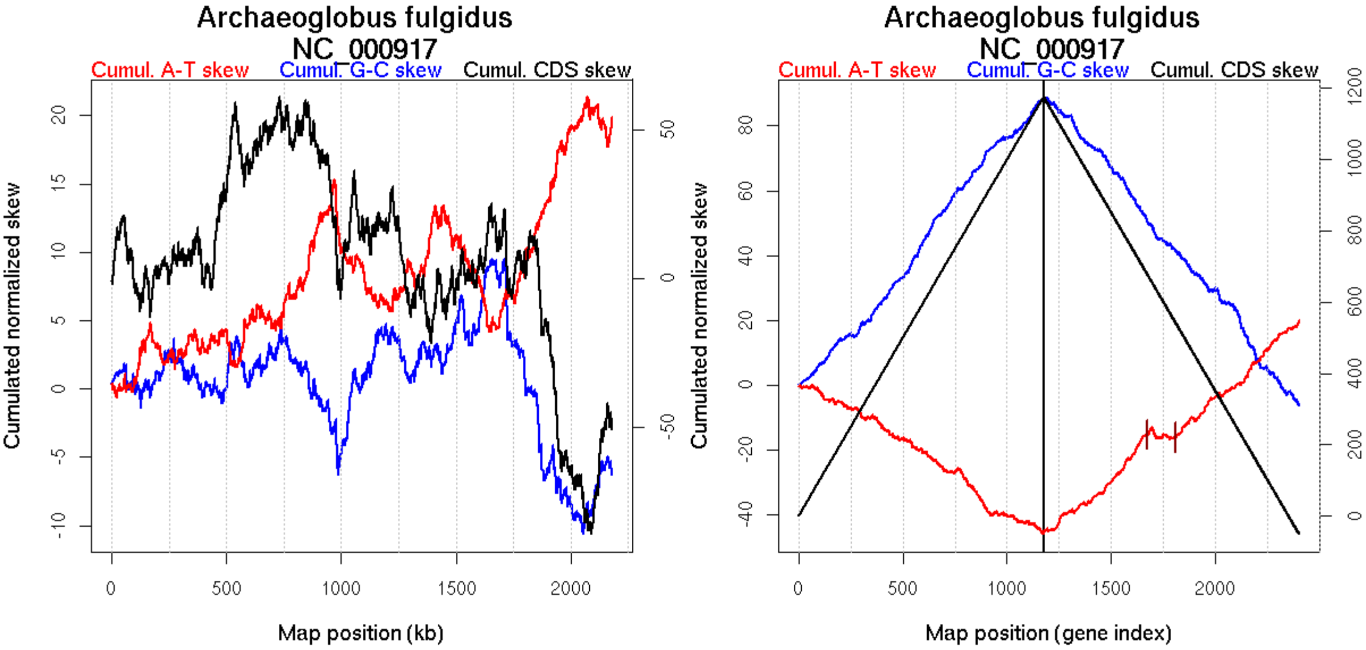
	Breakpoints	P-value	Chromosome coordinate (kb)
AT-skew forward	476	0.02333	926
	534	0	1018

Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
AT-skew forward	1 (0 kb)	476 (926.0125 kb)	NA	0.162
	477(927.7965 kb)	534 (1017.9545 kb)	lagging	0.048
	535(1019.07 kb)	813 (1551.092 kb)	lagging	0.193

20 Archaeoglobus fulgidus

Archaea; Euryarchaeota; Archaeoglobi; Archaeoglobales; Archaeoglobaceae; Archaeoglobus.
Accession number: NC_000917; **Genome size (bp)**: 2178400.
Number of genes: 2403.
Oriloc predictions: Origin NA Terminus NA
Worning et al., 2006: Origin 1682 kb Terminus 539 kb
Position(s) of the ORC/Cdc6 gene(s): 220.31 kb, 473.3 kb, 628.53 kb, 1145.3 kb, 1158 kb, 1888.65 kb
Consensus predictions: Origin NA Terminus NA



Significant breakpoints (p-value <0.05):

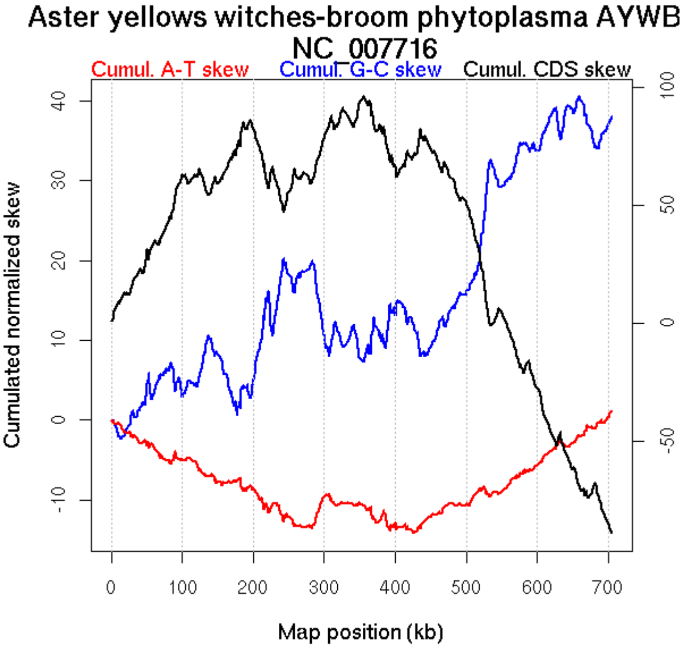
	Breakpoints	P-value	Chromosome coordinate (kb)
AT-skew reverse	1672	0.04	948
	1808	0.04	1158

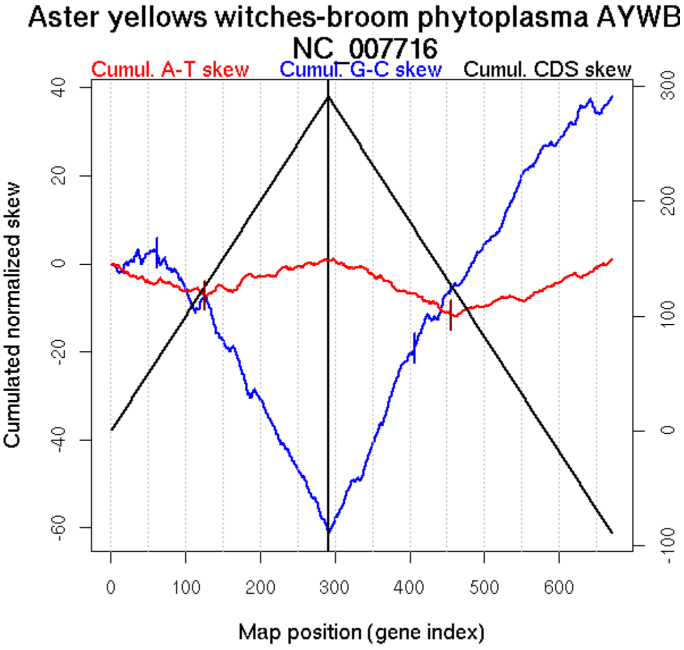
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
AT-skew reverse	1177 (0 kb)	1672 (947.752 kb)	NA	0.059
	1673(948.916 kb)	1808(1157.736 kb)	NA	-0.016
	1809(1158.364 kb)	2403(2178.146 kb)	NA	0.06

21 Aster yellows witches-broom phytoplasma AYWB

Bacteria; Firmicutes; Mollicutes; Acholeplasmatales; Acholeplasmataceae; Candidatus Phytoplasma; Candidatus Phytoplasma asteris.
Accession number: NC_007716; **Genome size (bp)**: 706569.
Number of genes: 671.
Oriloc predictions: Origin 0 kb Terminus 393 kb
Worning et al., 2006: Origin 705 kb Terminus 446 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 149.369 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.76 kb, 81.68 kb
Consensus predictions: Origin 0 kb Terminus 393 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	61	0.02	88
GC-skew reverse	406	0	337
AT-skew forward	126	0.02667	191
AT-skew reverse	456	0	402

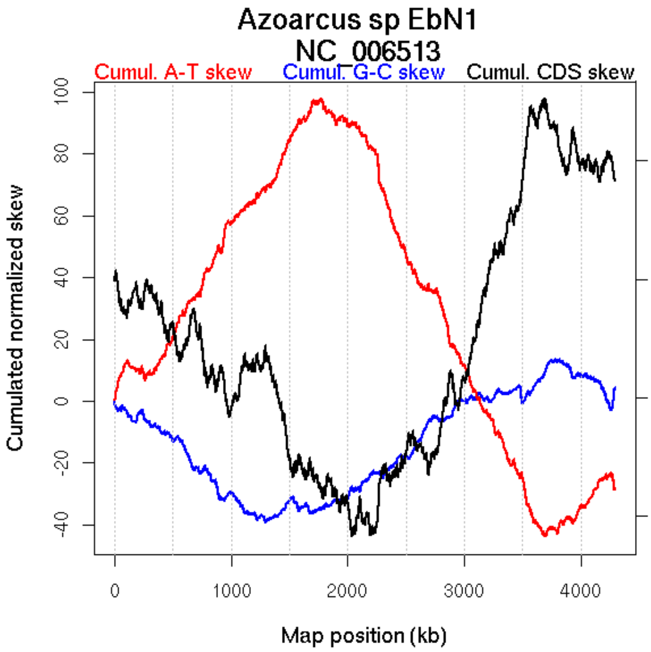
Segments:

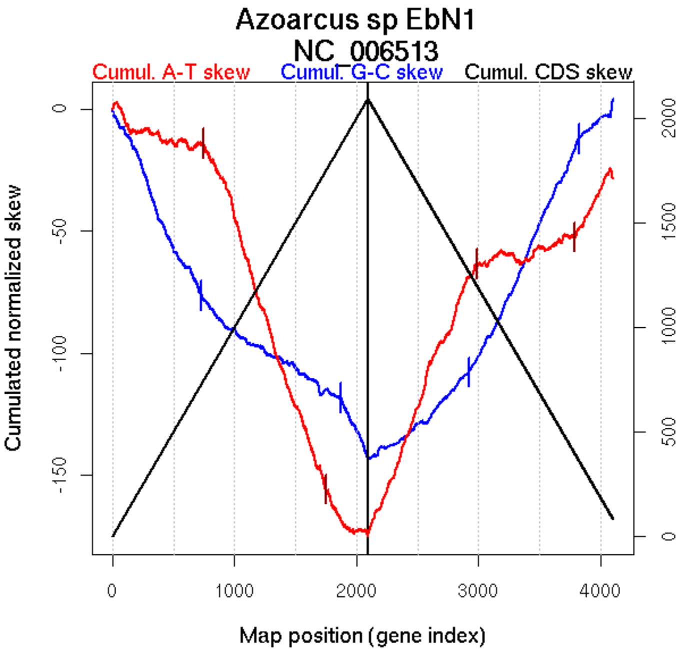
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	61 (87.868 kb)	leading	0.076
	62(88.4665 kb)	291 (705.696 kb)	NA	-0.276
GC-skew reverse	292 (0 kb)	406 (336.9875 kb)	leading	0.384
	407(338.89 kb)	671 (705.696 kb)	lagging	0.227
AT-skew forward	1 (0 kb)	126 (191.3645 kb)	leading	-0.048
	127(192.708 kb)	291 (705.696 kb)	NA	0.047
AT-skew reverse	292 (0 kb)	456 (401.617 kb)	leading	-0.078
	457(407.615 kb)	671(705.696 kb)	lagging	0.056

More T than A on the leading strand for replication - for reverse encoded genes.
More G than C on the leading strand for replication - for reverse encoded genes.

22 Azoarcus sp EbN1

Bacteria; Proteobacteria; Betaproteobacteria; Rhodocyclales; Rhodocyclaceae; Azoarcus.
Accession number: NC_006513; **Genome size (bp)**: 4296230.
Number of genes: 4104.
Oriloc predictions: Origin 1767 kb Terminus 3790 kb
Worning et al., 2006: Origin 1791 kb Terminus 3689 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1678.007 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1694.68 kb
Consensus predictions: Origin 1767 kb Terminus 3790 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	728	0.00667	1728
	1868	0.00667	3764
GC-skew reverse	2921	0.01333	1596
	3825	0.01333	3745
AT-skew forward	742	0	1766
	1747	0.00667	3540
AT-skew reverse	2987	0	1725
	3792	0.01	3694

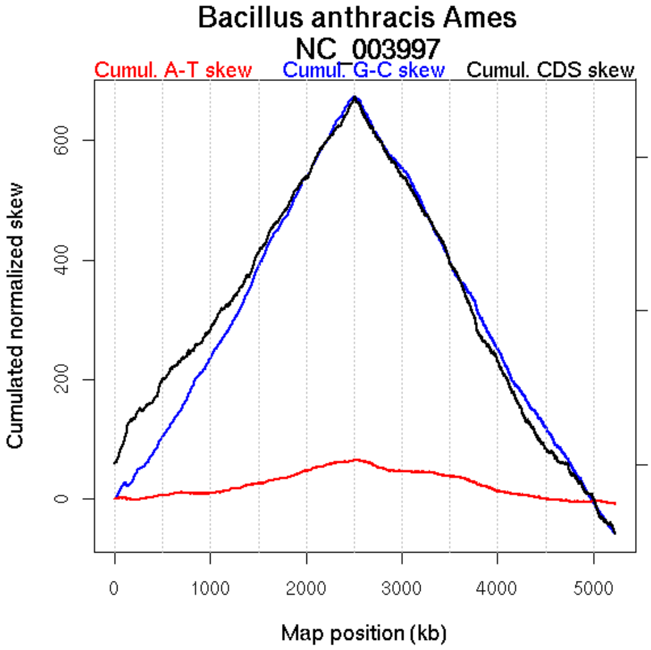
Segments:

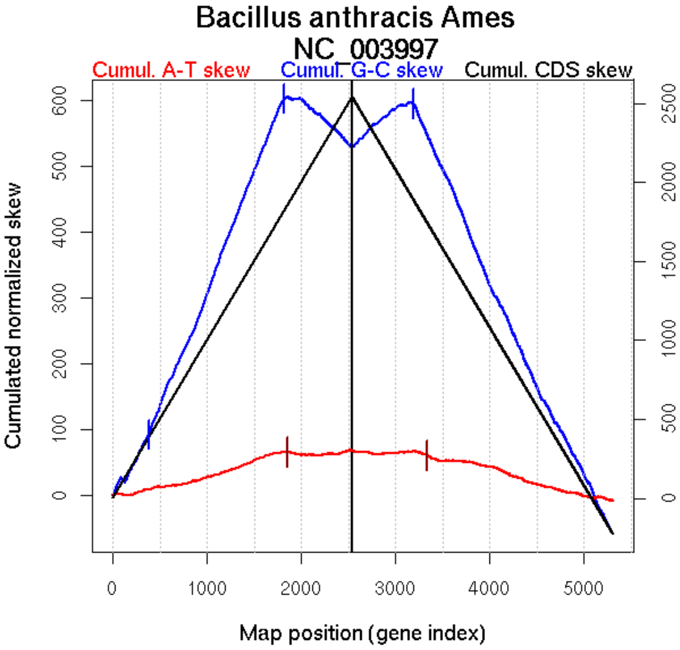
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	728 (1728.3005 kb)	lagging	-0.109
	729(1730.429 kb)	1868 (3764.391 kb)	leading	-0.034
	1869(3765.4115 kb)	2094 (4296.226 kb)	lagging	-0.103
GC-skew reverse	2095 (0 kb)	2921 (1596.304 kb)	lagging	0.043
	2922(1597.1375 kb)	3825 (3744.558 kb)	leading	0.109
	3826(3747.419 kb)	4104 (4296.226 kb)	lagging	0.042
AT-skew forward	1 (0 kb)	742 (1765.6785 kb)	lagging	-0.021
	743(1773.0925 kb)	1747 (3540.017 kb)	leading	-0.147
	1748(3540.3455 kb)	2094 (4296.226 kb)	NA	-0.049
AT-skew reverse	2095 (0 kb)	2987 (1724.932 kb)	lagging	0.129
	2988(1728.3575 kb)	3792(3693.6025 kb)	leading	0.014
	3793(3694.356 kb)	4104(4296.226 kb)	NA	0.093

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

23 Bacillus anthracis Ames

Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.
Accession number: NC_003997; **Genome size (bp)**: 5227293.
Number of genes: 5309.
Oriloc predictions: Origin 0 kb Terminus 2503 kb
Worning et al., 2006: Origin 1 kb Terminus 2506 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 5199.31 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1.08 kb
Consensus predictions: Origin 0 kb Terminus 2503 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	380	0.01667	513
	1824	0	2495
GC-skew reverse	3185	0	2513
AT-skew forward	1854	0.00667	2588
AT-skew reverse	3337	0.00667	2696

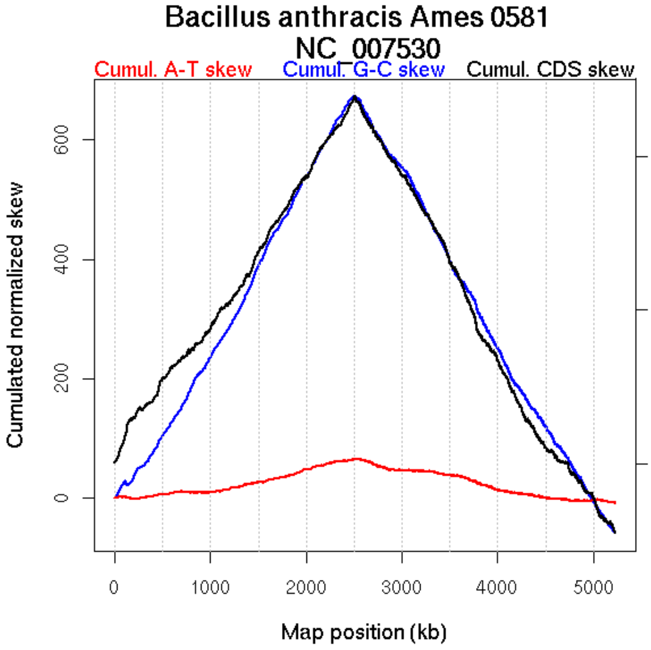
Segments:

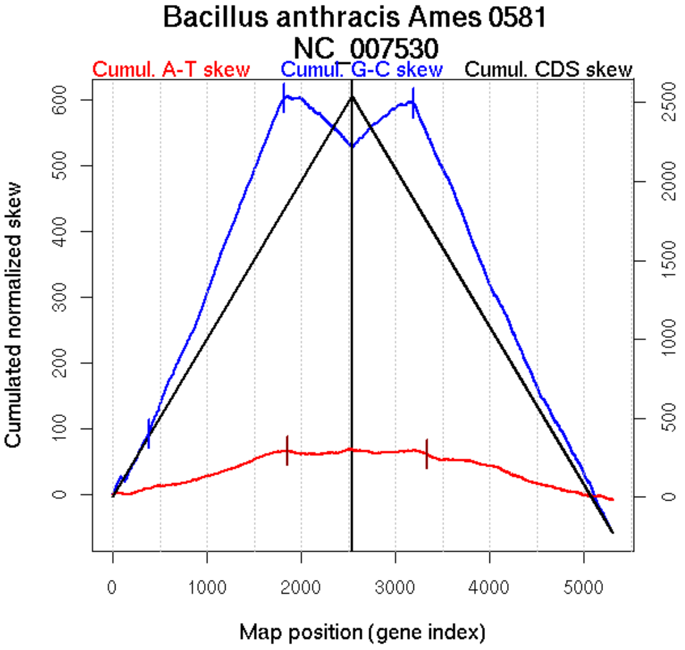
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	380 (513.29 kb)	leading	0.231
	381(514.404 kb)	1824 (2494.726 kb)	leading	0.36
	1825(2495.1445 kb)	2541 (5227.135 kb)	lagging	-0.114
GC-skew reverse	2542 (0 kb)	3185 (2512.6575 kb)	leading	0.111
	3186(2513.8755 kb)	5309 (5227.135 kb)	lagging	-0.311
AT-skew forward	1 (0 kb)	1854 (2588.41 kb)	leading	0.039
	1855(2592.57 kb)	2541 (5227.135 kb)	lagging	0.005
AT-skew reverse	2542 (0 kb)	3337 (2696.231 kb)	NA	-0.001
	3338(2696.93 kb)	5309(5227.135 kb)	lagging	-0.038

More A than T on the leading strand for replication - for forward encoded genes.
More G than C on the leading strand for replication.

24 Bacillus anthracis Ames 0581

Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.
Accession number: NC_007530; **Genome size (bp)**: 5227419.
Number of genes: 5307.
Oriloc predictions: Origin 0 kb Terminus 2503 kb
Worning et al., 2006: Origin 1 kb Terminus 2506 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 5199.436 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1.08 kb
Consensus predictions: Origin 0 kb Terminus 2503 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	380	NA	513
	1823	NA	2495
GC-skew reverse	3184	NA	2513
AT-skew forward	1853	NA	2589
AT-skew reverse	3335	NA	2696

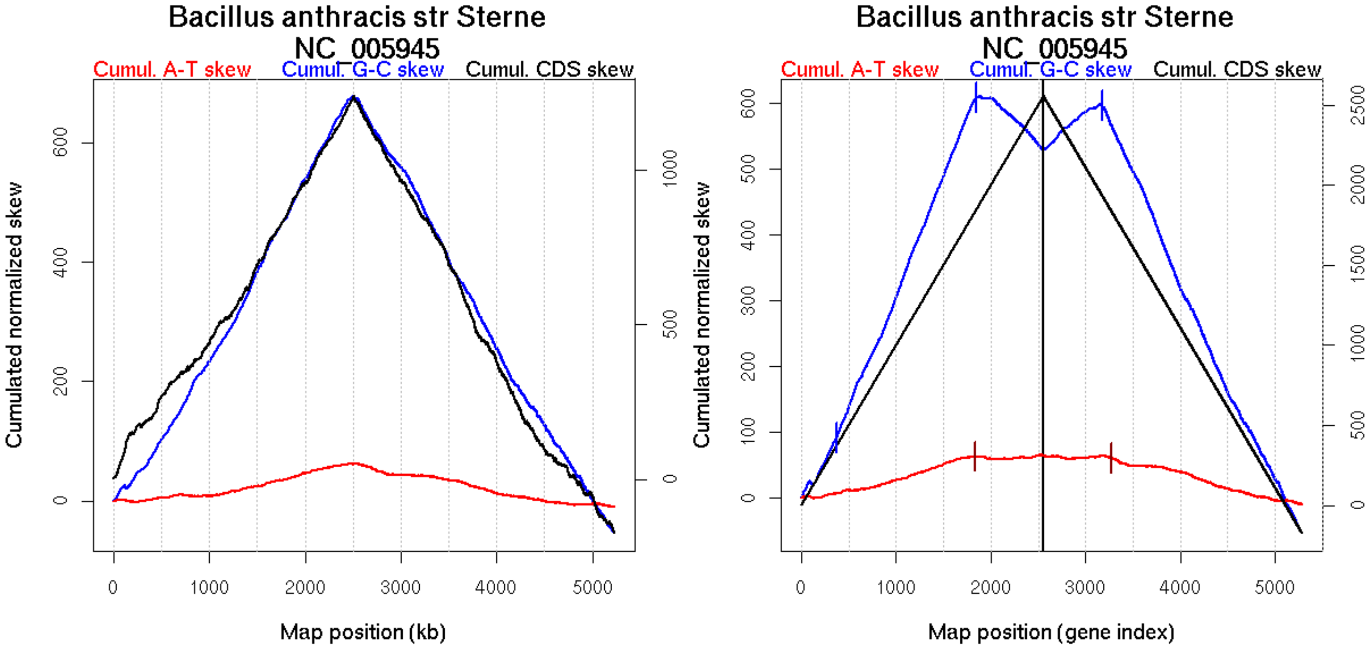
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	380 (513.29 kb)	leading	0.231
	381(514.404 kb)	1823 (2494.85 kb)	leading	0.36
	1824(2495.2685 kb)	2540 (5227.261 kb)	lagging	-0.114
GC-skew reverse	2541 (0 kb)	3184 (2512.7815 kb)	leading	0.111
	3185(2513.9995 kb)	5307 (5227.261 kb)	lagging	-0.311
AT-skew forward	1 (0 kb)	1853 (2588.534 kb)	leading	0.039
	1854(2592.694 kb)	2540 (5227.261 kb)	lagging	0.005
AT-skew reverse	2541 (0 kb)	3335 (2696.359 kb)	NA	-0.001
	3336(2697.058 kb)	5307(5227.261 kb)	lagging	-0.038

More A than T on the leading strand for replication - for forward encoded genes.
More G than C on the leading strand for replication.

25 Bacillus anthracis str Sterne

Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.
Accession number: NC_005945; **Genome size (bp)**: 5228663.
Number of genes: 5286.
Oriloc predictions: Origin 0 kb Terminus 2489 kb
Worning et al., 2006: Origin 1 kb Terminus 2507 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 5200.681 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1.08 kb
Consensus predictions: Origin 0 kb Terminus 2489 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	373	NA	510
	1844	NA	2495
GC-skew reverse	3173	NA	2498
AT-skew forward	1833	NA	2480
AT-skew reverse	3278	NA	2629

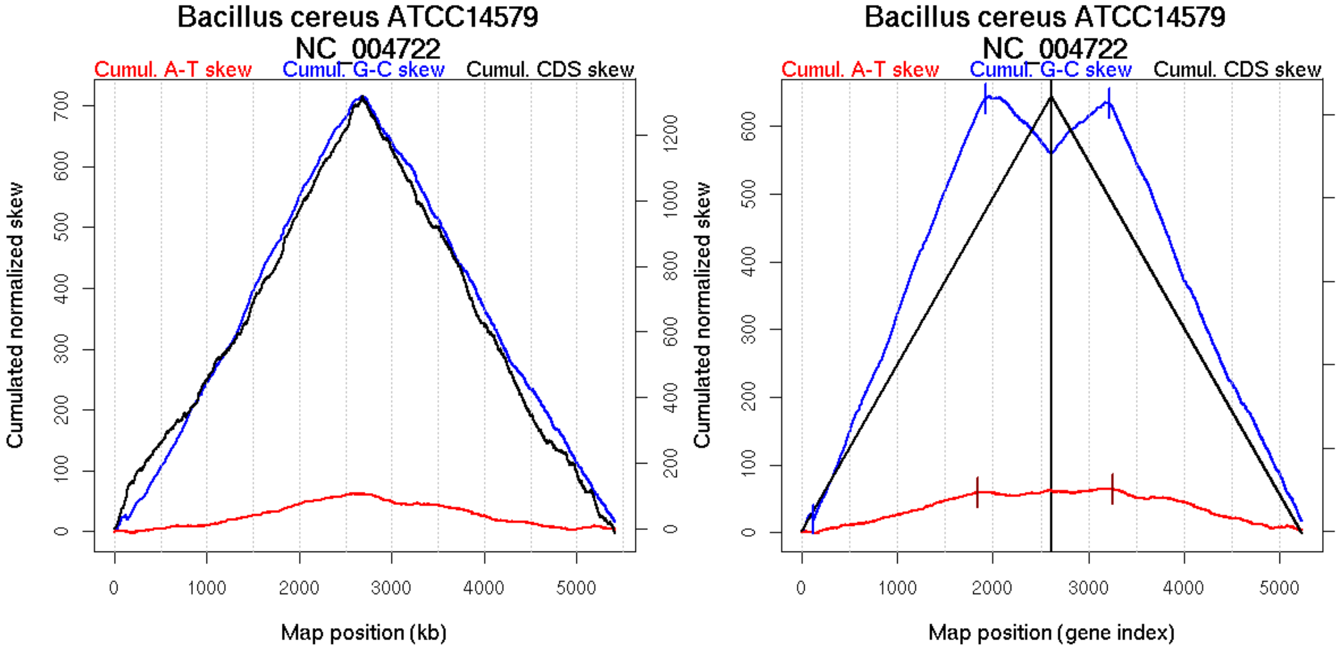
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	373 (510.0975 kb)	leading	0.236
	374(512.7405 kb)	1844 (2494.7715 kb)	leading	0.355
	1845(2495.1975 kb)	2556 (5228.506 kb)	lagging	-0.121
GC-skew reverse	2557 (0 kb)	3173 (2497.537 kb)	leading	0.118
	3174(2506.3505 kb)	5286 (5228.506 kb)	lagging	-0.312
AT-skew forward	1 (0 kb)	1833 (2479.965 kb)	leading	0.038
	1834(2481.8915 kb)	2556 (5228.506 kb)	lagging	0.003
AT-skew reverse	2557 (0 kb)	3278 (2629.2945 kb)	leading	0
	3279(2630.271 kb)	5286(5228.506 kb)	lagging	-0.037

More A than T on the leading strand for replication.
More G than C on the leading strand for replication.

26 Bacillus cereus ATCC14579

Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.
Accession number: NC_004722; **Genome size (bp)**: 5411809.
Number of genes: 5234.
Oriloc predictions: Origin 0 kb Terminus 2676 kb
Worning et al., 2006: Origin 1 kb Terminus 2681 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 5383.817 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.95 kb, 4525.58 kb
Consensus predictions: Origin 0 kb Terminus 2676 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	124	NA	141
	1927	NA	2677
GC-skew reverse	3213	NA	2631
AT-skew forward	1837	NA	2547
AT-skew reverse	3252	NA	2720

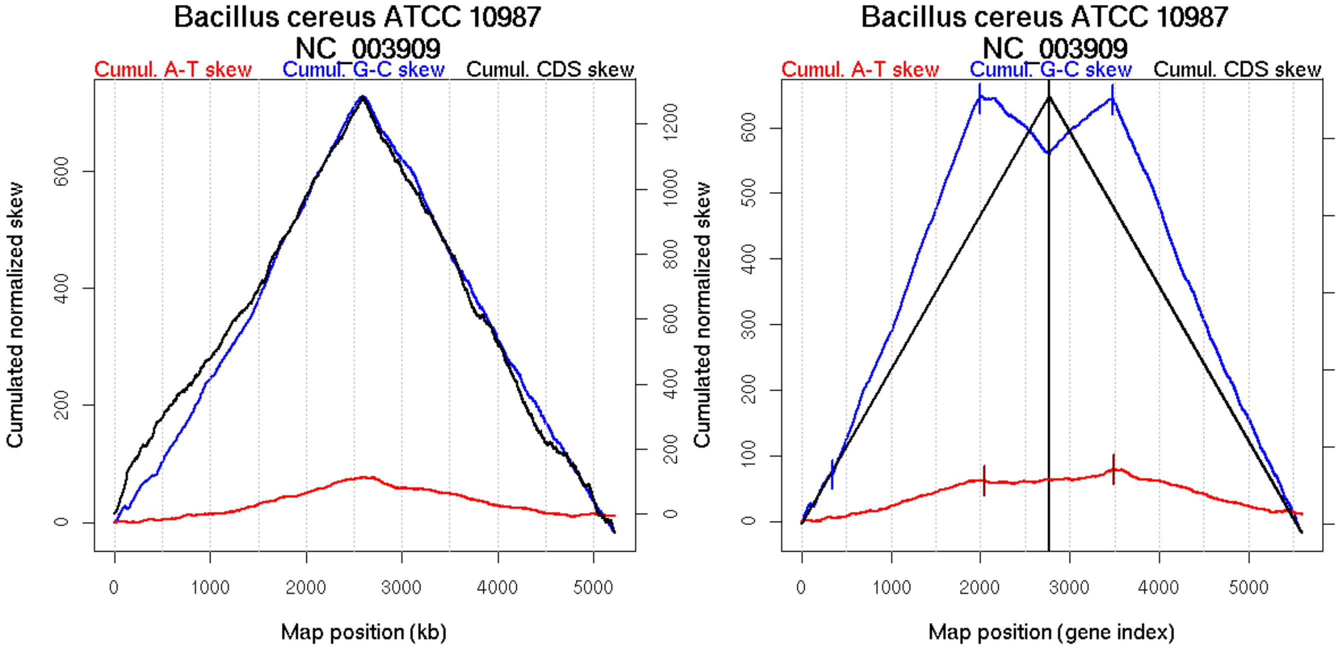
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	124 (140.7915 kb)	leading	0.2
	125(141.2235 kb)	1927 (2677.208 kb)	leading	0.355
	1928(2678.8765 kb)	2610 (5411.527 kb)	lagging	-0.133
GC-skew reverse	2611 (0 kb)	3213 (2631.3125 kb)	leading	0.125
	3214(2632.799 kb)	5234 (5411.527 kb)	lagging	-0.31
AT-skew forward	1 (0 kb)	1837 (2546.794 kb)	leading	0.034
	1838(2547.121 kb)	2610 (5411.527 kb)	lagging	0.002
AT-skew reverse	2611 (0 kb)	3252 (2719.717 kb)	leading	0.008
	3253(2722.8415 kb)	5234(5411.527 kb)	lagging	-0.032

More A than T on the leading strand for replication.
More G than C on the leading strand for replication.

27 Bacillus cereus ATCC 10987

Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.
Accession number: NC_003909; **Genome size (bp)**: 5224283.
Number of genes: 5600.
Oriloc predictions: Origin 0 kb Terminus 2575 kb
Worning et al., 2006: Origin 2 kb Terminus 2590 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 5196.309 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1.08 kb
Consensus predictions: Origin 0 kb Terminus 2575 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	345	NA	432
	1995	NA	2602
GC-skew reverse	3478	NA	2582
AT-skew forward	2041	NA	2755
AT-skew reverse	3495	NA	2604

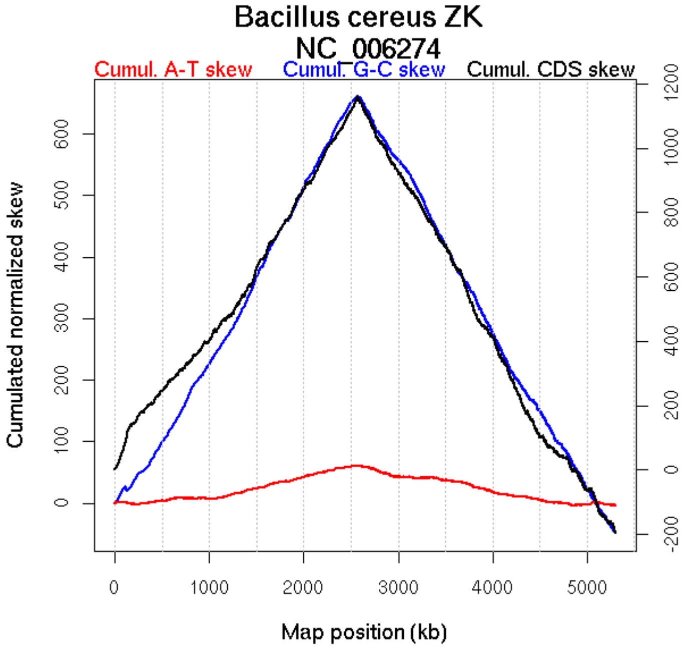
Segments:

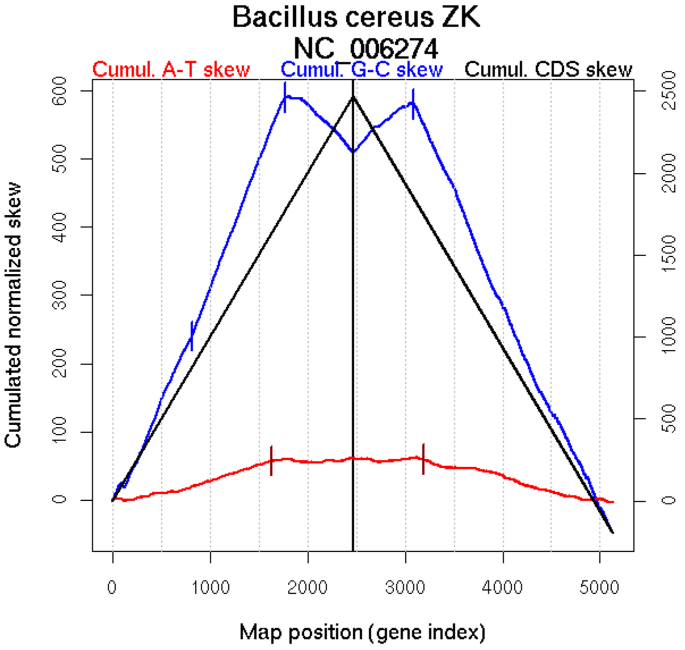
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	345 (431.9995 kb)	leading	0.212
	346(432.4325 kb)	1995 (2602.2435 kb)	leading	0.353
	1996(2605.729 kb)	2771 (5224.125 kb)	lagging	-0.12
GC-skew reverse	2772 (0 kb)	3478 (2581.7965 kb)	leading	0.117
	3479(2589.113 kb)	5600 (5224.125 kb)	lagging	-0.316
AT-skew forward	1 (0 kb)	2041 (2755.447 kb)	leading	0.034
	2042(2756.0725 kb)	2771 (5224.125 kb)	lagging	0.004
AT-skew reverse	2772 (0 kb)	3495 (2603.886 kb)	leading	0.02
	3496(2605.107 kb)	5600(5224.125 kb)	lagging	-0.034

More A than T on the leading strand for replication.
More G than C on the leading strand for replication.

28 Bacillus cereus ZK

Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.
Accession number: NC_006274; **Genome size (bp)**: 5300915.
Number of genes: 5134.
Oriloc predictions: Origin 0 kb Terminus 2557 kb
Worning et al., 2006: Origin 0 kb Terminus 2572 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 5273.051 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1.08 kb
Consensus predictions: Origin 0 kb Terminus 2557 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	817	NA	1265
	1771	NA	2563
GC-skew reverse	3088	NA	2555
AT-skew forward	1633	NA	2373
AT-skew reverse	3185	NA	2681

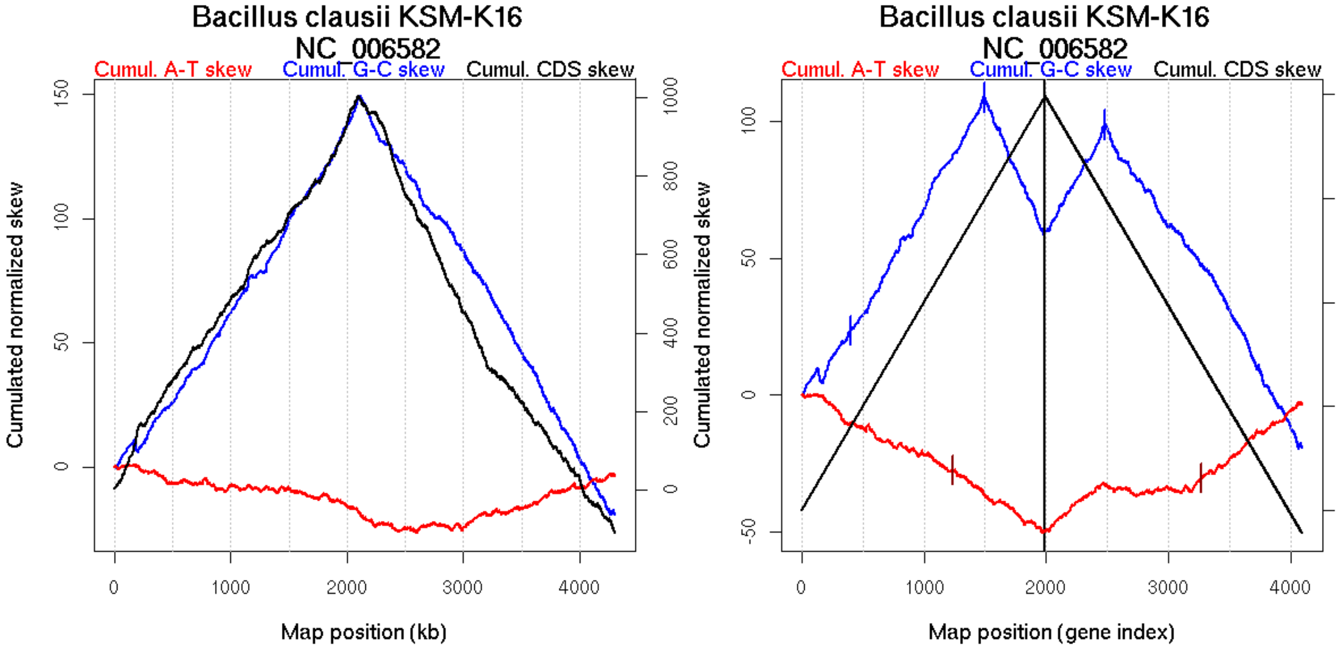
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	817 (1264.878 kb)	leading	0.314
	818(1265.355 kb)	1771 (2562.592 kb)	leading	0.372
	1772(2562.9585 kb)	2469 (5300.757 kb)	lagging	-0.125
GC-skew reverse	2470 (0 kb)	3088 (2555.093 kb)	leading	0.118
	3089(2557.905 kb)	5134 (5300.757 kb)	lagging	-0.311
AT-skew forward	1 (0 kb)	1633 (2373.1535 kb)	leading	0.037
	1634(2376.467 kb)	2469 (5300.757 kb)	NA	0
AT-skew reverse	2470 (0 kb)	3185 (2681.4695 kb)	leading	0.002
	3186(2682.446 kb)	5134(5300.757 kb)	lagging	-0.034

More A than T on the leading strand for replication - for reverse encoded genes.
More G than C on the leading strand for replication.

29 Bacillus clausii KSM-K16

Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
Accession number: NC_006582; **Genome size (bp)**: 4303871.
Number of genes: 4095.
Oriloc predictions: Origin 0 kb Terminus 2110 kb
Worning et al., 2006: Origin 0 kb Terminus 2097 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 3562.847 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.86 kb, 2177.89 kb, 2834.86 kb
Consensus predictions: Origin 0 kb Terminus 2110 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	397	NA	555
	1496	NA	2143
GC-skew reverse	2483	NA	2112
AT-skew forward	1234	NA	1806
AT-skew reverse	3267	NA	3094

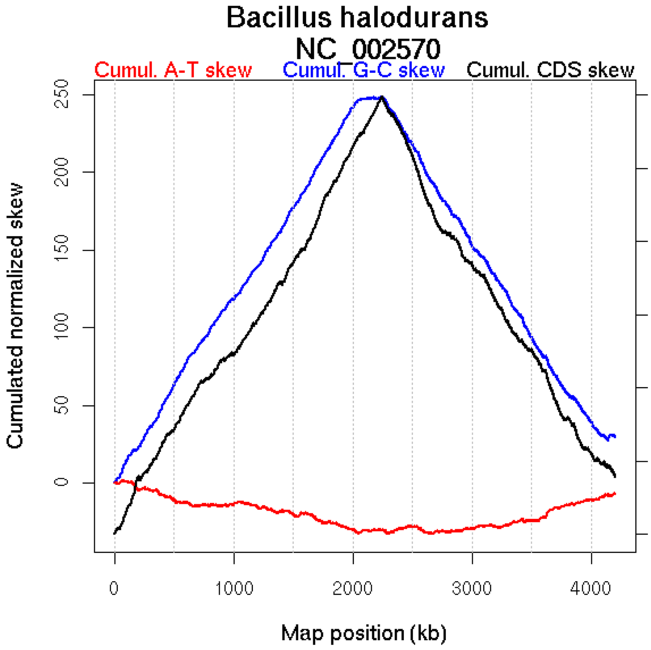
Segments:

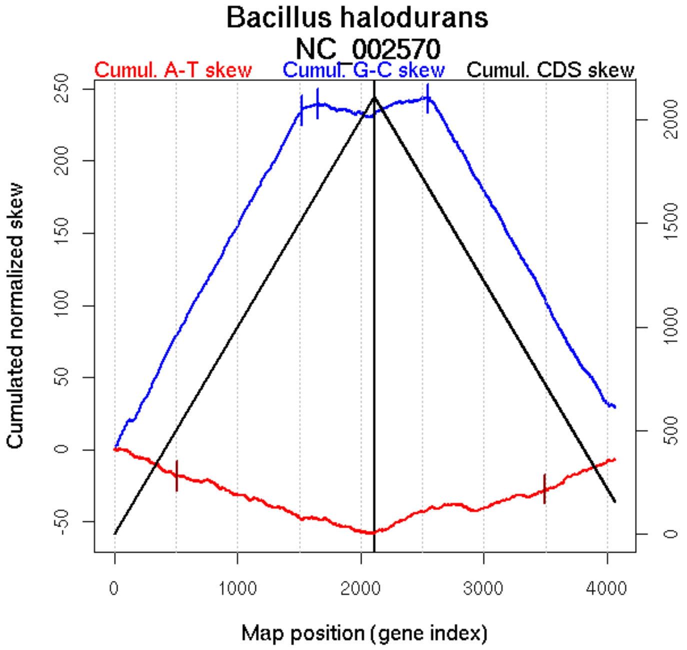
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	397 (554.9855 kb)	leading	0.055
	398(555.668 kb)	1496 (2143.1175 kb)	leading	0.079
	1497(2145.9975 kb)	1992 (4303.523 kb)	lagging	-0.101
GC-skew reverse	1993 (0 kb)	2483 (2111.7725 kb)	leading	0.078
	2484(2112.5385 kb)	4095 (4303.523 kb)	lagging	-0.071
AT-skew forward	1 (0 kb)	1234 (1806.2185 kb)	leading	-0.024
	1235(1808.407 kb)	1992 (4303.523 kb)	NA	-0.03
AT-skew reverse	1993 (0 kb)	3267 (3093.7655 kb)	NA	0.009
	3268(3095.159 kb)	4095(4303.523 kb)	lagging	0.035

More G than C on the leading strand for replication.

30 Bacillus halodurans

Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
Accession number: NC_002570; **Genome size (bp)**: 4202352.
Number of genes: 4065.
Oriloc predictions: Origin 0 kb Terminus 2239 kb
Worning et al., 2006: Origin 2 kb Terminus 2243 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 496.824 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1.26 kb, 3261.12 kb
Consensus predictions: Origin 0 kb Terminus 2239 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1521	NA	2054
	1650	NA	2238
GC-skew reverse	2549	NA	2064
AT-skew forward	504	NA	677
AT-skew reverse	3493	NA	3420

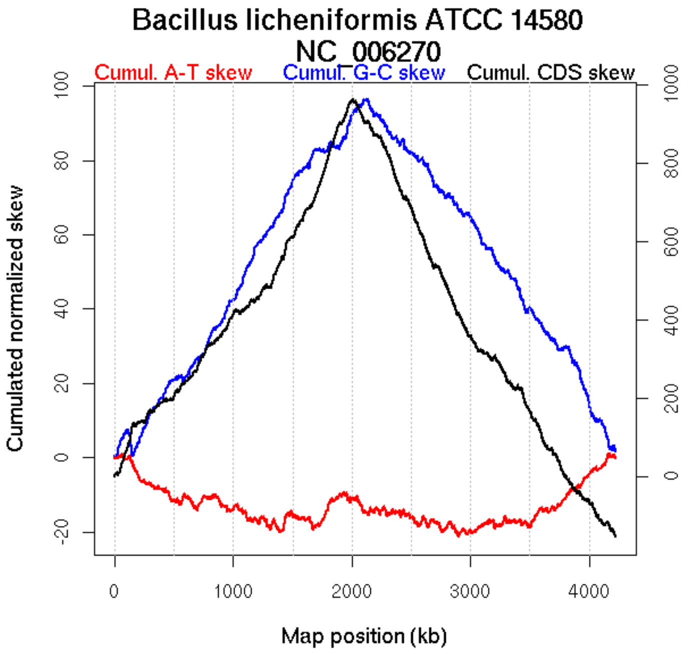
Segments:

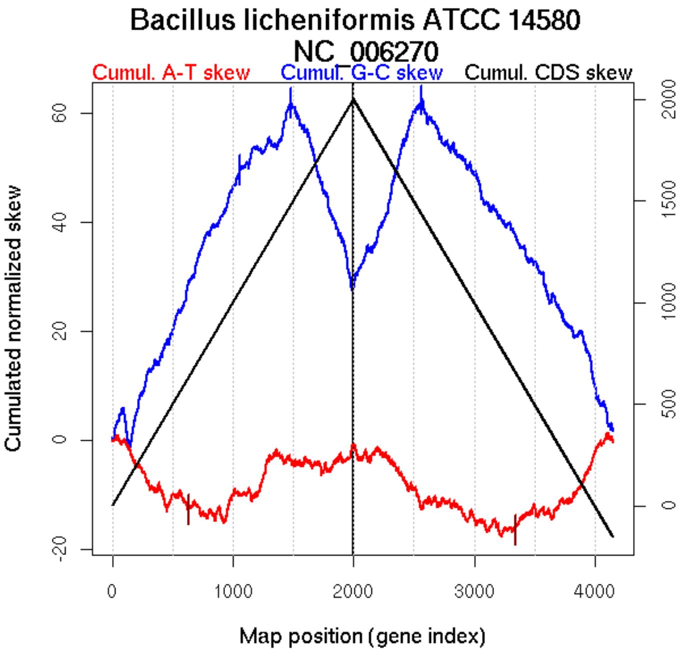
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1521 (2054.137 kb)	leading	0.155
	1522(2055.8855 kb)	1650 (2237.8505 kb)	leading	0.028
	1651(2238.925 kb)	2111 (4202.338 kb)	lagging	-0.019
GC-skew reverse	2112 (0 kb)	2549 (2064.4105 kb)	leading	0.022
	2550(2065.255 kb)	4065 (4202.338 kb)	lagging	-0.149
AT-skew forward	1 (0 kb)	504 (677.206 kb)	leading	-0.04
	505(678.3605 kb)	2111 (4202.338 kb)	NA	-0.027
AT-skew reverse	2112 (0 kb)	3493 (3419.768 kb)	NA	0.017
	3494(3420.614 kb)	4065(4202.338 kb)	lagging	0.039

More G than C on the leading strand for replication.

31 Bacillus licheniformis ATCC 14580

Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
Accession number: NC_006270; **Genome size (bp)**: 4222334.
Number of genes: 4152.
Oriloc predictions: Origin 0 kb Terminus 2118 kb
Worning et al., 2006: Origin 1 kb Terminus 2010 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 3842.647 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): NA
Consensus predictions: Origin 0 kb Terminus 2118 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1057	NA	1540
	1474	NA	2122
GC-skew reverse	2558	NA	2099
AT-skew forward	629	NA	954
AT-skew reverse	3340	NA	3047

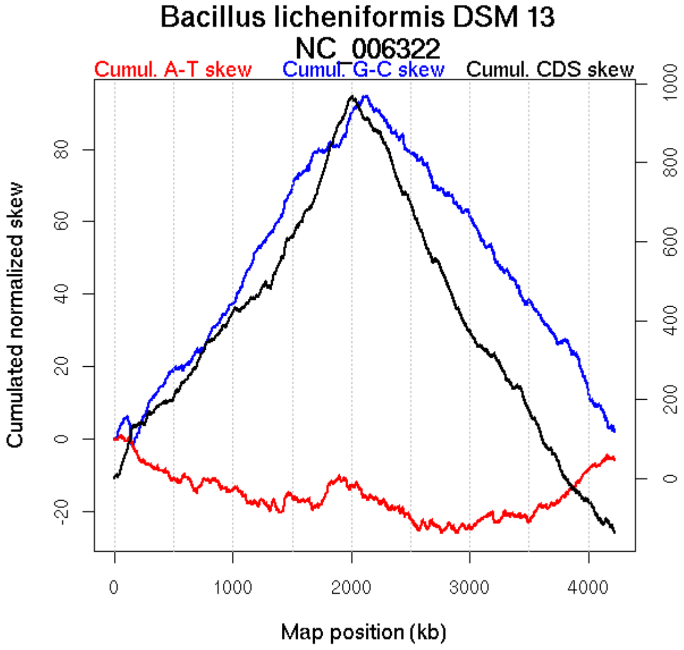
Segments:

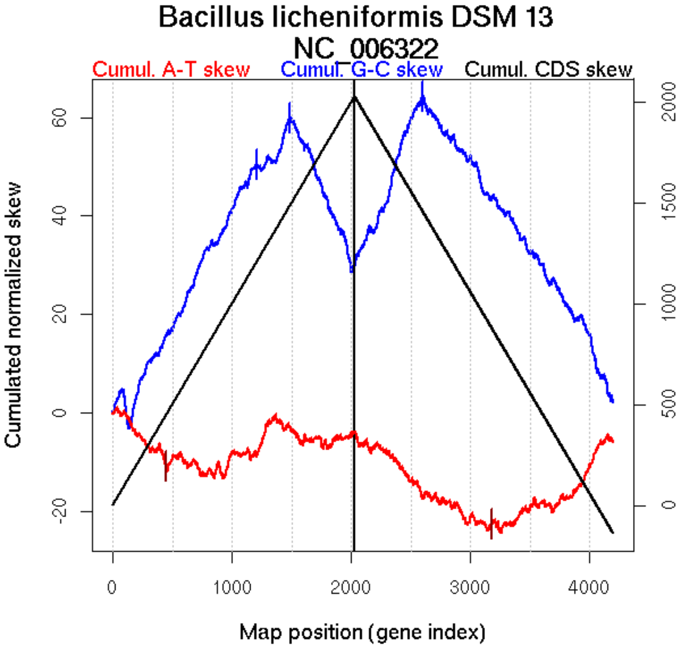
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1057 (1540.473 kb)	leading	0.049
	1058(1541.701 kb)	1474 (2121.938 kb)	leading	0.021
	1475(2123.662 kb)	1999 (4222.201 kb)	lagging	-0.066
GC-skew reverse	2000 (0 kb)	2558 (2099.24 kb)	leading	0.065
	2559(2100.594 kb)	4152 (4222.201 kb)	lagging	-0.035
AT-skew forward	1 (0 kb)	629 (953.544 kb)	leading	-0.022
	630(955.2415 kb)	1999 (4222.201 kb)	NA	0.009
AT-skew reverse	2000 (0 kb)	3340 (3046.995 kb)	NA	-0.013
	3341(3049.702 kb)	4152(4222.201 kb)	lagging	0.02

More G than C on the leading strand for replication.

32 Bacillus licheniformis DSM 13

Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
Accession number: NC_006322; **Genome size (bp)**: 4222645.
Number of genes: 4196.
Oriloc predictions: Origin 0 kb Terminus 2119 kb
Worning et al., 2006: Origin 0 kb Terminus 2013 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 3842.814 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.98 kb
Consensus predictions: Origin 0 kb Terminus 2119 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1206	NA	1724
	1484	NA	2122
GC-skew reverse	2595	NA	2101
AT-skew forward	448	NA	675
AT-skew reverse	3181	NA	2809

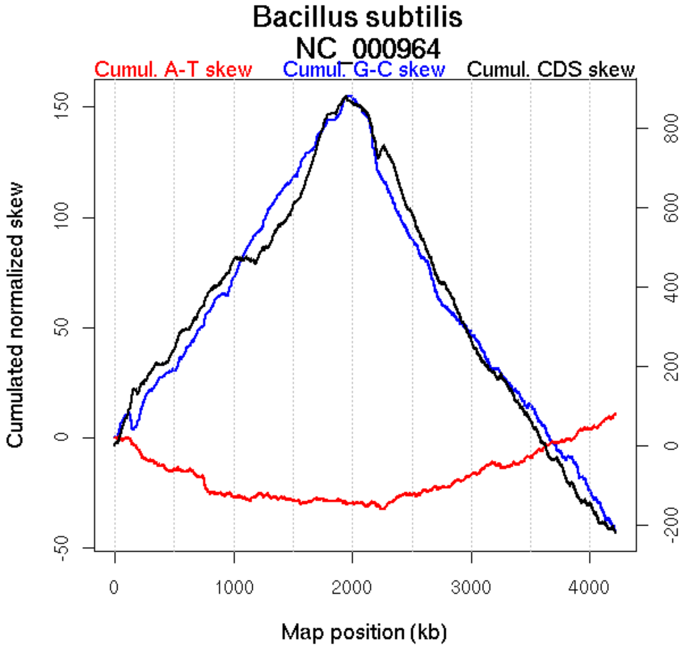
Segments:

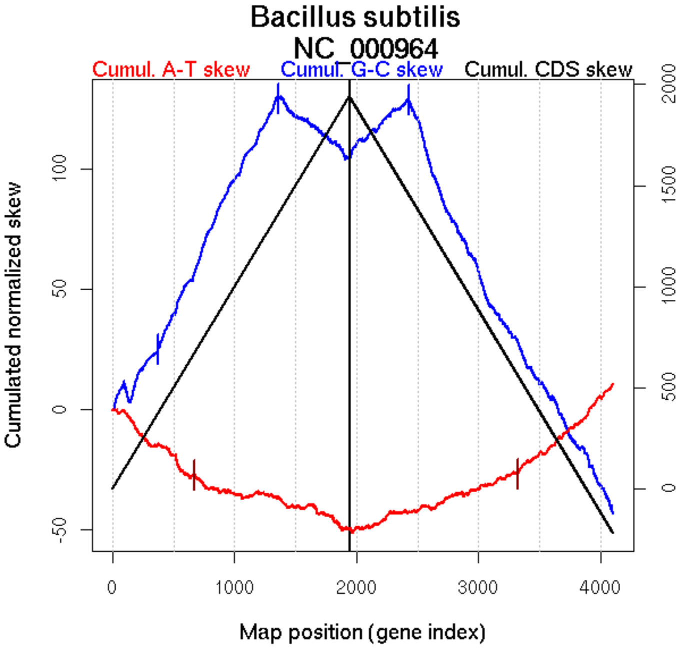
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1206 (1724.366 kb)	leading	0.045
	1207(1725.8435 kb)	1484 (2122.2405 kb)	leading	0.033
	1485(2122.782 kb)	2029 (4222.316 kb)	lagging	-0.058
GC-skew reverse	2030 (0 kb)	2595 (2101.438 kb)	leading	0.064
	2596(2102.324 kb)	4196 (4222.316 kb)	lagging	-0.036
AT-skew forward	1 (0 kb)	448 (674.994 kb)	leading	-0.025
	449(677.095 kb)	2029 (4222.316 kb)	NA	0.005
AT-skew reverse	2030 (0 kb)	3181 (2808.6135 kb)	NA	-0.017
	3182(2809.302 kb)	4196(4222.316 kb)	lagging	0.018

More G than C on the leading strand for replication.

33 Bacillus subtilis

Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
Accession number: NC_000964; **Genome size (bp)**: 4214630.
Number of genes: 4102.
Oriloc predictions: Origin 0 kb Terminus 1961 kb
Worning et al., 2006: Origin 0 kb Terminus 1947 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 3793.177 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1.08 kb
Consensus predictions: Origin 0 kb Terminus 1961 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	376	NA	532
	1362	NA	2035
GC-skew reverse	2426	NA	1999
AT-skew forward	667	NA	969
AT-skew reverse	3317	NA	3057

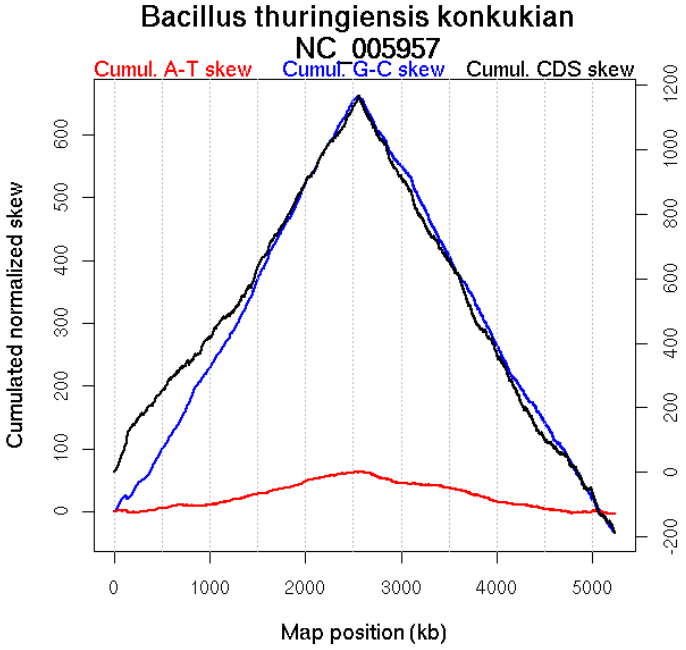
Segments:

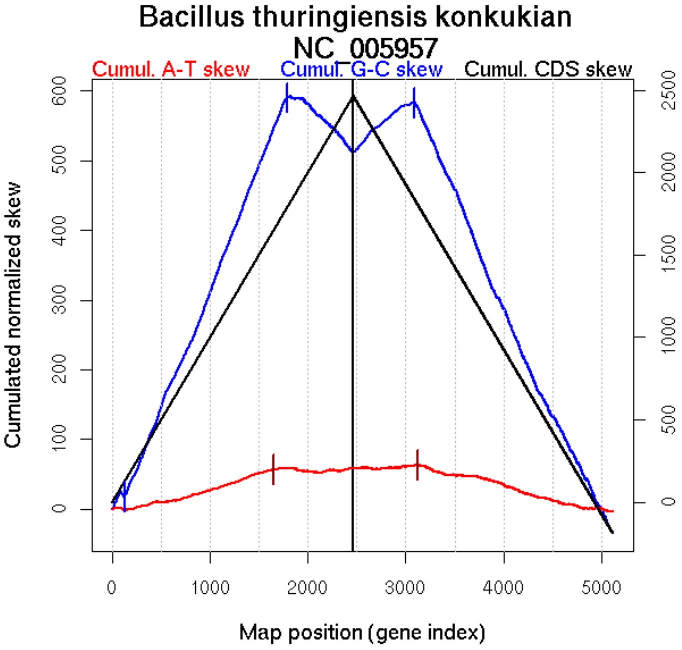
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	376 (532.2965 kb)	leading	0.063
	377(532.8795 kb)	1362 (2035.118 kb)	leading	0.107
	1363(2037.905 kb)	1941 (4214.413 kb)	lagging	-0.041
GC-skew reverse	1942 (0 kb)	2426 (1998.7935 kb)	leading	0.046
	2427(2000.3105 kb)	4102 (4214.413 kb)	lagging	-0.096
AT-skew forward	1 (0 kb)	667 (969.4515 kb)	leading	-0.045
	668(969.9775 kb)	1941 (4214.413 kb)	NA	-0.013
AT-skew reverse	1942 (0 kb)	3317 (3057.1755 kb)	NA	0.017
	3318(3058.46 kb)	4102(4214.413 kb)	lagging	0.046

More G than C on the leading strand for replication.

34 Bacillus thuringiensis konkukian

Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.
Accession number: NC_005957; **Genome size (bp)**: 5237682.
Number of genes: 5117.
Oriloc predictions: Origin 0 kb Terminus 2558 kb
Worning et al., 2006: Origin 0 kb Terminus 2561 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 5209.697 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1.08 kb
Consensus predictions: Origin 0 kb Terminus 2558 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	124	NA	141
	1784	NA	2547
GC-skew reverse	3093	NA	2537
AT-skew forward	1647	NA	2360
AT-skew reverse	3121	NA	2581

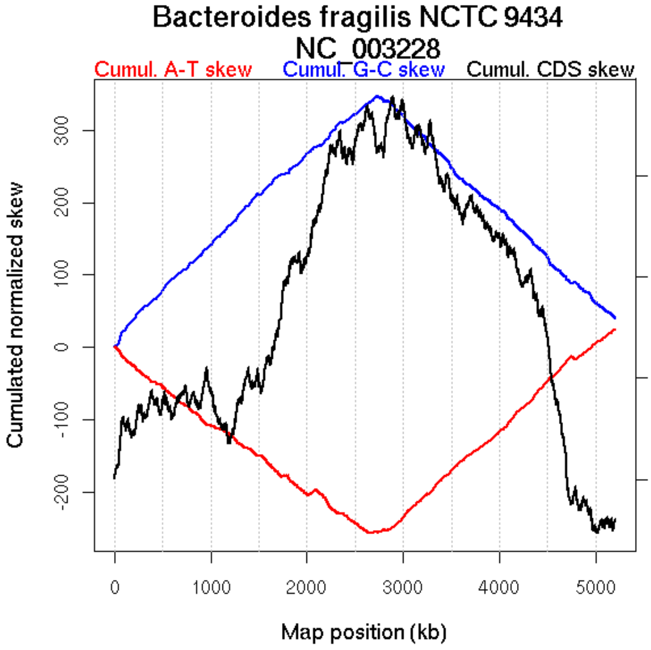
Segments:

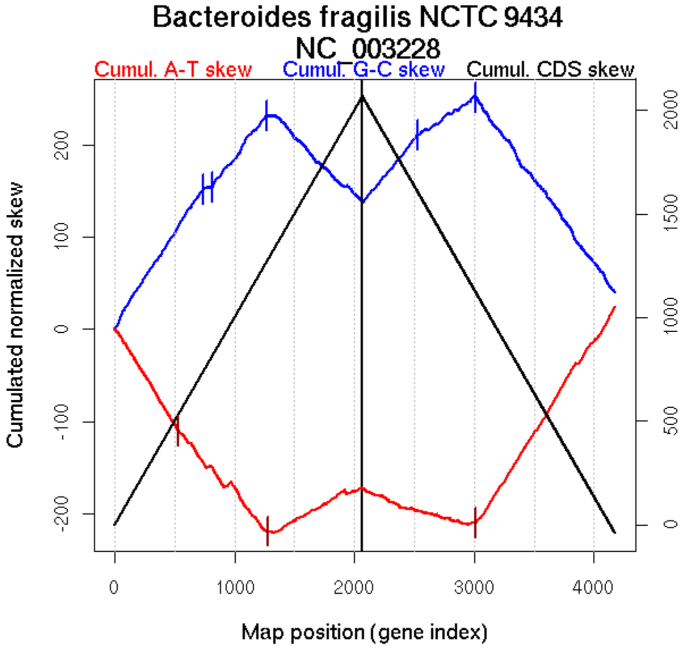
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	124 (141.4055 kb)	leading	0.179
	125(142.3175 kb)	1784 (2546.581 kb)	leading	0.348
	1785(2547.108 kb)	2464 (5237.314 kb)	lagging	-0.125
GC-skew reverse	2465 (0 kb)	3093 (2537.3935 kb)	leading	0.117
	3094(2541.5785 kb)	5117 (5237.314 kb)	lagging	-0.309
AT-skew forward	1 (0 kb)	1647 (2359.857 kb)	leading	0.037
	1648(2360.678 kb)	2464 (5237.314 kb)	NA	-0.002
AT-skew reverse	2465 (0 kb)	3121 (2581.384 kb)	leading	0.007
	3122(2584.222 kb)	5117(5237.314 kb)	lagging	-0.035

More A than T on the leading strand for replication - for reverse encoded genes.
More G than C on the leading strand for replication.

35 Bacteroides fragilis NCTC 9434

Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales; Bacteroidaceae; Bacteroides.
Accession number: NC_003228; **Genome size (bp)**: 5205140.
Number of genes: 4176.
Oriloc predictions: Origin 0 kb Terminus 2730 kb
Worning et al., 2006: Origin 5205 kb Terminus 2716 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1371.344 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 4269.64 kb
Consensus predictions: Origin 0 kb Terminus 2730 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	741	0	1699
	811	0	1790
	1269	0	2734
GC-skew reverse	2527	0.03667	1314
	3010	0	2733
AT-skew forward	533	0.03667	1302
	1277	0	2748
AT-skew reverse	3010	0	2733

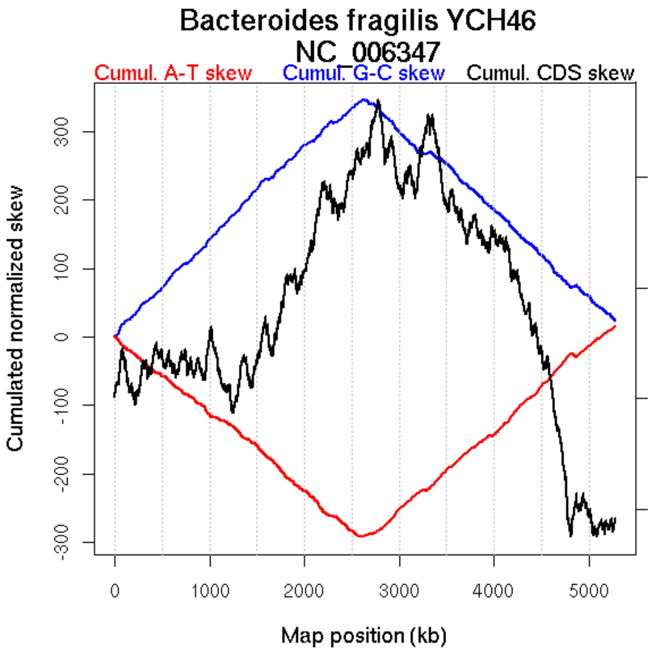
Segments:

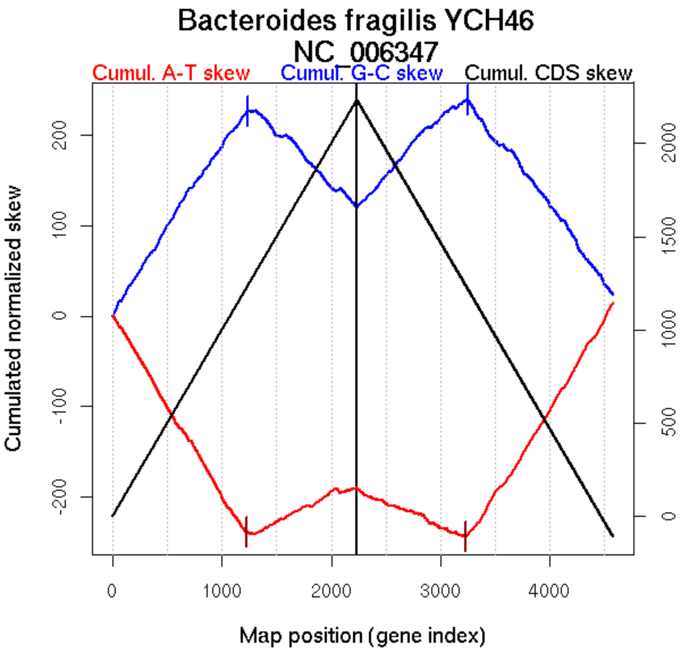
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	741 (1698.6775 kb)	leading	0.202
	742(1699.965 kb)	811 (1789.9265 kb)	leading	0.028
	812(1791.197 kb)	1269 (2733.988 kb)	leading	0.171
	1270(2738.1565 kb)	2068 (5204.75 kb)	lagging	-0.128
GC-skew reverse	2069 (0 kb)	2527 (1314.3715 kb)	leading	0.159
	2528(1318.607 kb)	3010 (2732.8295 kb)	leading	0.086
	3011(2734.082 kb)	4176 (5204.75 kb)	lagging	-0.182
AT-skew forward	1 (0 kb)	533 (1301.9185 kb)	leading	-0.211
	534(1304.147 kb)	1277 (2748.4195 kb)	leading	-0.145
	1278(2749.816 kb)	2068 (5204.75 kb)	lagging	0.068
AT-skew reverse	2069 (0 kb)	3010 (2732.8295 kb)	leading	-0.041
	3011(2734.082 kb)	4176(5204.75 kb)	lagging	0.204

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

36 Bacteroides fragilis YCH46

Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales; Bacteroidaceae; Bacteroides.
Accession number: NC_006347; **Genome size (bp)**: 5277274.
Number of genes: 4578.
Oriloc predictions: Origin 0 kb Terminus 2615 kb
Worning et al., 2006: Origin 5277 kb Terminus 2617 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 272.461 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 4363.71 kb
Consensus predictions: Origin 0 kb Terminus 2615 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1231	NA	2614
GC-skew reverse	3248	NA	2626
AT-skew forward	1222	NA	2601
AT-skew reverse	3231	NA	2580

Segments:

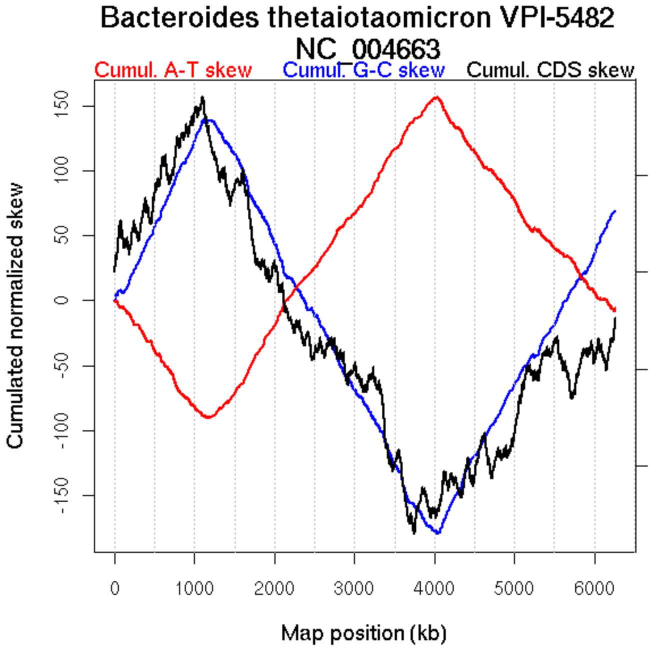
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1231 (2613.6105 kb)	leading	0.184
	1232(2613.847 kb)	2234 (5276.884 kb)	lagging	-0.114
GC-skew reverse	2235 (0 kb)	3248 (2626.3315 kb)	leading	0.124
	3249(2627.1425 kb)	4578 (5276.884 kb)	lagging	-0.159
AT-skew forward	1 (0 kb)	1222 (2600.862 kb)	leading	-0.2
	1223(2602.6225 kb)	2234 (5276.884 kb)	lagging	0.058
AT-skew reverse	2235 (0 kb)	3231 (2580.253 kb)	leading	-0.052
	3232(2583.1175 kb)	4578(5276.884 kb)	lagging	0.194

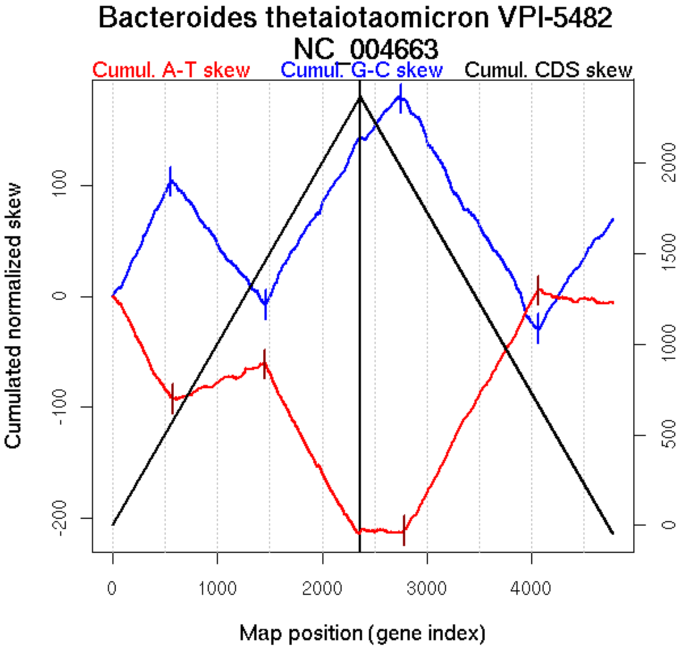
More T than A on the leading strand for replication.

More G than C on the leading strand for replication.

37 Bacteroides thetaiotaomicron VPI-5482

Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales; Bacteroidaceae; Bacteroides.
Accession number: NC_004663; **Genome size (bp)**: 6260361.
Number of genes: 4778.
Oriloc predictions: Origin 4034 kb Terminus 1173 kb
Worning et al., 2006: Origin 4038 kb Terminus 1185 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 362.736 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 2698.16 kb
Consensus predictions: Origin 4034 kb Terminus 1173 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	558	NA	1226
	1462	NA	4045
GC-skew reverse	2751	NA	1146
	4068	NA	4024
AT-skew forward	573	NA	1329
	1457	NA	4032
AT-skew reverse	2782	NA	1192
	4067	NA	4018

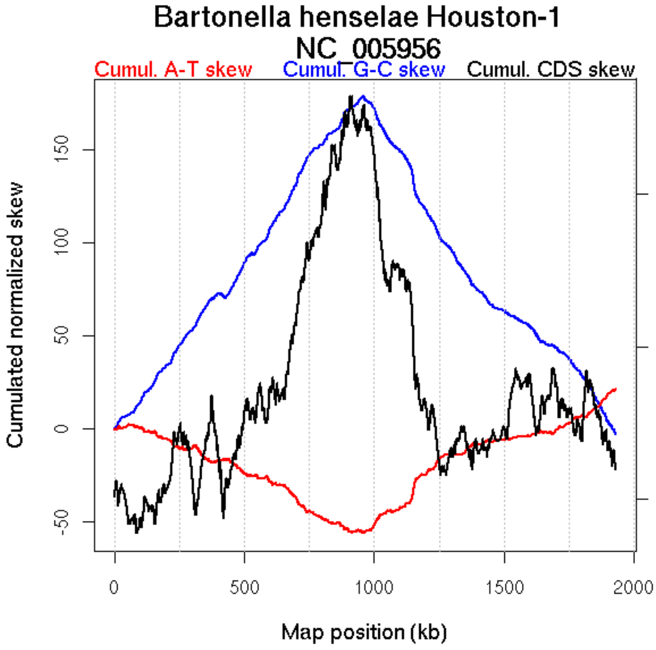
Segments:

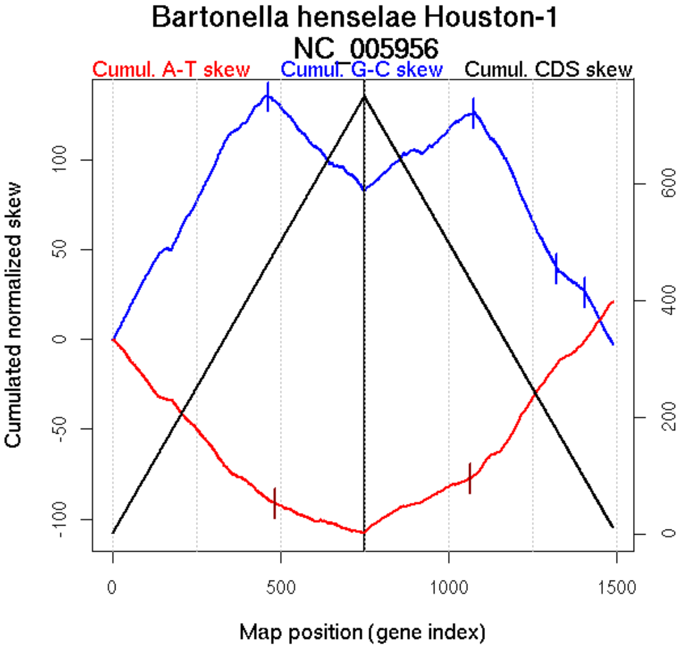
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	558 (1226.1965 kb)	leading	0.196
	559(1235.1475 kb)	1462 (4044.664 kb)	lagging	-0.127
	1463(4049.998 kb)	2365 (6259.965 kb)	leading	0.159
GC-skew reverse	2366 (0 kb)	2751 (1146.193 kb)	leading	0.114
	2752(1147.3055 kb)	4068 (4024.0495 kb)	lagging	-0.16
	4069(4032.048 kb)	4778 (6259.965 kb)	leading	0.138
AT-skew forward	1 (0 kb)	573 (1329.471 kb)	leading	-0.176
	574(1330.614 kb)	1457 (4032.2535 kb)	lagging	0.037
	1458(4035.0895 kb)	2365 (6259.965 kb)	leading	-0.171
AT-skew reverse	2366 (0 kb)	2782 (1191.9245 kb)	leading	-0.006
	2783(1192.68 kb)	4067(4017.578 kb)	lagging	0.171
	4068(4024.0495 kb)	4778(6259.965 kb)	leading	-0.013

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

38 Bartonella henselae Houston-1

Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Bartonellaceae; Bartonella.
Accession number: NC_005956; **Genome size (bp)**: 1931047.
Number of genes: 1488.
Oriloc predictions: Origin 0 kb Terminus 957 kb
Worning et al., 2006: Origin 1931 kb Terminus 974 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1930.908 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 159.56 kb
Consensus predictions: Origin 0 kb Terminus 957 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	463	0	983
GC-skew reverse	1074	0	944
	1321	0.02444	1464
	1405	0.03111	1742
AT-skew forward	483	0.00667	1066
AT-skew reverse	1062	0	924

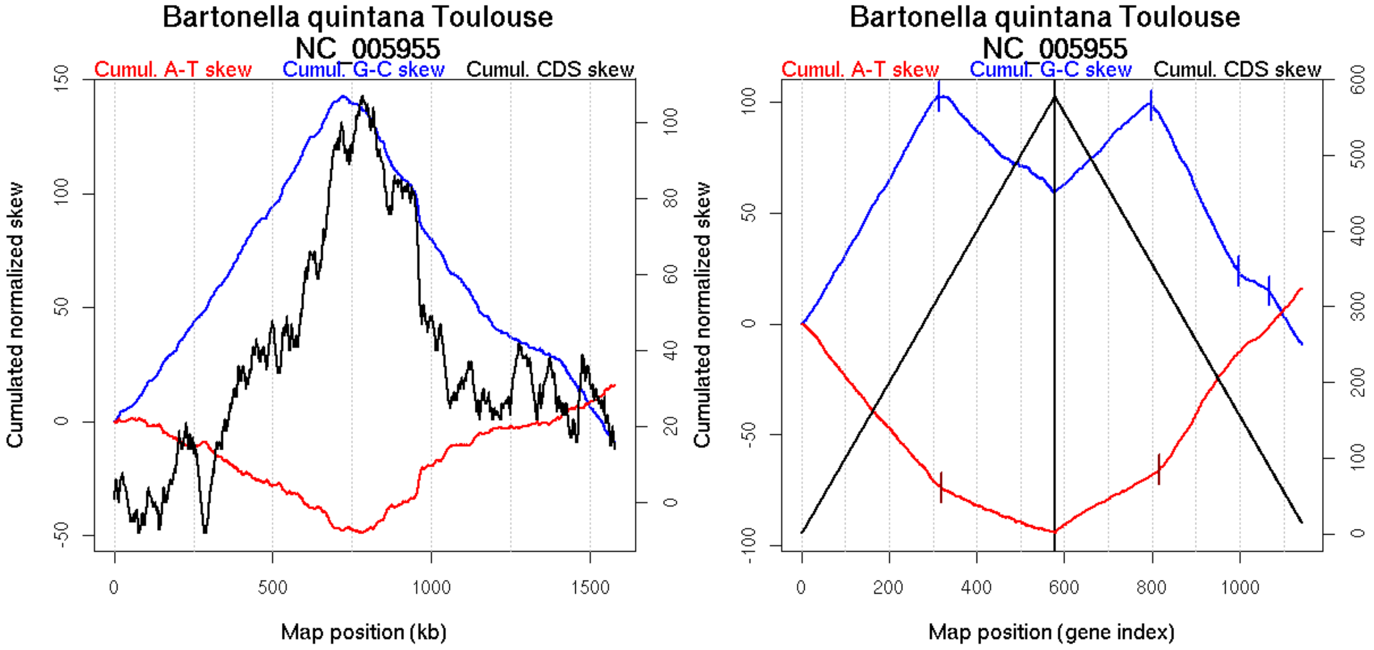
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	463 (982.769 kb)	leading	0.303
	464(999.642 kb)	749 (1930.402 kb)	lagging	-0.183
GC-skew reverse	750 (0 kb)	1074 (944.3505 kb)	leading	0.127
	1075(947.1655 kb)	1321 (1464.478 kb)	lagging	-0.369
	1322(1469.286 kb)	1405 (1742.241 kb)	lagging	-0.147
	1406(1743.5405 kb)	1488 (1930.402 kb)	lagging	-0.361
AT-skew forward	1 (0 kb)	483 (1066.477 kb)	leading	-0.194
	484(1068.857 kb)	749 (1930.402 kb)	lagging	-0.061
AT-skew reverse	750 (0 kb)	1062 (923.6905 kb)	leading	0.089
	1063(924.942 kb)	1488(1930.402 kb)	lagging	0.238

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

39 Bartonella quintana Toulouse

Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Bartonellaceae; Bartonella.
Accession number: NC_005955; **Genome size (bp)**: 1581384.
Number of genes: 1142.
Oriloc predictions: Origin 0 kb Terminus 715 kb
Worning et al., 2006: Origin 0 kb Terminus 723 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1581.243 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 146.98 kb
Consensus predictions: Origin 0 kb Terminus 715 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	313	NA	725
GC-skew reverse	799	NA	731
	997	NA	1193
	1066	NA	1410
AT-skew forward	319	NA	745
AT-skew reverse	817	NA	798

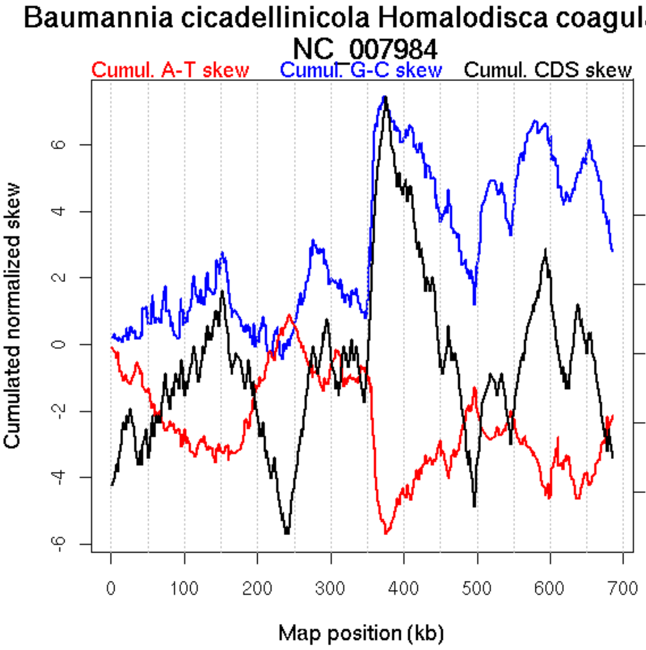
Segments:

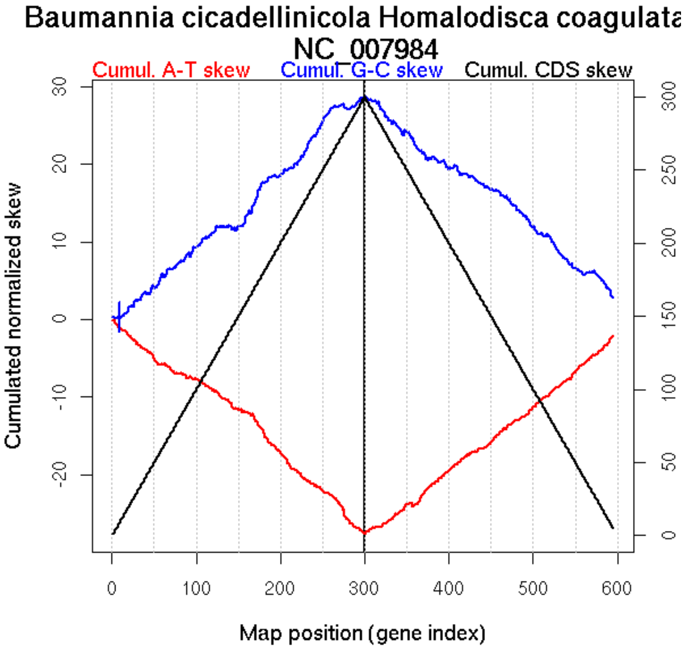
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	313 (725.141 kb)	leading	0.342
	314(734.092 kb)	578 (1580.794 kb)	lagging	-0.166
GC-skew reverse	579 (0 kb)	799 (731.202 kb)	leading	0.192
	800(734.7545 kb)	997 (1193.123 kb)	lagging	-0.4
	998(1195.087 kb)	1066 (1409.761 kb)	lagging	-0.104
	1067(1411.6525 kb)	1142 (1580.794 kb)	lagging	-0.332
AT-skew forward	1 (0 kb)	319 (744.7185 kb)	leading	-0.238
	320(745.775 kb)	578 (1580.794 kb)	lagging	-0.078
AT-skew reverse	579 (0 kb)	817 (797.8245 kb)	leading	0.111
	818(801.0195 kb)	1142(1580.794 kb)	lagging	0.249

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

40 Baumannia cicadellinicola Homalodisca coagulata

Bacteria; Proteobacteria; Gammaproteobacteria; Candidatus Baumannia.
Accession number: NC_007984; **Genome size (bp)**: 686194.
Number of genes: 595.
Oriloc predictions: Origin NA Terminus NA
Worning et al., 2006: Origin NA kb Terminus NA kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 20.052 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): NA
Consensus predictions: Origin NA Terminus NA





Significant breakpoints (p-value <0.05):

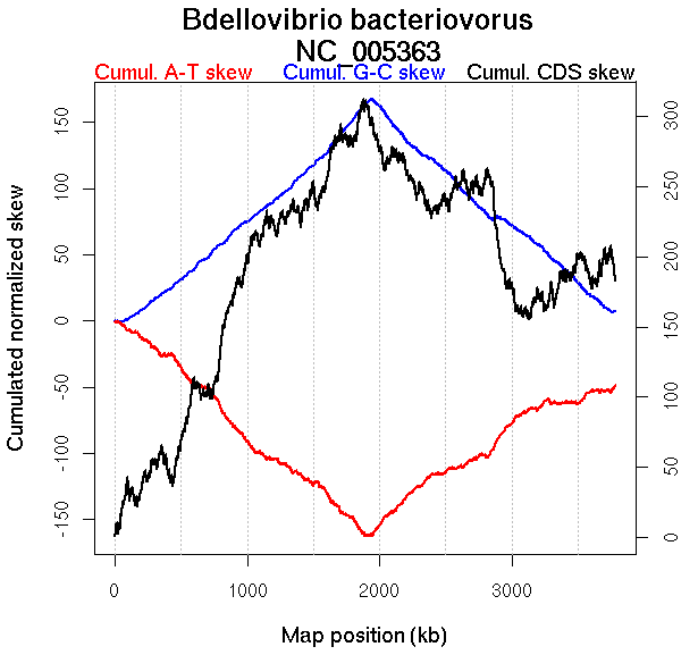
	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	9	0	15

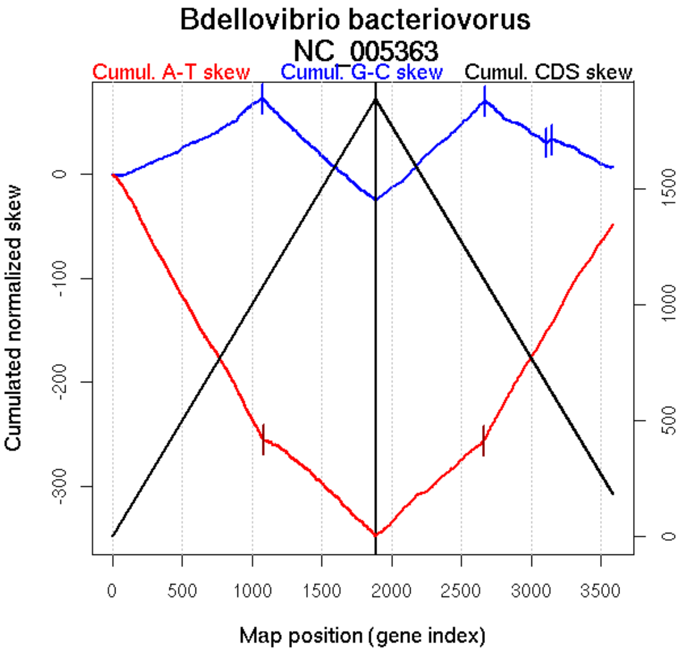
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	9 (14.623 kb)	NA	-0.004
	10(16.0995 kb)	300 (685.999 kb)	NA	0.101

41 Bdellovibrio bacteriovorus

Bacteria; Proteobacteria; Deltaproteobacteria; Bdellovibrionales; Bdellovibrionaceae; Bdellovibrio.
Accession number: NC_005363; **Genome size (bp)**: 3782950.
Number of genes: 3587.
Oriloc predictions: Origin 0 kb Terminus 1942 kb
Worning et al., 2006: Origin 3781 kb Terminus 1941 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1679.937 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.71 kb
Consensus predictions: Origin 0 kb Terminus 1942 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1074	0	1937
GC-skew reverse	2665	0	1943
	3108	0	2853
	3150	0	2893
AT-skew forward	1083	0	1963
AT-skew reverse	2659	0	1930

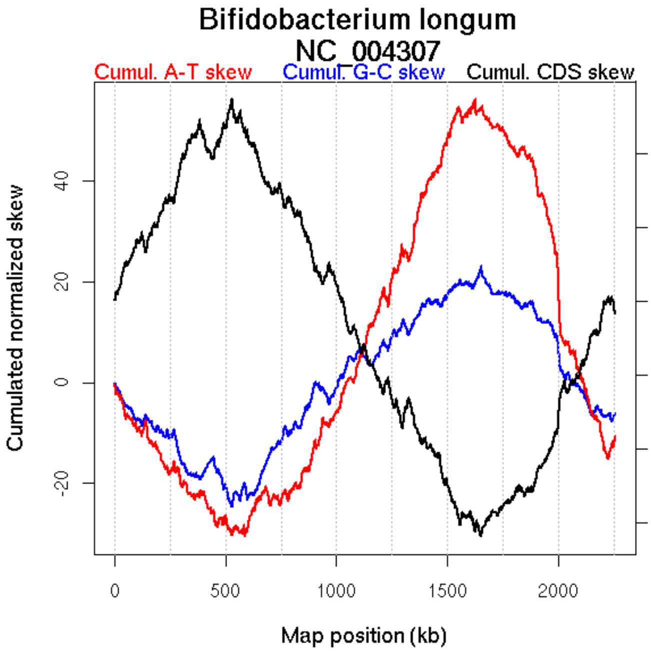
Segments:

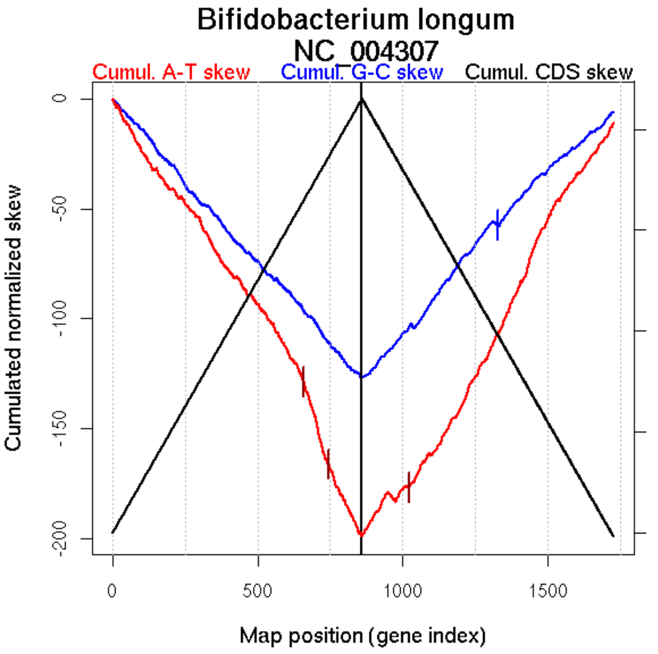
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1074 (1937.2435 kb)	leading	0.07
	1075(1938.498 kb)	1885 (3782.767 kb)	lagging	-0.12
GC-skew reverse	1886 (0 kb)	2665 (1942.722 kb)	leading	0.124
	2666(1944.3395 kb)	3108 (2853.187 kb)	lagging	-0.087
	3109(2856.749 kb)	3150 (2893.008 kb)	lagging	0.087
	3151(2893.882 kb)	3587 (3782.767 kb)	lagging	-0.068
AT-skew forward	1 (0 kb)	1083 (1962.6025 kb)	leading	-0.239
	1084(1965.6815 kb)	1885 (3782.767 kb)	lagging	-0.12
AT-skew reverse	1886 (0 kb)	2659 (1930.0265 kb)	leading	0.118
	2660(1931.2165 kb)	3587(3782.767 kb)	lagging	0.226

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

42 Bifidobacterium longum

Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales; Bifidobacteriaceae; Bifidobacterium.
Accession number: NC_004307; **Genome size (bp)**: 2256640.
Number of genes: 1727.
Oriloc predictions: Origin 1651 kb Terminus 528 kb
Worning et al., 2006: Origin 1653 kb Terminus 530 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1572.246 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1625.01 kb
Consensus predictions: Origin 1651 kb Terminus 528 kb





Significant breakpoints (p-value <0.05):

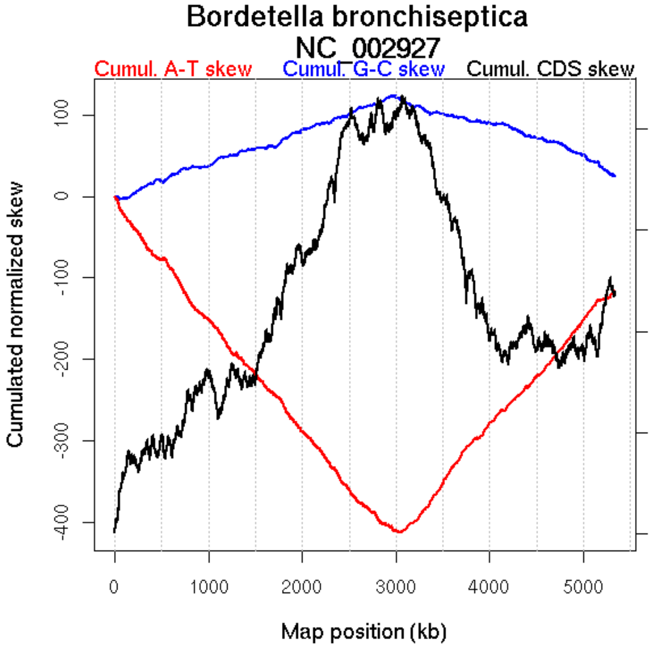
	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew reverse	1329	0.03333	1153
AT-skew forward	660	0.00333	1901
	743	0.02	2033
AT-skew reverse	1022	0.00667	576

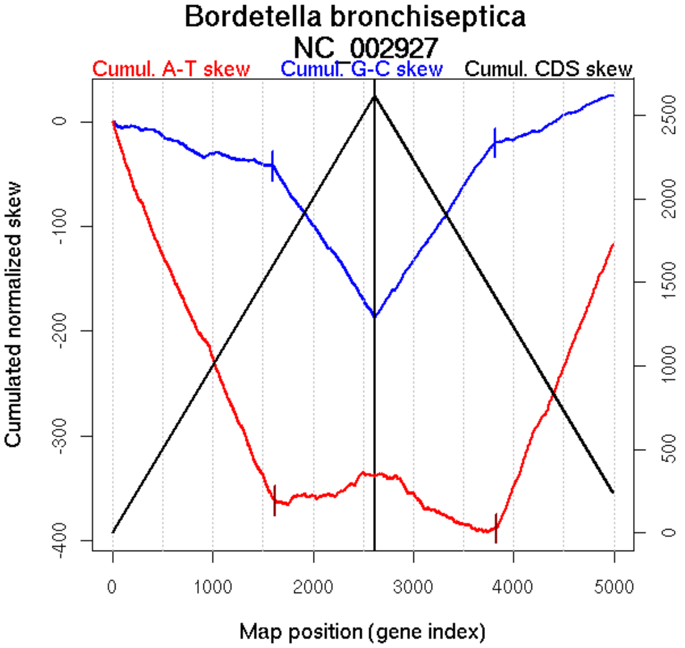
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew reverse	861 (0 kb)	1329 (1153.4815 kb)	NA	0.161
	1330(1154.8595 kb)	1727 (2256.529 kb)	NA	0.122
AT-skew forward	1 (0 kb)	660 (1900.6875 kb)	NA	-0.184
	661(1901.083 kb)	743 (2032.687 kb)	leading	-0.476
	744(2038.6605 kb)	860 (2256.529 kb)	leading	-0.281
AT-skew reverse	861 (0 kb)	1022 (575.5075 kb)	NA	0.133
	1023(576.564 kb)	1727(2256.529 kb)	NA	0.25

43 Bordetella bronchiseptica

Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales; Alcaligenaceae; Bordetella.
Accession number: NC_002927; **Genome size (bp)**: 5339179.
Number of genes: 4993.
Oriloc predictions: Origin 38 kb Terminus 2999 kb
Worning et al., 2006: Origin 5332 kb Terminus 2977 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1806.278 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 5310.85 kb
Consensus predictions: Origin 0 kb Terminus 2999 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1602	0	2973
GC-skew reverse	3811	0	2986
AT-skew forward	1617	0	3005
AT-skew reverse	3830	0	3034

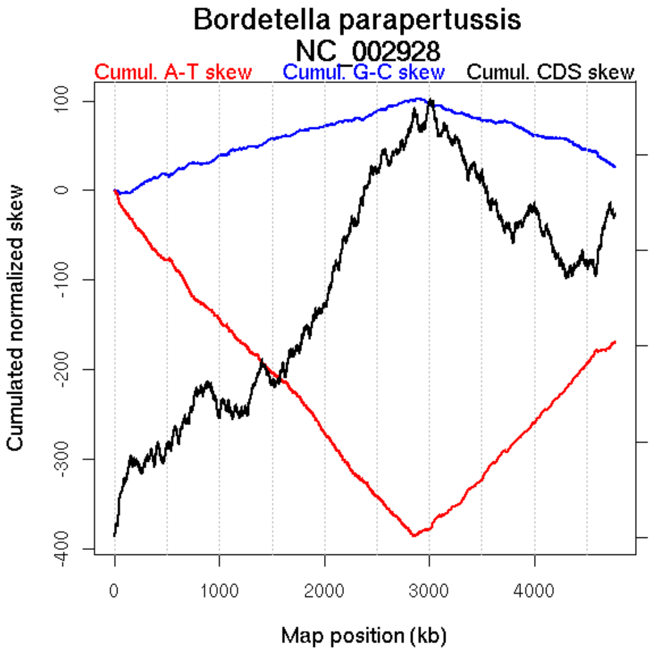
Segments:

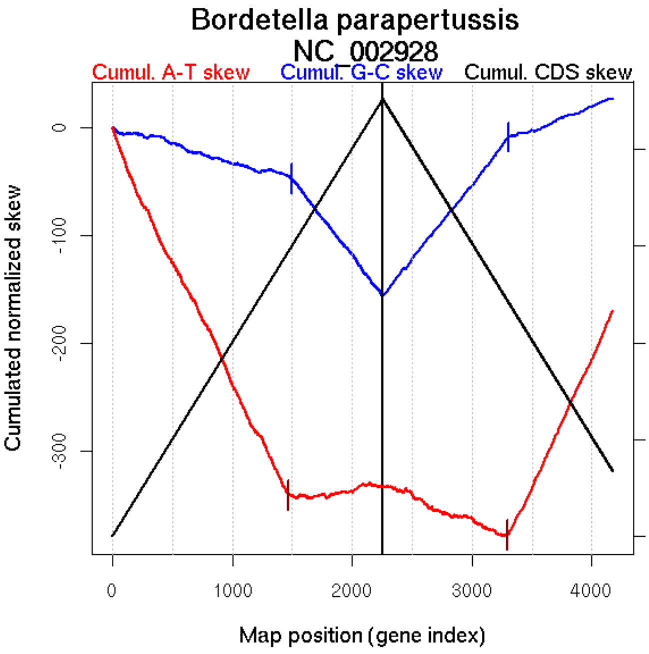
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1602 (2973.384 kb)	leading	-0.028
	1603(2973.803 kb)	2616 (5337.385 kb)	lagging	-0.138
GC-skew reverse	2617 (0 kb)	3811 (2985.65 kb)	leading	0.141
	3812(2987.0905 kb)	4993 (5337.385 kb)	lagging	0.042
AT-skew forward	1 (0 kb)	1617 (3004.985 kb)	leading	-0.217
	1618(3005.221 kb)	2616 (5337.385 kb)	lagging	0.028
AT-skew reverse	2617 (0 kb)	3830 (3034.317 kb)	leading	-0.053
	3831(3044.481 kb)	4993(5337.385 kb)	lagging	0.232

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

44 Bordetella parapertussis

Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales; Alcaligenaceae; Bordetella.
Accession number: NC_002928; **Genome size (bp)**: 4773551.
Number of genes: 4176.
Oriloc predictions: Origin 51 kb Terminus 2912 kb
Worning et al., 2006: Origin 4764 kb Terminus 2868 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 2413.881 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 4745.23 kb
Consensus predictions: Origin 0 kb Terminus 2912 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1497	NA	2928
GC-skew reverse	3302	NA	2883
AT-skew forward	1473	NA	2852
AT-skew reverse	3299	NA	2875

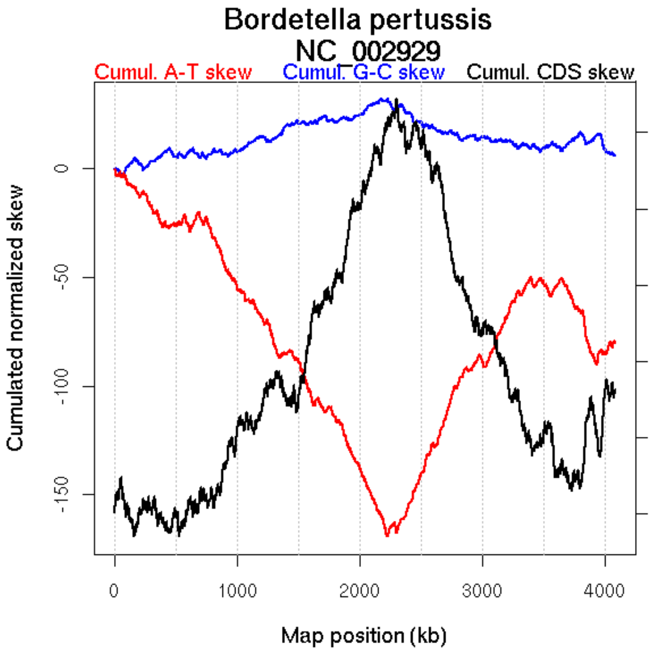
Segments:

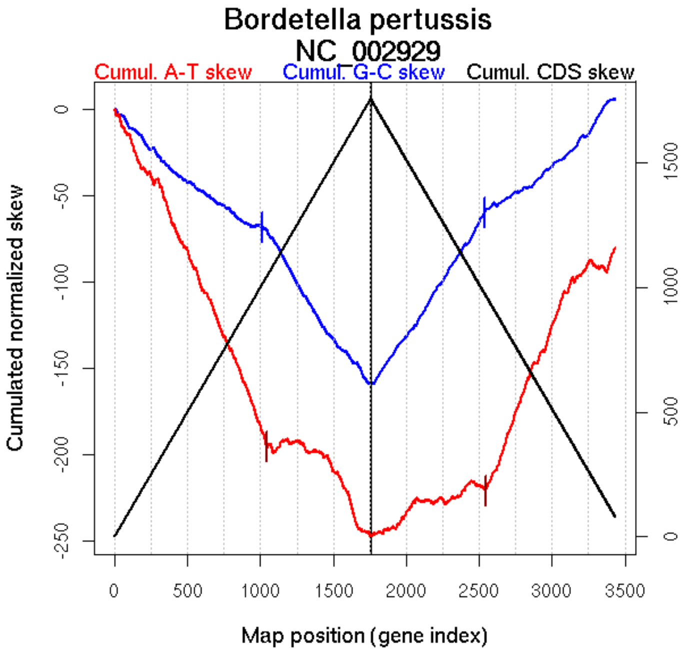
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1497 (2928.328 kb)	leading	-0.031
	1498(2929.384 kb)	2257 (4771.757 kb)	lagging	-0.143
GC-skew reverse	2258 (0 kb)	3302 (2883.0435 kb)	leading	0.139
	3303(2886.208 kb)	4176 (4771.757 kb)	lagging	0.044
AT-skew forward	1 (0 kb)	1473 (2852.0855 kb)	leading	-0.226
	1474(2853.914 kb)	2257 (4771.757 kb)	lagging	0.017
AT-skew reverse	2258 (0 kb)	3299 (2875.2195 kb)	leading	-0.047
	3300(2878.3485 kb)	4176(4771.757 kb)	lagging	0.239

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

45 Bordetella pertussis

Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales; Alcaligenaceae; Bordetella.
Accession number: NC_002929; **Genome size (bp)**: 4086189.
Number of genes: 3433.
Oriloc predictions: Origin 69 kb Terminus 2227 kb
Worning et al., 2006: Origin 3464 kb Terminus 2230 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1642.294 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 505.27 kb
Consensus predictions: Origin 0 kb Terminus 2227 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1015	NA	2178
GC-skew reverse	2538	NA	2171
AT-skew forward	1045	NA	2228
AT-skew reverse	2548	NA	2226

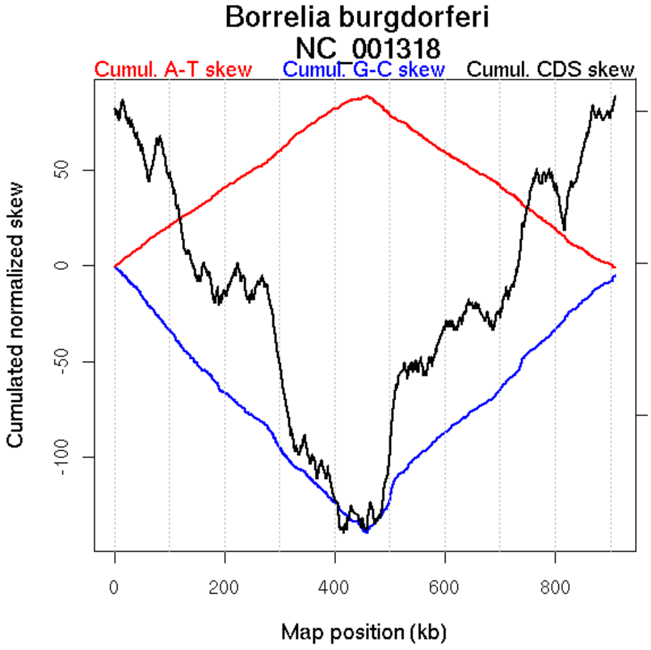
Segments:

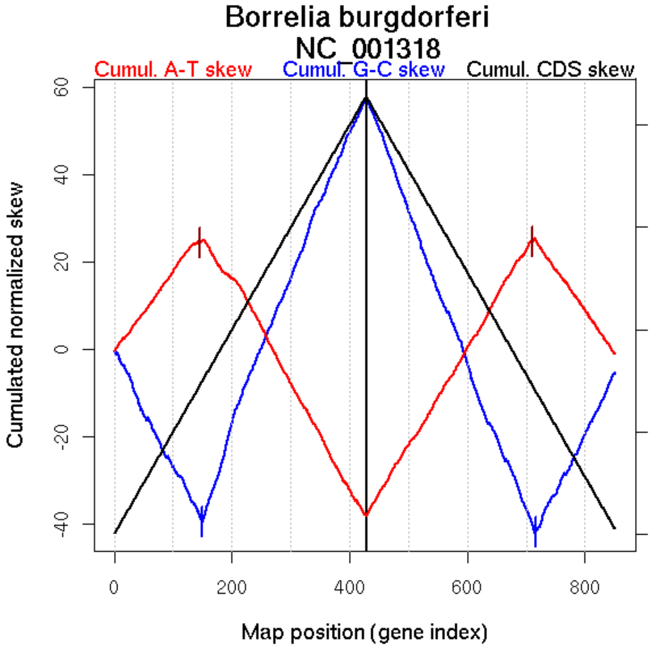
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1015 (2178.225 kb)	leading	-0.069
	1016(2178.686 kb)	1757 (4084.462 kb)	lagging	-0.127
GC-skew reverse	1758 (0 kb)	2538 (2171.0675 kb)	leading	0.128
	2539(2180.808 kb)	3433 (4084.462 kb)	lagging	0.073
AT-skew forward	1 (0 kb)	1045 (2227.971 kb)	leading	-0.183
	1046(2229.0815 kb)	1757 (4084.462 kb)	lagging	-0.078
AT-skew reverse	1758 (0 kb)	2548 (2226.1425 kb)	leading	0.039
	2549(2234.295 kb)	3433(4084.462 kb)	lagging	0.164

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

46 Borrelia burgdorferi

Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia; Borrelia burgdorferi group.
Accession number: NC_001318; **Genome size (bp)**: 910724.
Number of genes: 851.
Oriloc predictions: Origin 457 kb Terminus 0 kb
Worning et al., 2006: Origin NA kb Terminus NA kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 491.712 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): NA
Consensus predictions: Origin 457 kb Terminus 0 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	150	0	458
GC-skew reverse	716	0	467
AT-skew forward	145	0	446
AT-skew reverse	710	0	448

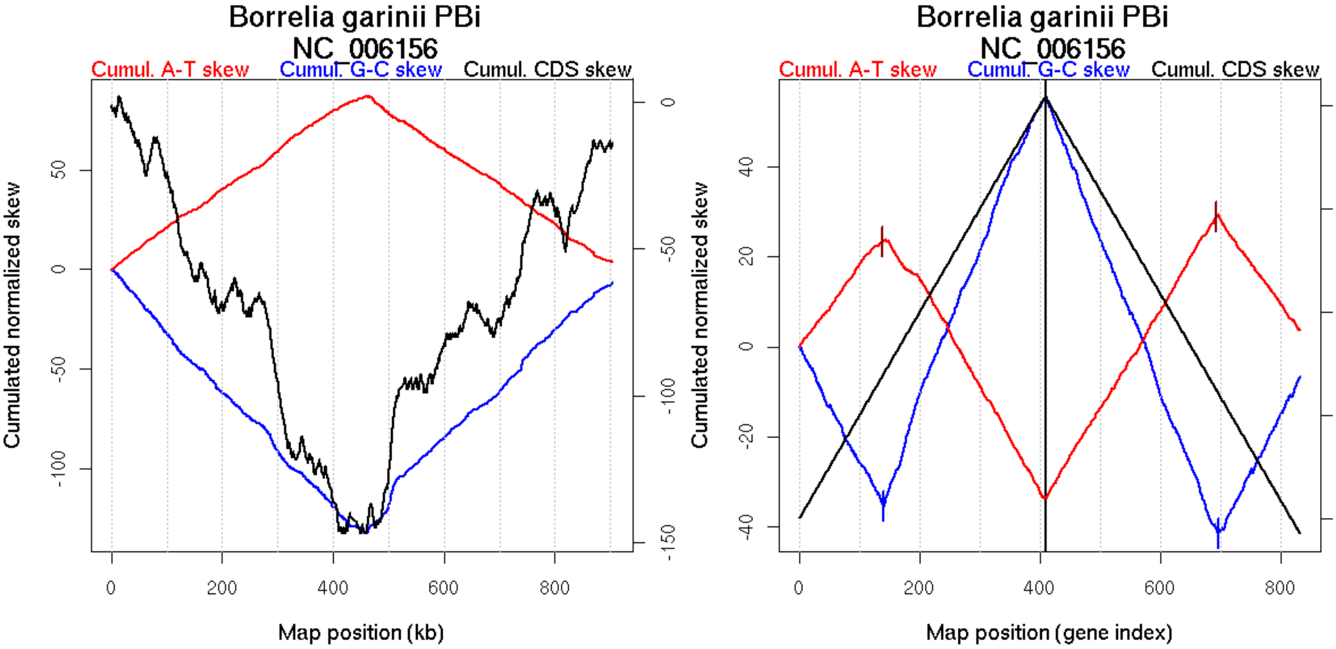
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	150 (458.155 kb)	lagging	-0.26
	151(459.478 kb)	428 (909.588 kb)	leading	0.343
GC-skew reverse	429 (0 kb)	716 (467.454 kb)	lagging	-0.349
	717(468.475 kb)	851 (909.588 kb)	leading	0.268
AT-skew forward	1 (0 kb)	145 (446.0755 kb)	lagging	0.183
	146(448.437 kb)	428 (909.588 kb)	leading	-0.236
AT-skew reverse	429 (0 kb)	710 (447.7815 kb)	lagging	0.225
	711(449.6375 kb)	851(909.588 kb)	leading	-0.19

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

47 Borrelia garinii PBi

Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia; Borrelia burgdorferi group.
Accession number: NC_006156; **Genome size (bp)**: 904246.
Number of genes: 832.
Oriloc predictions: Origin 459 kb Terminus 0 kb
Worning et al., 2006: Origin NA kb Terminus NA kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 790.251 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 459.52 kb
Consensus predictions: Origin 459 kb Terminus 0 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	141	NA	460
GC-skew reverse	696	NA	463
AT-skew forward	139	NA	452
AT-skew reverse	692	NA	450

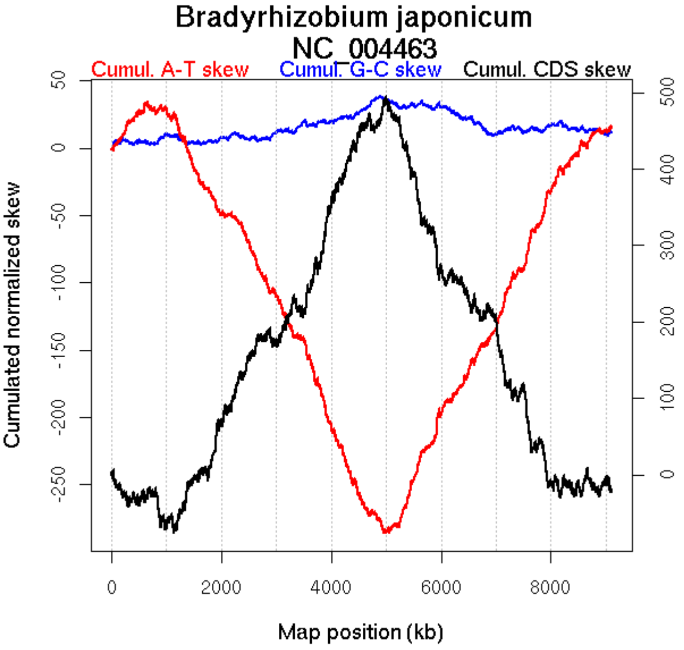
Segments:

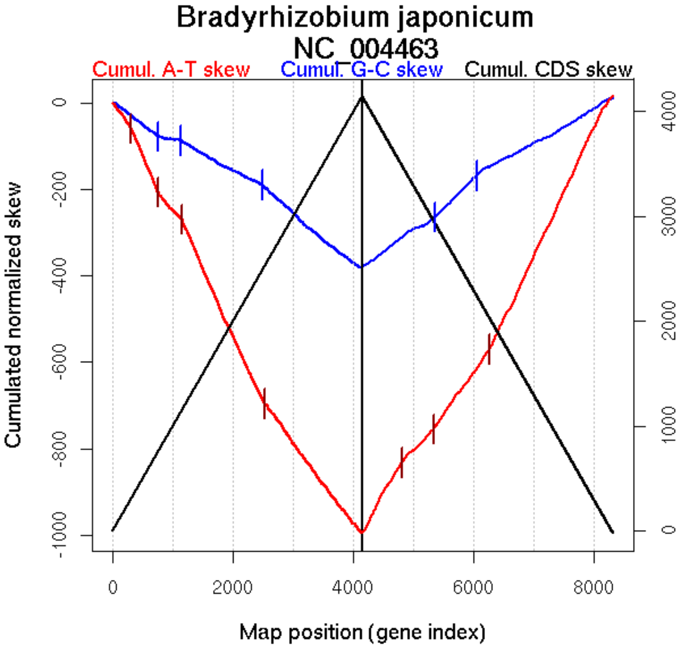
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	141 (460.362 kb)	lagging	-0.251
	142(461.689 kb)	409 (903.762 kb)	leading	0.339
GC-skew reverse	410 (0 kb)	696 (463.127 kb)	lagging	-0.34
	697(469.729 kb)	832 (903.762 kb)	leading	0.259
AT-skew forward	1 (0 kb)	139 (452.368 kb)	lagging	0.178
	140(455.935 kb)	409 (903.762 kb)	leading	-0.223
AT-skew reverse	410 (0 kb)	692 (449.976 kb)	lagging	0.221
	693(452.2665 kb)	832(903.762 kb)	leading	-0.185

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

48 Bradyrhizobium japonicum

Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae; Bradyrhizobium.
Accession number: NC_004463; **Genome size (bp)**: 9105828.
Number of genes: 8317.
Oriloc predictions: Origin 684 kb Terminus 4926 kb
Worning et al., 2006: Origin 328 kb Terminus 5002 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 68.858 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 894.42 kb
Consensus predictions: Origin 684 kb Terminus 4926 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	757	0	1646
	1135	0.00667	2319
	2482	0.01333	4958
GC-skew reverse	5358	0.00667	2859
	6050	0	4707
AT-skew forward	306	0	681
	754	0	1641
	1146	0	2335
	2531	0	5076
AT-skew reverse	4802	0	1407
	5330	0.04889	2795
	6266	0.00222	5211

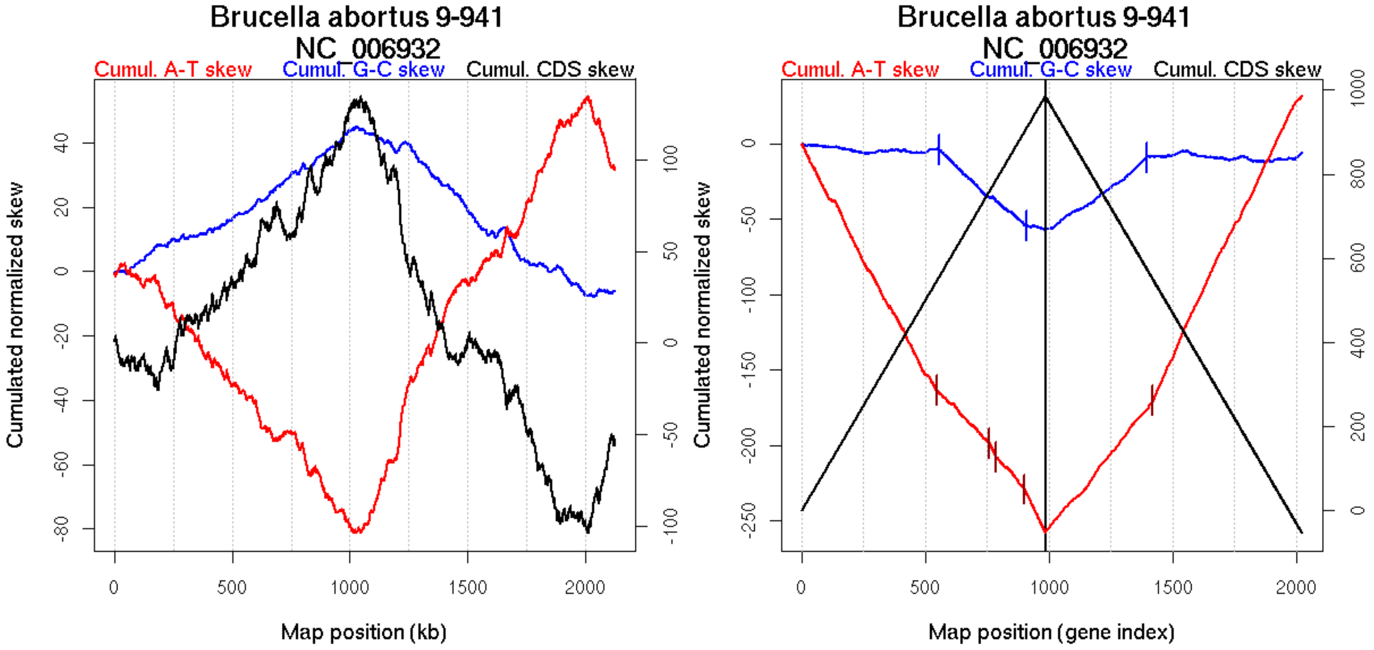
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	757 (1645.778 kb)	NA	-0.107
	758(1648.5805 kb)	1135 (2319.173 kb)	leading	-0.02
	1136(2320.658 kb)	2482 (4957.524 kb)	leading	-0.076
	2483(4958.895 kb)	4147 (9105.797 kb)	lagging	-0.118
GC-skew reverse	4148 (0 kb)	5358 (2859.041 kb)	NA	0.097
	5359(2859.841 kb)	6050 (4707.2085 kb)	leading	0.141
	6051(4710.0715 kb)	8317 (9105.797 kb)	lagging	0.078
AT-skew forward	1 (0 kb)	306 (680.5335 kb)	lagging	-0.189
	307(685.99 kb)	754 (1641.0115 kb)	leading	-0.331
	755(1641.4245 kb)	1146 (2334.5915 kb)	leading	-0.153
	1147(2337.9065 kb)	2531 (5076.3265 kb)	leading	-0.311
	2532(5079.429 kb)	4147 (9105.797 kb)	lagging	-0.189
AT-skew reverse	4148 (0 kb)	4802 (1407.391 kb)	NA	0.255
	4803(1408.4165 kb)	5330(2794.706 kb)	leading	0.138
	5331(2796.3425 kb)	6266(5211.3115 kb)	leading	0.194
	6267(5212.6245 kb)	8317(9105.797 kb)	lagging	0.295

More T than A on the leading strand for replication.
More G than C on the leading strand for replication - for forward encoded genes.

49 Brucella abortus 9-941

Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Brucellaceae; Brucella.
Accession number: NC_006932; **Genome size (bp)**: 2124241.
Number of genes: 2023.
Oriloc predictions: Origin 2010 kb Terminus 1027 kb
Worning et al., 2006: Origin 2011 kb Terminus 1046 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 2010.838 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1.53 kb
Consensus predictions: Origin 2010 kb Terminus 1027 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	554	0.00667	1043
	909	0.01	2015
GC-skew reverse	1393	0	1005
AT-skew forward	545	0.04833	1021
	759	0.01833	1615
	786	0.03333	1686
	901	0.01833	1997
AT-skew reverse	1418	0	1067

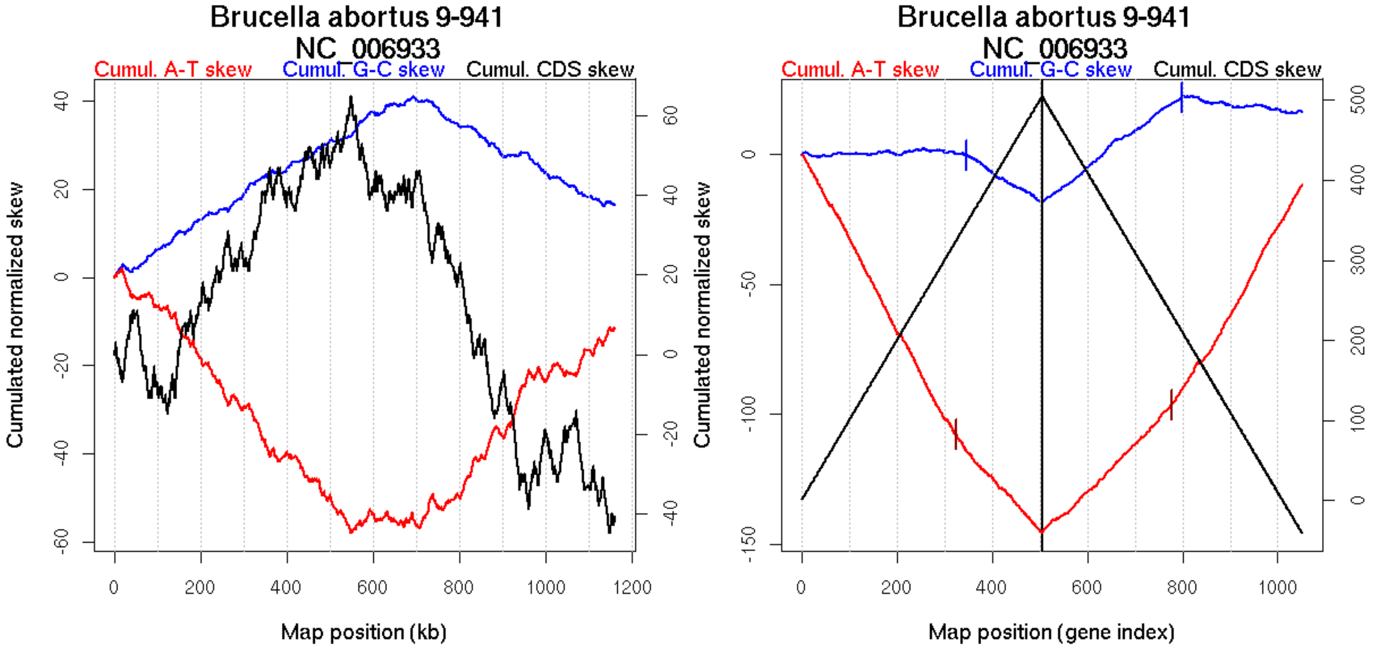
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	554 (1042.68 kb)	leading	-0.008
	555(1043.438 kb)	909 (2015.303 kb)	lagging	-0.141
	910(2016.7215 kb)	985 (2124.032 kb)	leading	-0.029
GC-skew reverse	986 (0 kb)	1393 (1005.0665 kb)	leading	0.116
	1394(1009.921 kb)	2023 (2124.032 kb)	lagging	-0.006
AT-skew forward	1 (0 kb)	545 (1021.3115 kb)	leading	-0.301
	546(1022.173 kb)	759 (1614.897 kb)	lagging	-0.166
	760(1617.307 kb)	786 (1685.762 kb)	lagging	-0.331
	787(1687.349 kb)	901 (1997.142 kb)	lagging	-0.185
	902(1998.0155 kb)	985 (2124.032 kb)	leading	-0.348
AT-skew reverse	986 (0 kb)	1418 (1066.688 kb)	leading	0.201
	1419(1071.351 kb)	2023(2124.032 kb)	lagging	0.338

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

50 Brucella abortus 9-941

Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Brucellaceae; Brucella.
Accession number: NC_006933; **Genome size (bp)**: 1162204.
Number of genes: 1051.
Oriloc predictions: Origin 1 kb Terminus 695 kb
Worning et al., 2006: Origin 1161 kb Terminus 672 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1162.128 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.75 kb
Consensus predictions: Origin 0 kb Terminus 695 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	346	0	708
GC-skew reverse	799	0	687
AT-skew forward	324	0	665
AT-skew reverse	777	0	631

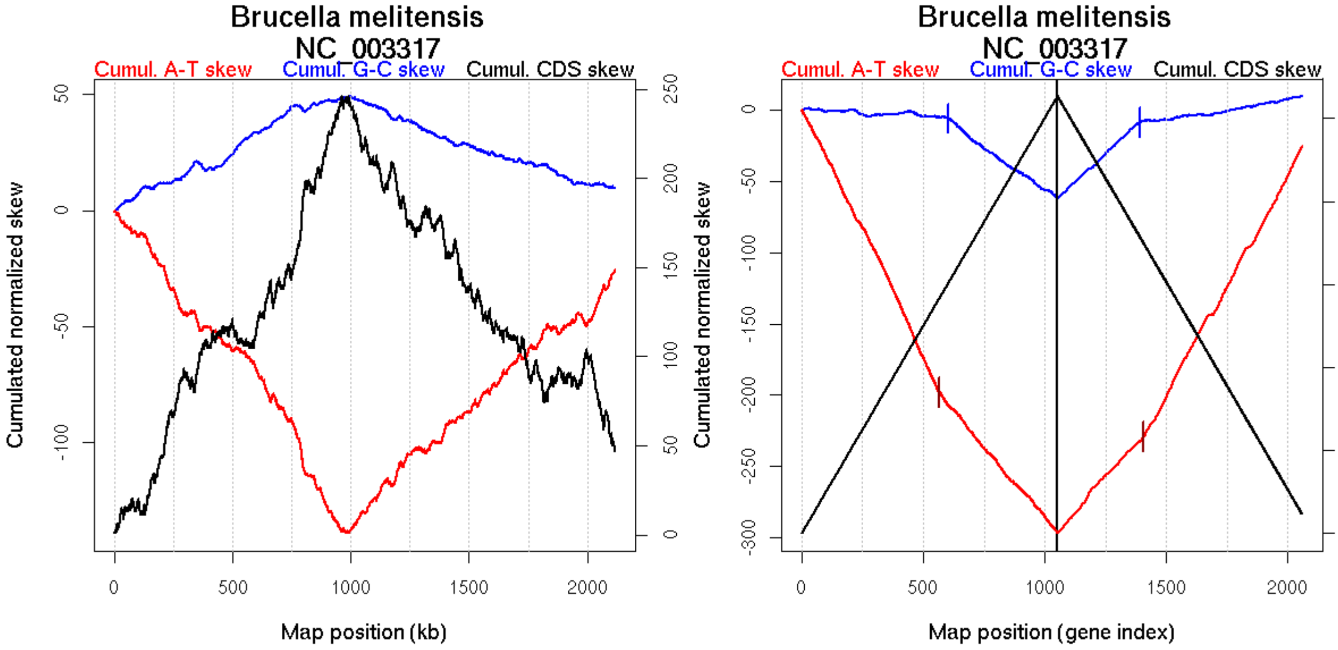
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	346 (708.004 kb)	leading	0.004
	347(714.8105 kb)	505 (1161.987 kb)	lagging	-0.114
GC-skew reverse	506 (0 kb)	799 (687.029 kb)	leading	0.141
	800(688.226 kb)	1051 (1161.987 kb)	lagging	-0.024
AT-skew forward	1 (0 kb)	324 (664.6885 kb)	leading	-0.342
	325(667.086 kb)	505 (1161.987 kb)	lagging	-0.2
AT-skew reverse	506 (0 kb)	777 (631.197 kb)	leading	0.181
	778(632.981 kb)	1051(1161.987 kb)	lagging	0.317

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

51 Brucella melitensis

Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Brucellaceae; Brucella.
Accession number: NC_003317; **Genome size (bp)**: 2117144.
Number of genes: 2059.
Oriloc predictions: Origin 0 kb Terminus 978 kb
Worning et al., 2006: Origin 0 kb Terminus 960 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 2117.016 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 2001.87 kb
Consensus predictions: Origin 0 kb Terminus 978 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	603	NA	1012
GC-skew reverse	1394	NA	960
AT-skew forward	567	NA	935
AT-skew reverse	1408	NA	992

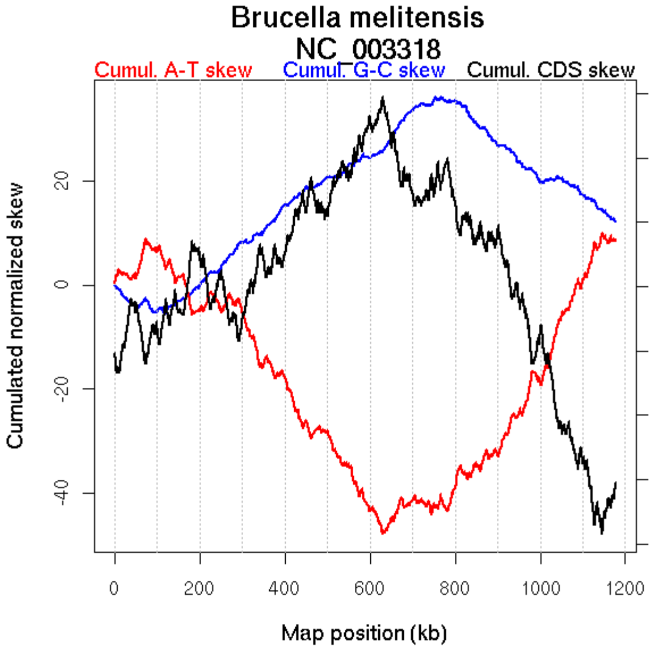
Segments:

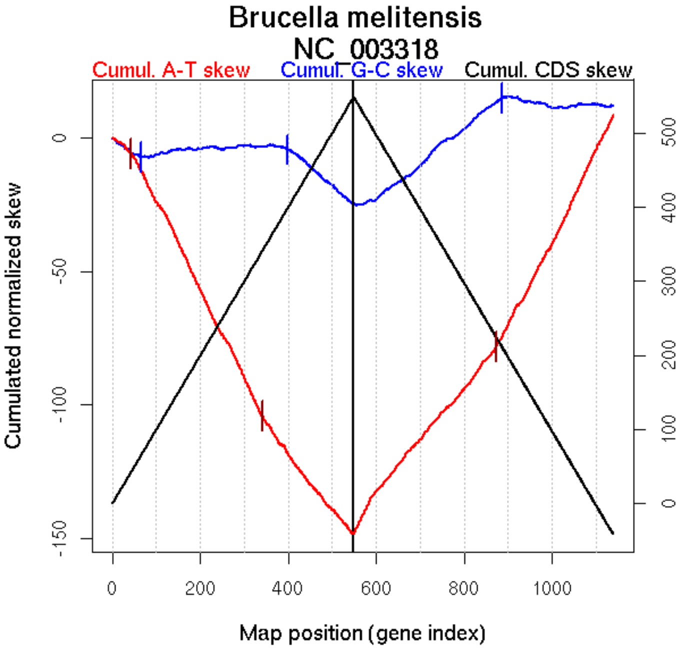
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	603 (1011.9425 kb)	leading	-0.009
	604(1017.222 kb)	1053 (2116.943 kb)	lagging	-0.121
GC-skew reverse	1054 (0 kb)	1394 (959.5415 kb)	leading	0.159
	1395(963.171 kb)	2059 (2116.943 kb)	lagging	0.027
AT-skew forward	1 (0 kb)	567 (935.298 kb)	leading	-0.35
	568(935.7025 kb)	1053 (2116.943 kb)	lagging	-0.199
AT-skew reverse	1054 (0 kb)	1408 (992.029 kb)	leading	0.193
	1409(992.78 kb)	2059(2116.943 kb)	lagging	0.307

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

52 Brucella melitensis

Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Brucellaceae; Brucella.
Accession number: NC_003318; **Genome size (bp)**: 1177787.
Number of genes: 1139.
Oriloc predictions: Origin 93 kb Terminus 767 kb
Worning et al., 2006: Origin 94 kb Terminus 748 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 878.595 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): NA
Consensus predictions: Origin 93 kb Terminus 767 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	65	NA	119
	398	NA	775
GC-skew reverse	887	NA	765
AT-skew forward	43	NA	84
	342	NA	654
AT-skew reverse	873	NA	742

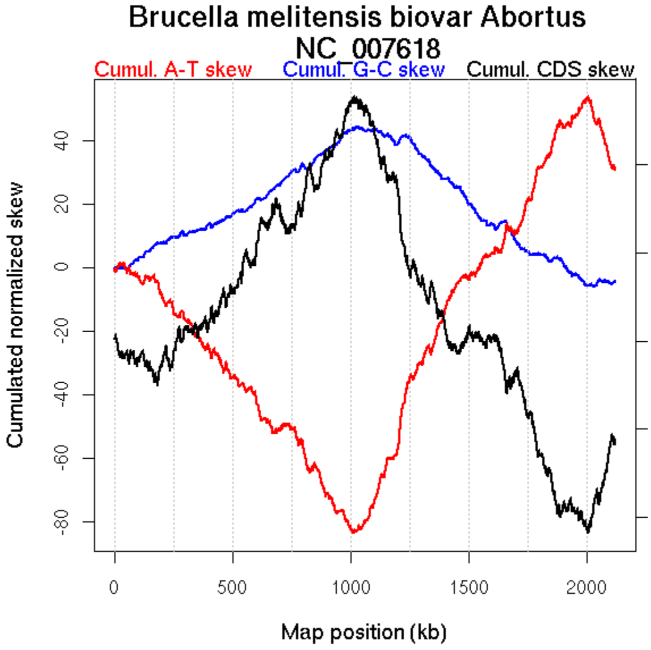
Segments:

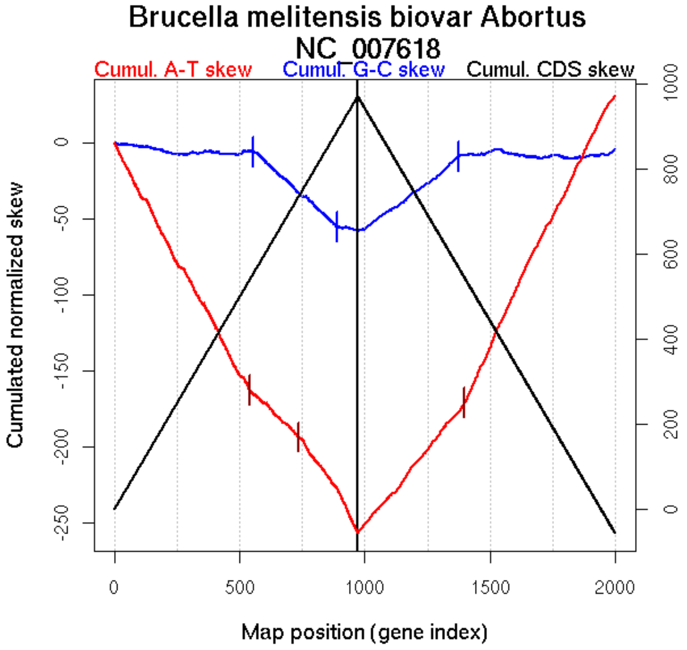
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	65 (118.8585 kb)	NA	-0.113
	66(119.693 kb)	398 (775.3905 kb)	leading	0.011
	399(776.9275 kb)	549 (1177.47 kb)	lagging	-0.142
GC-skew reverse	550 (0 kb)	887 (764.6755 kb)	leading	0.129
	888(765.787 kb)	1139 (1177.47 kb)	lagging	-0.012
AT-skew forward	1 (0 kb)	43 (83.8505 kb)	lagging	-0.14
	44(84.36 kb)	342 (653.739 kb)	leading	-0.333
	343(654.2525 kb)	549 (1177.47 kb)	NA	-0.211
AT-skew reverse	550 (0 kb)	873 (741.8825 kb)	leading	0.201
	874(746.3605 kb)	1139(1177.47 kb)	lagging	0.328

More T than A on the leading strand for replication - for reverse encoded genes.
More G than C on the leading strand for replication.

53 Brucella melitensis biovar Abortus

Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Brucellaceae; Brucella.
Accession number: NC_007618; **Genome size (bp)**: 2121359.
Number of genes: 2000.
Oriloc predictions: Origin 2007 kb Terminus 1024 kb
Worning et al., 2006: Origin NA kb Terminus NA kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 2007.957 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1.53 kb, 584.02 kb, 1099.13 kb
Consensus predictions: Origin 2007 kb Terminus 1024 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	555	NA	1047
	890	NA	2006
GC-skew reverse	1373	NA	999
AT-skew forward	542	NA	1013
	735	NA	1559
AT-skew reverse	1399	NA	1058

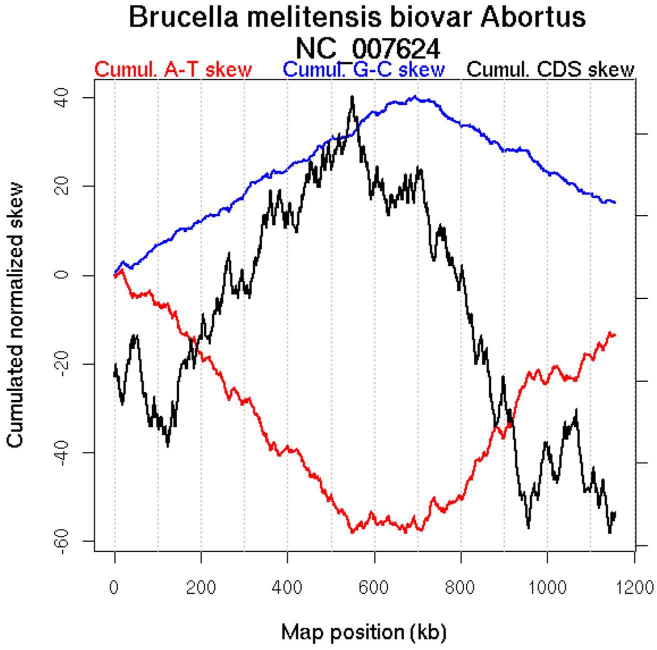
Segments:

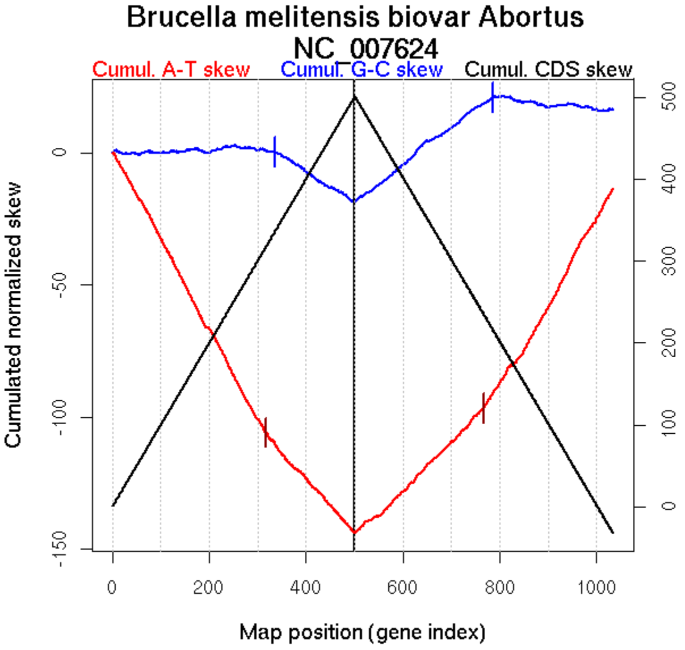
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	555 (1046.9695 kb)	leading	-0.011
	556(1053.557 kb)	890 (2006.217 kb)	lagging	-0.148
	891(2008.926 kb)	972 (2121.15 kb)	leading	-0.026
GC-skew reverse	973 (0 kb)	1373 (998.8635 kb)	leading	0.122
	1374(1002.1865 kb)	2000 (2121.15 kb)	lagging	-0.003
AT-skew forward	1 (0 kb)	542 (1012.669 kb)	leading	-0.299
	543(1013.036 kb)	735 (1559.4045 kb)	lagging	-0.156
	736(1561.8305 kb)	972 (2121.15 kb)	NA	-0.259
AT-skew reverse	973 (0 kb)	1399 (1058.3955 kb)	leading	0.201
	1400(1059.286 kb)	2000(2121.15 kb)	lagging	0.339

More T than A on the leading strand for replication - for reverse encoded genes.
More G than C on the leading strand for replication.

54 Brucella melitensis biovar Abortus

Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Brucellaceae; Brucella.
Accession number: NC_007624; **Genome size (bp)**: 1156948.
Number of genes: 1034.
Oriloc predictions: Origin 0 kb Terminus 695 kb
Worning et al., 2006: Origin NA kb Terminus NA kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1156.872 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): NA
Consensus predictions: Origin 0 kb Terminus 695 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	337	NA	697
GC-skew reverse	787	NA	688
AT-skew forward	317	NA	659
AT-skew reverse	766	NA	637

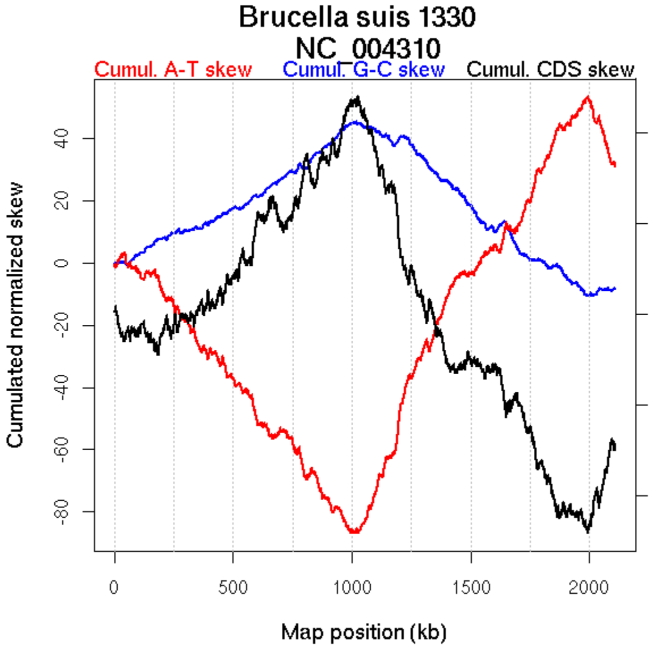
Segments:

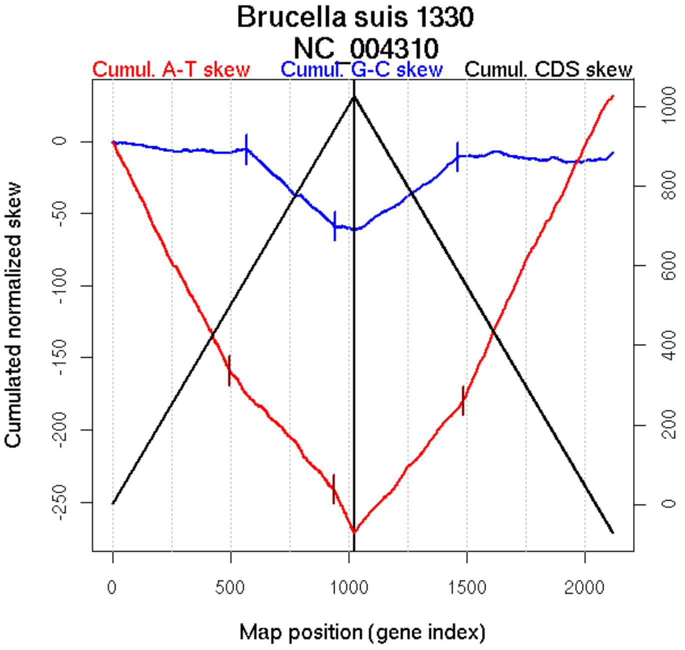
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	337 (696.788 kb)	leading	0.006
	338(697.8015 kb)	501 (1156.731 kb)	lagging	-0.117
GC-skew reverse	502 (0 kb)	787 (688.214 kb)	leading	0.142
	788(689.425 kb)	1034 (1156.731 kb)	lagging	-0.021
AT-skew forward	1 (0 kb)	317 (659.335 kb)	leading	-0.341
	318(661.39 kb)	501 (1156.731 kb)	lagging	-0.201
AT-skew reverse	502 (0 kb)	766 (636.9795 kb)	leading	0.181
	767(639.8225 kb)	1034(1156.731 kb)	lagging	0.317

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

55 Brucella suis 1330

Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Brucellaceae; Brucella.
Accession number: NC_004310; **Genome size (bp)**: 2107794.
Number of genes: 2122.
Oriloc predictions: Origin 1993 kb Terminus 1008 kb
Worning et al., 2006: Origin 1989 kb Terminus 1010 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1994.176 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1.53 kb
Consensus predictions: Origin 1993 kb Terminus 1008 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	567	NA	1023
	944	NA	1997
GC-skew reverse	1465	NA	997
AT-skew forward	497	NA	910
	937	NA	1979
AT-skew reverse	1487	NA	1041

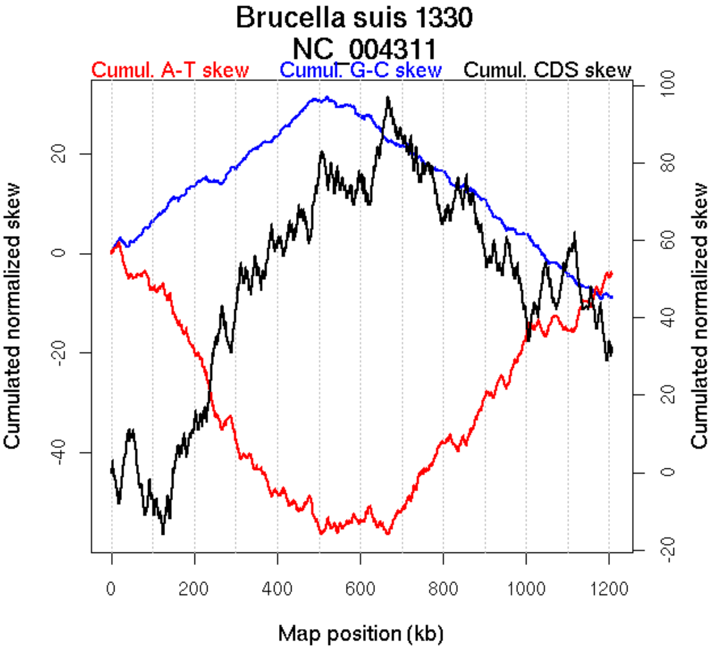
Segments:

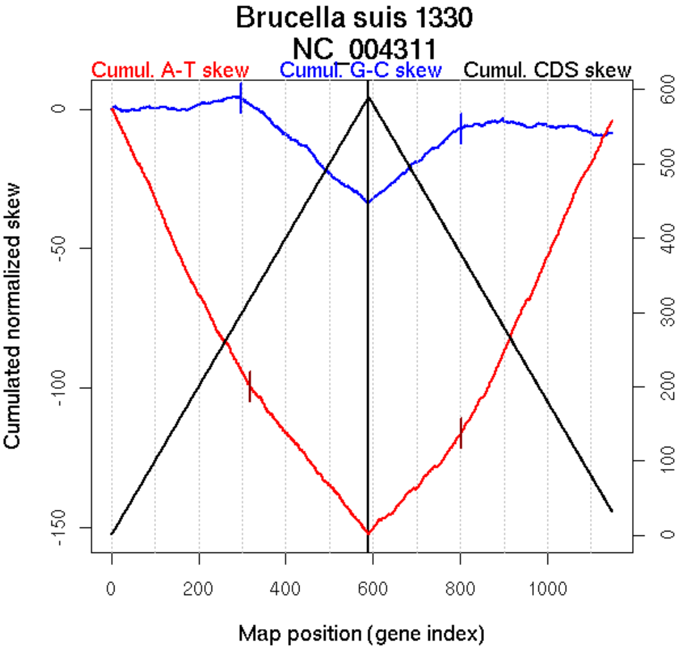
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	567 (1022.605 kb)	leading	-0.012
	568(1023.72 kb)	944 (1996.603 kb)	lagging	-0.14
	945(1997.2245 kb)	1025 (2107.585 kb)	leading	-0.028
GC-skew reverse	1026 (0 kb)	1465 (996.532 kb)	leading	0.115
	1466(998.5145 kb)	2122 (2107.585 kb)	lagging	-0.007
AT-skew forward	1 (0 kb)	497 (910.0405 kb)	leading	-0.316
	498(911.7055 kb)	937 (1979.2755 kb)	lagging	-0.182
	938(1980.48 kb)	1025 (2107.585 kb)	leading	-0.346
AT-skew reverse	1026 (0 kb)	1487 (1041.082 kb)	leading	0.198
	1488(1042.74 kb)	2122(2107.585 kb)	lagging	0.335

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

56 Brucella suis 1330

Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Brucellaceae; Brucella.
Accession number: NC_004311; **Genome size (bp)**: 1207381.
Number of genes: 1148.
Oriloc predictions: Origin 0 kb Terminus 512 kb
Worning et al., 2006: Origin 11 kb Terminus 543 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 410.441 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.75 kb
Consensus predictions: Origin 0 kb Terminus 512 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	297	NA	518
GC-skew reverse	802	NA	502
AT-skew forward	318	NA	573
AT-skew reverse	802	NA	502

Segments:

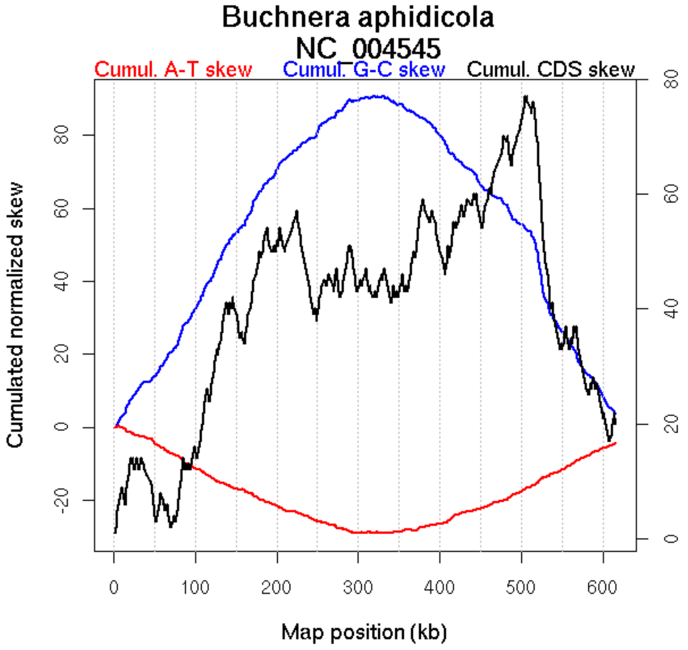
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	297 (517.587 kb)	leading	0.015
	298(523.3945 kb)	590 (1207.164 kb)	lagging	-0.132
GC-skew reverse	591 (0 kb)	802 (501.544 kb)	leading	0.128
	803(507.9615 kb)	1148 (1207.164 kb)	lagging	-0.011
AT-skew forward	1 (0 kb)	318 (572.9915 kb)	leading	-0.32
	319(575.1075 kb)	590 (1207.164 kb)	lagging	-0.192
AT-skew reverse	591 (0 kb)	802 (501.544 kb)	leading	0.163
	803(507.9615 kb)	1148(1207.164 kb)	lagging	0.335

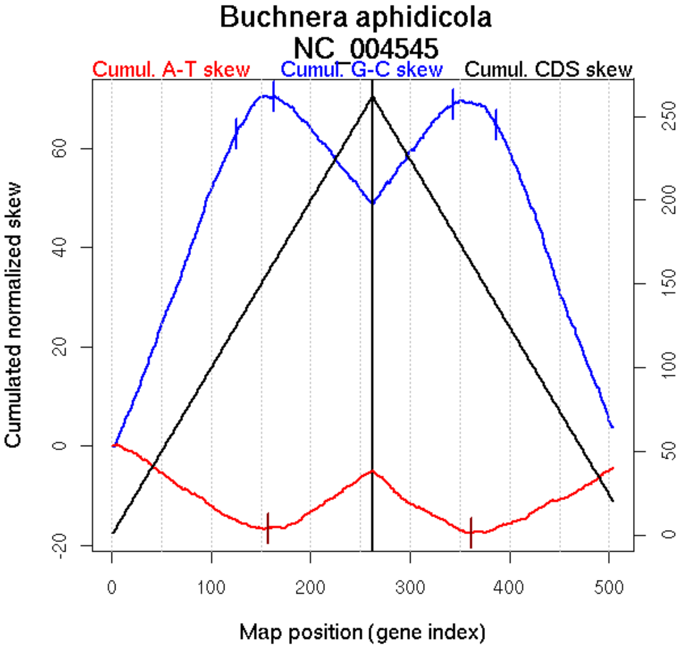
More T than A on the leading strand for replication.

More G than C on the leading strand for replication.

57 Buchnera aphidicola

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Buchnera.
Accession number: NC_004545; **Genome size (bp)**: 615980.
Number of genes: 504.
Oriloc predictions: Origin 4 kb Terminus 336 kb
Worning et al., 2006: Origin 3 kb Terminus 320 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 86.816 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 13.8 kb
Consensus predictions: Origin 0 kb Terminus 336 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	125	0.02333	256
	163	0.00333	354
GC-skew reverse	343	0.04333	255
	387	0.00333	384
AT-skew forward	157	0	342
AT-skew reverse	361	0	298

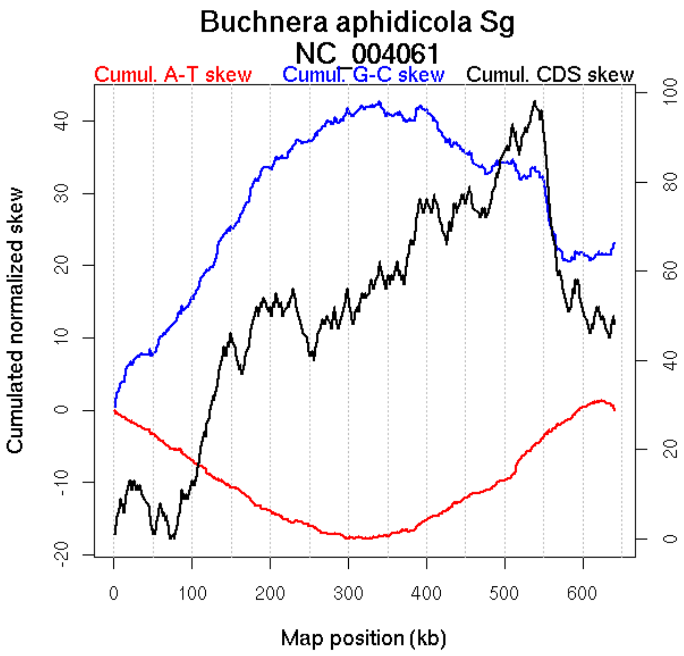
Segments:

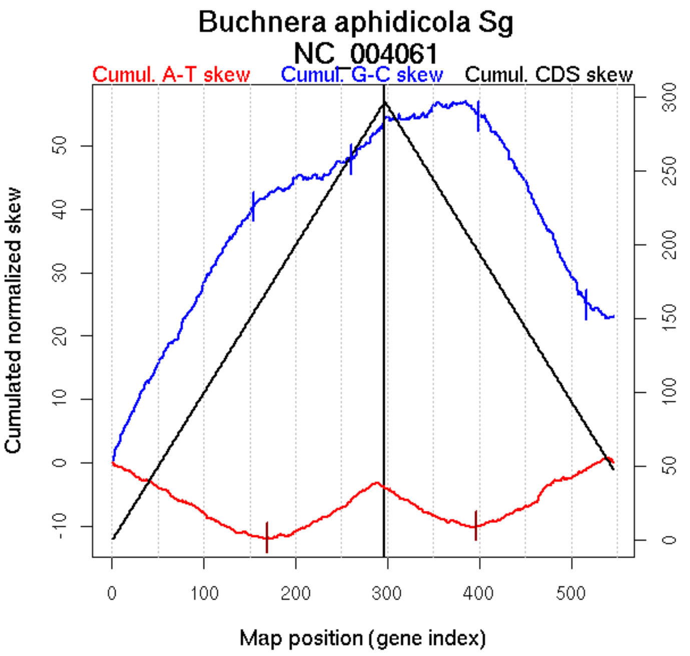
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	125 (255.741 kb)	leading	0.529
	126(260.2555 kb)	163 (354.121 kb)	NA	0.197
	164(355.9595 kb)	262 (615.98 kb)	lagging	-0.231
GC-skew reverse	263 (0 kb)	343 (254.7085 kb)	leading	0.258
	344(262.909 kb)	387 (383.894 kb)	NA	-0.092
	388(385.1935 kb)	504 (615.98 kb)	lagging	-0.542
AT-skew forward	1 (0 kb)	157 (342.212 kb)	leading	-0.123
	158(342.4955 kb)	262 (615.98 kb)	lagging	0.123
AT-skew reverse	263 (0 kb)	361 (297.918 kb)	leading	-0.126
	362(301.2495 kb)	504(615.98 kb)	lagging	0.095

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

58 Buchnera aphidicola Sg

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Buchnera.
Accession number: NC_004061; **Genome size (bp)**: 641454.
Number of genes: 546.
Oriloc predictions: Origin 0 kb Terminus 329 kb
Worning et al., 2006: Origin 628 kb Terminus 331 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 121.963 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 13.08 kb
Consensus predictions: Origin 0 kb Terminus 329 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	154	NA	308
	260	NA	522
GC-skew reverse	399	NA	304
	516	NA	576
AT-skew forward	169	NA	339
AT-skew reverse	397	NA	302

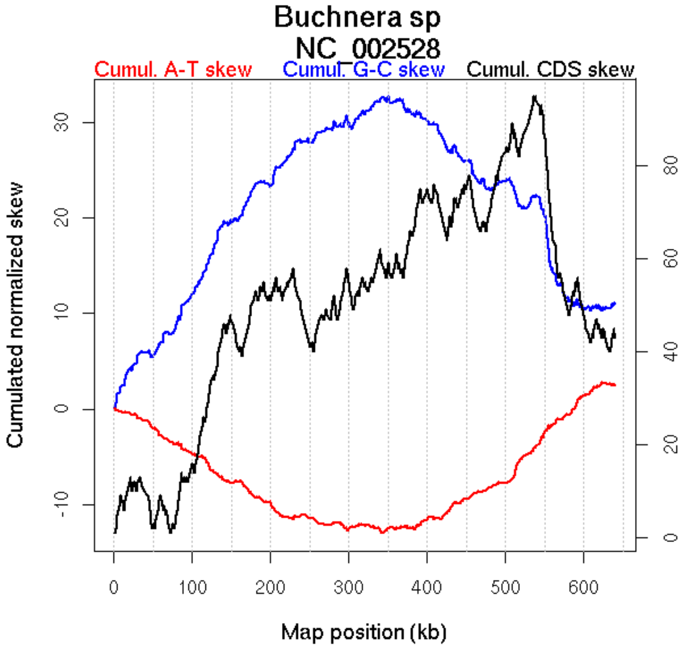
Segments:

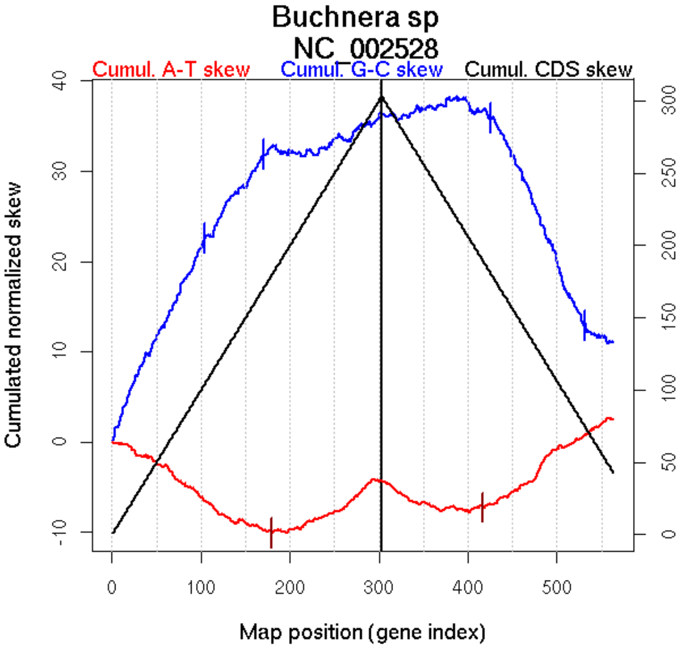
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	154 (308.427 kb)	leading	0.255
	155(309.5565 kb)	260 (521.7875 kb)	lagging	0.062
	261(523.2085 kb)	297 (641.021 kb)	lagging	0.162
GC-skew reverse	298 (0 kb)	399 (304.2175 kb)	leading	0.027
	400(305.3405 kb)	516 (576.395 kb)	lagging	-0.269
	517(577.5765 kb)	546 (641.021 kb)	lagging	-0.083
AT-skew forward	1 (0 kb)	169 (338.815 kb)	leading	-0.076
	170(339.9225 kb)	297 (641.021 kb)	lagging	0.078
AT-skew reverse	298 (0 kb)	397 (302.0995 kb)	leading	-0.064
	398(303.12 kb)	546(641.021 kb)	lagging	0.081

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

59 Buchnera sp

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Buchnera.
Accession number: NC_002528; **Genome size (bp)**: 640681.
Number of genes: 563.
Oriloc predictions: Origin 0 kb Terminus 342 kb
Worning et al., 2006: Origin 627 kb Terminus 331 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 38.44 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 13.24 kb
Consensus predictions: Origin 0 kb Terminus 342 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	104	NA	180
	171	NA	337
GC-skew reverse	425	NA	362
	531	NA	579
AT-skew forward	180	NA	359
AT-skew reverse	417	NA	342

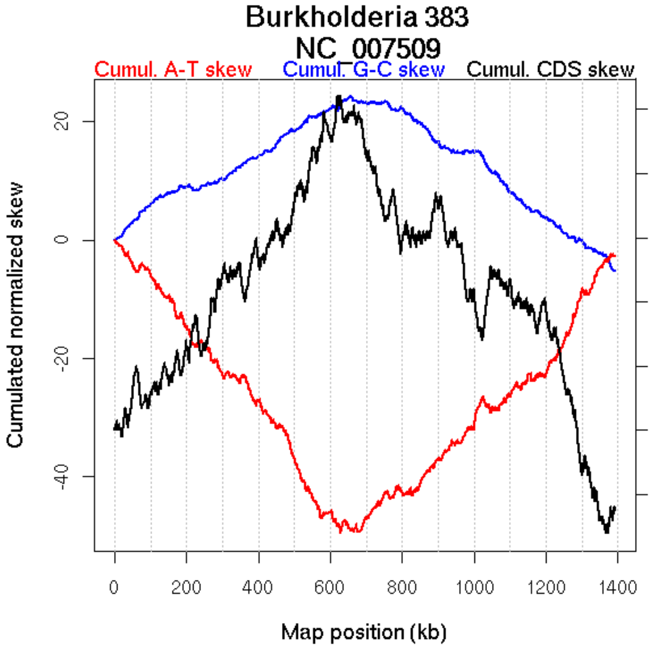
Segments:

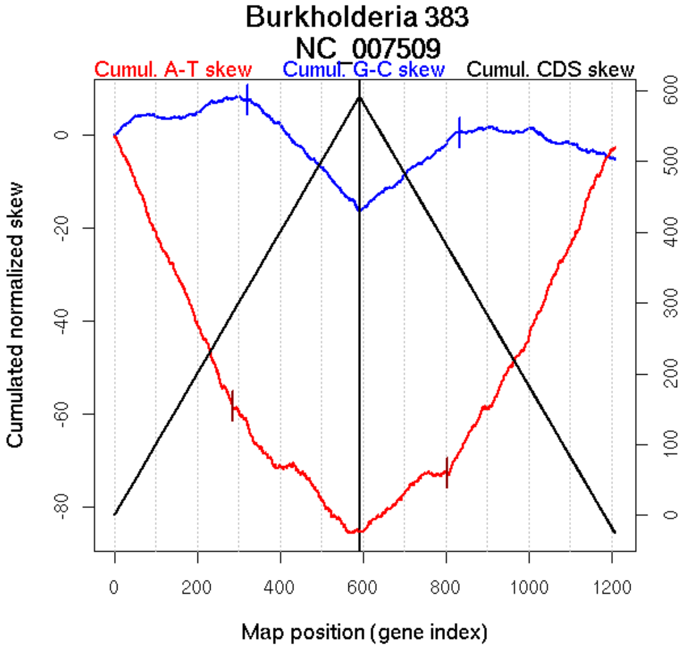
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	104 (180.0005 kb)	leading	0.205
	105(183.1675 kb)	171 (337.1975 kb)	leading	0.141
	172(338.0335 kb)	303 (640.441 kb)	lagging	0.031
GC-skew reverse	304 (0 kb)	425 (361.99 kb)	leading	0.009
	426(362.4875 kb)	531 (578.632 kb)	lagging	-0.233
	532(580.5415 kb)	563 (640.441 kb)	lagging	-0.049
AT-skew forward	1 (0 kb)	180 (358.896 kb)	leading	-0.064
	181(360.6275 kb)	303 (640.441 kb)	lagging	0.052
AT-skew reverse	304 (0 kb)	417 (341.8505 kb)	leading	-0.025
	418(343.1015 kb)	563(640.441 kb)	lagging	0.075

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

60 Burkholderia 383

Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
Accession number: NC_007509; **Genome size (bp)**: 1395069.
Number of genes: 1209.
Oriloc predictions: Origin 0 kb Terminus 658 kb
Worning et al., 2006: Origin 77 kb Terminus 2012 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 142.365 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): NA
Consensus predictions: Origin 0 kb Terminus 658 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	321	0	634
GC-skew reverse	833	0	682
AT-skew forward	285	0	571
AT-skew reverse	805	0.00667	626

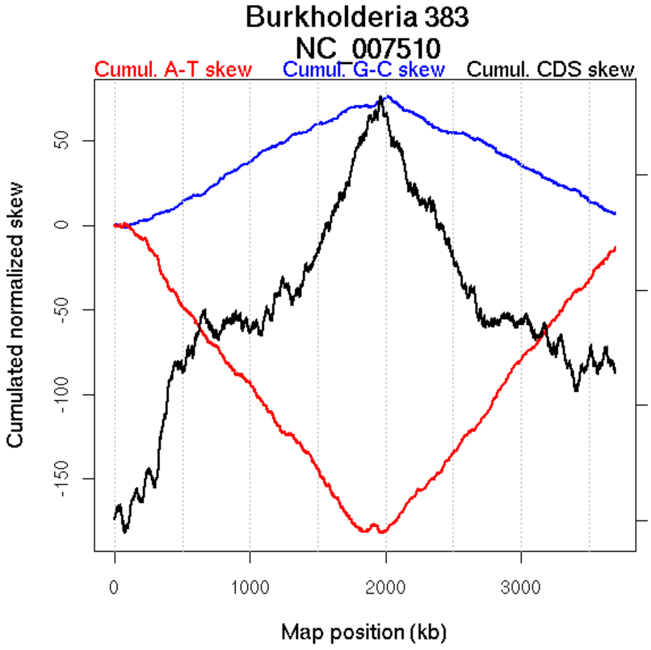
Segments:

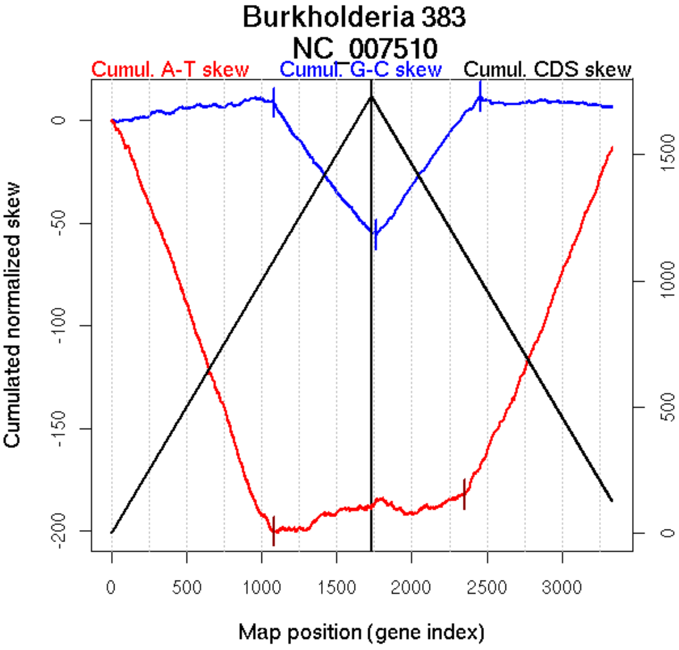
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	321 (634.067 kb)	leading	0.02
	322(639.984 kb)	592 (1392.995 kb)	lagging	-0.09
GC-skew reverse	593 (0 kb)	833 (681.6045 kb)	leading	0.07
	834(683.4015 kb)	1209 (1392.995 kb)	lagging	-0.017
AT-skew forward	1 (0 kb)	285 (570.8625 kb)	leading	-0.204
	286(571.7255 kb)	592 (1392.995 kb)	lagging	-0.087
AT-skew reverse	593 (0 kb)	805 (625.688 kb)	leading	0.069
	806(626.1925 kb)	1209(1392.995 kb)	lagging	0.178

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

61 Burkholderia 383

Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
Accession number: NC_007510; **Genome size (bp)**: 3694126.
Number of genes: 3334.
Oriloc predictions: Origin 84 kb Terminus 2010 kb
Worning et al., 2006: Origin 2 kb Terminus 1786 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 31.445 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.86 kb
Consensus predictions: Origin 0 kb Terminus 2010 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1079	0	2054
GC-skew reverse	1765	0	72
	2454	0	2014
AT-skew forward	1082	0	2058
AT-skew reverse	2354	0	1718

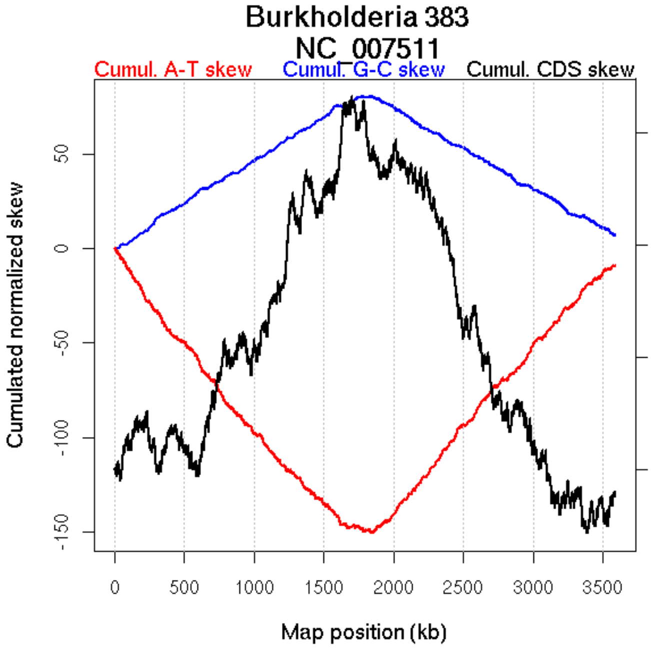
Segments:

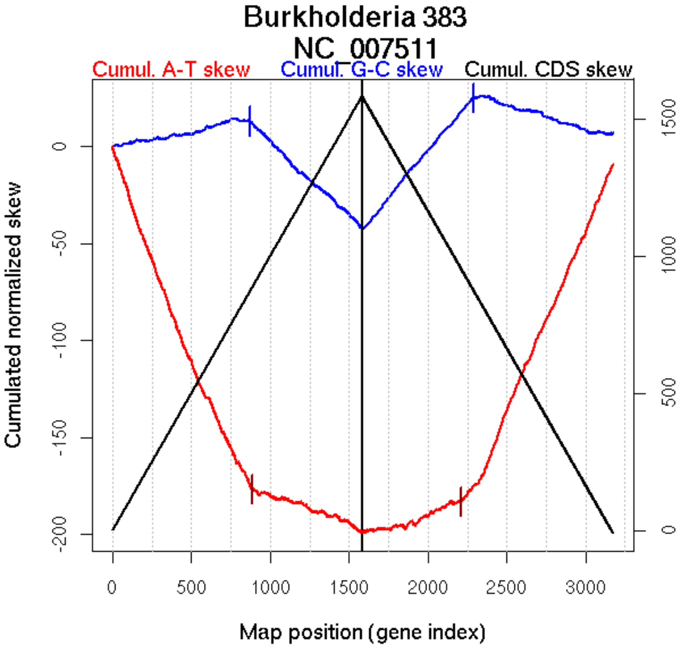
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1079 (2054.0745 kb)	leading	0.01
	1080(2054.7685 kb)	1731 (3693.781 kb)	lagging	-0.097
GC-skew reverse	1732 (0 kb)	1765 (72.126 kb)	leading	-0.014
	1766(73.415 kb)	2454 (2014.0375 kb)	leading	0.1
	2455(2015.7355 kb)	3334 (3693.781 kb)	lagging	-0.002
AT-skew forward	1 (0 kb)	1082 (2057.5185 kb)	leading	-0.199
	1083(2062.124 kb)	1731 (3693.781 kb)	lagging	0.023
AT-skew reverse	1732 (0 kb)	2354 (1717.7815 kb)	leading	0.005
	2355(1719.701 kb)	3334(3693.781 kb)	lagging	0.176

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

62 Burkholderia 383

Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
Accession number: NC_007511; **Genome size (bp)**: 3587082.
Number of genes: 3174.
Oriloc predictions: Origin 0 kb Terminus 1775 kb
Worning et al., 2006: Origin 2 kb Terminus 667 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 869.516 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): NA
Consensus predictions: Origin 0 kb Terminus 1775 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	874	0	1835
GC-skew reverse	2289	0	1791
AT-skew forward	886	0	1862
AT-skew reverse	2212	0	1584

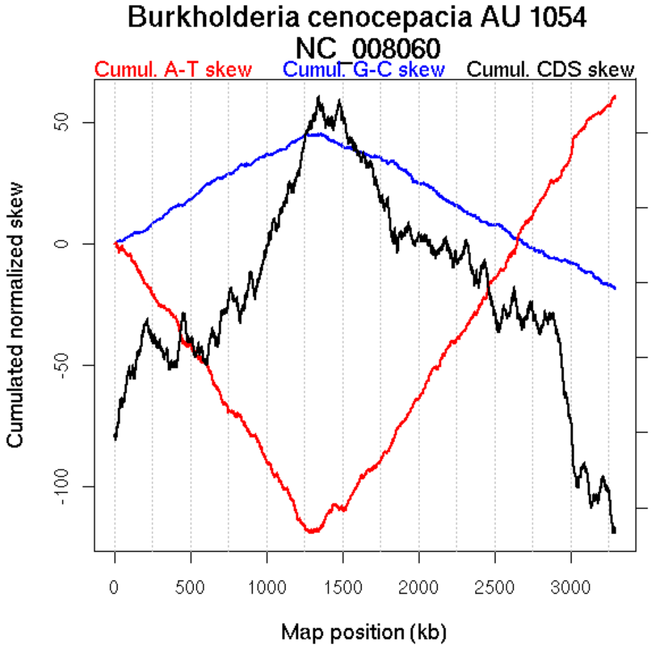
Segments:

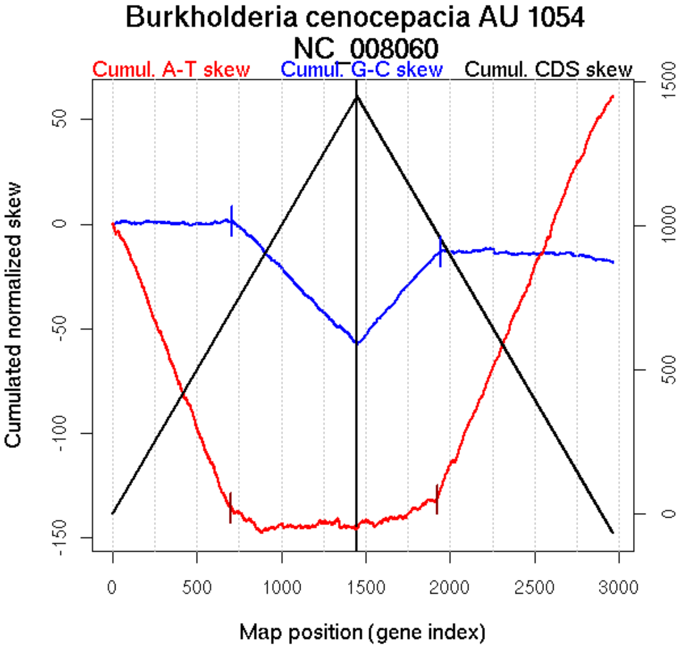
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	874 (1835.114 kb)	leading	0.017
	875(1838.037 kb)	1582 (3587.014 kb)	lagging	-0.076
GC-skew reverse	1583 (0 kb)	2289 (1790.561 kb)	leading	0.097
	2290(1793.215 kb)	3174 (3587.014 kb)	lagging	-0.025
AT-skew forward	1 (0 kb)	886 (1862.364 kb)	leading	-0.2
	887(1863.0115 kb)	1582 (3587.014 kb)	lagging	-0.029
AT-skew reverse	1583 (0 kb)	2212 (1584.3295 kb)	leading	0.027
	2213(1587.152 kb)	3174(3587.014 kb)	lagging	0.188

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

63 Burkholderia cenocepacia AU 1054

Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
Accession number: NC_008060; **Genome size (bp)**: 3294563.
Number of genes: 2965.
Oriloc predictions: Origin 0 kb Terminus 1262 kb
Worning et al., 2006: Origin 5 kb Terminus 1348 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 53.538 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 302.53 kb, 2803.09 kb
Consensus predictions: Origin 0 kb Terminus 1262 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	708	NA	1334
GC-skew reverse	1945	NA	1345
AT-skew forward	699	NA	1321
AT-skew reverse	1921	NA	1248

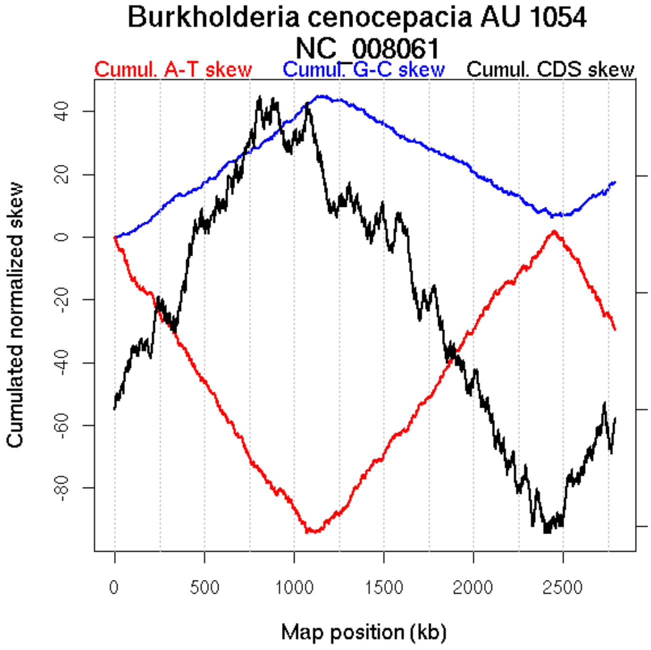
Segments:

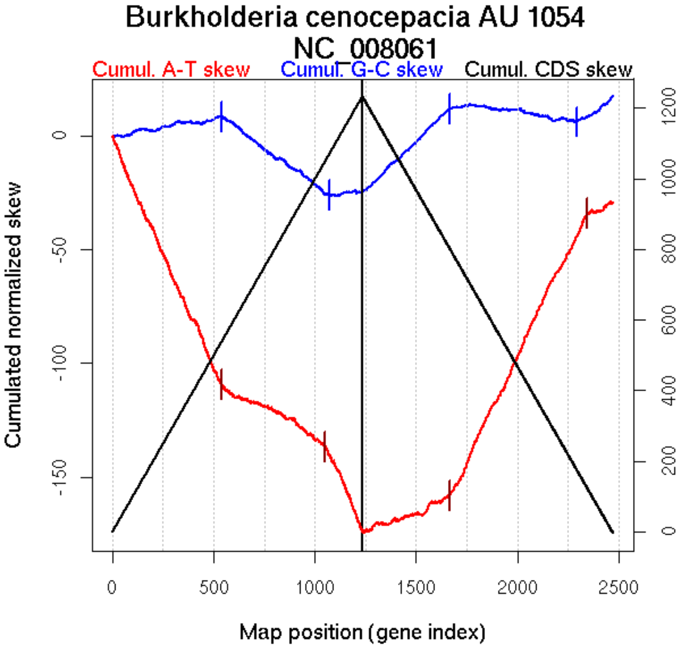
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	708 (1333.6525 kb)	leading	0
	709(1334.2875 kb)	1449 (3294.336 kb)	lagging	-0.081
GC-skew reverse	1450 (0 kb)	1945 (1345.499 kb)	leading	0.092
	1946(1345.8775 kb)	2965 (3294.336 kb)	lagging	-0.004
AT-skew forward	1 (0 kb)	699 (1320.843 kb)	leading	-0.203
	700(1322.306 kb)	1449 (3294.336 kb)	lagging	-0.005
AT-skew reverse	1450 (0 kb)	1921 (1247.63 kb)	leading	0.027
	1922(1254.052 kb)	2965(3294.336 kb)	lagging	0.19

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

64 Burkholderia cenocepacia AU 1054

Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
Accession number: NC_008061; **Genome size (bp)**: 2788459.
Number of genes: 2472.
Oriloc predictions: Origin 2453 kb Terminus 1180 kb
Worning et al., 2006: Origin 2459 kb Terminus 1094 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 552.795 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): NA
Consensus predictions: Origin 2453 kb Terminus 1180 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	537	NA	1119
	1072	NA	2487
GC-skew reverse	1663	NA	1131
	2292	NA	2368
AT-skew forward	538	NA	1123
	1048	NA	2438
AT-skew reverse	1667	NA	1135
	2345	NA	2470

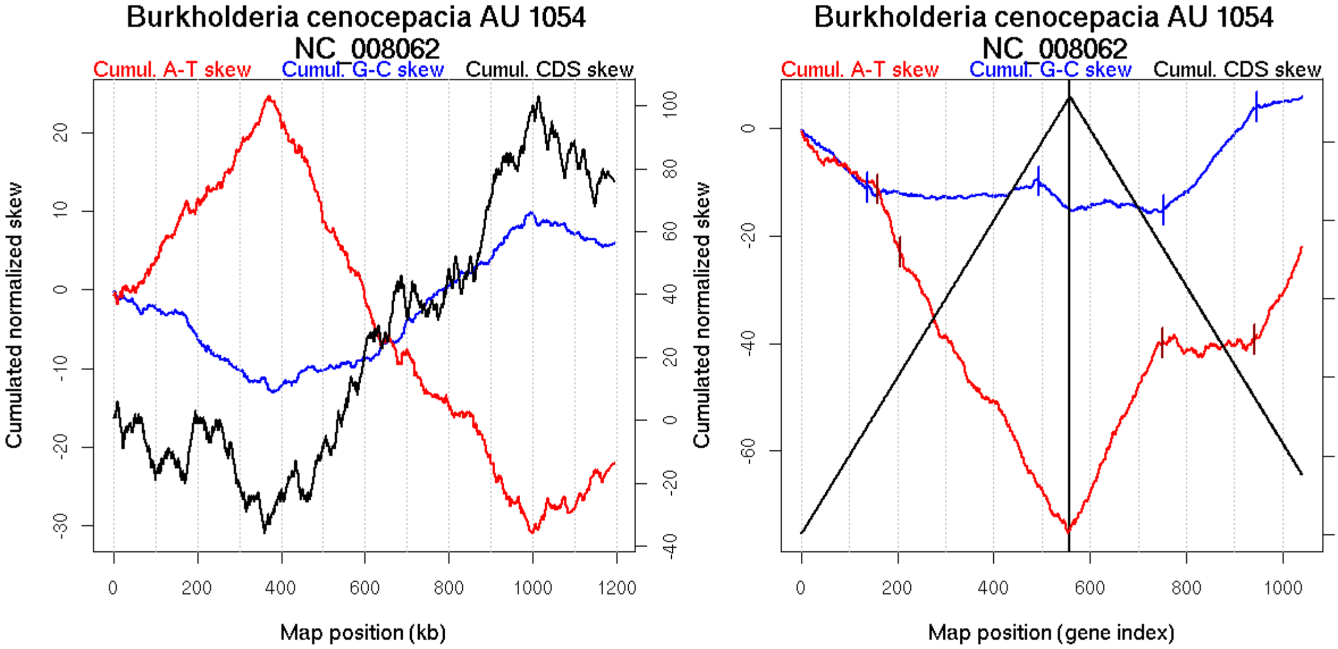
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	537 (1119.4725 kb)	leading	0.016
	538(1123.2275 kb)	1072 (2486.767 kb)	lagging	-0.065
	1073(2491.099 kb)	1234 (2788.442 kb)	leading	0.013
GC-skew reverse	1235 (0 kb)	1663 (1131.421 kb)	leading	0.087
	1664(1132.2995 kb)	2292 (2368.0175 kb)	lagging	-0.012
	2293(2369.55 kb)	2472 (2788.442 kb)	NA	0.06
AT-skew forward	1 (0 kb)	538 (1123.2275 kb)	leading	-0.2
	539(1124.561 kb)	1048 (2437.8655 kb)	lagging	-0.047
	1049(2439.6285 kb)	1234 (2788.442 kb)	leading	-0.203
AT-skew reverse	1235 (0 kb)	1667 (1135.3685 kb)	leading	0.035
	1668(1136.515 kb)	2345(2470.411 kb)	lagging	0.185
	2346(2473.4115 kb)	2472(2788.442 kb)	leading	0.04

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

65 Burkholderia cenocepacia AU 1054

Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
Accession number: NC_008062; **Genome size (bp)**: 1196094.
Number of genes: 1040.
Oriloc predictions: Origin 384 kb Terminus 995 kb
Worning et al., 2006: Origin 384 kb Terminus 1001 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 421.149 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): NA
Consensus predictions: Origin 384 kb Terminus 995 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	138	NA	333
	493	NA	1006
GC-skew reverse	752	NA	411
	946	NA	973
AT-skew forward	159	NA	387
	205	NA	481
AT-skew reverse	750	NA	404
	942	NA	958

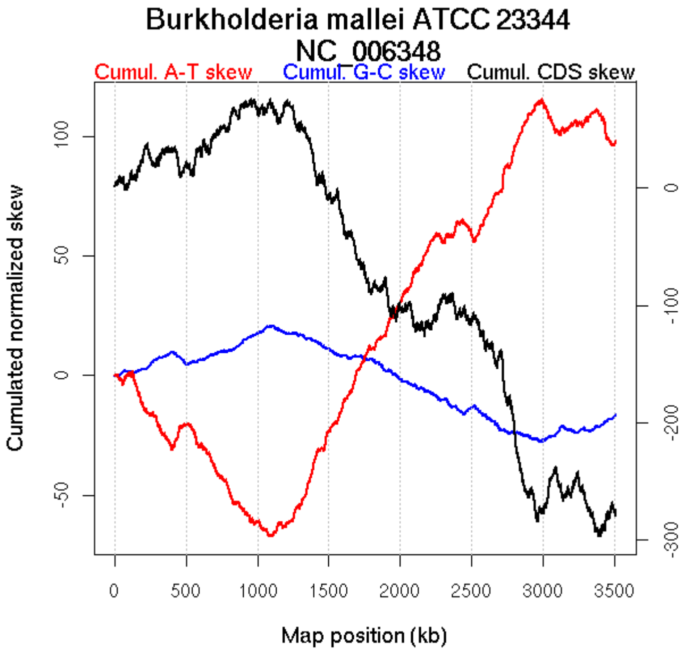
Segments:

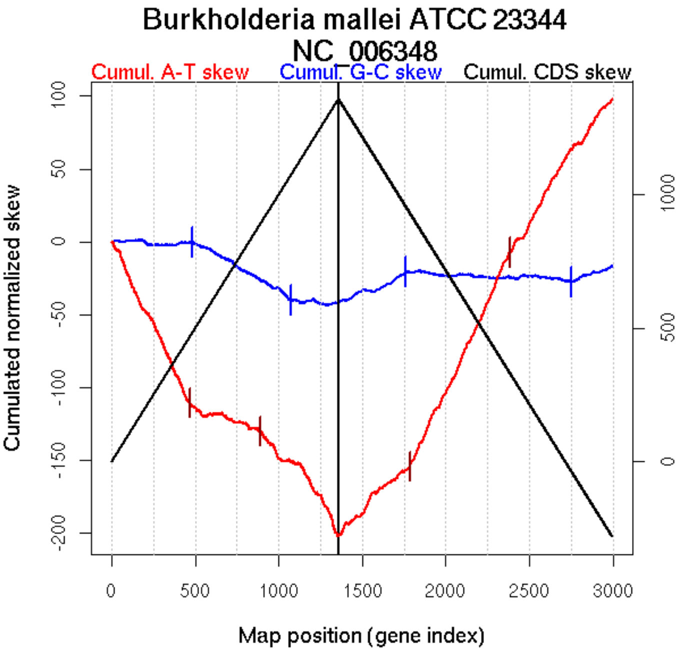
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	138 (333.165 kb)	lagging	-0.081
	139(335.41 kb)	493 (1006.456 kb)	leading	0.002
	494(1007.875 kb)	558 (1195.505 kb)	lagging	-0.083
GC-skew reverse	559 (0 kb)	752 (411.3665 kb)	lagging	-0.004
	753(421.559 kb)	946 (972.5365 kb)	leading	0.102
	947(974.2945 kb)	1040 (1195.505 kb)	lagging	0.017
AT-skew forward	1 (0 kb)	159 (386.861 kb)	lagging	-0.055
	160(388.7885 kb)	205 (480.776 kb)	leading	-0.259
	206(482.12 kb)	558 (1195.505 kb)	NA	-0.145
AT-skew reverse	559 (0 kb)	750 (403.8945 kb)	lagging	0.19
	751(404.8815 kb)	942(958.123 kb)	leading	0.001
	943(961.0035 kb)	1040(1195.505 kb)	lagging	0.171

More T than A on the leading strand for replication - for reverse encoded genes.
More G than C on the leading strand for replication.

66 Burkholderia mallei ATCC 23344

Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia.
Accession number: NC_006348; **Genome size (bp)**: 3510148.
Number of genes: 2995.
Oriloc predictions: Origin 3009 kb Terminus 1086 kb
Worning et al., 2006: Origin 2960 kb Terminus 1081 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1552.022 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.85 kb
Consensus predictions: Origin 3009 kb Terminus 1086 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	483	NA	1106
	1071	NA	2759
GC-skew reverse	1761	NA	1085
	2750	NA	2953
AT-skew forward	468	NA	1070
	891	NA	2267
AT-skew reverse	1784	NA	1132
	2386	NA	2350

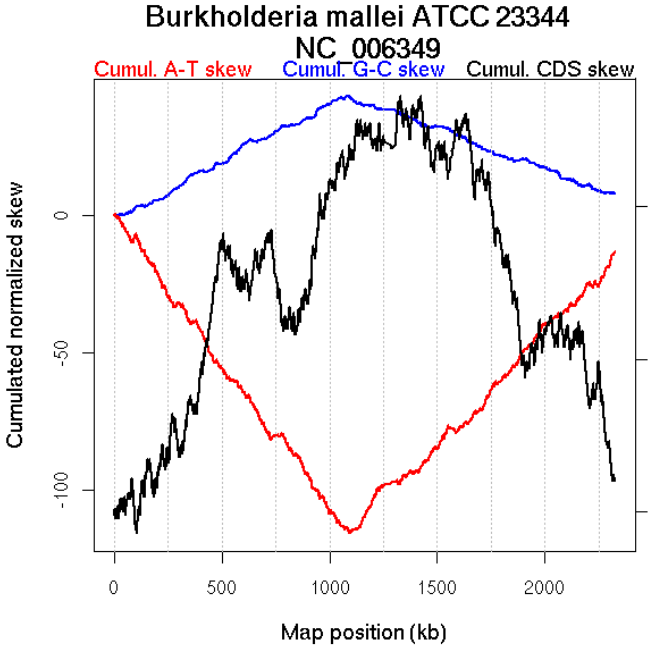
Segments:

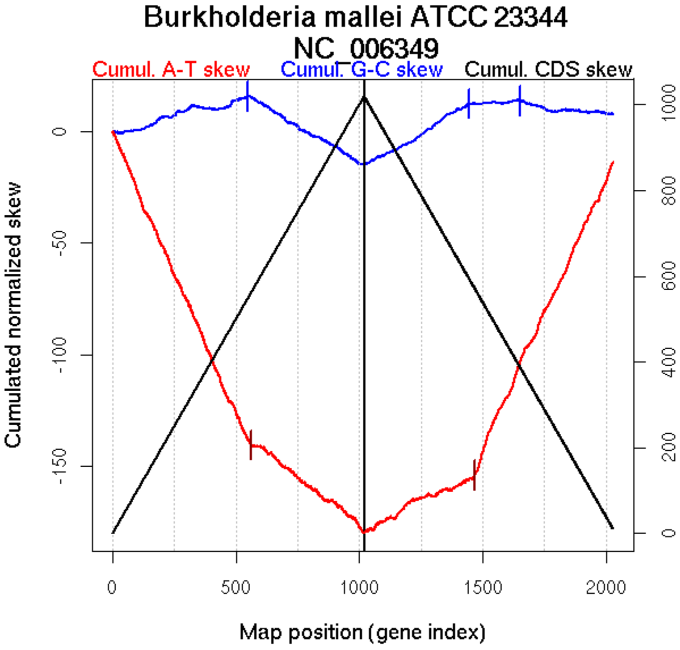
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	483 (1106.126 kb)	leading	-0.005
	484(1113.578 kb)	1071 (2759.2005 kb)	lagging	-0.066
	1072(2760.262 kb)	1358 (3509.727 kb)	NA	-0.01
GC-skew reverse	1359 (0 kb)	1761 (1085.097 kb)	leading	0.046
	1762(1089.9365 kb)	2750 (2952.766 kb)	lagging	-0.005
	2751(2953.251 kb)	2995 (3509.727 kb)	leading	0.04
AT-skew forward	1 (0 kb)	468 (1069.507 kb)	leading	-0.238
	469(1072.2365 kb)	891 (2266.6955 kb)	lagging	-0.037
	892(2267.078 kb)	1358 (3509.727 kb)	NA	-0.135
AT-skew reverse	1359 (0 kb)	1784 (1131.6835 kb)	leading	0.113
	1785(1133.125 kb)	2386(2349.6165 kb)	lagging	0.244
	2387(2350.6115 kb)	2995(3509.727 kb)	NA	0.178

More G than C on the leading strand for replication.

67 Burkholderia mallei ATCC 23344

Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia.
Accession number: NC_006349; **Genome size (bp)**: 2325379.
Number of genes: 2029.
Oriloc predictions: Origin 6 kb Terminus 1088 kb
Worning et al., 2006: Origin 4 kb Terminus 1089 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 856.553 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): NA
Consensus predictions: Origin 0 kb Terminus 1088 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	548	NA	1073
GC-skew reverse	1446	NA	1042
	1654	NA	1549
AT-skew forward	560	NA	1092
AT-skew reverse	1468	NA	1104

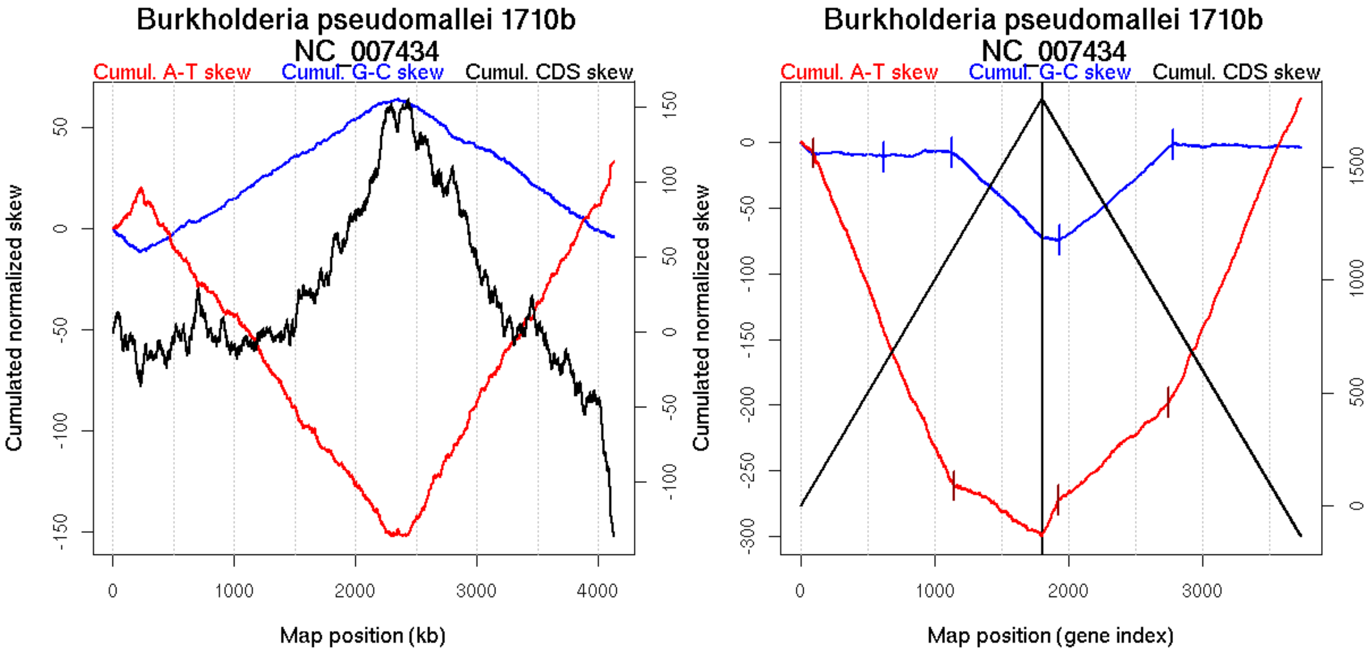
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	548 (1073.254 kb)	leading	0.03
	549(1074.07 kb)	1020 (2324.451 kb)	lagging	-0.066
GC-skew reverse	1021 (0 kb)	1446 (1042.0975 kb)	leading	0.067
	1447(1042.4855 kb)	1654 (1549.3515 kb)	lagging	0.007
	1655(1568.6775 kb)	2029 (2324.451 kb)	lagging	-0.012
AT-skew forward	1 (0 kb)	560 (1092.239 kb)	leading	-0.252
	561(1095.5475 kb)	1020 (2324.451 kb)	lagging	-0.085
AT-skew reverse	1021 (0 kb)	1468 (1104.4155 kb)	leading	0.055
	1469(1107.213 kb)	2029(2324.451 kb)	lagging	0.242

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

68 Burkholderia pseudomallei 1710b

Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; pseudomallei group.
Accession number: NC_007434; **Genome size (bp)**: 4126292.
Number of genes: 3736.
Oriloc predictions: Origin 222 kb Terminus 2344 kb
Worning et al., 2006: Origin 225 kb Terminus 2390 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 2786.353 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 311.44 kb
Consensus predictions: Origin 222 kb Terminus 2344 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	620	NA	1302
	1124	NA	2346
GC-skew reverse	1928	NA	247
	2776	NA	2323
AT-skew forward	91	NA	236
	1145	NA	2405
AT-skew reverse	1926	NA	241
	2749	NA	2237

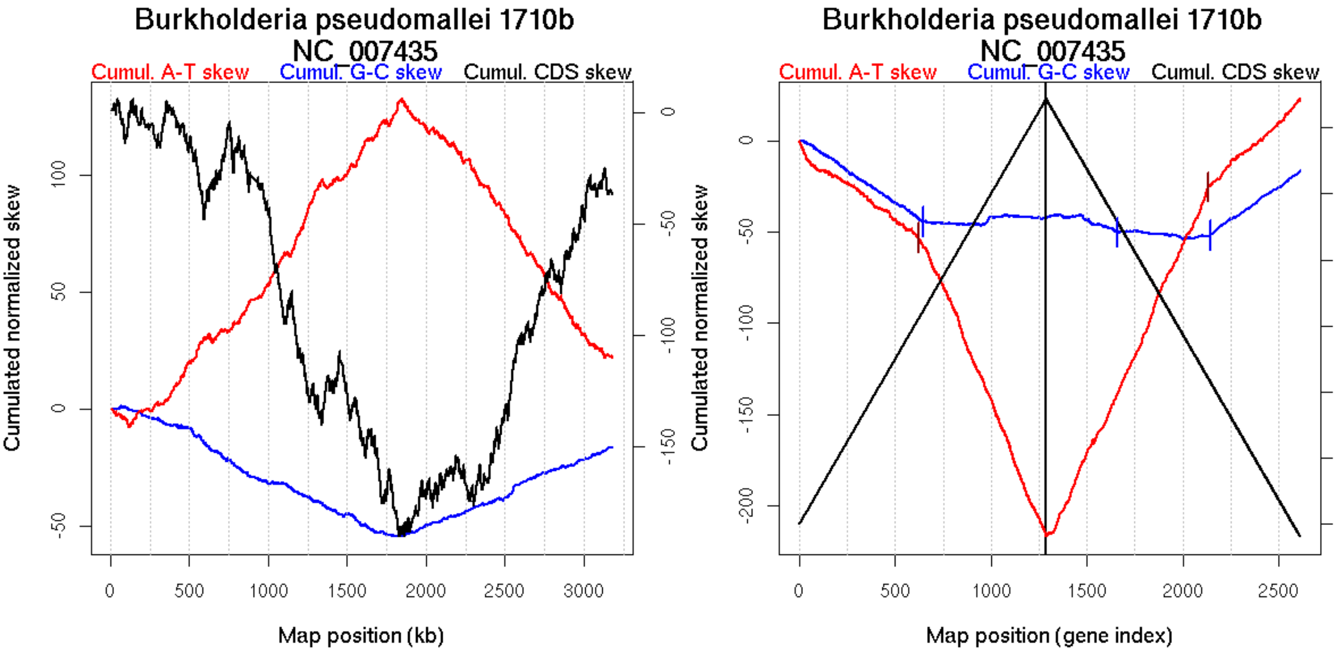
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	620 (1302.4425 kb)	leading	-0.008
	621(1304.166 kb)	1124 (2346.049 kb)	leading	0.009
	1125(2347.94 kb)	1801 (4125.633 kb)	lagging	-0.097
GC-skew reverse	1802 (0 kb)	1928 (246.892 kb)	lagging	-0.017
	1929(251.843 kb)	2776 (2322.7165 kb)	leading	0.088
	2777(2324.561 kb)	3736 (4125.633 kb)	lagging	-0.002
AT-skew forward	1 (0 kb)	91 (236.4735 kb)	lagging	-0.086
	92(237.258 kb)	1145 (2404.721 kb)	leading	-0.247
	1146(2408.569 kb)	1801 (4125.633 kb)	lagging	-0.063
AT-skew reverse	1802 (0 kb)	1926 (240.538 kb)	lagging	0.222
	1927(244.3055 kb)	2749(2237.1635 kb)	leading	0.092
	2750(2238.079 kb)	3736(4125.633 kb)	lagging	0.242

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

69 Burkholderia pseudomallei 1710b

Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; pseudomallei group.
Accession number: NC_007435; **Genome size (bp)**: 3181762.
Number of genes: 2611.
Oriloc predictions: Origin 1843 kb Terminus 89 kb
Worning et al., 2006: Origin 1842 kb Terminus 121 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 2693.125 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): NA
Consensus predictions: Origin 1843 kb Terminus 89 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	645	NA	1778
GC-skew reverse	1658	NA	945
	2142	NA	1856
AT-skew forward	621	NA	1729
AT-skew reverse	2134	NA	1842

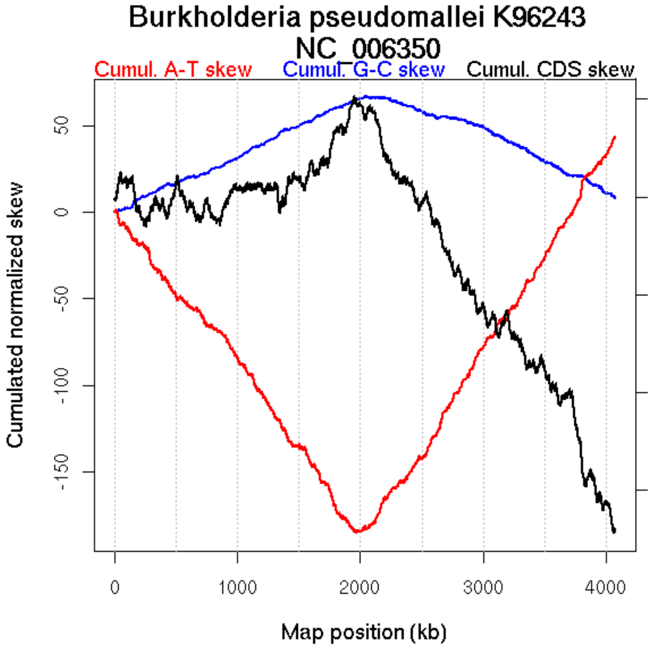
Segments:

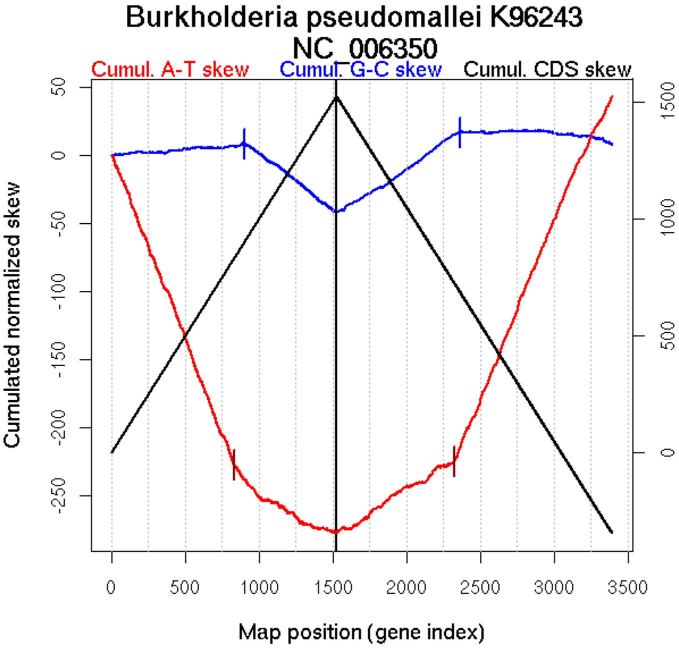
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	645 (1778.4525 kb)	lagging	-0.071
	646(1783.175 kb)	1287 (3179.266 kb)	leading	0.008
GC-skew reverse	1288 (0 kb)	1658 (945.0435 kb)	lagging	-0.024
	1659(946.451 kb)	2142 (1856.0875 kb)	lagging	-0.008
	2143(1857.189 kb)	2611 (3179.266 kb)	leading	0.073
AT-skew forward	1 (0 kb)	621 (1729.054 kb)	lagging	-0.074
	622(1731.644 kb)	1287 (3179.266 kb)	leading	-0.253
AT-skew reverse	1288 (0 kb)	2134 (1842.1005 kb)	lagging	0.231
	2135(1843.68 kb)	2611(3179.266 kb)	leading	0.096

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

70 Burkholderia pseudomallei K96243

Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; pseudomallei group.
Accession number: NC_006350; **Genome size (bp)**: 4074542.
Number of genes: 3395.
Oriloc predictions: Origin 1 kb Terminus 2039 kb
Worning et al., 2006: Origin 4 kb Terminus 1994 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 2526.57 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 86.15 kb
Consensus predictions: Origin 0 kb Terminus 2039 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	900	NA	2054
GC-skew reverse	2366	NA	2125
AT-skew forward	834	NA	1866
AT-skew reverse	2323	NA	2018

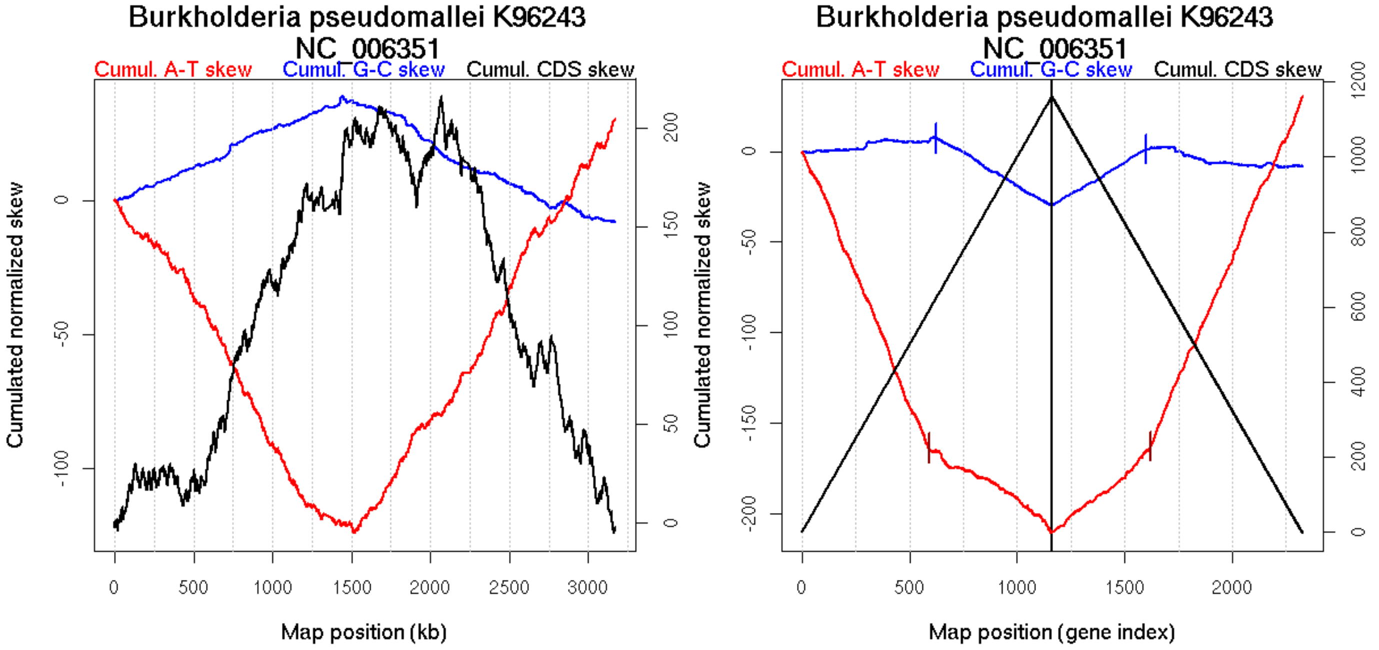
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	900 (2053.767 kb)	leading	0.008
	901(2055.3165 kb)	1526 (4074.029 kb)	lagging	-0.083
GC-skew reverse	1527 (0 kb)	2366 (2125.471 kb)	leading	0.073
	2367(2127.681 kb)	3395 (4074.029 kb)	lagging	-0.006
AT-skew forward	1 (0 kb)	834 (1866.239 kb)	leading	-0.276
	835(1867.976 kb)	1526 (4074.029 kb)	lagging	-0.067
AT-skew reverse	1527 (0 kb)	2323 (2018.337 kb)	leading	0.069
	2324(2020.015 kb)	3395(4074.029 kb)	lagging	0.256

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

71 Burkholderia pseudomallei K96243

Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; pseudomallei group.
Accession number: NC_006351; **Genome size (bp)**: 3173005.
Number of genes: 2327.
Oriloc predictions: Origin 0 kb Terminus 1440 kb
Worning et al., 2006: Origin 3161 kb Terminus 1518 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 873.516 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): NA
Consensus predictions: Origin 0 kb Terminus 1440 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	621	NA	1446
GC-skew reverse	1600	NA	1444
AT-skew forward	590	NA	1412
AT-skew reverse	1622	NA	1522

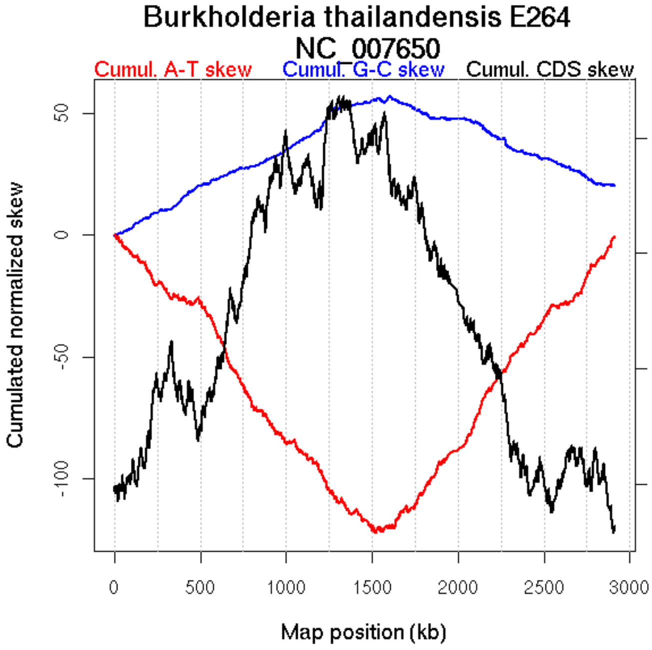
Segments:

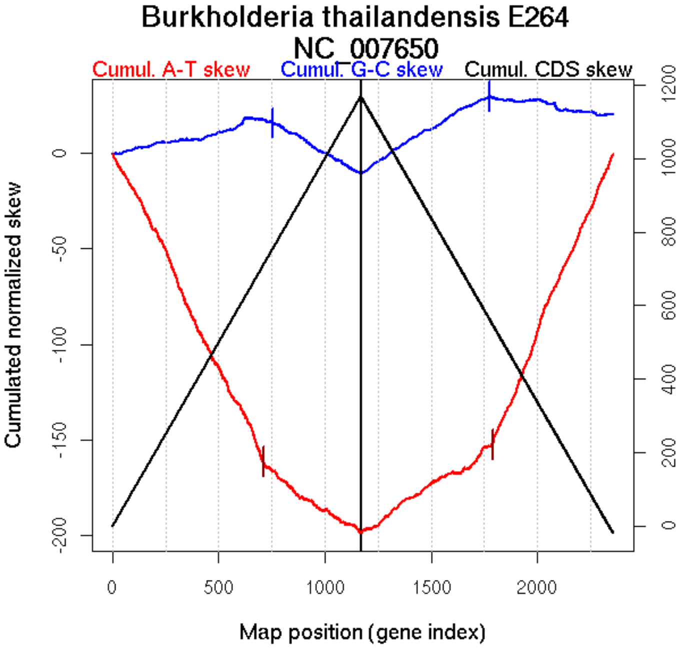
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	621 (1446.399 kb)	leading	0.013
	622(1446.589 kb)	1162 (3170.031 kb)	lagging	-0.071
GC-skew reverse	1163 (0 kb)	1600 (1444.1415 kb)	leading	0.071
	1601(1455.908 kb)	2327 (3170.031 kb)	lagging	-0.017
AT-skew forward	1 (0 kb)	590 (1412.152 kb)	leading	-0.284
	591(1420.35 kb)	1162 (3170.031 kb)	lagging	-0.072
AT-skew reverse	1163 (0 kb)	1622 (1522.1755 kb)	leading	0.098
	1623(1525.5875 kb)	2327(3170.031 kb)	lagging	0.27

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

72 Burkholderia thailandensis E264

Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; pseudomallei group.
Accession number: NC_007650; **Genome size (bp)**: 2914771.
Number of genes: 2357.
Oriloc predictions: Origin 5 kb Terminus 1599 kb
Worning et al., 2006: Origin 9 kb Terminus 2649 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 2135 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): NA
Consensus predictions: Origin 0 kb Terminus 1599 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	756	NA	1646
GC-skew reverse	1773	NA	1599
AT-skew forward	710	NA	1518
AT-skew reverse	1790	NA	1631

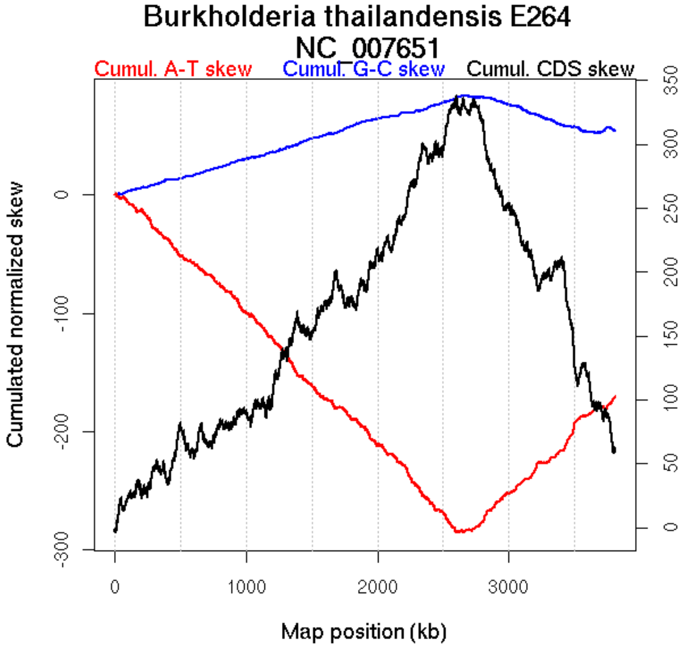
Segments:

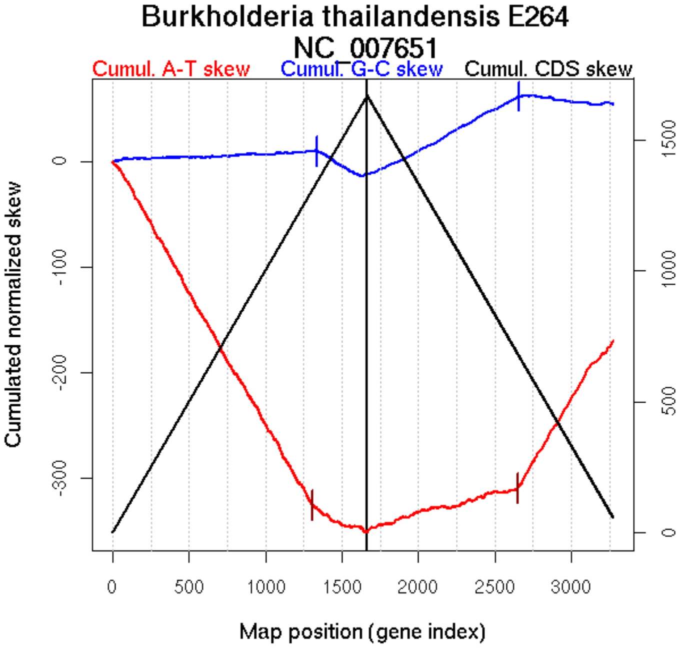
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	756 (1646.121 kb)	leading	0.025
	757(1648.081 kb)	1169 (2911.815 kb)	lagging	-0.066
GC-skew reverse	1170 (0 kb)	1773 (1599.0185 kb)	leading	0.067
	1774(1602.1695 kb)	2357 (2911.815 kb)	lagging	-0.018
AT-skew forward	1 (0 kb)	710 (1517.942 kb)	leading	-0.229
	711(1518.6215 kb)	1169 (2911.815 kb)	lagging	-0.076
AT-skew reverse	1170 (0 kb)	1790 (1631.303 kb)	leading	0.072
	1791(1632.677 kb)	2357(2911.815 kb)	lagging	0.268

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

73 Burkholderia thailandensis E264

Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; pseudomallei group.
Accession number: NC_007651; **Genome size (bp)**: 3809201.
Number of genes: 3275.
Oriloc predictions: Origin 1 kb Terminus 2649 kb
Worning et al., 2006: Origin 4 kb Terminus 1519 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 2360.432 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 3691.15 kb
Consensus predictions: Origin 0 kb Terminus 2649 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1334	NA	2709
GC-skew reverse	2656	NA	2646
AT-skew forward	1308	NA	2620
AT-skew reverse	2652	NA	2629

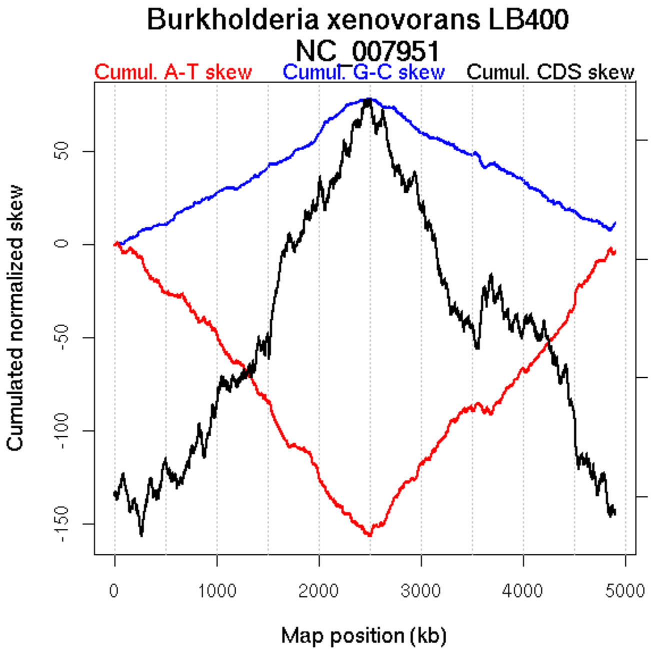
Segments:

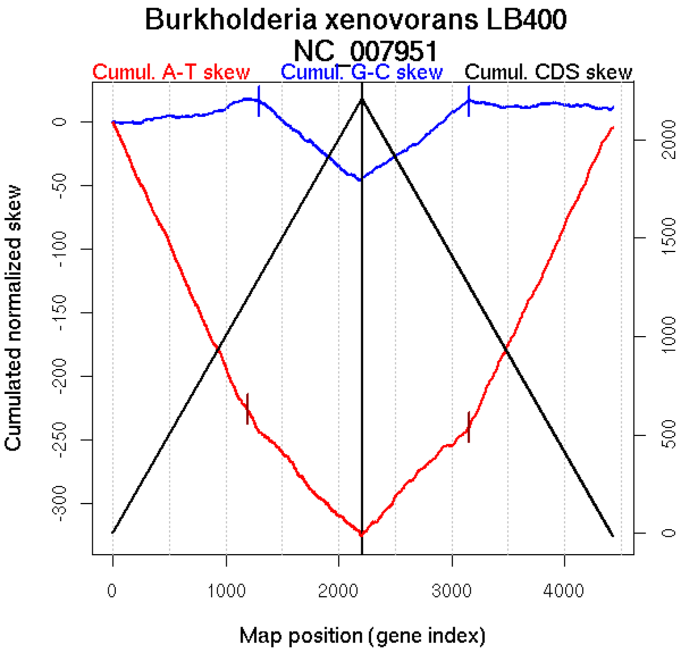
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1334 (2709.46 kb)	leading	0.006
	1335(2710.307 kb)	1667 (3808.859 kb)	lagging	-0.079
GC-skew reverse	1668 (0 kb)	2656 (2646.1865 kb)	leading	0.077
	2657(2651.4055 kb)	3275 (3808.859 kb)	lagging	-0.015
AT-skew forward	1 (0 kb)	1308 (2620.339 kb)	leading	-0.253
	1309(2625.2545 kb)	1667 (3808.859 kb)	lagging	-0.064
AT-skew reverse	1668 (0 kb)	2652 (2629.3945 kb)	leading	0.039
	2653(2631.4555 kb)	3275(3808.859 kb)	lagging	0.229

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

74 Burkholderia xenovorans LB400

Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia.
Accession number: NC_007951; **Genome size (bp)**: 4895836.
Number of genes: 4430.
Oriloc predictions: Origin 2 kb Terminus 2499 kb
Worning et al., 2006: Origin 260 kb Terminus 2500 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 4844.087 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1.01 kb
Consensus predictions: Origin 0 kb Terminus 2499 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1297	NA	2539
GC-skew reverse	3154	NA	2482
AT-skew forward	1192	NA	2316
AT-skew reverse	3156	NA	2485

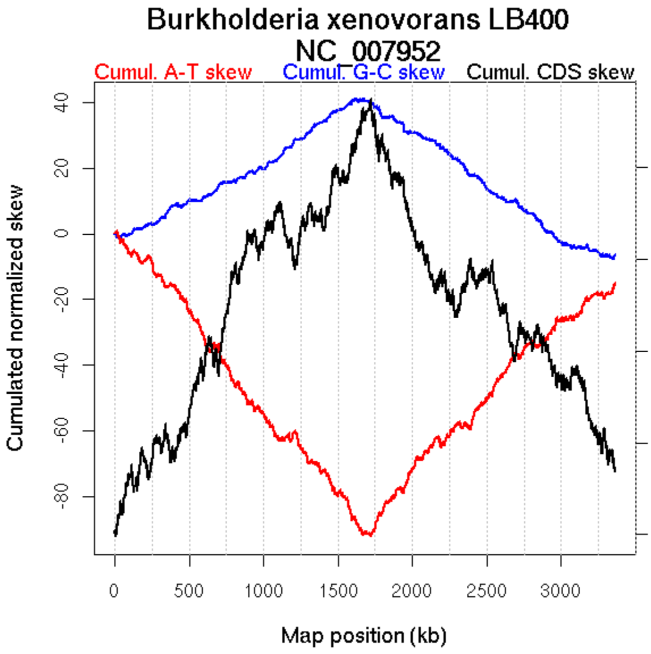
Segments:

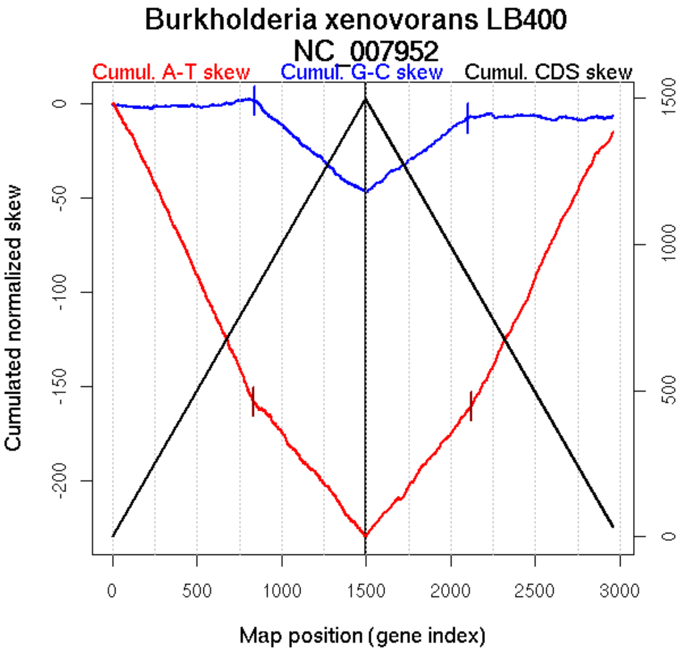
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1297 (2538.9415 kb)	leading	0.015
	1298(2540.004 kb)	2207 (4895.635 kb)	lagging	-0.072
GC-skew reverse	2208 (0 kb)	3154 (2482.261 kb)	leading	0.065
	3155(2483.609 kb)	4430 (4895.635 kb)	lagging	-0.002
AT-skew forward	1 (0 kb)	1192 (2315.639 kb)	leading	-0.193
	1193(2316.5435 kb)	2207 (4895.635 kb)	lagging	-0.096
AT-skew reverse	2208 (0 kb)	3156 (2485.027 kb)	leading	0.09
	3157(2487.3125 kb)	4430(4895.635 kb)	lagging	0.188

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

75 Burkholderia xenovorans LB400

Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia.
Accession number: NC_007952; **Genome size (bp)**: 3363523.
Number of genes: 2960.
Oriloc predictions: Origin 31 kb Terminus 1677 kb
Worning et al., 2006: Origin 9 kb Terminus 1691 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 3357.362 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): NA
Consensus predictions: Origin 0 kb Terminus 1677 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	841	NA	1665
GC-skew reverse	2103	NA	1647
AT-skew forward	836	NA	1660
AT-skew reverse	2120	NA	1692

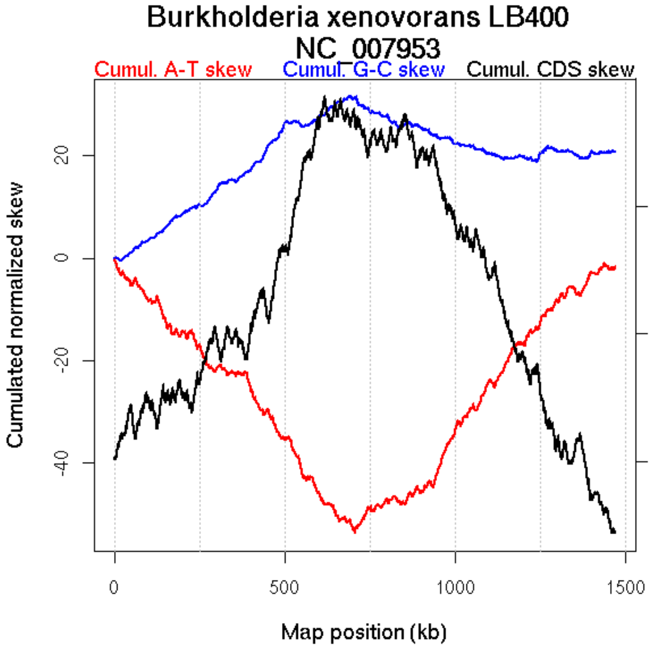
Segments:

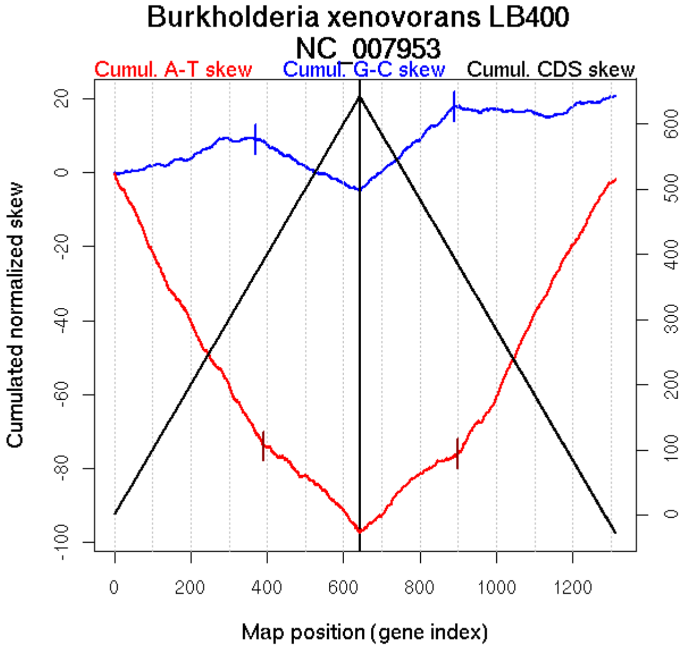
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	841 (1665.4565 kb)	leading	0.004
	842(1666.8515 kb)	1497 (3363.376 kb)	lagging	-0.075
GC-skew reverse	1498 (0 kb)	2103 (1646.909 kb)	leading	0.065
	2104(1649.9635 kb)	2960 (3363.376 kb)	lagging	-0.002
AT-skew forward	1 (0 kb)	836 (1660.262 kb)	leading	-0.192
	837(1661.207 kb)	1497 (3363.376 kb)	lagging	-0.109
AT-skew reverse	1498 (0 kb)	2120 (1692.1305 kb)	leading	0.11
	2121(1701.174 kb)	2960(3363.376 kb)	lagging	0.181

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

76 Burkholderia xenovorans LB400

Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia.
Accession number: NC_007953; **Genome size (bp)**: 1471779.
Number of genes: 1312.
Oriloc predictions: Origin 16 kb Terminus 691 kb
Worning et al., 2006: Origin 1440 kb Terminus 704 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 903.896 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): NA
Consensus predictions: Origin 0 kb Terminus 691 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	371	NA	659
GC-skew reverse	891	NA	691
AT-skew forward	391	NA	710
AT-skew reverse	900	NA	709

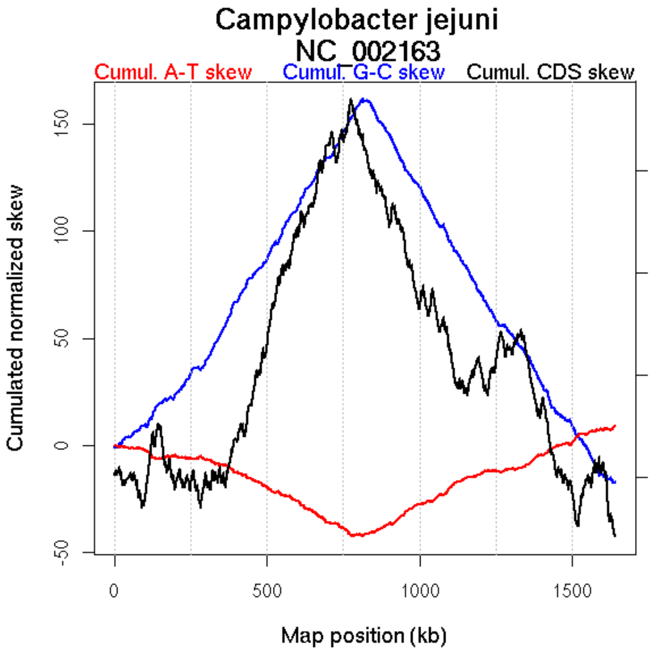
Segments:

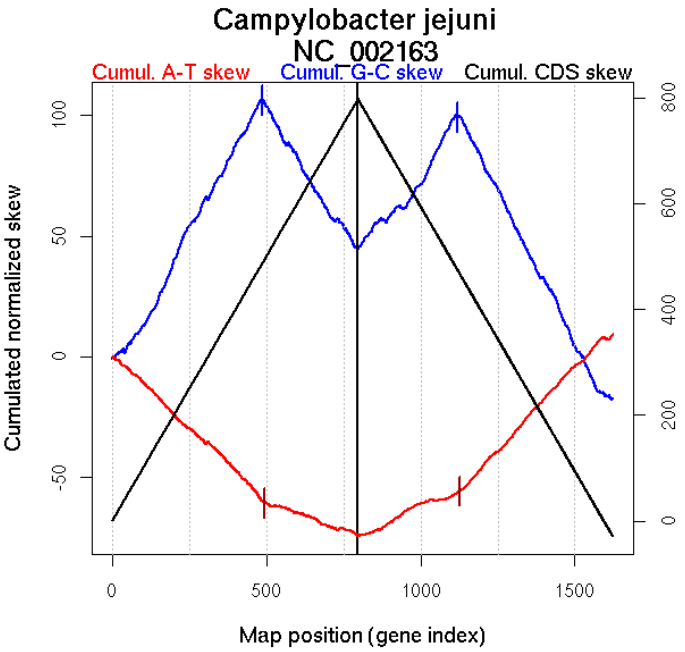
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	371 (659.453 kb)	leading	0.031
	372(660.2655 kb)	642 (1471.524 kb)	lagging	-0.052
GC-skew reverse	643 (0 kb)	891 (691.4125 kb)	leading	0.09
	892(692.5065 kb)	1312 (1471.524 kb)	lagging	0.006
AT-skew forward	1 (0 kb)	391 (710.39 kb)	leading	-0.187
	392(711.468 kb)	642 (1471.524 kb)	lagging	-0.09
AT-skew reverse	643 (0 kb)	900 (709.004 kb)	leading	0.087
	901(709.318 kb)	1312(1471.524 kb)	lagging	0.191

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

77 Campylobacter jejuni

Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter.
Accession number: NC_002163; **Genome size (bp)**: 1641481.
Number of genes: 1623.
Oriloc predictions: Origin 0 kb Terminus 813 kb
Worning et al., 2006: Origin 1 kb Terminus 775 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1262.127 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.66 kb
Consensus predictions: Origin 0 kb Terminus 813 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	486	0	830
GC-skew reverse	1120	0	818
AT-skew forward	495	0	861
AT-skew reverse	1126	0	829

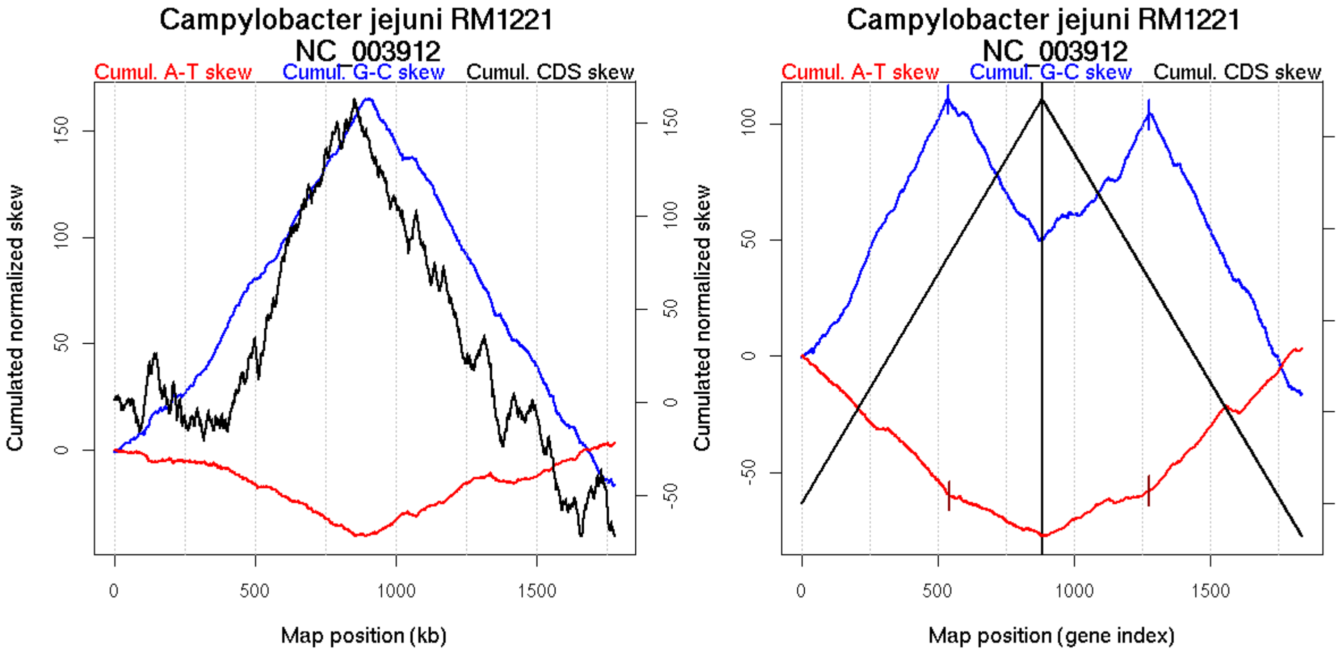
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	486 (830.069 kb)	leading	0.237
	487(840.3345 kb)	797 (1641.386 kb)	lagging	-0.2
GC-skew reverse	798 (0 kb)	1120 (818.14 kb)	leading	0.165
	1121(818.866 kb)	1623 (1641.386 kb)	lagging	-0.248
AT-skew forward	1 (0 kb)	495 (860.7225 kb)	leading	-0.121
	496(861.053 kb)	797 (1641.386 kb)	lagging	-0.045
AT-skew reverse	798 (0 kb)	1126 (829.177 kb)	leading	0.06
	1127(830.6035 kb)	1623(1641.386 kb)	lagging	0.136

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

78 Campylobacter jejuni RM1221

Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales; Campylobacteraceae; Campylobacter.
Accession number: NC_003912; **Genome size (bp)**: 1777831.
Number of genes: 1838.
Oriloc predictions: Origin 0 kb Terminus 893 kb
Worning et al., 2006: Origin 7 kb Terminus 853 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1346.536 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.66 kb
Consensus predictions: Origin 0 kb Terminus 893 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	537	NA	896
GC-skew reverse	1276	NA	896
AT-skew forward	544	NA	926
AT-skew reverse	1277	NA	897

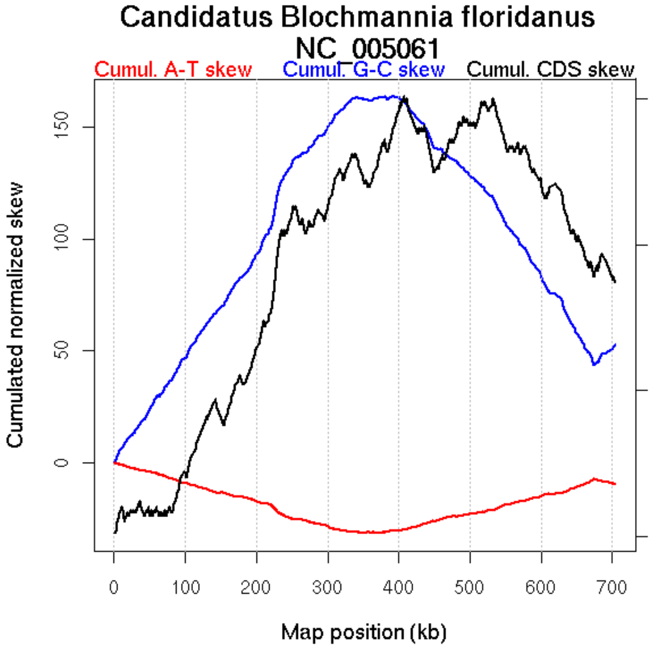
Segments:

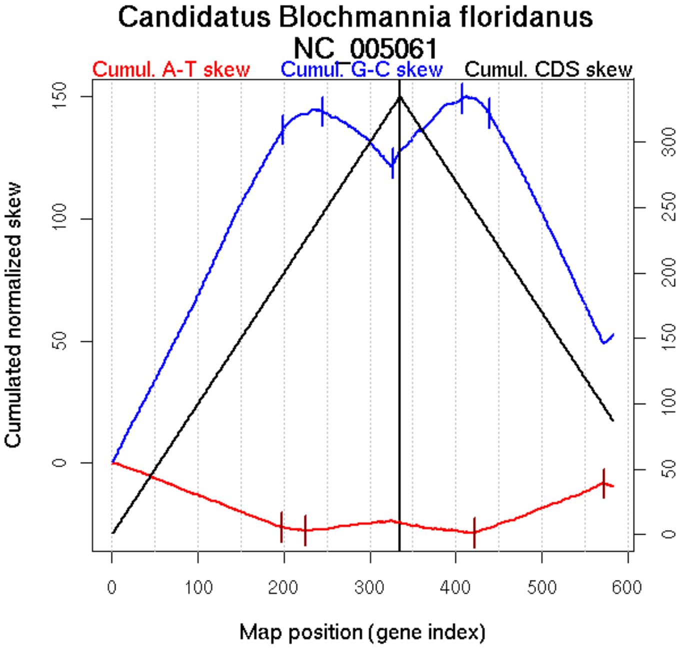
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	537 (896.1895 kb)	leading	0.22
	538(908.256 kb)	883 (1777.736 kb)	lagging	-0.191
GC-skew reverse	884 (0 kb)	1276 (896.328 kb)	leading	0.124
	1277(897.054 kb)	1838 (1777.736 kb)	lagging	-0.224
AT-skew forward	1 (0 kb)	544 (926.03 kb)	leading	-0.106
	545(928.251 kb)	883 (1777.736 kb)	lagging	-0.053
AT-skew reverse	884 (0 kb)	1277 (897.054 kb)	leading	0.051
	1278(899.8135 kb)	1838(1777.736 kb)	lagging	0.107

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

79 Candidatus Blochmannia floridanus

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; ant endosymbionts; Candidatus Blochmannia.
Accession number: NC_005061; **Genome size (bp)**: 705557.
Number of genes: 583.
Oriloc predictions: Origin 675 kb Terminus 376 kb
Worning et al., 2006: Origin 675 kb Terminus 372 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 255.113 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): NA
Consensus predictions: Origin 675 kb Terminus 376 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	199	0.02	324
	245	0.04444	403
	327	0	678
GC-skew reverse	408	0.03	320
	439	0.03667	415
AT-skew forward	197	0.04	316
	226	0.04667	378
AT-skew reverse	422	0.02333	351
	573	0.01	688

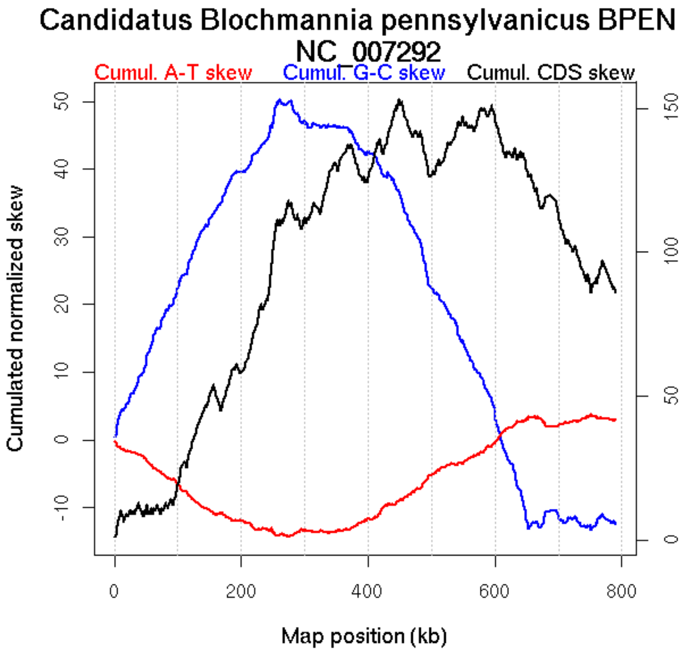
Segments:

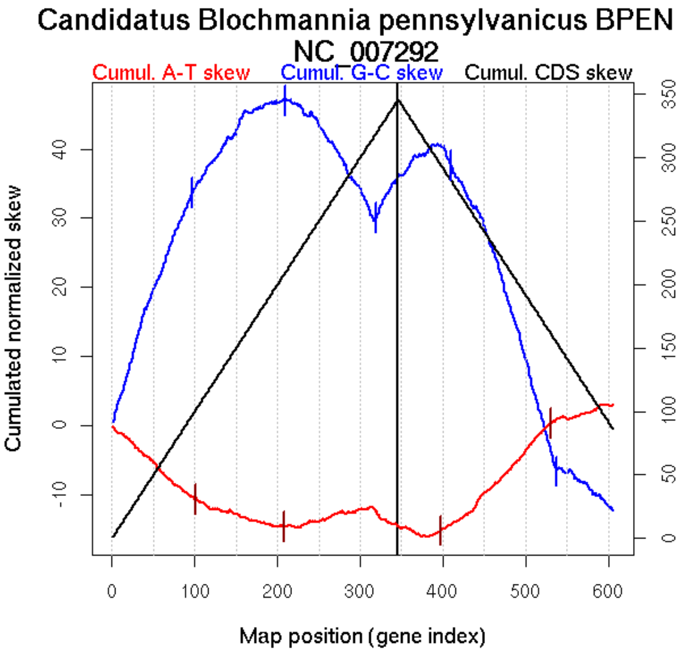
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	199 (323.94 kb)	leading	0.701
	200(324.8235 kb)	245 (403.289 kb)	NA	0.147
	246(404.311 kb)	327 (678.025 kb)	lagging	-0.279
	328(679.958 kb)	335 (704.748 kb)	leading	0.655
GC-skew reverse	336 (0 kb)	408 (319.584 kb)	leading	0.307
	409(321.129 kb)	439 (415.1275 kb)	NA	-0.223
	440(416.7295 kb)	583 (704.748 kb)	lagging	-0.703
AT-skew forward	1 (0 kb)	197 (315.7665 kb)	leading	-0.137
	198(320.158 kb)	226 (378.097 kb)	leading	-0.045
	227(379.5185 kb)	335 (704.748 kb)	lagging	0.039
AT-skew reverse	336 (0 kb)	422 (351.387 kb)	leading	-0.043
	423(353.3365 kb)	573(688.219 kb)	lagging	0.134
	574(690.9225 kb)	583(704.748 kb)	leading	-0.107

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

80 Candidatus Blochmannia pennsylvanicus BPEN

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; ant endosymbionts; Candidatus Blochmannia.
Accession number: NC_007292; **Genome size (bp)**: 791654.
Number of genes: 606.
Oriloc predictions: Origin 0 kb Terminus 270 kb
Worning et al., 2006: Origin 749 kb Terminus 280 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 330.744 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): NA
Consensus predictions: Origin 0 kb Terminus 270 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	97	NA	182
	210	NA	359
	319	NA	670
GC-skew reverse	410	NA	292
	537	NA	655
AT-skew forward	101	NA	190
	208	NA	355
AT-skew reverse	397	NA	262
	531	NA	648

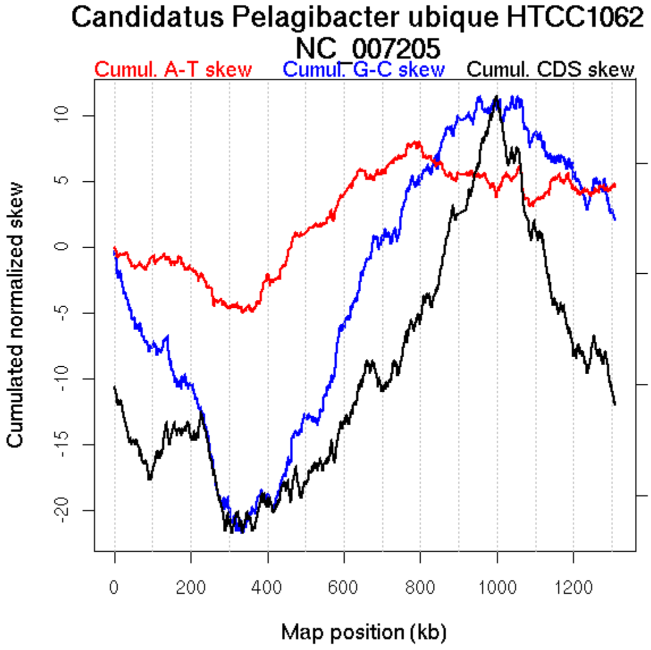
Segments:

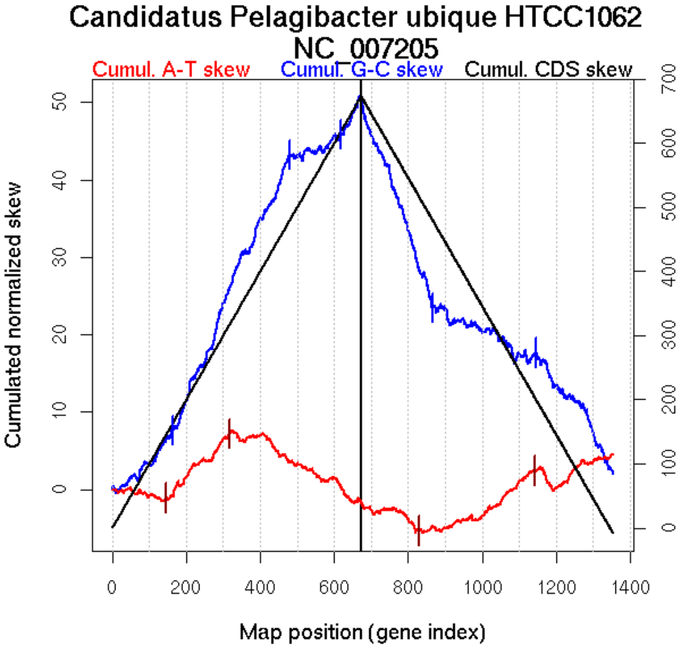
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	97 (182.487 kb)	leading	0.345
	98(183.7985 kb)	210 (359.223 kb)	NA	0.123
	211(363.0835 kb)	319 (669.8115 kb)	lagging	-0.169
	320(675.0555 kb)	346 (790.625 kb)	lagging	0.211
GC-skew reverse	347 (0 kb)	410 (292.448 kb)	NA	0.054
	411(293.64 kb)	537 (655.146 kb)	lagging	-0.358
	538(657.8235 kb)	606 (790.625 kb)	lagging	-0.093
AT-skew forward	1 (0 kb)	101 (190.285 kb)	leading	-0.109
	102(191.613 kb)	208 (355.1035 kb)	NA	-0.036
	209(356.9935 kb)	346 (790.625 kb)	lagging	0.011
AT-skew reverse	347 (0 kb)	397 (261.687 kb)	leading	-0.022
	398(263.5255 kb)	531(647.5475 kb)	lagging	0.123
	532(648.2815 kb)	606(790.625 kb)	lagging	0.035

More T than A on the leading strand for replication.
More G than C on the leading strand for replication - for forward encoded genes.

81 Candidatus Pelagibacter ubique HTCC1062

Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales; SAR11 cluster; Candidatus Pelagibacter.
Accession number: NC_007205; **Genome size (bp)**: 1308759.
Number of genes: 1354.
Oriloc predictions: Origin NA Terminus NA
Worning et al., 2006: Origin 335 kb Terminus 996 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 774.747 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 399.58 kb, 704.8 kb
Consensus predictions: Origin 335 kb Terminus 996 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	162	NA	376
	480	NA	870
	619	NA	1168
GC-skew reverse	867	NA	326
	1147	NA	1040
AT-skew forward	146	NA	346
	318	NA	635
AT-skew reverse	831	NA	273
	1142	NA	1027

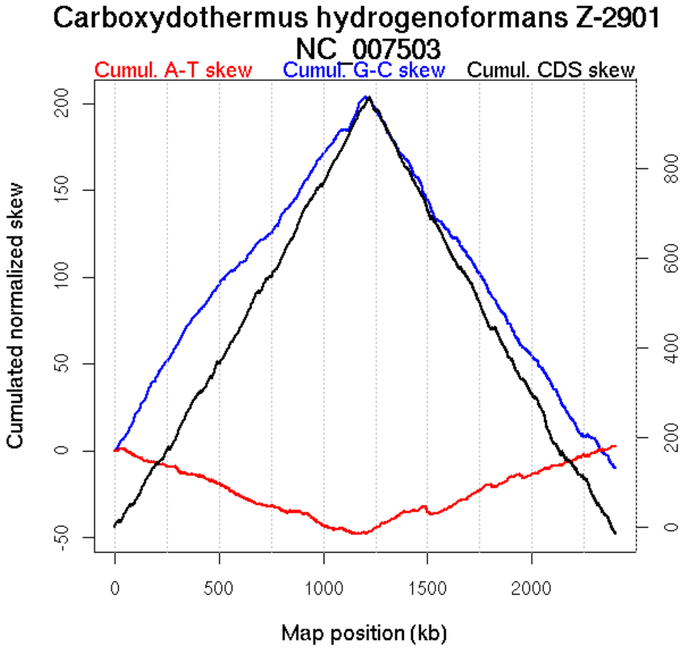
Segments:

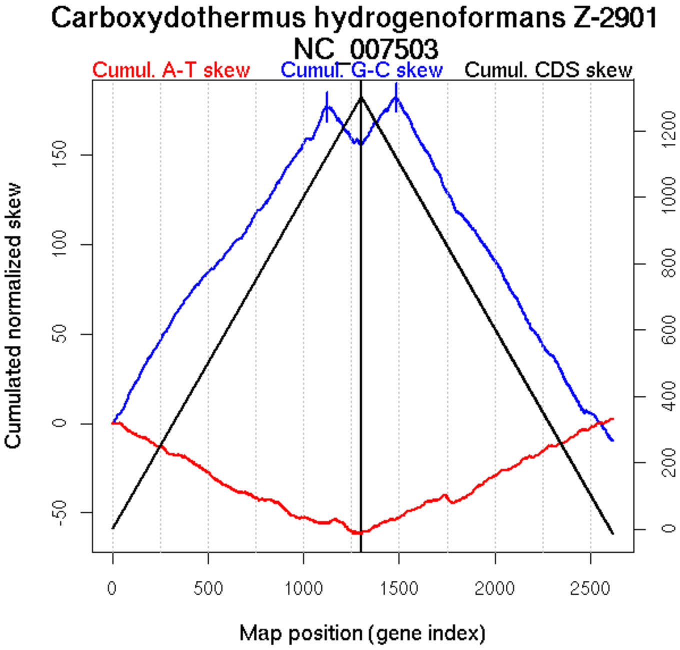
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	162 (375.9785 kb)	lagging	0.048
	163(377.52 kb)	480 (869.7445 kb)	leading	0.113
	481(873.2175 kb)	619 (1168.1975 kb)	NA	0.02
	620(1171.209 kb)	673 (1308.716 kb)	lagging	0.099
GC-skew reverse	674 (0 kb)	867 (326.099 kb)	lagging	-0.133
	868(326.7875 kb)	1147 (1040.49 kb)	NA	-0.025
	1148(1041.505 kb)	1354 (1308.716 kb)	lagging	-0.07
AT-skew forward	1 (0 kb)	146 (346.3965 kb)	lagging	-0.009
	147(349.6355 kb)	318 (634.859 kb)	leading	0.047
	319(635.4895 kb)	673 (1308.716 kb)	NA	-0.027
AT-skew reverse	674 (0 kb)	831 (272.6625 kb)	lagging	-0.016
	832(273.5665 kb)	1142(1027.0385 kb)	NA	0.026
	1143(1028.139 kb)	1354(1308.716 kb)	lagging	0.017

More G than C on the leading strand for replication - for forward encoded genes.

82 Carboxydothermus hydrogenoformans Z-2901

Bacteria; Firmicutes; Clostridia; Clostridiales; Peptococcaceae; Carboxydothermus.
Accession number: NC_007503; **Genome size (bp)**: 2401520.
Number of genes: 2619.
Oriloc predictions: Origin 0 kb Terminus 1199 kb
Worning et al., 2006: Origin 2399 kb Terminus 1219 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 639.063 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 2400.62 kb
Consensus predictions: Origin 0 kb Terminus 1199 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1123	0	1202
GC-skew reverse	1483	0	1220

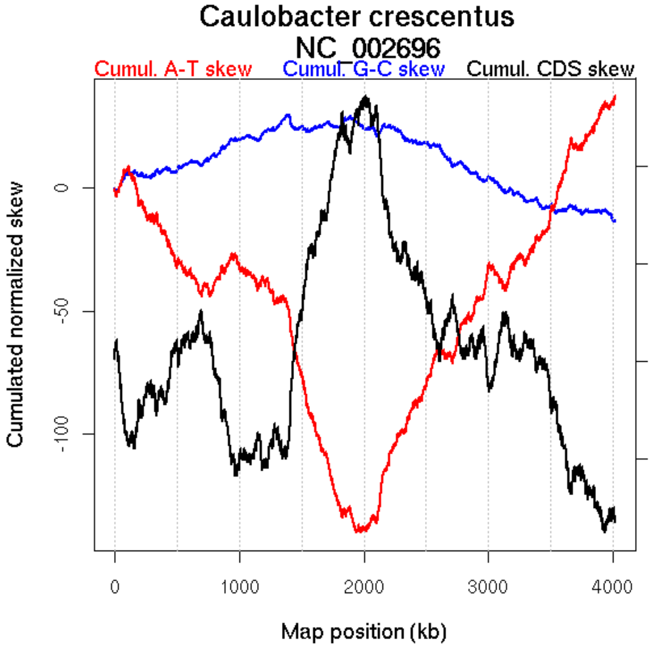
Segments:

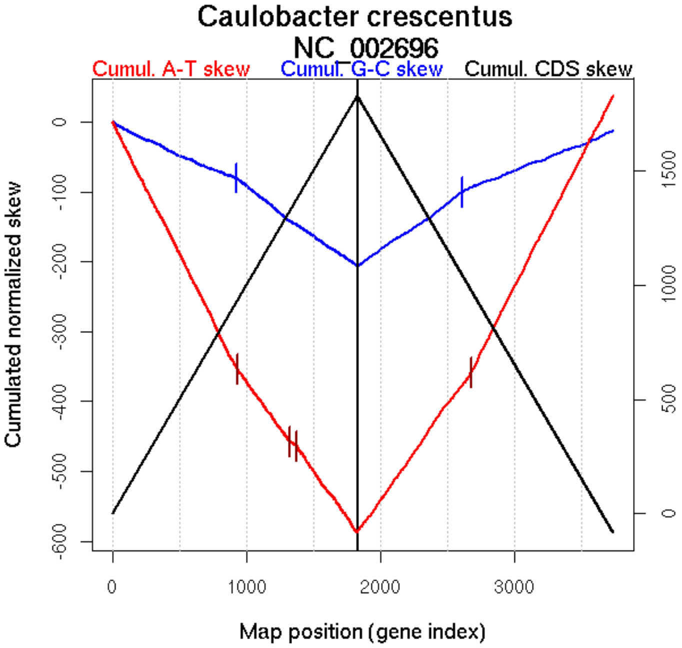
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1123 (1201.721 kb)	leading	0.149
	1124(1204.054 kb)	1302 (2401.301 kb)	lagging	-0.132
GC-skew reverse	1303 (0 kb)	1483 (1220.0635 kb)	leading	0.148
	1484(1220.885 kb)	2619 (2401.301 kb)	lagging	-0.171

More G than C on the leading strand for replication.

83 Caulobacter crescentus

Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales; Caulobacteraceae; Caulobacter.
Accession number: NC_002696; **Genome size (bp)**: 4016947.
Number of genes: 3737.
Oriloc predictions: Origin 0 kb Terminus 1891 kb
Worning et al., 2006: Origin 113 kb Terminus 2026 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 2914.721 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 6.37 kb, 1885.73 kb
Consensus predictions: Origin 0 kb Terminus 1891 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	920	0	1910
GC-skew reverse	2610	0	1865
AT-skew forward	932	0.02889	1929
	1324	0.01333	2879
	1374	0.00444	2996
AT-skew reverse	2676	0	2039

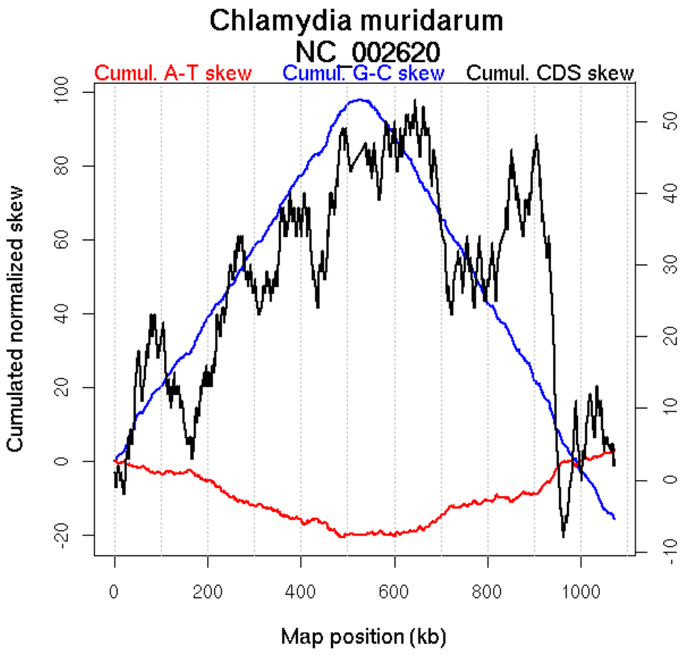
Segments:

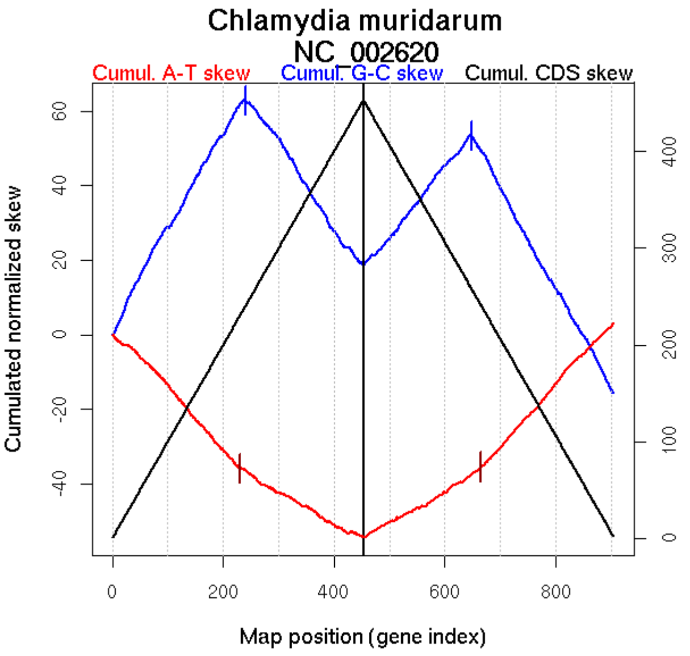
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	920 (1909.5035 kb)	leading	-0.086
	921(1910.869 kb)	1827 (4016.702 kb)	lagging	-0.139
GC-skew reverse	1828 (0 kb)	2610 (1864.6755 kb)	leading	0.133
	2611(1866.9765 kb)	3737 (4016.702 kb)	lagging	0.075
AT-skew forward	1 (0 kb)	932 (1929.154 kb)	leading	-0.38
	933(1930.629 kb)	1324 (2879.223 kb)	lagging	-0.264
	1325(2883.787 kb)	1374 (2996.0375 kb)	lagging	-0.127
	1375(2997.456 kb)	1827 (4016.702 kb)	lagging	-0.269
AT-skew reverse	1828 (0 kb)	2676 (2039.4515 kb)	leading	0.273
	2677(2041.5365 kb)	3737(4016.702 kb)	lagging	0.373

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

84 Chlamydia muridarum

Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
Accession number: NC_002620; **Genome size (bp)**: 1072950.
Number of genes: 904.
Oriloc predictions: Origin 0 kb Terminus 531 kb
Worning et al., 2006: Origin 1 kb Terminus 534 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 545.141 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 630.75 kb, 657.23 kb
Consensus predictions: Origin 0 kb Terminus 531 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	240	0	546
GC-skew reverse	649	0	547
AT-skew forward	231	0	492
AT-skew reverse	665	0.00667	589

Segments:

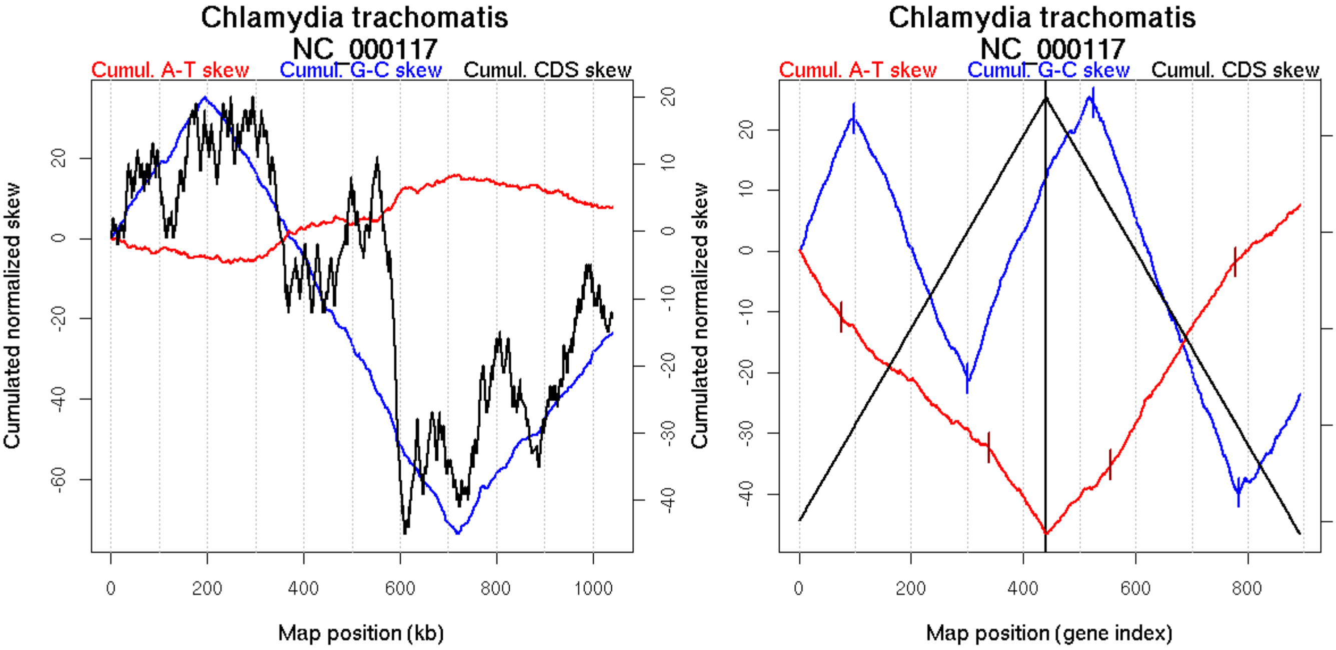
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	240 (545.5405 kb)	leading	0.261
	241(547.3605 kb)	453 (1072.918 kb)	lagging	-0.224
GC-skew reverse	454 (0 kb)	649 (547.3015 kb)	leading	0.186
	650(548.521 kb)	904 (1072.918 kb)	lagging	-0.268
AT-skew forward	1 (0 kb)	231 (492.1385 kb)	leading	-0.162
	232(493.8495 kb)	453 (1072.918 kb)	lagging	-0.085
AT-skew reverse	454 (0 kb)	665 (588.721 kb)	leading	0.085
	666(589.3765 kb)	904(1072.918 kb)	lagging	0.166

More T than A on the leading strand for replication.

More G than C on the leading strand for replication.

85 Chlamydia trachomatis

Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
Accession number: NC_000117; **Genome size (bp)**: 1042519.
Number of genes: 893.
Oriloc predictions: Origin 719 kb Terminus 194 kb
Worning et al., 2006: Origin 720 kb Terminus 197 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 66.916 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 280.57 kb, 307.12 kb
Consensus predictions: Origin 719 kb Terminus 194 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	97	NA	202
	301	NA	714
GC-skew reverse	524	NA	202
	784	NA	722
AT-skew forward	75	NA	157
	338	NA	787
AT-skew reverse	556	NA	276
	777	NA	711

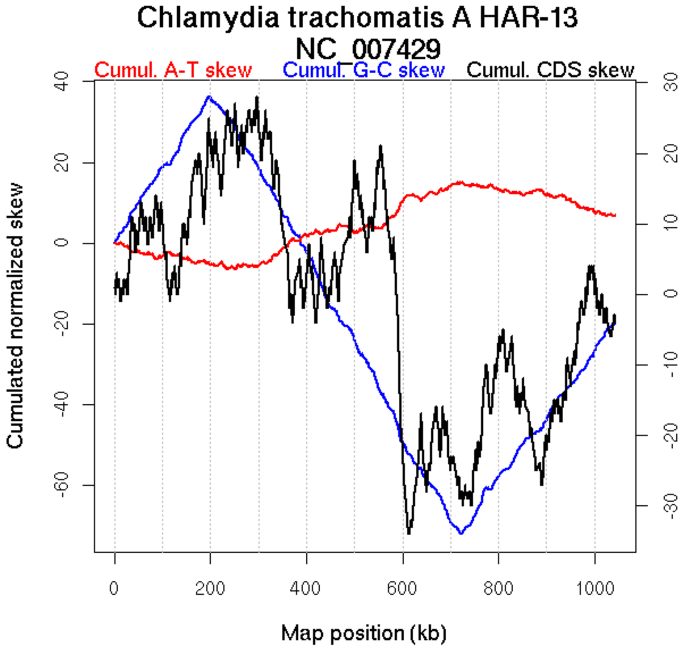
Segments:

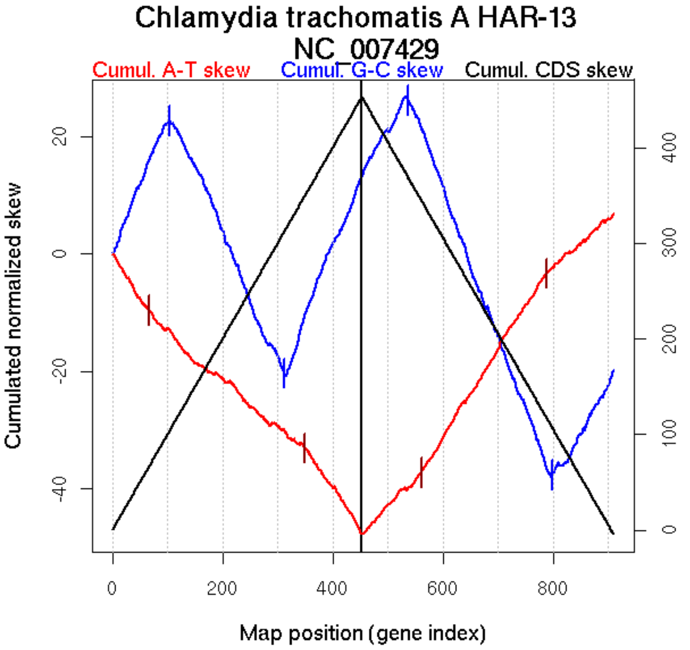
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	97 (202.3195 kb)	leading	0.237
	98(204.4395 kb)	301 (713.8745 kb)	lagging	-0.224
	302(716.68 kb)	440 (1041.646 kb)	leading	0.24
GC-skew reverse	441 (0 kb)	524 (201.6305 kb)	leading	0.152
	525(202.4675 kb)	784 (722.241 kb)	lagging	-0.252
	785(726.816 kb)	893 (1041.646 kb)	leading	0.145
AT-skew forward	1 (0 kb)	75 (156.5485 kb)	leading	-0.148
	76(158.0535 kb)	338 (786.775 kb)	NA	-0.081
	339(787.5455 kb)	440 (1041.646 kb)	leading	-0.134
AT-skew reverse	441 (0 kb)	556 (275.7385 kb)	NA	0.094
	557(279.0735 kb)	777(710.708 kb)	lagging	0.153
	778(712.361 kb)	893(1041.646 kb)	leading	0.079

More G than C on the leading strand for replication.

86 Chlamydia trachomatis A HAR-13

Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
Accession number: NC_007429; **Genome size (bp)**: 1044459.
Number of genes: 910.
Oriloc predictions: Origin 721 kb Terminus 199 kb
Worning et al., 2006: Origin 723 kb Terminus 197 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 67.641 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 282.83 kb, 309.37 kb
Consensus predictions: Origin 721 kb Terminus 199 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	103	NA	198
	313	NA	717
GC-skew reverse	538	NA	204
	799	NA	730
AT-skew forward	67	NA	141
	350	NA	790
AT-skew reverse	561	NA	256
	788	NA	706

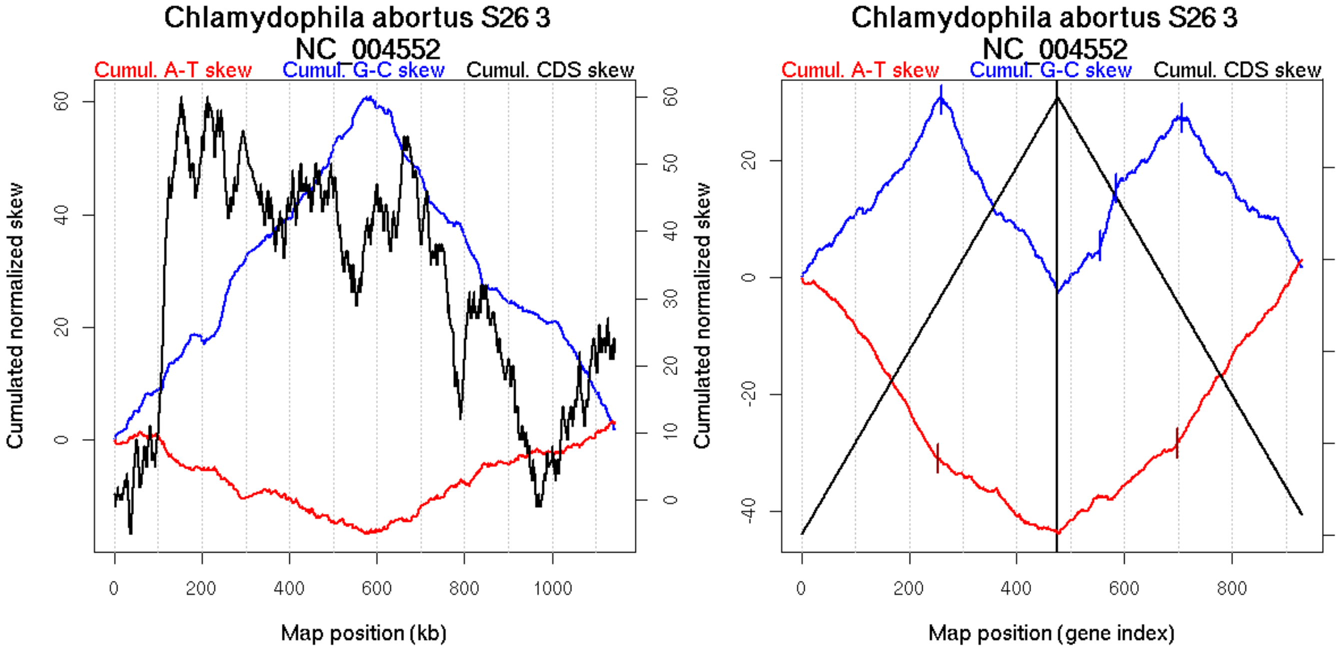
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	103 (198.004 kb)	leading	0.231
	104(201.349 kb)	313 (716.594 kb)	lagging	-0.219
	314(719.399 kb)	453 (1044.185 kb)	leading	0.241
GC-skew reverse	454 (0 kb)	538 (203.8885 kb)	leading	0.155
	539(204.7255 kb)	799 (729.5355 kb)	lagging	-0.252
	800(733.5895 kb)	910 (1044.185 kb)	leading	0.161
AT-skew forward	1 (0 kb)	67 (140.5995 kb)	leading	-0.152
	68(142.086 kb)	350 (790.2925 kb)	NA	-0.081
	351(791.478 kb)	453 (1044.185 kb)	leading	-0.137
AT-skew reverse	454 (0 kb)	561 (256.237 kb)	NA	0.095
	562(257.0545 kb)	788(705.6485 kb)	lagging	0.15
	789(709.404 kb)	910(1044.185 kb)	leading	0.082

More T than A on the leading strand for replication - for reverse encoded genes.
More G than C on the leading strand for replication.

87 Chlamydophila abortus S26 3

Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
Accession number: NC_004552; **Genome size (bp)**: 1144377.
Number of genes: 930.
Oriloc predictions: Origin 0 kb Terminus 574 kb
Worning et al., 2006: Origin 0 kb Terminus 574 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 822.392 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 413.48 kb, 529.73 kb
Consensus predictions: Origin 0 kb Terminus 574 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	261	0	583
GC-skew reverse	556	0.02	243
	585	0.02444	324
	706	0.03333	605
AT-skew forward	253	0.00667	568
AT-skew reverse	698	0	584

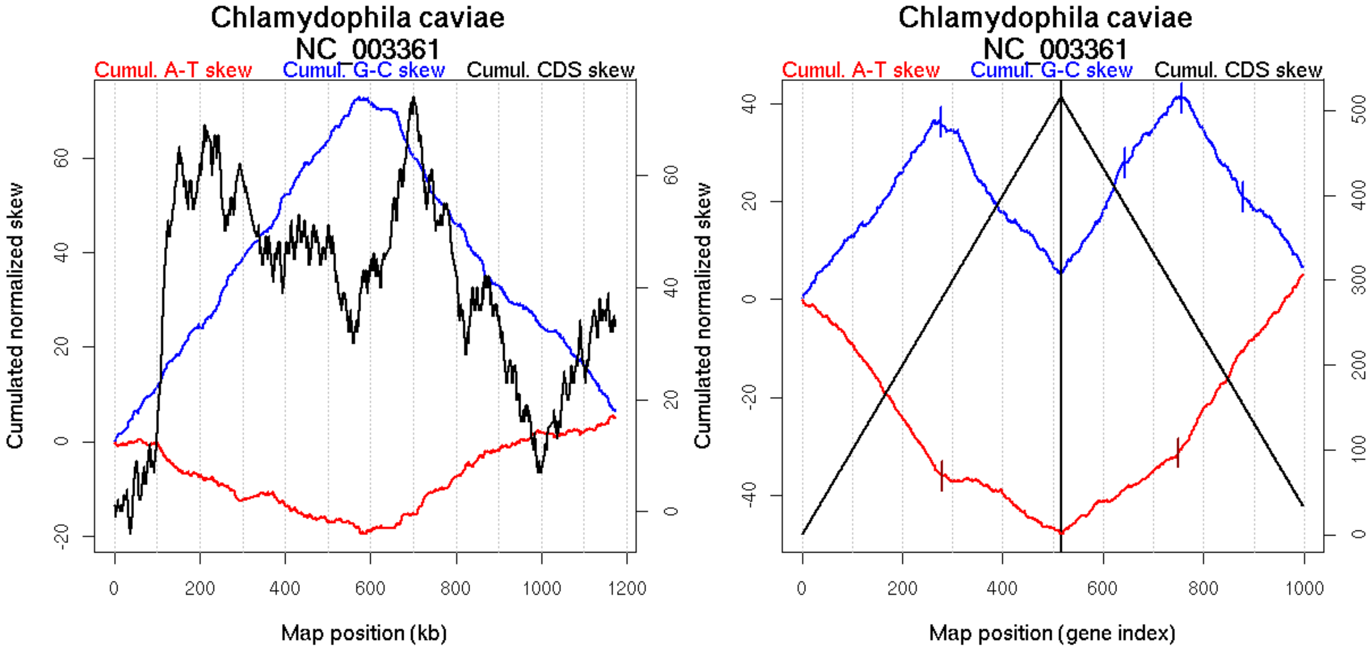
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	261 (582.5295 kb)	leading	0.11
	262(584.7255 kb)	476 (1144.231 kb)	lagging	-0.142
GC-skew reverse	477 (0 kb)	556 (242.7695 kb)	leading	0.094
	557(245.623 kb)	585 (324.2265 kb)	leading	0.345
	586(327.6995 kb)	706 (604.8715 kb)	leading	0.103
	707(607.287 kb)	930 (1144.231 kb)	lagging	-0.105
AT-skew forward	1 (0 kb)	253 (568.3425 kb)	leading	-0.129
	254(568.8215 kb)	476 (1144.231 kb)	lagging	-0.061
AT-skew reverse	477 (0 kb)	698 (584.2575 kb)	leading	0.067
	699(585.388 kb)	930(1144.231 kb)	lagging	0.13

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

88 Chlamydophila caviae

Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
Accession number: NC_003361; **Genome size (bp)**: 1173390.
Number of genes: 998.
Oriloc predictions: Origin 0 kb Terminus 588 kb
Worning et al., 2006: Origin NA kb Terminus NA kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 857.337 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 420.13 kb, 536.29 kb
Consensus predictions: Origin 0 kb Terminus 588 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	276	NA	594
GC-skew reverse	643	NA	357
	756	NA	604
	878	NA	884
AT-skew forward	279	NA	598
AT-skew reverse	749	NA	590

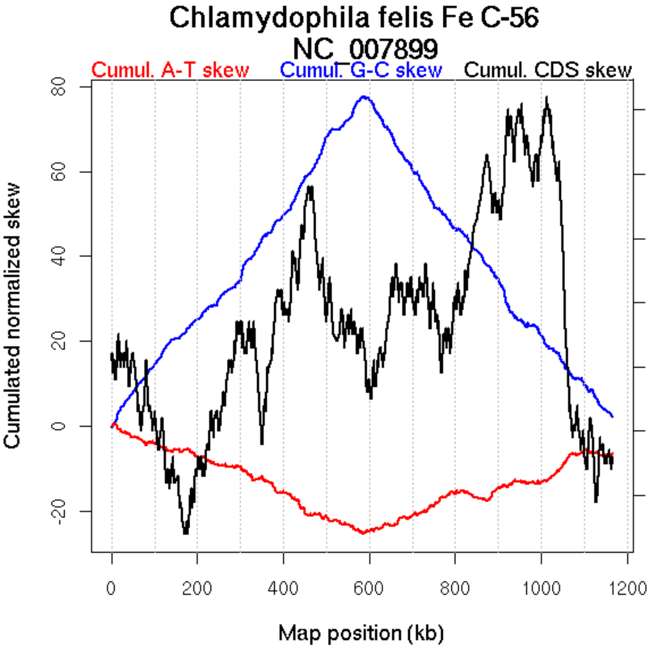
Segments:

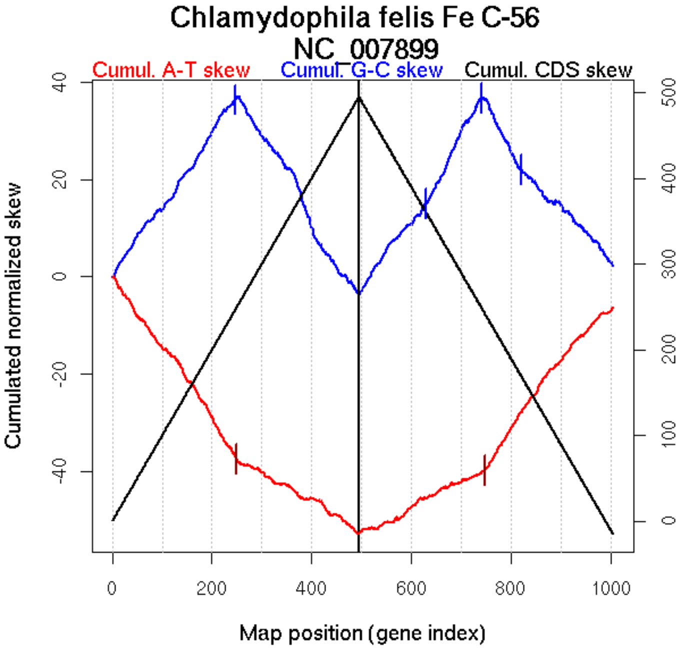
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	276 (594.1435 kb)	leading	0.132
	277(595.182 kb)	516 (1173.383 kb)	lagging	-0.132
GC-skew reverse	517 (0 kb)	643 (357.184 kb)	leading	0.179
	644(358.1525 kb)	756 (604.281 kb)	leading	0.124
	757(606.7115 kb)	878 (883.852 kb)	lagging	-0.171
	879(884.8165 kb)	998 (1173.383 kb)	lagging	-0.117
AT-skew forward	1 (0 kb)	279 (597.6135 kb)	leading	-0.136
	280(598.553 kb)	516 (1173.383 kb)	lagging	-0.055
AT-skew reverse	517 (0 kb)	749 (590.329 kb)	leading	0.067
	750(591.5175 kb)	998(1173.383 kb)	lagging	0.144

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

89 Chlamydophila felis Fe C-56

Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
Accession number: NC_007899; **Genome size (bp)**: 1166239.
Number of genes: 1005.
Oriloc predictions: Origin 4 kb Terminus 583 kb
Worning et al., 2006: Origin 9 kb Terminus 585 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 834.256 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 628.12 kb, 743.51 kb
Consensus predictions: Origin 0 kb Terminus 583 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	246	NA	575
GC-skew reverse	630	NA	323
	742	NA	585
	820	NA	762
AT-skew forward	250	NA	582
AT-skew reverse	747	NA	592

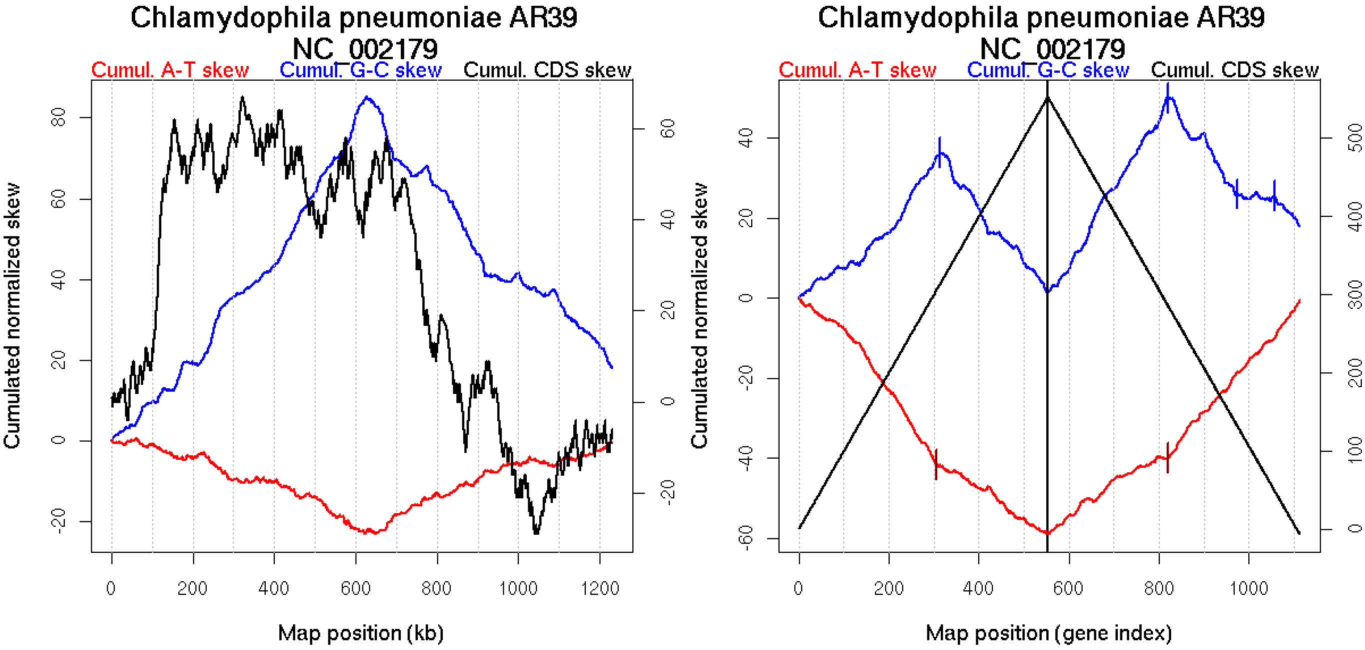
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	246 (574.893 kb)	leading	0.146
	247(576.994 kb)	495 (1166.159 kb)	lagging	-0.177
GC-skew reverse	496 (0 kb)	630 (322.862 kb)	leading	0.133
	631(324.3555 kb)	742 (584.8685 kb)	leading	0.204
	743(586.553 kb)	820 (761.9185 kb)	lagging	-0.206
	821(762.9495 kb)	1005 (1166.159 kb)	lagging	-0.101
AT-skew forward	1 (0 kb)	250 (582.3145 kb)	leading	-0.146
	251(583.5945 kb)	495 (1166.159 kb)	lagging	-0.059
AT-skew reverse	496 (0 kb)	747 (591.8665 kb)	leading	0.054
	748(592.565 kb)	1005(1166.159 kb)	lagging	0.132

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

90 Chlamydophila pneumoniae AR39

Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
Accession number: NC_002179; **Genome size (bp)**: 1229853.
Number of genes: 1112.
Oriloc predictions: Origin 0 kb Terminus 624 kb
Worning et al., 2006: Origin 0 kb Terminus 626 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 493.236 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 370.93 kb, 491 kb
Consensus predictions: Origin 0 kb Terminus 624 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	314	NA	626
GC-skew reverse	821	NA	622
	973	NA	930
	1057	NA	1089
AT-skew forward	307	NA	621
AT-skew reverse	819	NA	617

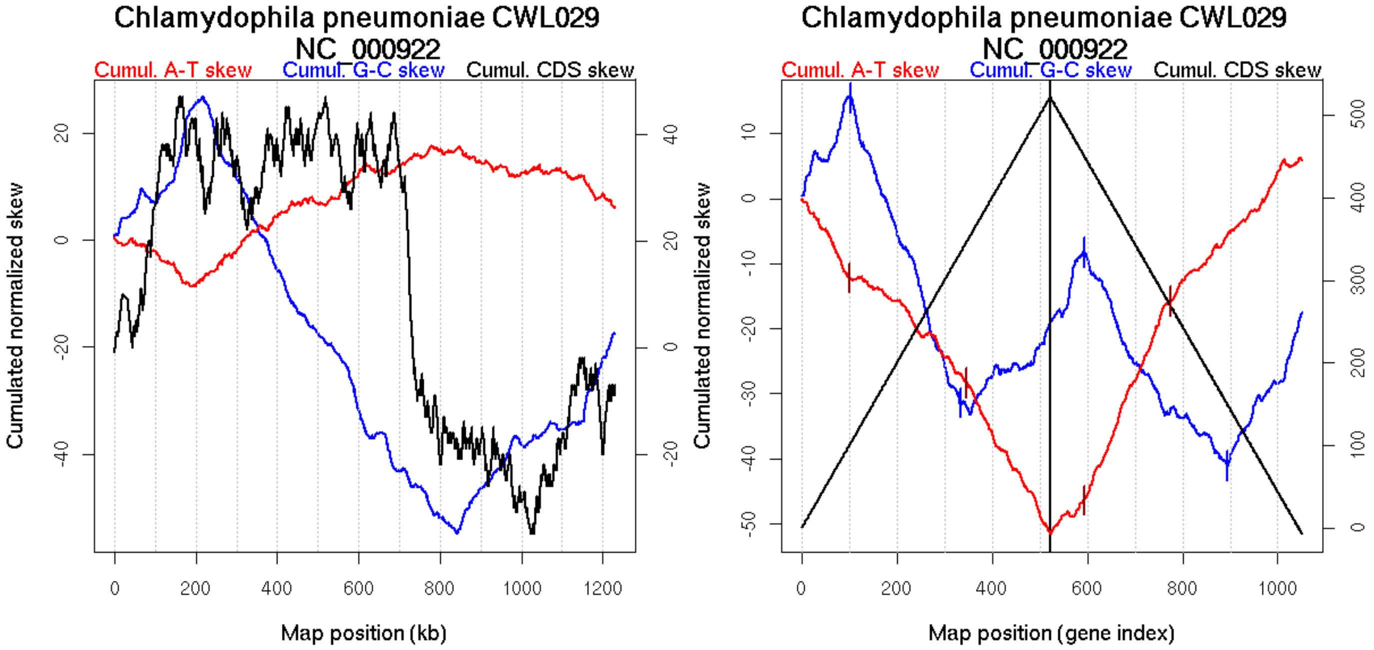
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	314 (625.9915 kb)	leading	0.11
	315(628.214 kb)	553 (1229.83 kb)	lagging	-0.14
GC-skew reverse	554 (0 kb)	821 (622.2255 kb)	leading	0.185
	822(625.581 kb)	973 (930.082 kb)	lagging	-0.152
	974(930.7055 kb)	1057 (1089.136 kb)	lagging	-0.008
	1058(1094.9365 kb)	1112 (1229.83 kb)	lagging	-0.115
AT-skew forward	1 (0 kb)	307 (620.594 kb)	leading	-0.138
	308(622.0345 kb)	553 (1229.83 kb)	lagging	-0.075
AT-skew reverse	554 (0 kb)	819 (617.317 kb)	leading	0.075
	820(617.8865 kb)	1112(1229.83 kb)	lagging	0.128

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

91 Chlamydophila pneumoniae CWL029

Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
Accession number: NC_000922; **Genome size (bp)**: 1230230.
Number of genes: 1051.
Oriloc predictions: Origin 840 kb Terminus 215 kb
Worning et al., 2006: Origin 841 kb Terminus 216 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 348.047 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 350.28 kb, 470.29 kb
Consensus predictions: Origin 840 kb Terminus 215 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	103	NA	220
	334	NA	784
GC-skew reverse	594	NA	218
	894	NA	841
AT-skew forward	101	NA	215
	347	NA	819
AT-skew reverse	594	NA	218
	775	NA	644

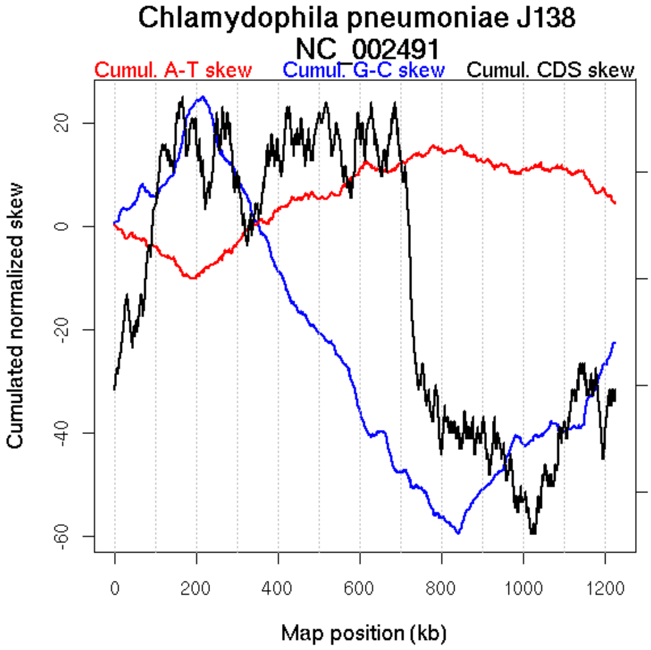
Segments:

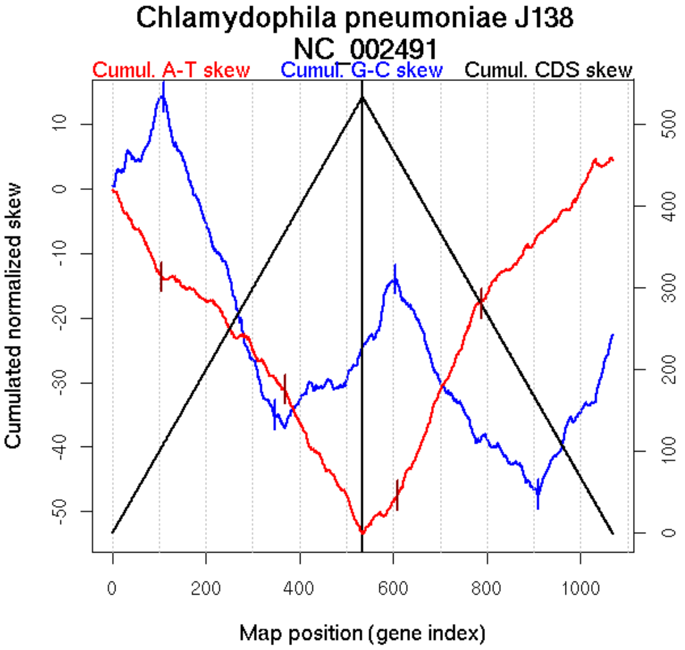
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	103 (219.7085 kb)	leading	0.129
	104(224.158 kb)	334 (784.1915 kb)	lagging	-0.201
	335(784.909 kb)	522 (1229.832 kb)	leading	0.057
GC-skew reverse	523 (0 kb)	594 (218.481 kb)	leading	0.179
	595(218.765 kb)	894 (841.146 kb)	lagging	-0.104
	895(843.3645 kb)	1051 (1229.832 kb)	leading	0.127
AT-skew forward	1 (0 kb)	101 (214.811 kb)	leading	-0.122
	102(215.2805 kb)	347 (818.8895 kb)	lagging	-0.069
	348(821.929 kb)	522 (1229.832 kb)	leading	-0.127
AT-skew reverse	523 (0 kb)	594 (218.481 kb)	leading	0.059
	595(218.765 kb)	775(644.3215 kb)	lagging	0.175
	776(645.251 kb)	1051(1229.832 kb)	NA	0.081

More T than A on the leading strand for replication - for forward encoded genes.
More G than C on the leading strand for replication.

92 Chlamydophila pneumoniae J138

Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
Accession number: NC_002491; **Genome size (bp)**: 1226565.
Number of genes: 1069.
Oriloc predictions: Origin 840 kb Terminus 215 kb
Worning et al., 2006: Origin 840 kb Terminus 217 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 347.669 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 349.9 kb, 470 kb
Consensus predictions: Origin 840 kb Terminus 215 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	110	NA	224
	347	NA	784
GC-skew reverse	603	NA	218
	909	NA	840
AT-skew forward	105	NA	207
	368	NA	845
AT-skew reverse	608	NA	221
	787	NA	641

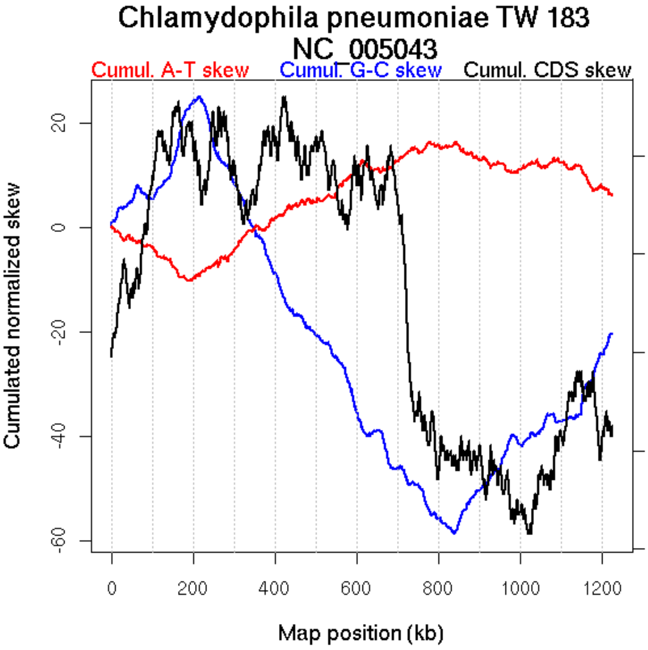
Segments:

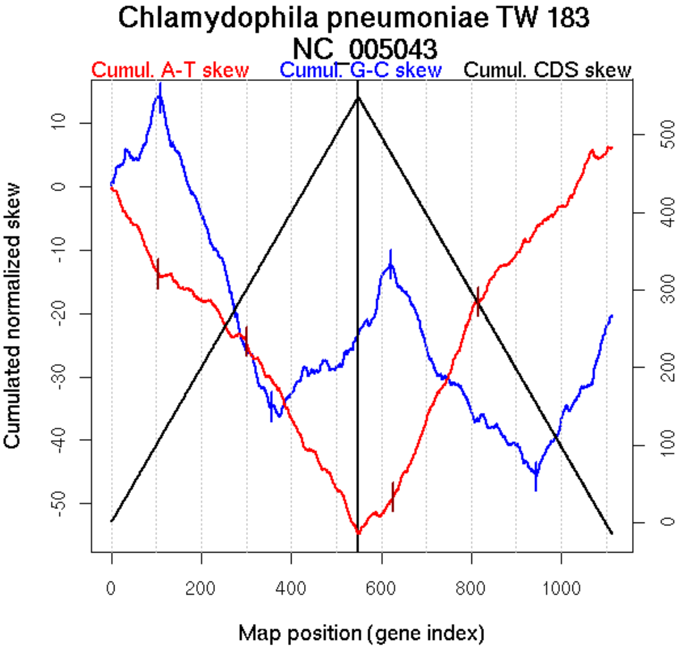
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	110 (223.781 kb)	leading	0.114
	111(224.701 kb)	347 (784.23 kb)	lagging	-0.206
	348(784.925 kb)	534 (1226.167 kb)	leading	0.049
GC-skew reverse	535 (0 kb)	603 (217.719 kb)	leading	0.182
	604(218.104 kb)	909 (840.467 kb)	lagging	-0.105
	910(842.2505 kb)	1069 (1226.167 kb)	leading	0.132
AT-skew forward	1 (0 kb)	105 (207.229 kb)	leading	-0.128
	106(210.7325 kb)	368 (844.557 kb)	lagging	-0.071
	369(847.84 kb)	534 (1226.167 kb)	leading	-0.124
AT-skew reverse	535 (0 kb)	608 (220.858 kb)	leading	0.066
	609(221.459 kb)	787(640.914 kb)	lagging	0.174
	788(641.568 kb)	1069(1226.167 kb)	NA	0.08

More T than A on the leading strand for replication - for forward encoded genes.
More G than C on the leading strand for replication.

93 Chlamydophila pneumoniae TW 183

Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
Accession number: NC_005043; **Genome size (bp)**: 1225935.
Number of genes: 1113.
Oriloc predictions: Origin 838 kb Terminus 213 kb
Worning et al., 2006: Origin 837 kb Terminus 215 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 345.461 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 347.7 kb, 467.79 kb
Consensus predictions: Origin 838 kb Terminus 213 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	109	NA	217
	357	NA	801
GC-skew reverse	622	NA	216
	944	NA	838
AT-skew forward	105	NA	206
	300	NA	626
AT-skew reverse	627	NA	219
	815	NA	633

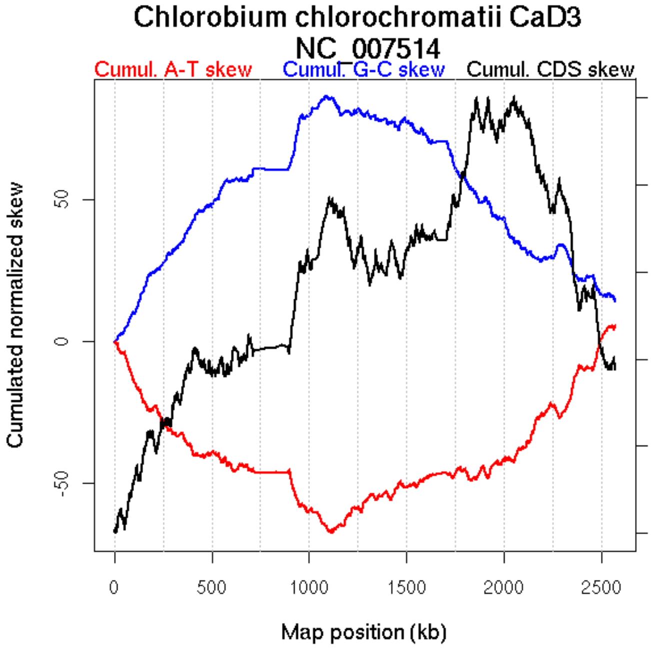
Segments:

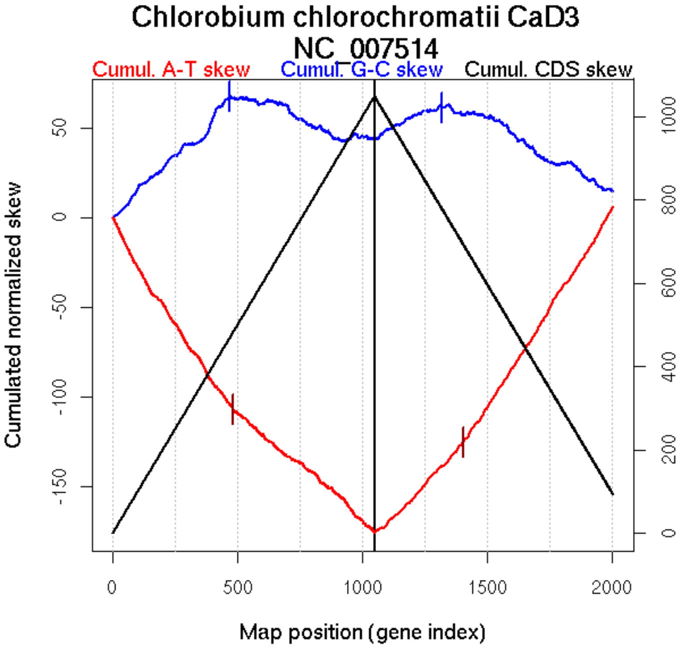
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	109 (217.1155 kb)	leading	0.113
	110(221.565 kb)	357 (800.7725 kb)	lagging	-0.197
	358(802.263 kb)	549 (1225.537 kb)	leading	0.054
GC-skew reverse	550 (0 kb)	622 (215.888 kb)	leading	0.173
	623(216.172 kb)	944 (838.452 kb)	lagging	-0.095
	945(840.6785 kb)	1113 (1225.537 kb)	leading	0.137
AT-skew forward	1 (0 kb)	105 (206.2135 kb)	leading	-0.13
	106(209.425 kb)	300 (626.05 kb)	lagging	-0.059
	301(627.9345 kb)	549 (1225.537 kb)	NA	-0.117
AT-skew reverse	550 (0 kb)	627 (219.243 kb)	leading	0.06
	628(224.285 kb)	815(633.4645 kb)	lagging	0.167
	816(634.305 kb)	1113(1225.537 kb)	NA	0.083

More G than C on the leading strand for replication.

94 Chlorobium chlorochromatii CaD3

Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae; Chlorobium/Pelodictyon group; Chlorobium.
Accession number: NC_007514; **Genome size (bp)**: 2572079.
Number of genes: 2002.
Oriloc predictions: Origin 0 kb Terminus 1118 kb
Worning et al., 2006: Origin 2559 kb Terminus 1110 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 0.059 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1.08 kb
Consensus predictions: Origin 0 kb Terminus 1118 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	468	0	1083
GC-skew reverse	1318	0	972
AT-skew forward	484	0	1114
AT-skew reverse	1402	0	1217

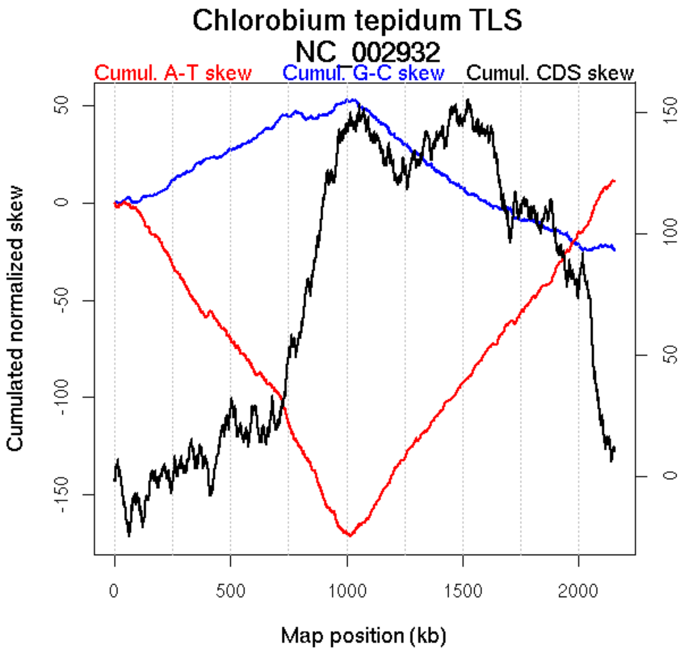
Segments:

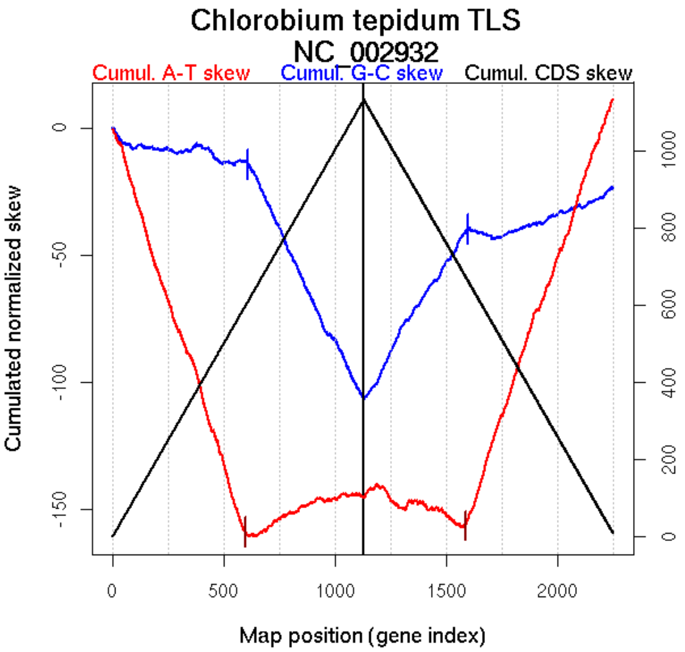
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	468 (1082.9745 kb)	leading	0.136
	469(1087.22 kb)	1048 (2571.844 kb)	lagging	-0.051
GC-skew reverse	1049 (0 kb)	1318 (971.8045 kb)	leading	0.067
	1319(973.574 kb)	2002 (2571.844 kb)	lagging	-0.076
AT-skew forward	1 (0 kb)	484 (1113.6855 kb)	leading	-0.216
	485(1114.7655 kb)	1048 (2571.844 kb)	lagging	-0.118
AT-skew reverse	1049 (0 kb)	1402 (1216.655 kb)	NA	0.145
	1403(1217.3005 kb)	2002(2571.844 kb)	lagging	0.218

More T than A on the leading strand for replication - for forward encoded genes.
More G than C on the leading strand for replication.

95 Chlorobium tepidum TLS

Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae; Chlorobaculum.
Accession number: NC_002932; **Genome size (bp)**: 2154946.
Number of genes: 2252.
Oriloc predictions: Origin 0 kb Terminus 1000 kb
Worning et al., 2006: Origin 2152 kb Terminus 1018 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 3.148 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 2.14 kb
Consensus predictions: Origin 0 kb Terminus 1000 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	610	NA	1031
GC-skew reverse	1598	NA	1033
AT-skew forward	598	NA	1006
AT-skew reverse	1587	NA	1018

Segments:

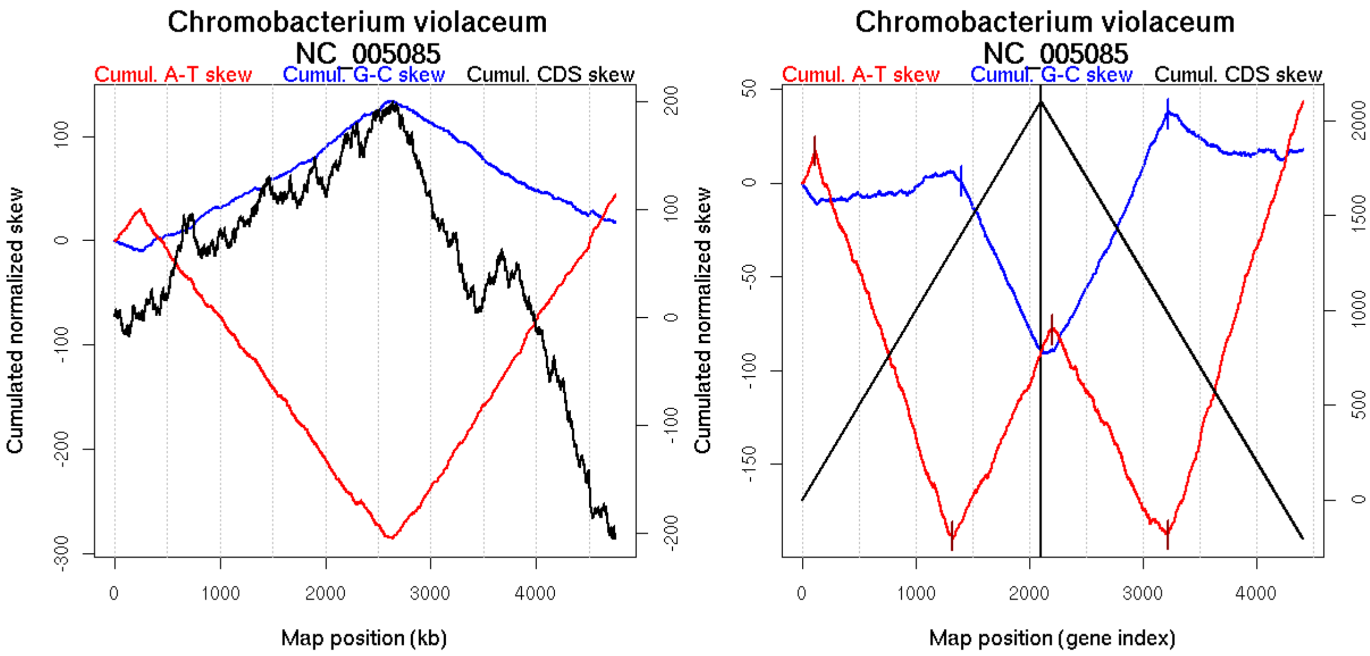
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	610 (1031.149 kb)	leading	-0.015
	611(1032.23 kb)	1131 (2154.932 kb)	lagging	-0.181
GC-skew reverse	1132 (0 kb)	1598 (1033.4485 kb)	leading	0.144
	1599(1035.4035 kb)	2252 (2154.932 kb)	lagging	0.028
AT-skew forward	1 (0 kb)	598 (1006.244 kb)	leading	-0.267
	599(1009.84 kb)	1131 (2154.932 kb)	lagging	0.035
AT-skew reverse	1132 (0 kb)	1587 (1018.1655 kb)	leading	-0.031
	1588(1018.972 kb)	2252(2154.932 kb)	lagging	0.253

More T than A on the leading strand for replication.

More G than C on the leading strand for replication.

96 Chromobacterium violaceum

Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae; Chromobacterium.
Accession number: NC_005085; **Genome size (bp)**: 4751080.
Number of genes: 4407.
Oriloc predictions: Origin 192 kb Terminus 2594 kb
Worning et al., 2006: Origin 244 kb Terminus 2612 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 236.463 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.95 kb
Consensus predictions: Origin 236 kb Terminus 2612 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1395	0	2852
GC-skew reverse	3217	0	2607
AT-skew forward	115	0	238
	1317	0	2624
AT-skew reverse	2204	0	222
	3218	0	2608

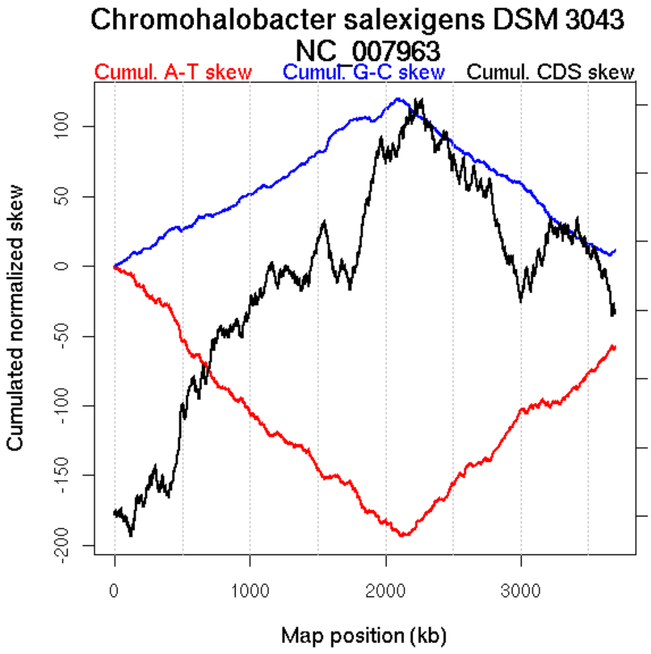
Segments:

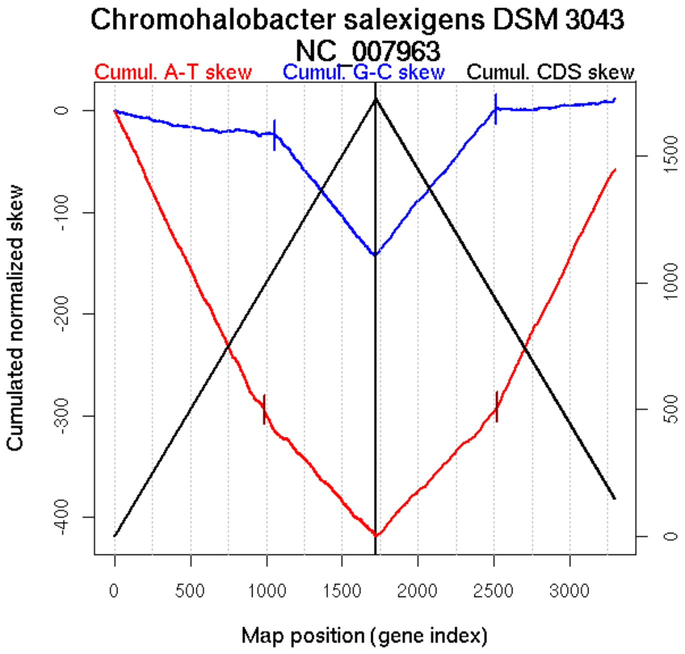
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1395 (2851.7175 kb)	leading	0.01
	1396(2856.591 kb)	2101 (4750.994 kb)	lagging	-0.131
GC-skew reverse	2102 (0 kb)	3217 (2606.9635 kb)	leading	0.123
	3218(2607.539 kb)	4407 (4750.994 kb)	lagging	-0.016
AT-skew forward	1 (0 kb)	115 (237.694 kb)	lagging	0.156
	116(241.255 kb)	1317 (2624.304 kb)	leading	-0.171
	1318(2627.63 kb)	2101 (4750.994 kb)	lagging	0.125
AT-skew reverse	2102 (0 kb)	2204 (222.114 kb)	lagging	0.128
	2205(222.642 kb)	3218(2607.539 kb)	leading	-0.116
	3219(2609.4035 kb)	4407(4750.994 kb)	lagging	0.199

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

97 Chromohalobacter salexigens DSM 3043

Bacteria; Proteobacteria; Gammaproteobacteria; Oceanospirillales; Halomonadaceae; Chromohalobacter.
Accession number: NC_007963; **Genome size (bp)**: 3696649.
Number of genes: 3298.
Oriloc predictions: Origin 5 kb Terminus 2099 kb
Worning et al., 2006: Origin 3673 kb Terminus 2128 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 3680.112 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.84 kb, 2380.22 kb
Consensus predictions: Origin 3680 kb Terminus 2128 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1057	0	2107
GC-skew reverse	2511	0	2127
AT-skew forward	986	0	1956
AT-skew reverse	2522	0	2160

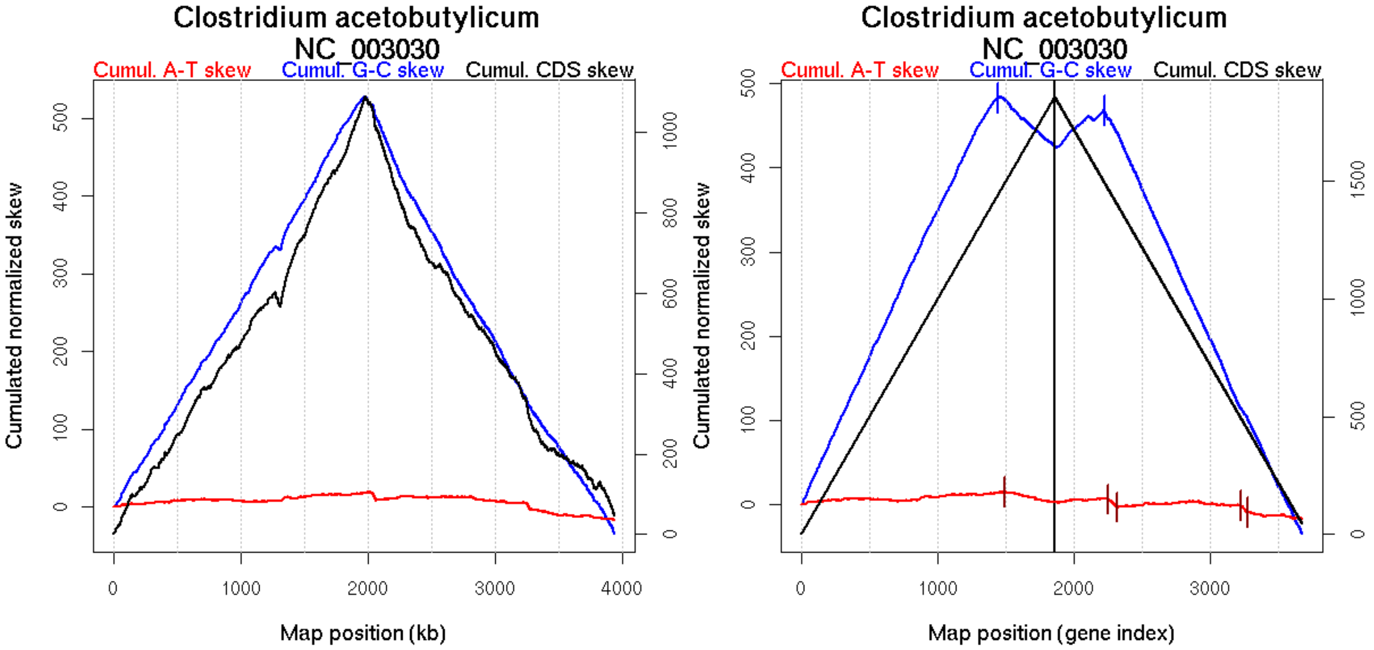
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1057 (2106.5855 kb)	leading	-0.021
	1058(2107.6905 kb)	1723 (3696.5 kb)	lagging	-0.185
GC-skew reverse	1724 (0 kb)	2511 (2127.0675 kb)	leading	0.181
	2512(2128.067 kb)	3298 (3696.5 kb)	lagging	0.011
AT-skew forward	1 (0 kb)	986 (1956.3495 kb)	leading	-0.304
	987(1957.4135 kb)	1723 (3696.5 kb)	lagging	-0.161
AT-skew reverse	1724 (0 kb)	2522 (2160.1915 kb)	leading	0.155
	2523(2161.304 kb)	3298(3696.5 kb)	lagging	0.304

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

98 Clostridium acetobutylicum

Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
Accession number: NC_003030; **Genome size (bp)**: 3940880.
Number of genes: 3672.
Oriloc predictions: Origin 0 kb Terminus 1979 kb
Worning et al., 2006: Origin 0 kb Terminus 1982 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 366.064 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1.14 kb, 2020.04 kb
Consensus predictions: Origin 0 kb Terminus 1979 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1442	0	1974
GC-skew reverse	2221	0	1986
AT-skew forward	1491	0.00667	2348
AT-skew reverse	2251	0	2024
	2317	0	2068
	3221	0	3252
	3272	0	3289

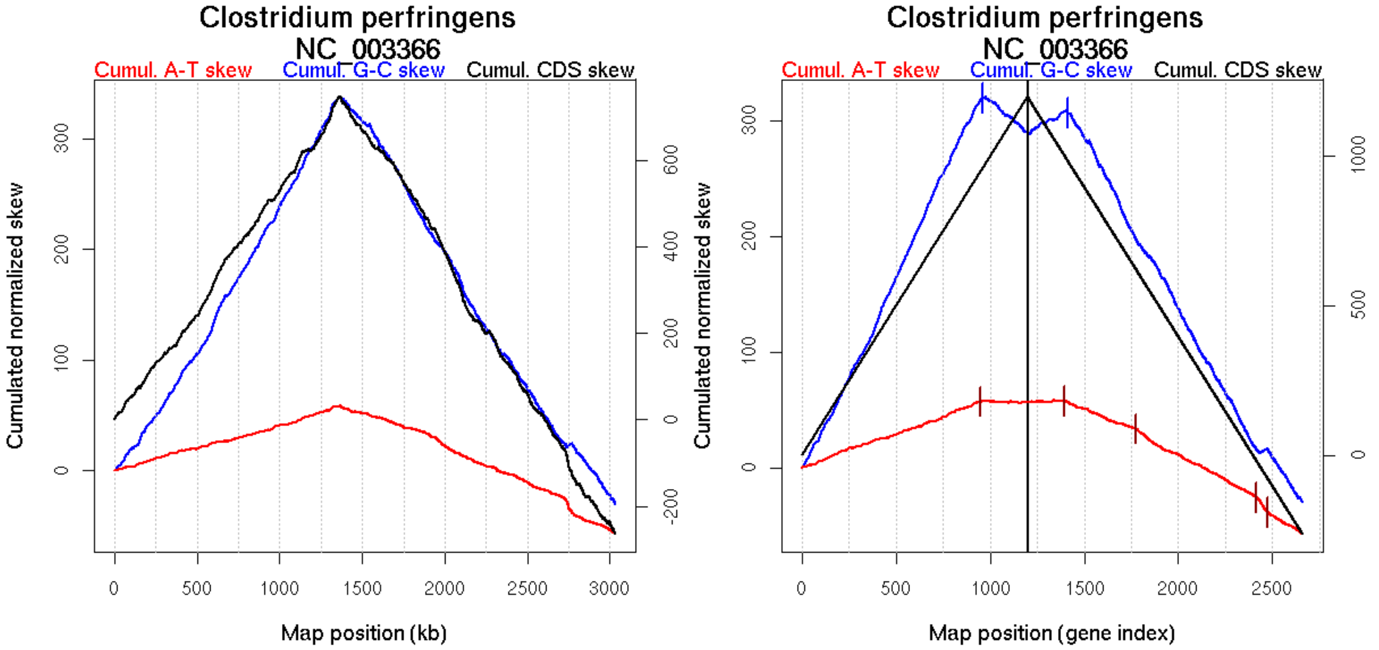
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1442 (1974.0355 kb)	leading	0.344
	1443(1976.4295 kb)	1859 (3940.781 kb)	lagging	-0.149
GC-skew reverse	1860 (0 kb)	2221 (1985.947 kb)	leading	0.12
	2222(1987.046 kb)	3672 (3940.781 kb)	lagging	-0.351
AT-skew forward	1 (0 kb)	1491 (2348.266 kb)	leading	0.007
	1492(2353.177 kb)	1859 (3940.781 kb)	lagging	-0.036
AT-skew reverse	1860 (0 kb)	2251 (2024.02 kb)	leading	0.01
	2252(2026.275 kb)	2317(2068.3815 kb)	lagging	-0.152
	2318(2070.7935 kb)	3221(3251.9705 kb)	lagging	0.002
	3222(3252.7725 kb)	3272(3289.4985 kb)	lagging	-0.173
	3273(3290.431 kb)	3672(3940.781 kb)	lagging	-0.015

More A than T on the leading strand for replication.
More G than C on the leading strand for replication.

99 Clostridium perfringens

Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
Accession number: NC_003366; **Genome size (bp)**: 3031430.
Number of genes: 2660.
Oriloc predictions: Origin 0 kb Terminus 1359 kb
Worning et al., 2006: Origin 0 kb Terminus 1361 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 0.143 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1.1 kb, 2988.68 kb
Consensus predictions: Origin 0 kb Terminus 1359 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	960	NA	1386
GC-skew reverse	1411	NA	1369
AT-skew forward	950	NA	1357
AT-skew reverse	1391	NA	1230
	1771	NA	1885
	2416	NA	2728
	2475	NA	2773

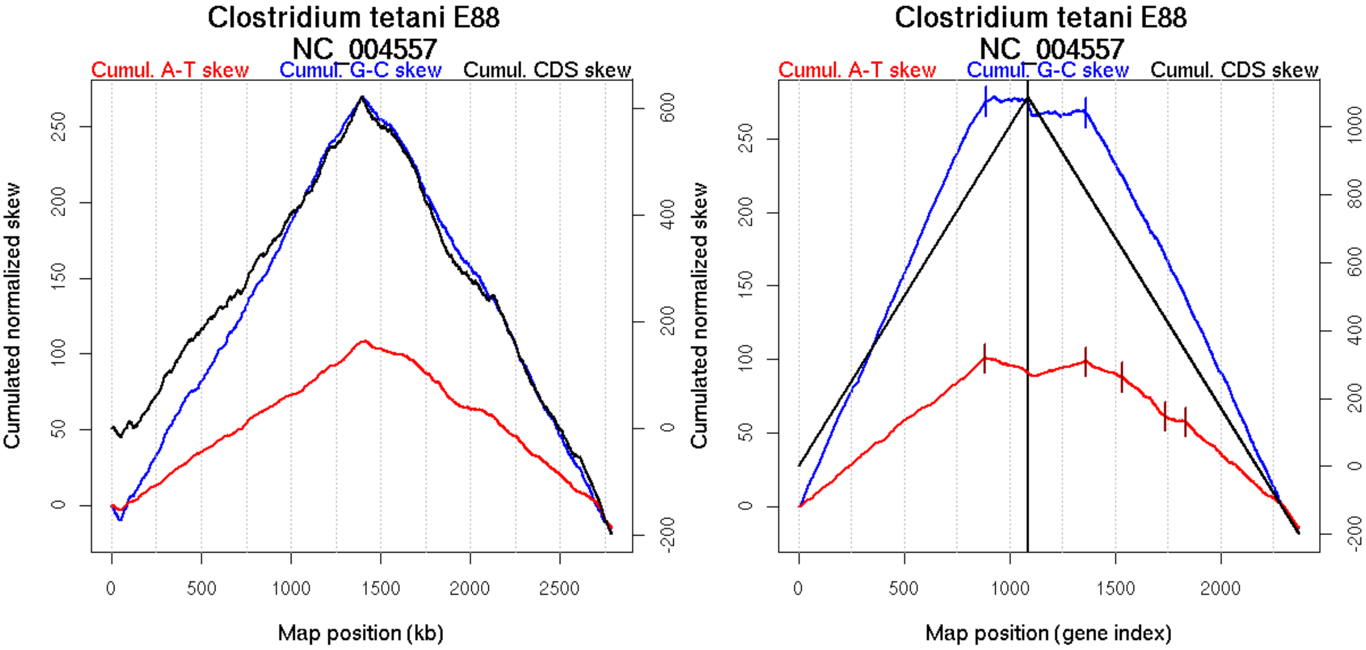
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	960 (1385.8015 kb)	leading	0.346
	961(1387.462 kb)	1198 (3030.809 kb)	lagging	-0.135
GC-skew reverse	1199 (0 kb)	1411 (1369.3125 kb)	leading	0.09
	1412(1369.9865 kb)	2660 (3030.809 kb)	lagging	-0.279
AT-skew forward	1 (0 kb)	950 (1356.7575 kb)	leading	0.059
	951(1357.074 kb)	1198 (3030.809 kb)	lagging	-0.005
AT-skew reverse	1199 (0 kb)	1391 (1230.337 kb)	leading	0.005
	1392(1233.2145 kb)	1771(1884.558 kb)	lagging	-0.064
	1772(1885.0355 kb)	2416(2728.434 kb)	lagging	-0.087
	2417(2730.371 kb)	2475(2773.477 kb)	lagging	-0.233
	2476(2774.6675 kb)	2660(3030.809 kb)	lagging	-0.093

More A than T on the leading strand for replication.
More G than C on the leading strand for replication.

100 Clostridium tetani E88

Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae; Clostridium.
Accession number: NC_004557; **Genome size (bp)**: 2799251.
Number of genes: 2373.
Oriloc predictions: Origin 0 kb Terminus 1395 kb
Worning et al., 2006: Origin 52 kb Terminus 1396 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 52.839 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 51.74 kb
Consensus predictions: Origin 0 kb Terminus 1395 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	889	NA	1450
GC-skew reverse	1360	NA	1409
AT-skew forward	882	NA	1391
AT-skew reverse	1360	NA	1409
	1533	NA	1677
	1740	NA	1916
	1833	NA	2074

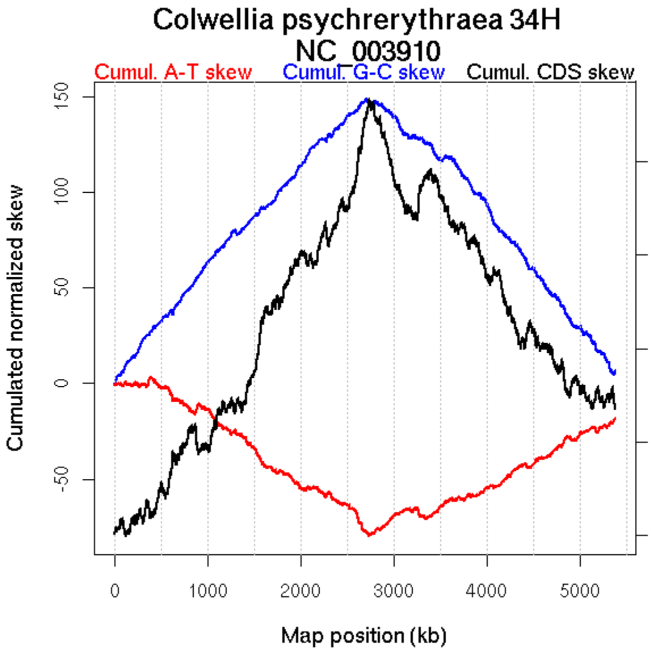
Segments:

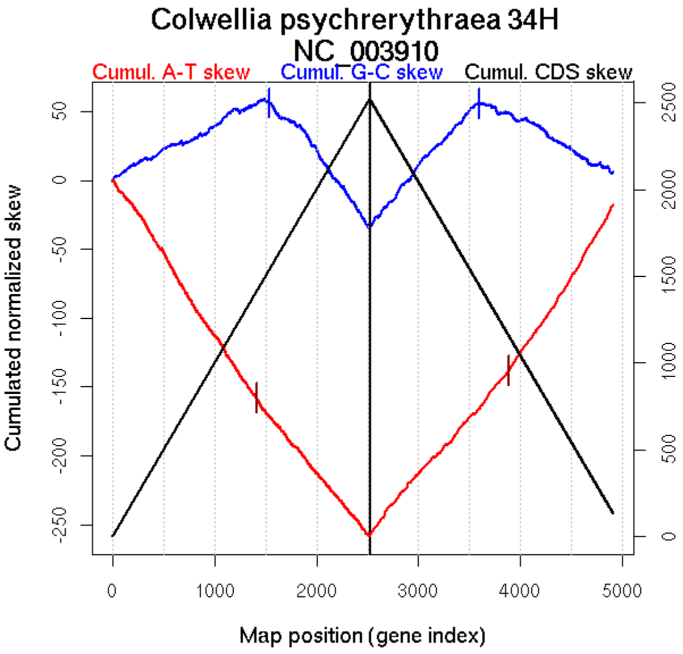
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	889 (1450.2155 kb)	leading	0.32
	890(1454.6505 kb)	1087 (2788.261 kb)	lagging	-0.003
GC-skew reverse	1088 (0 kb)	1360 (1409.31 kb)	leading	0.003
	1361(1411.6505 kb)	2373 (2788.261 kb)	lagging	-0.291
AT-skew forward	1 (0 kb)	882 (1391.146 kb)	leading	0.113
	883(1393.009 kb)	1087 (2788.261 kb)	lagging	-0.045
AT-skew reverse	1088 (0 kb)	1360 (1409.31 kb)	leading	0.037
	1361(1411.6505 kb)	1533(1677.3545 kb)	lagging	-0.058
	1534(1678.284 kb)	1740(1916.3525 kb)	lagging	-0.129
	1741(1917.0595 kb)	1833(2074.0985 kb)	lagging	-0.031
	1834(2075.985 kb)	2373(2788.261 kb)	lagging	-0.126

More A than T on the leading strand for replication.
More G than C on the leading strand for replication.

101 Colwellia psychrerythraea 34H

Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales; Colwelliaceae; Colwellia.
Accession number: NC_003910; **Genome size (bp)**: 5373180.
Number of genes: 4909.
Oriloc predictions: Origin 0 kb Terminus 2730 kb
Worning et al., 2006: Origin 5373 kb Terminus 2734 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 5367.814 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.76 kb
Consensus predictions: Origin 0 kb Terminus 2730 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1537	0	2815
GC-skew reverse	3594	0	2785
AT-skew forward	1410	0	2609
AT-skew reverse	3891	0	3343

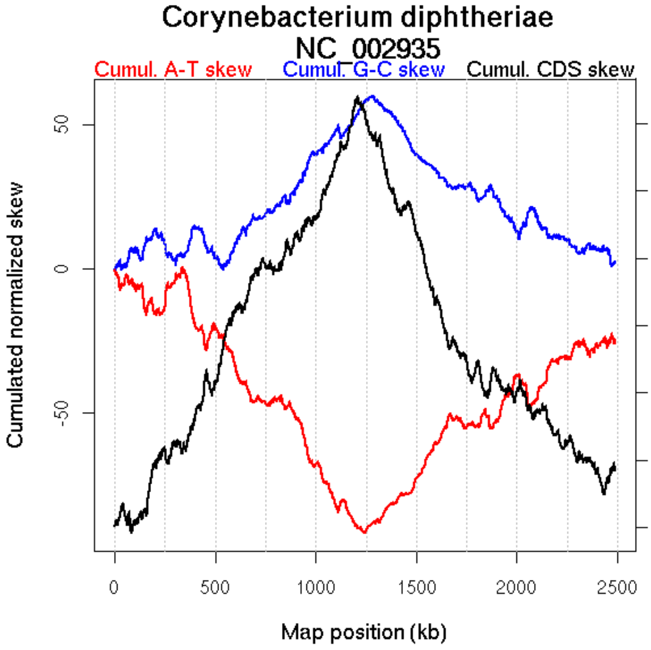
Segments:

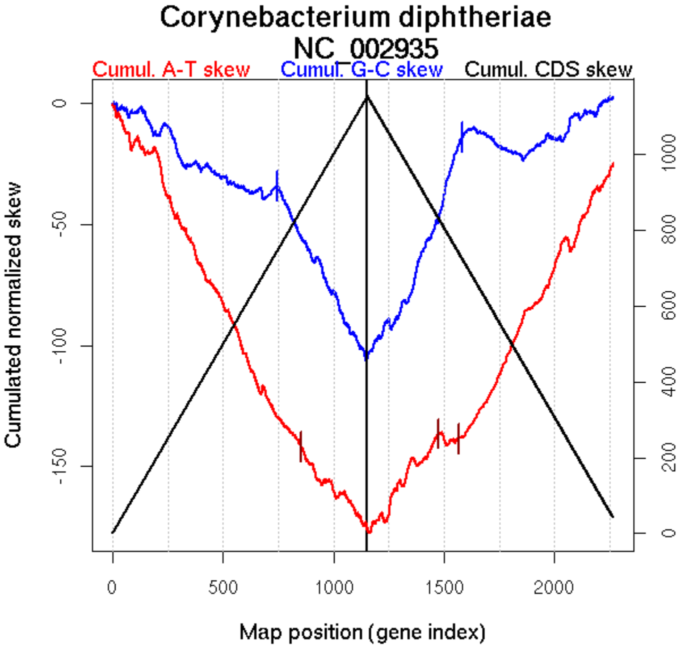
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1537 (2814.6735 kb)	leading	0.038
	1538(2819.677 kb)	2522 (5373.071 kb)	lagging	-0.094
GC-skew reverse	2523 (0 kb)	3594 (2784.9875 kb)	leading	0.085
	3595(2785.461 kb)	4909 (5373.071 kb)	lagging	-0.041
AT-skew forward	1 (0 kb)	1410 (2609.07 kb)	leading	-0.116
	1411(2609.5945 kb)	2522 (5373.071 kb)	lagging	-0.089
AT-skew reverse	2523 (0 kb)	3891 (3343.3525 kb)	NA	0.084
	3892(3343.7985 kb)	4909(5373.071 kb)	lagging	0.116

More T than A on the leading strand for replication - for forward encoded genes.
More G than C on the leading strand for replication.

102 Corynebacterium diphtheriae

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacteriaceae; Corynebacterium.
Accession number: NC_002935; **Genome size (bp)**: 2488635.
Number of genes: 2264.
Oriloc predictions: Origin 11 kb Terminus 1243 kb
Worning et al., 2006: Origin 2472 kb Terminus 1239 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 26.975 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.85 kb
Consensus predictions: Origin 0 kb Terminus 1243 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	743	0.00667	1240
GC-skew reverse	1584	0	1238
AT-skew forward	853	0.00667	1678
AT-skew reverse	1476	0.02	875
	1564	0	1194

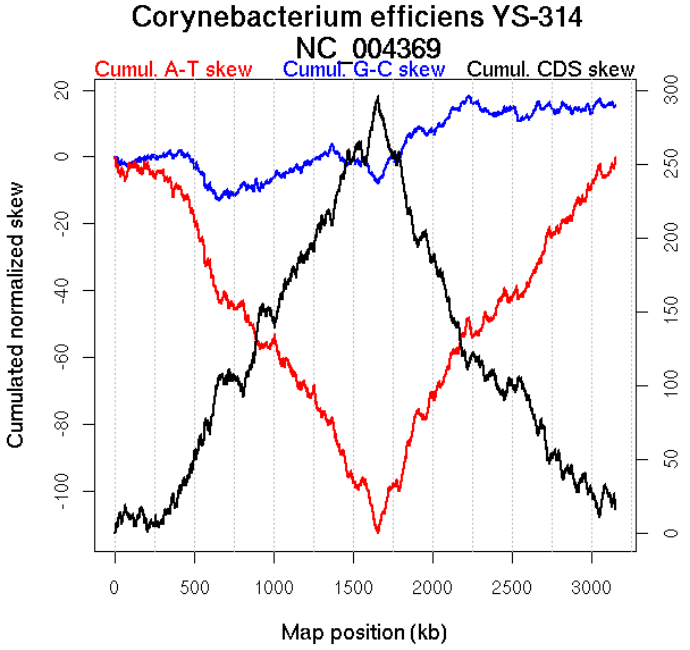
Segments:

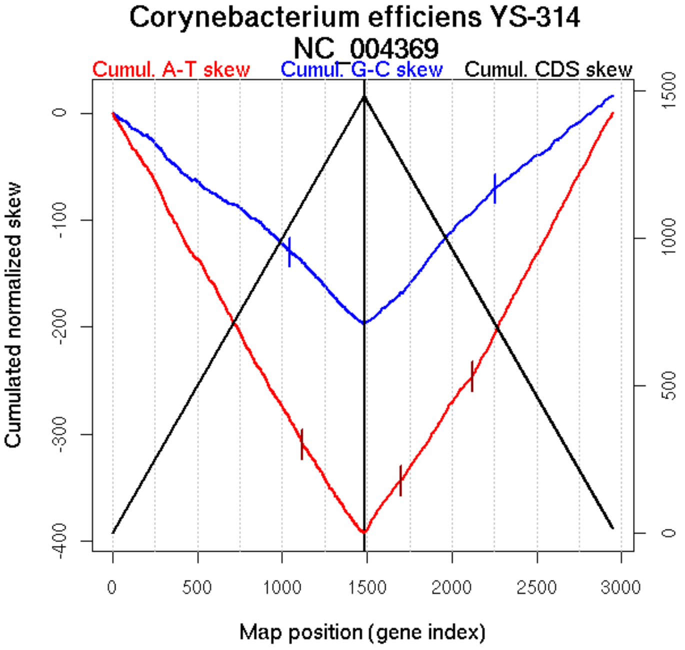
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	743 (1239.862 kb)	leading	-0.058
	744(1249.5765 kb)	1153 (2487.711 kb)	lagging	-0.175
GC-skew reverse	1154 (0 kb)	1584 (1237.8095 kb)	leading	0.214
	1585(1238.62 kb)	2264 (2487.711 kb)	lagging	0.023
AT-skew forward	1 (0 kb)	853 (1678.237 kb)	leading	-0.176
	854(1680.126 kb)	1153 (2487.711 kb)	lagging	-0.096
AT-skew reverse	1154 (0 kb)	1476 (874.758 kb)	leading	0.128
	1477(875.7435 kb)	1564(1194.0705 kb)	leading	-0.029
	1565(1200.519 kb)	2264(2487.711 kb)	lagging	0.168

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

103 Corynebacterium efficiens YS-314

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacteriaceae; Corynebacterium.
Accession number: NC_004369; **Genome size (bp)**: 3147090.
Number of genes: 2950.
Oriloc predictions: Origin 0 kb Terminus 1653 kb
Worning et al., 2006: Origin 3045 kb Terminus 1654 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 31.811 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.86 kb
Consensus predictions: Origin 0 kb Terminus 1653 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1047	NA	2024
GC-skew reverse	2254	NA	1858
AT-skew forward	1121	NA	2252
AT-skew reverse	1699	NA	533
	2120	NA	1637

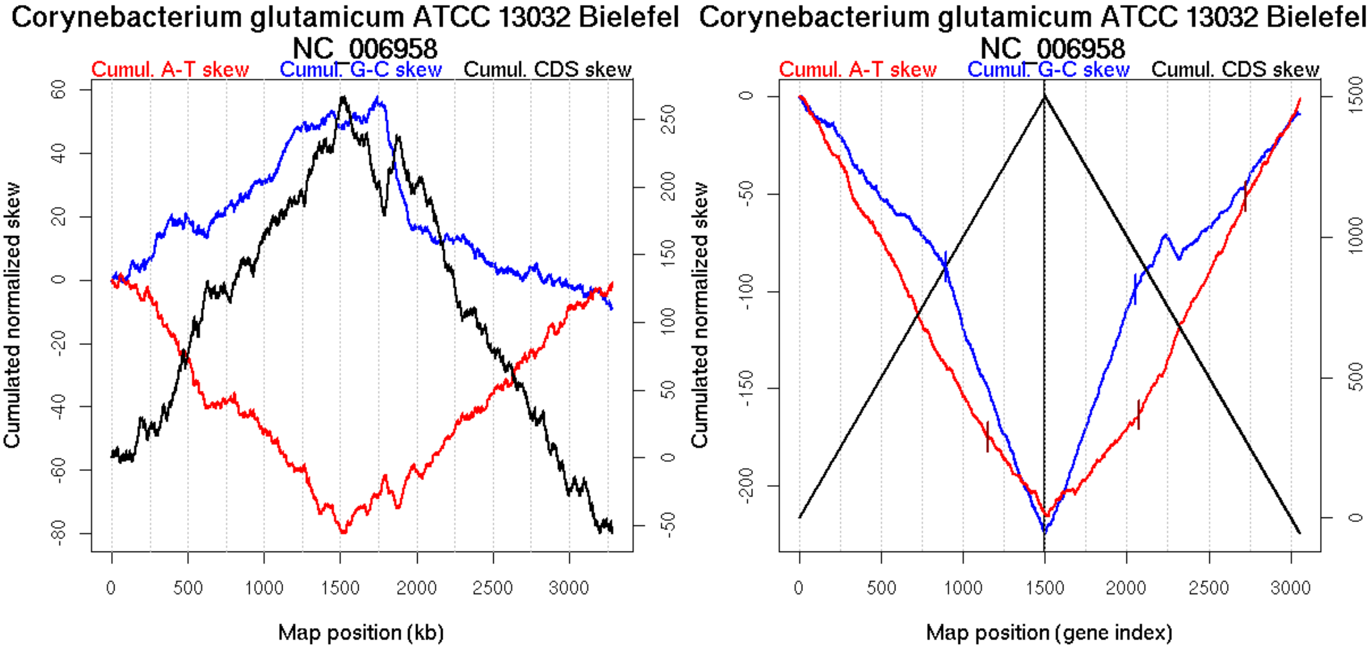
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1047 (2024.115 kb)	leading	-0.12
	1048(2028.468 kb)	1483 (3146.959 kb)	lagging	-0.165
GC-skew reverse	1484 (0 kb)	2254 (1857.714 kb)	NA	0.173
	2255(1859.058 kb)	2950 (3146.959 kb)	lagging	0.126
AT-skew forward	1 (0 kb)	1121 (2252.413 kb)	NA	-0.276
	1122(2253.512 kb)	1483 (3146.959 kb)	lagging	-0.239
AT-skew reverse	1484 (0 kb)	1699 (532.6115 kb)	leading	0.231
	1700(540.696 kb)	2120(1637.2635 kb)	leading	0.239
	2121(1642.051 kb)	2950(3146.959 kb)	lagging	0.299

More T than A on the leading strand for replication - for reverse encoded genes.
More G than C on the leading strand for replication - for forward encoded genes.

104 Corynebacterium glutamicum ATCC 13032 Bielefeld

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacteriaceae; Corynebacterium.
Accession number: NC_006958; **Genome size (bp)**: 3282708.
Number of genes: 3057.
Oriloc predictions: Origin 0 kb Terminus 1742 kb
Worning et al., 2006: Origin 3266 kb Terminus 1536 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 35.94 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.79 kb
Consensus predictions: Origin 35 kb Terminus 1742 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	893	NA	1652
GC-skew reverse	2050	NA	1407
AT-skew forward	1150	NA	2350
AT-skew reverse	2071	NA	1443
	2726	NA	2691

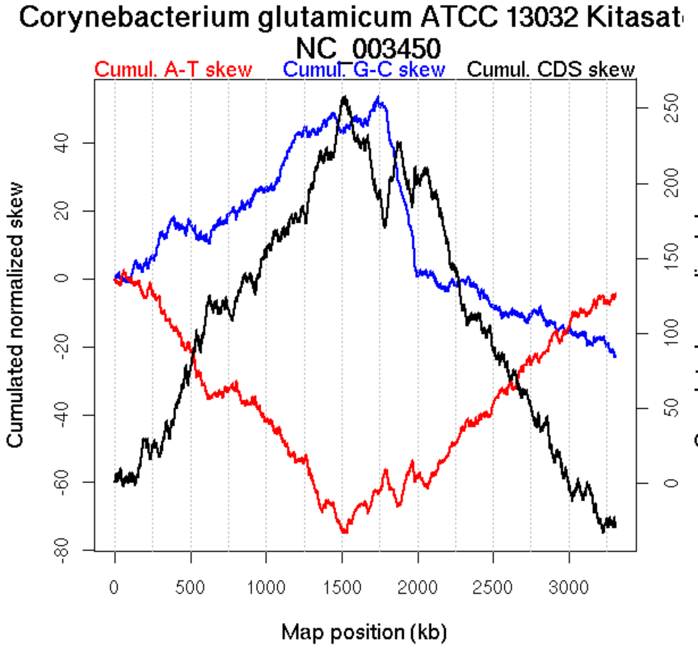
Segments:

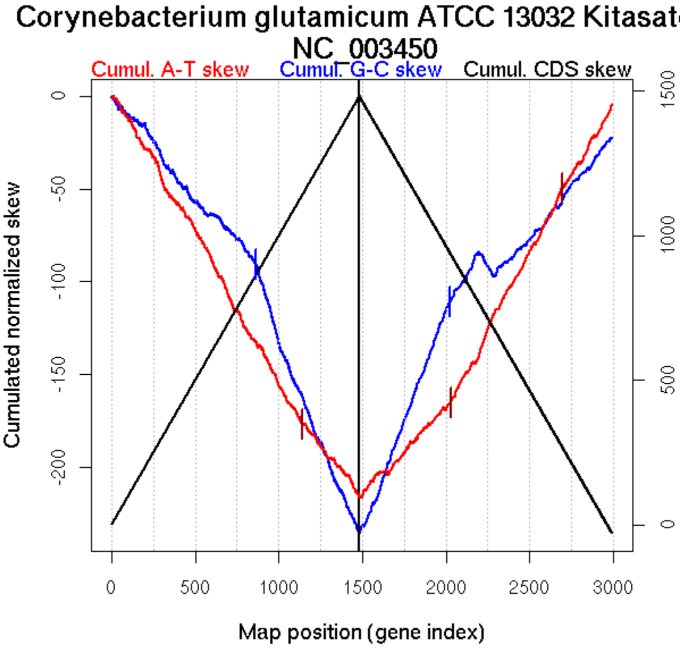
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	893 (1651.9665 kb)	leading	-0.097
	894(1657.143 kb)	1501 (3282.629 kb)	lagging	-0.22
GC-skew reverse	1502 (0 kb)	2050 (1406.9365 kb)	leading	0.235
	2051(1407.6815 kb)	3057 (3282.629 kb)	NA	0.085
AT-skew forward	1 (0 kb)	1150 (2349.957 kb)	NA	-0.156
	1151(2350.6965 kb)	1501 (3282.629 kb)	lagging	-0.108
AT-skew reverse	1502 (0 kb)	2071 (1443.0005 kb)	leading	0.09
	2072(1446.0865 kb)	2726(2690.5165 kb)	NA	0.169
	2727(2691.5025 kb)	3057(3282.629 kb)	lagging	0.146

More G than C on the leading strand for replication - for forward encoded genes.

105 Corynebacterium glutamicum ATCC 13032 Kitasato

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacteriaceae; Corynebacterium.
Accession number: NC_003450; **Genome size (bp)**: 3309401.
Number of genes: 2993.
Oriloc predictions: Origin 0 kb Terminus 1740 kb
Worning et al., 2006: Origin 4 kb Terminus 1563 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 35.94 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.79 kb
Consensus predictions: Origin 35 kb Terminus 1740 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	863	NA	1651
GC-skew reverse	2025	NA	1424
AT-skew forward	1143	NA	2389
AT-skew reverse	2029	NA	1432
	2694	NA	2732

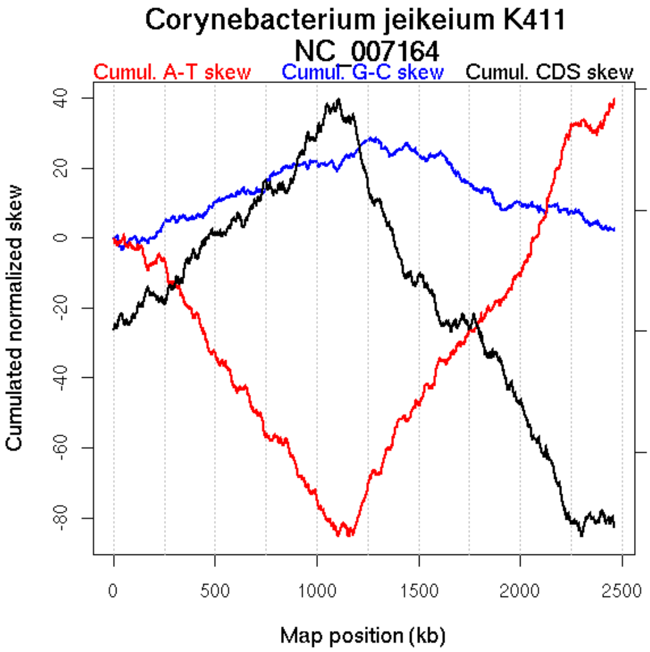
Segments:

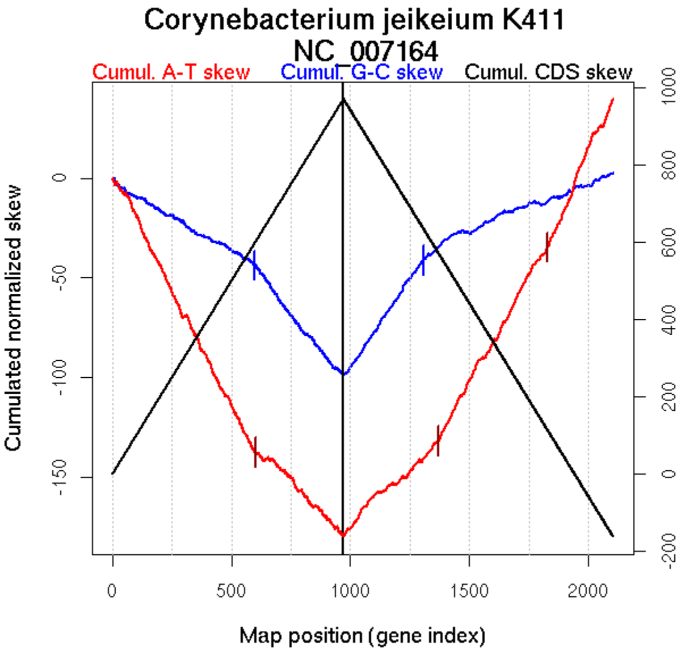
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	863 (1650.5655 kb)	leading	-0.105
	864(1655.676 kb)	1482 (3308.553 kb)	lagging	-0.228
GC-skew reverse	1483 (0 kb)	2025 (1423.9405 kb)	leading	0.238
	2026(1428.2675 kb)	2993 (3308.553 kb)	NA	0.085
AT-skew forward	1 (0 kb)	1143 (2388.8305 kb)	NA	-0.158
	1144(2391.5175 kb)	1482 (3308.553 kb)	lagging	-0.111
AT-skew reverse	1483 (0 kb)	2029 (1431.6355 kb)	leading	0.093
	2030(1434.412 kb)	2694(2731.8025 kb)	NA	0.171
	2695(2734.3205 kb)	2993(3308.553 kb)	lagging	0.149

More G than C on the leading strand for replication - for forward encoded genes.

106 Corynebacterium jeikeium K411

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Corynebacteriaceae; Corynebacterium.
Accession number: NC_007164; **Genome size (bp)**: 2462499.
Number of genes: 2104.
Oriloc predictions: Origin 0 kb Terminus 1234 kb
Worning et al., 2006: Origin 0 kb Terminus 1084 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 2462.344 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.88 kb
Consensus predictions: Origin 0 kb Terminus 1234 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	599	NA	1286
GC-skew reverse	1308	NA	992
AT-skew forward	602	NA	1290
AT-skew reverse	1369	NA	1148
	1829	NA	1949

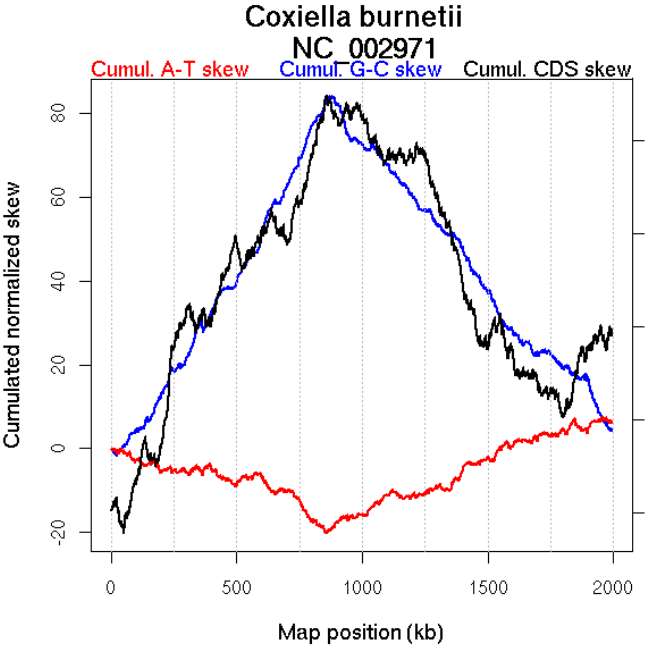
Segments:

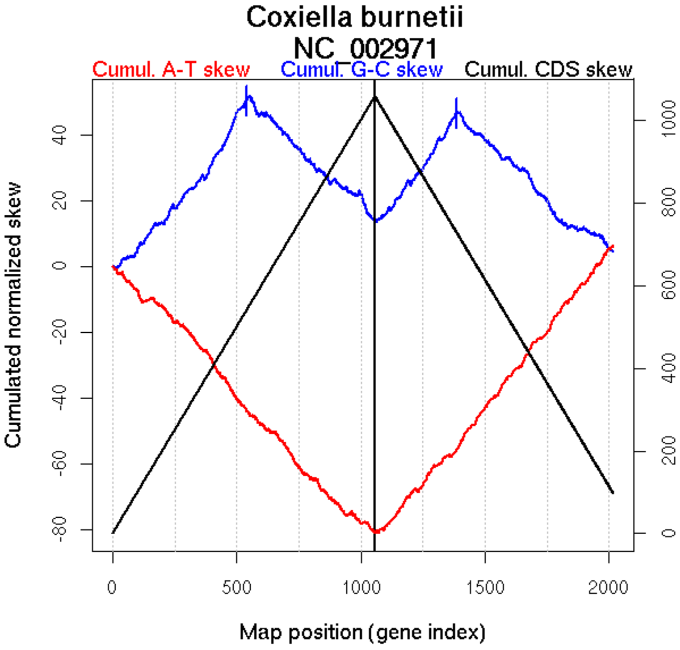
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	599 (1285.7225 kb)	leading	-0.068
	600(1286.3445 kb)	971 (2461.792 kb)	lagging	-0.15
GC-skew reverse	972 (0 kb)	1308 (992.135 kb)	leading	0.178
	1309(1002.5695 kb)	2104 (2461.792 kb)	lagging	0.048
AT-skew forward	1 (0 kb)	602 (1289.7125 kb)	leading	-0.235
	603(1291.5965 kb)	971 (2461.792 kb)	lagging	-0.119
AT-skew reverse	972 (0 kb)	1369 (1147.763 kb)	leading	0.109
	1370(1154.1415 kb)	1829(1948.814 kb)	lagging	0.212
	1830(1953.699 kb)	2104(2461.792 kb)	lagging	0.274

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

107 Coxiella burnetii

Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales; Coxiellaceae; Coxiella.
Accession number: NC_002971; **Genome size (bp)**: 1995281.
Number of genes: 2016.
Oriloc predictions: Origin 0 kb Terminus 861 kb
Worning et al., 2006: Origin 36 kb Terminus 861 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1080.164 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.82 kb
Consensus predictions: Origin 0 kb Terminus 861 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	539	0	850
GC-skew reverse	1387	0	868

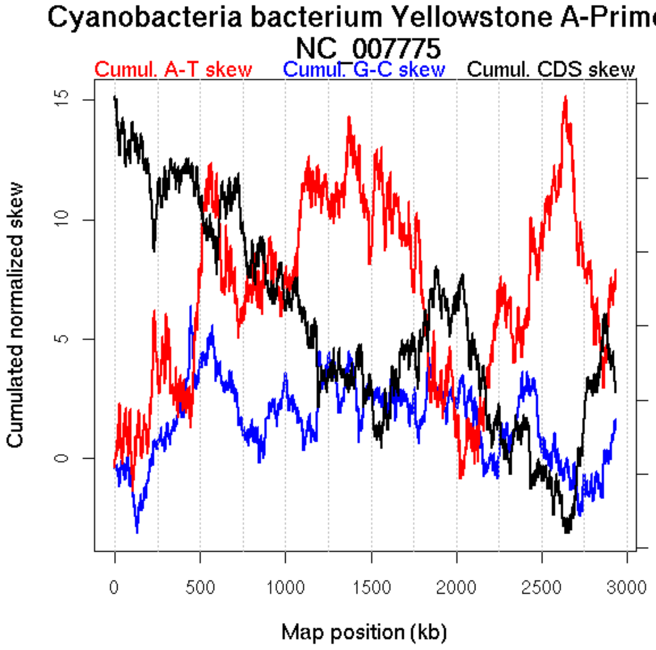
Segments:

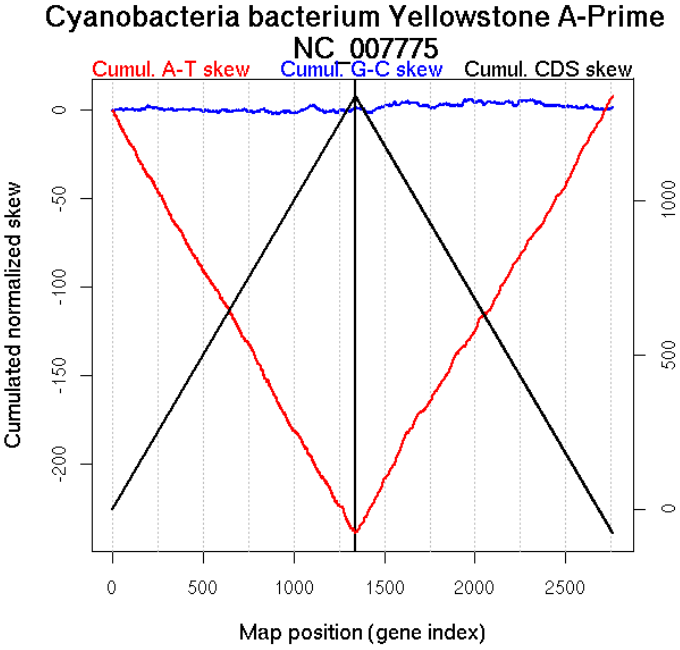
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	539 (849.53 kb)	leading	0.093
	540(849.848 kb)	1057 (1995.196 kb)	lagging	-0.069
GC-skew reverse	1058 (0 kb)	1387 (868.404 kb)	leading	0.102
	1388(873.233 kb)	2016 (1995.196 kb)	lagging	-0.068

More G than C on the leading strand for replication.

108 Cyanobacteria bacterium Yellowstone A-Prime

Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
Accession number: NC_007775; **Genome size (bp)**: 2932766.
Number of genes: 2760.
Oriloc predictions: Origin NA Terminus NA
Worning et al., 2006: Origin 1149 kb Terminus 264 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1647.947 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.77 kb
Consensus predictions: Origin 1647 kb Terminus 3050 kb

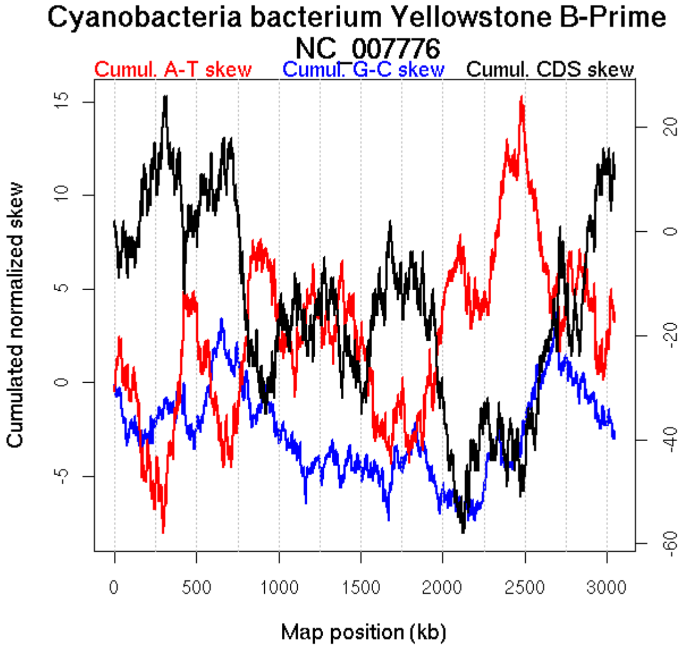


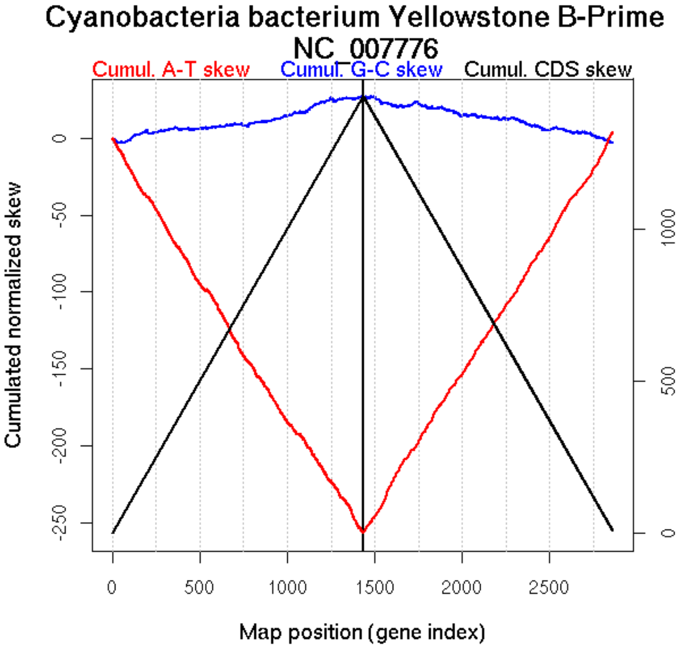


No significant breakpoints.

109 Cyanobacteria bacterium Yellowstone B-Prime

Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
Accession number: NC_007776; **Genome size (bp)**: 3046682.
Number of genes: 2862.
Oriloc predictions: Origin NA Terminus NA
Worning et al., 2006: Origin 1277 kb Terminus 2295 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1616.831 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.77 kb
Consensus predictions: Origin 1616 kb Terminus 3050 kb

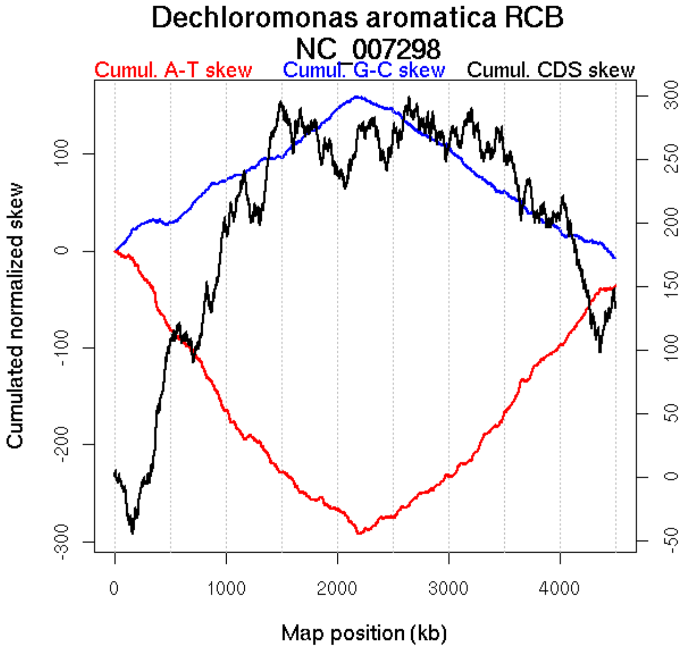


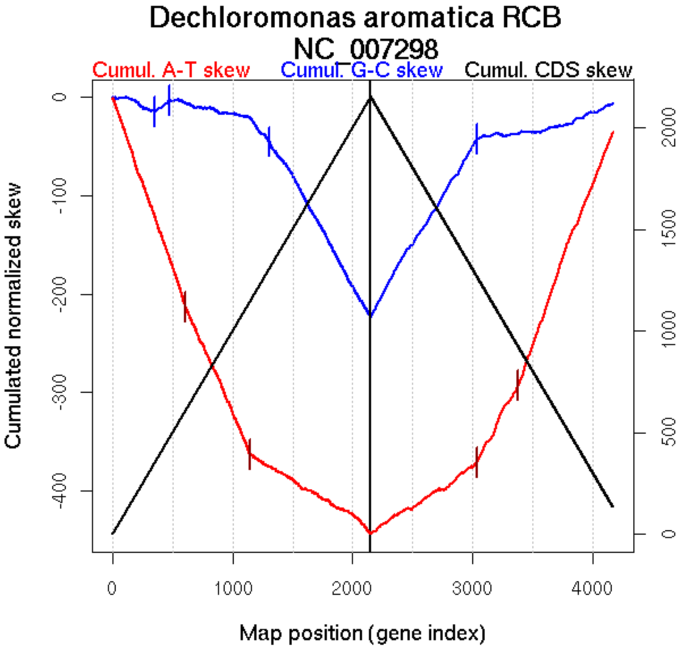


No significant breakpoints.

110 Dechloromonas aromatica RCB

Bacteria; Proteobacteria; Betaproteobacteria; Rhodocyclales; Rhodocyclaceae; Dechloromona
Accession number: NC_007298; **Genome size (bp)**: 4501104.
Number of genes: 4171.
Oriloc predictions: Origin 4 kb Terminus 2193 kb
Worning et al., 2006: Origin 4501 kb Terminus 2194 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 2687.74 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.85 kb
Consensus predictions: Origin 4 kb Terminus 2193 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	354	0	675
	473	0	882
	1307	0	2557
GC-skew reverse	3040	0	2223
AT-skew forward	609	0.04667	1097
	1147	0.00667	2187
AT-skew reverse	3035	0	2215
	3382	0.02333	2957

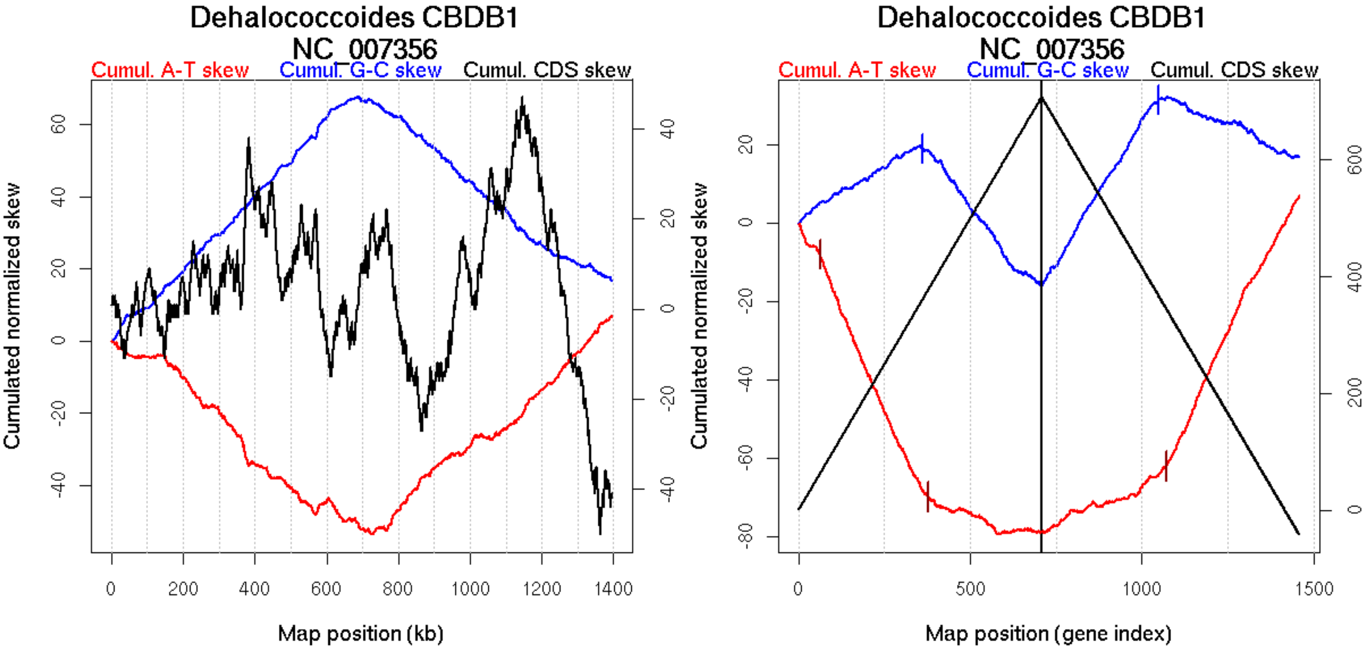
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	354 (675.027 kb)	leading	-0.048
	355(678.2485 kb)	473 (881.921 kb)	leading	0.093
	474(882.4175 kb)	1307 (2557.494 kb)	NA	-0.04
	1308(2557.76 kb)	2152 (4501.019 kb)	lagging	-0.217
GC-skew reverse	2153 (0 kb)	3040 (2223.1145 kb)	leading	0.198
	3041(2227.331 kb)	4171 (4501.019 kb)	lagging	0.029
AT-skew forward	1 (0 kb)	609 (1097.21 kb)	leading	-0.346
	610(1097.9375 kb)	1147 (2186.6865 kb)	leading	-0.275
	1148(2188.2145 kb)	2152 (4501.019 kb)	lagging	-0.074
AT-skew reverse	2153 (0 kb)	3035 (2215.2505 kb)	leading	0.078
	3036(2216.2995 kb)	3382(2957.422 kb)	lagging	0.229
	3383(2958.58 kb)	4171(4501.019 kb)	lagging	0.327

More T than A on the leading strand for replication.
More G than C on the leading strand for replication - for reverse encoded genes.

111 Dehalococcoides CBDB1

Bacteria; Chloroflexi; Dehalococcoidetes; Dehalococcoides.
Accession number: NC_007356; **Genome size (bp)**: 1395502.
Number of genes: 1458.
Oriloc predictions: Origin 0 kb Terminus 724 kb
Worning et al., 2006: Origin 1 kb Terminus 725 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 852.281 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.93 kb
Consensus predictions: Origin 0 kb Terminus 724 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	361	0	696
GC-skew reverse	1050	0.00667	660
AT-skew forward	62	0.03333	151
	376	0.00667	720
AT-skew reverse	1071	0	721

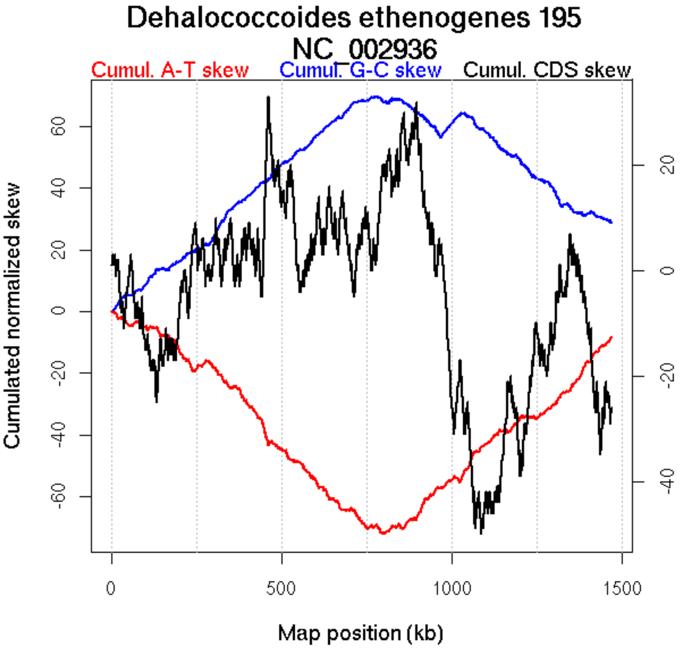
Segments:

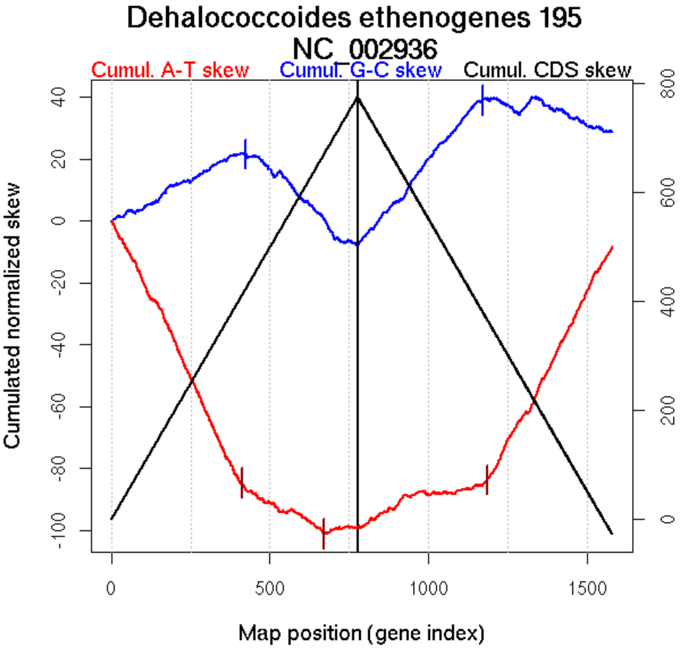
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	361 (696.4655 kb)	leading	0.053
	362(697.701 kb)	708 (1395.47 kb)	lagging	-0.112
GC-skew reverse	709 (0 kb)	1050 (659.93 kb)	leading	0.143
	1051(661.281 kb)	1458 (1395.47 kb)	lagging	-0.04
AT-skew forward	1 (0 kb)	62 (150.968 kb)	leading	-0.109
	63(151.5415 kb)	376 (720.0955 kb)	leading	-0.199
	377(720.621 kb)	708 (1395.47 kb)	lagging	-0.028
AT-skew reverse	709 (0 kb)	1071 (720.7535 kb)	leading	0.04
	1072(728.918 kb)	1458(1395.47 kb)	lagging	0.181

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

112 Dehalococcoides ethenogenes 195

Bacteria; Chloroflexi; Dehalococcoidetes; Dehalococcoides.
Accession number: NC_002936; **Genome size (bp)**: 1469720.
Number of genes: 1579.
Oriloc predictions: Origin 0 kb Terminus 791 kb
Worning et al., 2006: Origin 2 kb Terminus 793 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 444.38 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.93 kb
Consensus predictions: Origin 0 kb Terminus 791 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	423	NA	791
GC-skew reverse	1171	NA	756
AT-skew forward	412	NA	780
	670	NA	1272
AT-skew reverse	1184	NA	777

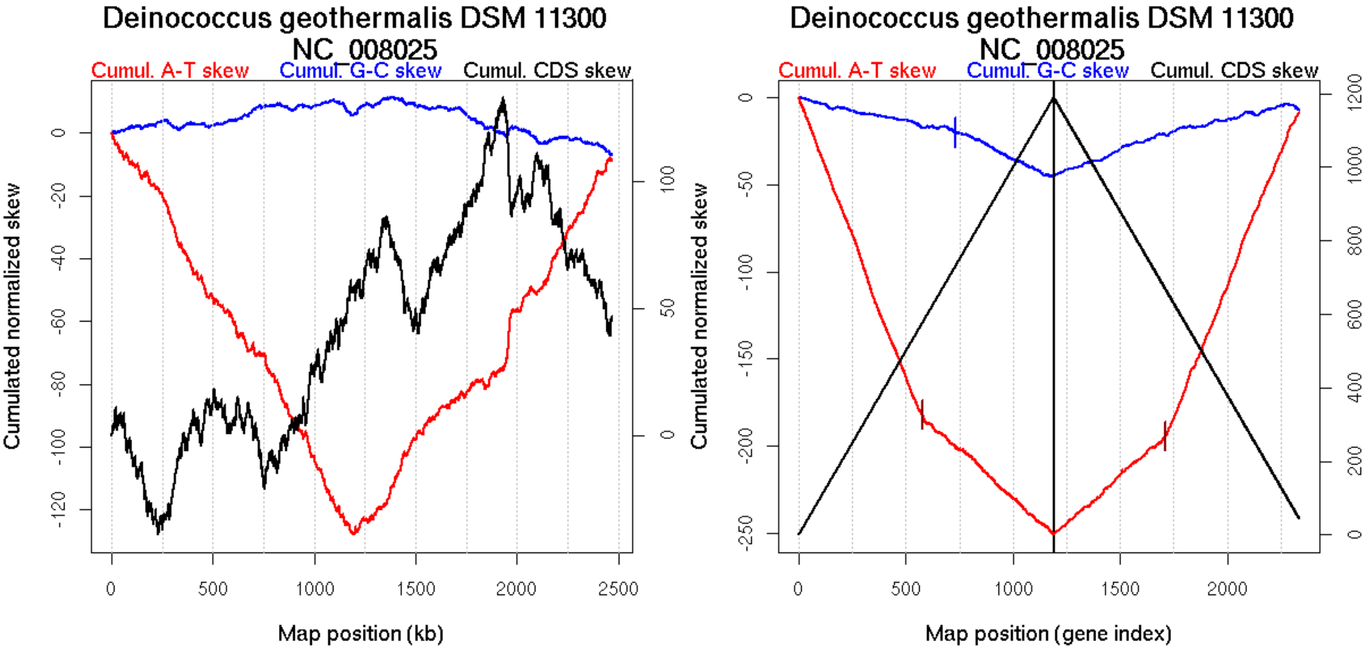
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	423 (791.188 kb)	leading	0.056
	424(791.6765 kb)	776 (1469.688 kb)	lagging	-0.096
GC-skew reverse	777 (0 kb)	1171 (756.3965 kb)	leading	0.124
	1172(756.8935 kb)	1579 (1469.688 kb)	lagging	-0.026
AT-skew forward	1 (0 kb)	412 (779.7365 kb)	leading	-0.212
	413(780.6305 kb)	670 (1272.0355 kb)	lagging	-0.052
	671(1276.4295 kb)	776 (1469.688 kb)	lagging	0.019
AT-skew reverse	777 (0 kb)	1184 (777.418 kb)	leading	0.032
	1185(788.166 kb)	1579(1469.688 kb)	lagging	0.196

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

113 Deinococcus geothermalis DSM 11300

Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales; Deinococcaceae; Deinococcus.
Accession number: NC_008025; **Genome size (bp)**: 2467205.
Number of genes: 2335.
Oriloc predictions: Origin 2 kb Terminus 1257 kb
Worning et al., 2006: Origin 6 kb Terminus 1153 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 2391.621 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.93 kb
Consensus predictions: Origin 0 kb Terminus 1257 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	729	0.02	1516
AT-skew forward	578	0	1177
AT-skew reverse	1711	0	1175

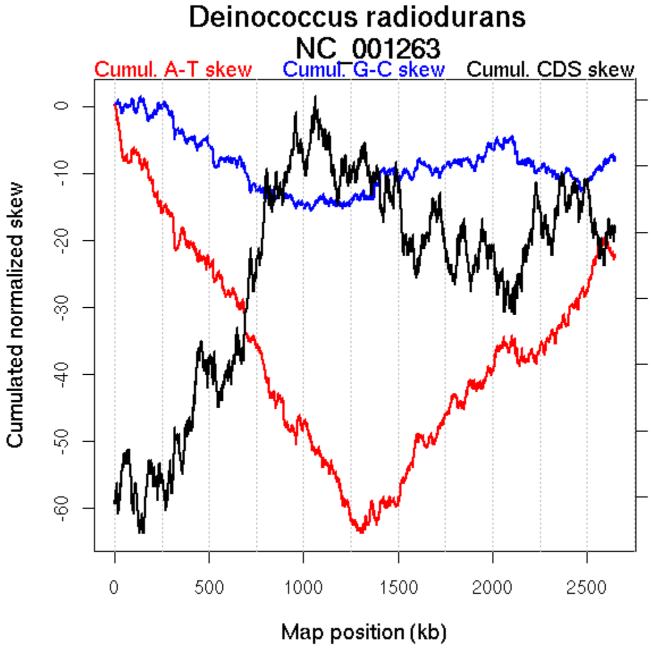
Segments:

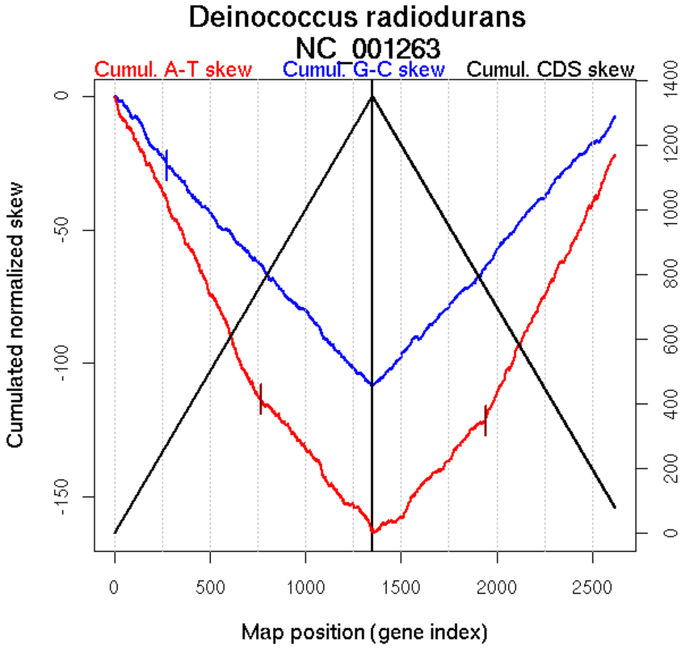
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	729 (1515.771 kb)	leading	-0.025
	730(1517.149 kb)	1190 (2467.021 kb)	lagging	-0.06
AT-skew forward	1 (0 kb)	578 (1176.723 kb)	leading	-0.322
	579(1177.654 kb)	1190 (2467.021 kb)	lagging	-0.11
AT-skew reverse	1191 (0 kb)	1711 (1175.052 kb)	leading	0.109
	1712(1180.8095 kb)	2335(2467.021 kb)	lagging	0.305

More T than A on the leading strand for replication.
More G than C on the leading strand for replication - for forward encoded genes.

114 Deinococcus radiodurans

Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales; Deinococcaceae; Deinococcus.
Accession number: NC_001263; **Genome size (bp)**: 2648638.
Number of genes: 2620.
Oriloc predictions: Origin 0 kb Terminus 1345 kb
Worning et al., 2006: Origin 2479 kb Terminus 1350 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1.722 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 2.59 kb
Consensus predictions: Origin 0 kb Terminus 1345 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	276	NA	523
AT-skew forward	766	NA	1449
AT-skew reverse	1941	NA	1296

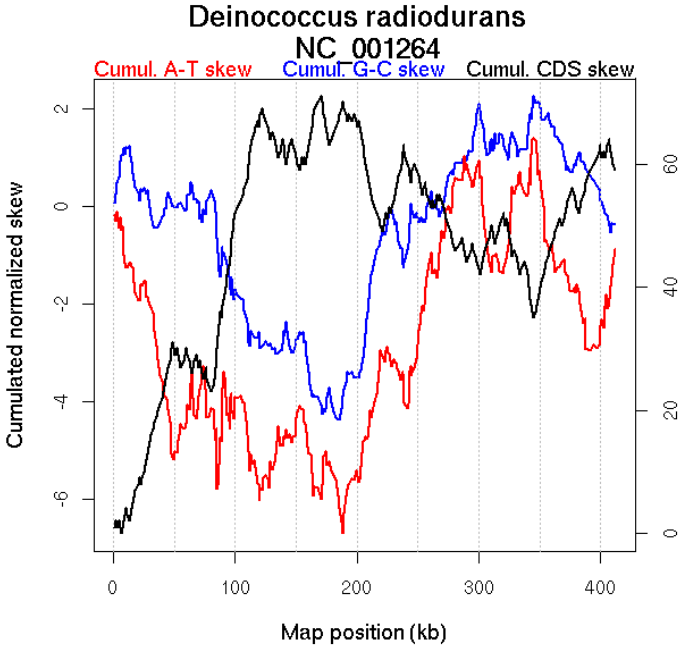
Segments:

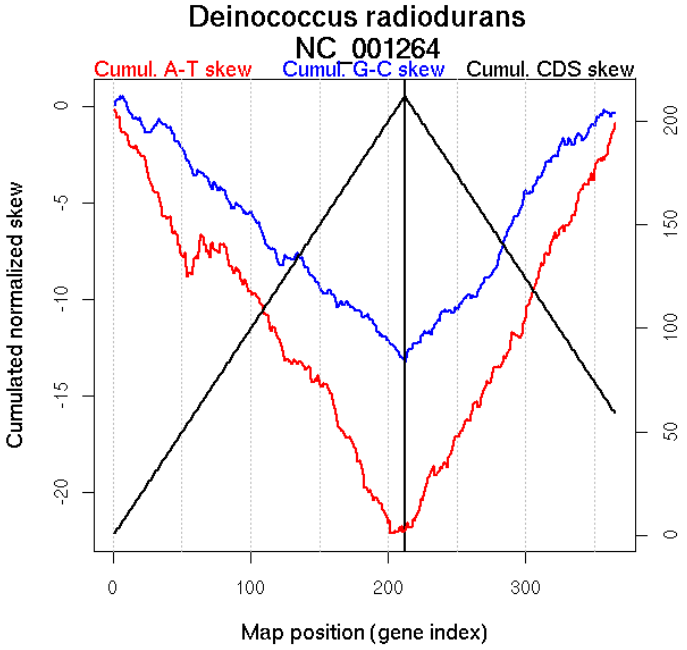
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	276 (523.277 kb)	leading	-0.097
	277(524.08 kb)	1350 (2648.524 kb)	NA	-0.077
AT-skew forward	1 (0 kb)	766 (1448.786 kb)	leading	-0.149
	767(1452.042 kb)	1350 (2648.524 kb)	lagging	-0.085
AT-skew reverse	1351 (0 kb)	1941 (1296.4735 kb)	leading	0.078
	1942(1299.7385 kb)	2620(2648.524 kb)	lagging	0.142

More T than A on the leading strand for replication.

115 Deinococcus radiodurans

Bacteria; Deinococcus-Thermus; Deinococci; Deinococcales; Deinococcaceae; Deinococcus.
Accession number: NC_001264; **Genome size (bp)**: 412348.
Number of genes: 365.
Oriloc predictions: Origin NA Terminus NA
Worning et al., 2006: Origin 171 kb Terminus 301 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 42.917 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): NA
Consensus predictions: Origin NA Terminus NA

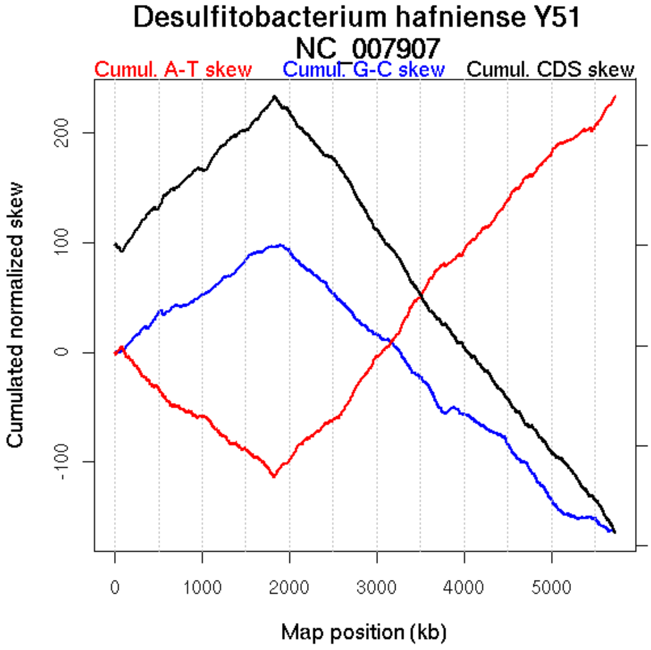


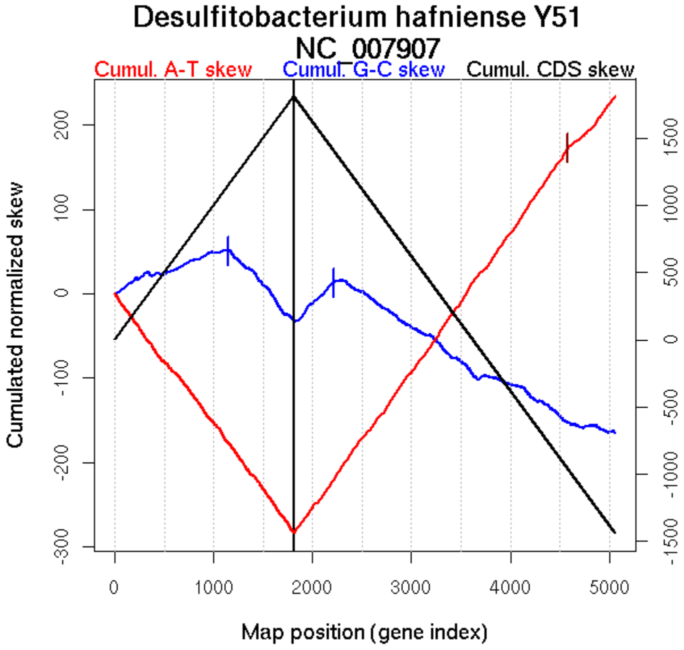


No significant breakpoints.

116 Desulfitobacterium hafniense Y51

Bacteria; Firmicutes; Clostridia; Clostridiales; Peptococcaceae; Desulfitobacterium.
Accession number: NC_007907; **Genome size (bp)**: 5727534.
Number of genes: 5060.
Oriloc predictions: Origin 0 kb Terminus 1825 kb
Worning et al., 2006: Origin 79 kb Terminus 1858 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 4540.614 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.68 kb
Consensus predictions: Origin 79 kb Terminus 1825 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1153	0	1820
GC-skew reverse	2210	0	1730
AT-skew reverse	4584	0	5090

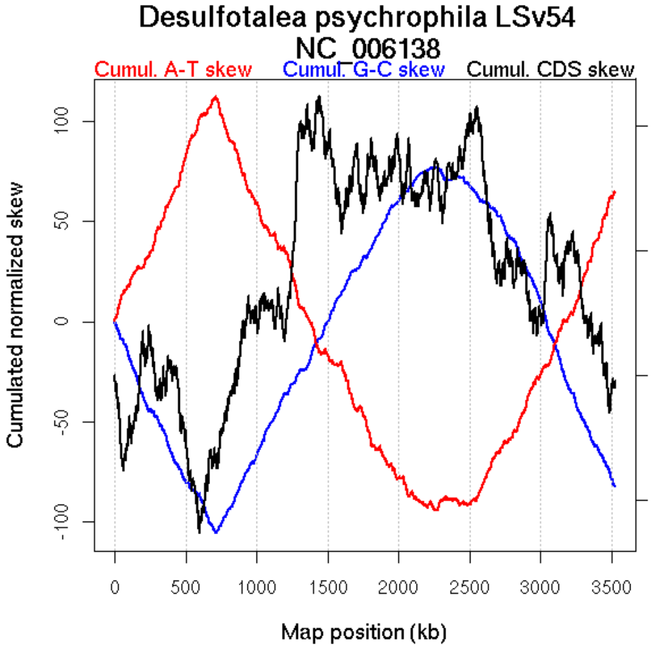
Segments:

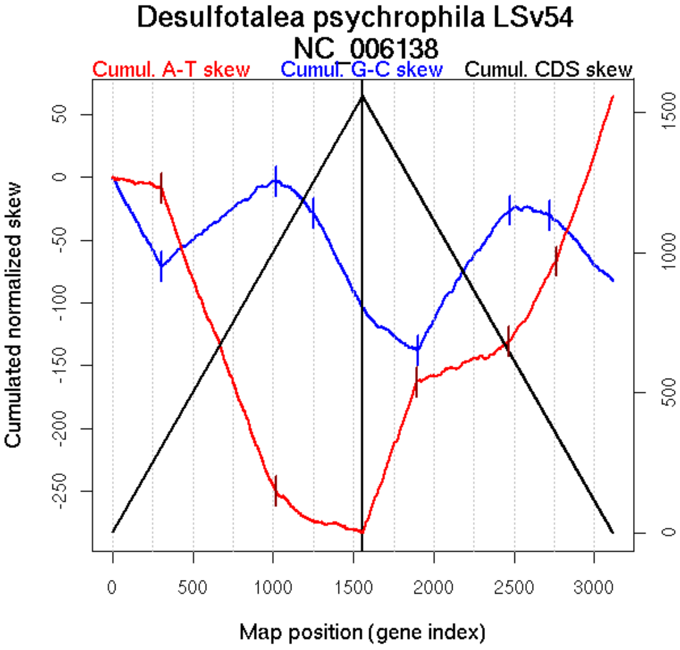
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1153 (1820.1805 kb)	leading	0.043
	1154(1821.0975 kb)	1811 (5727.179 kb)	lagging	-0.131
GC-skew reverse	1812 (0 kb)	2210 (1730.1935 kb)	leading	0.122
	2211(1730.9995 kb)	5060 (5727.179 kb)	lagging	-0.068
AT-skew reverse	1812 (0 kb)	4584 (5089.528 kb)	lagging	0.164
	4585(5090.958 kb)	5060(5727.179 kb)	lagging	0.13

More G than C on the leading strand for replication.

117 Desulfotalea psychrophila LSv54

Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobacterales; Desulfobulbaceae; Desulfotalea.
Accession number: NC_006138; **Genome size (bp)**: 3523383.
Number of genes: 3116.
Oriloc predictions: Origin 709 kb Terminus 2260 kb
Worning et al., 2006: Origin 710 kb Terminus 2476 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 709.722 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 302.57 kb
Consensus predictions: Origin 709 kb Terminus 2260 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	307	0	711
	1018	0	2233
	1253	0.01333	2817
GC-skew reverse	1901	0	719
	2476	0	2166
	2719	0.00444	2708
AT-skew forward	305	0	702
	1016	0	2228
AT-skew reverse	1895	0	707
	2468	0	2132
	2763	0.00222	2802

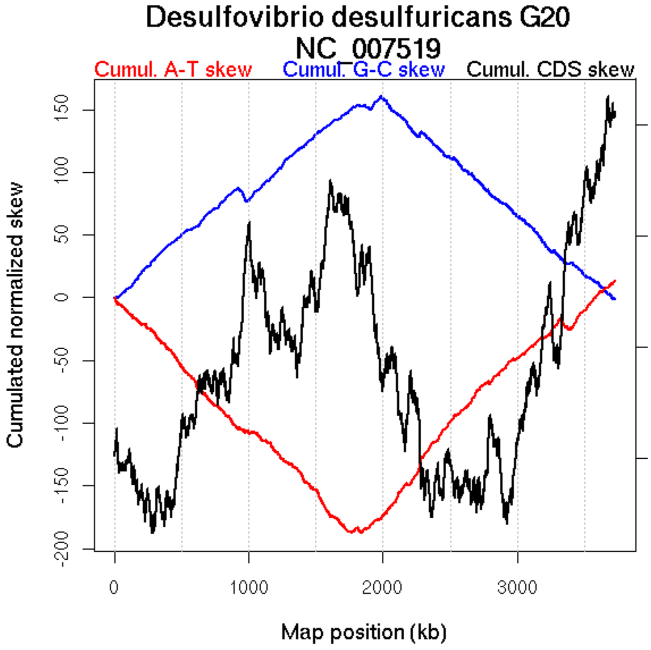
Segments:

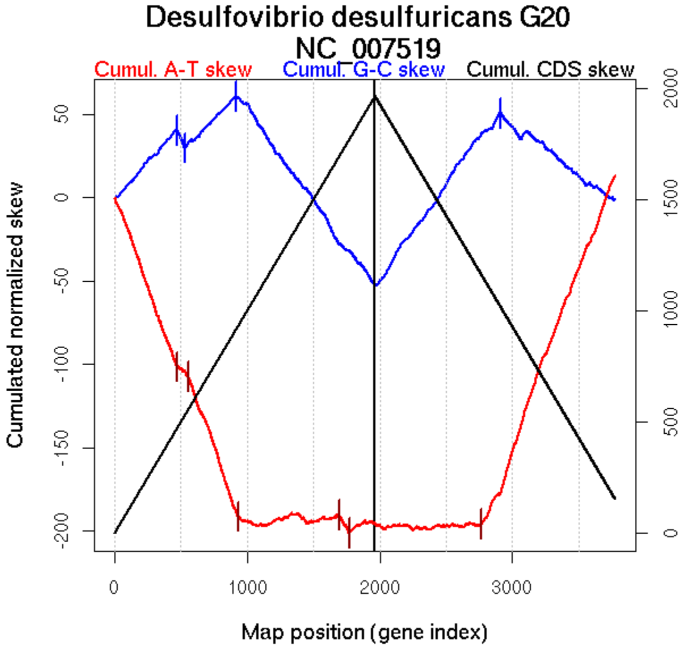
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	307 (711.083 kb)	lagging	-0.231
	308(713.589 kb)	1018 (2232.6825 kb)	leading	0.097
	1019(2234.514 kb)	1253 (2817.2865 kb)	lagging	-0.112
	1254(2822.8175 kb)	1557 (3523.092 kb)	lagging	-0.251
GC-skew reverse	1558 (0 kb)	1901 (718.9925 kb)	lagging	-0.094
	1902(719.795 kb)	2476 (2166.3905 kb)	leading	0.194
	2477(2167.4695 kb)	2719 (2707.699 kb)	lagging	-0.022
	2720(2708.2195 kb)	3116 (3523.092 kb)	lagging	-0.14
AT-skew forward	1 (0 kb)	305 (702.146 kb)	lagging	-0.024
	306(706.3935 kb)	1016 (2228.0955 kb)	leading	-0.338
	1017(2229.0175 kb)	1557 (3523.092 kb)	lagging	-0.053
AT-skew reverse	1558 (0 kb)	1895 (707.0055 kb)	lagging	0.354
	1896(707.5455 kb)	2468(2132.4265 kb)	leading	0.052
	2469(2135.0975 kb)	2763(2802.347 kb)	lagging	0.225
	2764(2804.1815 kb)	3116(3523.092 kb)	lagging	0.37

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

118 Desulfovibrio desulfuricans G20

Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales; Desulfovibrionaceae; Desulfovibrio.
Accession number: NC_007519; **Genome size (bp)**: 3730232.
Number of genes: 3775.
Oriloc predictions: Origin 6 kb Terminus 1983 kb
Worning et al., 2006: Origin 8 kb Terminus 1984 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 272.232 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.84 kb, 2337.94 kb
Consensus predictions: Origin 6 kb Terminus 1983 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	470	0	925
	527	0	984
	913	0	1814
GC-skew reverse	2915	0	1990
AT-skew forward	468	0.01467	923
	555	0.012	1062
	935	0	1836
	1693	0.01867	3324
	1770	0.012	3408
AT-skew reverse	2768	0	1772

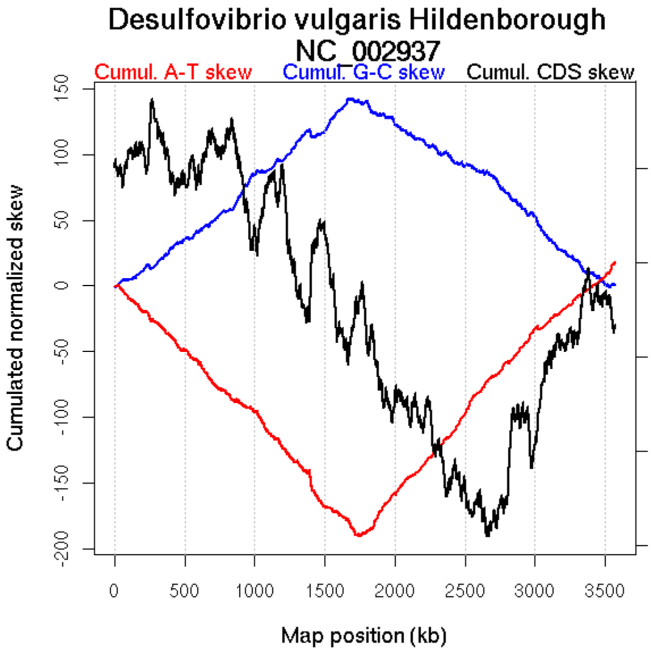
Segments:

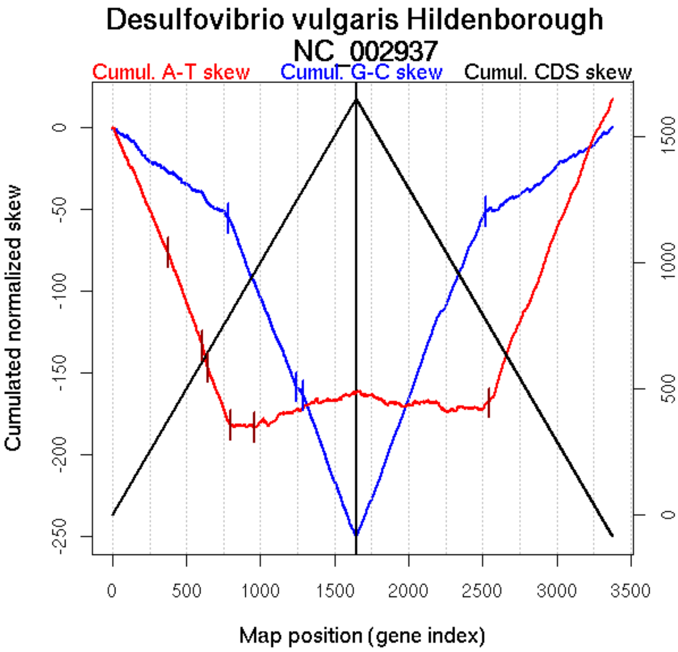
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	470 (924.9485 kb)	leading	0.09
	471(925.4135 kb)	527 (984.287 kb)	leading	-0.186
	528(984.98 kb)	913 (1814.0545 kb)	leading	0.081
	914(1815.594 kb)	1965 (3730.118 kb)	lagging	-0.111
GC-skew reverse	1966 (0 kb)	2915 (1989.514 kb)	leading	0.112
	2916(1990.4055 kb)	3775 (3730.118 kb)	lagging	-0.06
AT-skew forward	1 (0 kb)	468 (922.856 kb)	leading	-0.222
	469(923.369 kb)	555 (1061.802 kb)	leading	-0.071
	556(1063.891 kb)	935 (1836.4945 kb)	leading	-0.226
	936(1838.0905 kb)	1693 (3324.1175 kb)	lagging	0.004
	1694(3325.019 kb)	1770 (3408.031 kb)	lagging	-0.13
	1771(3408.3015 kb)	1965 (3730.118 kb)	lagging	0.027
AT-skew reverse	1966 (0 kb)	2768 (1771.7605 kb)	leading	0.001
	2769(1773.5585 kb)	3775(3730.118 kb)	lagging	0.215

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

119 Desulfovibrio vulgaris Hildenborough

Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales; Desulfovibrionaceae; Desulfovibrio.
Accession number: NC_002937; **Genome size (bp)**: 3570858.
Number of genes: 3378.
Oriloc predictions: Origin 0 kb Terminus 1666 kb
Worning et al., 2006: Origin 9 kb Terminus 1747 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 2271.812 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.81 kb, 2348.45 kb
Consensus predictions: Origin 0 kb Terminus 1666 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	783	NA	1722
	1242	NA	2787
	1287	NA	2830
GC-skew reverse	2520	NA	1770
AT-skew forward	375	NA	823
	609	NA	1393
	644	NA	1412
	795	NA	1746
	961	NA	2137
AT-skew reverse	2540	NA	1790

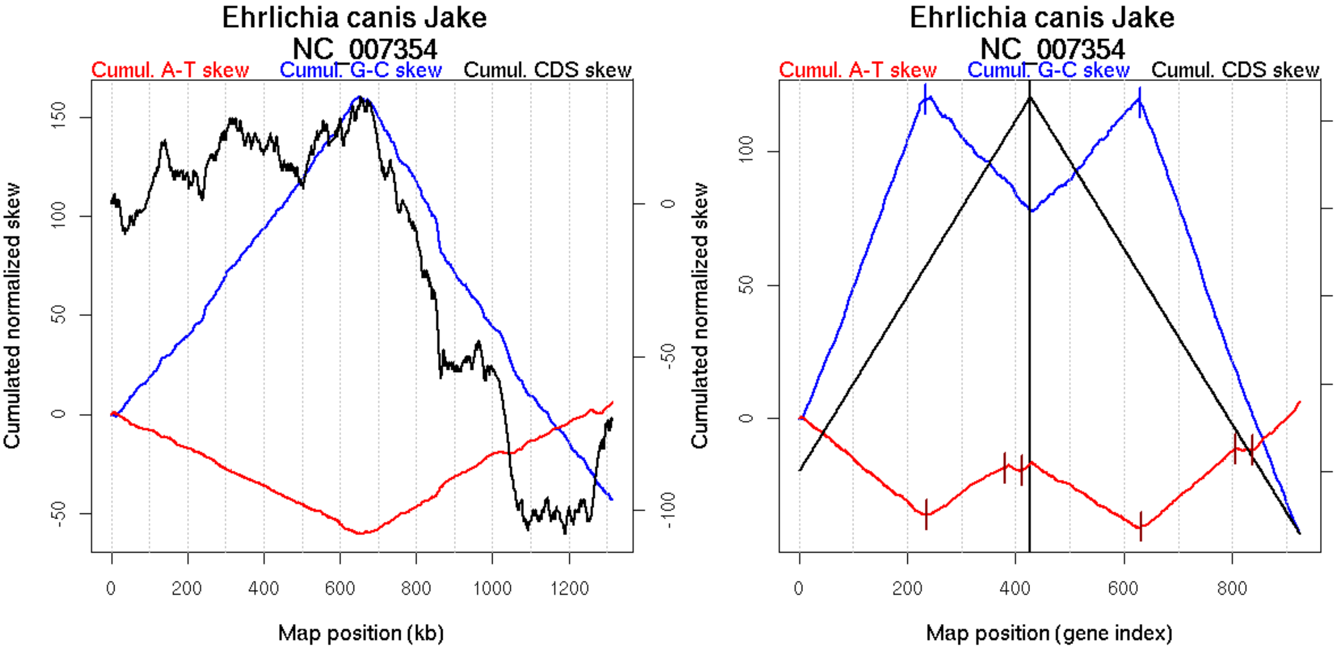
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	783 (1721.9025 kb)	leading	-0.069
	784(1724.112 kb)	1242 (2787.0295 kb)	lagging	-0.224
	1243(2787.9375 kb)	1287 (2829.9325 kb)	lagging	-0.099
	1288(2830.997 kb)	1647 (3570.714 kb)	lagging	-0.247
GC-skew reverse	1648 (0 kb)	2520 (1769.8165 kb)	leading	0.232
	2521(1770.351 kb)	3378 (3570.714 kb)	lagging	0.062
AT-skew forward	1 (0 kb)	375 (822.632 kb)	leading	-0.206
	376(825.193 kb)	609 (1392.81 kb)	leading	-0.242
	610(1393.226 kb)	644 (1411.882 kb)	leading	-0.403
	645(1413.2 kb)	795 (1745.8345 kb)	NA	-0.232
	796(1748.2385 kb)	961 (2136.605 kb)	lagging	-0.002
	962(2136.799 kb)	1647 (3570.714 kb)	lagging	0.03
AT-skew reverse	1648 (0 kb)	2540 (1790.389 kb)	leading	-0.009
	2541(1791.715 kb)	3378(3570.714 kb)	lagging	0.225

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

120 Ehrlichia canis Jake

Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales; Anaplasmataceae; Ehrlichia.
Accession number: NC_007354; **Genome size (bp)**: 1315030.
Number of genes: 925.
Oriloc predictions: Origin 9 kb Terminus 654 kb
Worning et al., 2006: Origin 11 kb Terminus 655 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 769.927 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 291.26 kb, 414.2 kb
Consensus predictions: Origin 9 kb Terminus 654 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	233	0	653
GC-skew reverse	629	0	660
AT-skew forward	236	0	663
	381	0.00667	1239
	412	0.00222	1291
AT-skew reverse	631	0	664
	805	0.01333	1018
	837	0.00444	1052

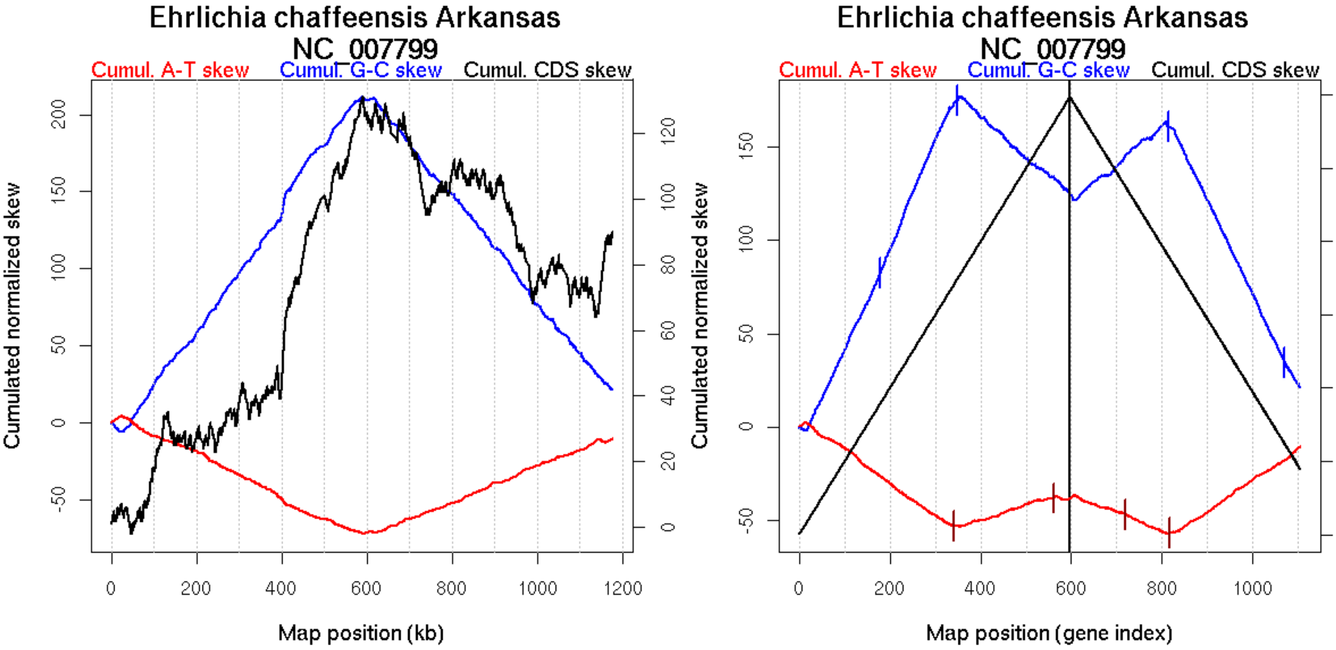
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	233 (652.6085 kb)	leading	0.542
	234(654.0135 kb)	427 (1314.671 kb)	lagging	-0.22
GC-skew reverse	428 (0 kb)	629 (659.7175 kb)	leading	0.22
	630(662.2105 kb)	925 (1314.671 kb)	lagging	-0.56
AT-skew forward	1 (0 kb)	236 (662.9015 kb)	leading	-0.164
	237(667.8425 kb)	381 (1238.531 kb)	lagging	0.133
	382(1245.5865 kb)	412 (1290.544 kb)	lagging	-0.077
	413(1293.292 kb)	427 (1314.671 kb)	lagging	0.173
AT-skew reverse	428 (0 kb)	631 (663.835 kb)	leading	-0.122
	632(664.7825 kb)	805(1017.829 kb)	lagging	0.173
	806(1019.4905 kb)	837(1051.9545 kb)	lagging	-0.02
	838(1053.402 kb)	925(1314.671 kb)	lagging	0.198

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

121 Ehrlichia chaffeensis Arkansas

Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales; Anaplasmataceae; Ehrlichia.
Accession number: NC_007799; **Genome size (bp)**: 1176248.
Number of genes: 1104.
Oriloc predictions: Origin 25 kb Terminus 592 kb
Worning et al., 2006: Origin 22 kb Terminus 599 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 27.125 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 823.18 kb
Consensus predictions: Origin 25 kb Terminus 592 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	179	NA	328
	348	NA	602
GC-skew reverse	815	NA	595
	1070	NA	1098
AT-skew forward	341	NA	587
	561	NA	1126
AT-skew reverse	719	NA	280
	817	NA	598

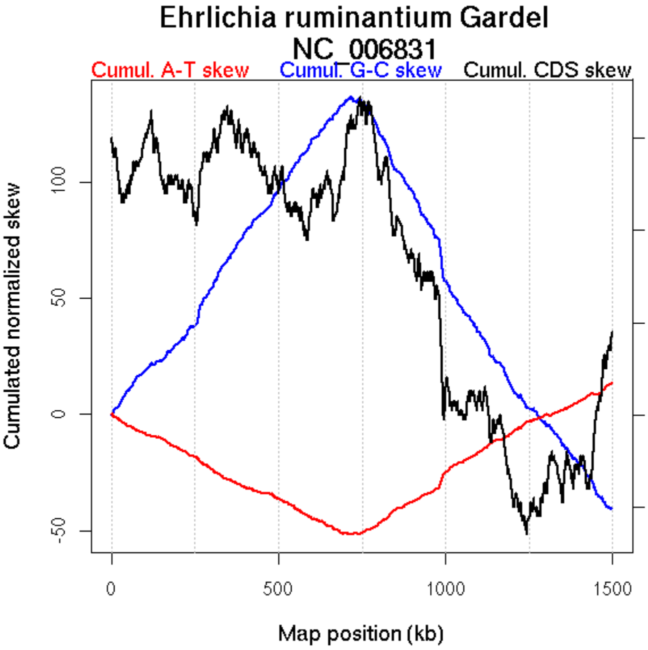
Segments:

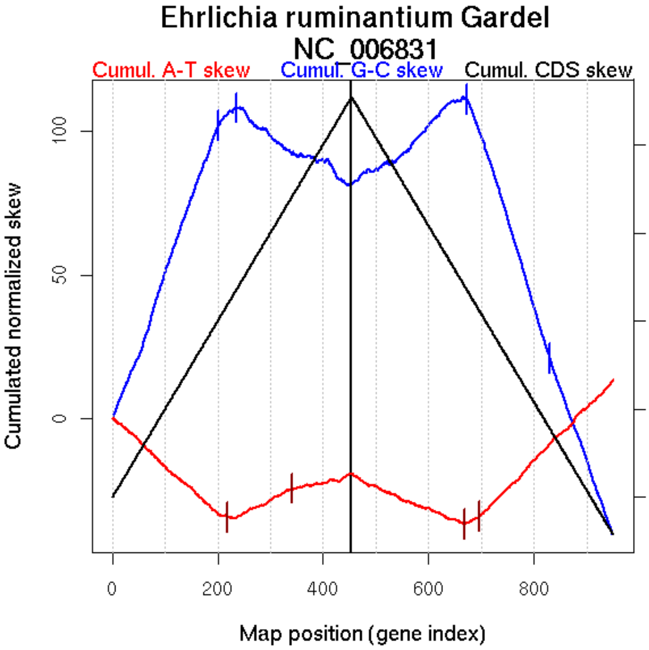
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	179 (328.25 kb)	leading	0.503
	180(328.482 kb)	348 (602.13 kb)	leading	0.569
	349(604.763 kb)	597 (1176.237 kb)	lagging	-0.212
GC-skew reverse	598 (0 kb)	815 (594.993 kb)	leading	0.2
	816(595.907 kb)	1070 (1097.7335 kb)	lagging	-0.507
	1071(1101.7515 kb)	1104 (1176.237 kb)	lagging	-0.388
AT-skew forward	1 (0 kb)	341 (586.906 kb)	leading	-0.174
	342(588.3665 kb)	561 (1125.746 kb)	lagging	0.078
	562(1130.678 kb)	597 (1176.237 kb)	lagging	-0.053
AT-skew reverse	598 (0 kb)	719 (279.827 kb)	leading	-0.083
	720(281.422 kb)	817(597.696 kb)	leading	-0.109
	818(598.9195 kb)	1104(1176.237 kb)	lagging	0.164

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

122 Ehrlichia ruminantium Gardel

Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales; Anaplasmataceae; Ehrlichia.
Accession number: NC_006831; **Genome size (bp)**: 1499920.
Number of genes: 950.
Oriloc predictions: Origin 0 kb Terminus 716 kb
Worning et al., 2006: Origin 1496 kb Terminus 701 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 4.28 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 484.36 kb
Consensus predictions: Origin 0 kb Terminus 716 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	201	NA	684
	235	NA	754
GC-skew reverse	672	NA	715
	830	NA	1105
AT-skew forward	219	NA	710
	340	NA	1209
AT-skew reverse	668	NA	693
	697	NA	789

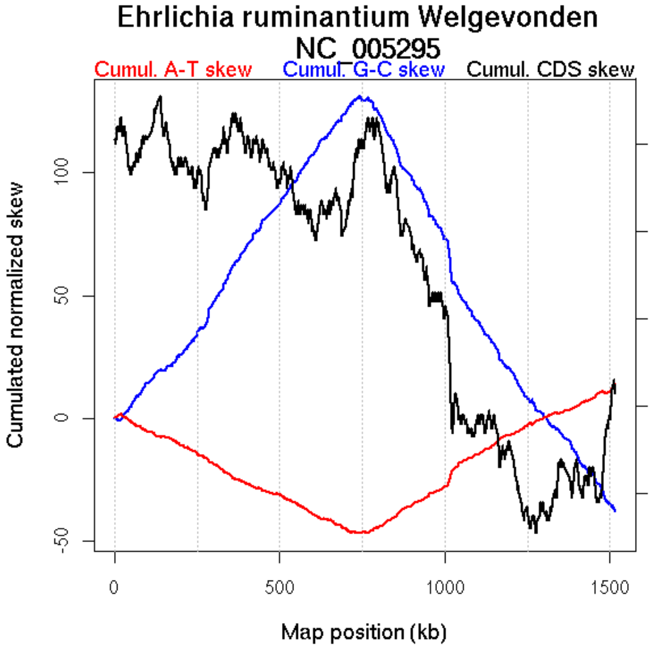
Segments:

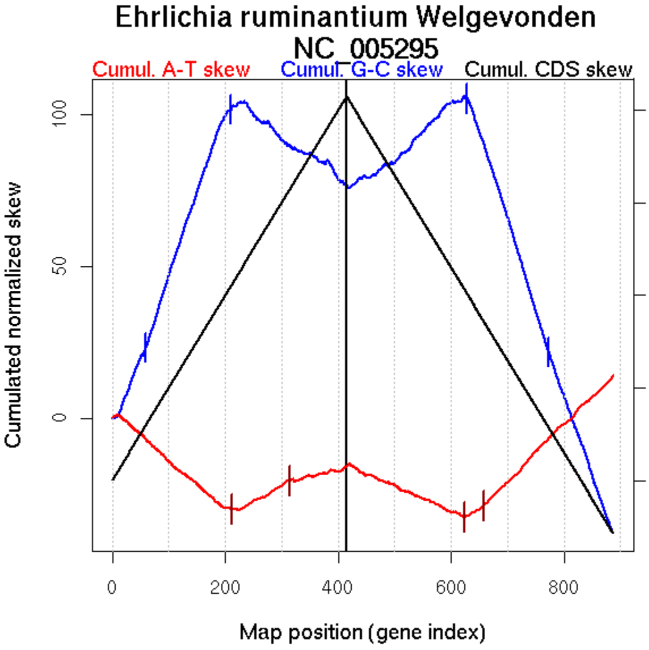
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	201 (684.444 kb)	leading	0.524
	202(685.5225 kb)	235 (754.001 kb)	NA	0.171
	236(755.8925 kb)	454 (1499.902 kb)	lagging	-0.115
GC-skew reverse	455 (0 kb)	672 (714.5835 kb)	leading	0.151
	673(718.888 kb)	830 (1105.1435 kb)	lagging	-0.589
	831(1107.057 kb)	950 (1499.902 kb)	lagging	-0.51
AT-skew forward	1 (0 kb)	219 (709.603 kb)	leading	-0.166
	220(713.4405 kb)	340 (1209.259 kb)	lagging	0.091
	341(1217.9525 kb)	454 (1499.902 kb)	lagging	0.041
AT-skew reverse	455 (0 kb)	668 (692.678 kb)	leading	-0.078
	669(694.3815 kb)	697(789.1565 kb)	lagging	0.091
	698(790.8825 kb)	950(1499.902 kb)	lagging	0.187

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

123 Ehrlichia ruminantium Welgevonden

Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales; Anaplasmataceae; Ehrlichia.
Accession number: NC_005295; **Genome size (bp)**: 1516355.
Number of genes: 887.
Oriloc predictions: Origin 0 kb Terminus 740 kb
Worning et al., 2006: Origin 15 kb Terminus 730 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1261.994 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 507.29 kb
Consensus predictions: Origin 0 kb Terminus 740 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	60	NA	223
	210	NA	734
GC-skew reverse	627	NA	734
	773	NA	1111
AT-skew forward	212	NA	738
	314	NA	1191
AT-skew reverse	624	NA	715
	658	NA	823

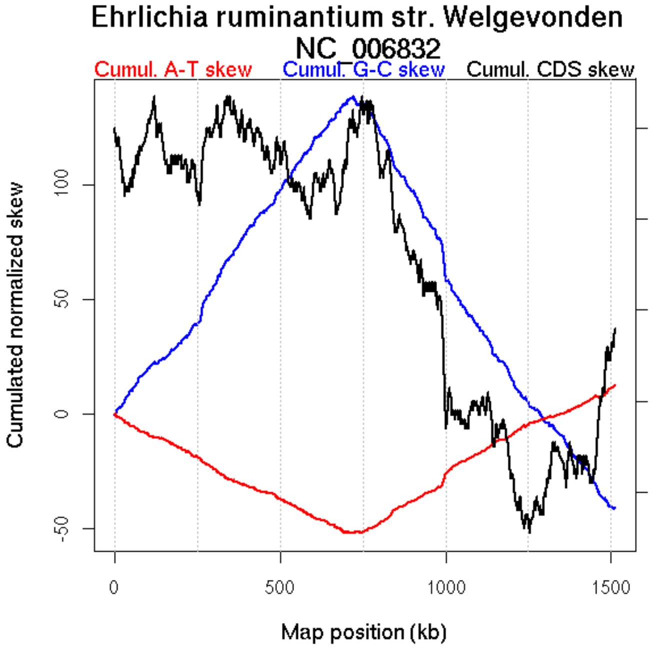
Segments:

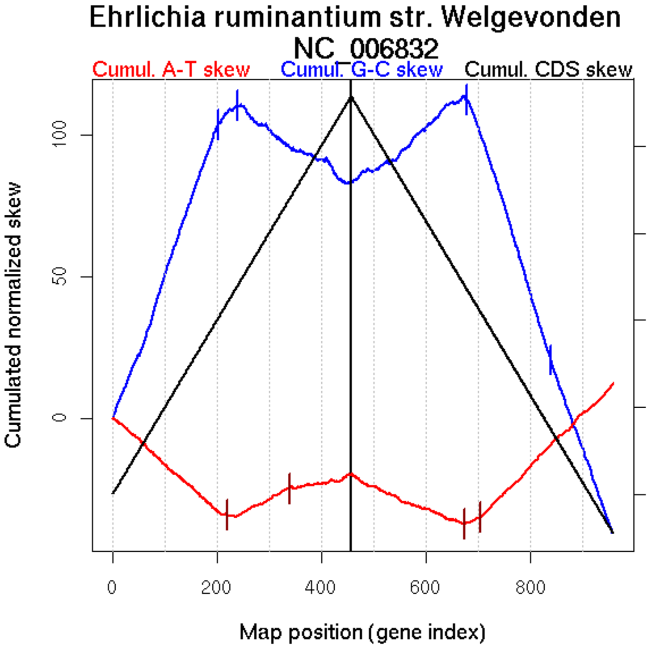
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	60 (222.5755 kb)	leading	0.439
	61(225.6805 kb)	210 (733.5285 kb)	leading	0.547
	211(737.9065 kb)	415 (1516.329 kb)	lagging	-0.134
GC-skew reverse	416 (0 kb)	627 (733.991 kb)	leading	0.157
	628(739.0425 kb)	773 (1110.7055 kb)	lagging	-0.591
	774(1114.939 kb)	887 (1516.329 kb)	lagging	-0.521
AT-skew forward	1 (0 kb)	212 (738.2305 kb)	leading	-0.162
	213(740.293 kb)	314 (1191.397 kb)	lagging	0.103
	315(1194.01 kb)	415 (1516.329 kb)	lagging	0.042
AT-skew reverse	416 (0 kb)	624 (715.246 kb)	leading	-0.083
	625(718.904 kb)	658(822.5705 kb)	lagging	0.11
	659(823.4865 kb)	887(1516.329 kb)	lagging	0.186

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

124 Ehrlichia ruminantium str. Welgevonden

Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales; Anaplasmataceae; Ehrlichia.
Accession number: NC_006832; **Genome size (bp)**: 1512977.
Number of genes: 958.
Oriloc predictions: Origin 0 kb Terminus 720 kb
Worning et al., 2006: Origin 1509 kb Terminus 703 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1240.088 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 487.15 kb
Consensus predictions: Origin 0 kb Terminus 720 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	202	NA	688
	239	NA	757
GC-skew reverse	678	NA	718
	839	NA	1115
AT-skew forward	221	NA	713
	339	NA	1201
AT-skew reverse	674	NA	697
	704	NA	789

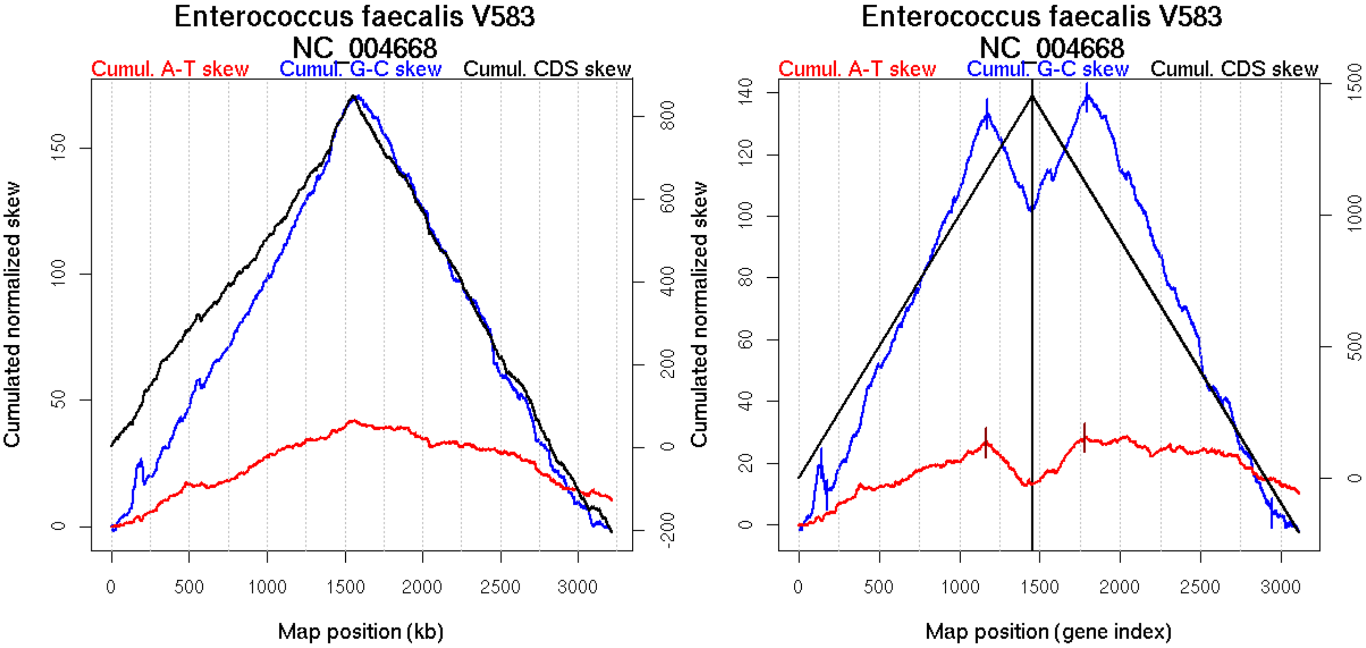
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	202 (687.8325 kb)	leading	0.528
	203(688.816 kb)	239 (757.468 kb)	NA	0.175
	240(759.3595 kb)	457 (1512.959 kb)	lagging	-0.123
GC-skew reverse	458 (0 kb)	678 (717.828 kb)	leading	0.149
	679(721.748 kb)	839 (1114.9655 kb)	lagging	-0.591
	840(1116.985 kb)	958 (1512.959 kb)	lagging	-0.511
AT-skew forward	1 (0 kb)	221 (713.3755 kb)	leading	-0.165
	222(717.7535 kb)	339 (1200.762 kb)	lagging	0.092
	340(1210.731 kb)	457 (1512.959 kb)	lagging	0.036
AT-skew reverse	458 (0 kb)	674 (697.0685 kb)	leading	-0.078
	675(698.751 kb)	704(789.4945 kb)	lagging	0.086
	705(791.279 kb)	958(1512.959 kb)	lagging	0.184

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

125 Enterococcus faecalis V583

Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.
Accession number: NC_004668; **Genome size (bp)**: 3218031.
Number of genes: 3113.
Oriloc predictions: Origin 0 kb Terminus 1587 kb
Worning et al., 2006: Origin 3217 kb Terminus 1551 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1.449 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.73 kb
Consensus predictions: Origin 0 kb Terminus 1587 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	140	0	190
	175	0	213
	1172	0	1549
GC-skew reverse	1792	0.00667	1577
	2946	0.04667	2979
AT-skew forward	1167	0	1543
AT-skew reverse	1783	0	1563

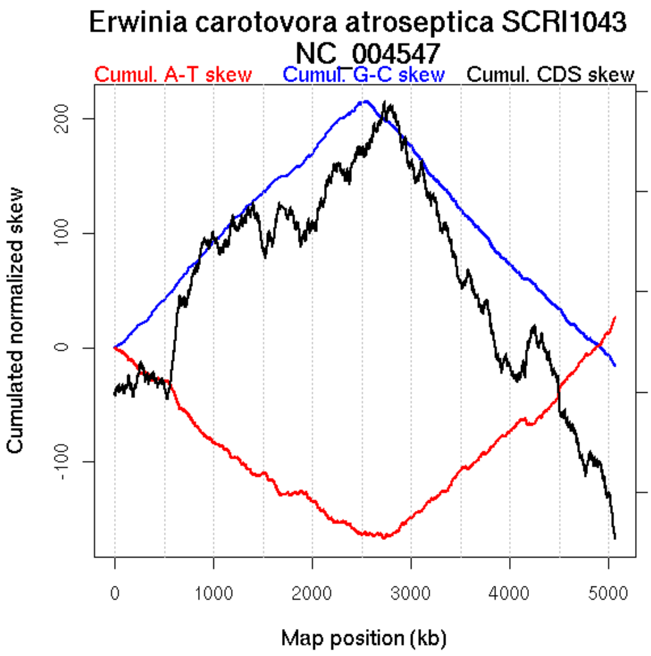
Segments:

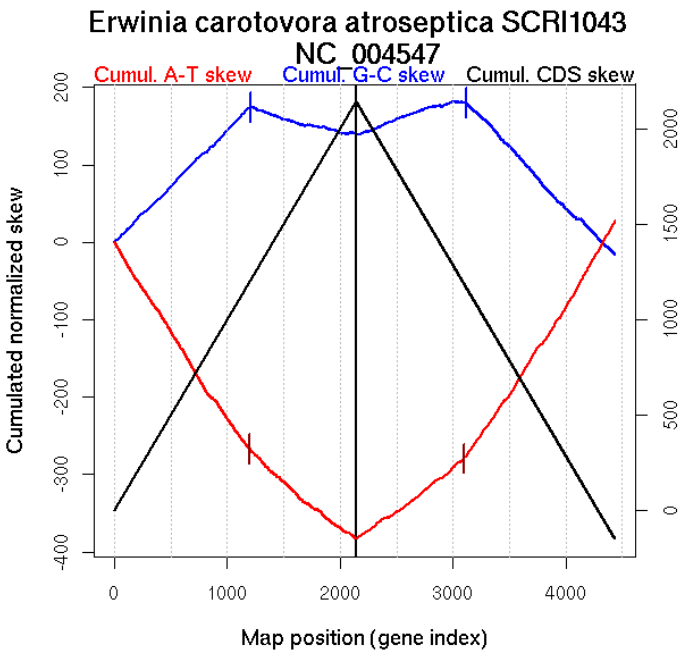
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	140 (189.9815 kb)	leading	0.164
	141(191.7025 kb)	175 (212.876 kb)	leading	-0.316
	176(214.2415 kb)	1172 (1548.855 kb)	leading	0.123
	1173(1553.8395 kb)	1453 (3217.567 kb)	lagging	-0.118
GC-skew reverse	1454 (0 kb)	1792 (1577.2375 kb)	leading	0.104
	1793(1577.6035 kb)	2946 (2979.2805 kb)	lagging	-0.121
	2947(2980.752 kb)	3113 (3217.567 kb)	lagging	-0.037
AT-skew forward	1 (0 kb)	1167 (1543.0155 kb)	leading	0.022
	1168(1545.265 kb)	1453 (3217.567 kb)	lagging	-0.054
AT-skew reverse	1454 (0 kb)	1783 (1562.545 kb)	leading	0.05
	1784(1565.168 kb)	3113(3217.567 kb)	lagging	-0.012

More A than T on the leading strand for replication.
More G than C on the leading strand for replication.

126 Erwinia carotovora atroseptica SCRI1043

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Pectobacterium.
Accession number: NC_004547; **Genome size (bp)**: 5064019.
Number of genes: 4435.
Oriloc predictions: Origin 0 kb Terminus 2554 kb
Worning et al., 2006: Origin 5062 kb Terminus 2553 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 426.996 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1430.99 kb, 4984.4 kb
Consensus predictions: Origin 0 kb Terminus 2554 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1207	0	2541
GC-skew reverse	3114	0	2542
AT-skew forward	1194	0	2510
AT-skew reverse	3096	0	2512

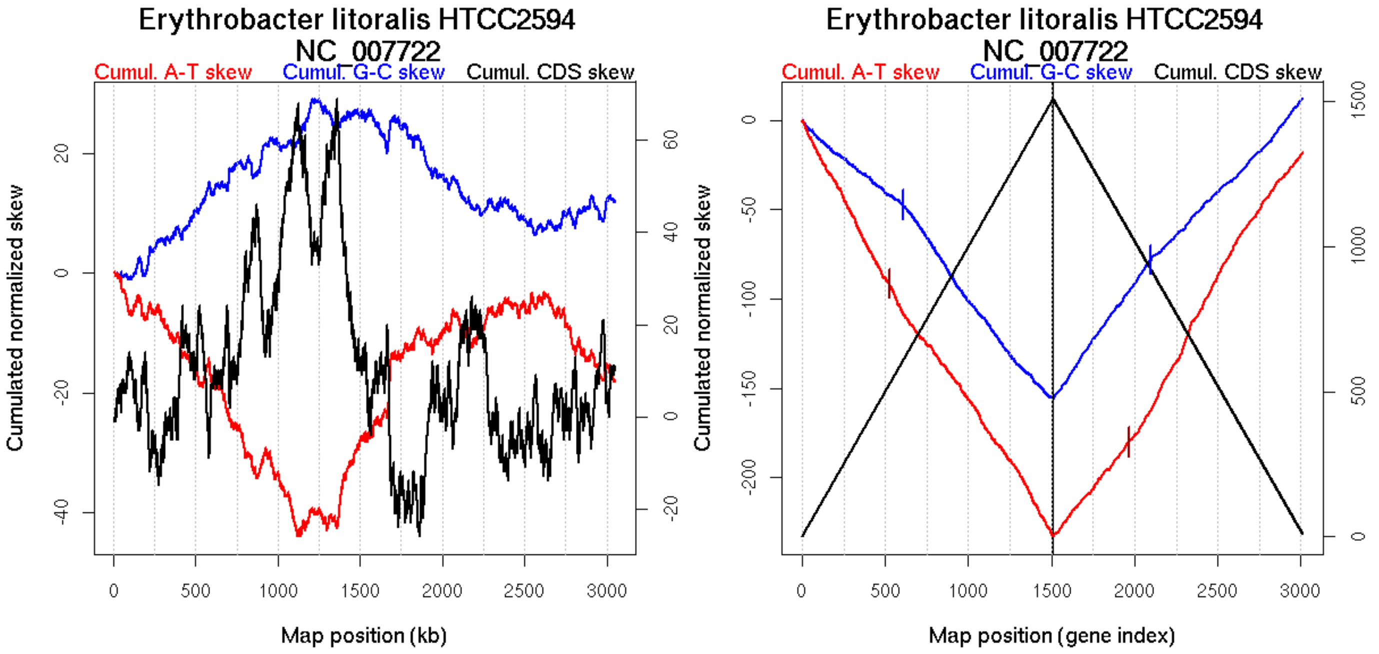
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1207 (2540.5065 kb)	leading	0.145
	1208(2542.335 kb)	2144 (5063.659 kb)	lagging	-0.037
GC-skew reverse	2145 (0 kb)	3114 (2542.156 kb)	leading	0.048
	3115(2544.1555 kb)	4435 (5063.659 kb)	lagging	-0.151
AT-skew forward	1 (0 kb)	1194 (2509.856 kb)	leading	-0.225
	1195(2517.955 kb)	2144 (5063.659 kb)	lagging	-0.122
AT-skew reverse	2145 (0 kb)	3096 (2512.203 kb)	leading	0.107
	3097(2512.853 kb)	4435(5063.659 kb)	lagging	0.228

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

127 Erythrobacter litoralis HTCC2594

Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales; Erythrobacteraceae; Erythrobacter.
Accession number: NC_007722; **Genome size (bp)**: 3052398.
Number of genes: 3010.
Oriloc predictions: Origin 0 kb Terminus 1207 kb
Worning et al., 2006: Origin 2626 kb Terminus 1298 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1188.291 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 2143.12 kb
Consensus predictions: Origin 0 kb Terminus 1207 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	607	0	1218
GC-skew reverse	2097	0.02	1251
AT-skew forward	523	0.04	1032
AT-skew reverse	1963	0.02667	958

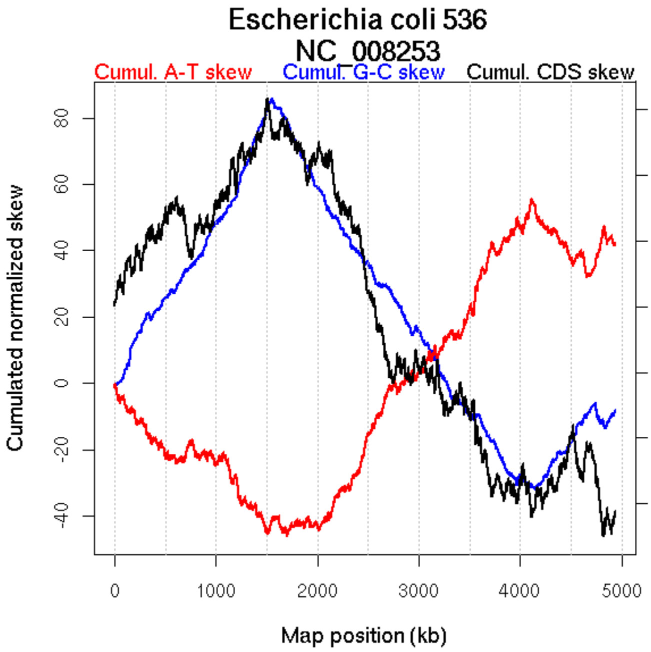
Segments:

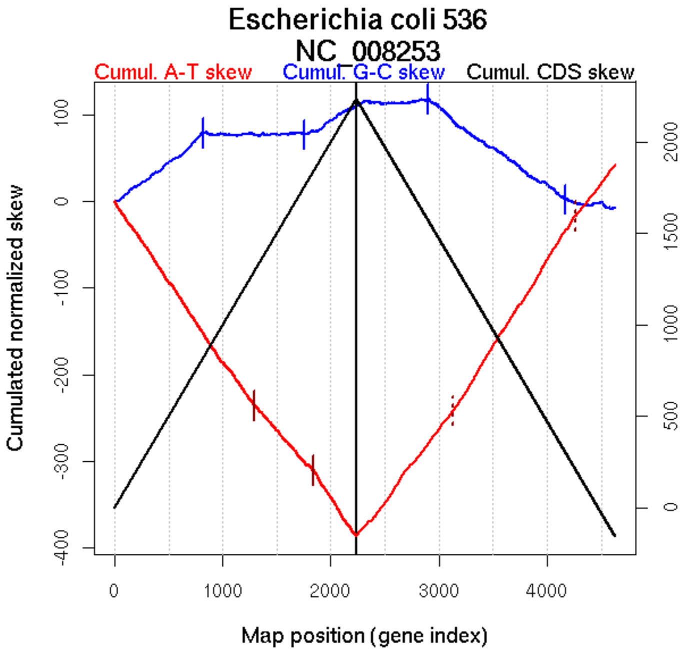
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	607 (1218.236 kb)	leading	-0.075
	608(1218.7185 kb)	1510 (3050.991 kb)	lagging	-0.124
GC-skew reverse	1511 (0 kb)	2097 (1250.7195 kb)	leading	0.133
	2098(1254.263 kb)	3010 (3050.991 kb)	lagging	0.097
AT-skew forward	1 (0 kb)	523 (1032.082 kb)	leading	-0.176
	524(1035.2365 kb)	1510 (3050.991 kb)	lagging	-0.136
AT-skew reverse	1511 (0 kb)	1963 (957.807 kb)	leading	0.115
	1964(961.255 kb)	3010(3050.991 kb)	lagging	0.164

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

128 Escherichia coli 536

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.
Accession number: NC_008253; **Genome size (bp)**: 4938920.
Number of genes: 4629.
Oriloc predictions: Origin 4114 kb Terminus 1522 kb
Worning et al., 2006: Origin 4107 kb Terminus 1536 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1916.035 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 4067.49 kb
Consensus predictions: Origin 4114 kb Terminus 1522 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	817	0.00667	1588
	1750	0.01667	3885
GC-skew reverse	2899	0.00667	1548
	4166	0.01333	3963
AT-skew forward	1294	0.03333	2829
	1840	0.01	4036
AT-skew reverse	3134	0.09	2014
	4263	0.07333	4171

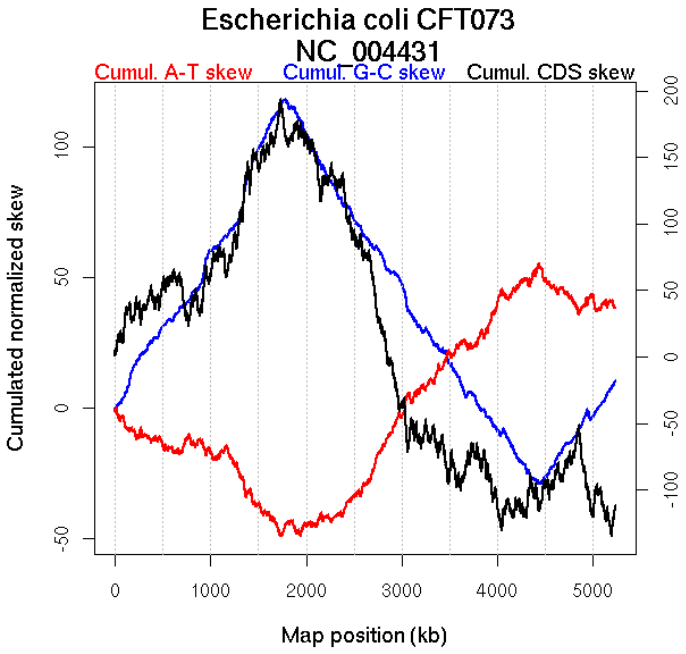
Segments:

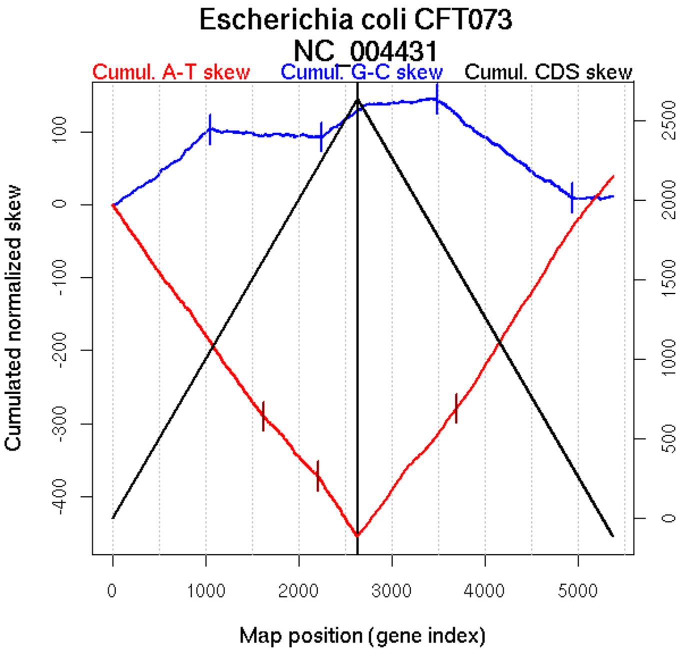
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	817 (1587.5645 kb)	leading	0.095
	818(1590.594 kb)	1750 (3884.9965 kb)	lagging	0.001
	1751(3886.8575 kb)	2236 (4937.574 kb)	NA	0.075
GC-skew reverse	2237 (0 kb)	2899 (1547.5595 kb)	leading	0.005
	2900(1548.0685 kb)	4166 (3963.42 kb)	lagging	-0.089
	4167(3964.9955 kb)	4629 (4937.574 kb)	NA	-0.017
AT-skew forward	1 (0 kb)	1294 (2828.5695 kb)	NA	-0.183
	1295(2829.439 kb)	1840 (4035.9385 kb)	lagging	-0.141
	1841(4040.9405 kb)	2236 (4937.574 kb)	leading	-0.195
AT-skew reverse	2237 (0 kb)	3134 (2014.04 kb)	NA	0.165
	3135(2017.628 kb)	4263(4170.7365 kb)	lagging	0.2
	4264(4171.717 kb)	4629(4937.574 kb)	leading	0.162

More G than C on the leading strand for replication.

129 Escherichia coli CFT073

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.
Accession number: NC_004431; **Genome size (bp)**: 5231428.
Number of genes: 5378.
Oriloc predictions: Origin 4431 kb Terminus 1749 kb
Worning et al., 2006: Origin 4428 kb Terminus 1730 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 3066.718 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 2875.41 kb
Consensus predictions: Origin 4431 kb Terminus 1749 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1045	NA	1832
	2250	NA	4469
GC-skew reverse	3486	NA	1778
	4943	NA	4377
AT-skew forward	1623	NA	3227
	2209	NA	4382
AT-skew reverse	3698	NA	2141

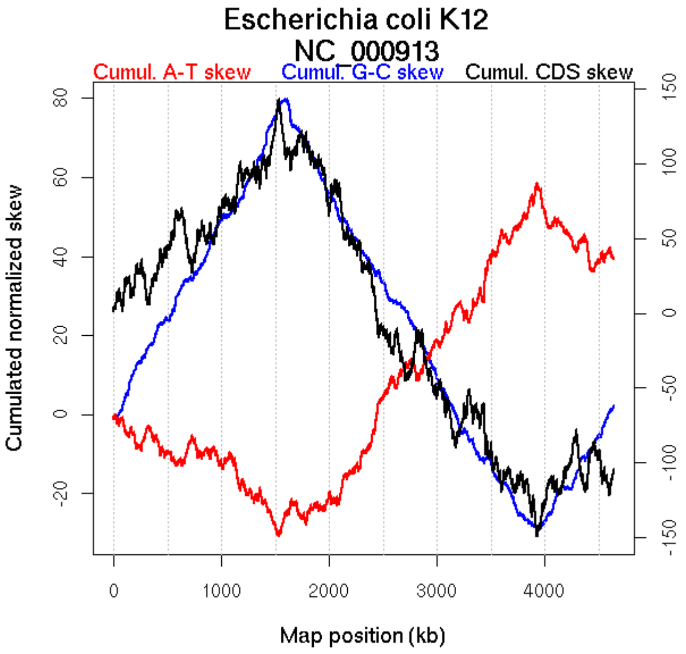
Segments:

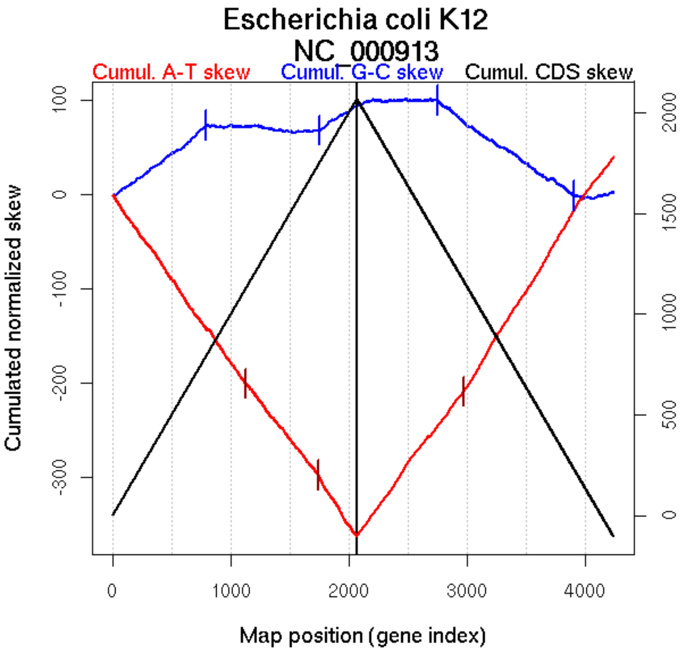
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1045 (1832.2345 kb)	leading	0.1
	1046(1832.561 kb)	2250 (4469.186 kb)	lagging	-0.007
	2251(4470.2465 kb)	2633 (5231.401 kb)	leading	0.092
GC-skew reverse	2634 (0 kb)	3486 (1778.068 kb)	leading	0.013
	3487(1779.359 kb)	4943 (4377.4495 kb)	lagging	-0.092
	4944(4378.5445 kb)	5378 (5231.401 kb)	leading	0.005
AT-skew forward	1 (0 kb)	1623 (3227.144 kb)	NA	-0.179
	1624(3228.8315 kb)	2209 (4381.926 kb)	lagging	-0.146
	2210(4386.22 kb)	2633 (5231.401 kb)	leading	-0.197
AT-skew reverse	2634 (0 kb)	3698 (2140.5635 kb)	NA	0.163
	3699(2142.165 kb)	5378(5231.401 kb)	NA	0.195

More G than C on the leading strand for replication.

130 Escherichia coli K12

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.
Accession number: NC_000913; **Genome size (bp)**: 4639675.
Number of genes: 4242.
Oriloc predictions: Origin 3928 kb Terminus 1549 kb
Worning et al., 2006: Origin 3925 kb Terminus 1550 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 3923.969 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 3179.02 kb, 3752.29 kb
Consensus predictions: Origin 3928 kb Terminus 1549 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	789	NA	1605
	1753	NA	3962
GC-skew reverse	2750	NA	1603
	3909	NA	3858
AT-skew forward	1124	NA	2428
	1737	NA	3911
AT-skew reverse	2972	NA	2003

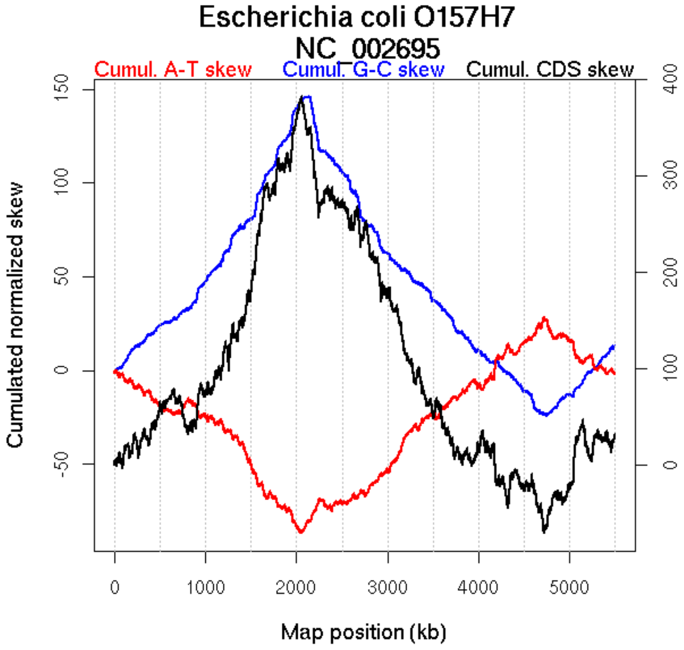
Segments:

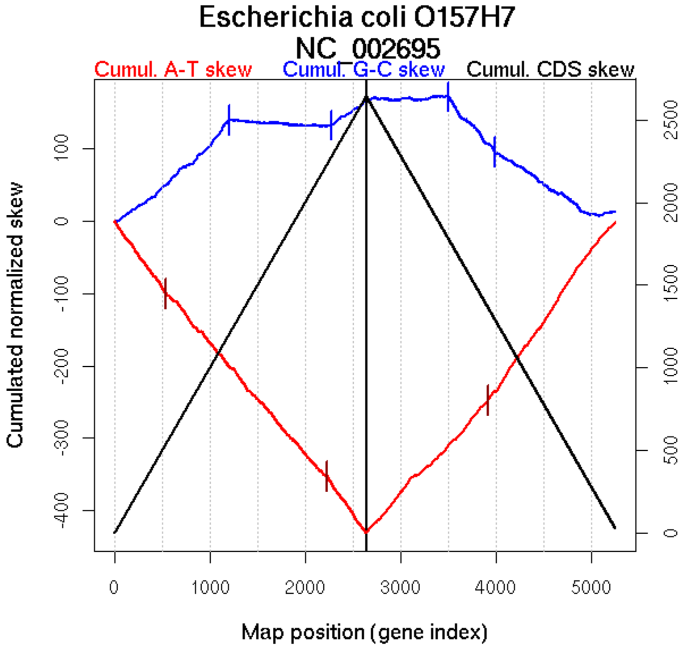
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	789 (1605.0095 kb)	leading	0.093
	790(1605.34 kb)	1753 (3962.251 kb)	lagging	-0.008
	1754(3964.182 kb)	2069 (4639.648 kb)	leading	0.08
GC-skew reverse	2070 (0 kb)	2750 (1602.6805 kb)	leading	0.005
	2751(1607.4195 kb)	3909 (3858.2185 kb)	lagging	-0.085
	3910(3859.935 kb)	4242 (4639.648 kb)	leading	0.012
AT-skew forward	1 (0 kb)	1124 (2428.296 kb)	NA	-0.177
	1125(2438.375 kb)	1737 (3910.9035 kb)	lagging	-0.158
	1738(3927.753 kb)	2069 (4639.648 kb)	leading	-0.199
AT-skew reverse	2070 (0 kb)	2972 (2003.1255 kb)	NA	0.17
	2973(2008.0395 kb)	4242(4639.648 kb)	NA	0.2

More G than C on the leading strand for replication.

131 Escherichia coli O157H7

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.
Accession number: NC_002695; **Genome size (bp)**: 5498450.
Number of genes: 5252.
Oriloc predictions: Origin 4723 kb Terminus 2073 kb
Worning et al., 2006: Origin 4725 kb Terminus 2074 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 470.531 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 3334.59 kb, 4669.26 kb
Consensus predictions: Origin 4723 kb Terminus 2073 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1206	NA	2131
	2275	NA	4767
GC-skew reverse	3506	NA	2141
	3991	NA	2926
AT-skew forward	538	NA	1104
	2225	NA	4629
AT-skew reverse	3921	NA	2806

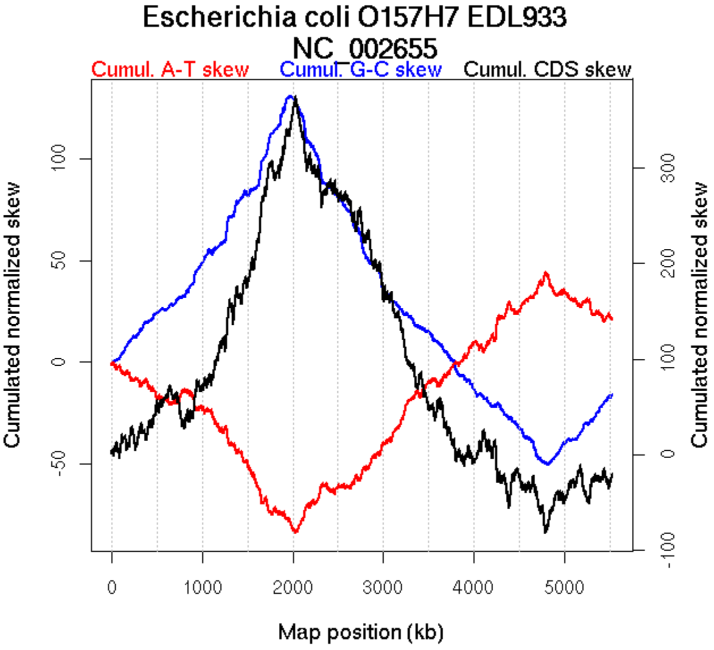
Segments:

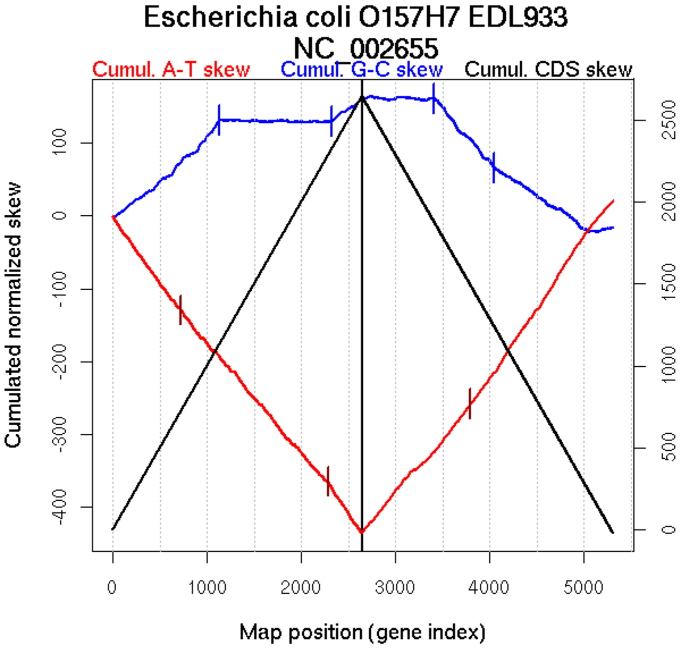
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1206 (2131.238 kb)	leading	0.115
	1207(2135.619 kb)	2275 (4767.003 kb)	lagging	-0.008
	2276(4767.947 kb)	2642 (5498.423 kb)	leading	0.088
GC-skew reverse	2643 (0 kb)	3506 (2140.5245 kb)	leading	0.004
	3507(2144.1035 kb)	3991 (2925.7145 kb)	lagging	-0.145
	3992(2926.535 kb)	5252 (5498.423 kb)	NA	-0.078
AT-skew forward	1 (0 kb)	538 (1103.961 kb)	leading	-0.181
	539(1105.272 kb)	2225 (4628.6505 kb)	NA	-0.153
	2226(4630.03 kb)	2642 (5498.423 kb)	leading	-0.19
AT-skew reverse	2643 (0 kb)	3921 (2806.242 kb)	NA	0.139
	3922(2807.0805 kb)	5252(5498.423 kb)	NA	0.191

More G than C on the leading strand for replication - for forward encoded genes.

132 Escherichia coli O157H7 EDL933

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.
Accession number: NC_002655; **Genome size (bp)**: 5528445.
Number of genes: 5306.
Oriloc predictions: Origin 4788 kb Terminus 2014 kb
Worning et al., 2006: Origin 4783 kb Terminus 2010 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 470.533 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 3404.43 kb, 4738.24 kb
Consensus predictions: Origin 4788 kb Terminus 2014 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1133	NA	1952
	2327	NA	4841
GC-skew reverse	3405	NA	1872
	4044	NA	2998
AT-skew forward	728	NA	1367
	2282	NA	4735
AT-skew reverse	3794	NA	2600

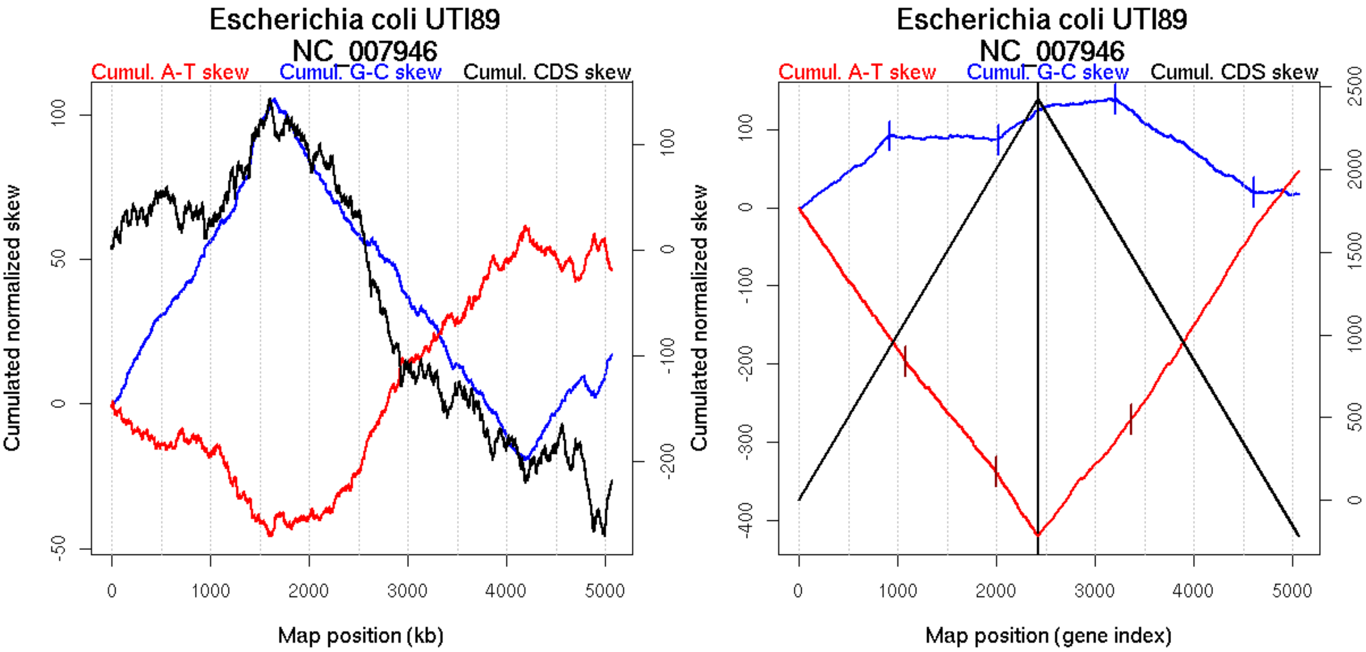
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1133 (1951.7345 kb)	leading	0.114
	1134(1952.178 kb)	2327 (4840.992 kb)	lagging	-0.002
	2328(4842.344 kb)	2643 (5528.418 kb)	leading	0.088
GC-skew reverse	2644 (0 kb)	3405 (1871.685 kb)	leading	-0.003
	3406(1873.7945 kb)	4044 (2998.4425 kb)	lagging	-0.149
	4045(2999.0045 kb)	5306 (5528.418 kb)	NA	-0.077
AT-skew forward	1 (0 kb)	728 (1367.1115 kb)	leading	-0.179
	729(1367.871 kb)	2282 (4735.4295 kb)	NA	-0.152
	2283(4739.699 kb)	2643 (5528.418 kb)	leading	-0.196
AT-skew reverse	2644 (0 kb)	3794 (2600.049 kb)	NA	0.148
	3795(2601.0175 kb)	5306(5528.418 kb)	NA	0.192

More G than C on the leading strand for replication - for forward encoded genes.

133 Escherichia coli UTI89

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.
Accession number: NC_007946; **Genome size (bp)**: 5065741.
Number of genes: 5066.
Oriloc predictions: Origin 4191 kb Terminus 1626 kb
Worning et al., 2006: Origin 4186 kb Terminus 1601 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 2037.206 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 4144.6 kb
Consensus predictions: Origin 4191 kb Terminus 1626 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	916	NA	1684
	2020	NA	4229
GC-skew reverse	3209	NA	1651
	4606	NA	4137
AT-skew forward	1079	NA	2017
	1994	NA	4164
AT-skew reverse	3362	NA	1934

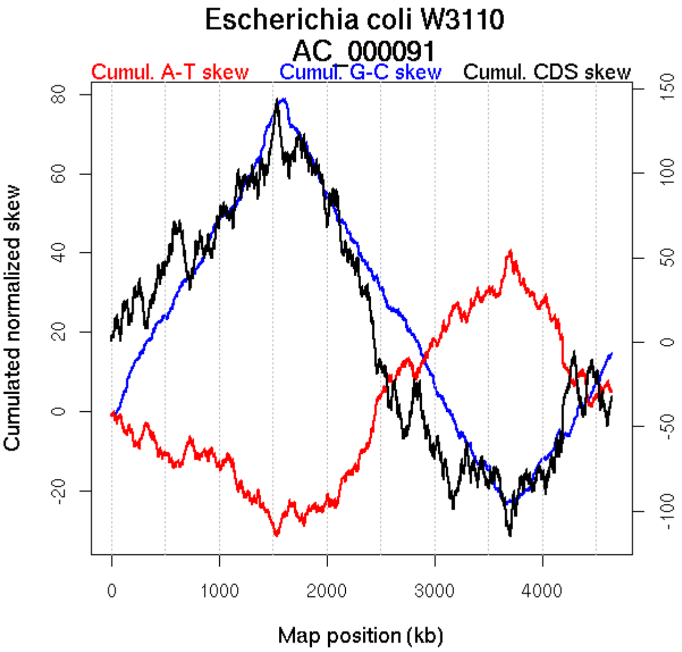
Segments:

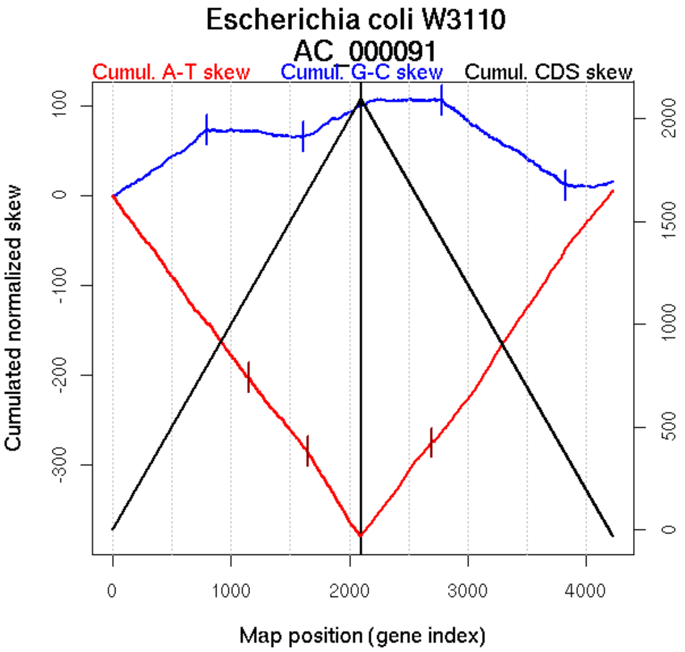
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	916 (1683.722 kb)	leading	0.098
	917(1687.4815 kb)	2020 (4229.016 kb)	lagging	-0.002
	2021(4230.0765 kb)	2424 (5065.714 kb)	leading	0.084
GC-skew reverse	2425 (0 kb)	3209 (1651.014 kb)	leading	0.014
	3210(1651.9535 kb)	4606 (4137.2815 kb)	lagging	-0.083
	4607(4138.3765 kb)	5066 (5065.714 kb)	leading	-0.004
AT-skew forward	1 (0 kb)	1079 (2017.1065 kb)	NA	-0.18
	1080(2023.8325 kb)	1994 (4163.5715 kb)	lagging	-0.153
	1995(4172.0245 kb)	2424 (5065.714 kb)	leading	-0.195
AT-skew reverse	2425 (0 kb)	3362 (1933.5335 kb)	NA	0.155
	3363(1934.099 kb)	5066(5065.714 kb)	NA	0.193

More G than C on the leading strand for replication.

134 Escherichia coli W3110

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Escherichia.
Accession number: AC_000091; **Genome size (bp)**: 4646332.
Number of genes: 4226.
Oriloc predictions: Origin 3677 kb Terminus 1558 kb
Worning et al., 2006: Origin 3714 kb Terminus 1554 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 3710.735 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 3295.96 kb, 3757.39 kb
Consensus predictions: Origin 3677 kb Terminus 1558 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	792	NA	1609
	1614	NA	3635
GC-skew reverse	2777	NA	1599
	3828	NA	3676
AT-skew forward	1150	NA	2503
	1645	NA	3721
AT-skew reverse	2692	NA	1400

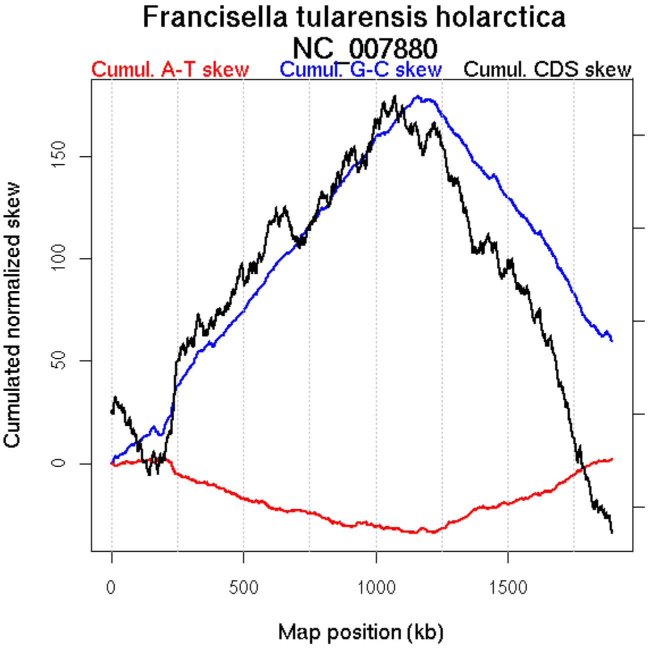
Segments:

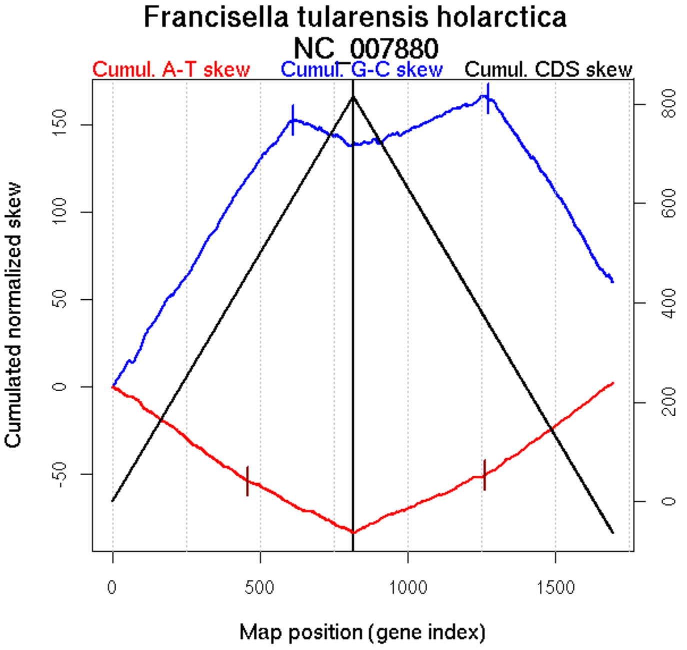
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	792 (1608.6995 kb)	leading	0.091
	793(1609.03 kb)	1614 (3634.942 kb)	lagging	-0.011
	1615(3639.504 kb)	2097 (4646.305 kb)	leading	0.073
GC-skew reverse	2098 (0 kb)	2777 (1598.8745 kb)	leading	0.004
	2778(1601.6445 kb)	3828 (3676.3485 kb)	lagging	-0.087
	3829(3679.2945 kb)	4226 (4646.305 kb)	leading	0.008
AT-skew forward	1 (0 kb)	1150 (2503.0625 kb)	NA	-0.177
	1151(2505.82 kb)	1645 (3721.303 kb)	lagging	-0.161
	1646(3722.9305 kb)	2097 (4646.305 kb)	leading	-0.214
AT-skew reverse	2098 (0 kb)	2692 (1400.3145 kb)	leading	0.178
	2693(1401.2205 kb)	4226(4646.305 kb)	NA	0.191

More G than C on the leading strand for replication.

135 Francisella tularensis holarctica

Bacteria; Proteobacteria; Gammaproteobacteria; Thiotrichales; Francisellaceae; Francisella.
Accession number: NC_007880; **Genome size (bp)**: 1895994.
Number of genes: 1696.
Oriloc predictions: Origin 0 kb Terminus 1150 kb
Worning et al., 2006: Origin 7 kb Terminus 1223 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 283.261 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1.01 kb
Consensus predictions: Origin 0 kb Terminus 1150 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	613	0	1191
GC-skew reverse	1275	0	1174
AT-skew forward	458	0.01333	879
AT-skew reverse	1263	0	1157

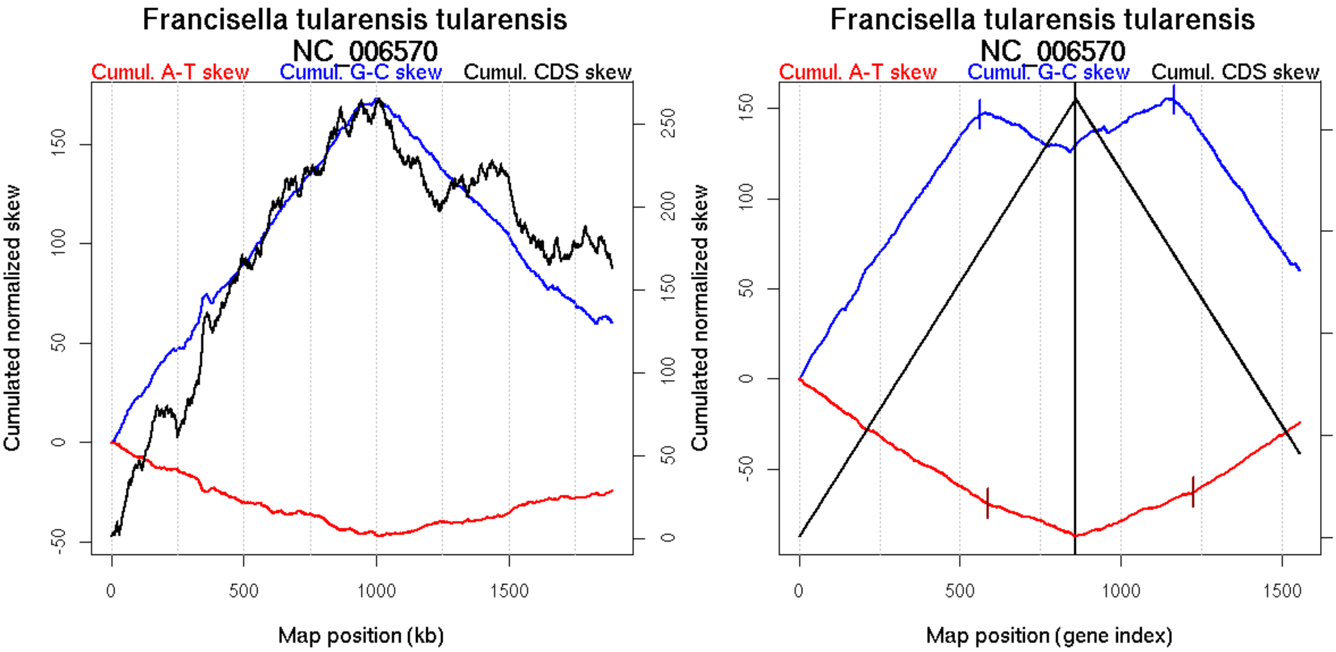
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	613 (1191.31 kb)	leading	0.256
	614(1191.8145 kb)	816 (1895.783 kb)	lagging	-0.074
GC-skew reverse	817 (0 kb)	1275 (1174.0465 kb)	leading	0.066
	1276(1174.53 kb)	1696 (1895.783 kb)	lagging	-0.259
AT-skew forward	1 (0 kb)	458 (879.309 kb)	leading	-0.122
	459(881.0635 kb)	816 (1895.783 kb)	NA	-0.083
AT-skew reverse	817 (0 kb)	1263 (1157.493 kb)	leading	0.073
	1264(1158.7425 kb)	1696(1895.783 kb)	lagging	0.123

More T than A on the leading strand for replication - for reverse encoded genes.
More G than C on the leading strand for replication.

136 Francisella tularensis tularensis

Bacteria; Proteobacteria; Gammaproteobacteria; Thiotrichales; Francisellaceae; Francisella.
Accession number: NC_006570; **Genome size (bp)**: 1892819.
Number of genes: 1557.
Oriloc predictions: Origin 0 kb Terminus 1009 kb
Worning et al., 2006: Origin 0 kb Terminus 1003 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1550.394 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.76 kb
Consensus predictions: Origin 0 kb Terminus 1009 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	561	NA	995
GC-skew reverse	1164	NA	992
AT-skew forward	586	NA	1063
AT-skew reverse	1226	NA	1100

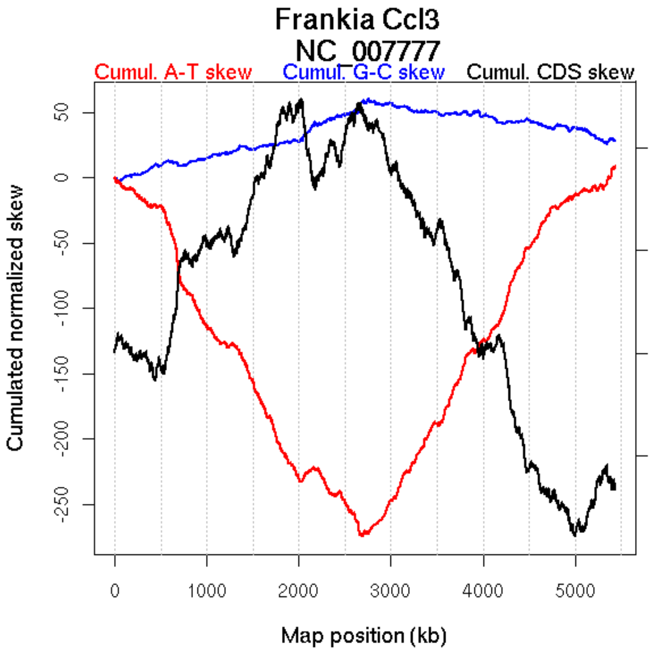
Segments:

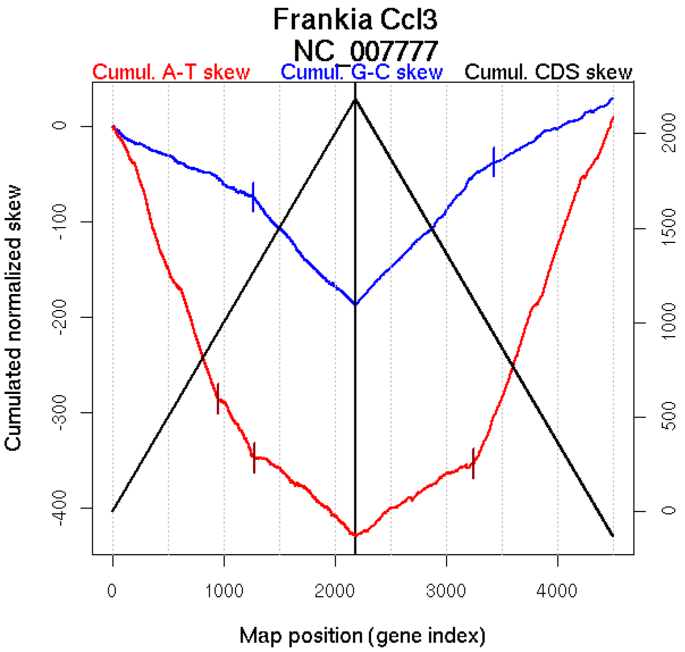
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	561 (994.7165 kb)	leading	0.263
	562(995.8195 kb)	860 (1892.386 kb)	lagging	-0.08
GC-skew reverse	861 (0 kb)	1164 (992.3655 kb)	leading	0.08
	1165(999.284 kb)	1557 (1892.386 kb)	lagging	-0.256
AT-skew forward	1 (0 kb)	586 (1063.196 kb)	leading	-0.117
	587(1072.27 kb)	860 (1892.386 kb)	lagging	-0.064
AT-skew reverse	861 (0 kb)	1226 (1099.693 kb)	NA	0.07
	1227(1101.7905 kb)	1557(1892.386 kb)	lagging	0.118

More T than A on the leading strand for replication - for forward encoded genes.
More G than C on the leading strand for replication.

137 Frankia CcI3

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Frankineae; Frankiaceae; Frankia.
Accession number: NC_007777; **Genome size (bp)**: 5433628.
Number of genes: 4499.
Oriloc predictions: Origin 32 kb Terminus 2755 kb
Worning et al., 2006: Origin 45 kb Terminus 2755 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 5307.541 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.88 kb
Consensus predictions: Origin 0 kb Terminus 2755 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1269	0	2713
GC-skew reverse	3432	0	3170
AT-skew forward	949	0.02	2009
	1275	0.02667	2727
AT-skew reverse	3249	0	2759

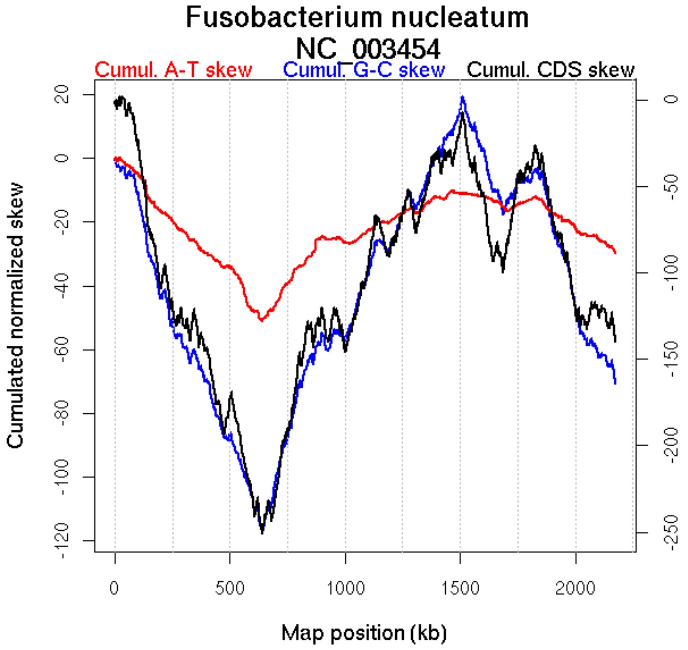
Segments:

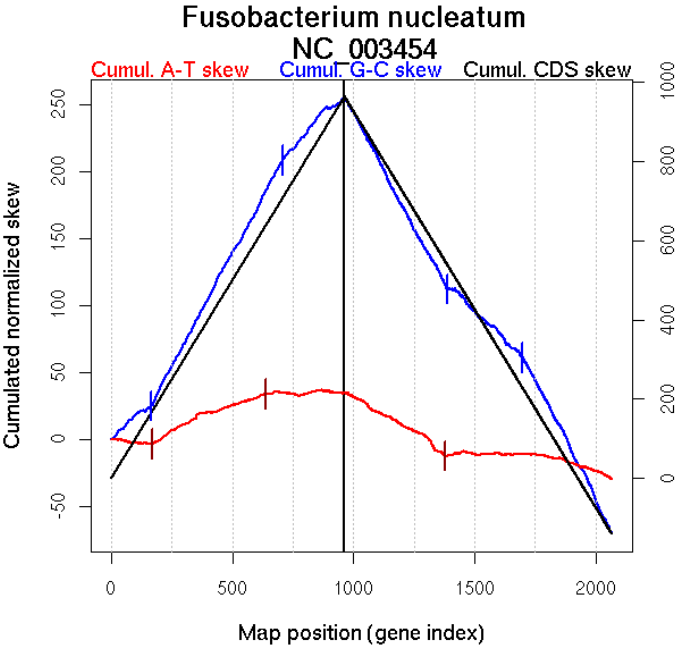
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1269 (2712.858 kb)	leading	-0.055
	1270(2713.326 kb)	2183 (5432.789 kb)	lagging	-0.122
GC-skew reverse	2184 (0 kb)	3432 (3169.5545 kb)	leading	0.123
	3433(3175.75 kb)	4499 (5432.789 kb)	lagging	0.061
AT-skew forward	1 (0 kb)	949 (2008.5885 kb)	leading	-0.311
	950(2009.8335 kb)	1275 (2727.4375 kb)	leading	-0.198
	1276(2728.9515 kb)	2183 (5432.789 kb)	lagging	-0.095
AT-skew reverse	2184 (0 kb)	3249 (2758.7295 kb)	leading	0.074
	3250(2763.4515 kb)	4499(5432.789 kb)	lagging	0.299

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

138 Fusobacterium nucleatum

Bacteria; Fusobacteria; Fusobacterales; Fusobacteriaceae; Fusobacterium.
Accession number: NC_003454; **Genome size (bp)**: 2174500.
Number of genes: 2066.
Oriloc predictions: Origin 642 kb Terminus 1509 kb
Worning et al., 2006: Origin 641 kb Terminus 1828 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 511.353 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 640.91 kb
Consensus predictions: Origin 642 kb Terminus 1509 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	166	0.01	615
	707	0.02	1509
GC-skew reverse	1386	0.00333	653
	1696	0	1528
AT-skew forward	169	0.00333	619
	637	0.03333	1390
AT-skew reverse	1377	0	632

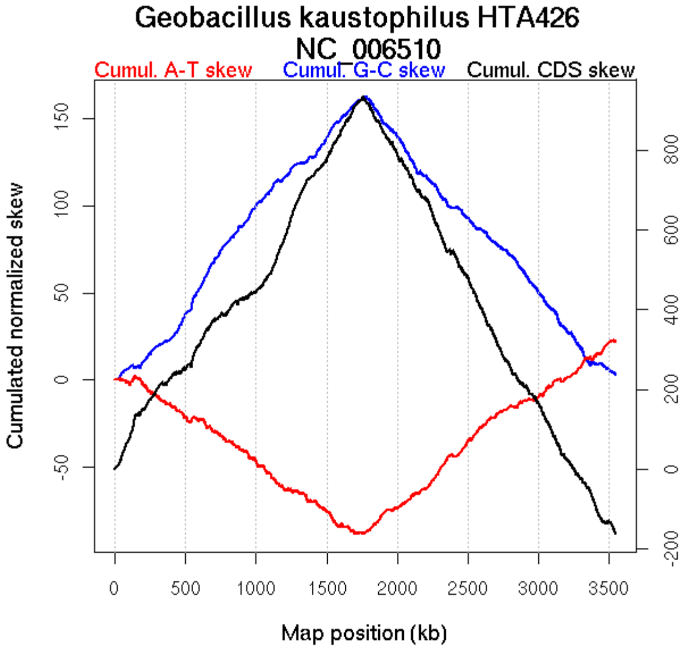
Segments:

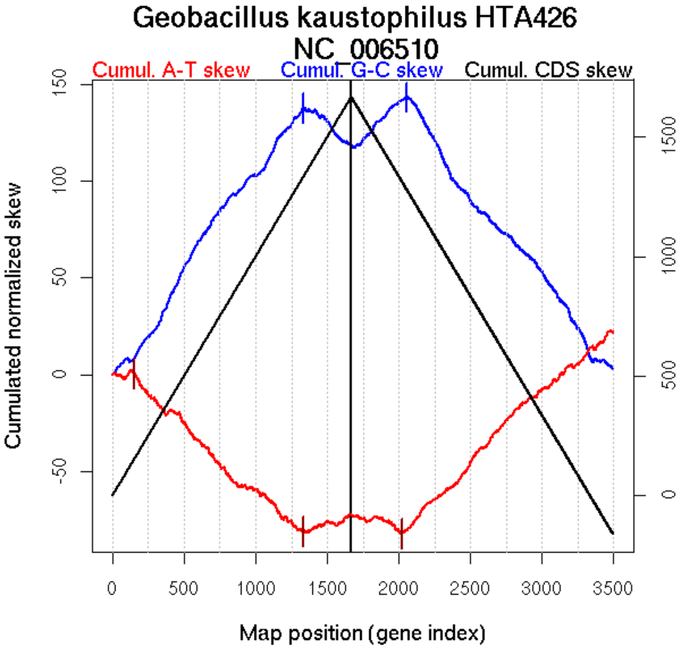
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	166 (614.829 kb)	lagging	0.154
	167(616.46 kb)	707 (1509.051 kb)	leading	0.337
	708(1509.65 kb)	963 (2174.476 kb)	lagging	0.188
GC-skew reverse	964 (0 kb)	1386 (652.65 kb)	lagging	-0.341
	1387(654.7915 kb)	1696 (1528.16 kb)	leading	-0.174
	1697(1528.963 kb)	2066 (2174.476 kb)	lagging	-0.357
AT-skew forward	1 (0 kb)	169 (619.4575 kb)	lagging	-0.023
	170(620.9865 kb)	637 (1389.6505 kb)	leading	0.075
	638(1390.944 kb)	963 (2174.476 kb)	NA	0.004
AT-skew reverse	964 (0 kb)	1377 (631.6025 kb)	lagging	-0.109
	1378(633.0515 kb)	2066(2174.476 kb)	NA	-0.022

More A than T on the leading strand for replication - for forward-encoded genes.
More G than C on the leading strand for replication.

139 Geobacillus kaustophilus HTA426

Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.
Accession number: NC_006510; **Genome size (bp)**: 3544776.
Number of genes: 3498.
Oriloc predictions: Origin 0 kb Terminus 1755 kb
Worning et al., 2006: Origin 0 kb Terminus 1756 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 258.377 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.76 kb, 2215.22 kb, 2744.08 kb
Consensus predictions: Origin 0 kb Terminus 1755 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1332	0	1766
GC-skew reverse	2057	0	1725
AT-skew forward	155	0.03667	183
	1333	0.02	1766
AT-skew reverse	2023	0	1584

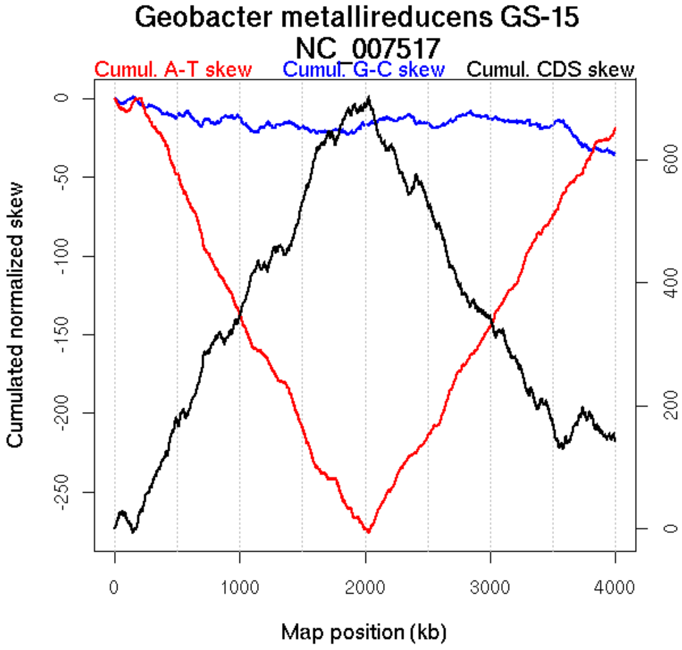
Segments:

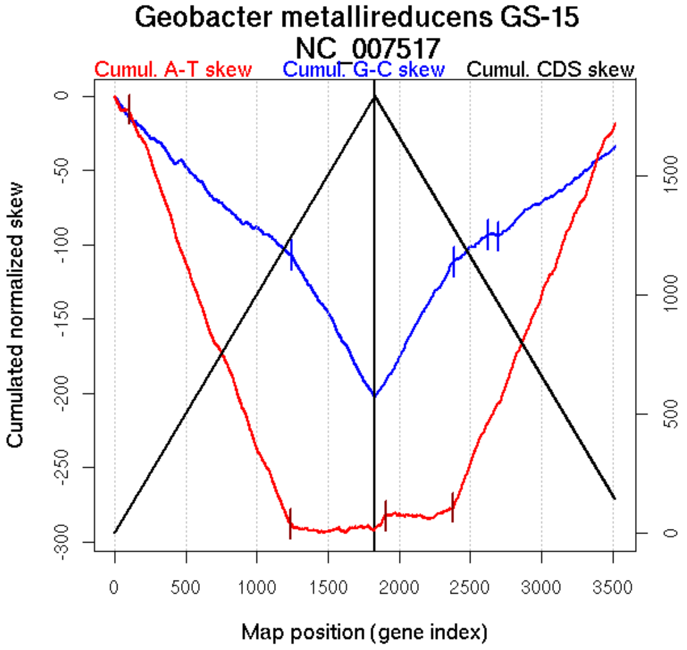
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1332 (1765.627 kb)	leading	0.108
	1333(1765.8845 kb)	1668 (3544.385 kb)	lagging	-0.066
GC-skew reverse	1669 (0 kb)	2057 (1725.403 kb)	leading	0.076
	2058(1728.061 kb)	3498 (3544.385 kb)	lagging	-0.095
AT-skew forward	1 (0 kb)	155 (182.9765 kb)	leading	0.009
	156(183.729 kb)	1333 (1765.8845 kb)	leading	-0.068
	1334(1771.659 kb)	1668 (3544.385 kb)	lagging	0.023
AT-skew reverse	1669 (0 kb)	2023 (1584.3815 kb)	leading	-0.019
	2024(1587.848 kb)	3498(3544.385 kb)	lagging	0.072

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

140 Geobacter metallireducens GS-15

Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales; Geobacteraceae; Geobacter.
Accession number: NC_007517; **Genome size (bp)**: 3997420.
Number of genes: 3519.
Oriloc predictions: Origin 146 kb Terminus 1912 kb
Worning et al., 2006: Origin 1 kb Terminus 2032 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 0.211 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.94 kb, 821.02 kb
Consensus predictions: Origin 0 kb Terminus 2032 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1244	0	2027
GC-skew reverse	2384	0.02667	2037
	2627	0.02667	2456
	2699	0.02667	2560
AT-skew forward	102	0.00667	209
	1239	0	2021
AT-skew reverse	1910	0.00667	237
	2382	0	2035

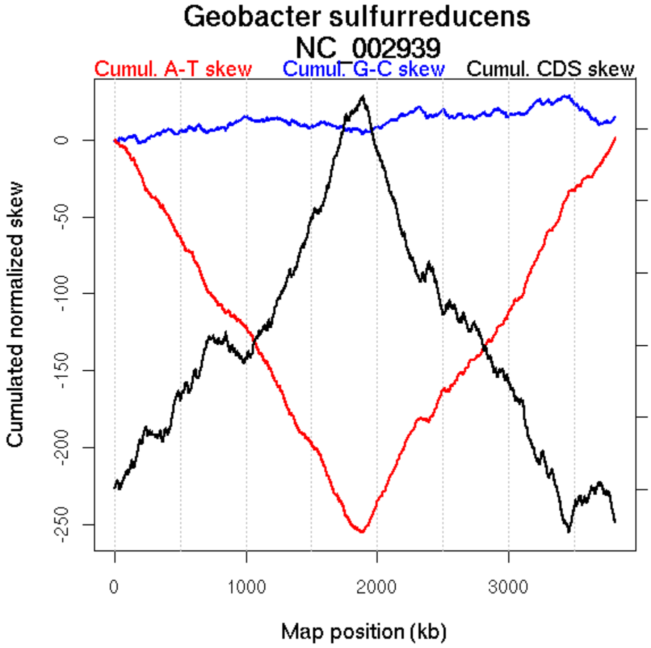
Segments:

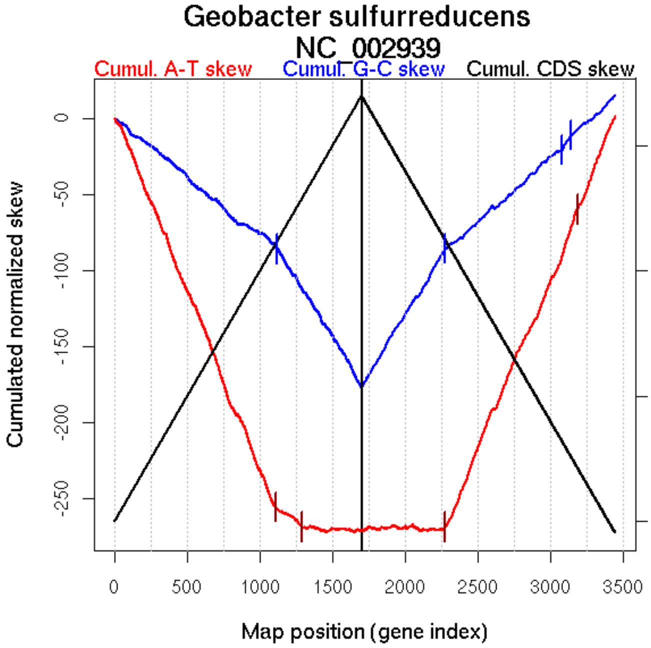
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1244 (2027.1055 kb)	leading	-0.084
	1245(2027.834 kb)	1831 (3997.4 kb)	lagging	-0.165
GC-skew reverse	1832 (0 kb)	2384 (2036.886 kb)	leading	0.169
	2385(2037.6275 kb)	2627 (2456.311 kb)	lagging	0.075
	2628(2458.008 kb)	2699 (2560.1135 kb)	lagging	-0.019
	2700(2561.3415 kb)	3519 (3997.4 kb)	lagging	0.07
AT-skew forward	1 (0 kb)	102 (209.3035 kb)	leading	-0.085
	103(209.9015 kb)	1239 (2021.4925 kb)	leading	-0.25
	1240(2022.2 kb)	1831 (3997.4 kb)	lagging	0.002
AT-skew reverse	1832 (0 kb)	1910 (236.752 kb)	leading	0.129
	1911(252.5165 kb)	2382(2034.943 kb)	leading	0.005
	2383(2035.767 kb)	3519(3997.4 kb)	lagging	0.229

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

141 Geobacter sulfurreducens

Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales; Geobacteraceae; Geobacter.
Accession number: NC_002939; **Genome size (bp)**: 3814139.
Number of genes: 3445.
Oriloc predictions: Origin 7 kb Terminus 1864 kb
Worning et al., 2006: Origin 2 kb Terminus 1896 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1279.286 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.7 kb, 1166.41 kb
Consensus predictions: Origin 0 kb Terminus 1864 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1121	NA	1879
GC-skew reverse	2277	NA	1857
	3082	NA	3145
	3145	NA	3258
AT-skew forward	1108	NA	1854
	1292	NA	2567
AT-skew reverse	2275	NA	1849
	3185	NA	3302

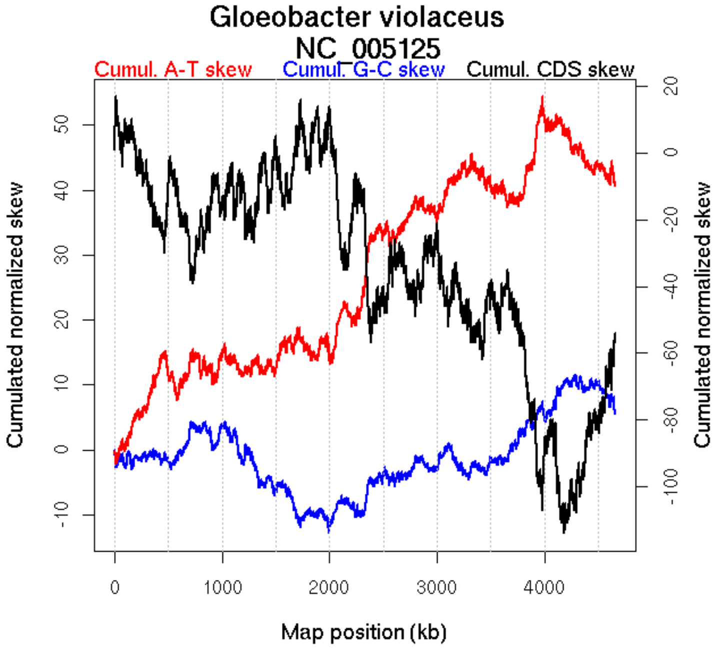
Segments:

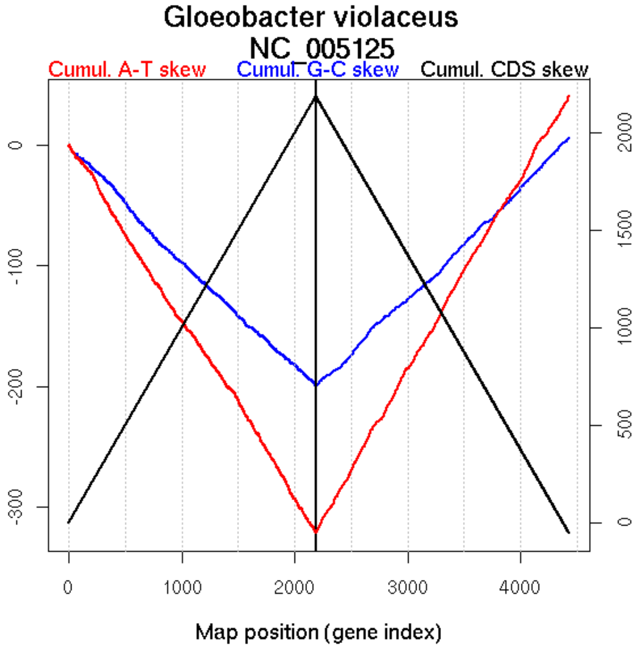
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1121 (1879.253 kb)	leading	-0.078
	1122(1881.159 kb)	1700 (3813.332 kb)	lagging	-0.154
GC-skew reverse	1701 (0 kb)	2277 (1857.2335 kb)	leading	0.156
	2278(1862.06 kb)	3082 (3144.7995 kb)	lagging	0.084
	3083(3145.151 kb)	3145 (3258.412 kb)	lagging	0.156
	3146(3259.2 kb)	3445 (3813.332 kb)	lagging	0.083
AT-skew forward	1 (0 kb)	1108 (1853.6475 kb)	leading	-0.235
	1109(1856.167 kb)	1292 (2567.212 kb)	lagging	-0.061
	1293(2567.597 kb)	1700 (3813.332 kb)	lagging	-0.005
AT-skew reverse	1701 (0 kb)	2275 (1849.4255 kb)	leading	-0.001
	2276(1853.5985 kb)	3185(3302.09 kb)	lagging	0.225
	3186(3302.7155 kb)	3445(3813.332 kb)	lagging	0.25

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

142 Gloeobacter violaceus

Bacteria; Cyanobacteria; Gloeobacteria; Gloeobacterales; Gloeobacter.
Accession number: NC_005125; **Genome size (bp)**: 4659019.
Number of genes: 4430.
Oriloc predictions: Origin NA Terminus NA
Worning et al., 2006: Origin 3785 kb Terminus 832 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 2722.088 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1584.42 kb
Consensus predictions: Origin NA Terminus NA

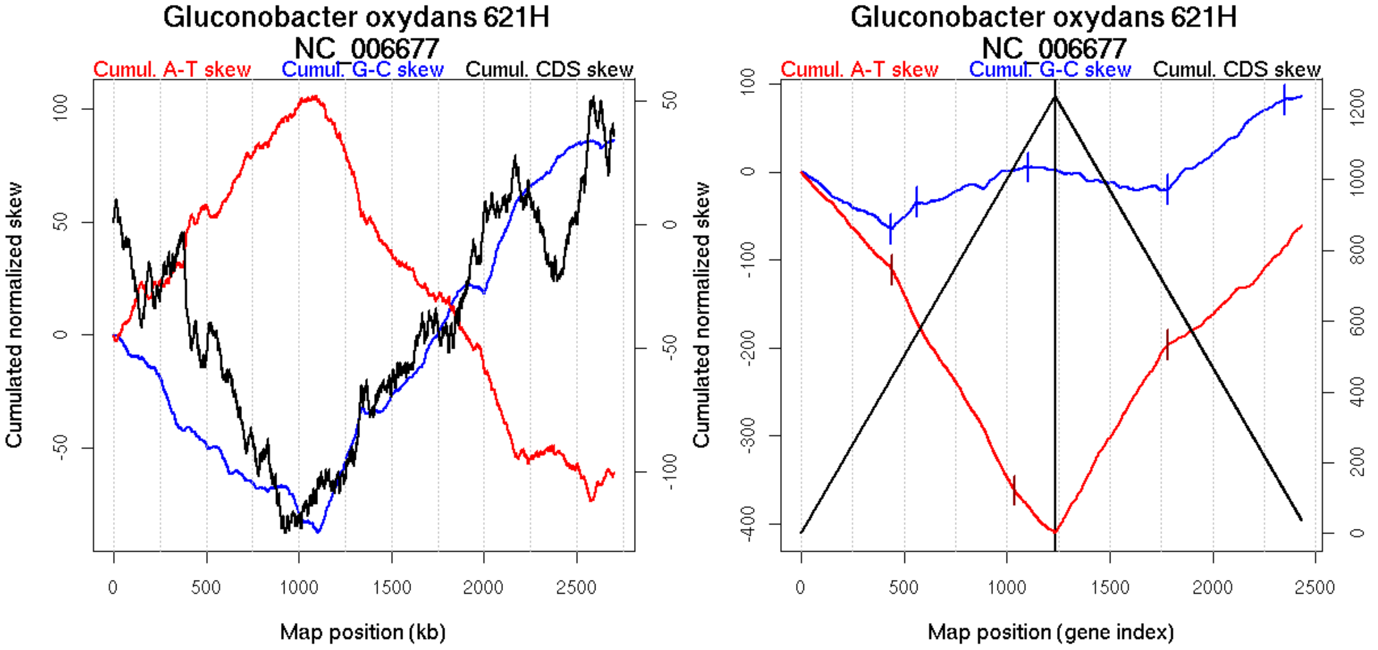




No significant breakpoints.

143 Gluconobacter oxydans 621H

Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales; Acetobacteraceae; Gluconobacter.
Accession number: NC_006677; **Genome size (bp)**: 2702173.
Number of genes: 2432.
Oriloc predictions: Origin 1101 kb Terminus 2586 kb
Worning et al., 2006: Origin 1102 kb Terminus 2571 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 447.934 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 2124.48 kb
Consensus predictions: Origin 1101 kb Terminus 2586 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	435	0	1101
	561	0.02	1338
	1101	0.03556	2486
GC-skew reverse	1783	0	1124
	2350	0	2536
AT-skew forward	443	0.00667	1116
	1039	0.00667	2371
AT-skew reverse	1782	0.00667	1117

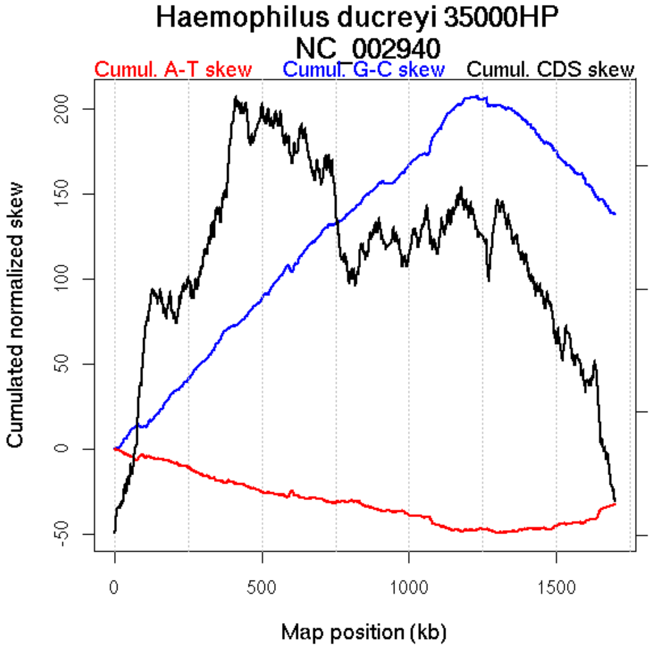
Segments:

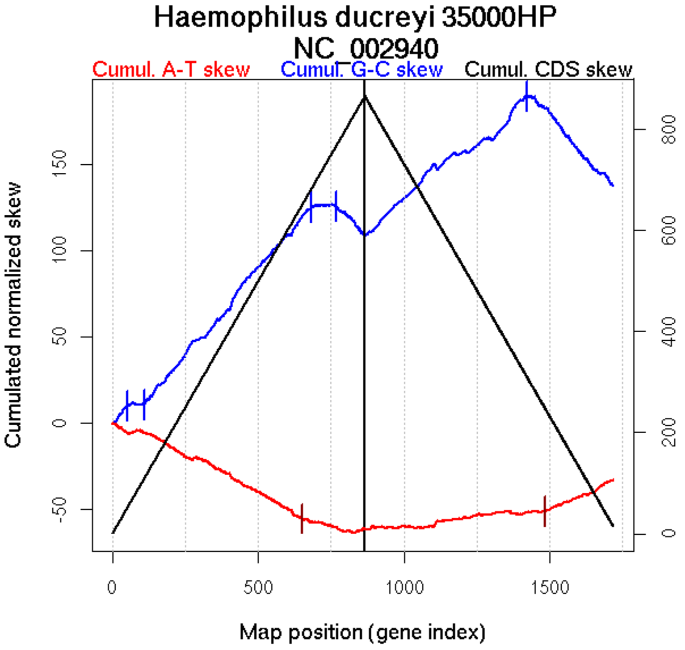
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	435 (1100.6995 kb)	lagging	-0.144
	436(1101.538 kb)	561 (1337.572 kb)	leading	0.237
	562(1338.2605 kb)	1101 (2486.177 kb)	leading	0.086
	1102(2488.612 kb)	1235 (2702 kb)	NA	-0.031
GC-skew reverse	1236 (0 kb)	1783 (1123.75 kb)	lagging	-0.042
	1784(1125.099 kb)	2350 (2536.484 kb)	leading	0.181
	2351(2539.1845 kb)	2432 (2702 kb)	lagging	0.044
AT-skew forward	1 (0 kb)	443 (1116.246 kb)	lagging	-0.253
	444(1117.5095 kb)	1039 (2371.359 kb)	leading	-0.404
	1040(2373.823 kb)	1235 (2702 kb)	NA	-0.253
AT-skew reverse	1236 (0 kb)	1782 (1116.5155 kb)	lagging	0.395
	1783(1123.75 kb)	2432(2702 kb)	leading	0.208

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

144 Haemophilus ducreyi 35000HP

Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Haemophilu
Accession number: NC_002940; **Genome size (bp)**: 1698955.
Number of genes: 1717.
Oriloc predictions: Origin 0 kb Terminus 1216 kb
Worning et al., 2006: Origin 0 kb Terminus 1178 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1698.947 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 679.1 kb
Consensus predictions: Origin 0 kb Terminus 1216 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	52	0.01167	71
	108	0.03167	109
	682	0.035	1187
	766	0.04667	1395
GC-skew reverse	1422	0	1201
AT-skew forward	650	0.01333	1129
AT-skew reverse	1482	0	1328

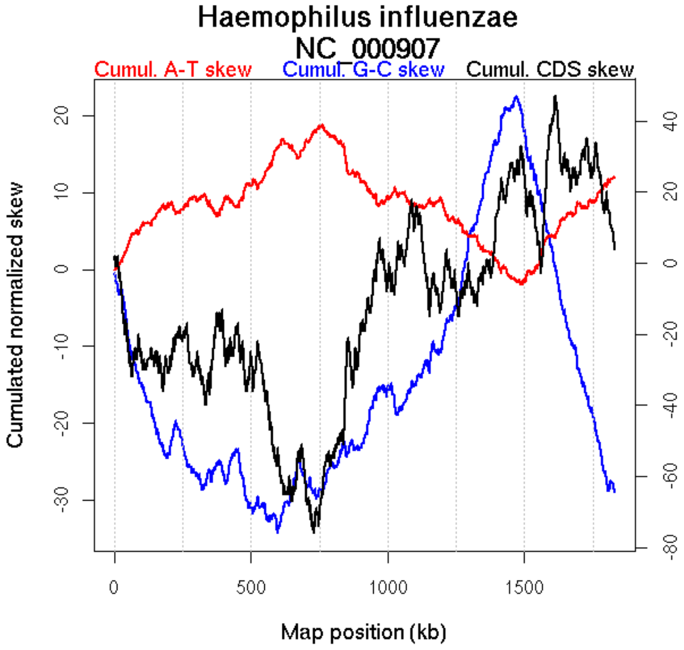
Segments:

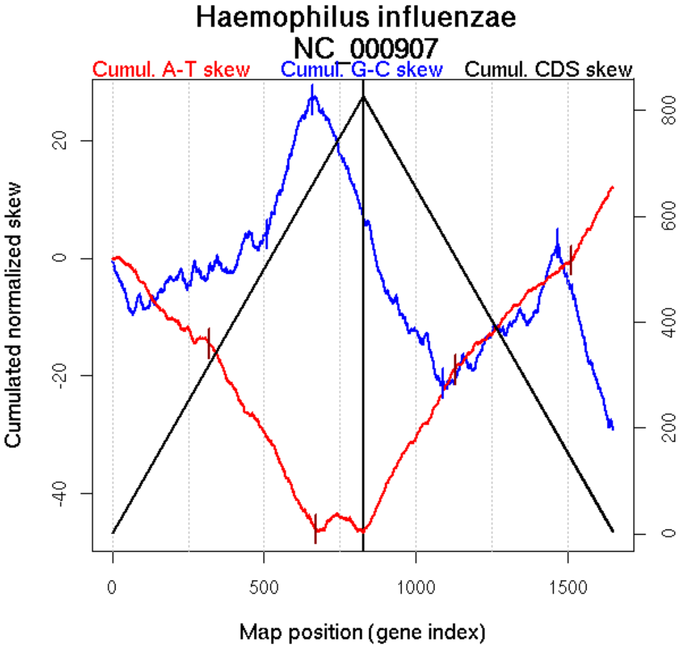
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	52 (70.889 kb)	leading	0.225
	53(72.1755 kb)	108 (108.766 kb)	leading	0.002
	109(109.6105 kb)	682 (1186.7265 kb)	leading	0.2
	683(1188.2945 kb)	766 (1395.4795 kb)	lagging	0.01
	767(1400.4895 kb)	866 (1698.704 kb)	lagging	-0.17
GC-skew reverse	867 (0 kb)	1422 (1201.151 kb)	leading	0.134
	1423(1202.06 kb)	1717 (1698.704 kb)	lagging	-0.191
AT-skew forward	1 (0 kb)	650 (1129.358 kb)	leading	-0.085
	651(1130.748 kb)	866 (1698.704 kb)	NA	-0.037
AT-skew reverse	867 (0 kb)	1482 (1327.985 kb)	leading	0.02
	1483(1329.267 kb)	1717(1698.704 kb)	lagging	0.075

More T than A on the leading strand for replication - for reverse encoded genes.
More G than C on the leading strand for replication.

145 Haemophilus influenzae

Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Haemophilu
Accession number: NC_000907; **Genome size (bp)**: 1830138.
Number of genes: 1650.
Oriloc predictions: Origin 757 kb Terminus 1472 kb
Worning et al., 2006: Origin 324 kb Terminus 1476 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1324.811 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1056.59 kb
Consensus predictions: Origin 757 kb Terminus 1472 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	511	NA	1124
	658	NA	1444
GC-skew reverse	1091	NA	548
	1467	NA	1469
AT-skew forward	319	NA	781
	672	NA	1482
AT-skew reverse	1129	NA	600
	1512	NA	1540

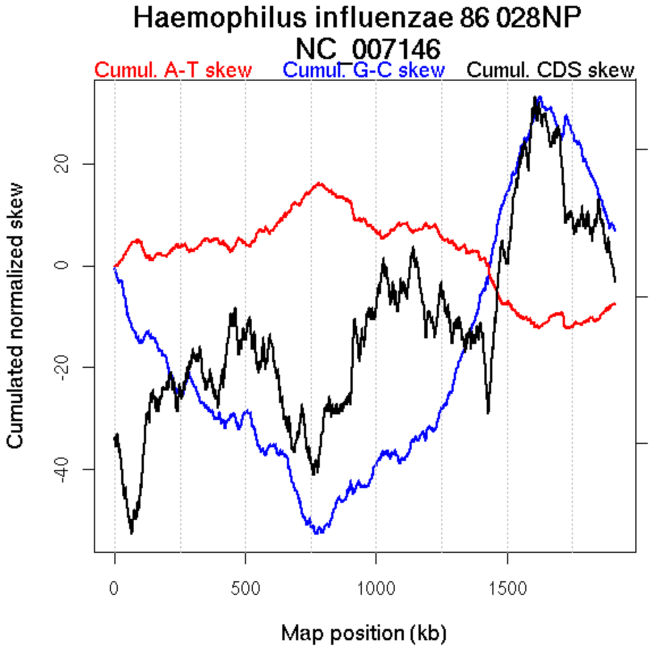
Segments:

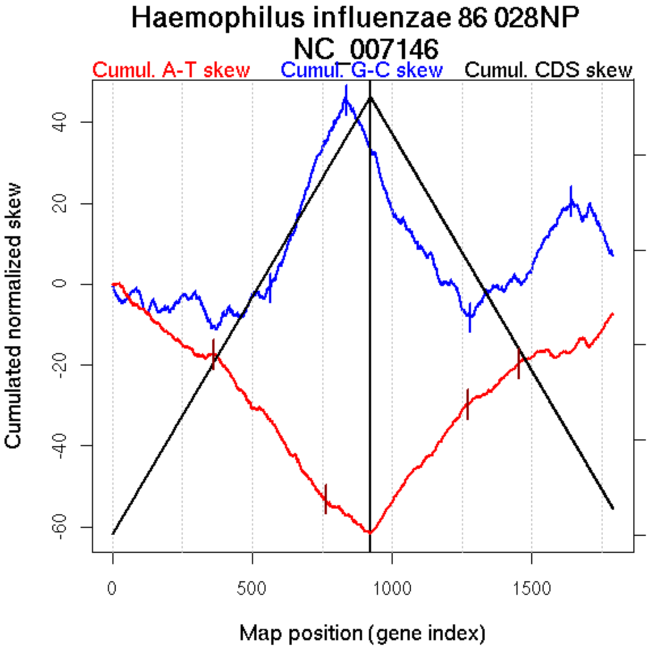
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	511 (1124.0155 kb)	NA	0.02
	512(1136.1955 kb)	658 (1444.0335 kb)	leading	0.162
	659(1446.7525 kb)	827 (1829.889 kb)	lagging	-0.123
GC-skew reverse	828 (0 kb)	1091 (548.3625 kb)	lagging	-0.098
	1092(549.4175 kb)	1467 (1469.1325 kb)	NA	0.053
	1468(1475.337 kb)	1650 (1829.889 kb)	lagging	-0.176
AT-skew forward	1 (0 kb)	319 (780.6195 kb)	lagging	-0.052
	320(782.522 kb)	672 (1482.4735 kb)	leading	-0.089
	673(1484.089 kb)	827 (1829.889 kb)	lagging	0
AT-skew reverse	828 (0 kb)	1129 (600.434 kb)	lagging	0.089
	1130(601.783 kb)	1512(1540.017 kb)	NA	0.049
	1513(1540.9185 kb)	1650(1829.889 kb)	lagging	0.092

More T than A on the leading strand for replication - for forward encoded genes.

146 Haemophilus influenzae 86 028NP

Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Haemophilu
Accession number: NC_007146; **Genome size (bp)**: 1913428.
Number of genes: 1791.
Oriloc predictions: Origin 774 kb Terminus 1621 kb
Worning et al., 2006: Origin 734 kb Terminus 1620 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 122.554 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1112.81 kb
Consensus predictions: Origin 774 kb Terminus 1621 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	566	NA	1192
	838	NA	1637
GC-skew reverse	1280	NA	753
	1642	NA	1619
AT-skew forward	363	NA	783
	763	NA	1531
AT-skew reverse	1273	NA	745
	1454	NA	1204

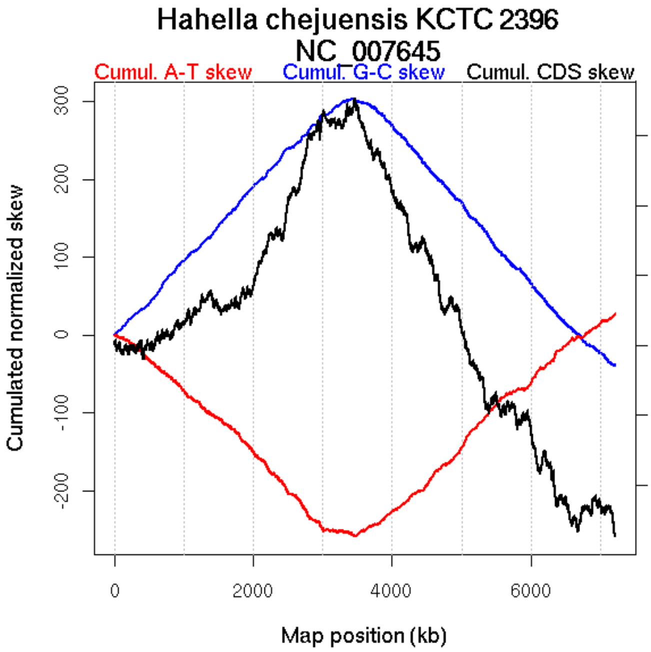
Segments:

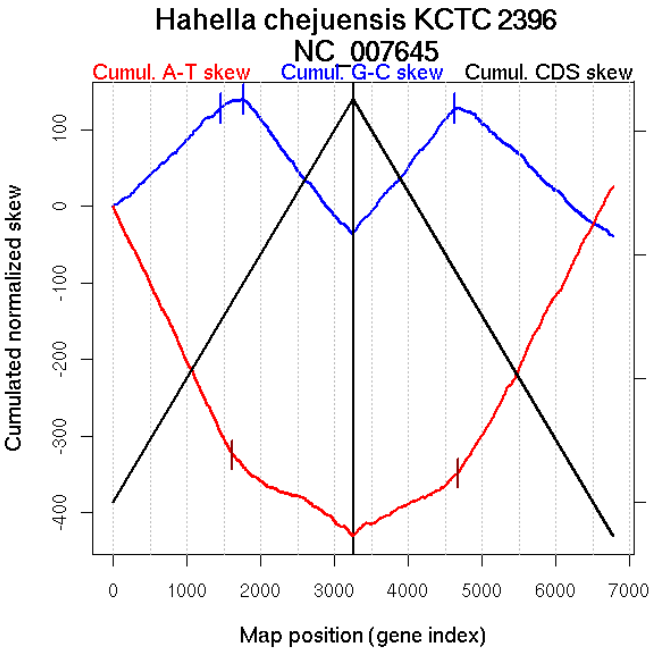
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	566 (1191.633 kb)	NA	-0.003
	567(1192.331 kb)	838 (1637.3735 kb)	leading	0.18
	839(1642.6725 kb)	923 (1913.179 kb)	lagging	-0.14
GC-skew reverse	924 (0 kb)	1280 (752.8205 kb)	lagging	-0.106
	1281(753.4345 kb)	1642 (1619.365 kb)	leading	0.073
	1643(1623.526 kb)	1791 (1913.179 kb)	lagging	-0.081
AT-skew forward	1 (0 kb)	363 (782.5735 kb)	lagging	-0.056
	364(783.918 kb)	763 (1530.6765 kb)	leading	-0.09
	764(1532.872 kb)	923 (1913.179 kb)	NA	-0.051
AT-skew reverse	924 (0 kb)	1273 (745.1355 kb)	lagging	0.09
	1274(746.8015 kb)	1454(1203.743 kb)	leading	0.055
	1455(1206.656 kb)	1791(1913.179 kb)	NA	0.027

More T than A on the leading strand for replication - for forward encoded genes.
More G than C on the leading strand for replication - for reverse encoded genes.

147 Hahella chejuensis KCTC 2396

Bacteria; Proteobacteria; Gammaproteobacteria; Oceanospirillales; Hahellaceae; Hahella.
Accession number: NC_007645; **Genome size (bp)**: 7215267.
Number of genes: 6778.
Oriloc predictions: Origin 0 kb Terminus 3439 kb
Worning et al., 2006: Origin 7213 kb Terminus 3403 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 2255.356 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1.08 kb, 1941.58 kb
Consensus predictions: Origin 0 kb Terminus 3439 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1453	0.01667	2821
	1761	0	3441
GC-skew reverse	4632	0	3360
AT-skew forward	1621	0	3174
AT-skew reverse	4676	0	3445

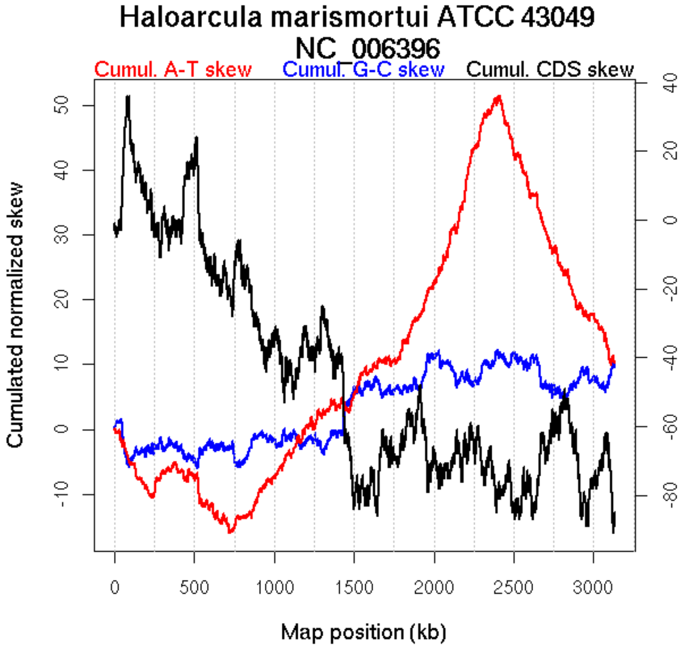
Segments:

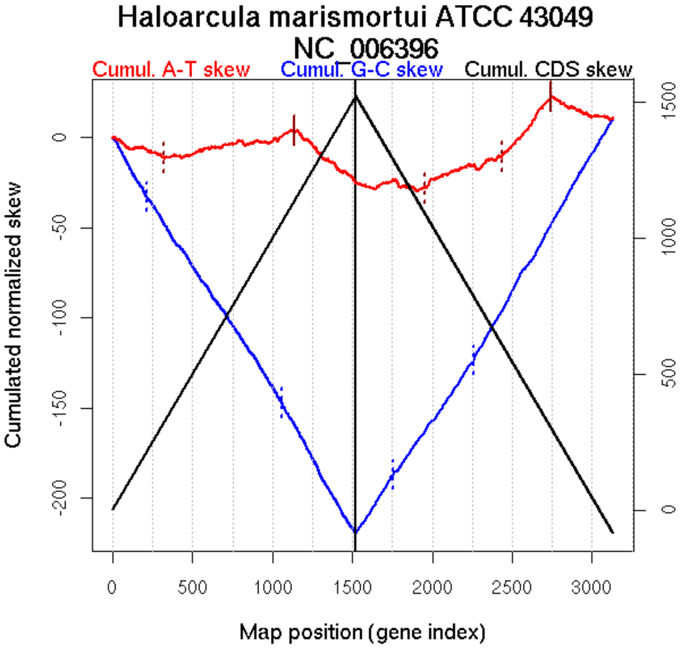
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1453 (2821.2505 kb)	leading	0.092
	1454(2822.3295 kb)	1761 (3440.6735 kb)	leading	0.034
	1762(3442.307 kb)	3253 (7214.957 kb)	lagging	-0.123
GC-skew reverse	3254 (0 kb)	4632 (3360.063 kb)	leading	0.118
	4633(3360.687 kb)	6778 (7214.957 kb)	lagging	-0.085
AT-skew forward	1 (0 kb)	1621 (3173.665 kb)	leading	-0.202
	1622(3174.0565 kb)	3253 (7214.957 kb)	lagging	-0.056
AT-skew reverse	3254 (0 kb)	4676 (3445.262 kb)	leading	0.051
	4677(3451.485 kb)	6778(7214.957 kb)	lagging	0.182

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

148 Haloarcula marismortui ATCC 43049

Archaea; Euryarchaeota; Halobacteria; Halobacteriales; Halobacteriaceae; Haloarcula.
Accession number: NC_006396; **Genome size (bp)**: 3131724.
Number of genes: 3131.
Oriloc predictions: Origin 2402 kb Terminus 786 kb
Worning et al., 2006: Origin 1471 kb Terminus 2412 kb
Position(s) of the ORC/Cdc6 gene(s): 2124.86 kb, 482.97 kb, 684.65 kb, 697.94 kb, 938.04 kb, 1129.35 kb, 1361.24 kb, 1402.02 kb, 1403.19 kb, 2065.9 kb, 2124.86 kb, 2414.82 kb, 2461.99 kb, 2542.96 kb
Consensus predictions: Origin 2402 kb Terminus 786 kb





Significant breakpoints (p-value <0.05):

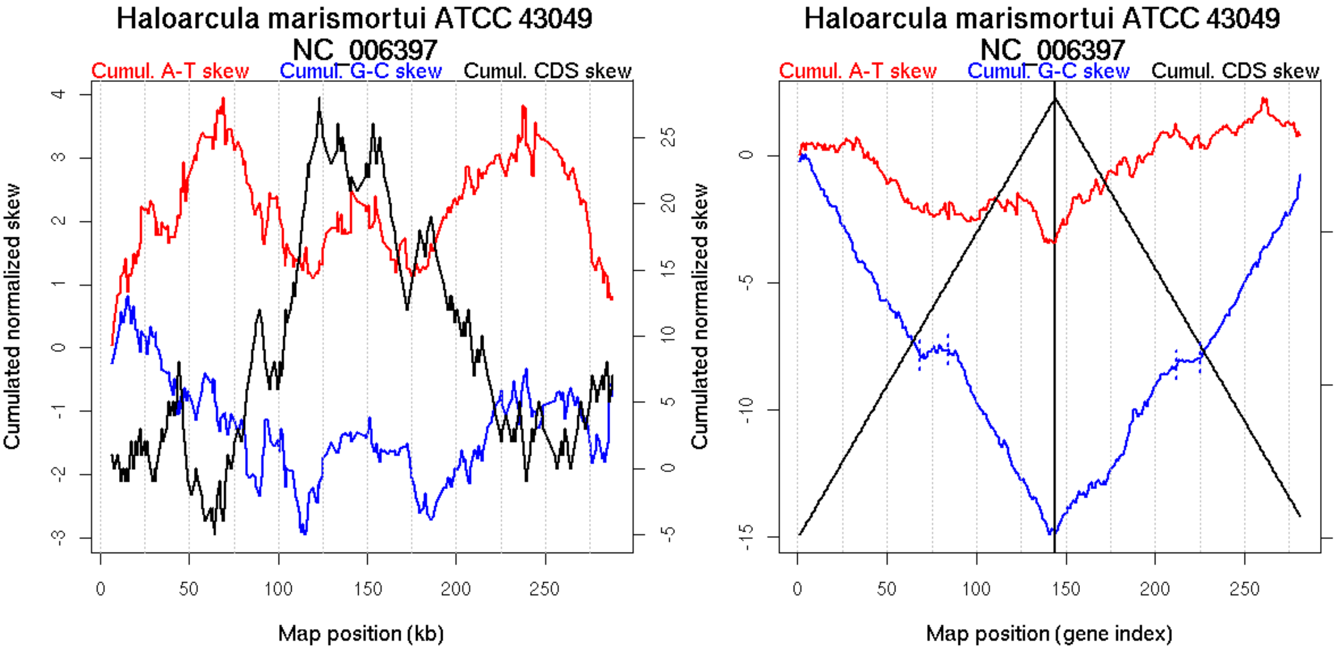
	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	211	0.25	430
	1059	0.27	2205
	211	0.25	430
	1059	0.27	2205
GC-skew reverse	1752	0.63667	477
	2258	0.25333	1432
AT-skew forward	323	0.21	654
	1133	0.00667	2353
AT-skew reverse	1952	0.44889	833
	2433	0.06222	1766
	2744	0.00444	2383

Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	211 (429.88 kb)	leading	-0.16
	212(430.553 kb)	211 (429.88 kb)	leading	0.046
	212(430.553 kb)	1059 (2205.091 kb)	NA	-0.133
	1060(2209.019 kb)	1059 (2205.091 kb)	lagging	0.103
	1060(2209.019 kb)	1523 (3131.71 kb)	NA	-0.16
GC-skew reverse	1524 (0 kb)	1752 (476.7125 kb)	leading	0.14
	1753(480.0495 kb)	2258 (1432.4445 kb)	NA	0.127
	2259(1432.9865 kb)	3131 (3131.71 kb)	NA	0.154
AT-skew forward	1 (0 kb)	323 (654.352 kb)	leading	-0.029
	324(660.357 kb)	1133 (2352.695 kb)	lagging	0.016
	1134(2353.162 kb)	1523 (3131.71 kb)	leading	-0.075
AT-skew reverse	1524 (0 kb)	1952 (833.2865 kb)	leading	-0.004
	1953(834.9045 kb)	2433(1765.5575 kb)	lagging	0.03
	2434(1767.34 kb)	2744(2383.1365 kb)	lagging	0.11
	2745(2384.2265 kb)	3131(3131.71 kb)	leading	-0.032

149 Haloarcula marismortui ATCC 43049

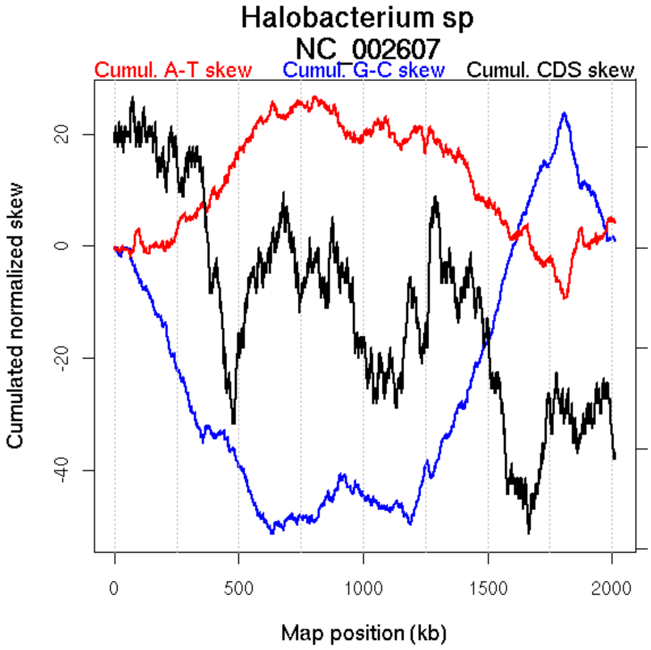
Archaea; Euryarchaeota; Halobacteria; Halobacteriales; Halobacteriaceae; Haloarcula.
Accession number: NC_006397; **Genome size (bp)**: 288050.
Number of genes: 281.
Oriloc predictions: Origin NA Terminus NA
Worning et al., 2006: Origin 231 kb Terminus 124 kb
Position(s) of the ORC/Cdc6 gene(s): 7.45 kb, 50.84 kb
Consensus predictions: Origin NA Terminus NA

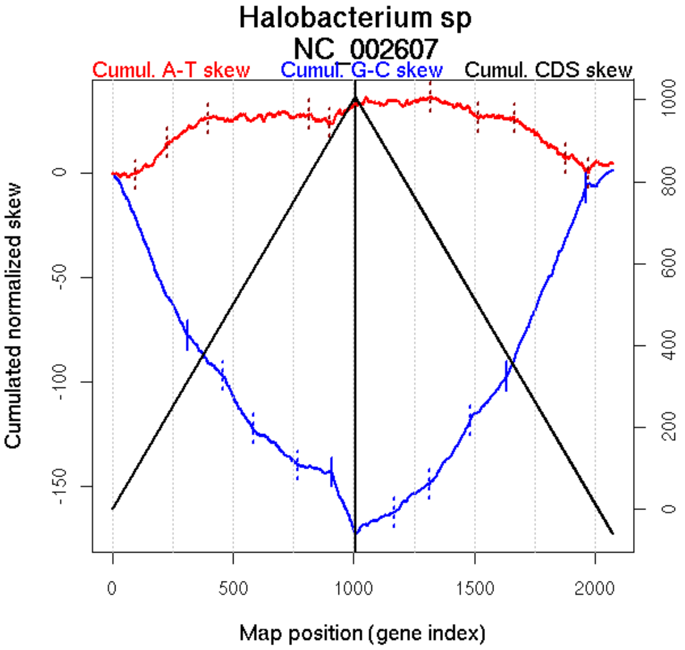


No significant breakpoints.

150 Halobacterium sp

Archaea; Euryarchaeota; Halobacteria; Halobacteriales; Halobacteriaceae; Halobacterium.
Accession number: NC_002607; **Genome size (bp)**: 2014239.
Number of genes: 2075.
Oriloc predictions: Origin 1806 kb Terminus 637 kb
Worning et al., 2006: Origin 1124 kb Terminus 1806 kb
Position(s) of the ORC/Cdc6 gene(s): 921.27 kb, 1808.01 kb, 1615.2 kb, 1691.83 kb
Consensus predictions: Origin NA Terminus NA





Significant breakpoints (p-value <0.05):

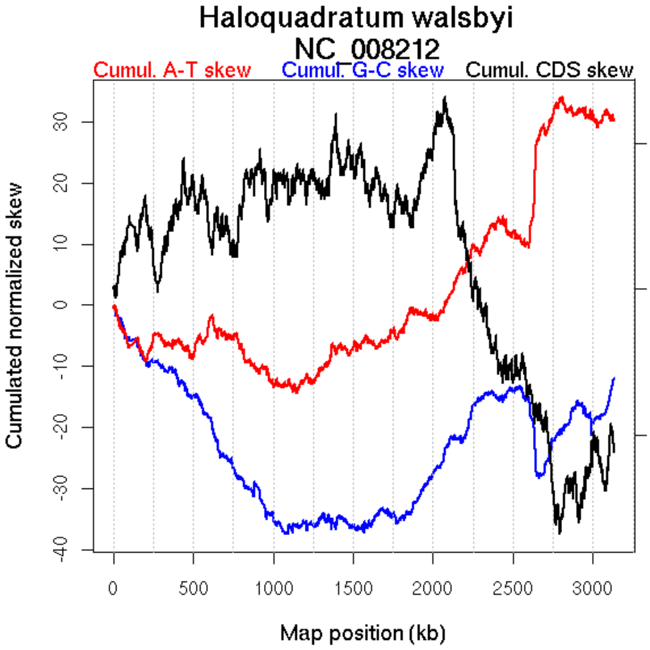
	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	311	0.044	630
	457	0.26267	910
	582	0.06133	1163
	769	0.32	1518
	907	0.00667	1805
GC-skew reverse	1168	0.588	317
	1315	0.14533	571
	1484	0.57333	900
	1633	0.01733	1186
	1962	0.00133	1802
AT-skew forward	96	0.268	199
	228	0.94267	490
	395	0.53467	796
	816	0.83733	1629
	899	0.24	1788
AT-skew reverse	1317	0.74267	577
	1514	0.87867	953
	1665	0.44	1235
	1876	1	1600
	1970	0.33467	1810

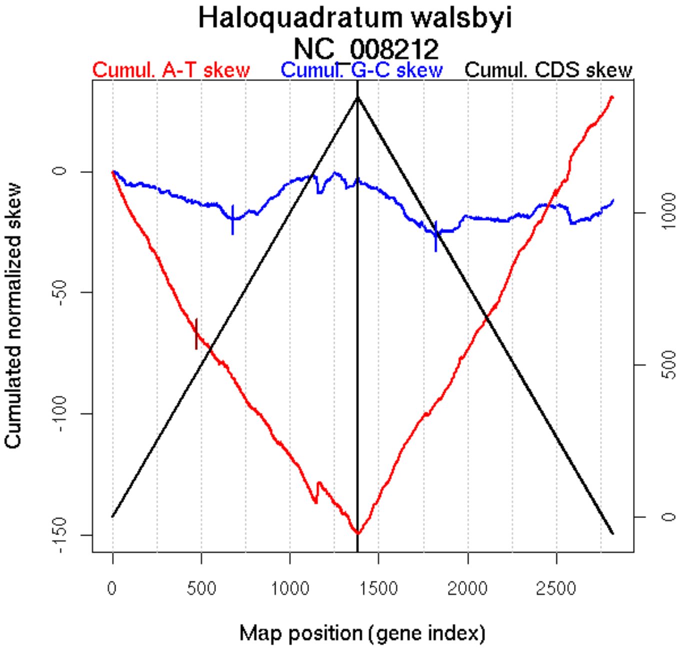
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	311 (629.955 kb)	NA	-0.264
	312(630.7415 kb)	457 (910.426 kb)	NA	-0.138
	458(911.6865 kb)	582 (1162.789 kb)	NA	-0.206
	583(1163.994 kb)	769 (1518.214 kb)	NA	-0.092
	770(1519.019 kb)	907 (1804.6575 kb)	NA	-0.028
	908(1809.2145 kb)	1007 (2014.236 kb)	NA	-0.285
GC-skew reverse	1008 (0 kb)	1168 (316.657 kb)	NA	0.055
	1169(319.028 kb)	1315 (571.411 kb)	NA	0.093
	1316(573.816 kb)	1484 (900.1975 kb)	NA	0.174
	1485(901.121 kb)	1633 (1186.4225 kb)	NA	0.136
	1634(1190.187 kb)	1962 (1801.5655 kb)	NA	0.271
	1963(1802.542 kb)	2075 (2014.236 kb)	NA	0.078
AT-skew forward	1 (0 kb)	96 (199.111 kb)	NA	-0.004
	97(201.0065 kb)	228 (489.8555 kb)	NA	0.105
	229(490.1245 kb)	395 (796.346 kb)	NA	0.078
	396(797.7195 kb)	816 (1629.1795 kb)	NA	0.005
	817(1631.7535 kb)	899 (1787.9925 kb)	NA	-0.033
	900(1790.153 kb)	1007 (2014.236 kb)	NA	0.081
AT-skew reverse	1008 (0 kb)	1317 (577.0025 kb)	NA	0.005
	1318(579.9445 kb)	1514(952.627 kb)	NA	-0.041
	1515(956.1005 kb)	1665(1235.1535 kb)	NA	-0.008
	1666(1235.833 kb)	1876(1600.4925 kb)	NA	-0.089
	1877(1602.2765 kb)	1970(1810.1095 kb)	NA	-0.081
	1971(1812.796 kb)	2075(2014.236 kb)	NA	0.017

151 Haloquadratum walsbyi

Archaea; Euryarchaeota; Halobacteria; Halobacteriales; Halobacteriaceae; Haloquadra.
Accession number: NC_008212; **Genome size (bp)**: 3132494.
Number of genes: 2820.
Oriloc predictions: Origin NA Terminus NA
Worning et al., 2006: Origin NA kb Terminus NA kb
Position(s) of the ORC/Cdc6 gene(s): 1.57 kb, 891.56 kb, 2252.85 kb, 2253.34 kb, 2255.32 kb, 2259.25 kb, 2604.48 kb, 2605.62 kb, 3064.63 kb
Consensus predictions: Origin NA Terminus NA





Significant breakpoints (p-value <0.05):

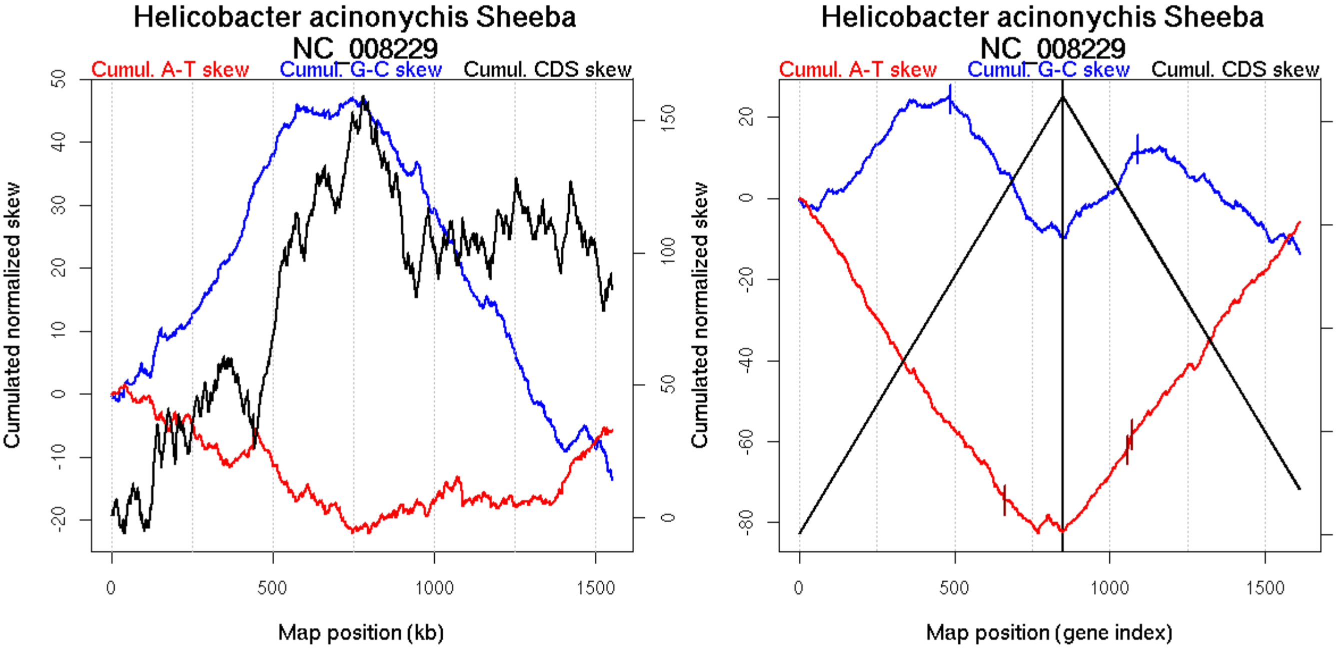
	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	679	0	1493
GC-skew reverse	1826	0	1075
AT-skew forward	476	0.01333	1064

Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	679 (1493.326 kb)	NA	-0.024
	680(1496.429 kb)	1382 (3132.269 kb)	NA	0.025
GC-skew reverse	1383 (0 kb)	1826 (1074.9205 kb)	NA	-0.056
	1827(1078.892 kb)	2820 (3132.269 kb)	NA	0.007
AT-skew forward	1 (0 kb)	476 (1064.494 kb)	NA	-0.139
	477(1065.5465 kb)	1382 (3132.269 kb)	NA	-0.092

152 Helicobacter acinonychis Sheeba

Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter.
Accession number: NC_008229; **Genome size (bp)**: 1553927.
Number of genes: 1612.
Oriloc predictions: Origin 0 kb Terminus 748 kb
Worning et al., 2006: Origin NA kb Terminus NA kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 141.352 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.68 kb, 662.74 kb
Consensus predictions: Origin 0 kb Terminus 748 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	485	0	794
GC-skew reverse	1088	0	576
AT-skew forward	661	0	1178
AT-skew reverse	1056	0.02333	435
	1072	0.02333	477

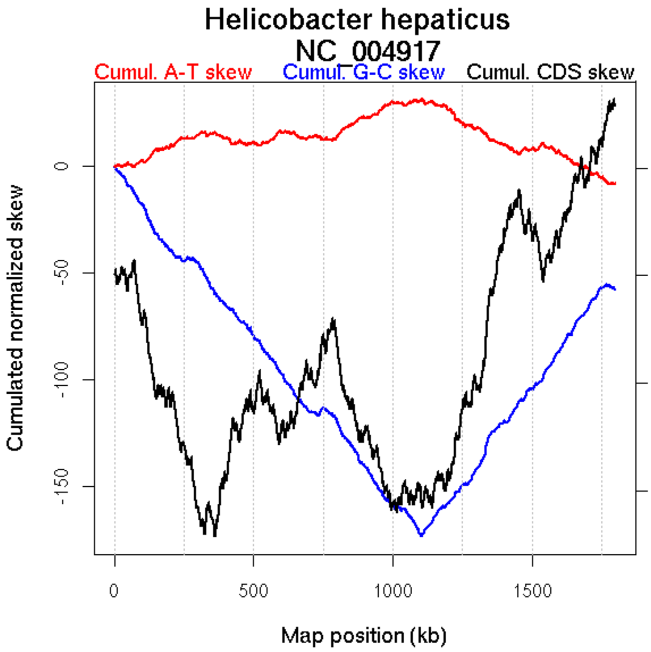
Segments:

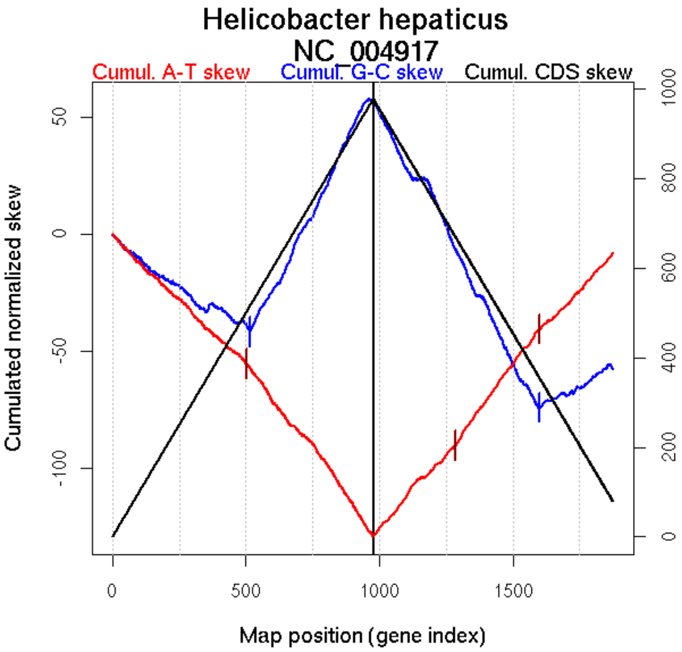
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	485 (793.6555 kb)	leading	0.07
	486(795.1175 kb)	849 (1553.786 kb)	lagging	-0.102
GC-skew reverse	850 (0 kb)	1088 (576.1375 kb)	leading	0.078
	1089(578.214 kb)	1612 (1553.786 kb)	lagging	-0.052
AT-skew forward	1 (0 kb)	661 (1177.6555 kb)	NA	-0.114
	662(1177.824 kb)	849 (1553.786 kb)	lagging	-0.033
AT-skew reverse	850 (0 kb)	1056 (435.134 kb)	leading	0.099
	1057(435.7355 kb)	1072(476.889 kb)	leading	0.254
	1073(509.53 kb)	1612(1553.786 kb)	NA	0.097

More G than C on the leading strand for replication.

153 Helicobacter hepaticus

Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter.
Accession number: NC_004917; **Genome size (bp)**: 1799146.
Number of genes: 1875.
Oriloc predictions: Origin 1105 kb Terminus 4 kb
Worning et al., 2006: Origin 1110 kb Terminus 1777 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1448.763 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1081.3 kb
Consensus predictions: Origin 1105 kb Terminus 4 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	516	NA	1107
GC-skew reverse	1597	NA	1104
AT-skew forward	502	NA	1079
AT-skew reverse	1283	NA	533
	1598	NA	1105

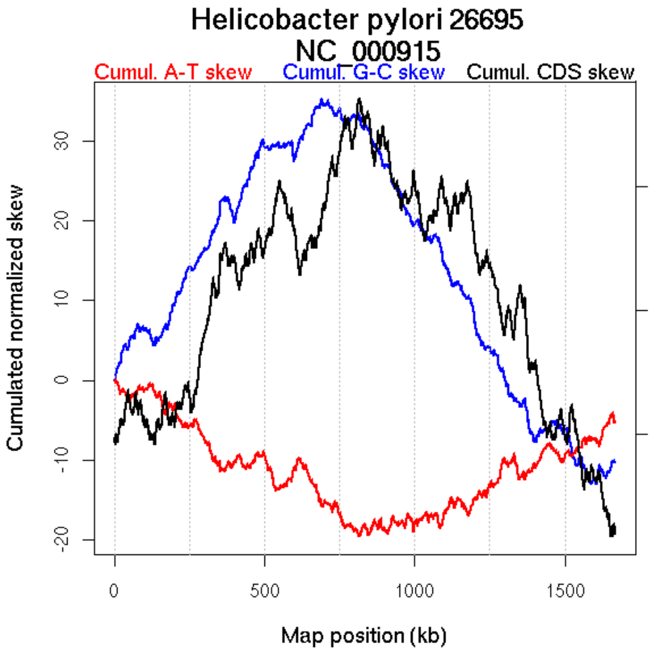
Segments:

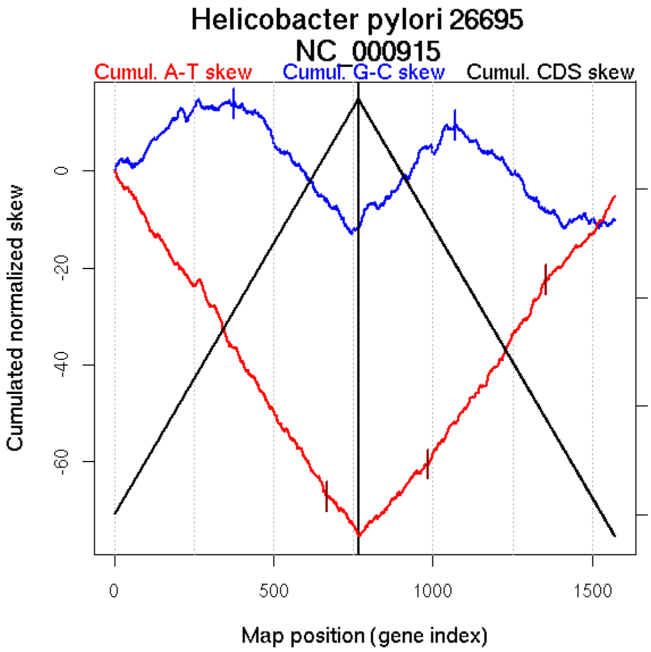
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	516 (1106.8705 kb)	lagging	-0.075
	517(1108.181 kb)	977 (1799.037 kb)	leading	0.227
GC-skew reverse	978 (0 kb)	1597 (1103.726 kb)	lagging	-0.214
	1598(1104.8485 kb)	1875 (1799.037 kb)	leading	0.064
AT-skew forward	1 (0 kb)	502 (1079.065 kb)	lagging	-0.109
	503(1080.6745 kb)	977 (1799.037 kb)	leading	-0.151
AT-skew reverse	978 (0 kb)	1283 (532.5885 kb)	lagging	0.126
	1284(532.984 kb)	1598(1104.8485 kb)	lagging	0.156
	1599(1105.672 kb)	1875(1799.037 kb)	leading	0.12

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

154 Helicobacter pylori 26695

Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter.
Accession number: NC_000915; **Genome size (bp)**: 1667867.
Number of genes: 1572.
Oriloc predictions: Origin 0 kb Terminus 813 kb
Worning et al., 2006: Origin 1655 kb Terminus 768 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1271.097 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1608.31 kb
Consensus predictions: Origin 0 kb Terminus 813 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	375	NA	710
GC-skew reverse	1070	NA	790
AT-skew forward	667	NA	1383
AT-skew reverse	984	NA	570
	1355	NA	1317

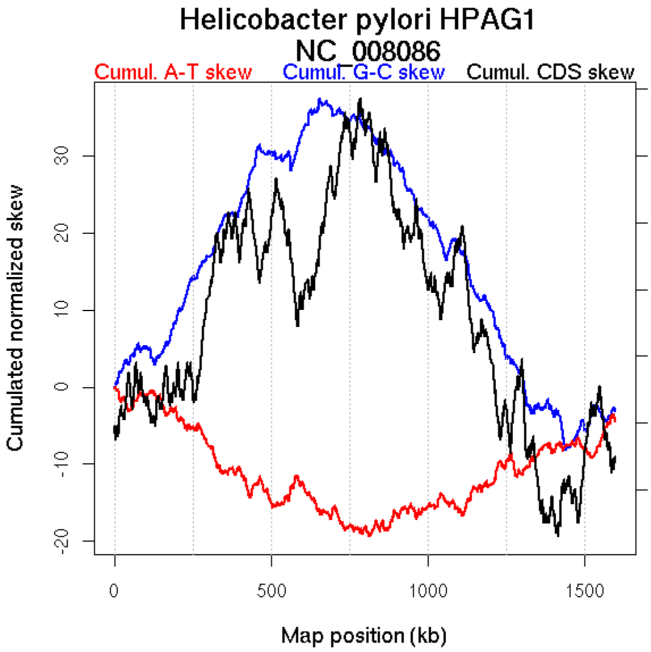
Segments:

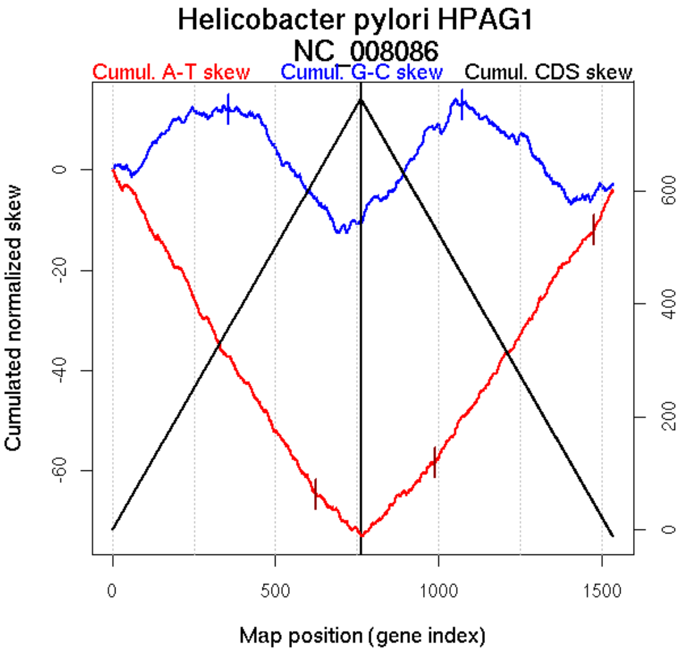
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	375 (709.967 kb)	leading	0.042
	376(710.692 kb)	766 (1667.8 kb)	NA	-0.075
GC-skew reverse	767 (0 kb)	1070 (790.2695 kb)	leading	0.068
	1071(791.489 kb)	1572 (1667.8 kb)	lagging	-0.045
AT-skew forward	1 (0 kb)	667 (1382.6155 kb)	NA	-0.1
	668(1384.5525 kb)	766 (1667.8 kb)	lagging	-0.078
AT-skew reverse	767 (0 kb)	984 (569.7705 kb)	leading	0.07
	985(571.799 kb)	1355(1317.115 kb)	NA	0.098
	1356(1319.218 kb)	1572(1667.8 kb)	lagging	0.076

More G than C on the leading strand for replication - for reverse encoded genes.

155 Helicobacter pylori HPAG1

Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter.
Accession number: NC_008086; **Genome size (bp)**: 1596366.
Number of genes: 1536.
Oriloc predictions: Origin 0 kb Terminus 764 kb
Worning et al., 2006: Origin 1438 kb Terminus 735 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1202.033 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1436.37 kb
Consensus predictions: Origin 0 kb Terminus 764 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	355	NA	674
GC-skew reverse	1073	NA	749
AT-skew forward	623	NA	1294
AT-skew reverse	991	NA	542
	1478	NA	1469

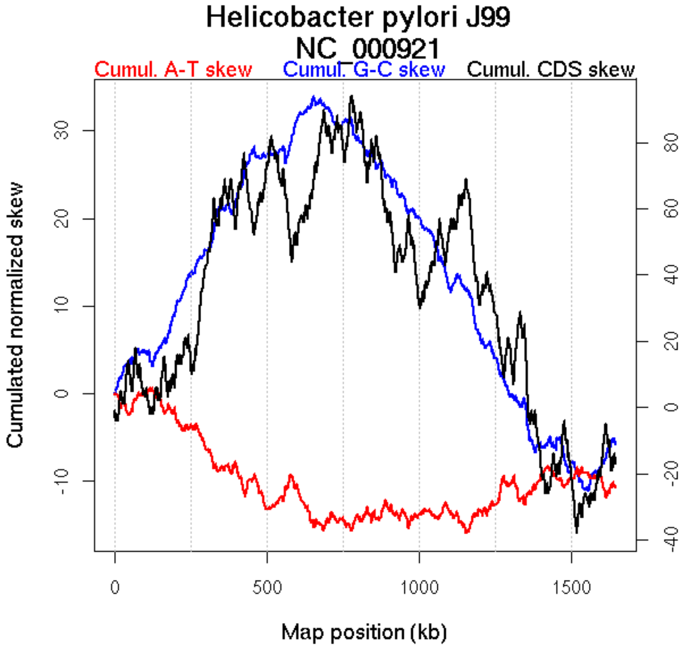
Segments:

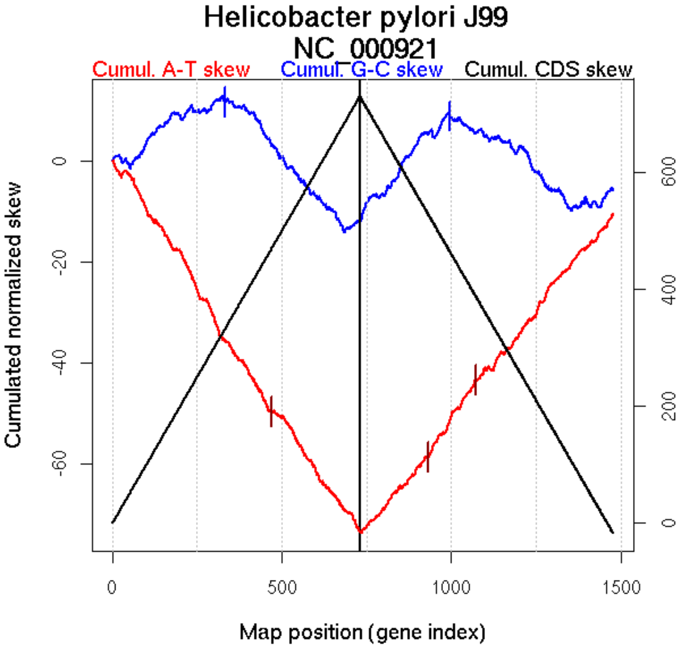
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	355 (674.13 kb)	leading	0.043
	356(674.559 kb)	762 (1596.29 kb)	lagging	-0.072
GC-skew reverse	763 (0 kb)	1073 (749.406 kb)	leading	0.079
	1074(750.4045 kb)	1536 (1596.29 kb)	lagging	-0.046
AT-skew forward	1 (0 kb)	623 (1293.987 kb)	NA	-0.106
	624(1294.989 kb)	762 (1596.29 kb)	lagging	-0.061
AT-skew reverse	763 (0 kb)	991 (541.5705 kb)	leading	0.066
	992(542.7915 kb)	1478(1469.263 kb)	NA	0.097
	1479(1470.6465 kb)	1536(1596.29 kb)	lagging	0.14

More G than C on the leading strand for replication.

156 Helicobacter pylori J99

Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Helicobacter.
Accession number: NC_000921; **Genome size (bp)**: 1643831.
Number of genes: 1477.
Oriloc predictions: Origin 0 kb Terminus 685 kb
Worning et al., 2006: Origin 1557 kb Terminus 685 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 120.75 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1558.48 kb
Consensus predictions: Origin 0 kb Terminus 685 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	331	NA	663
GC-skew reverse	995	NA	693
AT-skew forward	468	NA	1013
AT-skew reverse	933	NA	536
	1072	NA	850

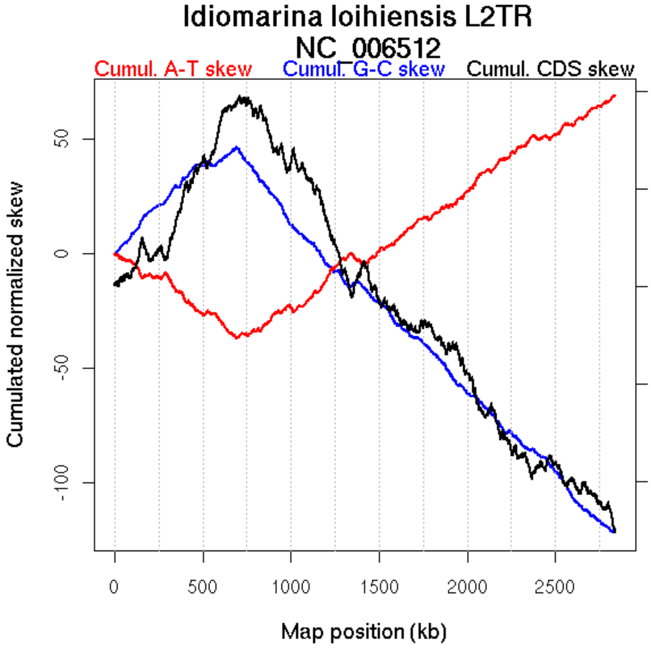
Segments:

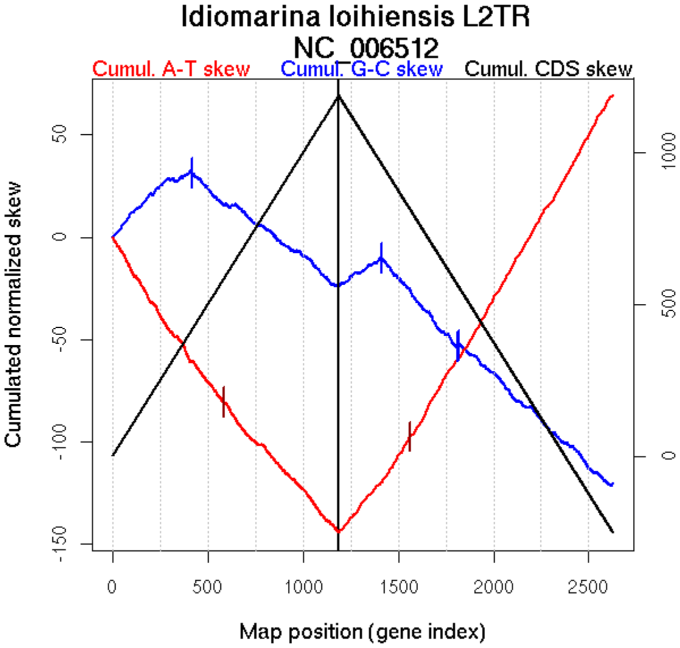
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	331 (663.138 kb)	leading	0.043
	332(665.9005 kb)	730 (1643.586 kb)	lagging	-0.074
GC-skew reverse	731 (0 kb)	995 (693.289 kb)	leading	0.078
	996(695.155 kb)	1477 (1643.586 kb)	lagging	-0.043
AT-skew forward	1 (0 kb)	468 (1013.4015 kb)	NA	-0.109
	469(1016.4615 kb)	730 (1643.586 kb)	lagging	-0.096
AT-skew reverse	731 (0 kb)	933 (536.4565 kb)	leading	0.077
	934(537.257 kb)	1072(849.739 kb)	NA	0.104
	1073(854.855 kb)	1477(1643.586 kb)	lagging	0.084

More T than A on the leading strand for replication - for reverse encoded genes.
More G than C on the leading strand for replication.

157 Idiomarina loihiensis L2TR

Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales; Idiomarinaceae; Idiomarina.
Accession number: NC_006512; **Genome size (bp)**: 2839318.
Number of genes: 2628.
Oriloc predictions: Origin 2829 kb Terminus 690 kb
Worning et al., 2006: Origin 2759 kb Terminus 772 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 2831.645 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1.04 kb, 1578.39 kb
Consensus predictions: Origin 0 kb Terminus 690 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	417	0	704
GC-skew reverse	1412	0.00889	695
	1812	0.00667	1338
	1821	0.00889	1354
AT-skew forward	582	0.04	1147
AT-skew reverse	1561	0.01333	952

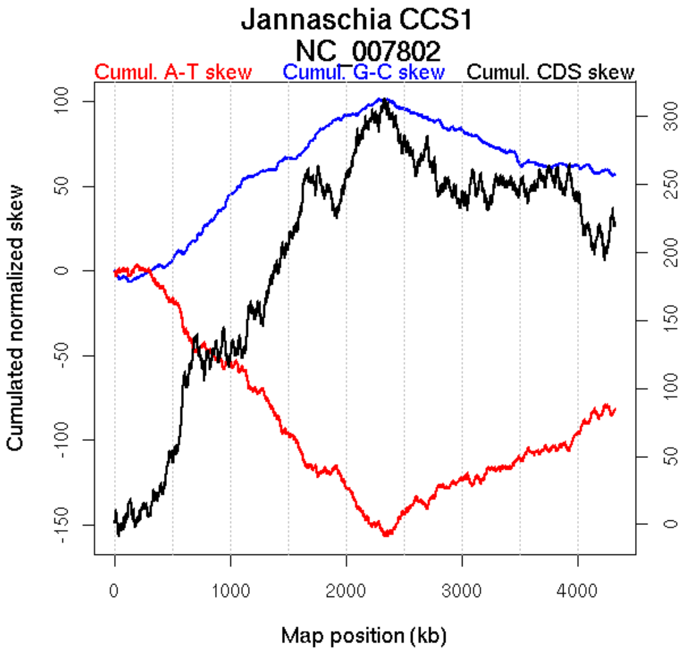
Segments:

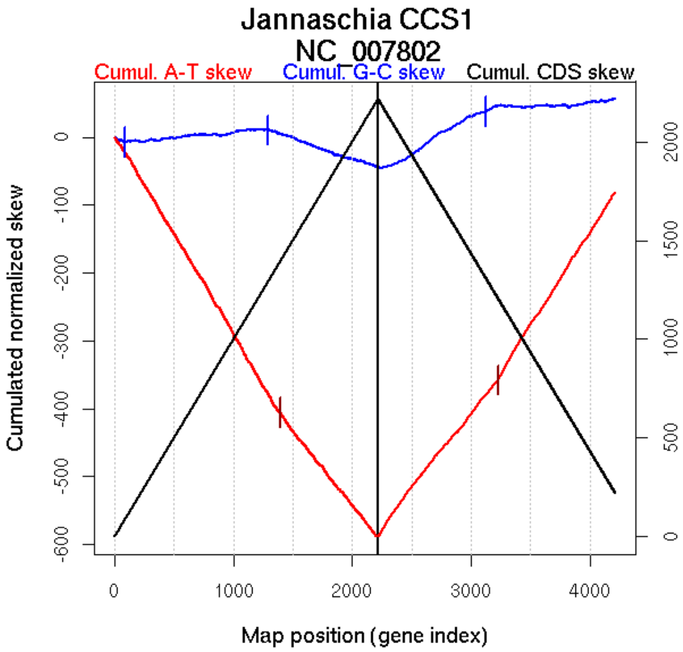
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	417 (703.908 kb)	leading	0.077
	418(705.464 kb)	1188 (2839.274 kb)	lagging	-0.069
GC-skew reverse	1189 (0 kb)	1412 (694.715 kb)	leading	0.06
	1413(699.4815 kb)	1812 (1338.4685 kb)	lagging	-0.111
	1813(1339.738 kb)	1821 (1354.2275 kb)	lagging	0.086
	1822(1369.523 kb)	2628 (2839.274 kb)	lagging	-0.088
AT-skew forward	1 (0 kb)	582 (1146.9815 kb)	NA	-0.138
	583(1150.96 kb)	1188 (2839.274 kb)	lagging	-0.102
AT-skew reverse	1189 (0 kb)	1561 (951.8 kb)	NA	0.122
	1562(952.912 kb)	2628(2839.274 kb)	lagging	0.158

More G than C on the leading strand for replication.

158 Jannaschia CCS1

Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Jannaschia.
Accession number: NC_007802; **Genome size (bp)**: 4317977.
Number of genes: 4212.
Oriloc predictions: Origin 136 kb Terminus 2352 kb
Worning et al., 2006: Origin 185 kb Terminus 2256 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 3425.348 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.76 kb, 1011.1 kb
Consensus predictions: Origin 136 kb Terminus 2352 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	82	0	138
	1294	0.00333	2294
GC-skew reverse	3125	0	2108
AT-skew forward	1391	0	2498
AT-skew reverse	3226	0.00667	2337

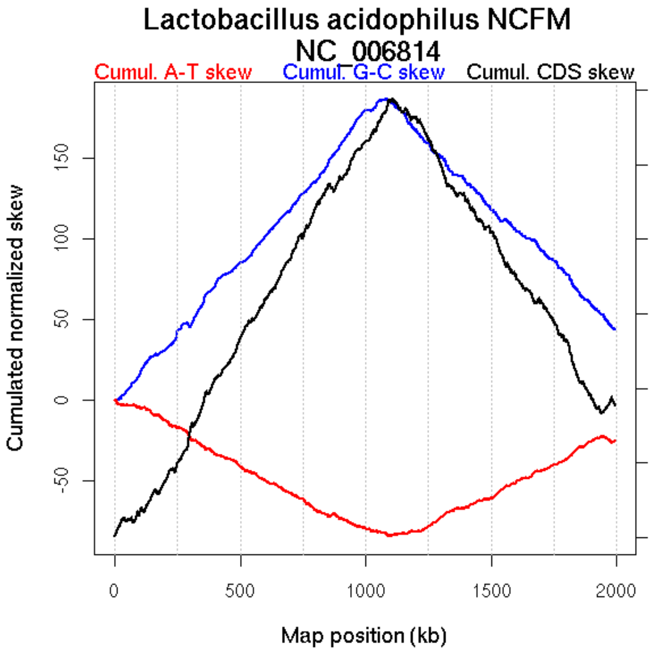
Segments:

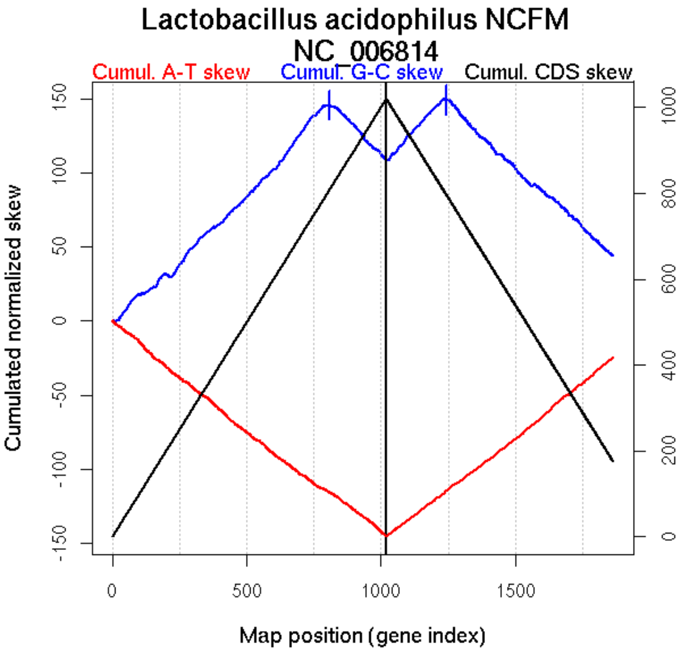
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	82 (138.344 kb)	lagging	-0.064
	83(147.3865 kb)	1294 (2293.7885 kb)	leading	0.016
	1295(2295.208 kb)	2217 (4317.478 kb)	lagging	-0.061
GC-skew reverse	2218 (0 kb)	3125 (2107.624 kb)	leading	0.105
	3126(2108.332 kb)	4212 (4317.478 kb)	lagging	0.009
AT-skew forward	1 (0 kb)	1391 (2497.936 kb)	leading	-0.295
	1392(2498.565 kb)	2217 (4317.478 kb)	lagging	-0.22
AT-skew reverse	2218 (0 kb)	3226 (2337.3905 kb)	leading	0.223
	3227(2338.165 kb)	4212(4317.478 kb)	lagging	0.276

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

159 Lactobacillus acidophilus NCFM

Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae; Lactobacillus.
Accession number: NC_006814; **Genome size (bp)**: 1993564.
Number of genes: 1864.
Oriloc predictions: Origin 0 kb Terminus 1104 kb
Worning et al., 2006: Origin 0 kb Terminus 1105 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1993.284 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.71 kb, 24.98 kb, 475.59 kb, 1535.59 kb
Consensus predictions: Origin 0 kb Terminus 1104 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	807	0	1085
GC-skew reverse	1242	0	1038

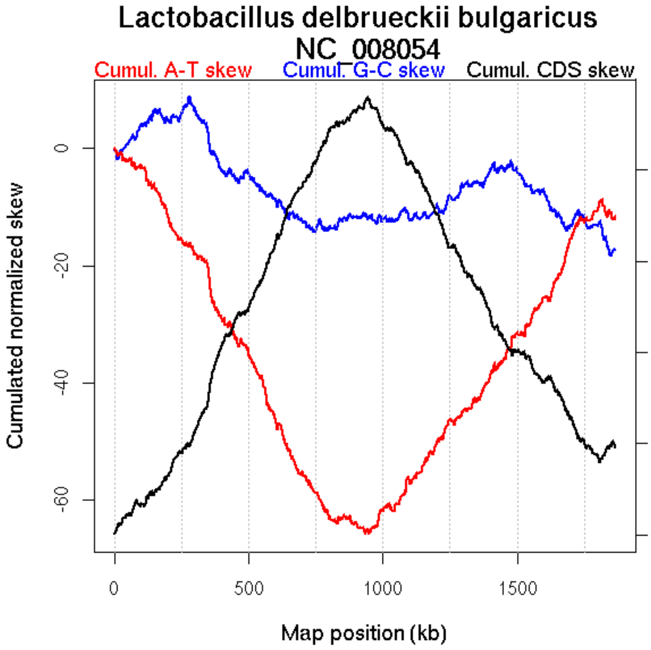
Segments:

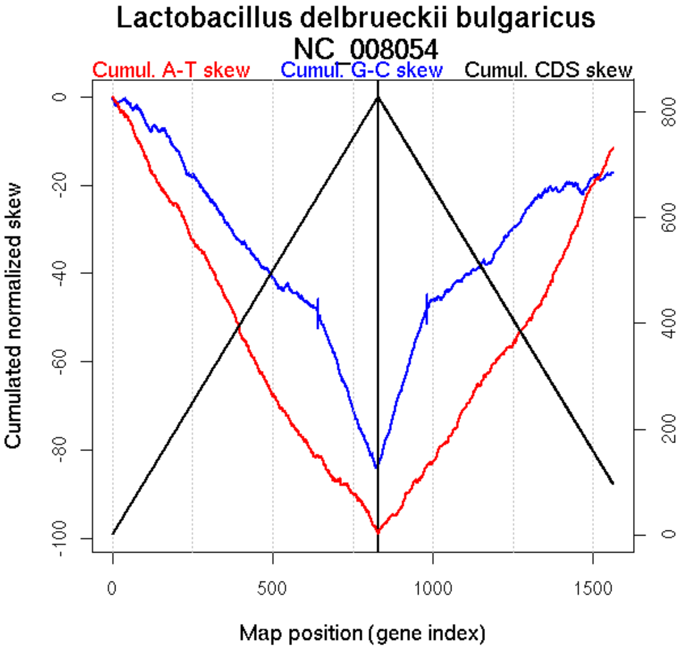
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	807 (1084.535 kb)	leading	0.183
	808(1084.669 kb)	1020 (1993.118 kb)	lagging	-0.186
GC-skew reverse	1021 (0 kb)	1242 (1038.1555 kb)	leading	0.198
	1243(1039.328 kb)	1864 (1993.118 kb)	lagging	-0.166

More G than C on the leading strand for replication.

160 Lactobacillus delbrueckii bulgaricus

Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae; Lactobacillus.
Accession number: NC_008054; **Genome size (bp)**: 1864998.
Number of genes: 1562.
Oriloc predictions: Origin 1805 kb Terminus 976 kb
Worning et al., 2006: Origin 1810 kb Terminus 911 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 180.898 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1 kb
Consensus predictions: Origin 1805 kb Terminus 976 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	642	NA	954
GC-skew reverse	981	NA	895

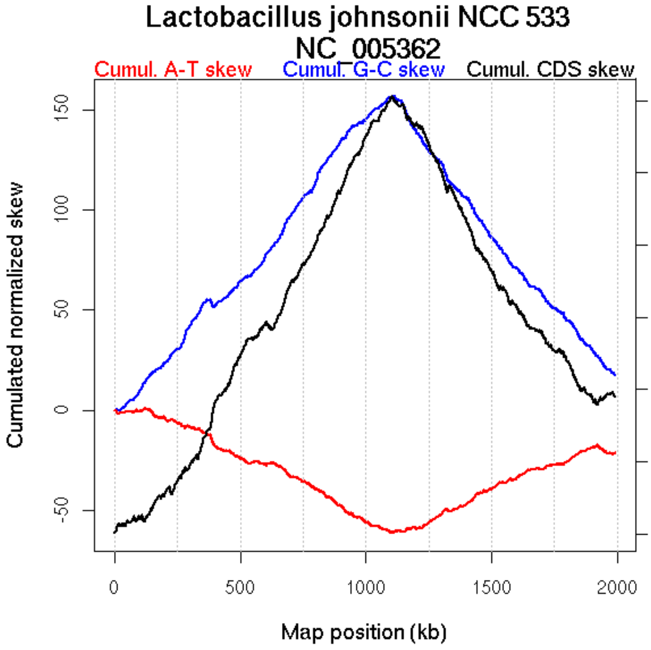
Segments:

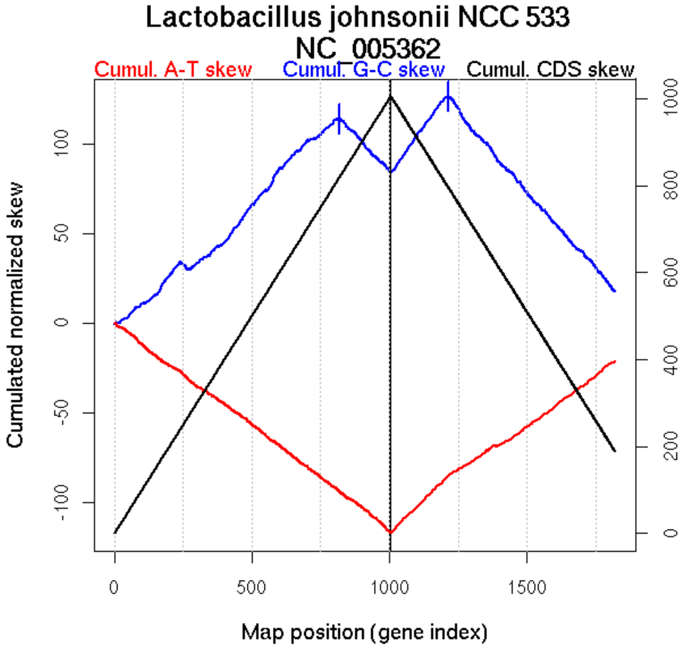
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	642 (954.4375 kb)	leading	-0.085
	643(960.876 kb)	829 (1864.845 kb)	NA	-0.196
GC-skew reverse	830 (0 kb)	981 (895.3115 kb)	leading	0.237
	982(899.036 kb)	1562 (1864.845 kb)	lagging	0.058

More G than C on the leading strand for replication - for reverse encoded genes.

161 Lactobacillus johnsonii NCC 533

Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae; Lactobacillus.
Accession number: NC_005362; **Genome size (bp)**: 1992676.
Number of genes: 1821.
Oriloc predictions: Origin 0 kb Terminus 1102 kb
Worning et al., 2006: Origin 0 kb Terminus 1100 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1767.509 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.68 kb
Consensus predictions: Origin 0 kb Terminus 1102 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	817	NA	1122
GC-skew reverse	1214	NA	1105

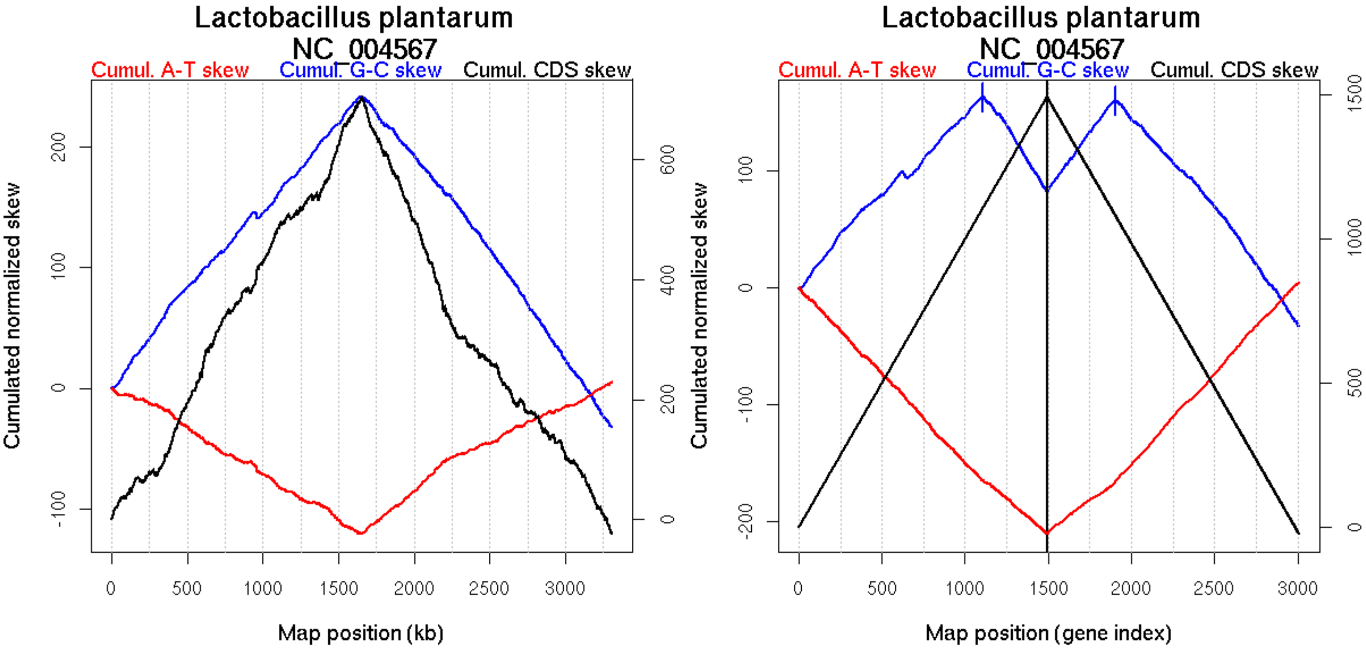
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	817 (1122.224 kb)	leading	0.148
	818(1131.2665 kb)	1005 (1992.002 kb)	lagging	-0.163
GC-skew reverse	1006 (0 kb)	1214 (1104.897 kb)	leading	0.214
	1215(1107.9505 kb)	1821 (1992.002 kb)	lagging	-0.176

More G than C on the leading strand for replication.

162 Lactobacillus plantarum

Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae; Lactobacillus.
Accession number: NC_004567; **Genome size (bp)**: 3308274.
Number of genes: 3009.
Oriloc predictions: Origin 0 kb Terminus 1646 kb
Worning et al., 2006: Origin 3 kb Terminus 1657 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1.412 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.68 kb
Consensus predictions: Origin 0 kb Terminus 1646 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1104	NA	1644
GC-skew reverse	1906	NA	1663

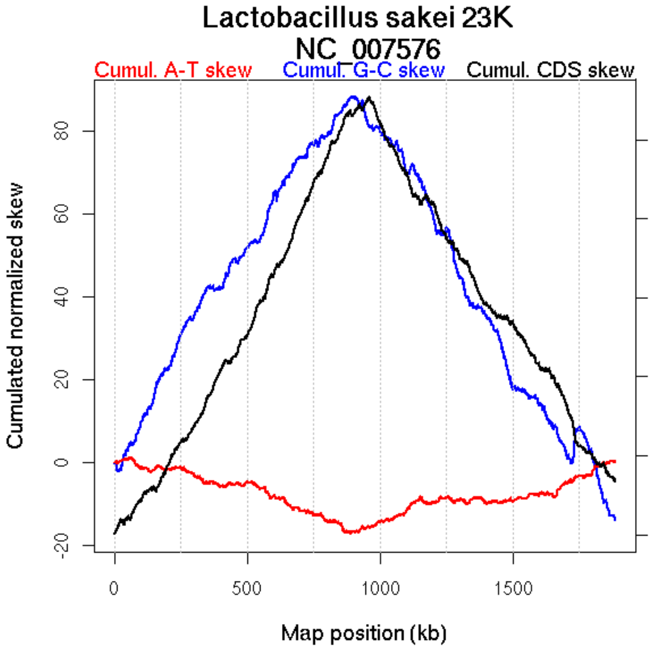
Segments:

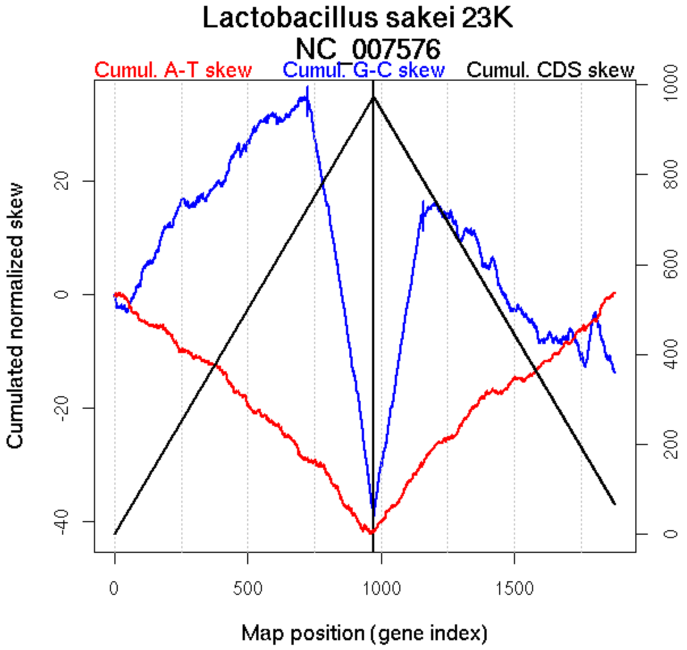
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1104 (1644.2495 kb)	leading	0.142
	1105(1645.365 kb)	1493 (3307.771 kb)	lagging	-0.217
GC-skew reverse	1494 (0 kb)	1906 (1662.5195 kb)	leading	0.194
	1907(1664.8435 kb)	3009 (3307.771 kb)	lagging	-0.173

More G than C on the leading strand for replication.

163 Lactobacillus sakei 23K

Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae; Lactobacillus.
Accession number: NC_007576; **Genome size (bp)**: 1884661.
Number of genes: 1879.
Oriloc predictions: Origin 0 kb Terminus 904 kb
Worning et al., 2006: Origin 0 kb Terminus 922 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 500.443 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.88 kb, 1368.77 kb
Consensus predictions: Origin 0 kb Terminus 904 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	724	NA	909
GC-skew reverse	1158	NA	893

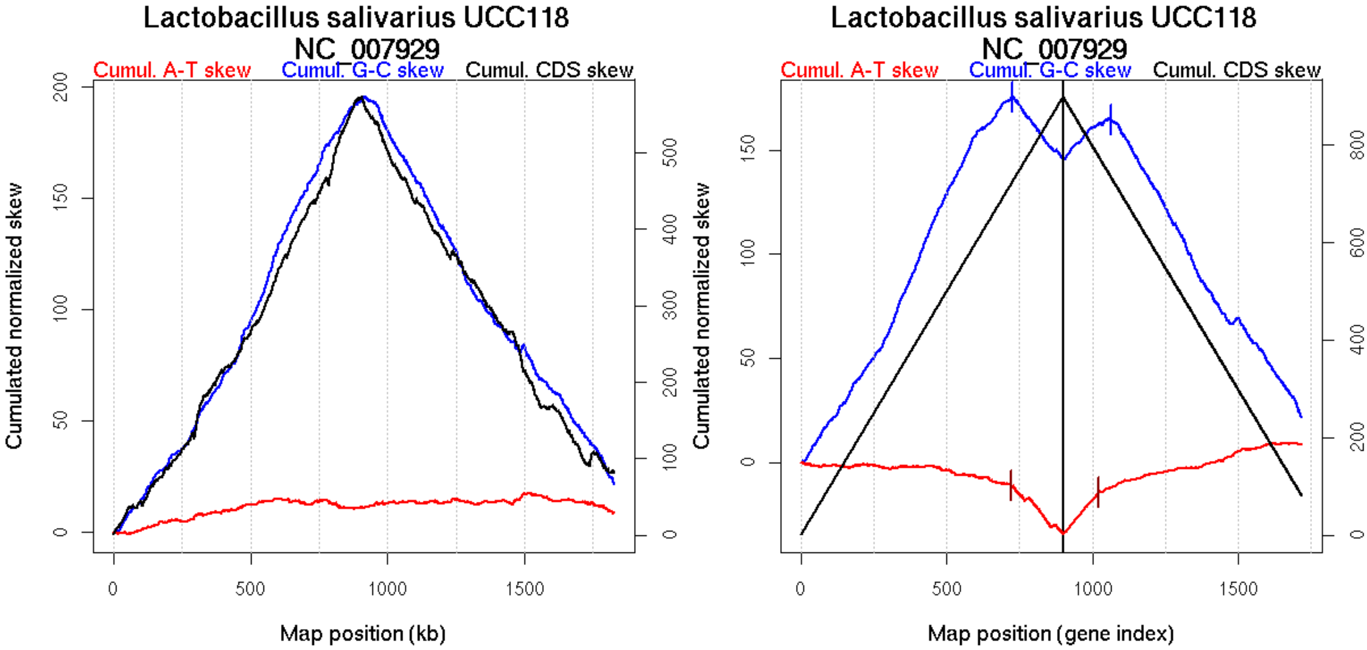
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	724 (909.183 kb)	leading	0.054
	725(911.3305 kb)	973 (1884.299 kb)	lagging	-0.295
GC-skew reverse	974 (0 kb)	1158 (892.8165 kb)	leading	0.292
	1159(901.43 kb)	1879 (1884.299 kb)	lagging	-0.042

More G than C on the leading strand for replication.

164 Lactobacillus salivarius UCC118

Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae; Lactobacillus.
Accession number: NC_007929; **Genome size (bp)**: 1827111.
Number of genes: 1717.
Oriloc predictions: Origin 2 kb Terminus 918 kb
Worning et al., 2006: Origin 0 kb Terminus 902 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 50.929 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.68 kb, 541.84 kb
Consensus predictions: Origin 2 kb Terminus 918 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	725	NA	949
GC-skew reverse	1063	NA	921
AT-skew forward	722	NA	924
AT-skew reverse	1020	NA	751

Segments:

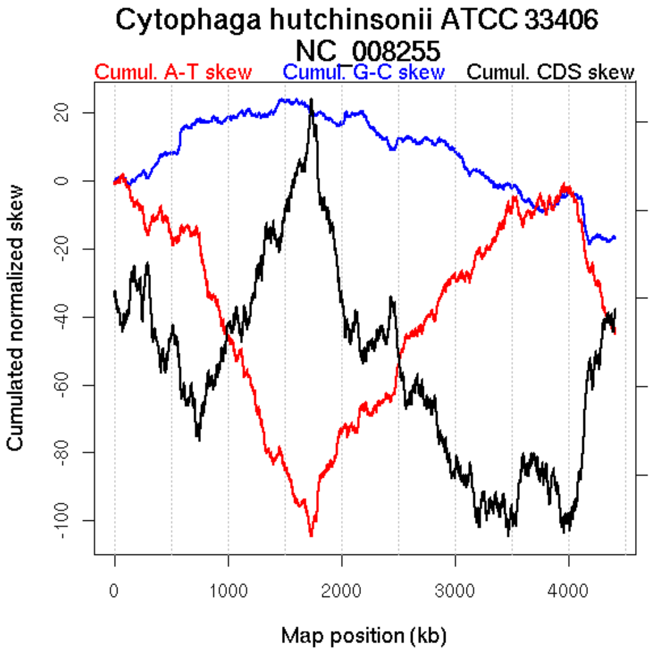
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	725 (949.2775 kb)	leading	0.267
	726(954.9685 kb)	899 (1826.624 kb)	lagging	-0.177
GC-skew reverse	900 (0 kb)	1063 (921.4205 kb)	leading	0.123
	1064(922.743 kb)	1717 (1826.624 kb)	lagging	-0.218
AT-skew forward	1 (0 kb)	722 (924.071 kb)	leading	-0.012
	723(934.747 kb)	899 (1826.624 kb)	lagging	-0.132
AT-skew reverse	900 (0 kb)	1020 (750.737 kb)	leading	0.167
	1021(755.523 kb)	1717(1826.624 kb)	lagging	0.035

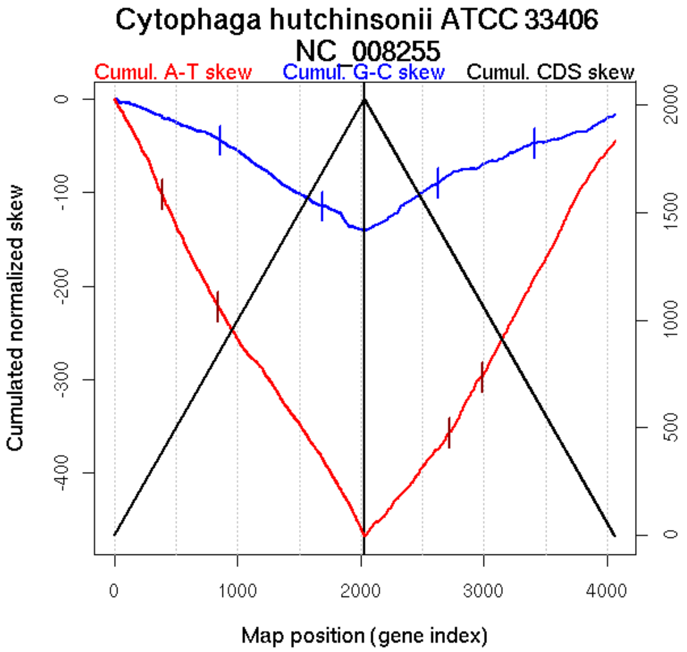
More A than T on the leading strand for replication.

More G than C on the leading strand for replication.

165 Cytophaga hutchinsonii ATCC 33406

Bacteria; Bacteroidetes; Sphingobacteria; Sphingobacteriales; Flexibacteraceae; Cytophaga.
Accession number: NC_008255; **Genome size (bp)**: 4433218.
Number of genes: 4064.
Oriloc predictions: Origin 3918 kb Terminus 1872 kb
Worning et al., 2006: Origin NA kb Terminus NA kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1144.741 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 3451.24 kb
Consensus predictions: Origin 3918 kb Terminus 1872 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	859	NA	1756
	1685	NA	3770
GC-skew reverse	2630	NA	1344
	3413	NA	2941
AT-skew forward	388	NA	911
	842	NA	1719
AT-skew reverse	2717	NA	1533
	2983	NA	2035

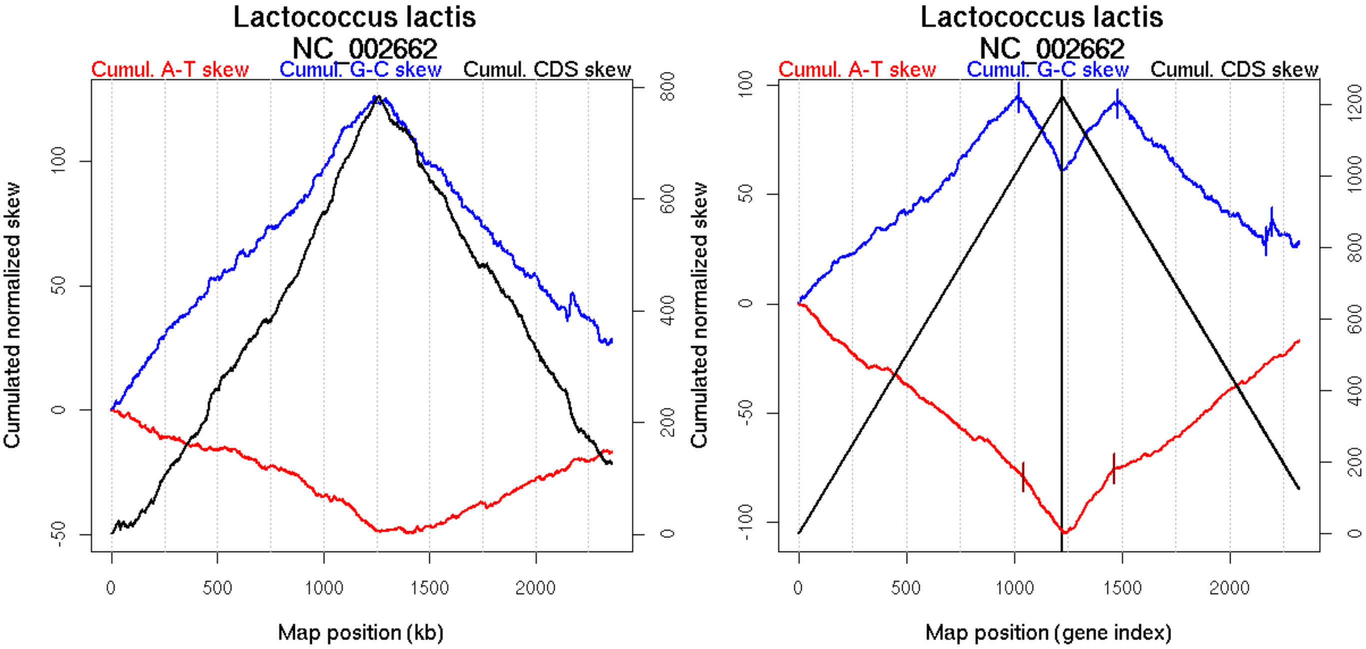
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	859 (1756.3405 kb)	leading	-0.051
	860(1765.5265 kb)	1685 (3770.3905 kb)	lagging	-0.089
	1686(3776.8965 kb)	2029 (4411.662 kb)	NA	-0.093
GC-skew reverse	2030 (0 kb)	2630 (1344.035 kb)	leading	0.092
	2631(1345.799 kb)	3413 (2940.942 kb)	NA	0.049
	3414(2945.9845 kb)	4064 (4411.662 kb)	NA	0.047
AT-skew forward	1 (0 kb)	388 (910.5005 kb)	leading	-0.261
	389(912.1885 kb)	842 (1718.6945 kb)	leading	-0.262
	843(1719.012 kb)	2029 (4411.662 kb)	NA	-0.197
AT-skew reverse	2030 (0 kb)	2717 (1532.636 kb)	leading	0.16
	2718(1533.053 kb)	2983(2035.0045 kb)	NA	0.247
	2984(2037.019 kb)	4064(4411.662 kb)	NA	0.242

More G than C on the leading strand for replication - for forward encoded genes.

166 Lactococcus lactis

Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
Accession number: NC_002662; **Genome size (bp)**: 2365589.
Number of genes: 2321.
Oriloc predictions: Origin 0 kb Terminus 1292 kb
Worning et al., 2006: Origin 0 kb Terminus 1265 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1963.115 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1.04 kb
Consensus predictions: Origin 0 kb Terminus 1292 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1019	0	1251
GC-skew reverse	1481	0.00444	1280
	2167	0	2155
	2193	0	2170
AT-skew forward	1045	0	1368
AT-skew reverse	1466	0.01333	1259

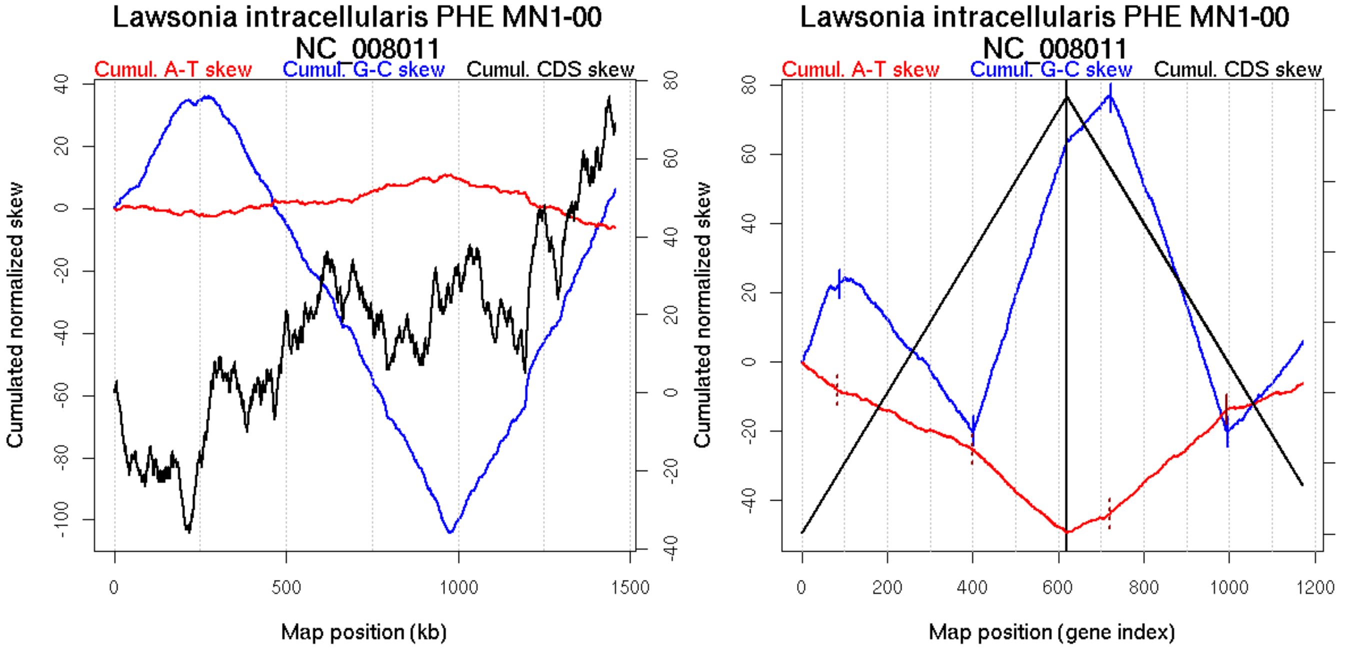
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1019 (1250.7845 kb)	leading	0.088
	1020(1252.1205 kb)	1223 (2359.847 kb)	lagging	-0.164
GC-skew reverse	1224 (0 kb)	1481 (1280.19 kb)	leading	0.132
	1482(1281.49 kb)	2167 (2155.186 kb)	lagging	-0.093
	2168(2156.06 kb)	2193 (2169.7995 kb)	lagging	0.366
	2194(2171.082 kb)	2321 (2359.847 kb)	lagging	-0.087
AT-skew forward	1 (0 kb)	1045 (1368.153 kb)	leading	-0.072
	1046(1372.944 kb)	1223 (2359.847 kb)	lagging	-0.137
AT-skew reverse	1224 (0 kb)	1466 (1259.2965 kb)	leading	0.133
	1467(1262.829 kb)	2321(2359.847 kb)	lagging	0.073

More A than T on the leading strand for replication.
More G than C on the leading strand for replication.

167 Lawsonia intracellularis PHE MN1-00

Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales; Desulfovibrionaceae; Lawsonia.
Accession number: NC_008011; **Genome size (bp)**: 1457619.
Number of genes: 1171.
Oriloc predictions: Origin 978 kb Terminus 214 kb
Worning et al., 2006: Origin 978 kb Terminus 218 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 166.882 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1.08 kb, 979.98 kb
Consensus predictions: Origin 978 kb Terminus 214 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	88	0	252
	401	0	984
GC-skew reverse	724	0	250
	995	0	979
AT-skew forward	83	0.14667	242
	399	0.05333	976
AT-skew reverse	719	0.05667	209
	994	0.03333	977

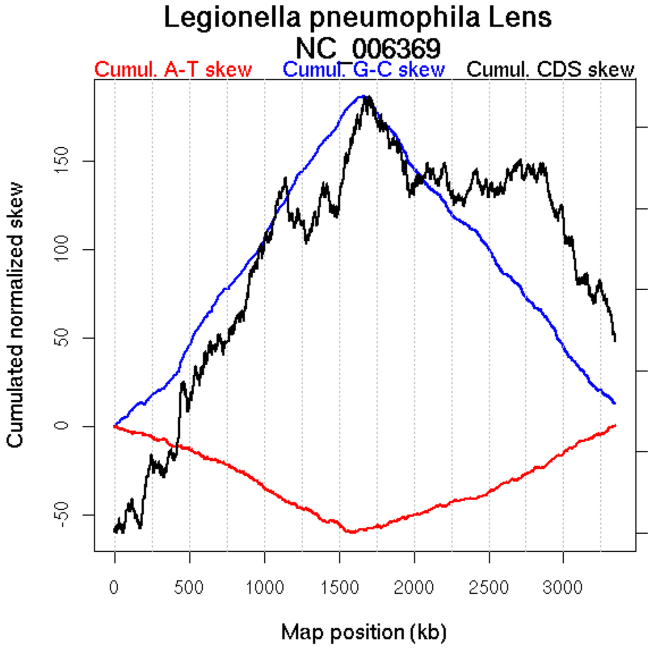
Segments:

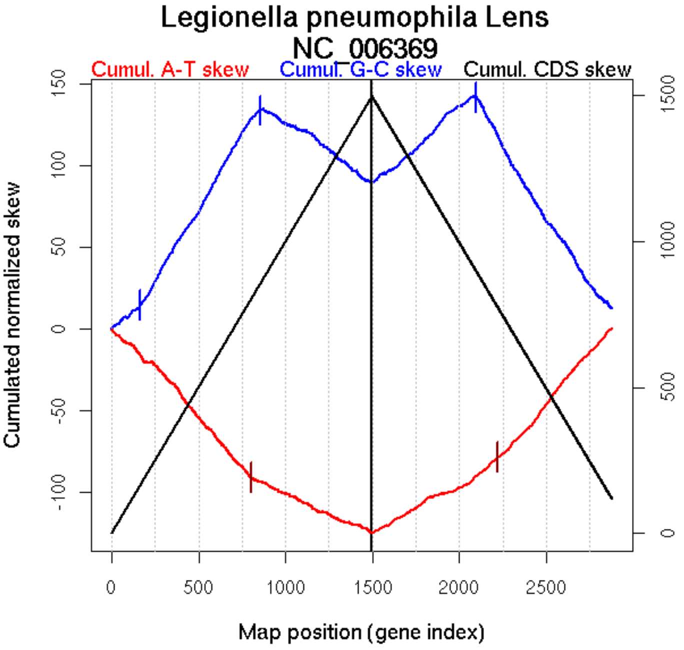
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	88 (252.029 kb)	NA	0.287
	89(255.014 kb)	401 (983.841 kb)	lagging	-0.15
	402(985.3895 kb)	620 (1457.486 kb)	leading	0.385
GC-skew reverse	621 (0 kb)	724 (250.2505 kb)	leading	0.134
	725(251.6875 kb)	995 (979.3405 kb)	lagging	-0.361
	996(986.582 kb)	1171 (1457.486 kb)	leading	0.147
AT-skew forward	1 (0 kb)	83 (241.5065 kb)	NA	-0.094
	84(242.876 kb)	399 (976.2955 kb)	lagging	-0.055
	400(982.237 kb)	620 (1457.486 kb)	leading	-0.112
AT-skew reverse	621 (0 kb)	719 (208.786 kb)	leading	0.052
	720(211.7655 kb)	994(977.403 kb)	lagging	0.106
	995(979.3405 kb)	1171(1457.486 kb)	leading	0.042

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

168 Legionella pneumophila Lens

Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales; Legionellaceae; Legionella.
Accession number: NC_006369; **Genome size (bp)**: 3345687.
Number of genes: 2878.
Oriloc predictions: Origin 8 kb Terminus 1622 kb
Worning et al., 2006: Origin NA kb Terminus NA kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 2894.446 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.88 kb
Consensus predictions: Origin 8 kb Terminus 1622 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	166	0.01333	349
	855	0	1652
GC-skew reverse	2095	0	1656
AT-skew forward	804	0	1570
AT-skew reverse	2220	0	1920

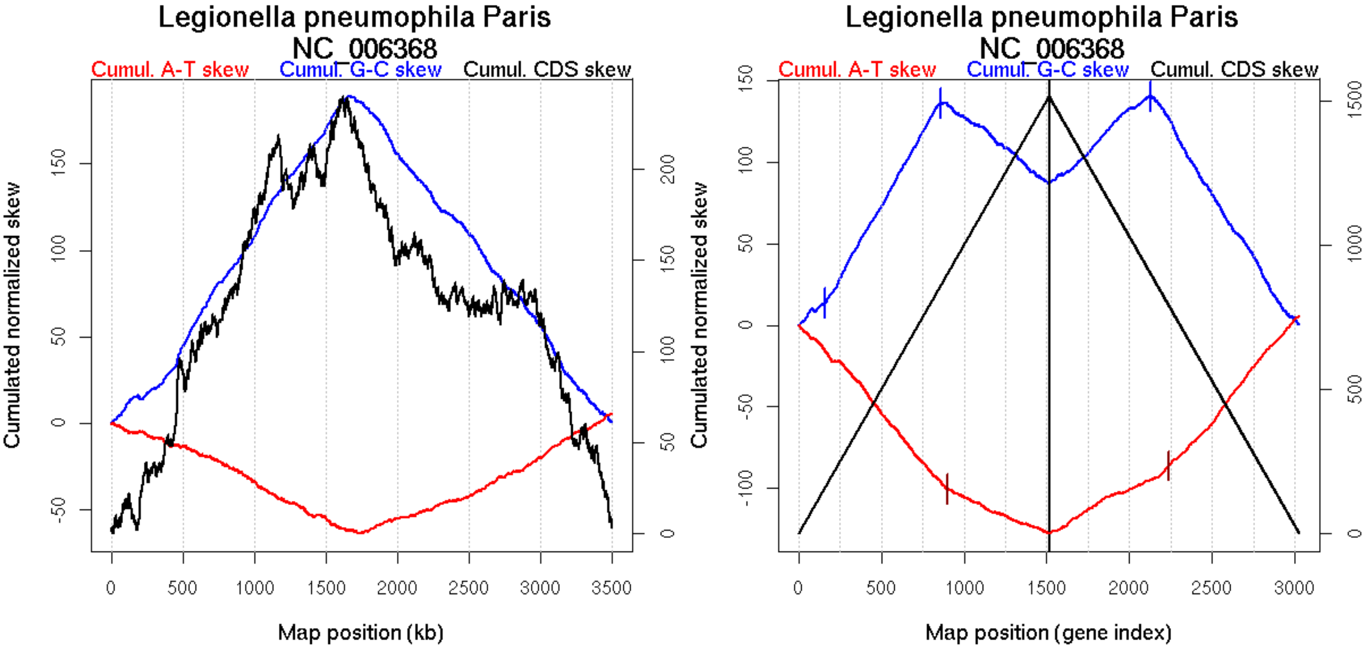
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	166 (349.323 kb)	leading	0.082
	167(350.042 kb)	855 (1652.1685 kb)	leading	0.179
	856(1653.338 kb)	1498 (3345.129 kb)	lagging	-0.073
GC-skew reverse	1499 (0 kb)	2095 (1656.323 kb)	leading	0.096
	2096(1657.352 kb)	2878 (3345.129 kb)	lagging	-0.168
AT-skew forward	1 (0 kb)	804 (1569.5595 kb)	leading	-0.116
	805(1571.673 kb)	1498 (3345.129 kb)	lagging	-0.049
AT-skew reverse	1499 (0 kb)	2220 (1919.672 kb)	NA	0.059
	2221(1920.2305 kb)	2878(3345.129 kb)	lagging	0.126

More T than A on the leading strand for replication - for forward encoded genes.
More G than C on the leading strand for replication.

169 Legionella pneumophila Paris

Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales; Legionellaceae; Legionella.
Accession number: NC_006368; **Genome size (bp)**: 3503610.
Number of genes: 3027.
Oriloc predictions: Origin 0 kb Terminus 1702 kb
Worning et al., 2006: Origin NA kb Terminus NA kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 3037.373 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.88 kb
Consensus predictions: Origin 0 kb Terminus 1702 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	159	NA	329
	859	NA	1698
GC-skew reverse	2130	NA	1665
AT-skew forward	897	NA	1836
AT-skew reverse	2237	NA	1859

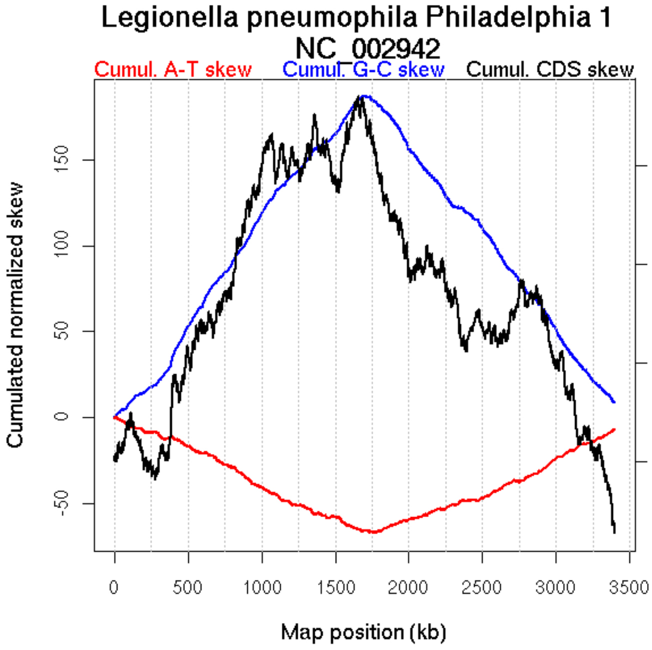
Segments:

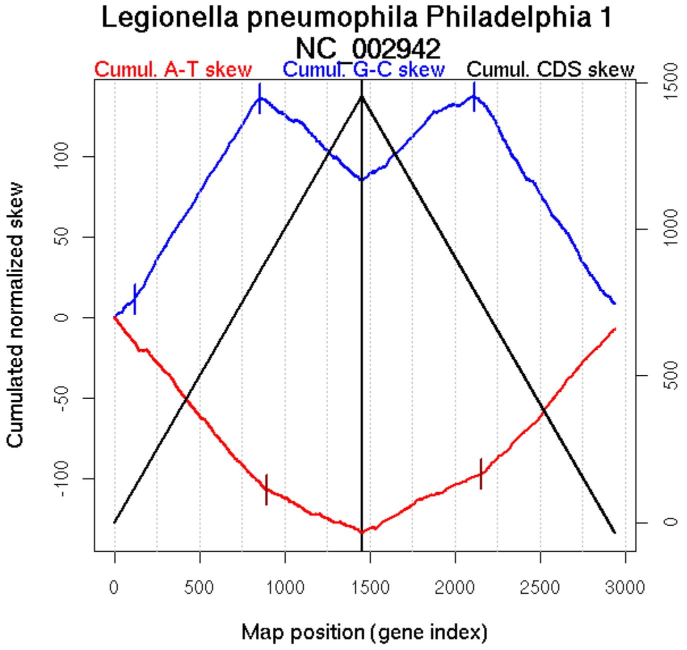
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	159 (329.259 kb)	leading	0.084
	160(331.2545 kb)	859 (1698.127 kb)	leading	0.178
	860(1699.195 kb)	1515 (3503.062 kb)	lagging	-0.078
GC-skew reverse	1516 (0 kb)	2130 (1665.302 kb)	leading	0.095
	2131(1666.756 kb)	3027 (3503.062 kb)	lagging	-0.163
AT-skew forward	1 (0 kb)	897 (1835.7645 kb)	leading	-0.115
	898(1839.9685 kb)	1515 (3503.062 kb)	lagging	-0.044
AT-skew reverse	1516 (0 kb)	2237 (1859.485 kb)	leading	0.054
	2238(1864.392 kb)	3027(3503.062 kb)	lagging	0.122

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

170 Legionella pneumophila Philadelphia 1

Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales; Legionellaceae; Legionella.
Accession number: NC_002942; **Genome size (bp)**: 3397754.
Number of genes: 2942.
Oriloc predictions: Origin 9 kb Terminus 1736 kb
Worning et al., 2006: Origin 0 kb Terminus 1692 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 2950.113 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1.33 kb, 3157.04 kb
Consensus predictions: Origin 9 kb Terminus 1736 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	120	NA	294
	852	NA	1727
GC-skew reverse	2115	NA	1695
AT-skew forward	894	NA	1886
AT-skew reverse	2158	NA	1764

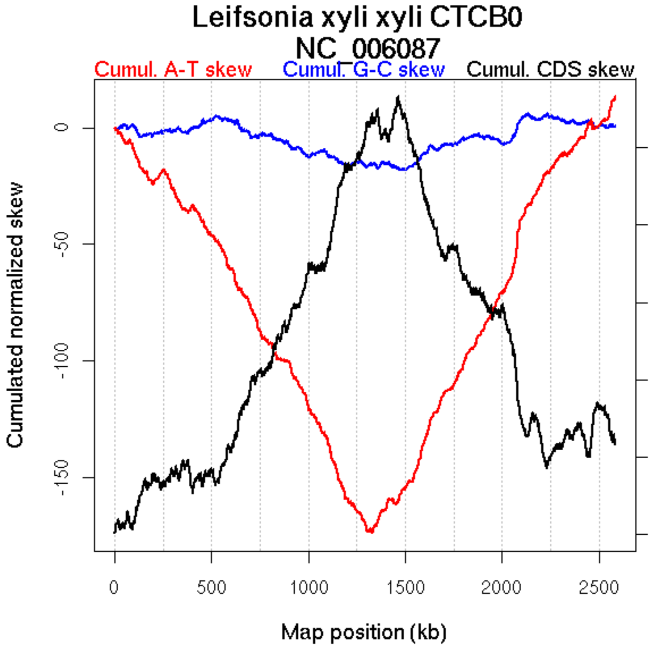
Segments:

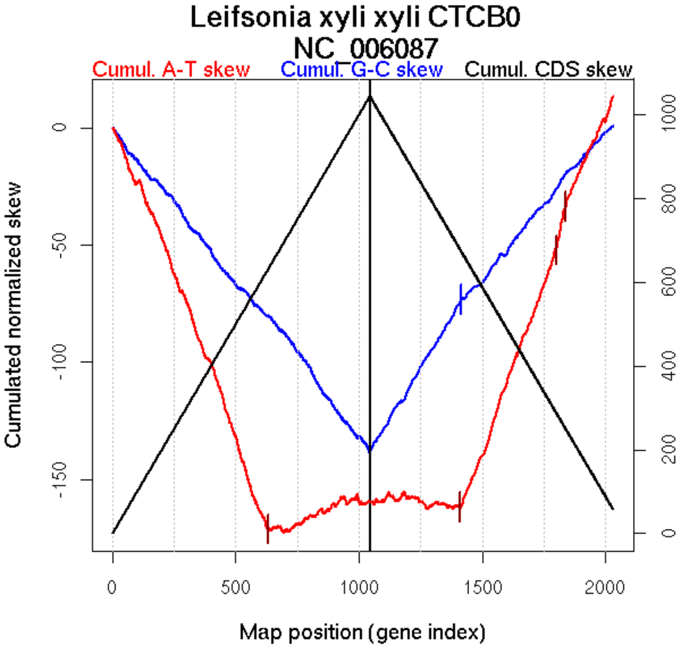
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	120 (293.8535 kb)	leading	0.094
	121(295.0025 kb)	852 (1727.19 kb)	leading	0.17
	853(1730.3415 kb)	1453 (3397.646 kb)	lagging	-0.089
GC-skew reverse	1454 (0 kb)	2115 (1694.588 kb)	leading	0.086
	2116(1696.29 kb)	2942 (3397.646 kb)	lagging	-0.163
AT-skew forward	1 (0 kb)	894 (1885.6575 kb)	leading	-0.122
	895(1889.512 kb)	1453 (3397.646 kb)	lagging	-0.047
AT-skew reverse	1454 (0 kb)	2158 (1763.6855 kb)	leading	0.053
	2159(1765.303 kb)	2942(3397.646 kb)	lagging	0.119

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

171 Leifsonia xyli xyli CTCB0

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Micrococcineae; Microbacteriaceae; Leifsonia.
Accession number: NC_006087; **Genome size (bp)**: 2584158.
Number of genes: 2030.
Oriloc predictions: Origin 30 kb Terminus 1301 kb
Worning et al., 2006: Origin 2573 kb Terminus 1329 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 17.296 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.94 kb
Consensus predictions: Origin 30 kb Terminus 1301 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew reverse	1416	0.01333	1334
AT-skew forward	629	0	1312
AT-skew reverse	1408	0	1311
	1799	0.00889	2072
	1838	0	2108

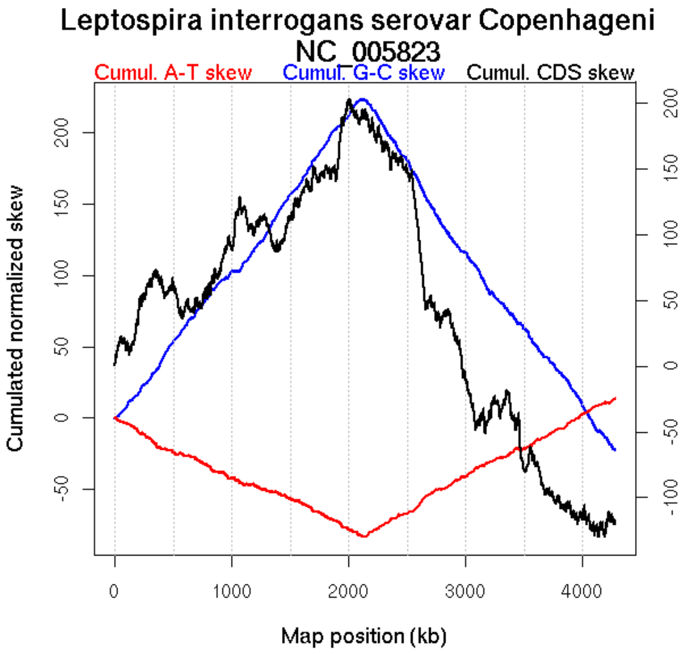
Segments:

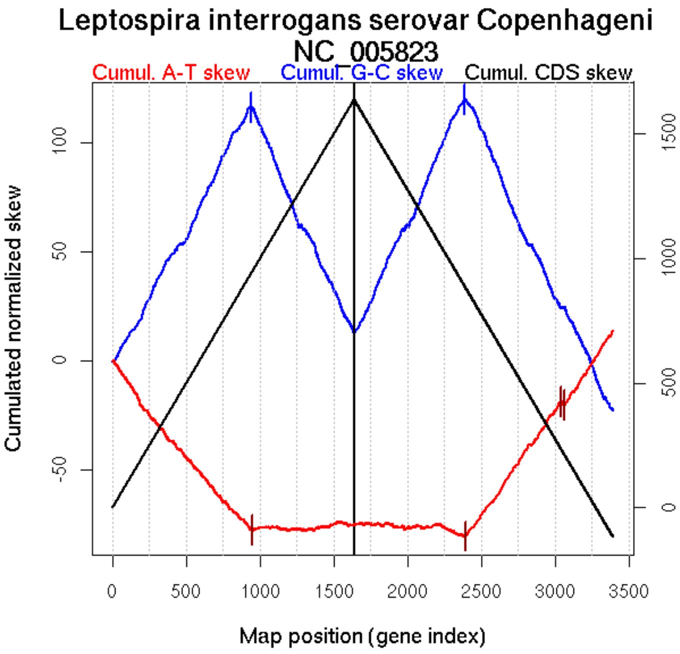
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew reverse	1045 (0 kb)	1416 (1333.8965 kb)	leading	0.173
	1417(1335.0235 kb)	2030 (2583.936 kb)	lagging	0.126
AT-skew forward	1 (0 kb)	629 (1312.3865 kb)	leading	-0.277
	630(1316.2955 kb)	1044 (2583.936 kb)	lagging	0.039
AT-skew reverse	1045 (0 kb)	1408 (1310.9005 kb)	leading	-0.01
	1409(1313.2485 kb)	1799(2071.5535 kb)	lagging	0.286
	1800(2072.037 kb)	1838(2108.4795 kb)	lagging	0.516
	1839(2112.21 kb)	2030(2583.936 kb)	lagging	0.228

More T than A on the leading strand for replication.
More G than C on the leading strand for replication - for reverse encoded genes.

172 Leptospira interrogans serovar Copenhageni

Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
Accession number: NC_005823; **Genome size (bp)**: 4277185.
Number of genes: 3394.
Oriloc predictions: Origin 0 kb Terminus 2132 kb
Worning et al., 2006: Origin 2 kb Terminus 2109 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 2510.365 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.96 kb
Consensus predictions: Origin 0 kb Terminus 2132 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	942	0	2130
GC-skew reverse	2390	0	2127
AT-skew forward	948	0	2138
AT-skew reverse	2394	0.01778	2145
	3040	0.00444	3458
	3061	0.00444	3467

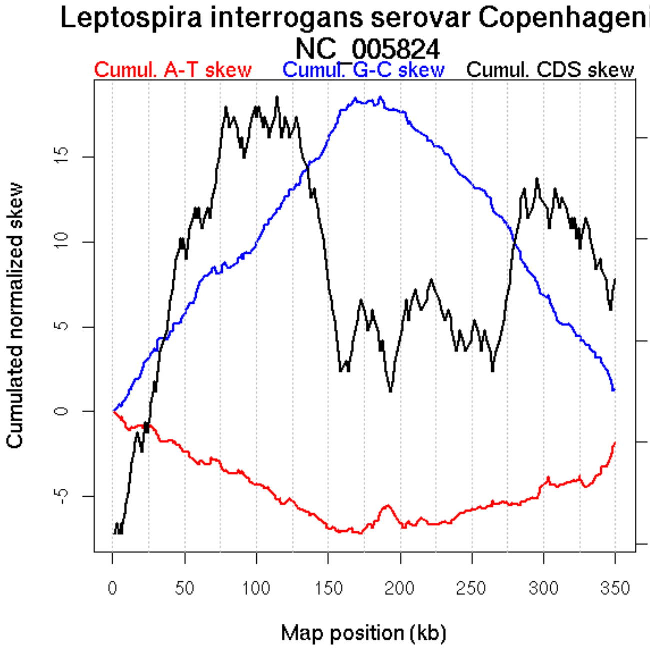
Segments:

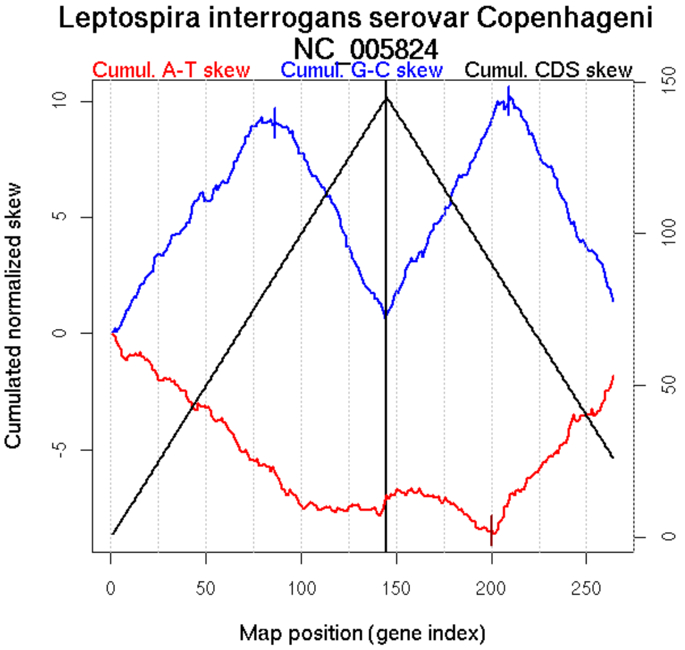
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	942 (2129.952 kb)	leading	0.127
	943(2130.3945 kb)	1638 (4277.01 kb)	lagging	-0.149
GC-skew reverse	1639 (0 kb)	2390 (2126.984 kb)	leading	0.147
	2391(2132.3645 kb)	3394 (4277.01 kb)	lagging	-0.144
AT-skew forward	1 (0 kb)	948 (2137.927 kb)	leading	-0.081
	949(2139.9205 kb)	1638 (4277.01 kb)	lagging	0.003
AT-skew reverse	1639 (0 kb)	2394 (2145.416 kb)	leading	-0.005
	2395(2147.942 kb)	3040(3457.5575 kb)	lagging	0.096
	3041(3457.8225 kb)	3061(3466.977 kb)	lagging	-0.071
	3062(3467.281 kb)	3394(4277.01 kb)	lagging	0.104

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

173 Leptospira interrogans serovar Copenhageni

Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
Accession number: NC_005824; **Genome size (bp)**: 350181.
Number of genes: 264.
Oriloc predictions: Origin 0 kb Terminus 202 kb
Worning et al., 2006: Origin 349 kb Terminus 203 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 34.642 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): NA
Consensus predictions: Origin 0 kb Terminus 202 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	86	0	195
GC-skew reverse	209	0	186
AT-skew reverse	200	0.00667	157

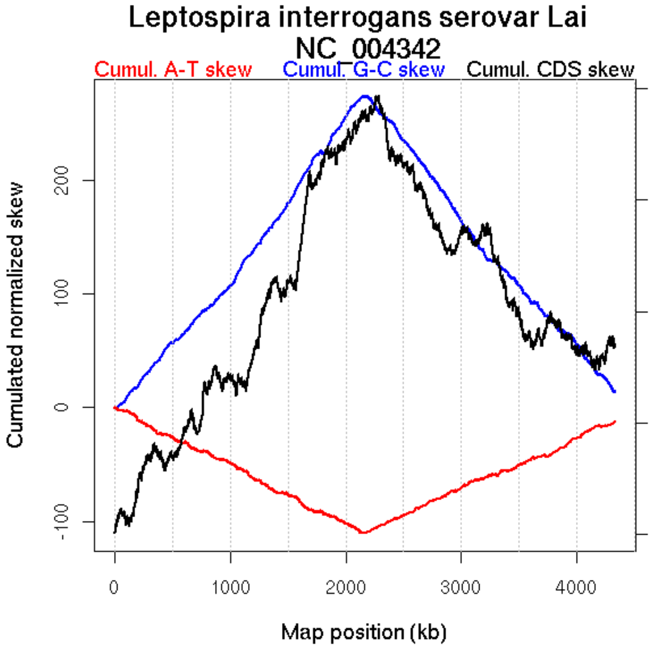
Segments:

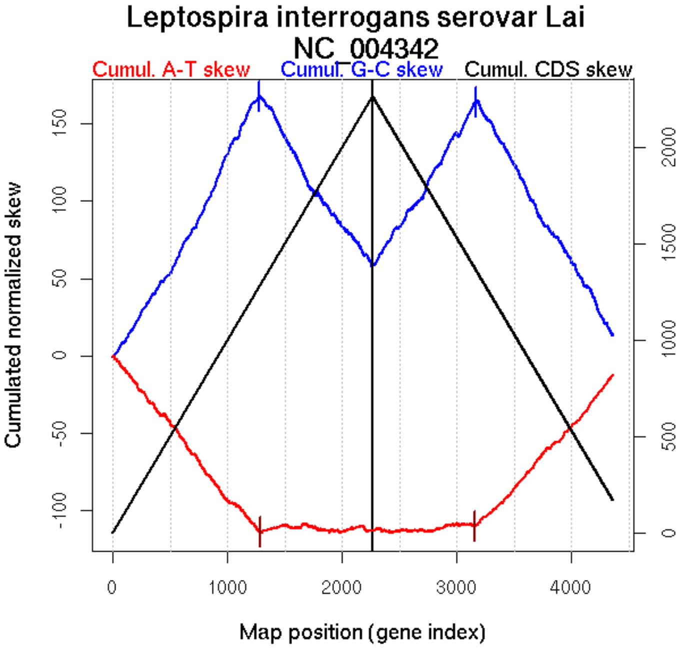
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	86 (195.3785 kb)	leading	0.111
	87(196.533 kb)	145 (350.166 kb)	lagging	-0.157
GC-skew reverse	146 (0 kb)	209 (185.9485 kb)	leading	0.147
	210(187.303 kb)	264 (350.166 kb)	lagging	-0.16
AT-skew reverse	146 (0 kb)	200 (157.1175 kb)	leading	-0.034
	201(158.09 kb)	264(350.166 kb)	NA	0.095

More G than C on the leading strand for replication.

174 Leptospira interrogans serovar Lai

Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
Accession number: NC_004342; **Genome size (bp)**: 4332241.
Number of genes: 4360.
Oriloc predictions: Origin 0 kb Terminus 2139 kb
Worning et al., 2006: Origin 4332 kb Terminus 2143 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1719.777 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.9 kb
Consensus predictions: Origin 0 kb Terminus 2139 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1280	NA	2156
GC-skew reverse	3169	NA	2161
AT-skew forward	1287	NA	2179
AT-skew reverse	3156	NA	2123

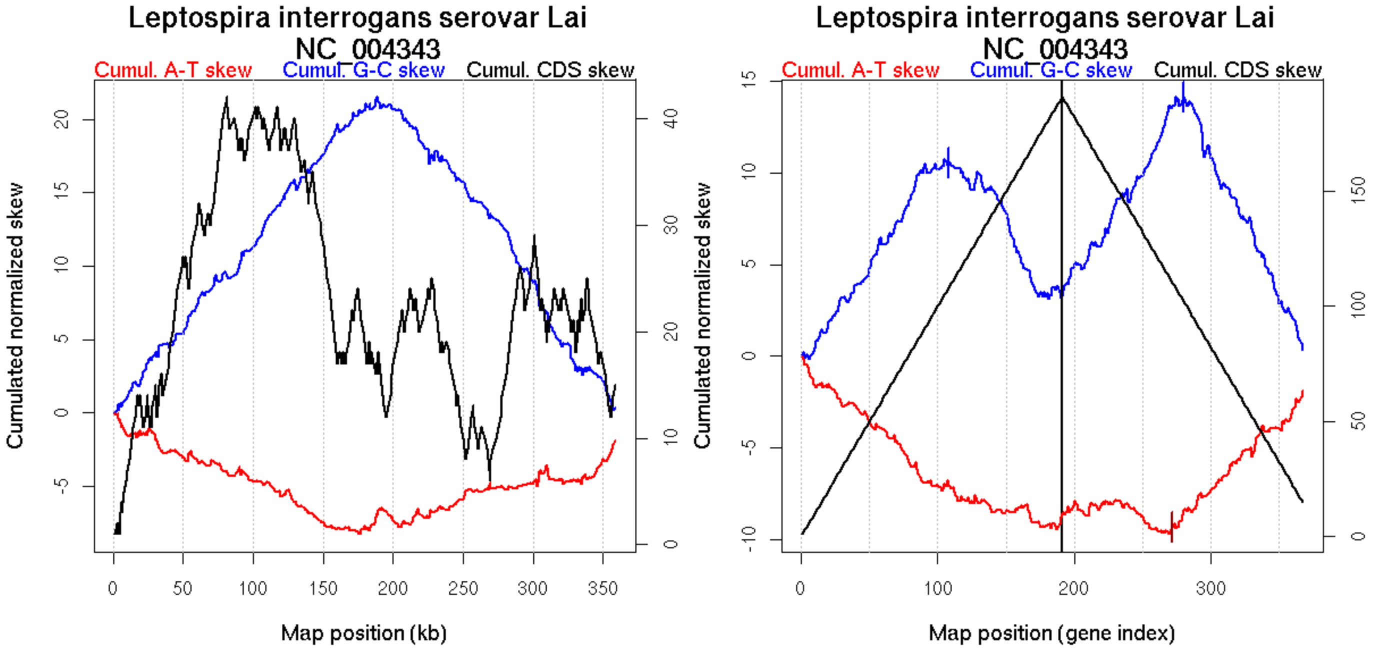
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1280 (2156.334 kb)	leading	0.136
	1281(2157.7455 kb)	2265 (4332.008 kb)	lagging	-0.113
GC-skew reverse	2266 (0 kb)	3169 (2161.46 kb)	leading	0.118
	3170(2168.856 kb)	4360 (4332.008 kb)	lagging	-0.127
AT-skew forward	1 (0 kb)	1287 (2179.2125 kb)	leading	-0.091
	1288(2181.025 kb)	2265 (4332.008 kb)	lagging	-0.001
AT-skew reverse	2266 (0 kb)	3156 (2123.4545 kb)	leading	0.005
	3157(2125.1305 kb)	4360(4332.008 kb)	lagging	0.081

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

175 Leptospira interrogans serovar Lai

Bacteria; Spirochaetes; Spirochaetales; Leptospiraceae; Leptospira.
Accession number: NC_004343; **Genome size (bp)**: 358943.
Number of genes: 367.
Oriloc predictions: Origin 0 kb Terminus 205 kb
Worning et al., 2006: Origin 357 kb Terminus 205 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 36.073 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): NA
Consensus predictions: Origin 0 kb Terminus 205 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	108	NA	197
GC-skew reverse	280	NA	189
AT-skew reverse	272	NA	179

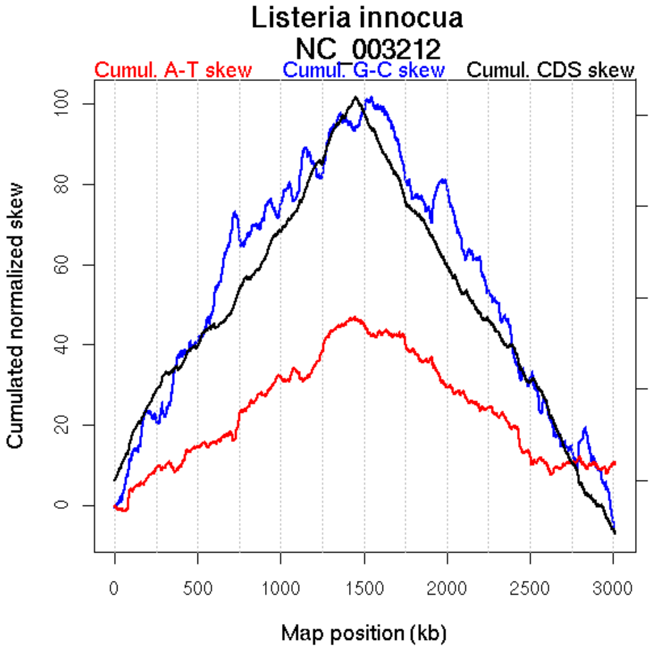
Segments:

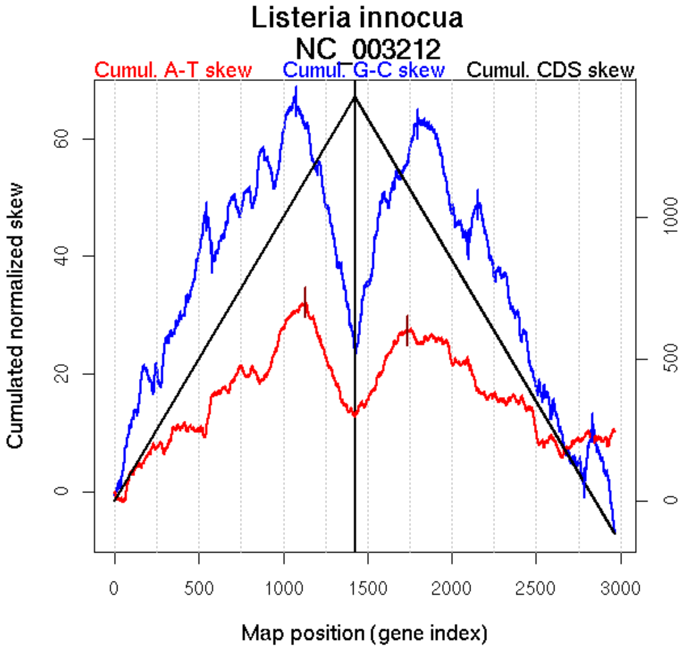
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	108 (197.1905 kb)	leading	0.111
	109(198.324 kb)	191 (358.928 kb)	lagging	-0.107
GC-skew reverse	192 (0 kb)	280 (189.115 kb)	leading	0.121
	281(190.3705 kb)	367 (358.928 kb)	lagging	-0.154
AT-skew reverse	192 (0 kb)	272 (178.8635 kb)	leading	-0.017
	273(180.0935 kb)	367(358.928 kb)	lagging	0.073

More T than A on the leading strand for replication - for reverse encoded genes.
More G than C on the leading strand for replication.

176 Listeria innocua

Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
Accession number: NC_003212; **Genome size (bp)**: 3011208.
Number of genes: 2967.
Oriloc predictions: Origin 0 kb Terminus 1419 kb
Worning et al., 2006: Origin 5 kb Terminus 1445 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1.725 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1 kb, 1603.59 kb
Consensus predictions: Origin 0 kb Terminus 1419 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	544	0	728
	582	0	768
	1074	0.00667	1366
GC-skew reverse	1796	0.02933	1533
	2100	0.00933	1914
	2151	0.012	1973
	2788	0.00667	2787
	2830	0.00533	2825
AT-skew forward	1132	0.00667	1442
AT-skew reverse	1735	0	1464

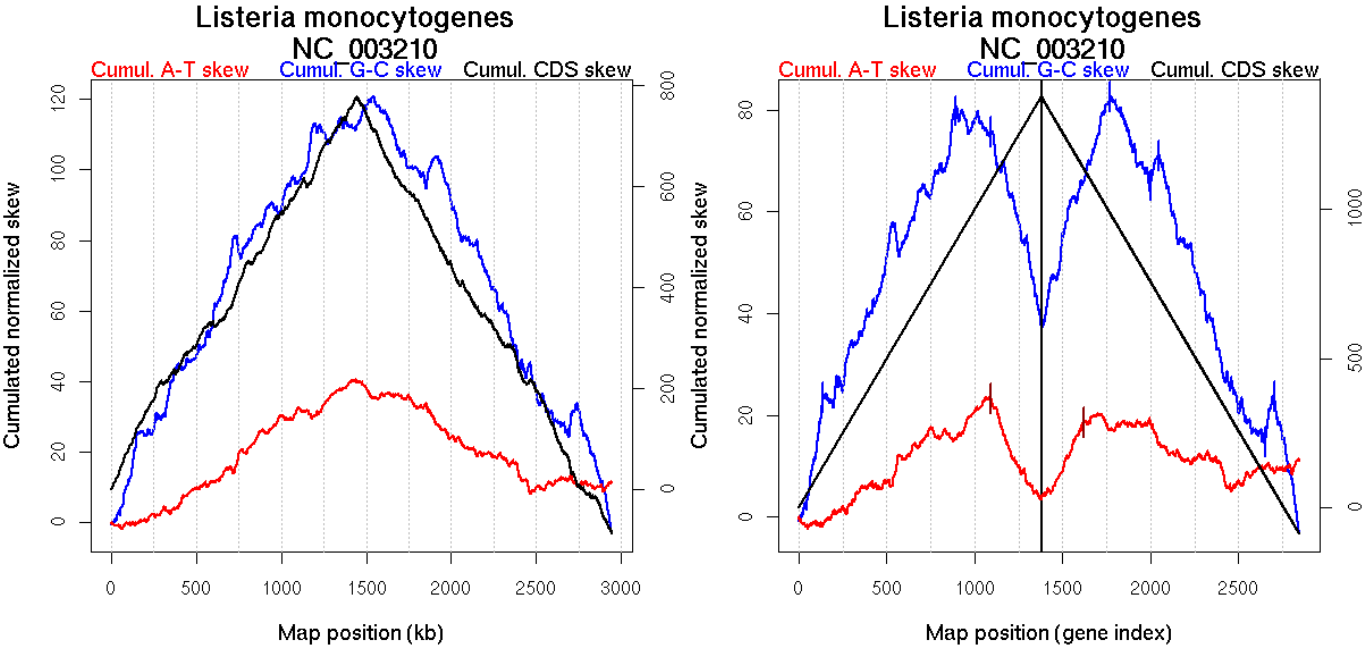
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	544 (727.876 kb)	leading	0.074
	545(728.3035 kb)	582 (767.6665 kb)	leading	-0.231
	583(768.346 kb)	1074 (1365.547 kb)	leading	0.047
	1075(1366.0085 kb)	1425 (3011.02 kb)	lagging	-0.119
GC-skew reverse	1426 (0 kb)	1796 (1532.541 kb)	NA	0.097
	1797(1533.204 kb)	2100 (1913.931 kb)	lagging	-0.084
	2101(1914.456 kb)	2151 (1973.41 kb)	lagging	0.141
	2152(1974.6145 kb)	2788 (2787.29 kb)	lagging	-0.074
	2789(2788.056 kb)	2830 (2824.8665 kb)	lagging	0.196
	2831(2825.541 kb)	2967 (3011.02 kb)	lagging	-0.12
AT-skew forward	1 (0 kb)	1132 (1442.3505 kb)	leading	0.027
	1133(1444.8335 kb)	1425 (3011.02 kb)	lagging	-0.07
AT-skew reverse	1426 (0 kb)	1735 (1464.4445 kb)	leading	0.052
	1736(1465.6445 kb)	2967(3011.02 kb)	lagging	-0.018

More A than T on the leading strand for replication.
More G than C on the leading strand for replication - for forward encoded genes.

177 Listeria monocytogenes

Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
Accession number: NC_003210; **Genome size (bp)**: 2944528.
Number of genes: 2846.
Oriloc predictions: Origin 0 kb Terminus 1485 kb
Worning et al., 2006: Origin 4 kb Terminus 1441 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1.724 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1 kb, 1599.12 kb
Consensus predictions: Origin 0 kb Terminus 1485 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	139	NA	153
	888	NA	1190
	1093	NA	1453
GC-skew reverse	1770	NA	1534
	2002	NA	1861
	2046	NA	1914
	2651	NA	2695
	2703	NA	2743
AT-skew forward	1089	NA	1441
AT-skew reverse	1619	NA	1136

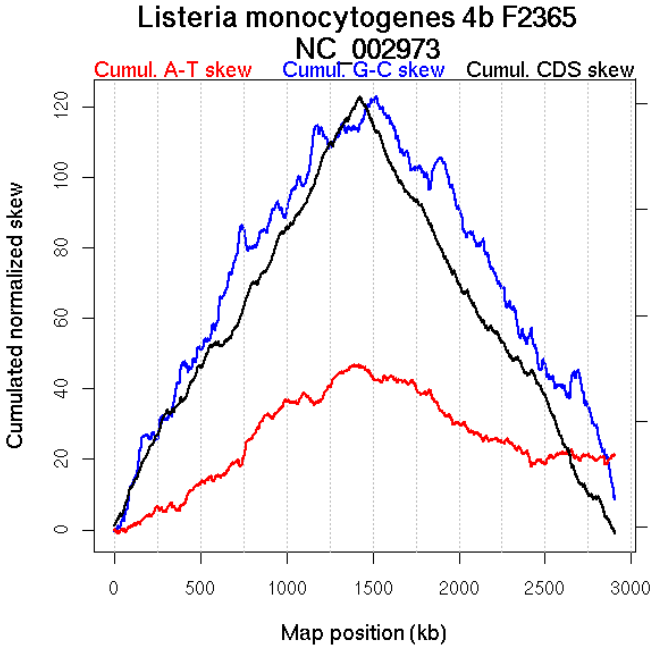
Segments:

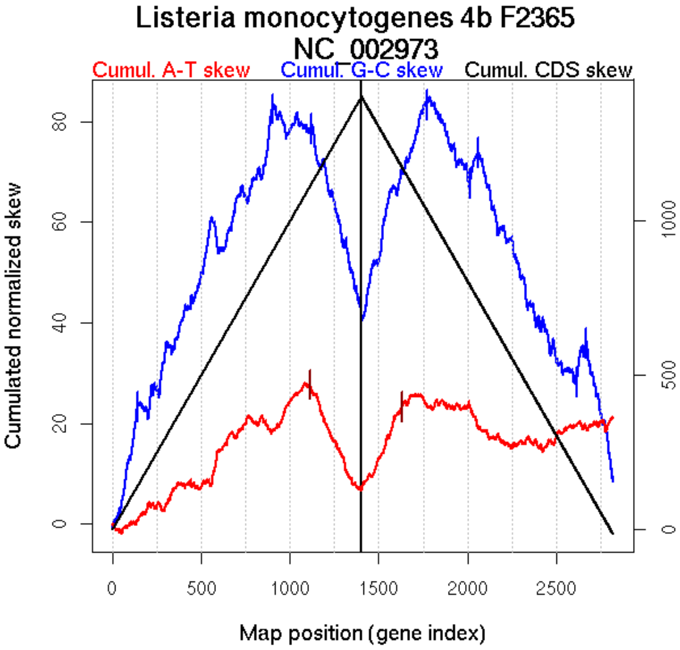
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	139 (153.125 kb)	leading	0.178
	140(155.9685 kb)	888 (1189.785 kb)	leading	0.074
	889(1190.265 kb)	1093 (1452.796 kb)	leading	-0.018
	1094(1458.0865 kb)	1379 (2944.341 kb)	lagging	-0.123
GC-skew reverse	1380 (0 kb)	1770 (1534.315 kb)	leading	0.113
	1771(1536.545 kb)	2002 (1861.227 kb)	lagging	-0.08
	2003(1863.2735 kb)	2046 (1914.0045 kb)	lagging	0.124
	2047(1914.998 kb)	2651 (2694.7915 kb)	lagging	-0.097
	2652(2695.7715 kb)	2703 (2742.5145 kb)	lagging	0.178
	2704(2743.9515 kb)	2846 (2944.341 kb)	lagging	-0.174
AT-skew forward	1 (0 kb)	1089 (1441.303 kb)	leading	0.024
	1090(1441.559 kb)	1379 (2944.341 kb)	lagging	-0.069
AT-skew reverse	1380 (0 kb)	1619 (1136.1715 kb)	leading	0.066
	1620(1138.225 kb)	2846(2944.341 kb)	lagging	-0.011

More A than T on the leading strand for replication.
More G than C on the leading strand for replication.

178 Listeria monocytogenes 4b F2365

Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
Accession number: NC_002973; **Genome size (bp)**: 2905187.
Number of genes: 2820.
Oriloc predictions: Origin 0 kb Terminus 1464 kb
Worning et al., 2006: Origin 0 kb Terminus 1434 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1.725 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1 kb
Consensus predictions: Origin 0 kb Terminus 1464 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	141	NA	159
	905	NA	1168
	1120	NA	1454
GC-skew reverse	1773	NA	1506
	2016	NA	1840
	2061	NA	1893
	2613	NA	2643
	2668	NA	2692
AT-skew forward	1111	NA	1419
AT-skew reverse	1632	NA	1073

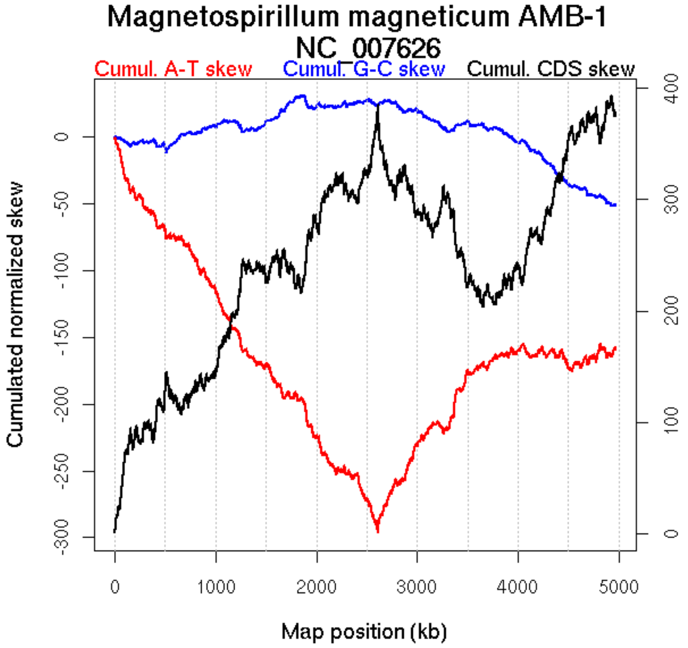
Segments:

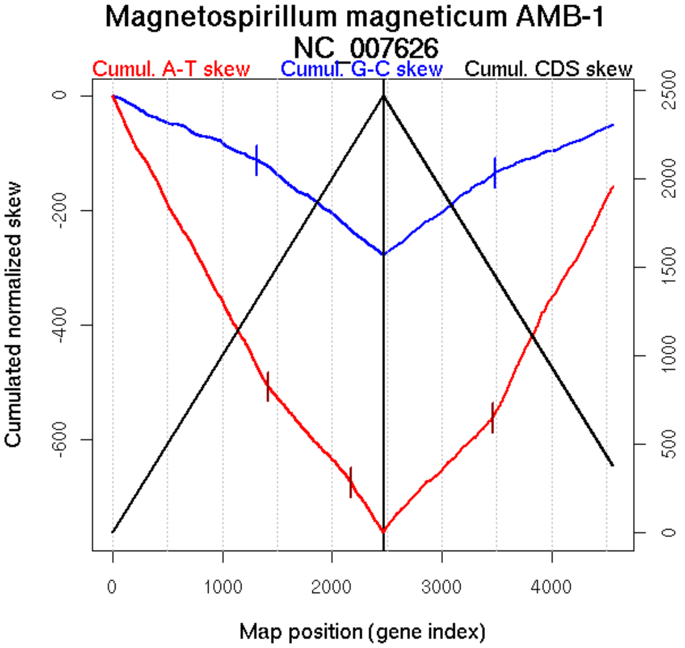
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	141 (158.736 kb)	leading	0.17
	142(160.689 kb)	905 (1167.717 kb)	leading	0.074
	906(1168.565 kb)	1120 (1454.4445 kb)	leading	-0.014
	1121(1455.6245 kb)	1403 (2905 kb)	lagging	-0.127
GC-skew reverse	1404 (0 kb)	1773 (1506.3955 kb)	leading	0.114
	1774(1507.0375 kb)	2016 (1840.4645 kb)	lagging	-0.072
	2017(1841.418 kb)	2061 (1893.3795 kb)	lagging	0.118
	2062(1894.373 kb)	2613 (2643.3295 kb)	lagging	-0.083
	2614(2644.3095 kb)	2668 (2692.1045 kb)	lagging	0.123
	2669(2692.82 kb)	2820 (2905 kb)	lagging	-0.165
AT-skew forward	1 (0 kb)	1111 (1418.781 kb)	leading	0.027
	1112(1420.398 kb)	1403 (2905 kb)	lagging	-0.077
AT-skew reverse	1404 (0 kb)	1632 (1073.4455 kb)	leading	0.075
	1633(1076.7195 kb)	2820(2905 kb)	lagging	-0.006

More A than T on the leading strand for replication.
More G than C on the leading strand for replication.

179 Magnetospirillum magneticum AMB-1

Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales; Rhodospirillaceae; Magnetospirillum.
Accession number: NC_007626; **Genome size (bp)**: 4967148.
Number of genes: 4559.
Oriloc predictions: Origin 0 kb Terminus 2611 kb
Worning et al., 2006: Origin 157 kb Terminus 2611 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 4958.066 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 3044.8 kb
Consensus predictions: Origin 0 kb Terminus 2611 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1317	0	2513
GC-skew reverse	3486	0	2611
AT-skew forward	1420	0.01333	2690
	2171	0.03333	4434
AT-skew reverse	3464	0	2522

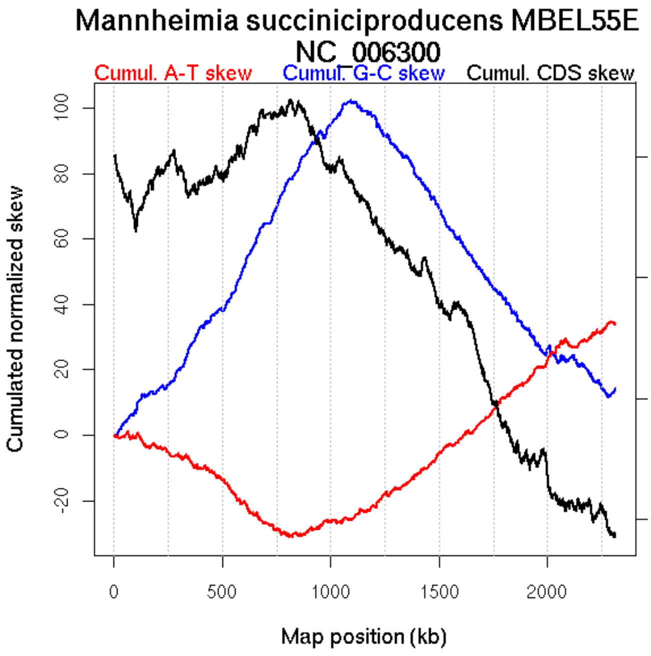
Segments:

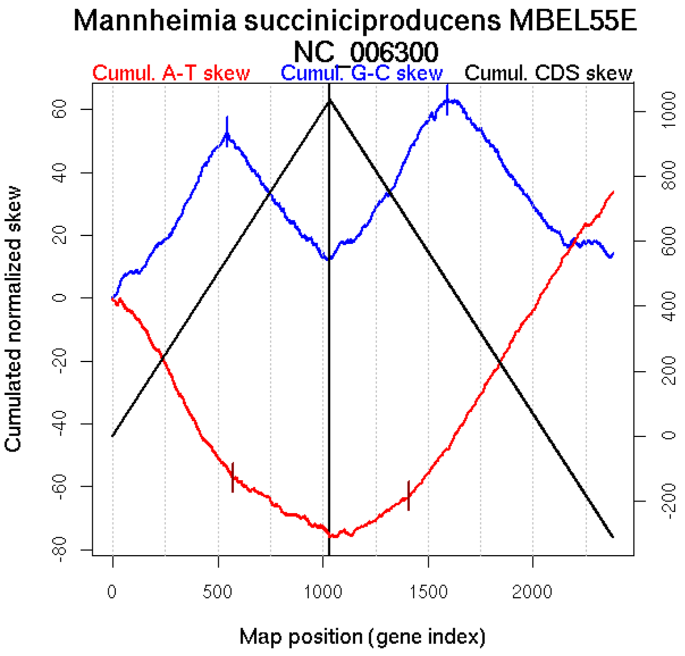
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1317 (2512.911 kb)	leading	-0.083
	1318(2514.1815 kb)	2468 (4967.145 kb)	lagging	-0.145
GC-skew reverse	2469 (0 kb)	3486 (2610.5265 kb)	leading	0.142
	3487(2611.3545 kb)	4559 (4967.145 kb)	lagging	0.075
AT-skew forward	1 (0 kb)	1420 (2690.2615 kb)	leading	-0.352
	1421(2691.626 kb)	2171 (4433.581 kb)	lagging	-0.217
	2172(4434.667 kb)	2468 (4967.145 kb)	lagging	-0.293
AT-skew reverse	2469 (0 kb)	3464 (2522.4585 kb)	leading	0.192
	3465(2528.039 kb)	4559(4967.145 kb)	lagging	0.362

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

180 Mannheimia succiniciproducens MBEL55E

Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Mannheimia
Accession number: NC_006300; **Genome size (bp)**: 2314078.
Number of genes: 2380.
Oriloc predictions: Origin 2280 kb Terminus 1079 kb
Worning et al., 2006: Origin 2303 kb Terminus 1052 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 376.717 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 448.65 kb
Consensus predictions: Origin 2280 kb Terminus 1079 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	544	0	1094
GC-skew reverse	1595	0	1087
AT-skew forward	574	0	1201
AT-skew reverse	1411	0	763

Segments:

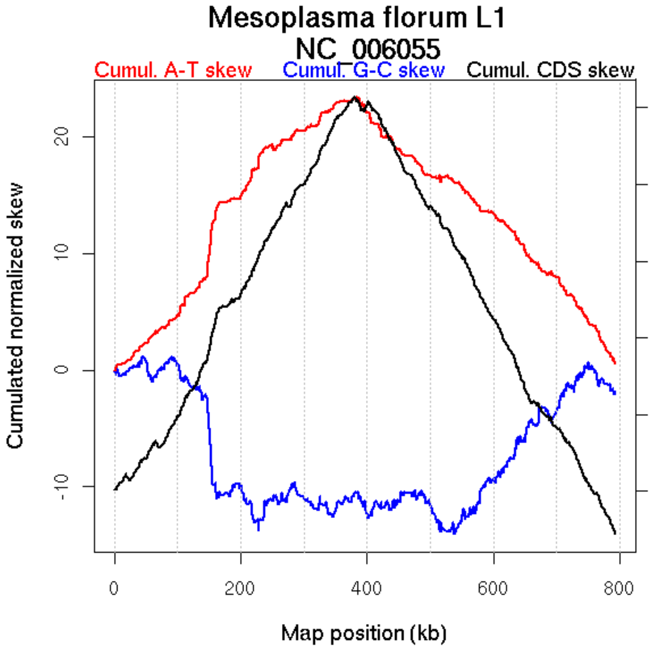
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	544 (1093.6305 kb)	leading	0.097
	545(1093.8035 kb)	1034 (2312.04 kb)	lagging	-0.084
GC-skew reverse	1035 (0 kb)	1595 (1087.3555 kb)	leading	0.099
	1596(1088.5005 kb)	2380 (2312.04 kb)	lagging	-0.071
AT-skew forward	1 (0 kb)	574 (1201.0155 kb)	leading	-0.11
	575(1202.9305 kb)	1034 (2312.04 kb)	lagging	-0.038
AT-skew reverse	1035 (0 kb)	1411 (762.6655 kb)	leading	0.036
	1412(766.1335 kb)	2380(2312.04 kb)	NA	0.104

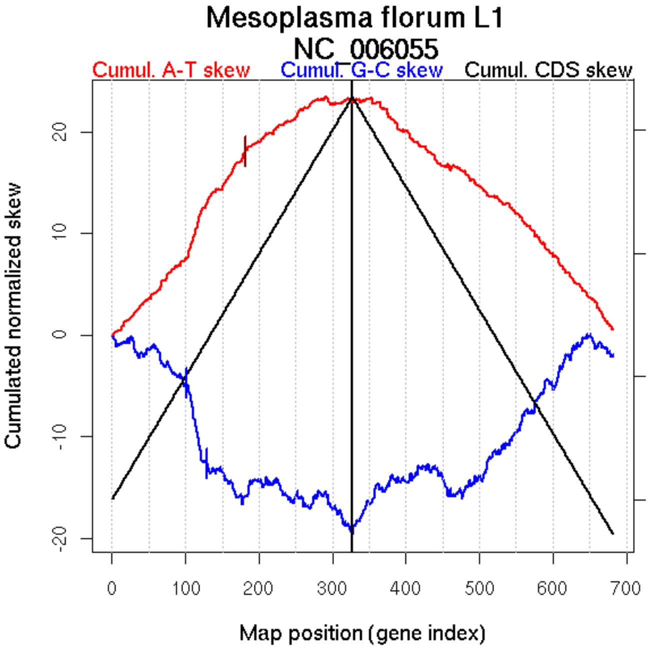
More T than A on the leading strand for replication - for forward encoded genes.

More G than C on the leading strand for replication.

181 Mesoplasma florum L1

Bacteria; Firmicutes; Mollicutes; Entomoplasmatales; Entomoplasmataceae; Mesoplasma.
Accession number: NC_006055; **Genome size (bp)**: 793224.
Number of genes: 682.
Oriloc predictions: Origin 0 kb Terminus 382 kb
Worning et al., 2006: Origin 0 kb Terminus 380 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 793.162 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.67 kb, 674.5 kb
Consensus predictions: Origin 0 kb Terminus 382 kb





Significant breakpoints (p-value <0.05):

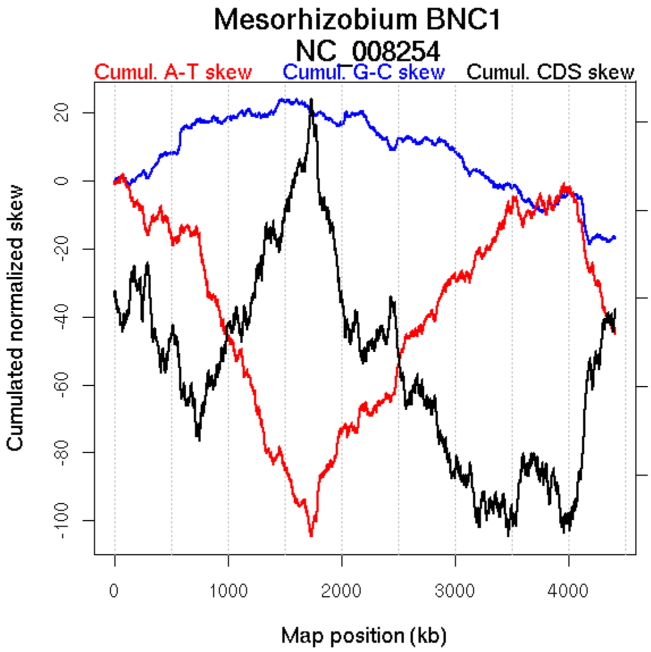
	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	101	0.00333	144
	129	0.00333	160
AT-skew forward	181	0.01333	232

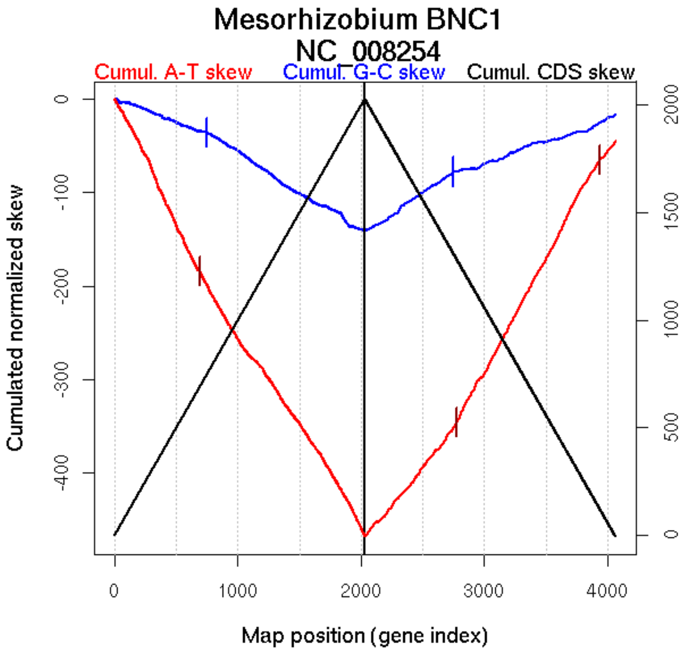
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	101 (143.6085 kb)	leading	-0.042
	102(146.028 kb)	129 (160.0735 kb)	leading	-0.328
	130(160.479 kb)	327 (792.924 kb)	NA	-0.021
AT-skew forward	1 (0 kb)	181 (231.5785 kb)	leading	0.105
	182(233.171 kb)	327 (792.924 kb)	NA	0.037

182 Mesorhizobium BNC1

Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Phyllobacteriaceae; Mesorhizobium.
Accession number: NC_008254; **Genome size (bp)**: 4412446.
Number of genes: 4064.
Oriloc predictions: Origin 3754 kb Terminus 1735 kb
Worning et al., 2006: Origin NA kb Terminus NA kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 3755.327 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.8 kb, 967.02 kb
Consensus predictions: Origin 3754 kb Terminus 1735 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	745	0	1540
GC-skew reverse	2750	0	1646
AT-skew forward	690	0	1456
AT-skew reverse	2778	0.01	1742
	3938	0.01	4035

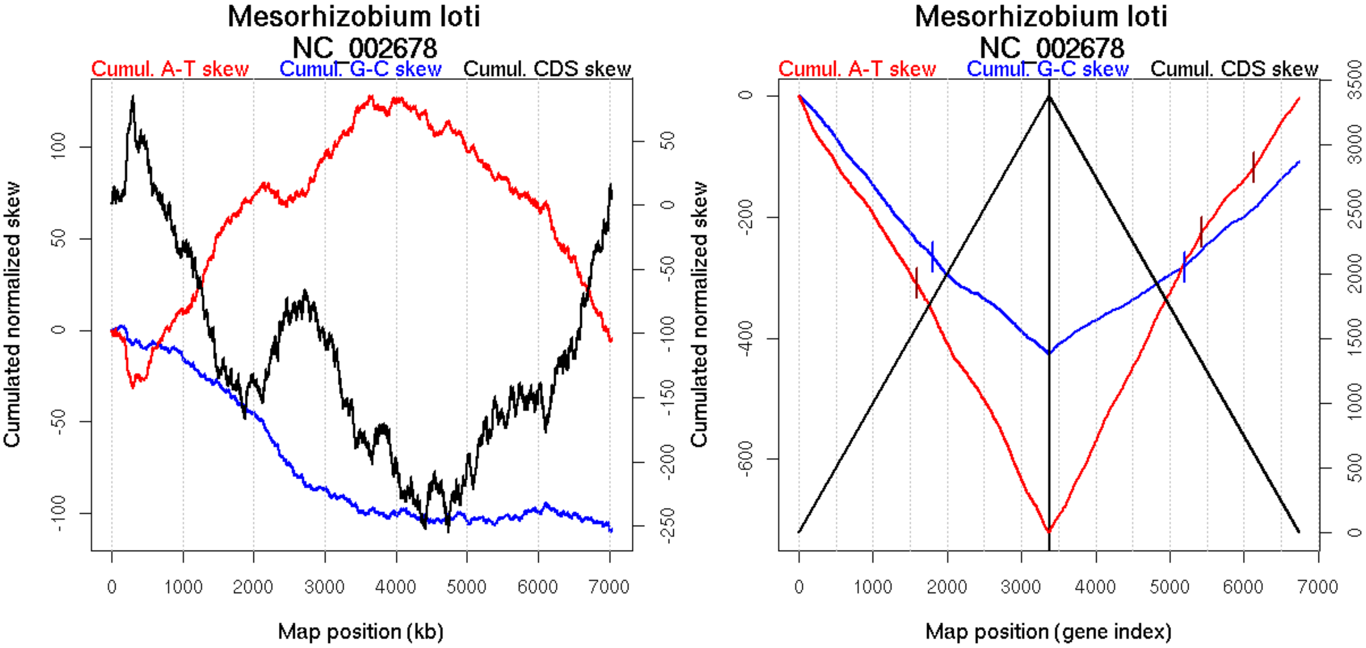
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	745 (1540.292 kb)	leading	-0.051
	746(1540.983 kb)	2029 (4411.662 kb)	NA	-0.084
GC-skew reverse	2030 (0 kb)	2750 (1645.506 kb)	leading	0.091
	2751(1646.596 kb)	4064 (4411.662 kb)	NA	0.046
AT-skew forward	1 (0 kb)	690 (1456.279 kb)	leading	-0.279
	691(1456.612 kb)	2029 (4411.662 kb)	NA	-0.199
AT-skew reverse	2030 (0 kb)	2778 (1741.6505 kb)	leading	0.162
	2779(1743.1055 kb)	3938(4035.232 kb)	lagging	0.245
	3939(4036.1585 kb)	4064(4411.662 kb)	leading	0.16

More T than A on the leading strand for replication - for reverse encoded genes.

183 Mesorhizobium loti

Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Phyllobacteriaceae; Mesorhizobium.
Accession number: NC_002678; **Genome size (bp)**: 7036071.
Number of genes: 6743.
Oriloc predictions: Origin NA Terminus NA
Worning et al., 2006: Origin 4738 kb Terminus 299 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 4479.559 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 4478.17 kb
Consensus predictions: Origin 4479 kb Terminus 146 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1810	NA	3930
GC-skew reverse	5195	NA	3578
AT-skew forward	1584	NA	3466
AT-skew reverse	5431	NA	4021
	6137	NA	5646

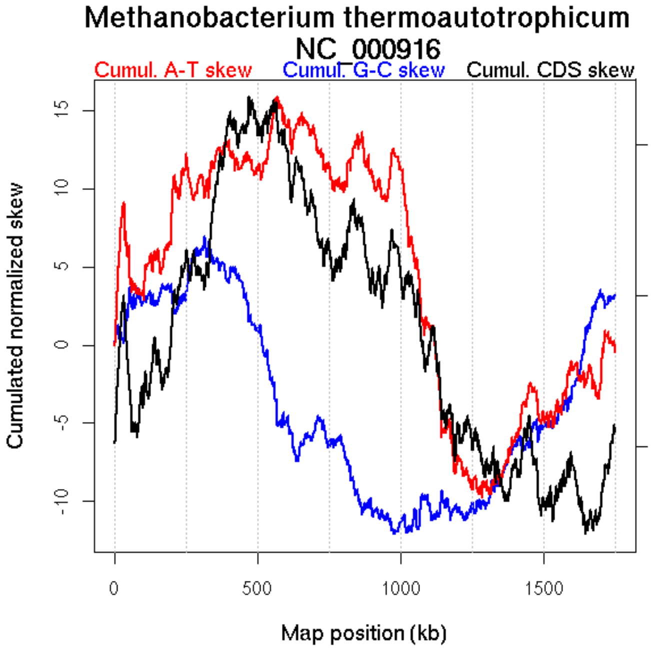
Segments:

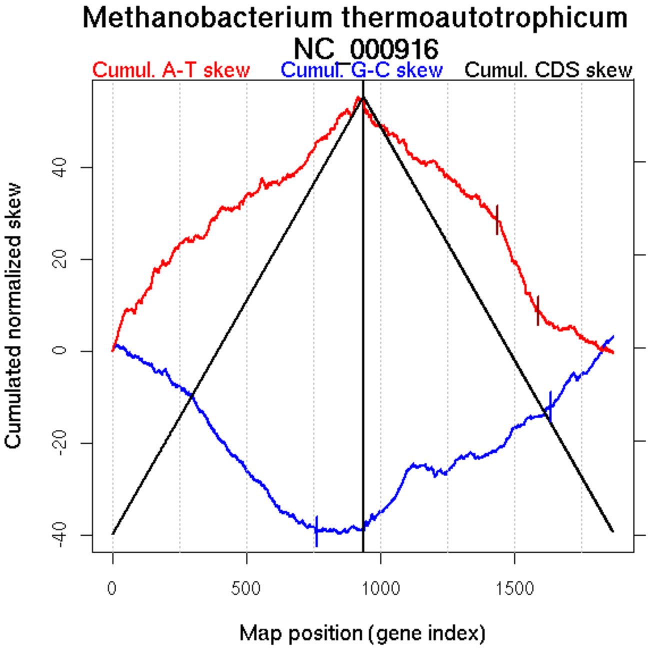
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1810 (3929.915 kb)	lagging	-0.153
	1811(3933.237 kb)	3374 (7035.848 kb)	NA	-0.096
GC-skew reverse	3375 (0 kb)	5195 (3577.8155 kb)	lagging	0.075
	5196(3579.008 kb)	6743 (7035.848 kb)	NA	0.108
AT-skew forward	1 (0 kb)	1584 (3465.658 kb)	lagging	-0.185
	1585(3467.7155 kb)	3374 (7035.848 kb)	NA	-0.227
AT-skew reverse	3375 (0 kb)	5431 (4020.913 kb)	lagging	0.245
	5432(4022.98 kb)	6137(5646.0345 kb)	NA	0.148
	6138(5647.274 kb)	6743(7035.848 kb)	leading	0.19

More T than A on the leading strand for replication - for reverse encoded genes.

184 Methanobacterium thermoautotrophicum

Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales; Methanobacteriaceae; Methanothermobacter.
Accession number: NC_000916; **Genome size (bp)**: 1751377.
Number of genes: 1870.
Oriloc predictions: Origin NA Terminus NA
Worning et al., 2006: Origin 1292 kb Terminus 404 kb
Position(s) of the ORC/Cdc6 gene(s): NA
Consensus predictions: Origin 1284 kb Terminus 566 kb





Significant breakpoints (p-value <0.05):

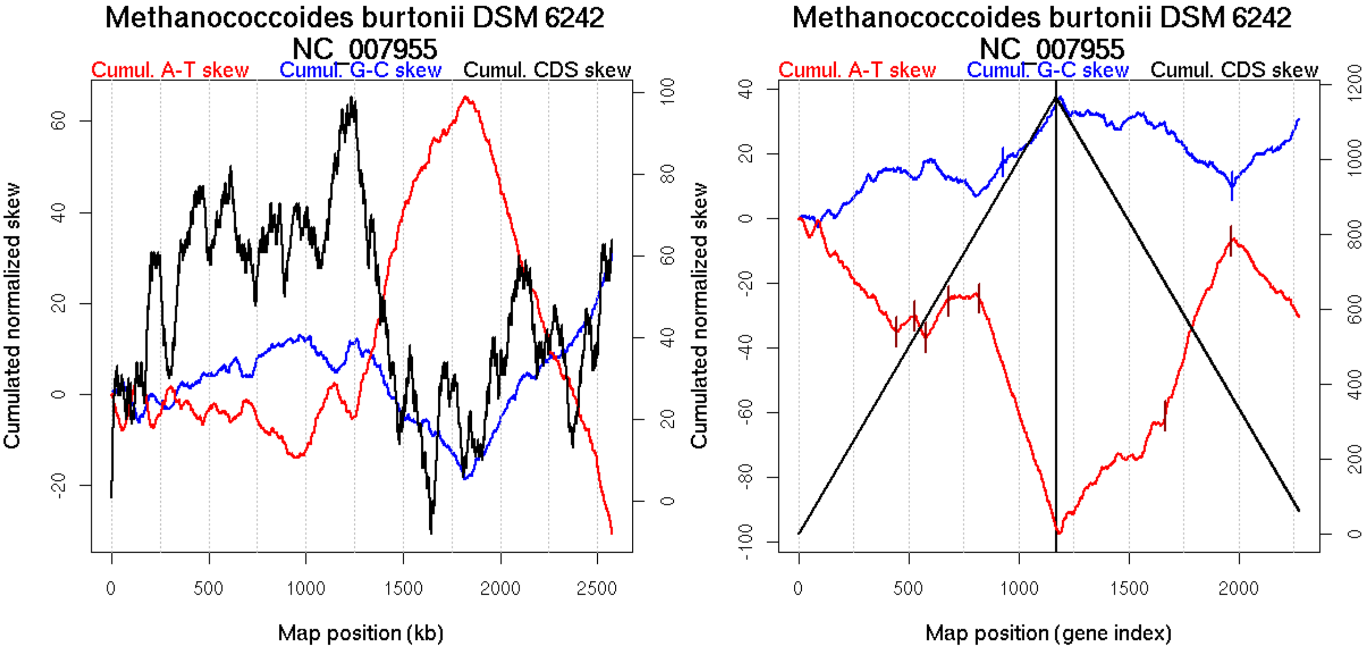
	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	763	0.00667	1428
GC-skew reverse	1639	0.03333	1293
AT-skew reverse	1436	0.02	996
	1591	0.01333	1207

Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	763 (1428.025 kb)	NA	-0.06
	764(1428.4165 kb)	938 (1751.364 kb)	leading	0.002
GC-skew reverse	939 (0 kb)	1639 (1292.5295 kb)	NA	0.032
	1640(1294.461 kb)	1870 (1751.364 kb)	leading	0.061
AT-skew reverse	939 (0 kb)	1436 (995.5585 kb)	NA	-0.045
	1437(996.241 kb)	1591(1206.6835 kb)	lagging	-0.135
	1592(1207.262 kb)	1870(1751.364 kb)	leading	-0.029

185 Methanococcoides burtonii DSM 6242

Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales; Methanosarcinaceae; Methanococcoides.
Accession number: NC_007955; **Genome size (bp)**: 2575032.
Number of genes: 2273.
Oriloc predictions: Origin 1820 kb Terminus 0 kb
Worning et al., 2006: Origin 1835 kb Terminus 55 kb
Position(s) of the ORC/Cdc6 gene(s): NA
Consensus predictions: Origin 1820 kb Terminus 0 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	929	0.00667	2057
GC-skew reverse	1969	0.01333	1850
AT-skew forward	443	0.00933	957
	528	0.00267	1147
	577	0	1250
	679	0.03067	1524
	821	0.00267	1848
AT-skew reverse	1665	0.02	1272
	1965	0	1828

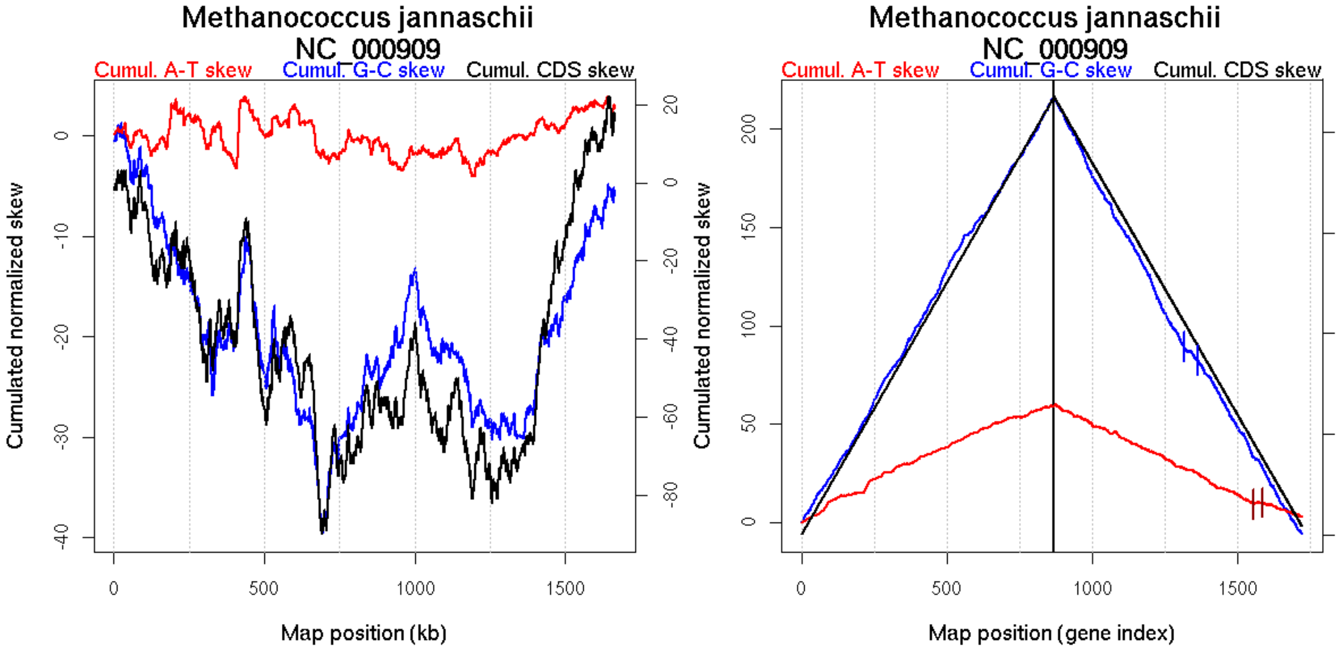
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	929 (2056.7765 kb)	lagging	0.014
	930(2059.6705 kb)	1168 (2574.796 kb)	leading	0.071
GC-skew reverse	1169 (0 kb)	1969 (1849.5445 kb)	lagging	-0.027
	1970(1850.5905 kb)	2273 (2574.796 kb)	leading	0.053
AT-skew forward	1 (0 kb)	443 (957.2505 kb)	lagging	-0.08
	444(961.6575 kb)	528 (1147.4695 kb)	lagging	0.062
	529(1149.0865 kb)	577 (1250.4995 kb)	lagging	-0.154
	578(1251.43 kb)	679 (1523.6625 kb)	lagging	0.125
	680(1526.353 kb)	821 (1847.54 kb)	lagging	0.005
	822(1852.2635 kb)	1168 (2574.796 kb)	leading	-0.202
AT-skew reverse	1169 (0 kb)	1665 (1272.164 kb)	lagging	0.065
	1666(1273.2755 kb)	1965(1828.394 kb)	lagging	0.182
	1966(1838.198 kb)	2273(2574.796 kb)	leading	-0.078

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

186 Methanococcus jannaschii

Archaea; Euryarchaeota; Methanococci; Methanococcales; Methanocaldococcaceae; Methanoc dococcus.
Accession number: NC_000909; **Genome size (bp)**: 1664970.
Number of genes: 1724.
Oriloc predictions: Origin NA Terminus NA
Worning et al., 2006: Origin 929 kb Terminus 1648 kb
Position(s) of the ORC/Cdc6 gene(s): 331 kb, 893.79 kb, 1095.76 kb, 1462.61 kb
Consensus predictions: Origin 691 kb Terminus 1642 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew reverse	1318	0.02333	731
	1365	0.04	839
AT-skew reverse	1556	0.01333	1224
	1586	0.02667	1271

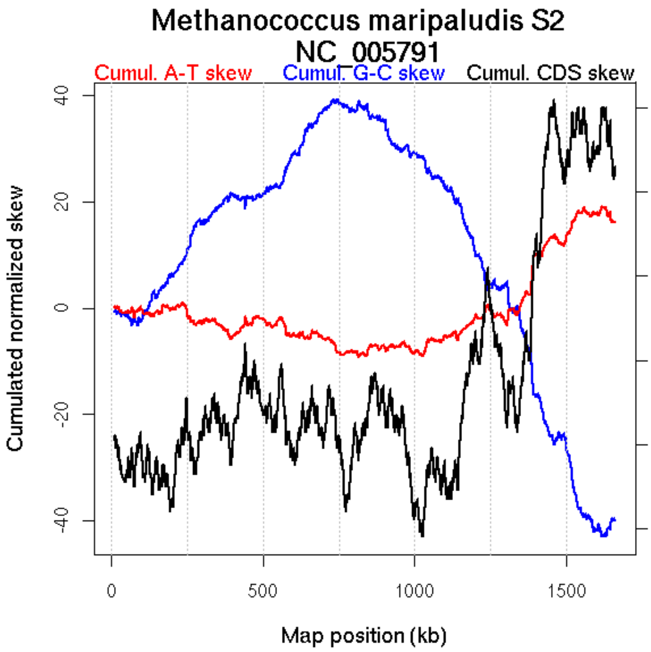
Segments:

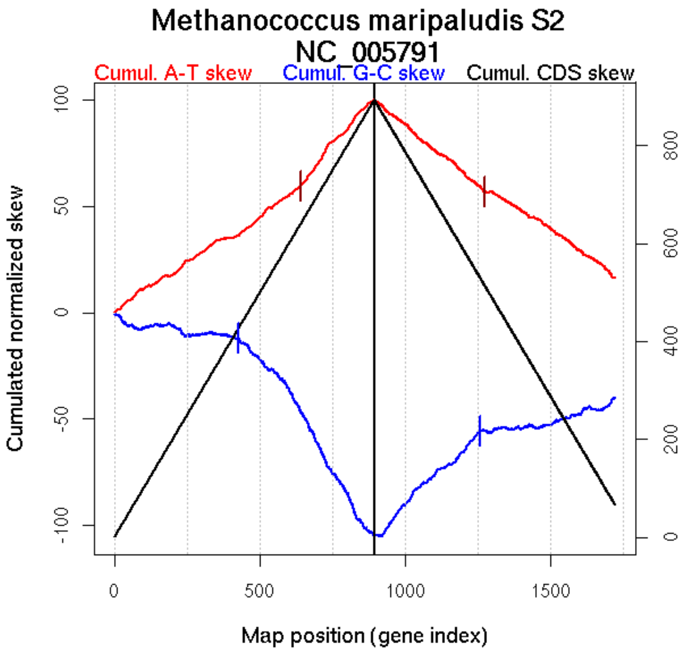
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew reverse	871 (0 kb)	1318 (730.675 kb)	lagging	-0.283
	1319(733.8075 kb)	1365 (839.012 kb)	leading	-0.127
	1366(842.457 kb)	1724 (1664.862 kb)	leading	-0.252
AT-skew reverse	871 (0 kb)	1556 (1223.728 kb)	NA	-0.073
	1557(1227.1155 kb)	1586(1270.8 kb)	leading	0.017
	1587(1272.4285 kb)	1724(1664.862 kb)	leading	-0.052

More G than C on the leading strand for replication - for reverse encoded genes.

187 Methanococcus maripaludis S2

Archaea; Euryarchaeota; Methanococci; Methanococcales; Methanococcaceae; Methanococcus.
Accession number: NC_005791; **Genome size (bp)**: 1661137.
Number of genes: 1722.
Oriloc predictions: Origin 1622 kb Terminus 814 kb
Worning et al., 2006: Origin 48 kb Terminus 905 kb
Position(s) of the ORC/Cdc6 gene(s): NA
Consensus predictions: Origin 1622 kb Terminus 814 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	427	NA	841
GC-skew reverse	1256	NA	726
AT-skew forward	640	NA	1231
AT-skew reverse	1275	NA	753

Segments:

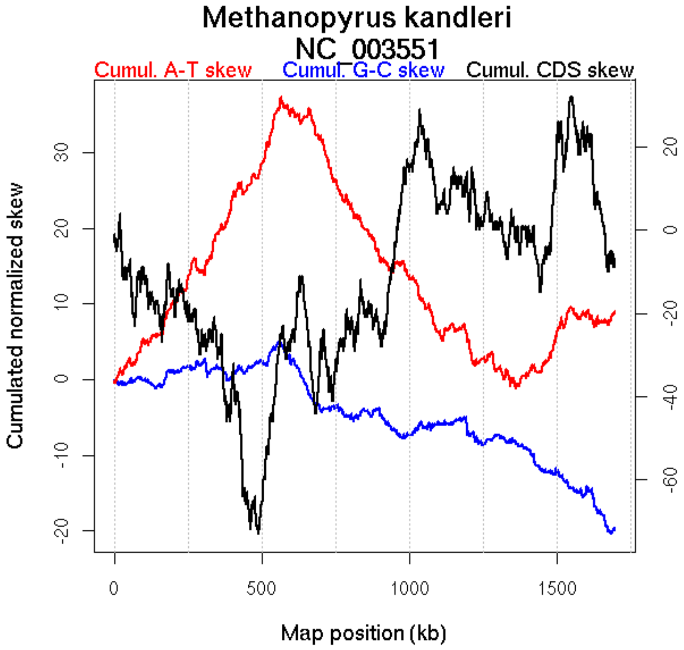
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	427 (841.279 kb)	leading	-0.019
	428(843.326 kb)	894 (1661.126 kb)	lagging	-0.215
GC-skew reverse	895 (0 kb)	1256 (726.0105 kb)	leading	0.135
	1257(728.6085 kb)	1722 (1661.126 kb)	NA	0.03
AT-skew forward	1 (0 kb)	640 (1231.204 kb)	NA	0.088
	641(1232.9355 kb)	894 (1661.126 kb)	lagging	0.163
AT-skew reverse	895 (0 kb)	1275 (753.3195 kb)	leading	-0.112
	1276(754.813 kb)	1722(1661.126 kb)	lagging	-0.092

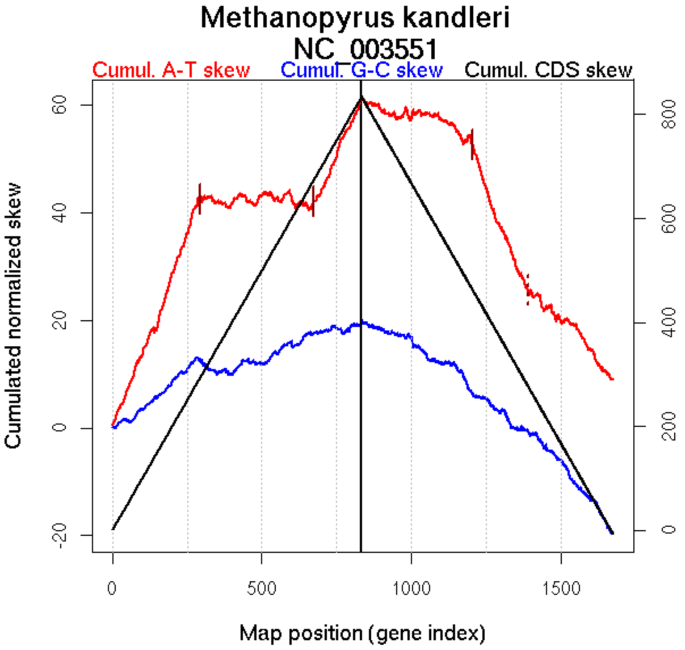
More T than A on the leading strand for replication - for reverse encoded genes.

More G than C on the leading strand for replication - for forward encoded genes.

188 Methanopyrus kandleri

Archaea; Euryarchaeota; Methanopyri; Methanopyrales; Methanopyraceae; Methanopyrus.
Accession number: NC_003551; **Genome size (bp)**: 1694969.
Number of genes: 1675.
Oriloc predictions: Origin 562 kb Terminus 1361 kb
Worning et al., 2006: Origin 492 kb Terminus 1211 kb
Position(s) of the ORC/Cdc6 gene(s): NA
Consensus predictions: Origin 562 kb Terminus 1361 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
AT-skew forward	292	0.00667	571
	672	0.02	1380
AT-skew reverse	1205	0.00333	675
	1389	0.05667	1100

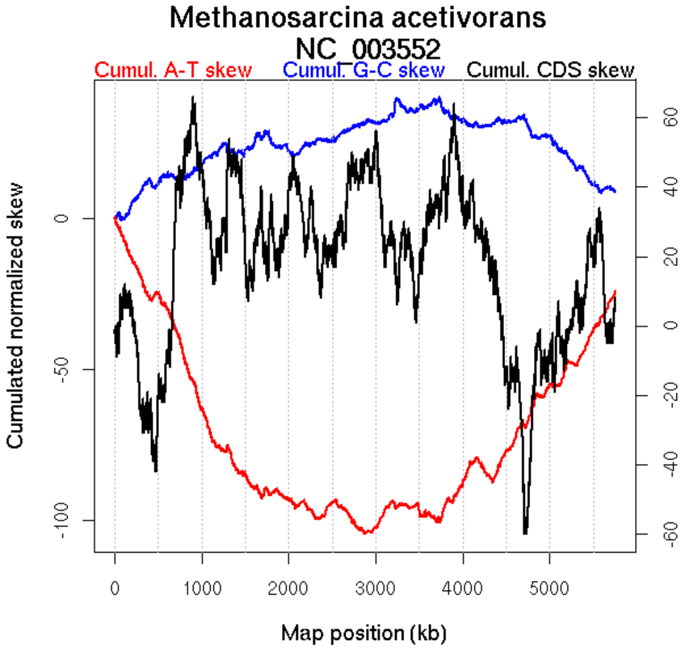
Segments:

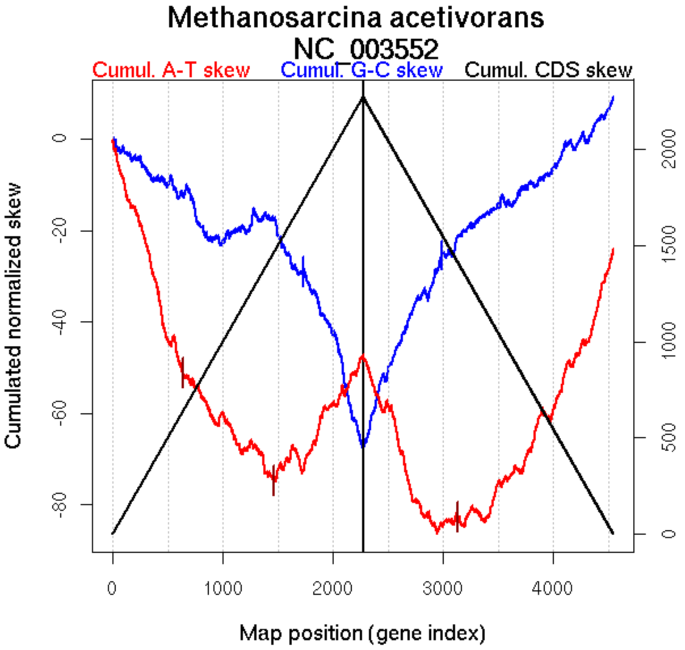
	From (index/coord.)	To (index/coord.)	Strand	Slope
AT-skew forward	1 (0 kb)	292 (570.704 kb)	lagging	0.146
	293(577.134 kb)	672 (1380.07 kb)	leading	-0.001
	673(1380.964 kb)	834 (1694.497 kb)	lagging	0.125
AT-skew reverse	835 (0 kb)	1205 (675.1585 kb)	NA	-0.016
	1206(676.4235 kb)	1389(1099.722 kb)	leading	-0.144
	1390(1102.377 kb)	1675(1694.497 kb)	NA	-0.058

More T than A on the leading strand for replication - for forward encoded genes.

189 Methanosarcina acetivorans

Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales; Methanosarcinaceae; Methanosarcina.
Accession number: NC_003552; **Genome size (bp)**: 5751492.
Number of genes: 4540.
Oriloc predictions: Origin 3 kb Terminus 3743 kb
Worning et al., 2006: Origin 5749 kb Terminus 3739 kb
Position(s) of the ORC/Cdc6 gene(s): 0.9 kb, 105.83 kb, 4363.58 kb, 5636.54 kb
Consensus predictions: Origin 3 kb Terminus 3743 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1730	0	4372
GC-skew reverse	2988	0.02667	1762
AT-skew forward	640	0.04333	1557
	1461	0.03	3706
AT-skew reverse	3133	0	2203

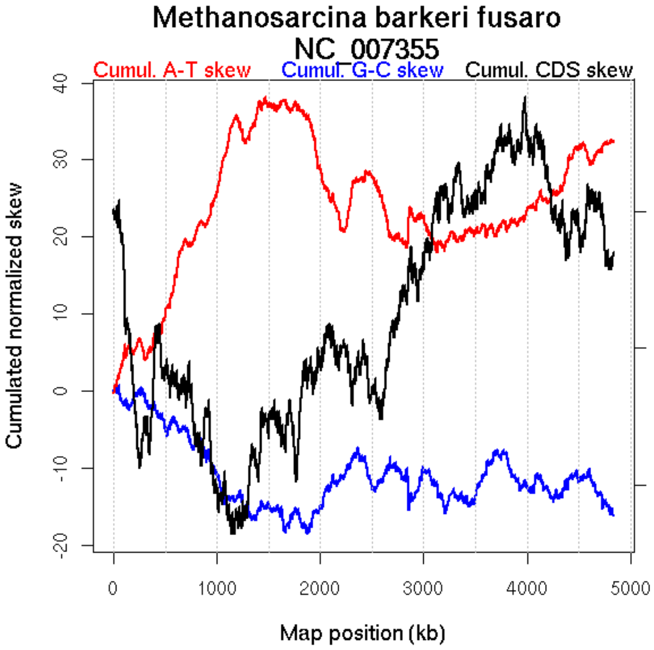
Segments:

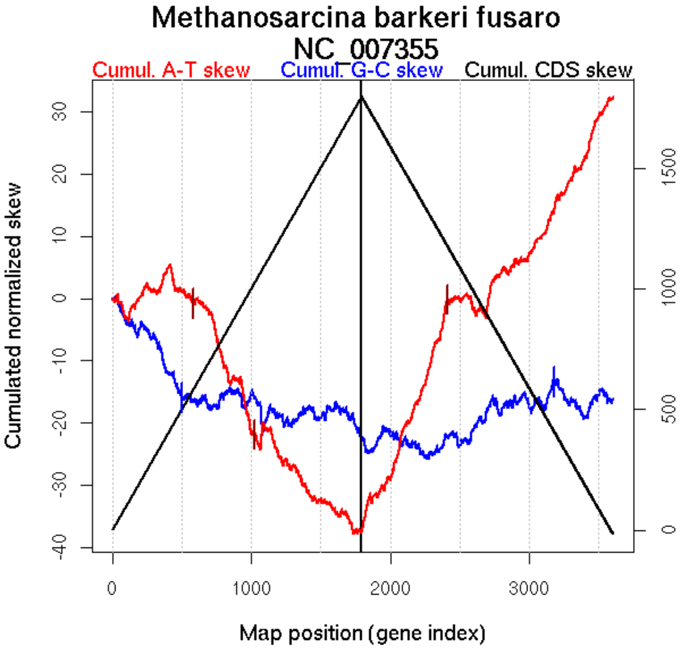
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1730 (4372.0815 kb)	leading	-0.014
	1731(4373.9145 kb)	2272 (5751.247 kb)	lagging	-0.072
GC-skew reverse	2273 (0 kb)	2988 (1762.436 kb)	leading	0.055
	2989(1763.53 kb)	4540 (5751.247 kb)	NA	0.02
AT-skew forward	1 (0 kb)	640 (1557.073 kb)	leading	-0.081
	641(1561.7505 kb)	1461 (3705.7845 kb)	leading	-0.027
	1462(3706.6385 kb)	2272 (5751.247 kb)	lagging	0.033
AT-skew reverse	2273 (0 kb)	3133 (2202.9005 kb)	leading	-0.048
	3134(2206.905 kb)	4540(5751.247 kb)	NA	0.041

More T than A on the leading strand for replication - for forward encoded genes.
More G than C on the leading strand for replication - for forward encoded genes.

190 Methanosarcina barkeri fusaro

Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales; Methanosarcinaceae; Methanosarcina.
Accession number: NC_007355; **Genome size (bp)**: 4837408.
Number of genes: 3606.
Oriloc predictions: Origin NA Terminus NA
Worning et al., 2006: Origin 1193 kb Terminus 4243 kb
Position(s) of the ORC/Cdc6 gene(s): 1100.3 kb, 1482.73 kb, 1963.22 kb, 2947.07 kb
Consensus predictions: Origin 1193 kb Terminus 0 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	500	NA	1377
GC-skew reverse	3180	NA	3708
AT-skew forward	584	NA	1583
	1024	NA	2730
AT-skew reverse	2416	NA	1471

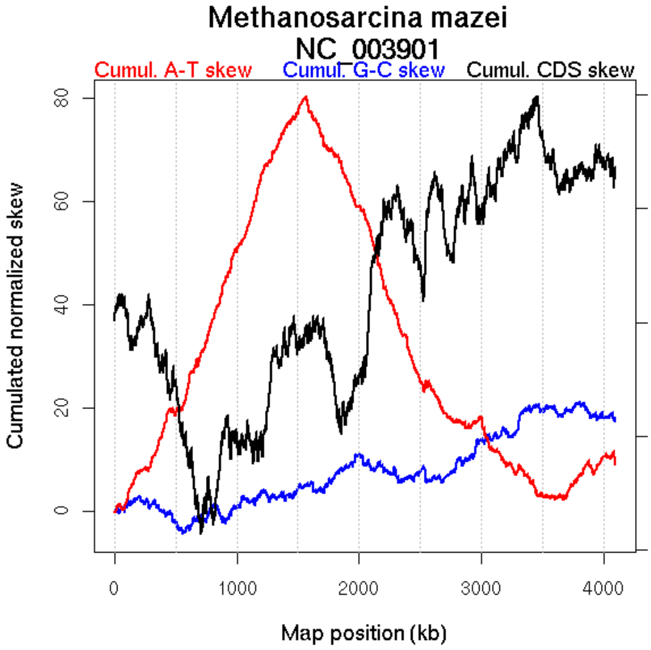
Segments:

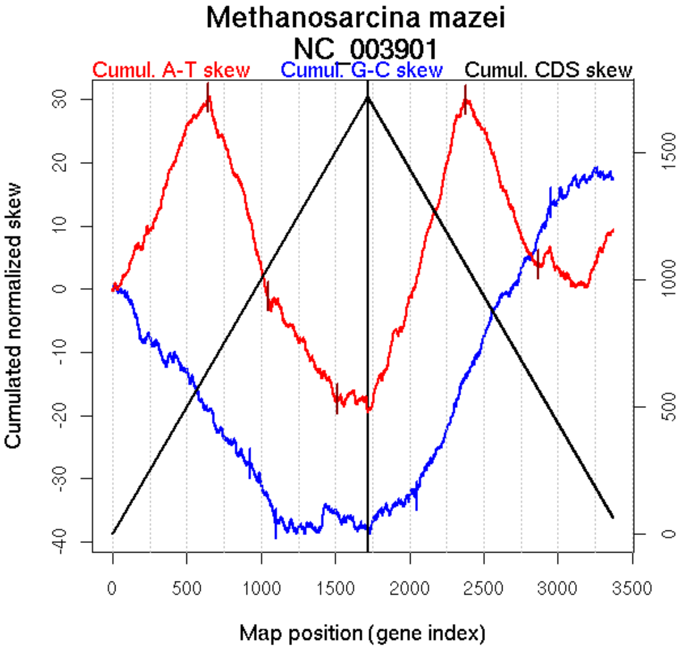
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	500 (1377.0235 kb)	NA	-0.029
	501(1378.509 kb)	1795 (4837.3 kb)	leading	-0.003
GC-skew reverse	1796 (0 kb)	3180 (3707.9715 kb)	NA	0.007
	3181(3709.752 kb)	3606 (4837.3 kb)	leading	-0.003
AT-skew forward	1 (0 kb)	584 (1582.761 kb)	NA	0.006
	585(1583.8545 kb)	1024 (2730.259 kb)	leading	-0.053
	1025(2734.616 kb)	1795 (4837.3 kb)	leading	-0.023
AT-skew reverse	1796 (0 kb)	2416 (1471.203 kb)	lagging	0.056
	2417(1474.346 kb)	3606(4837.3 kb)	leading	0.03

More T than A on the leading strand for replication - for reverse encoded genes.

191 Methanosarcina mazei

Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales; Methanosarcinaceae; Methanosarcina.
Accession number: NC_003901; **Genome size (bp)**: 4096345.
Number of genes: 3370.
Oriloc predictions: Origin 1564 kb Terminus 3624 kb
Worning et al., 2006: Origin 1573 kb Terminus 94 kb
Position(s) of the ORC/Cdc6 gene(s): 570.09 kb, 1655.64 kb, 2187.55 kb
Consensus predictions: Origin 1564 kb Terminus 3624 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	925	NA	2169
	1104	NA	2562
GC-skew reverse	2045	NA	695
	2949	NA	2991
AT-skew forward	646	NA	1550
	1044	NA	2458
	1515	NA	3574
AT-skew reverse	2381	NA	1577
	2865	NA	2798

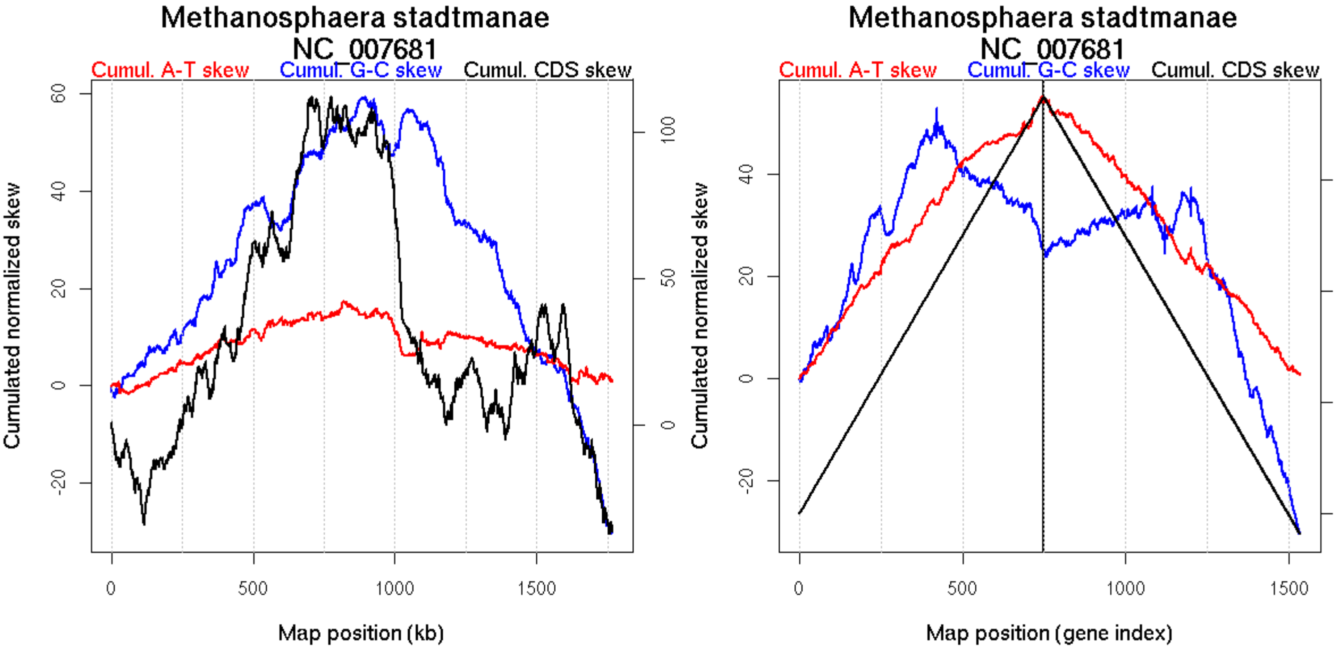
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	925 (2168.8935 kb)	NA	-0.031
	926(2171.7575 kb)	1104 (2562.0095 kb)	leading	-0.05
	1105(2566.0515 kb)	1718 (4096.173 kb)	NA	0.001
GC-skew reverse	1719 (0 kb)	2045 (695.3495 kb)	lagging	0.016
	2046(696.607 kb)	2949 (2990.5275 kb)	NA	0.049
	2950(2992.471 kb)	3370 (4096.173 kb)	NA	0.012
AT-skew forward	1 (0 kb)	646 (1549.585 kb)	lagging	0.052
	647(1550.551 kb)	1044 (2457.689 kb)	leading	-0.075
	1045(2458.404 kb)	1515 (3574.0565 kb)	leading	-0.035
	1516(3575.195 kb)	1718 (4096.173 kb)	lagging	-0.002
AT-skew reverse	1719 (0 kb)	2381 (1577.3975 kb)	lagging	0.077
	2382(1578.342 kb)	2865(2797.938 kb)	leading	-0.06
	2866(2802.044 kb)	3370(4096.173 kb)	NA	0.005

More T than A on the leading strand for replication - for forward encoded genes.

192 Methanosphaera stadtmanae

Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales; Methanobacteriaceae; Methanosphaera.
Accession number: NC_007681; **Genome size (bp)**: 1767403.
Number of genes: 1534.
Oriloc predictions: Origin 30 kb Terminus 836 kb
Worning et al., 2006: Origin 32 kb Terminus 874 kb
Position(s) of the ORC/Cdc6 gene(s): 396.58 kb, 1557.31 kb, 1.29 kb, 744.11 kb
Consensus predictions: Origin 30 kb Terminus 836 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	420	0	893
GC-skew reverse	1081	0.02889	928
	1120	0.00222	993
	1201	0.00222	1097

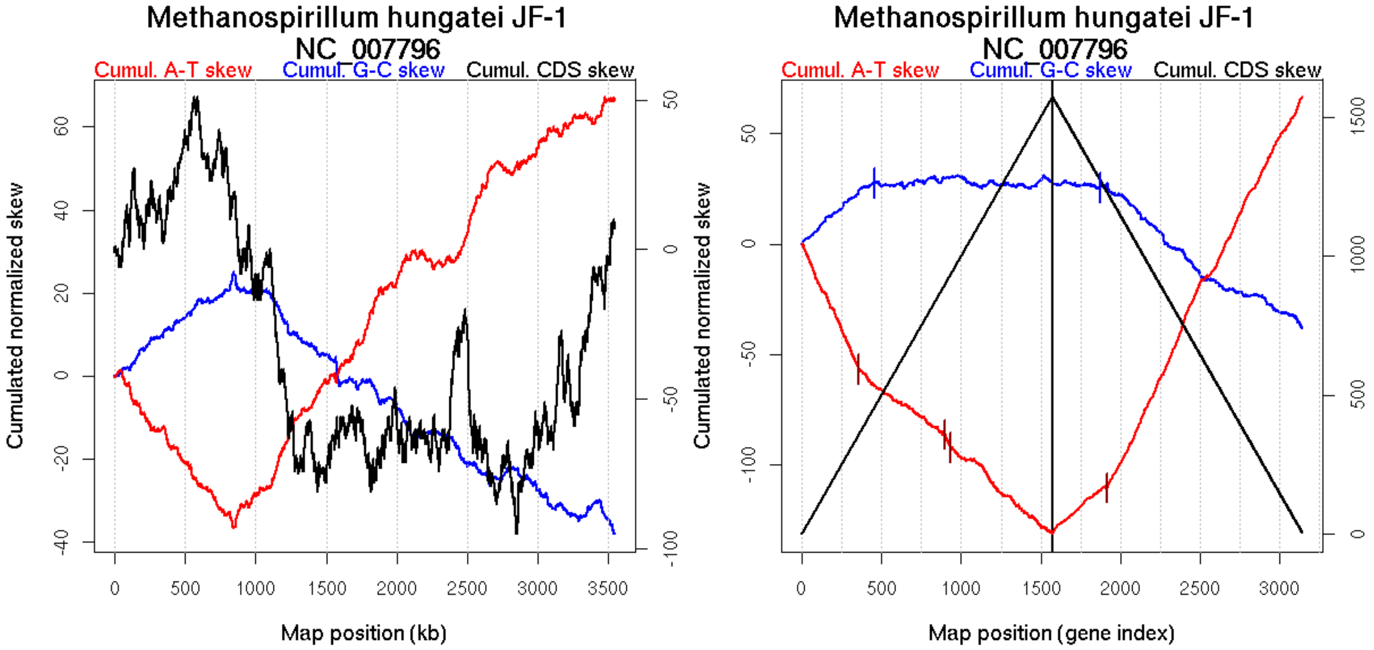
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	420 (893.3115 kb)	leading	0.122
	421(897.3195 kb)	749 (1767.356 kb)	lagging	-0.055
GC-skew reverse	750 (0 kb)	1081 (928.2365 kb)	NA	0.029
	1082(928.995 kb)	1120 (992.785 kb)	lagging	-0.204
	1121(993.823 kb)	1201 (1096.9145 kb)	lagging	0.117
	1202(1097.6935 kb)	1534 (1767.356 kb)	lagging	-0.192

More G than C on the leading strand for replication - for forward encoded genes.

193 Methanospirillum hungatei JF-1

Archaea; Euryarchaeota; Methanomicrobia; Methanomicrobiales; Methanospirillaceae; Methanospirillum.
Accession number: NC_007796; **Genome size (bp)**: 3544738.
Number of genes: 3139.
Oriloc predictions: Origin 0 kb Terminus 844 kb
Worning et al., 2006: Origin 3494 kb Terminus 1022 kb
Position(s) of the ORC/Cdc6 gene(s): 518.2 kb
Consensus predictions: Origin 0 kb Terminus 844 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	454	0	1052
GC-skew reverse	1870	0.02	759
AT-skew forward	359	0	838
	900	0	2176
	936	0.00222	2259
AT-skew reverse	1918	0	849

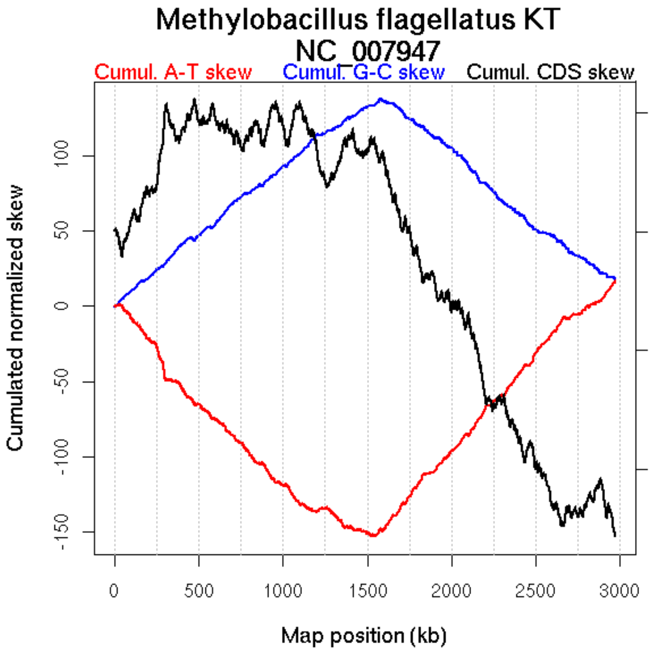
Segments:

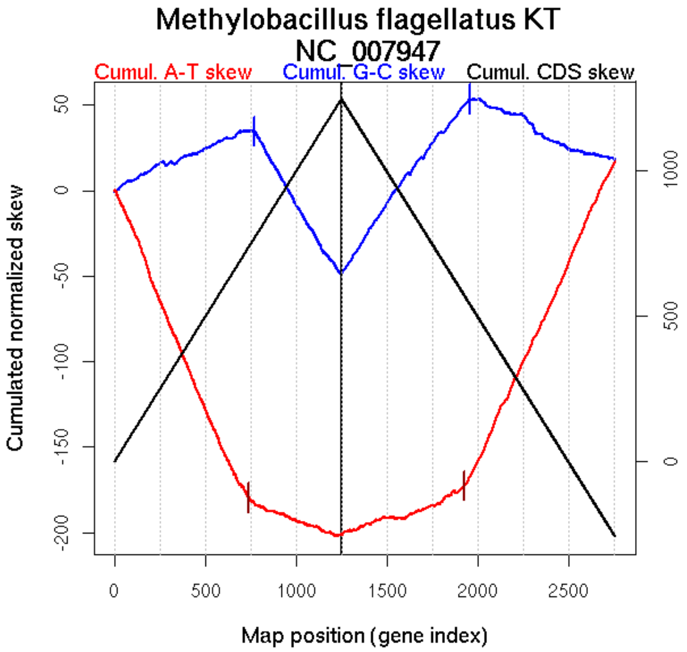
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	454 (1052.0045 kb)	NA	0.063
	455(1053.521 kb)	1573 (3544.709 kb)	lagging	0
GC-skew reverse	1574 (0 kb)	1870 (758.7745 kb)	leading	-0.005
	1871(760.5225 kb)	3139 (3544.709 kb)	lagging	-0.051
AT-skew forward	1 (0 kb)	359 (838.3355 kb)	leading	-0.156
	360(841.5225 kb)	900 (2175.9855 kb)	lagging	-0.052
	901(2177.611 kb)	936 (2259.1985 kb)	lagging	-0.157
	937(2260.5035 kb)	1573 (3544.709 kb)	lagging	-0.065
AT-skew reverse	1574 (0 kb)	1918 (849.12 kb)	leading	0.062
	1919(854.457 kb)	3139(3544.709 kb)	lagging	0.147

More T than A on the leading strand for replication.
More G than C on the leading strand for replication - for reverse encoded genes.

194 Methylobacillus flagellatus KT

Bacteria; Proteobacteria; Betaproteobacteria; Methylophilales; Methylophilaceae; Methylobacillus.
Accession number: NC_007947; **Genome size (bp)**: 2971517.
Number of genes: 2753.
Oriloc predictions: Origin 4 kb Terminus 1578 kb
Worning et al., 2006: Origin 5 kb Terminus 1578 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 2052.904 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.75 kb, 215.05 kb
Consensus predictions: Origin 4 kb Terminus 1578 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	767	0	1583
GC-skew reverse	1952	0	1584
AT-skew forward	738	0	1514
AT-skew reverse	1925	0	1546

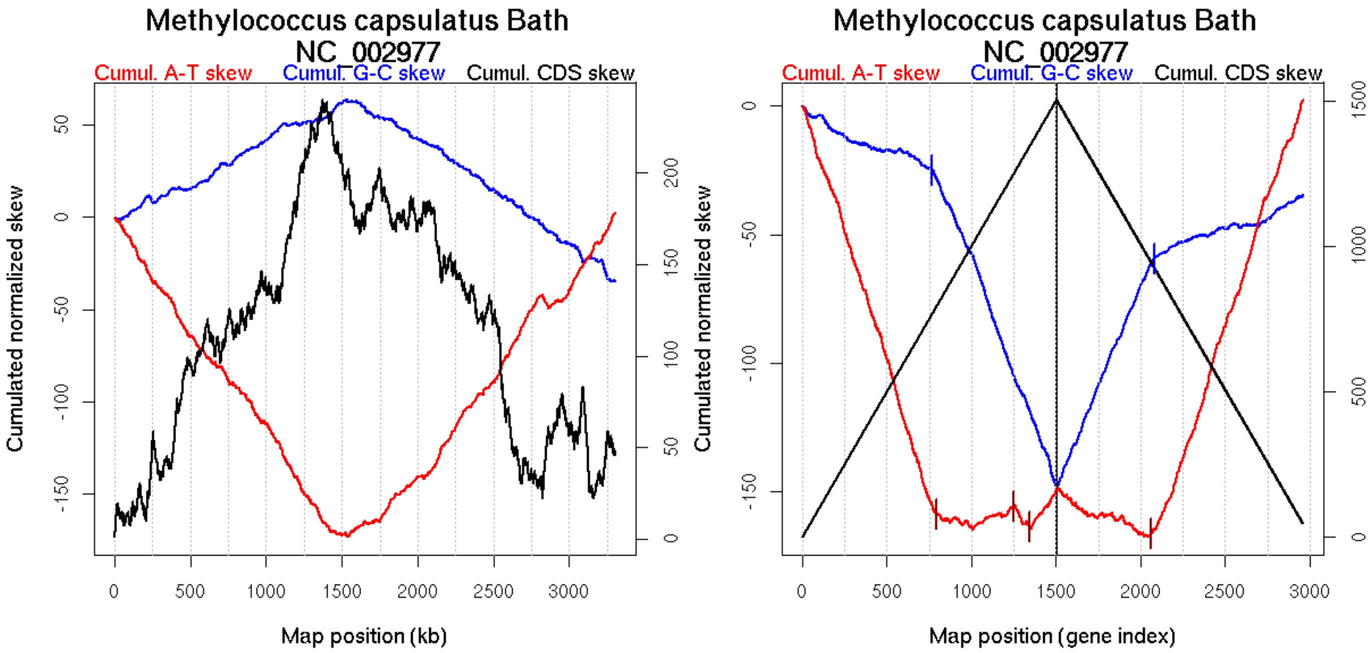
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	767 (1583.3605 kb)	leading	0.045
	768(1584.228 kb)	1248 (2971.284 kb)	lagging	-0.179
GC-skew reverse	1249 (0 kb)	1952 (1583.9045 kb)	leading	0.145
	1953(1586.2405 kb)	2753 (2971.284 kb)	lagging	-0.051
AT-skew forward	1 (0 kb)	738 (1513.565 kb)	leading	-0.254
	739(1514.016 kb)	1248 (2971.284 kb)	lagging	-0.041
AT-skew reverse	1249 (0 kb)	1925 (1546.012 kb)	leading	0.036
	1926(1546.443 kb)	2753(2971.284 kb)	lagging	0.234

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

195 Methylococcus capsulatus Bath

Bacteria; Proteobacteria; Gammaproteobacteria; Methylococcales; Methylococcaceae; Methylococcus.
Accession number: NC_002977; **Genome size (bp)**: 3304561.
Number of genes: 2959.
Oriloc predictions: Origin 0 kb Terminus 1522 kb
Worning et al., 2006: Origin 3302 kb Terminus 1536 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 2781.477 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1732.66 kb, 2698.35 kb, 3220.44 kb
Consensus predictions: Origin 0 kb Terminus 1522 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	768	0	1505
GC-skew reverse	2078	0	1520
AT-skew forward	793	0	1595
	1250	0.04889	2797
	1345	0.00222	2950
AT-skew reverse	2063	0	1499

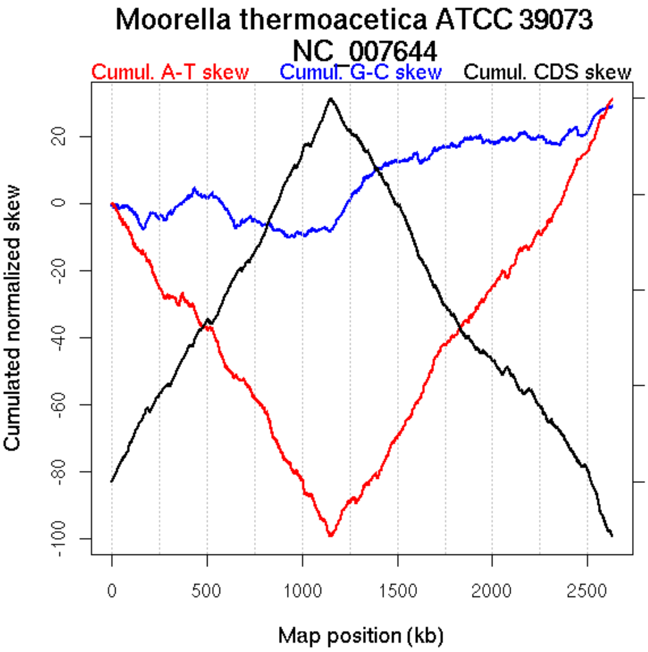
Segments:

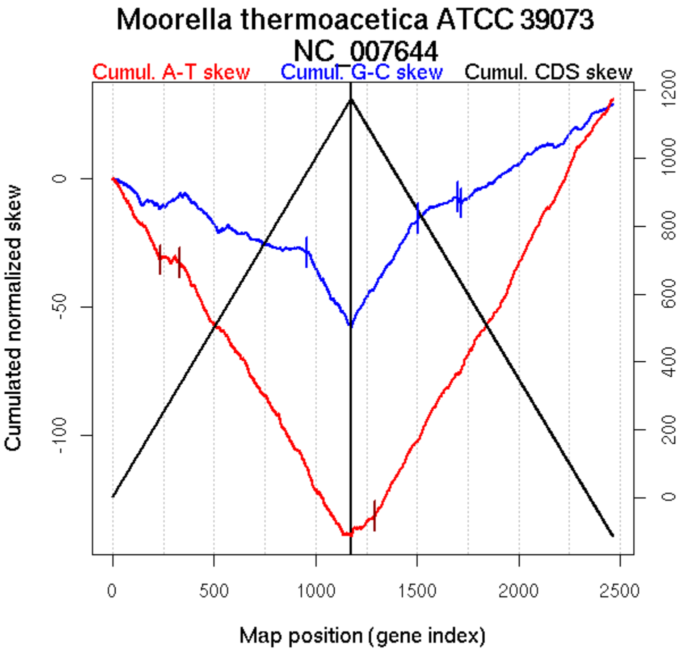
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	768 (1504.826 kb)	leading	-0.027
	769(1519.286 kb)	1503 (3304.518 kb)	lagging	-0.17
GC-skew reverse	1504 (0 kb)	2078 (1519.991 kb)	leading	0.157
	2079(1521.0245 kb)	2959 (3304.518 kb)	lagging	0.023
AT-skew forward	1 (0 kb)	793 (1595.2895 kb)	leading	-0.205
	794(1596.0675 kb)	1250 (2796.5785 kb)	lagging	0.007
	1251(2799.4965 kb)	1345 (2950.4055 kb)	lagging	-0.093
	1346(2953.6715 kb)	1503 (3304.518 kb)	lagging	0.088
AT-skew reverse	1504 (0 kb)	2063 (1499.313 kb)	leading	-0.029
	2064(1499.8875 kb)	2959(3304.518 kb)	lagging	0.197

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

196 Moorella thermoacetica ATCC 39073

Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales; Thermoanaerobacteriaceae; Moorella group; Moorella.
Accession number: NC_007644; **Genome size (bp)**: 2628784.
Number of genes: 2465.
Oriloc predictions: Origin 0 kb Terminus 1147 kb
Worning et al., 2006: Origin 1 kb Terminus 1148 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1166.999 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1.11 kb
Consensus predictions: Origin 0 kb Terminus 1147 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	956	0	1245
GC-skew reverse	1506	0.01778	1388
	1699	0	1606
	1716	0	1619
AT-skew forward	233	0.00667	283
	333	0.00667	401
AT-skew reverse	1294	0	939

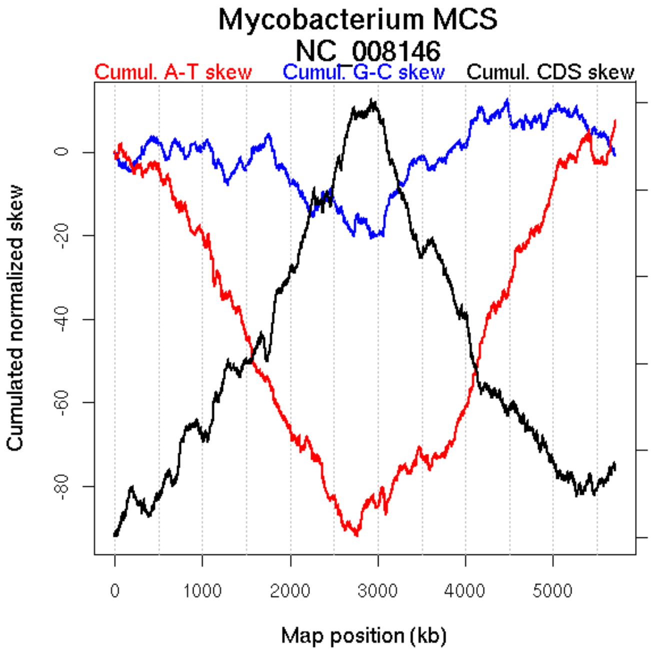
Segments:

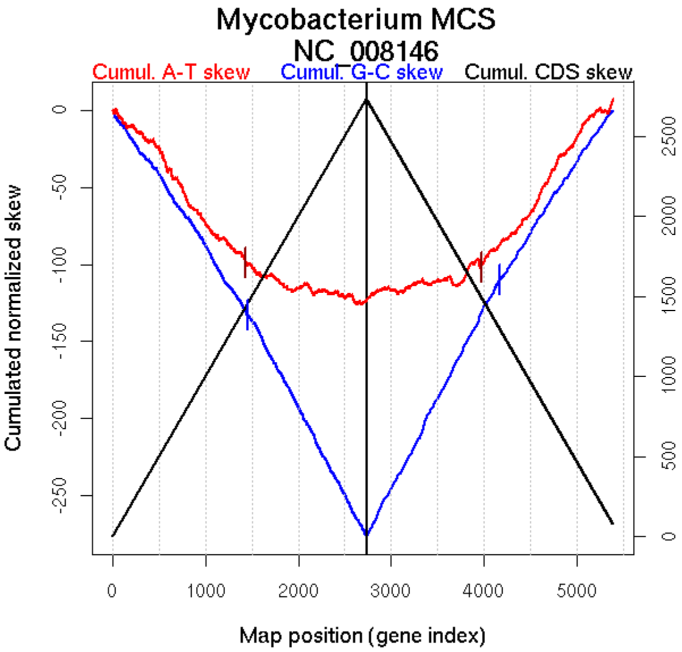
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	956 (1245.3885 kb)	leading	-0.031
	957(1246.805 kb)	1175 (2628.756 kb)	lagging	-0.134
GC-skew reverse	1176 (0 kb)	1506 (1388.105 kb)	NA	0.125
	1507(1388.6975 kb)	1699 (1606.0695 kb)	lagging	0.039
	1700(1606.4245 kb)	1716 (1618.614 kb)	lagging	-0.148
	1717(1619.487 kb)	2465 (2628.756 kb)	lagging	0.05
AT-skew forward	1 (0 kb)	233 (283.4095 kb)	leading	-0.131
	234(283.7385 kb)	333 (401.0435 kb)	leading	-0.015
	334(402.0475 kb)	1175 (2628.756 kb)	NA	-0.13
AT-skew reverse	1176 (0 kb)	1294 (938.6205 kb)	leading	0.056
	1295(946.949 kb)	2465(2628.756 kb)	lagging	0.14

More T than A on the leading strand for replication - for reverse encoded genes.
More G than C on the leading strand for replication - for forward encoded genes.

197 Mycobacterium MCS

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
Accession number: NC_008146; **Genome size (bp)**: 5705448.
Number of genes: 5391.
Oriloc predictions: Origin 0 kb Terminus 2672 kb
Worning et al., 2006: Origin NA kb Terminus NA kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 5654.273 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.76 kb
Consensus predictions: Origin 0 kb Terminus 2672 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1452	0.00667	2622
GC-skew reverse	4174	0.00667	3437
AT-skew forward	1432	0.00667	2594
AT-skew reverse	3975	0	3106

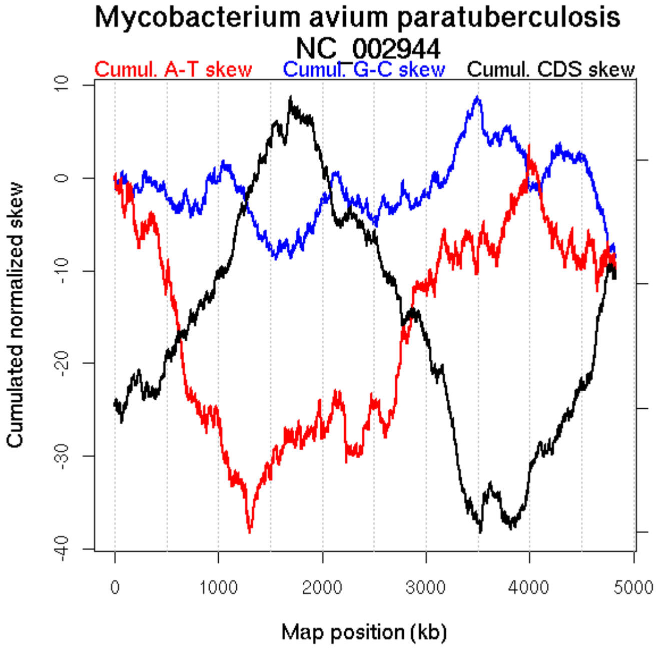
Segments:

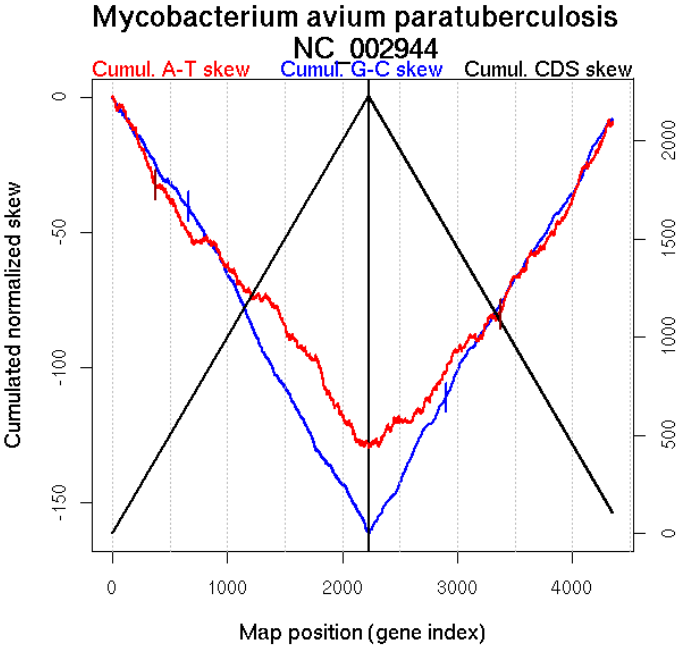
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1452 (2621.8515 kb)	leading	-0.091
	1453(2622.7795 kb)	2734 (5704.914 kb)	lagging	-0.114
GC-skew reverse	2735 (0 kb)	4174 (3436.8765 kb)	NA	0.117
	4175(3439.643 kb)	5391 (5704.914 kb)	lagging	0.092
AT-skew forward	1 (0 kb)	1432 (2593.722 kb)	leading	-0.074
	1433(2595.4805 kb)	2734 (5704.914 kb)	lagging	-0.017
AT-skew reverse	2735 (0 kb)	3975 (3106.034 kb)	NA	0.014
	3976(3107.885 kb)	5391(5704.914 kb)	lagging	0.081

More T than A on the leading strand for replication - for forward encoded genes.
More G than C on the leading strand for replication - for forward encoded genes.

198 Mycobacterium avium paratuberculosis

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium avium complex (MAC).
Accession number: NC_002944; **Genome size (bp)**: 4829781.
Number of genes: 4350.
Oriloc predictions: Origin 3996 kb Terminus 1331 kb
Worning et al., 2006: Origin 3775 kb Terminus 1902 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 14.701 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.77 kb
Consensus predictions: Origin 0 kb Terminus 2500 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	658	NA	1216
GC-skew reverse	2902	NA	1745
AT-skew forward	371	NA	703
AT-skew reverse	3370	NA	2685

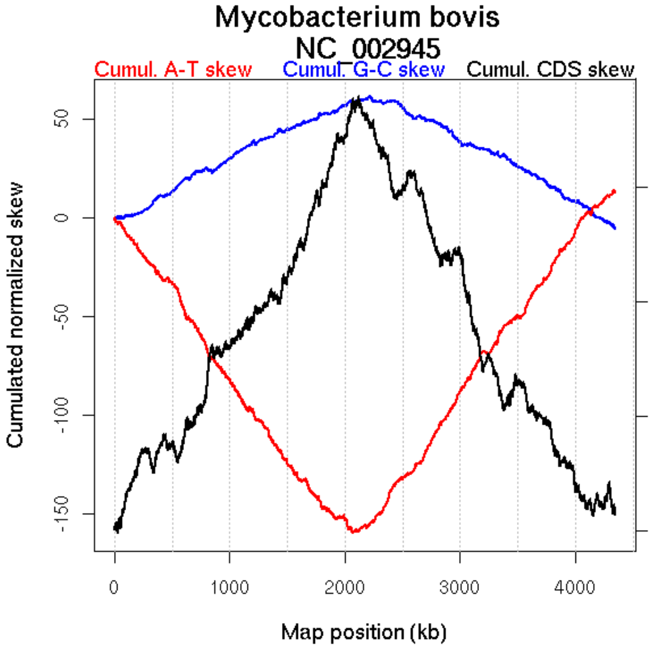
Segments:

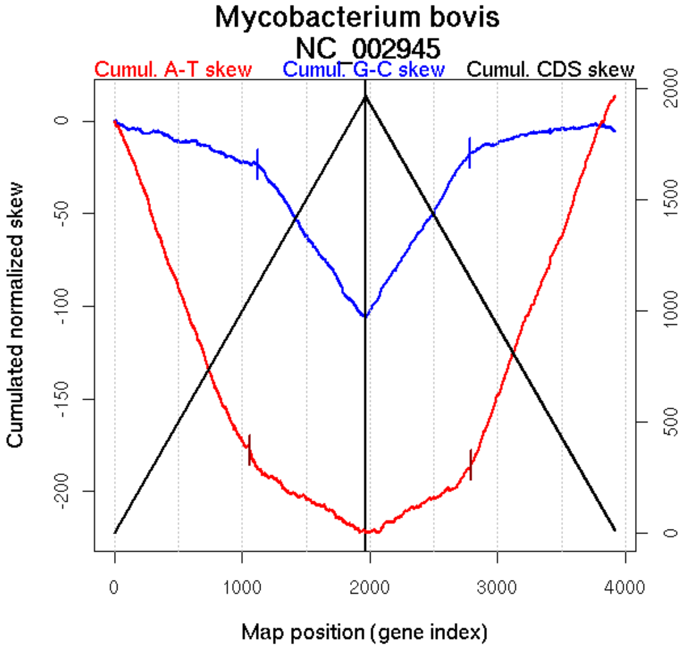
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	658 (1215.5775 kb)	leading	-0.063
	659(1218.5265 kb)	2227 (4829.176 kb)	NA	-0.078
GC-skew reverse	2228 (0 kb)	2902 (1744.918 kb)	leading	0.077
	2903(1746.049 kb)	4350 (4829.176 kb)	NA	0.069
AT-skew forward	1 (0 kb)	371 (702.773 kb)	leading	-0.086
	372(703.9095 kb)	2227 (4829.176 kb)	NA	-0.051
AT-skew reverse	2228 (0 kb)	3370 (2685.1975 kb)	leading	0.047
	3371(2686.451 kb)	4350(4829.176 kb)	lagging	0.069

More T than A on the leading strand for replication - for reverse encoded genes.

199 Mycobacterium bovis

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.
Accession number: NC_002945; **Genome size (bp)**: 4345492.
Number of genes: 3920.
Oriloc predictions: Origin 0 kb Terminus 2204 kb
Worning et al., 2006: Origin 2 kb Terminus 2127 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 60.159 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.76 kb
Consensus predictions: Origin 0 kb Terminus 2204 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1123	NA	2099
GC-skew reverse	2783	NA	2210
AT-skew forward	1061	NA	1994
AT-skew reverse	2794	NA	2230

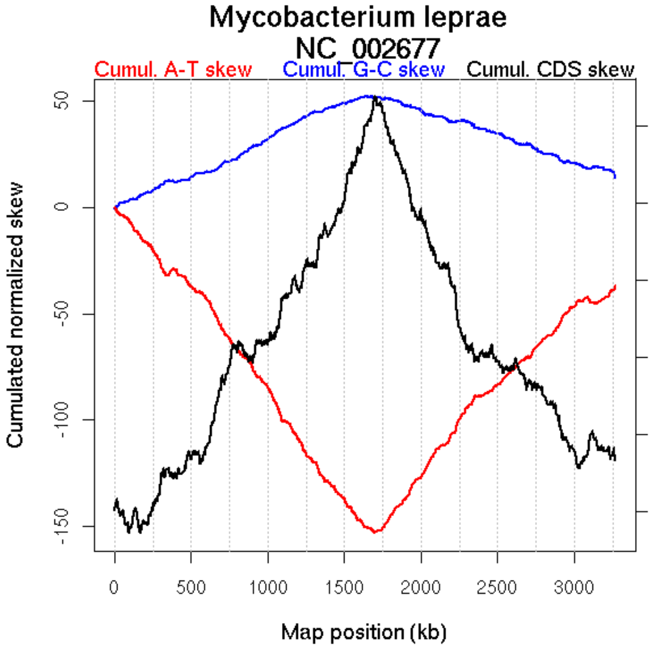
Segments:

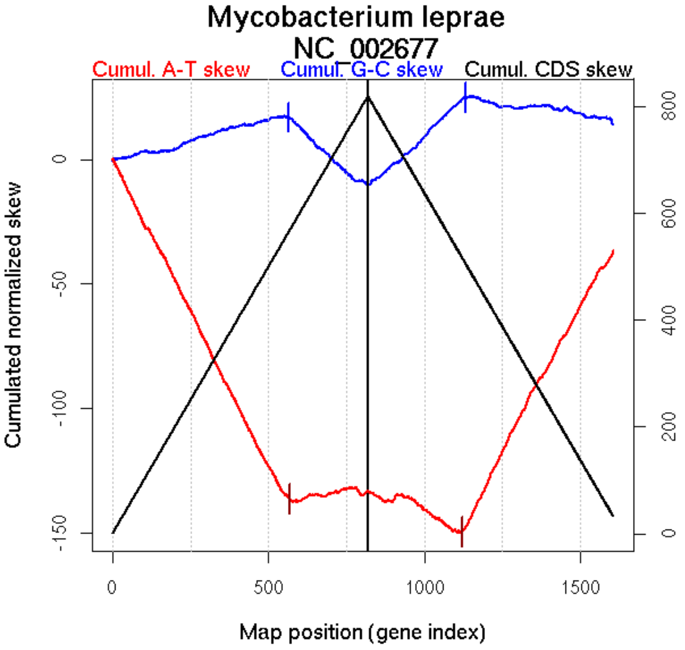
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1123 (2099.1455 kb)	leading	-0.02
	1124(2099.714 kb)	1967 (4344.889 kb)	lagging	-0.101
GC-skew reverse	1968 (0 kb)	2783 (2210.0625 kb)	leading	0.109
	2784(2212.1055 kb)	3920 (4344.889 kb)	lagging	0.012
AT-skew forward	1 (0 kb)	1061 (1994.3305 kb)	leading	-0.179
	1062(1995.619 kb)	1967 (4344.889 kb)	lagging	-0.042
AT-skew reverse	1968 (0 kb)	2794 (2229.598 kb)	leading	0.041
	2795(2232.6295 kb)	3920(4344.889 kb)	lagging	0.18

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

200 Mycobacterium leprae

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
Accession number: NC_002677; **Genome size (bp)**: 3268203.
Number of genes: 1605.
Oriloc predictions: Origin 0 kb Terminus 1706 kb
Worning et al., 2006: Origin 2 kb Terminus 1700 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 17.03 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.78 kb
Consensus predictions: Origin 0 kb Terminus 1706 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	563	NA	1681
GC-skew reverse	1133	NA	1737
AT-skew forward	569	NA	1692
AT-skew reverse	1121	NA	1657

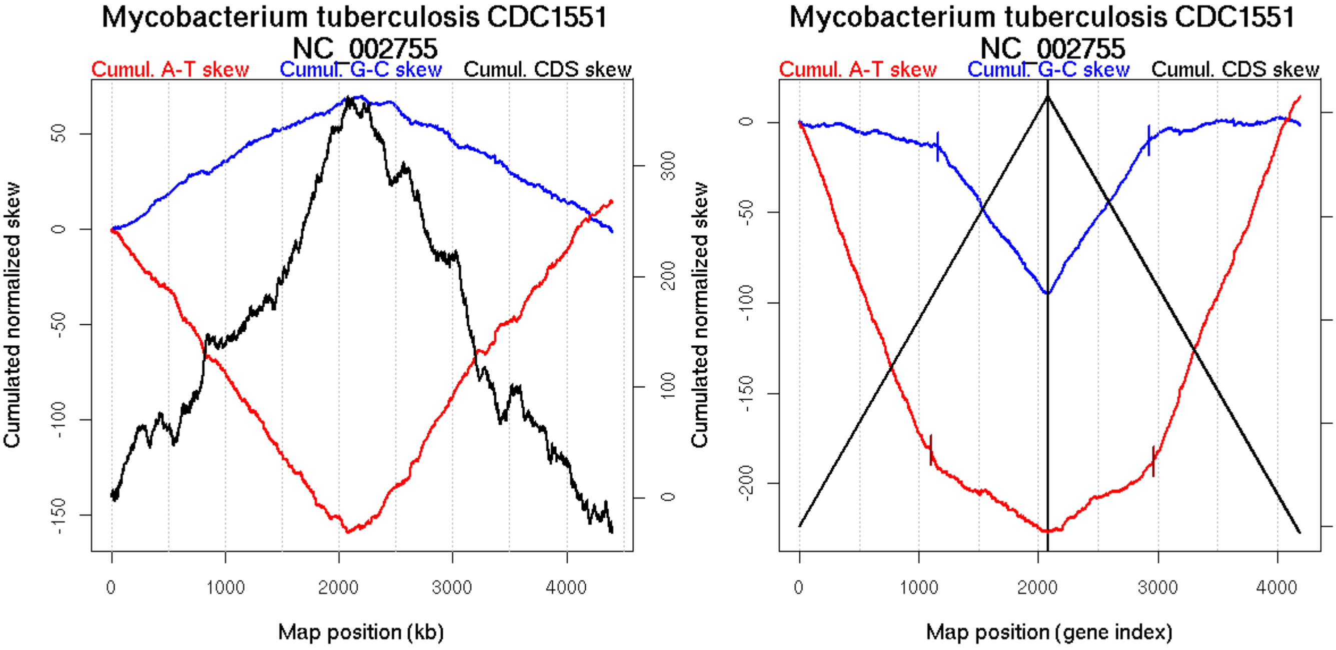
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	563 (1680.611 kb)	leading	0.034
	564(1682.086 kb)	819 (3267.653 kb)	lagging	-0.113
GC-skew reverse	820 (0 kb)	1133 (1737.1735 kb)	leading	0.118
	1134(1740.069 kb)	1605 (3267.653 kb)	lagging	-0.017
AT-skew forward	1 (0 kb)	569 (1692.1175 kb)	leading	-0.246
	570(1693.097 kb)	819 (3267.653 kb)	lagging	0.018
AT-skew reverse	820 (0 kb)	1121 (1657.49 kb)	leading	-0.055
	1122(1666.688 kb)	1605(3267.653 kb)	lagging	0.236

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

201 Mycobacterium tuberculosis CDC1551

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.
Accession number: NC_002755; **Genome size (bp)**: 4403837.
Number of genes: 4189.
Oriloc predictions: Origin 0 kb Terminus 2184 kb
Worning et al., 2006: Origin 2 kb Terminus 2125 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 60.113 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.76 kb
Consensus predictions: Origin 0 kb Terminus 2184 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1162	NA	2109
GC-skew reverse	2925	NA	2183
AT-skew forward	1101	NA	2001
AT-skew reverse	2960	NA	2244

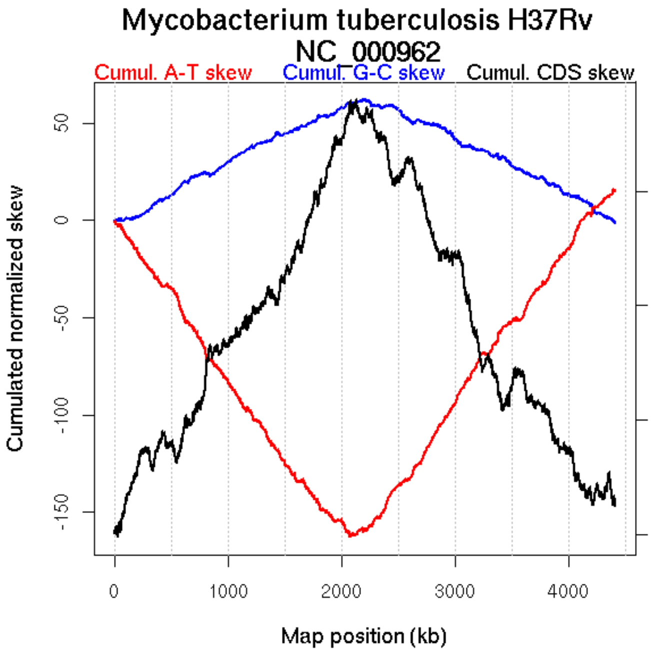
Segments:

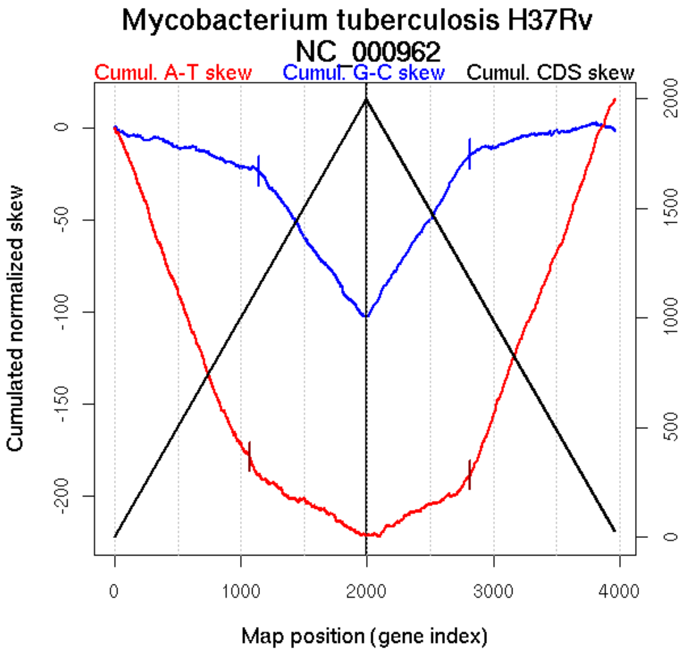
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1162 (2109.0425 kb)	leading	-0.012
	1163(2113.631 kb)	2079 (4403.468 kb)	lagging	-0.091
GC-skew reverse	2080 (0 kb)	2925 (2183.3925 kb)	leading	0.099
	2926(2187.9335 kb)	4189 (4403.468 kb)	lagging	0.007
AT-skew forward	1 (0 kb)	1101 (2001.2925 kb)	leading	-0.173
	1102(2002.581 kb)	2079 (4403.468 kb)	lagging	-0.039
AT-skew reverse	2080 (0 kb)	2960 (2243.9525 kb)	leading	0.041
	2961(2247.109 kb)	4189(4403.468 kb)	lagging	0.168

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

202 Mycobacterium tuberculosis H37Rv

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.
Accession number: NC_000962; **Genome size (bp)**: 4411532.
Number of genes: 3965.
Oriloc predictions: Origin 0 kb Terminus 2186 kb
Worning et al., 2006: Origin 2 kb Terminus 2128 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 60.169 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.76 kb
Consensus predictions: Origin 0 kb Terminus 2186 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1138	NA	2126
GC-skew reverse	2813	NA	2227
AT-skew forward	1071	NA	2007
AT-skew reverse	2819	NA	2236

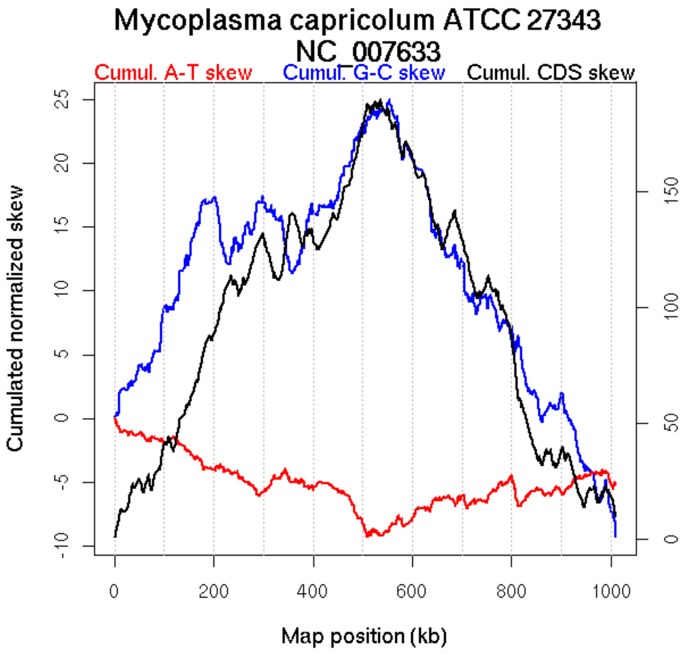
Segments:

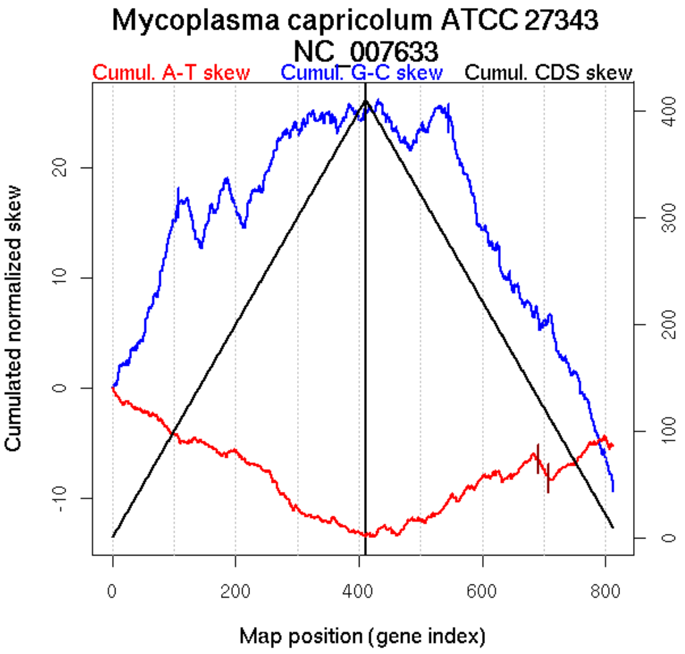
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1138 (2125.86 kb)	leading	-0.019
	1139(2127.993 kb)	1995 (4410.929 kb)	lagging	-0.096
GC-skew reverse	1996 (0 kb)	2813 (2226.9885 kb)	leading	0.108
	2814(2228.9065 kb)	3965 (4410.929 kb)	lagging	0.013
AT-skew forward	1 (0 kb)	1071 (2006.54 kb)	leading	-0.178
	1072(2007.388 kb)	1995 (4410.929 kb)	lagging	-0.039
AT-skew reverse	1996 (0 kb)	2819 (2235.807 kb)	leading	0.037
	2820(2236.2845 kb)	3965(4410.929 kb)	lagging	0.18

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

203 Mycoplasma capricolum ATCC 27343

Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
Accession number: NC_007633; **Genome size (bp)**: 1010023.
Number of genes: 812.
Oriloc predictions: Origin 0 kb Terminus 509 kb
Worning et al., 2006: Origin 0 kb Terminus 536 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1009.879 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.68 kb
Consensus predictions: Origin 0 kb Terminus 509 kb





Significant breakpoints (p-value <0.05):

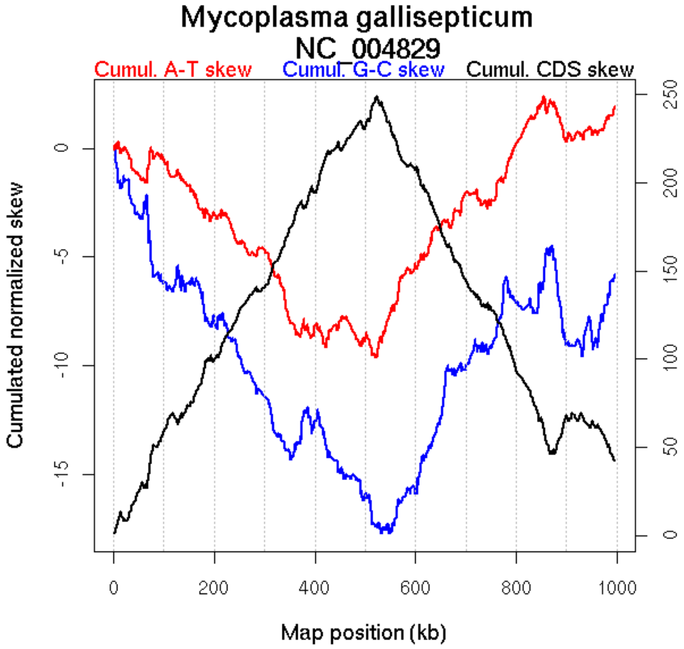
	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	107	0.02	177
GC-skew reverse	545	0.02	567
AT-skew reverse	691	0.02	804
	708	0.01333	813

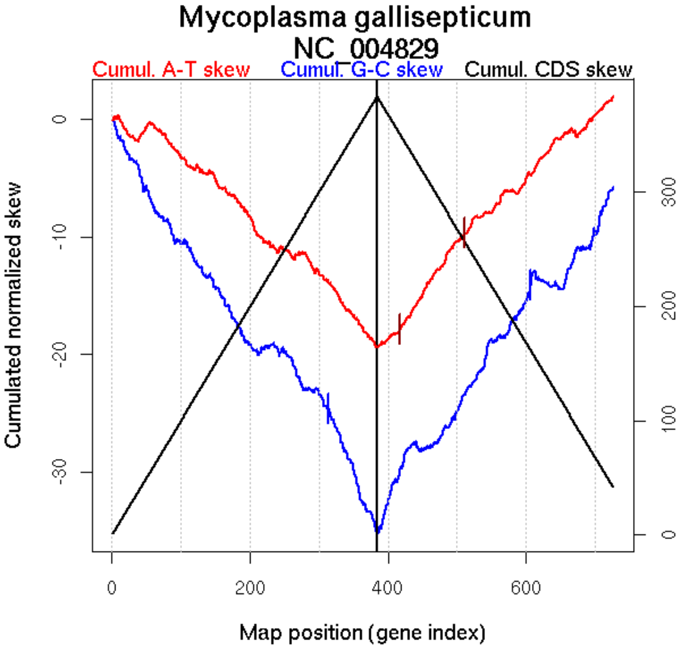
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	107 (176.665 kb)	leading	0.154
	108(177.2035 kb)	411 (1009.728 kb)	NA	0.042
GC-skew reverse	412 (0 kb)	545 (567.025 kb)	NA	-0.004
	546(568.0105 kb)	812 (1009.728 kb)	lagging	-0.106
AT-skew reverse	412 (0 kb)	691 (804.2 kb)	NA	0.028
	692(805.316 kb)	708(812.5855 kb)	lagging	-0.101
	709(813.0695 kb)	812(1009.728 kb)	lagging	0.038

204 Mycoplasma gallisepticum

Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
Accession number: NC_004829; **Genome size (bp)**: 996422.
Number of genes: 726.
Oriloc predictions: Origin 2 kb Terminus 521 kb
Worning et al., 2006: Origin 524 kb Terminus 0 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 79.183 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 3.86 kb
Consensus predictions: Origin 2 kb Terminus 521 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	314	NA	531
GC-skew reverse	606	NA	773
AT-skew reverse	417	NA	246
	511	NA	618

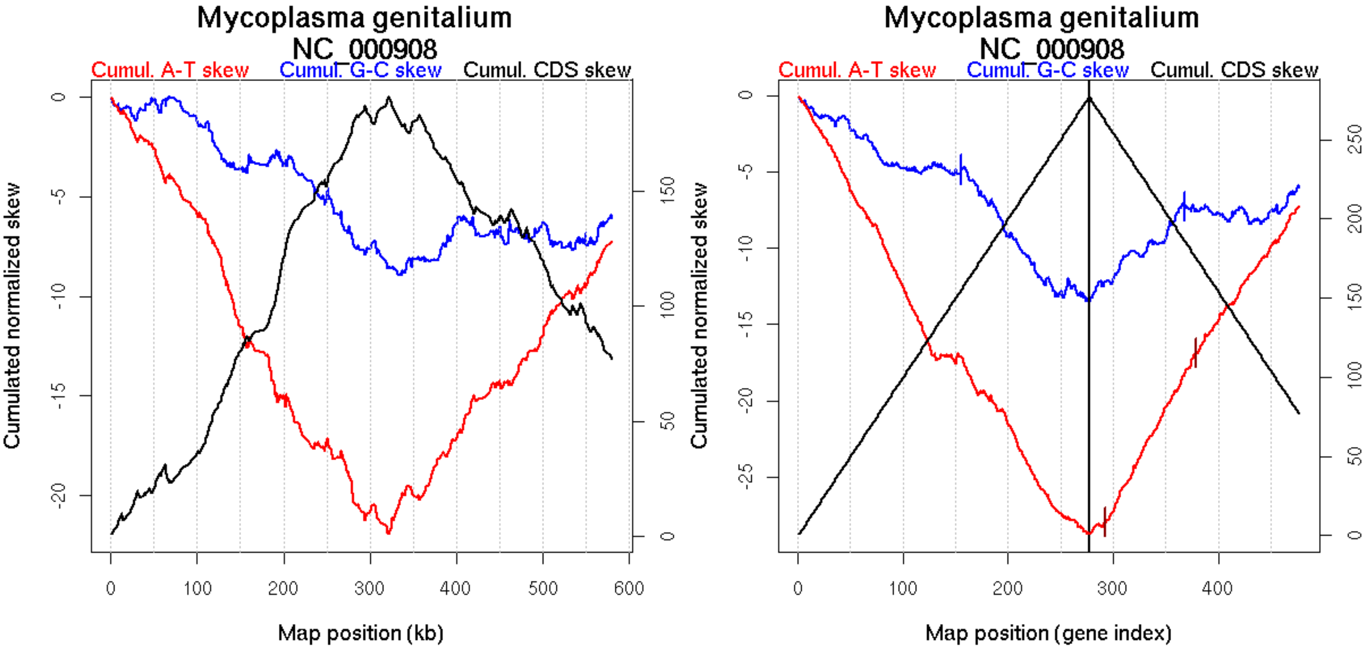
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	314 (531.4805 kb)	leading	-0.074
	315(539.8395 kb)	384 (996.422 kb)	lagging	-0.151
GC-skew reverse	385 (0 kb)	606 (773.091 kb)	NA	0.083
	607(775.0285 kb)	726 (996.422 kb)	lagging	0.067
AT-skew reverse	385 (0 kb)	417 (246.24 kb)	leading	0.044
	418(285.384 kb)	511(618.0915 kb)	NA	0.09
	512(619.1265 kb)	726(996.422 kb)	lagging	0.053

More G than C on the leading strand for replication - for forward encoded genes.

205 Mycoplasma genitalium

Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
Accession number: NC_000908; **Genome size (bp)**: 580076.
Number of genes: 477.
Oriloc predictions: Origin 0 kb Terminus 321 kb
Worning et al., 2006: Origin 580 kb Terminus 296 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 173.22 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 577.92 kb
Consensus predictions: Origin 0 kb Terminus 321 kb



Significant breakpoints (p-value <0.05):

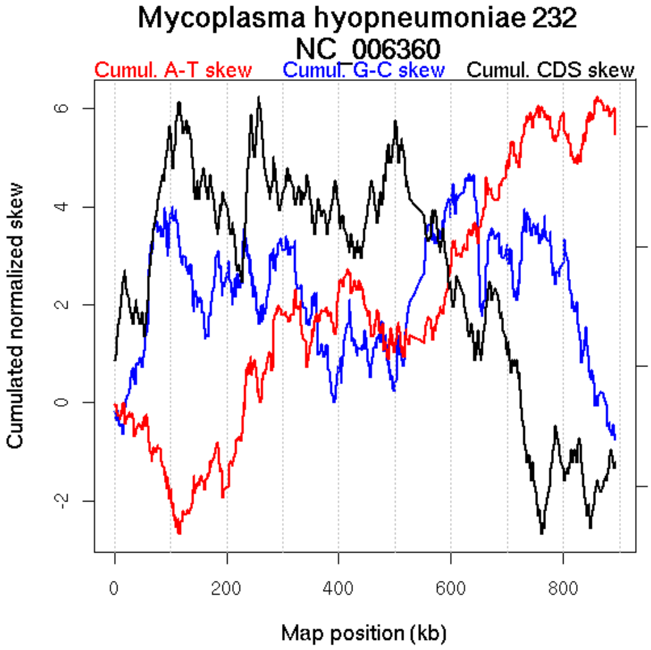
	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	155	NA	205
GC-skew reverse	368	NA	410
AT-skew reverse	293	NA	66
	379	NA	426

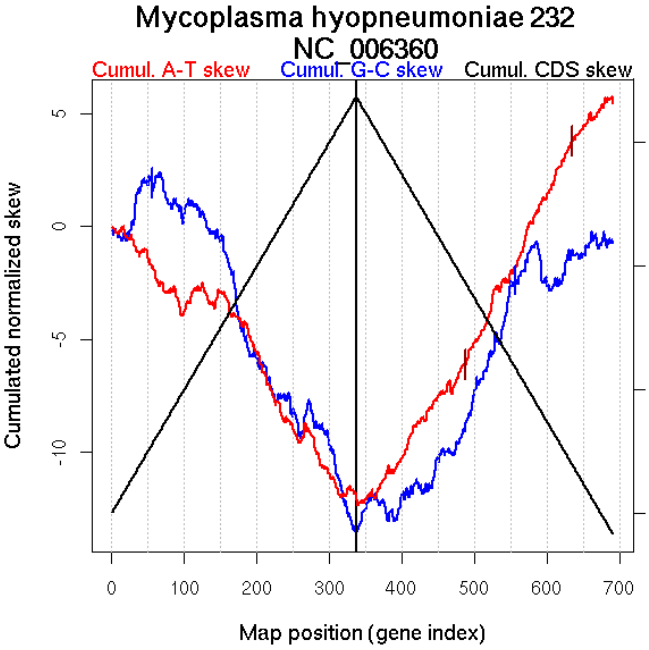
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	155 (204.877 kb)	leading	-0.034
	156(205.687 kb)	277 (580.033 kb)	NA	-0.077
GC-skew reverse	278 (0 kb)	368 (409.8255 kb)	NA	0.06
	369(411.404 kb)	477 (580.033 kb)	lagging	0.006
AT-skew reverse	278 (0 kb)	293 (66.47 kb)	leading	0.04
	294(66.9365 kb)	379(425.6075 kb)	NA	0.129
	380(430.7755 kb)	477(580.033 kb)	lagging	0.096

206 Mycoplasma hyopneumoniae 232

Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
Accession number: NC_006360; **Genome size (bp)**: 892758.
Number of genes: 691.
Oriloc predictions: Origin NA Terminus NA
Worning et al., 2006: Origin 513 kb Terminus 803 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 153.526 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): NA
Consensus predictions: Origin NA Terminus NA





Significant breakpoints (p-value <0.05):

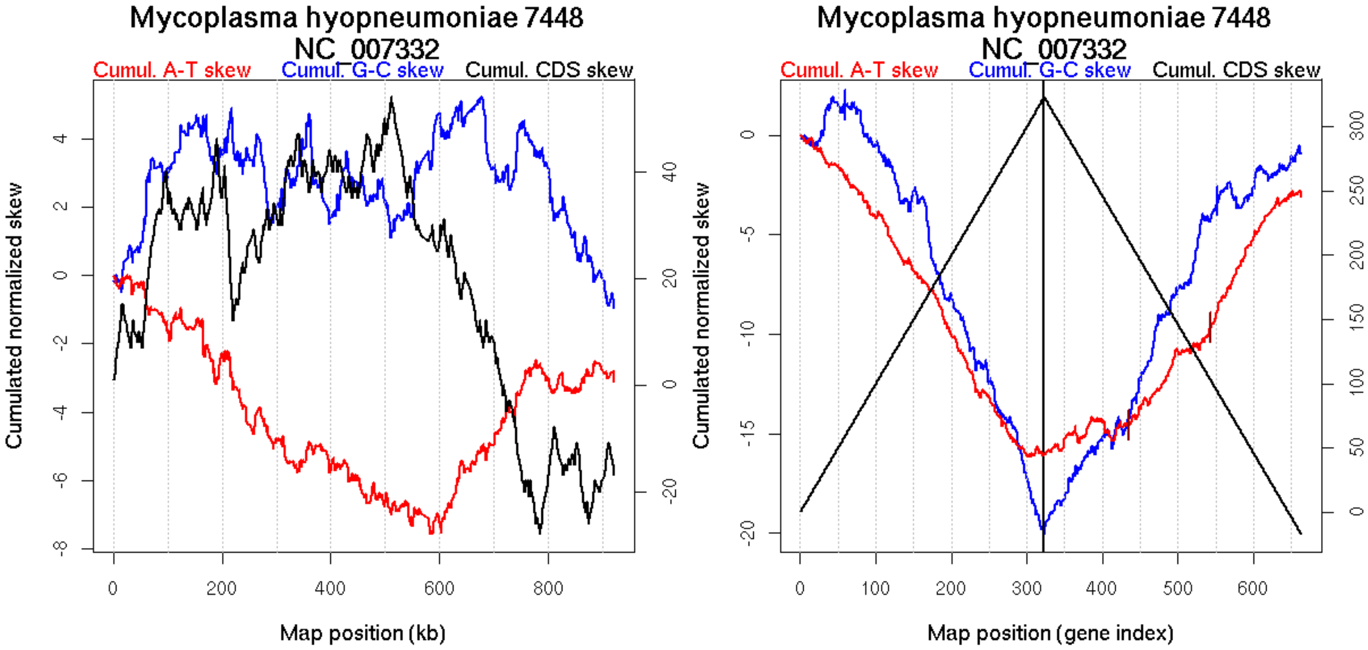
	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	55	NA	94
GC-skew reverse	557	NA	578
AT-skew reverse	488	NA	394
	635	NA	739

Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	55 (94.2295 kb)	NA	0.062
	56(94.538 kb)	337 (892.606 kb)	NA	-0.057
GC-skew reverse	338 (0 kb)	557 (578.338 kb)	NA	0.045
	558(580.26 kb)	691 (892.606 kb)	NA	0.011
AT-skew reverse	338 (0 kb)	488 (394.411 kb)	NA	0.045
	489(395.9235 kb)	635(738.8595 kb)	NA	0.067
	636(741.125 kb)	691(892.606 kb)	NA	0.035

207 Mycoplasma hyopneumoniae 7448

Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
Accession number: NC_007332; **Genome size (bp)**: 920079.
Number of genes: 663.
Oriloc predictions: Origin NA Terminus NA
Worning et al., 2006: Origin 511 kb Terminus 787 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 534.263 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): NA
Consensus predictions: Origin NA Terminus NA



Significant breakpoints (p-value <0.05):

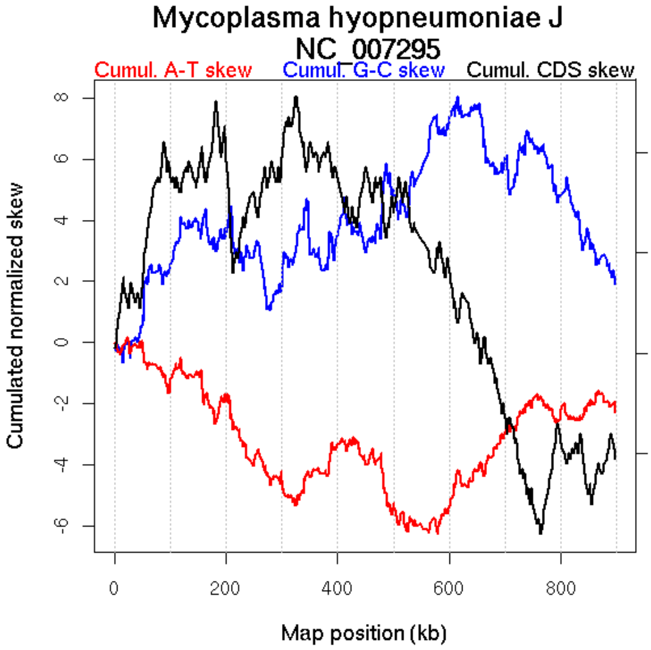
	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	60	NA	114
GC-skew reverse	552	NA	636
AT-skew reverse	435	NA	325
	543	NA	623

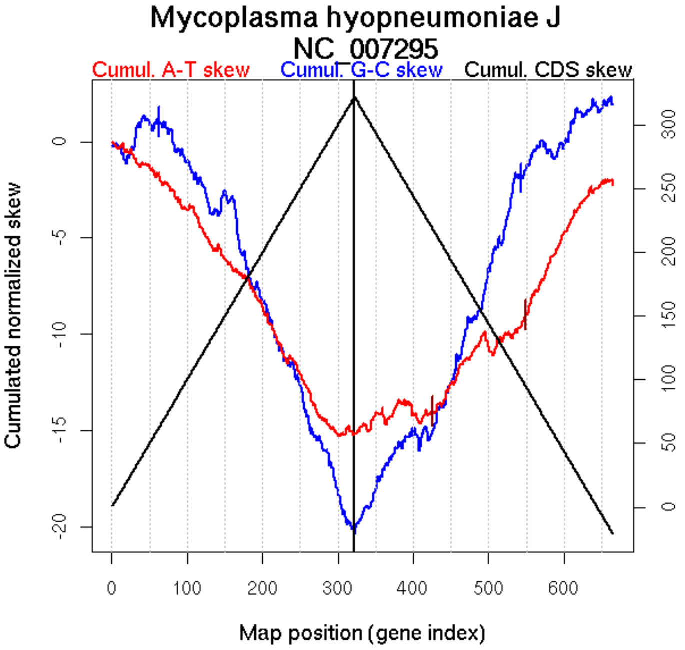
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	60 (113.937 kb)	NA	0.043
	61(119.5225 kb)	323 (920.079 kb)	NA	-0.083
GC-skew reverse	324 (0 kb)	552 (635.995 kb)	NA	0.071
	553(638.17 kb)	663 (920.079 kb)	NA	0.021
AT-skew reverse	324 (0 kb)	435 (325.102 kb)	NA	0.012
	436(328.6365 kb)	543(622.785 kb)	NA	0.044
	544(625.0725 kb)	663(920.079 kb)	NA	0.059

208 Mycoplasma hyopneumoniae J

Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
Accession number: NC_007295; **Genome size (bp)**: 897405.
Number of genes: 665.
Oriloc predictions: Origin NA Terminus NA
Worning et al., 2006: Origin 765 kb Terminus 451 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 288.356 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): NA
Consensus predictions: Origin NA Terminus NA





Significant breakpoints (p-value <0.05):

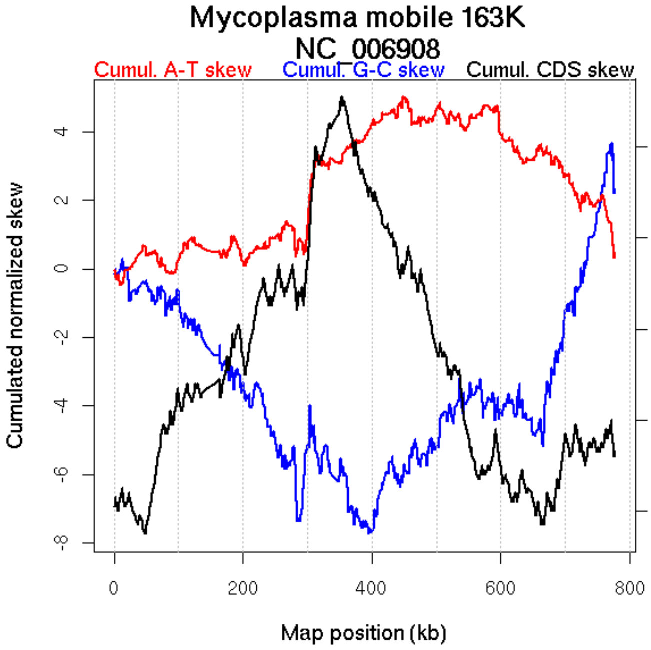
	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	63	NA	121
GC-skew reverse	543	NA	592
AT-skew reverse	426	NA	296
	549	NA	604

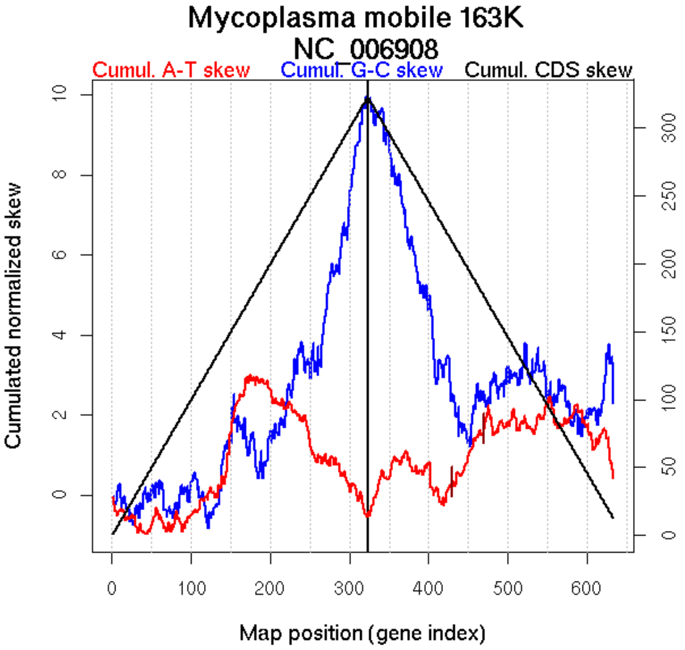
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	63 (120.7395 kb)	NA	0.033
	64(122.044 kb)	322 (897.405 kb)	NA	-0.085
GC-skew reverse	323 (0 kb)	543 (592.0195 kb)	NA	0.079
	544(594.982 kb)	665 (897.405 kb)	NA	0.032
AT-skew reverse	323 (0 kb)	426 (295.684 kb)	NA	0.009
	427(303.36 kb)	549(604.2765 kb)	NA	0.036
	550(605.319 kb)	665(897.405 kb)	NA	0.064

209 Mycoplasma mobile 163K

Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
Accession number: NC_006908; **Genome size (bp)**: 777079.
Number of genes: 633.
Oriloc predictions: Origin NA Terminus NA
Worning et al., 2006: Origin 354 kb Terminus 39 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 19.765 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): NA
Consensus predictions: Origin NA Terminus NA





Significant breakpoints (p-value <0.05):

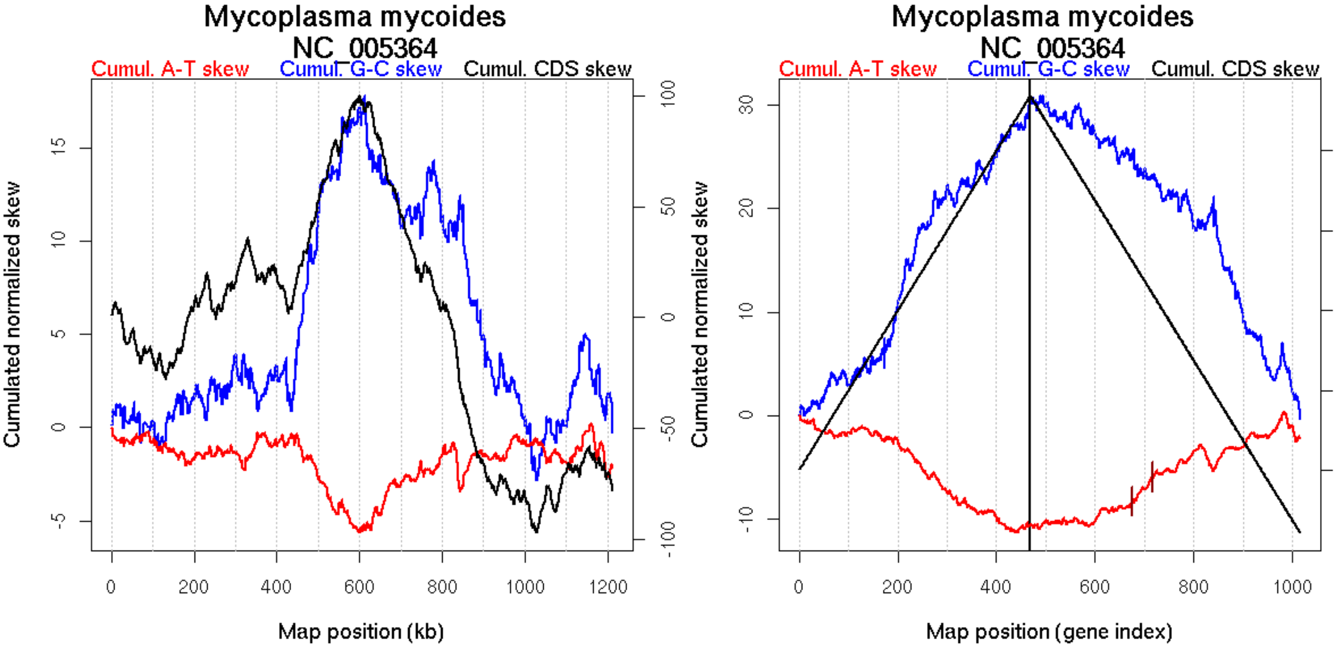
	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	261	NA	656
GC-skew reverse	438	NA	378
AT-skew reverse	430	NA	368
	470	NA	441

Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	261 (655.708 kb)	NA	0.014
	262(661.0755 kb)	323 (777.076 kb)	NA	0.106
GC-skew reverse	324 (0 kb)	438 (378.3985 kb)	NA	-0.076
	439(379.2175 kb)	633 (777.076 kb)	NA	0
AT-skew reverse	324 (0 kb)	430 (368.191 kb)	NA	-0.001
	431(369.233 kb)	470(440.7465 kb)	NA	0.04
	471(441.9965 kb)	633(777.076 kb)	NA	-0.003

210 Mycoplasma mycoides

Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
Accession number: NC_005364; **Genome size (bp)**: 1211703.
Number of genes: 1016.
Oriloc predictions: Origin NA Terminus NA
Worning et al., 2006: Origin 1075 kb Terminus 598 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1211.648 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.72 kb
Consensus predictions: Origin 0 kb Terminus 627 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	173	NA	387
GC-skew reverse	842	NA	847
AT-skew reverse	676	NA	610
	716	NA	665

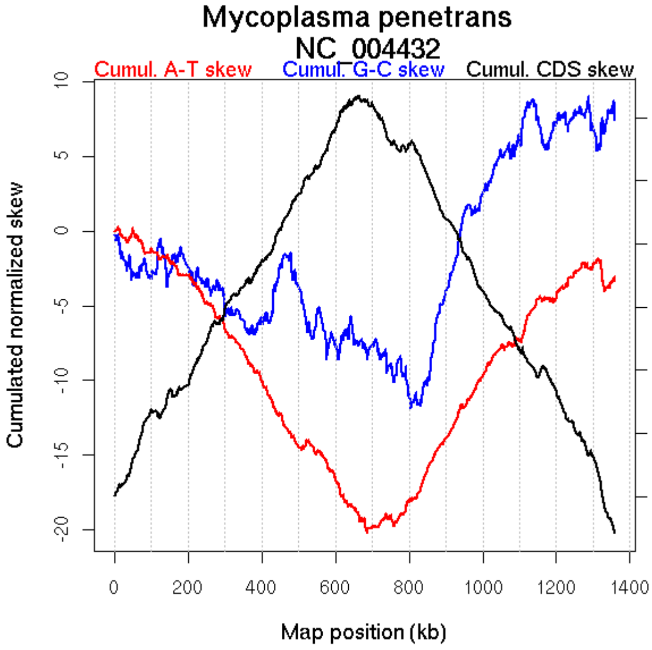
Segments:

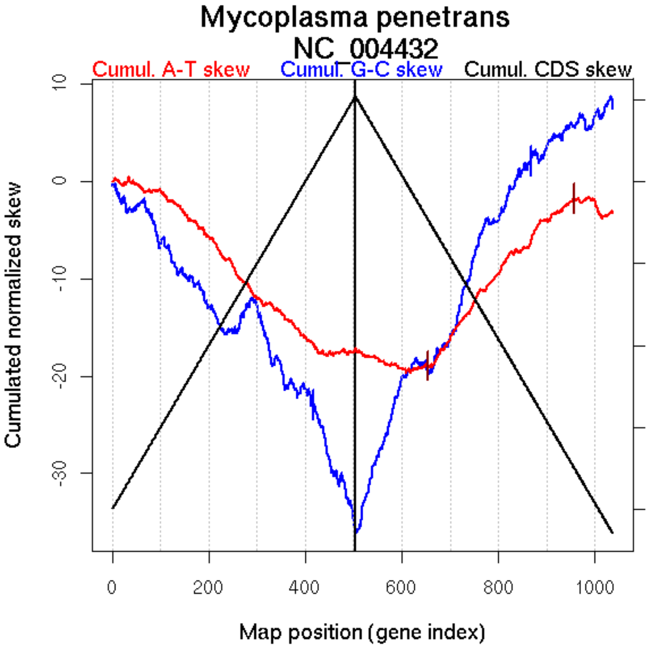
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	173 (386.8535 kb)	leading	0.033
	174(389.0915 kb)	469 (1211.534 kb)	NA	0.066
GC-skew reverse	470 (0 kb)	842 (846.5165 kb)	NA	-0.035
	843(847.5875 kb)	1016 (1211.534 kb)	lagging	-0.091
AT-skew reverse	470 (0 kb)	676 (610.114 kb)	leading	0.01
	677(611.492 kb)	716(664.7565 kb)	lagging	0.057
	717(665.367 kb)	1016(1211.534 kb)	lagging	0.017

More T than A on the leading strand for replication - for reverse encoded genes.

211 Mycoplasma penetrans

Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
Accession number: NC_004432; **Genome size (bp)**: 1358633.
Number of genes: 1037.
Oriloc predictions: Origin 0 kb Terminus 687 kb
Worning et al., 2006: Origin 0 kb Terminus 687 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 309.335 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.68 kb
Consensus predictions: Origin 0 kb Terminus 687 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	417	NA	660
GC-skew reverse	867	NA	1114
AT-skew reverse	653	NA	739
	958	NA	1278

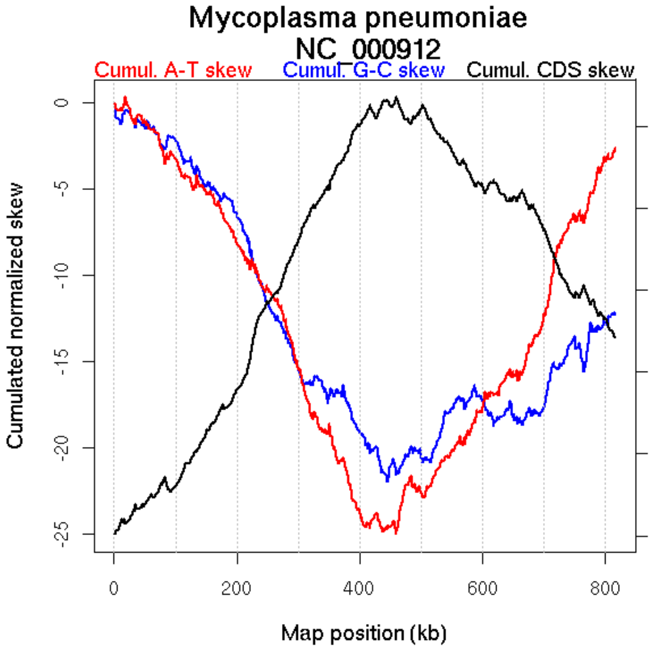
Segments:

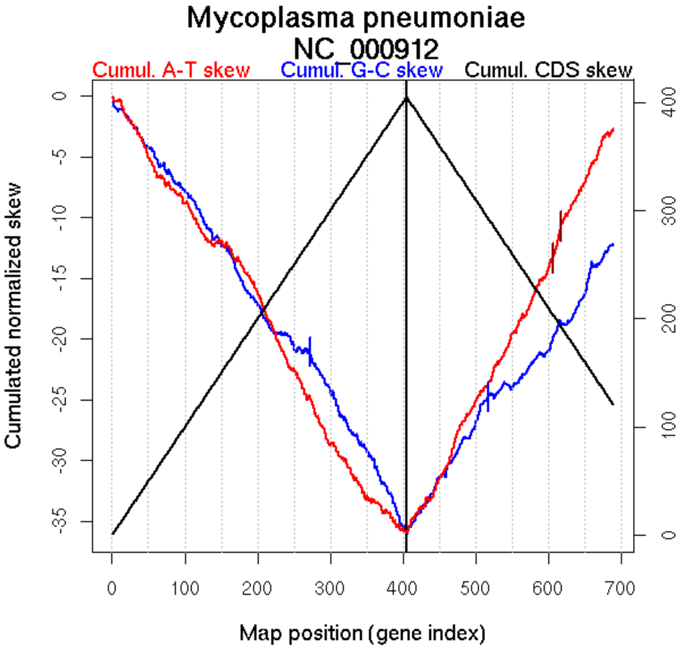
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	417 (660.269 kb)	leading	-0.052
	418(662.0785 kb)	504 (1358.463 kb)	lagging	-0.134
GC-skew reverse	505 (0 kb)	867 (1113.5705 kb)	NA	0.099
	868(1115.3355 kb)	1037 (1358.463 kb)	lagging	0.032
AT-skew reverse	505 (0 kb)	653 (739.333 kb)	NA	-0.013
	654(740.376 kb)	958(1277.5855 kb)	lagging	0.059
	959(1278.4845 kb)	1037(1358.463 kb)	lagging	-0.027

More G than C on the leading strand for replication - for forward encoded genes.

212 Mycoplasma pneumoniae

Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
Accession number: NC_000912; **Genome size (bp)**: 816394.
Number of genes: 689.
Oriloc predictions: Origin 0 kb Terminus 445 kb
Worning et al., 2006: Origin 446 kb Terminus 1 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 672.657 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 814.13 kb
Consensus predictions: Origin 0 kb Terminus 445 kb





Significant breakpoints (p-value <0.05):

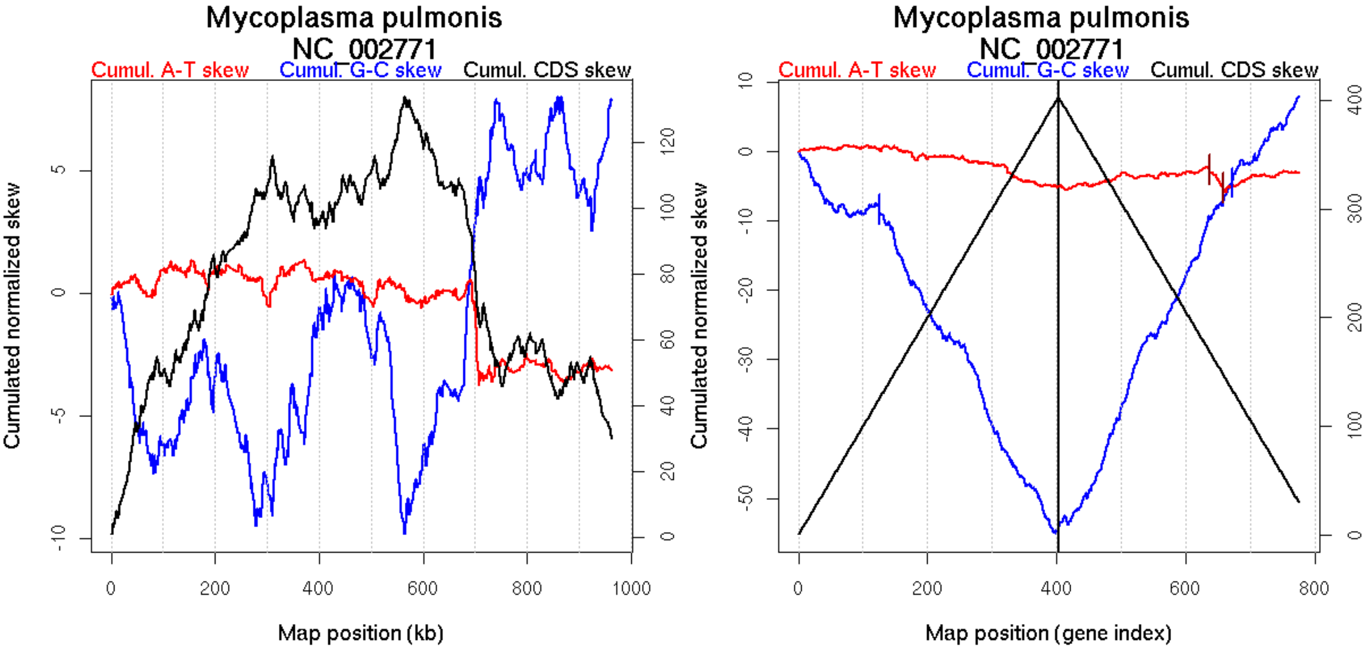
	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	272	NA	374
GC-skew reverse	517	NA	556
AT-skew reverse	606	NA	706
	617	NA	717

Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	272 (373.8325 kb)	leading	-0.083
	273(374.755 kb)	405 (816.338 kb)	NA	-0.106
GC-skew reverse	406 (0 kb)	517 (556.3135 kb)	NA	0.098
	518(557.594 kb)	689 (816.338 kb)	lagging	0.078
AT-skew reverse	406 (0 kb)	606 (706.3495 kb)	NA	0.113
	607(707.425 kb)	617(717.0645 kb)	lagging	0.243
	618(718.062 kb)	689(816.338 kb)	lagging	0.118

213 Mycoplasma pulmonis

Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
Accession number: NC_002771; **Genome size (bp)**: 963879.
Number of genes: 776.
Oriloc predictions: Origin NA Terminus NA
Worning et al., 2006: Origin 960 kb Terminus 570 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 0.105 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): NA
Consensus predictions: Origin NA Terminus NA



Significant breakpoints (p-value <0.05):

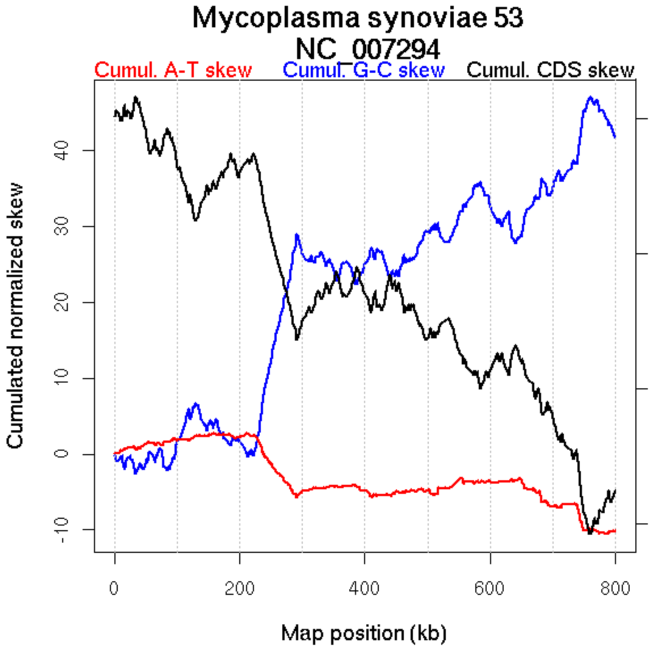
	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	125	NA	185
GC-skew reverse	672	NA	726
AT-skew reverse	637	NA	695
	658	NA	705

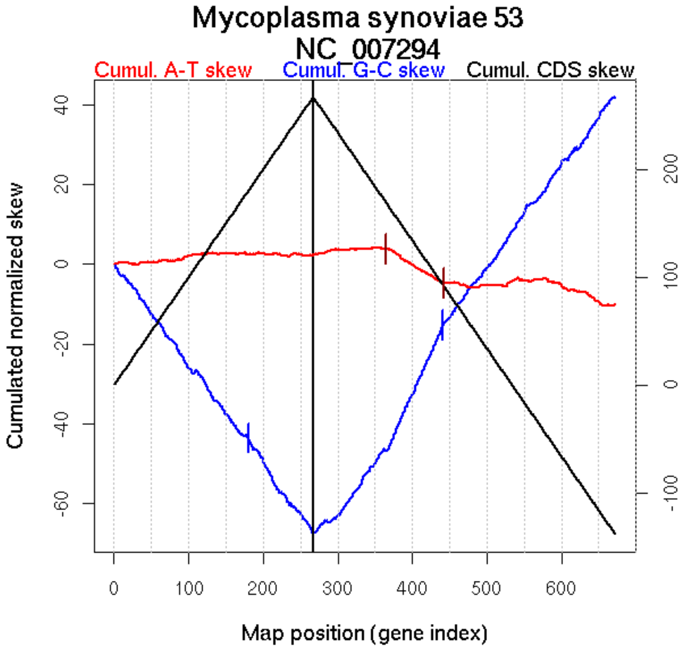
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	125 (185.113 kb)	NA	-0.06
	126(186.946 kb)	403 (963.879 kb)	NA	-0.168
GC-skew reverse	404 (0 kb)	672 (726.192 kb)	NA	0.197
	673(727.589 kb)	776 (963.879 kb)	NA	0.106
AT-skew reverse	404 (0 kb)	637 (695.0845 kb)	NA	0.011
	638(695.4375 kb)	658(705.216 kb)	NA	-0.121
	659(706.1135 kb)	776(963.879 kb)	NA	0.021

214 Mycoplasma synoviae 53

Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
Accession number: NC_007294; **Genome size (bp)**: 799476.
Number of genes: 672.
Oriloc predictions: Origin NA Terminus NA
Worning et al., 2006: Origin 292 kb Terminus 52 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 793.728 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.74 kb
Consensus predictions: Origin NA Terminus NA





Significant breakpoints (p-value <0.05):

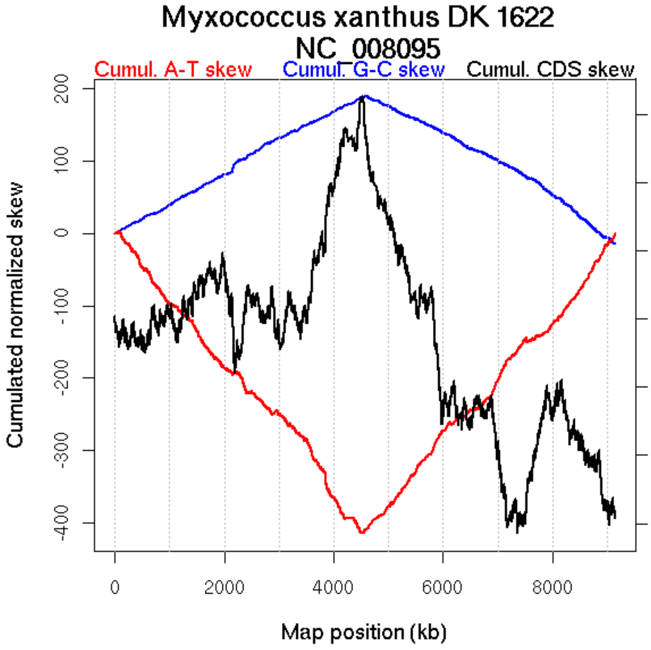
	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	180	NA	514
GC-skew reverse	441	NA	314
AT-skew reverse	364	NA	194
	442	NA	321

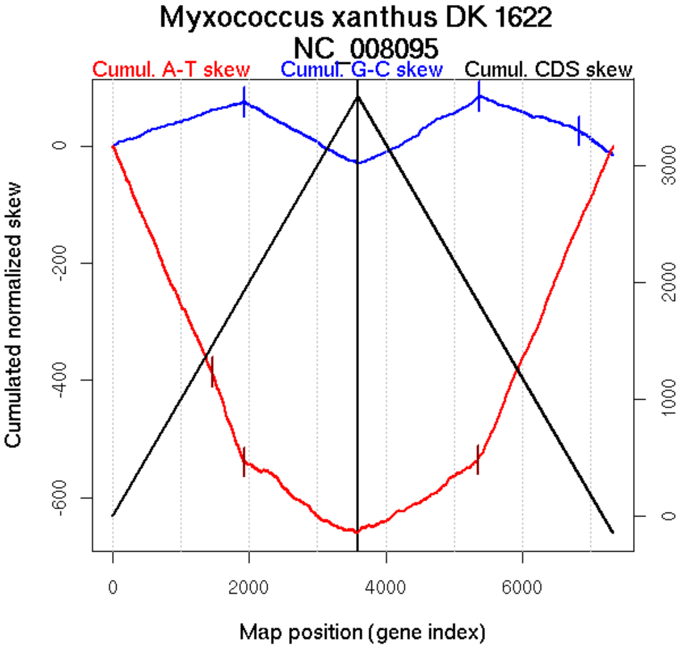
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	180 (513.876 kb)	NA	-0.25
	181(516.1825 kb)	267 (799.473 kb)	NA	-0.265
GC-skew reverse	268 (0 kb)	441 (313.8185 kb)	NA	0.303
	442(321.017 kb)	672 (799.473 kb)	NA	0.25
AT-skew reverse	268 (0 kb)	364 (194.042 kb)	NA	0.014
	365(195.3625 kb)	442(321.017 kb)	NA	-0.117
	443(328.598 kb)	672(799.473 kb)	NA	-0.019

215 Myxococcus xanthus DK 1622

Bacteria; Proteobacteria; Deltaproteobacteria; Myxococcales; Cystobacterineae; Myxococcaceae; Myxococcus.
Accession number: NC_008095; **Genome size (bp)**: 9139763.
Number of genes: 7330.
Oriloc predictions: Origin 0 kb Terminus 4570 kb
Worning et al., 2006: Origin 22 kb Terminus 4540 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 21.429 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.76 kb
Consensus predictions: Origin 0 kb Terminus 4570 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1925	0	4593
GC-skew reverse	5371	0	4568
	6841	0.01333	8141
AT-skew forward	1456	0.03	3508
	1923	0	4587
AT-skew reverse	5348	0	4497

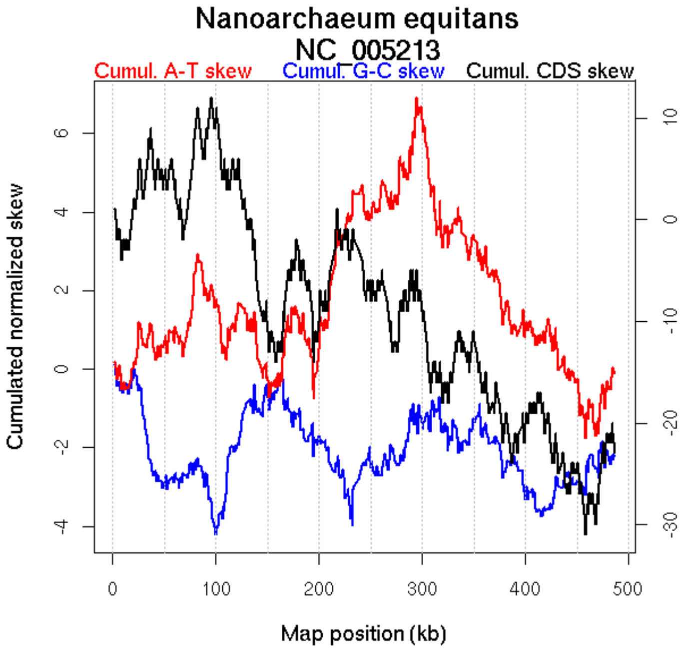
Segments:

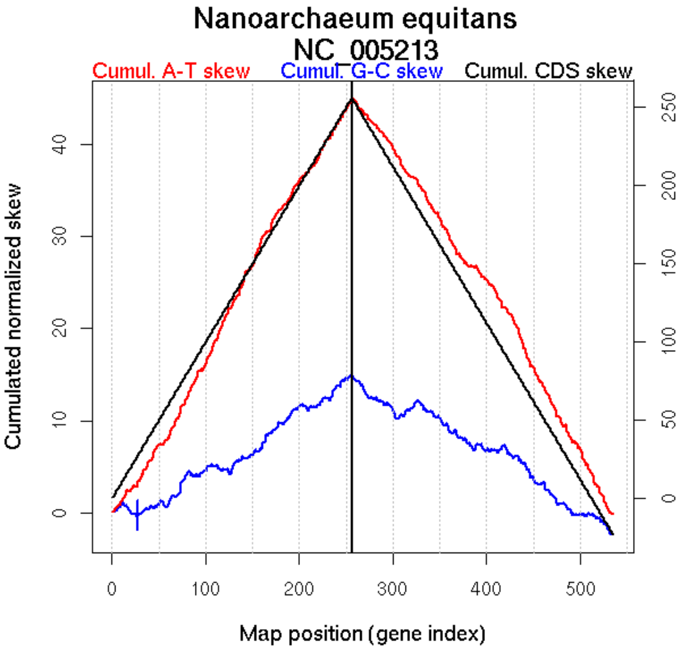
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1925 (4592.637 kb)	leading	0.039
	1926(4599.503 kb)	3593 (9139.599 kb)	lagging	-0.064
GC-skew reverse	3594 (0 kb)	5371 (4568.489 kb)	leading	0.066
	5372(4569.8415 kb)	6841 (8141.271 kb)	lagging	-0.038
	6842(8148.7405 kb)	7330 (9139.599 kb)	lagging	-0.085
AT-skew forward	1 (0 kb)	1456 (3508.406 kb)	leading	-0.265
	1457(3514.6655 kb)	1923 (4587.3395 kb)	leading	-0.334
	1924(4588.032 kb)	3593 (9139.599 kb)	lagging	-0.083
AT-skew reverse	3594 (0 kb)	5348 (4496.713 kb)	leading	0.07
	5349(4521.964 kb)	7330(9139.599 kb)	lagging	0.276

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

216 Nanoarchaeum equitans

Archaea; Nanoarchaeota; Nanoarchaeum.
Accession number: NC_005213; **Genome size (bp)**: 490885.
Number of genes: 535.
Oriloc predictions: Origin NA Terminus NA
Worning et al., 2006: Origin 387 kb Terminus 83 kb
Position(s) of the ORC/Cdc6 gene(s): NA
Consensus predictions: Origin NA Terminus NA





Significant breakpoints (p-value <0.05):

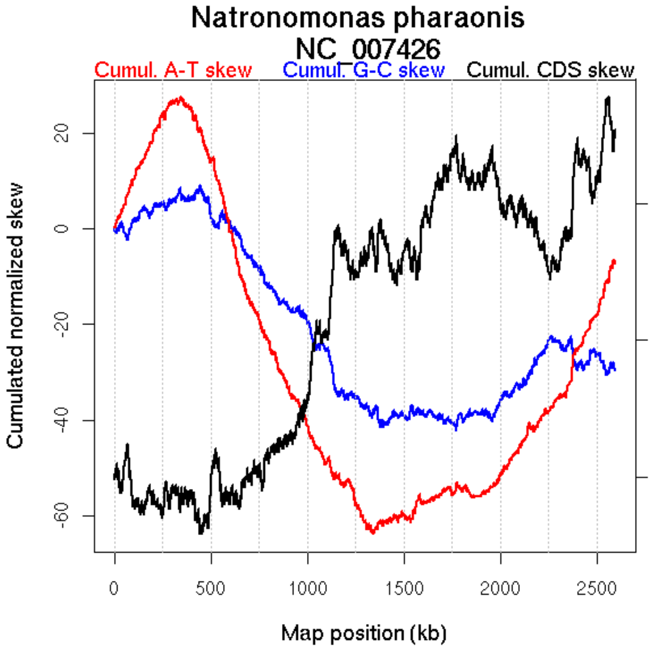
	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	28	0.04667	48

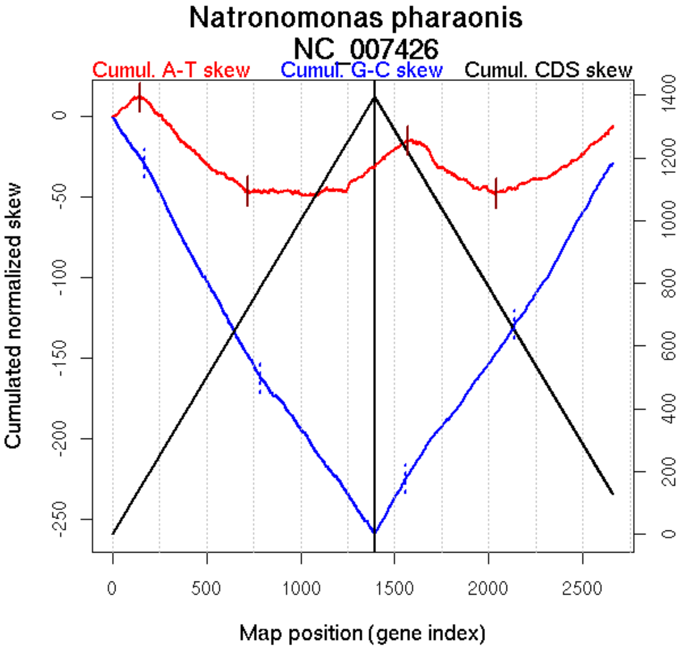
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	28 (47.892 kb)	NA	-0.028
	29(50.218 kb)	256 (486.962 kb)	NA	0.065

217 Natronomonas pharaonis

Archaea; Euryarchaeota; Halobacteria; Halobacteriales; Halobacteriaceae; Natronomonas.
Accession number: NC_007426; **Genome size (bp)**: 2595221.
Number of genes: 2661.
Oriloc predictions: Origin 339 kb Terminus 1320 kb
Worning et al., 2006: Origin 1334 kb Terminus 301 kb
Position(s) of the ORC/Cdc6 gene(s): 304.09 kb, 1488.11 kb, 1567.16 kb, 299.36 kb, 304.09 kb, 1488.11 kb, 1567.16 kb
Consensus predictions: Origin 339 kb Terminus 1320 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	168	0.06333	348
	788	0.05333	1465
	168	0.06333	348
	788	0.05333	1465
GC-skew reverse	1558	0.05333	333
	2139	0.11667	1533
	1558	0.05333	333
	2139	0.11667	1533
AT-skew forward	146	0.00333	307
	719	0.02333	1322
AT-skew reverse	1572	0.01333	354
	2039	0.02667	1343

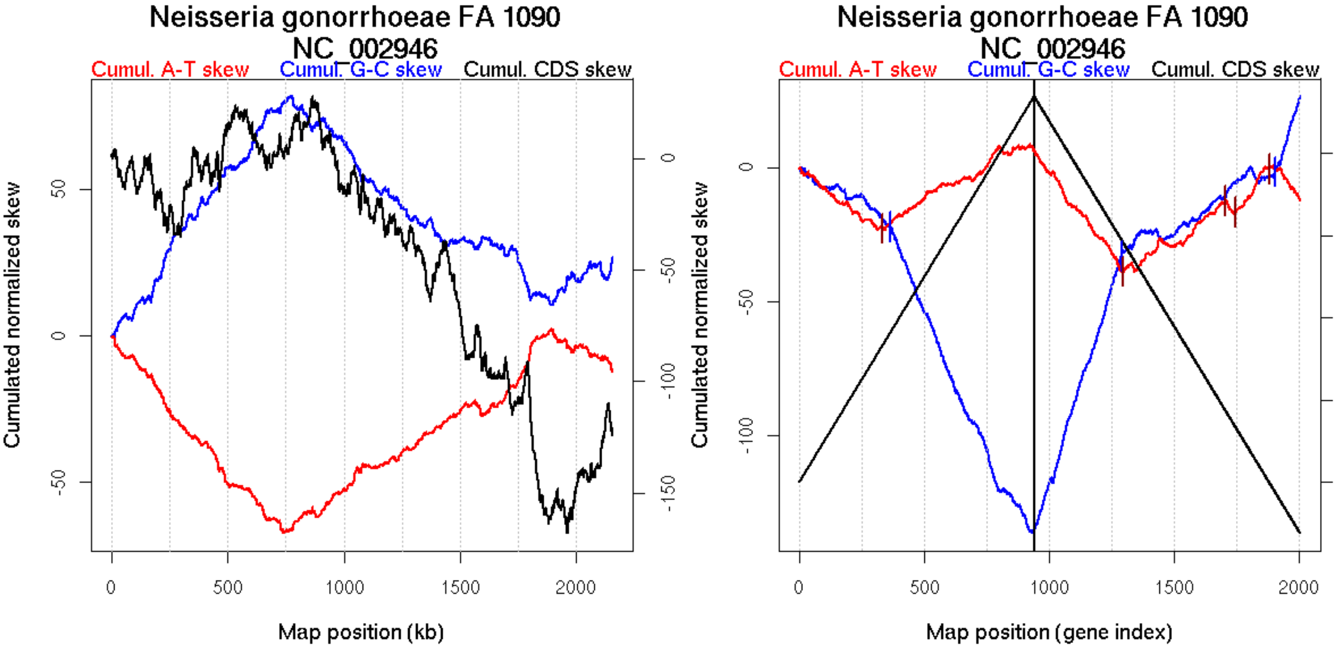
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	168 (347.948 kb)	lagging	-0.168
	169(350.9265 kb)	168 (347.948 kb)	leading	0.21
	169(350.9265 kb)	788 (1465.195 kb)	leading	-0.215
	789(1465.921 kb)	788 (1465.195 kb)	lagging	0.1
	789(1465.921 kb)	1394 (2595.209 kb)	lagging	-0.161
GC-skew reverse	1395 (0 kb)	1558 (332.7265 kb)	lagging	0.207
	1559(334.33 kb)	1558 (332.7265 kb)	lagging	-0.079
	1559(334.33 kb)	2139 (1533.052 kb)	NA	0.159
	2140(1534.0115 kb)	2139 (1533.052 kb)	lagging	-0.617
	2140(1534.0115 kb)	2661 (2595.209 kb)	lagging	0.199
AT-skew forward	1 (0 kb)	146 (306.632 kb)	lagging	0.093
	147(308.245 kb)	719 (1322.08 kb)	leading	-0.106
	720(1322.8535 kb)	1394 (2595.209 kb)	lagging	0.016
AT-skew reverse	1395 (0 kb)	1572 (354.3655 kb)	lagging	0.09
	1573(355.4835 kb)	2039(1342.621 kb)	leading	-0.078
	2040(1343.576 kb)	2661(2595.209 kb)	lagging	0.064

More T than A on the leading strand for replication.
More C than G on the leading strand for replication - for forward encoded genes.

218 Neisseria gonorrhoeae FA 1090

Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae; Neisseria.
Accession number: NC_002946; **Genome size (bp)**: 2153922.
Number of genes: 2002.
Oriloc predictions: Origin 11 kb Terminus 774 kb
Worning et al., 2006: Origin 1893 kb Terminus 761 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1233.358 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.94 kb
Consensus predictions: Origin 11 kb Terminus 774 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	365	0.00667	775
GC-skew reverse	1288	0	756
	1903	0	1917
AT-skew forward	332	0	717
AT-skew reverse	1294	0.02667	774
	1705	0.01833	1572
	1744	0.005	1618
	1878	0.00667	1848

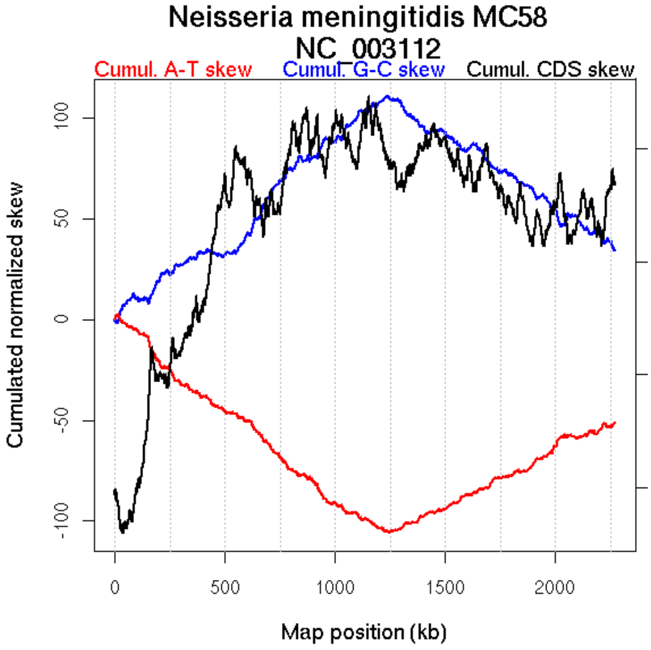
Segments:

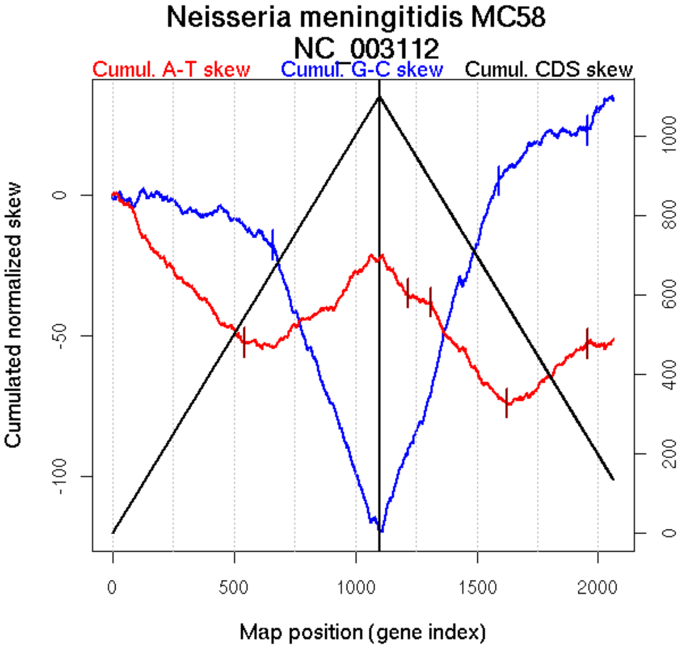
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	365 (774.99 kb)	leading	-0.051
	366(776.9635 kb)	939 (2153.788 kb)	lagging	-0.204
GC-skew reverse	940 (0 kb)	1288 (755.864 kb)	leading	0.294
	1289(757.2465 kb)	1903 (1916.5765 kb)	lagging	0.052
	1904(1918.323 kb)	2002 (2153.788 kb)	lagging	0.296
AT-skew forward	1 (0 kb)	332 (716.7335 kb)	leading	-0.071
	333(717.495 kb)	939 (2153.788 kb)	lagging	0.053
AT-skew reverse	940 (0 kb)	1294 (773.5205 kb)	leading	-0.122
	1295(776.304 kb)	1705(1572.0675 kb)	lagging	0.061
	1706(1574.3325 kb)	1744(1618.0545 kb)	lagging	-0.137
	1745(1619.8135 kb)	1878(1848.332 kb)	lagging	0.145
	1879(1852.491 kb)	2002(2153.788 kb)	lagging	-0.107

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

219 Neisseria meningitidis MC58

Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae; Neisseria.
Accession number: NC_003112; **Genome size (bp)**: 2272360.
Number of genes: 2063.
Oriloc predictions: Origin 12 kb Terminus 1246 kb
Worning et al., 2006: Origin 14 kb Terminus 1233 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1520.715 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 2005.17 kb
Consensus predictions: Origin 12 kb Terminus 1246 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	660	NA	1225
GC-skew reverse	1592	NA	1197
	1954	NA	2028
AT-skew forward	541	NA	979
AT-skew reverse	1217	NA	335
	1312	NA	621
	1625	NA	1253
	1958	NA	2033

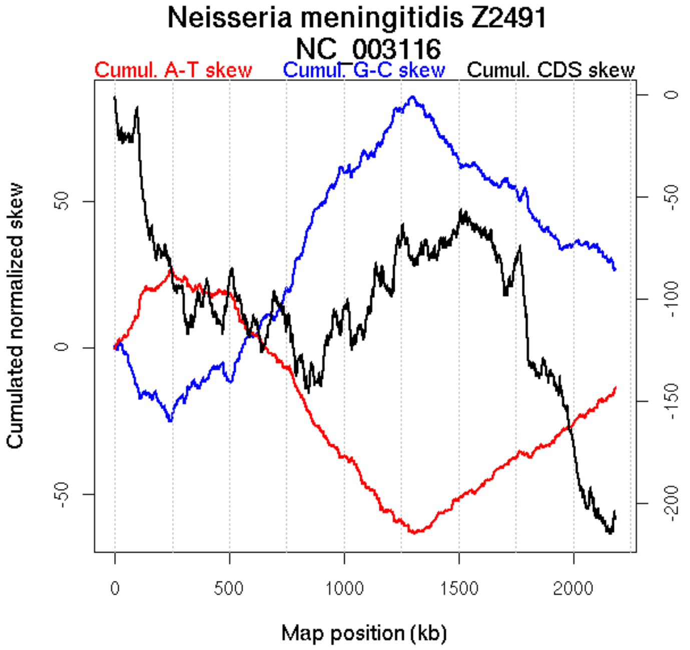
Segments:

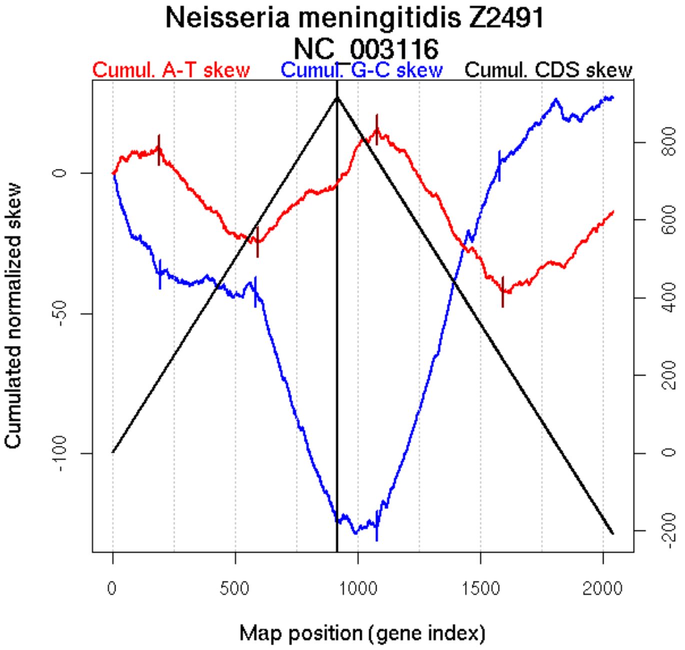
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	660 (1224.997 kb)	leading	-0.024
	661(1229.8305 kb)	1099 (2272.24 kb)	lagging	-0.231
GC-skew reverse	1100 (0 kb)	1592 (1196.904 kb)	leading	0.262
	1593(1198.027 kb)	1954 (2028.305 kb)	lagging	0.048
	1955(2029.0525 kb)	2063 (2272.24 kb)	lagging	0.115
AT-skew forward	1 (0 kb)	541 (978.745 kb)	leading	-0.1
	542(984.05 kb)	1099 (2272.24 kb)	NA	0.063
AT-skew reverse	1100 (0 kb)	1217 (335.003 kb)	leading	-0.125
	1218(337.182 kb)	1312(620.896 kb)	leading	-0.032
	1313(621.8015 kb)	1625(1252.7025 kb)	leading	-0.11
	1626(1253.258 kb)	1958(2032.6005 kb)	lagging	0.071
	1959(2033.2735 kb)	2063(2272.24 kb)	lagging	0.001

More T than A on the leading strand for replication - for reverse encoded genes.
More G than C on the leading strand for replication.

220 Neisseria meningitidis Z2491

Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales; Neisseriaceae; Neisseria.
Accession number: NC_003116; **Genome size (bp)**: 2184406.
Number of genes: 2040.
Oriloc predictions: Origin 239 kb Terminus 1290 kb
Worning et al., 2006: Origin 250 kb Terminus 1286 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1605.75 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 528.38 kb
Consensus predictions: Origin 220 kb Terminus 1290 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	194	NA	502
	582	NA	1255
GC-skew reverse	1079	NA	245
	1578	NA	1282
AT-skew forward	189	NA	497
	591	NA	1302
AT-skew reverse	1080	NA	246
	1593	NA	1310

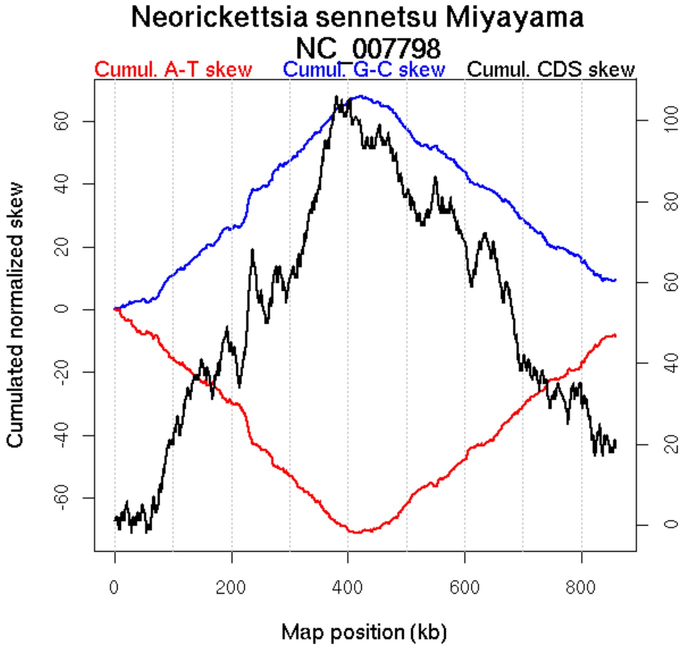
Segments:

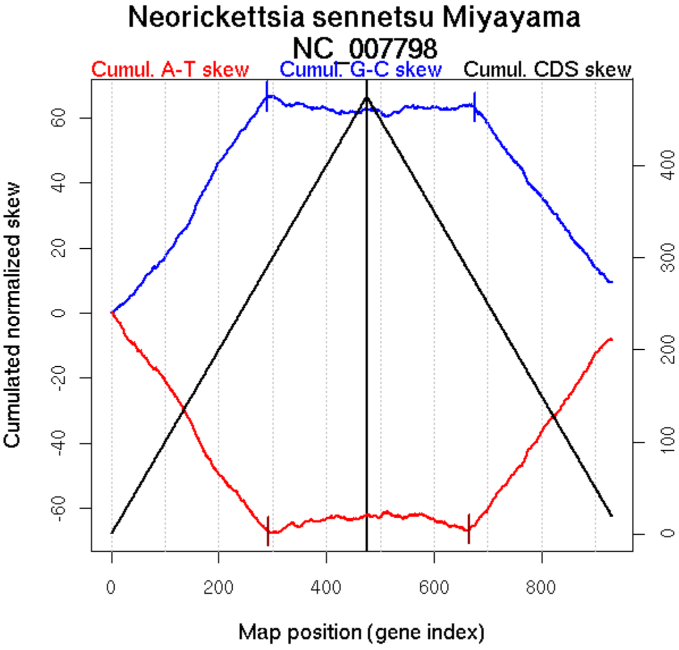
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	194 (502.309 kb)	NA	-0.163
	195(503.3815 kb)	582 (1254.9275 kb)	leading	-0.017
	583(1262.2445 kb)	916 (2184.369 kb)	lagging	-0.251
GC-skew reverse	917 (0 kb)	1079 (245.05 kb)	lagging	-0.016
	1080(246.0505 kb)	1578 (1282.228 kb)	leading	0.273
	1579(1282.9745 kb)	2040 (2184.369 kb)	lagging	0.044
AT-skew forward	1 (0 kb)	189 (496.5965 kb)	NA	0.034
	190(498.018 kb)	591 (1302.1965 kb)	leading	-0.086
	592(1304.272 kb)	916 (2184.369 kb)	lagging	0.064
AT-skew reverse	917 (0 kb)	1080 (246.0505 kb)	lagging	0.122
	1081(247.772 kb)	1593(1309.8255 kb)	leading	-0.119
	1594(1313.208 kb)	2040(2184.369 kb)	lagging	0.063

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

221 Neorickettsia sennetsu Miyayama

Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales; Anaplasmataceae; Neorickettsia.
Accession number: NC_007798; **Genome size (bp)**: 859006.
Number of genes: 931.
Oriloc predictions: Origin 0 kb Terminus 421 kb
Worning et al., 2006: Origin 855 kb Terminus 432 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 275.287 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 221.03 kb
Consensus predictions: Origin 0 kb Terminus 421 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	289	0	417
GC-skew reverse	675	0	437
AT-skew forward	293	0	431
AT-skew reverse	666	0	422

Segments:

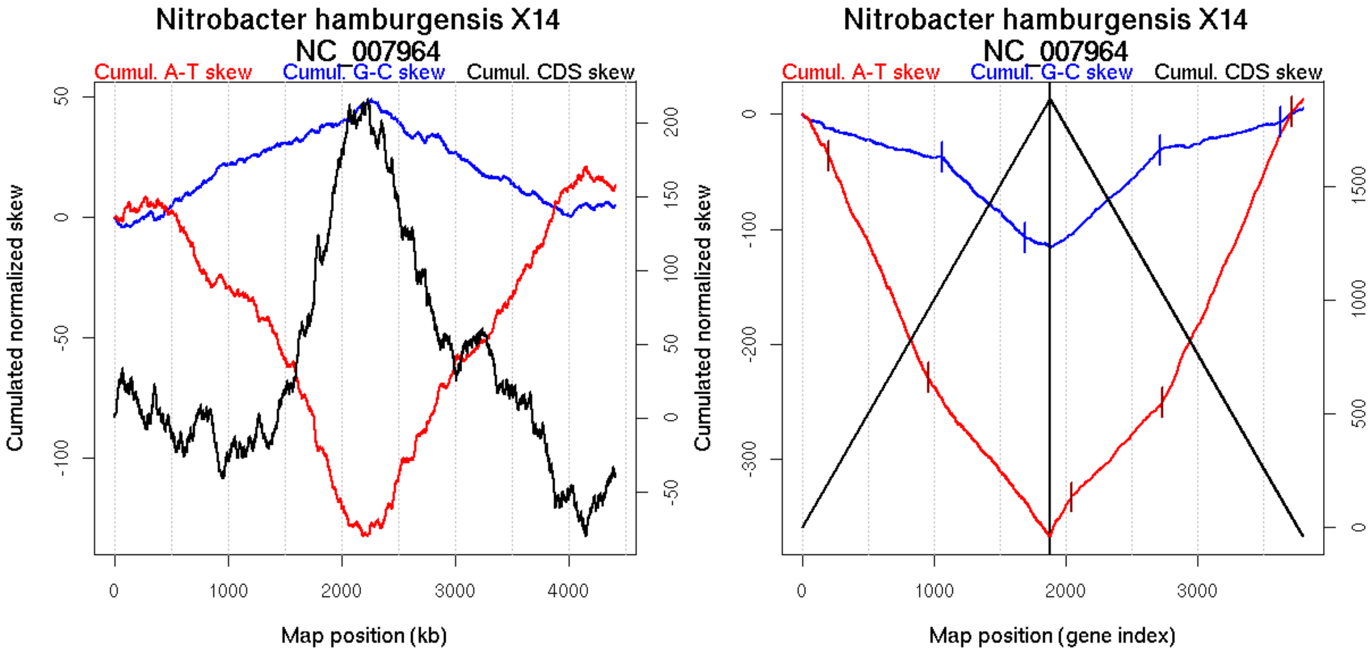
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	289 (417.3645 kb)	leading	0.246
	290(424.286 kb)	475 (858.852 kb)	lagging	-0.025
GC-skew reverse	476 (0 kb)	675 (437.4175 kb)	leading	0.01
	676(438.9625 kb)	931 (858.852 kb)	lagging	-0.217
AT-skew forward	1 (0 kb)	293 (431.2745 kb)	leading	-0.241
	294(436.523 kb)	475 (858.852 kb)	lagging	0.027
AT-skew reverse	476 (0 kb)	666 (421.7245 kb)	leading	-0.024
	667(423.2775 kb)	931(858.852 kb)	lagging	0.231

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

222 Nitrobacter hamburgensis X14

Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae; Nitrobacter.

Accession number: NC_007964; **Genome size (bp)**: 4406967.
Number of genes: 3804.
Oriloc predictions: Origin 130 kb Terminus 2244 kb
Worning et al., 2006: Origin 125 kb Terminus 2233 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 3026.606 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.82 kb
Consensus predictions: Origin 130 kb Terminus 2244 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1059	0.00667	2237
	1688	0.00667	3967
GC-skew reverse	2720	0.00667	2198
	3636	0.04333	3995
AT-skew forward	201	0.04667	459
	954	0.02	2018
AT-skew reverse	2044	0.03556	369
	2736	0.00222	2246
	3716	0.00222	4148

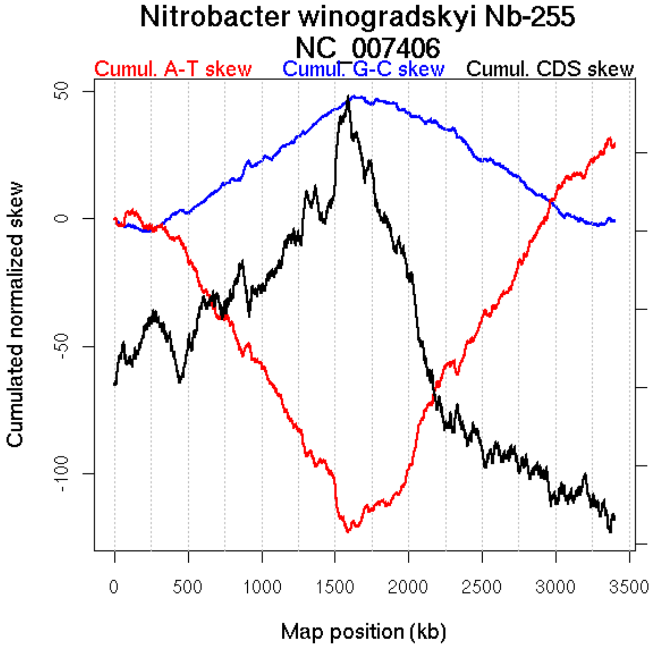
Segments:

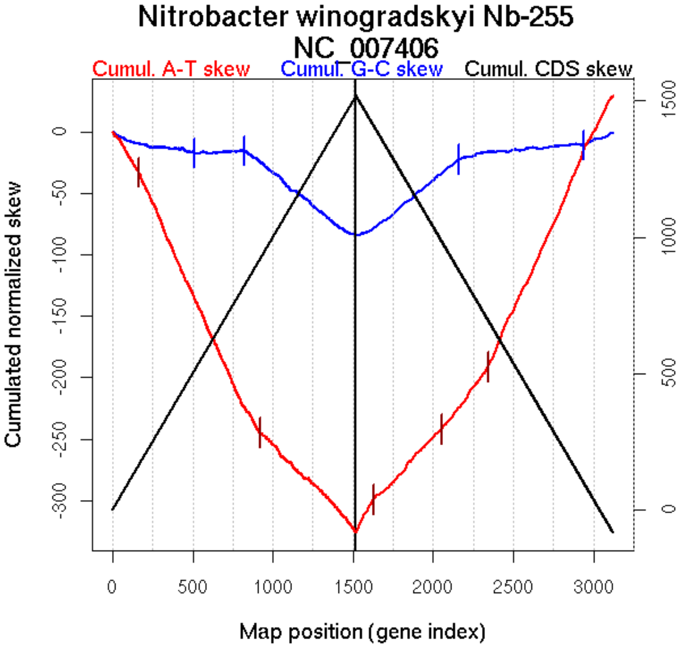
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1059 (2236.674 kb)	leading	-0.034
	1060(2242.7925 kb)	1688 (3966.516 kb)	lagging	-0.107
	1689(3969.062 kb)	1883 (4406.937 kb)	lagging	-0.039
GC-skew reverse	1884 (0 kb)	2720 (2198.5 kb)	leading	0.104
	2721(2200.975 kb)	3636 (3994.598 kb)	lagging	0.027
	3637(3995.303 kb)	3804 (4406.937 kb)	lagging	0.068
AT-skew forward	1 (0 kb)	201 (458.9955 kb)	NA	-0.188
	202(461.373 kb)	954 (2017.557 kb)	leading	-0.253
	955(2018.75 kb)	1883 (4406.937 kb)	lagging	-0.143
AT-skew reverse	1884 (0 kb)	2044 (368.7625 kb)	NA	0.202
	2045(369.912 kb)	2736(2245.9315 kb)	leading	0.12
	2737(2246.3055 kb)	3716(4148.3035 kb)	lagging	0.26
	3717(4152.2245 kb)	3804(4406.937 kb)	lagging	0.126

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

223 Nitrobacter winogradskyi Nb-255

Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae; Nitrobacter.
Accession number: NC_007406; **Genome size (bp)**: 3402093.
Number of genes: 3122.
Oriloc predictions: Origin 0 kb Terminus 1613 kb
Worning et al., 2006: Origin 241 kb Terminus 1591 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 2366.634 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1.28 kb, 2420.74 kb
Consensus predictions: Origin 0 kb Terminus 1613 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	511	NA	1053
	822	NA	1622
GC-skew reverse	2162	NA	1602
	2937	NA	3022
AT-skew forward	163	NA	329
	918	NA	1924
AT-skew reverse	1629	NA	297
	2052	NA	1292
	2341	NA	1903

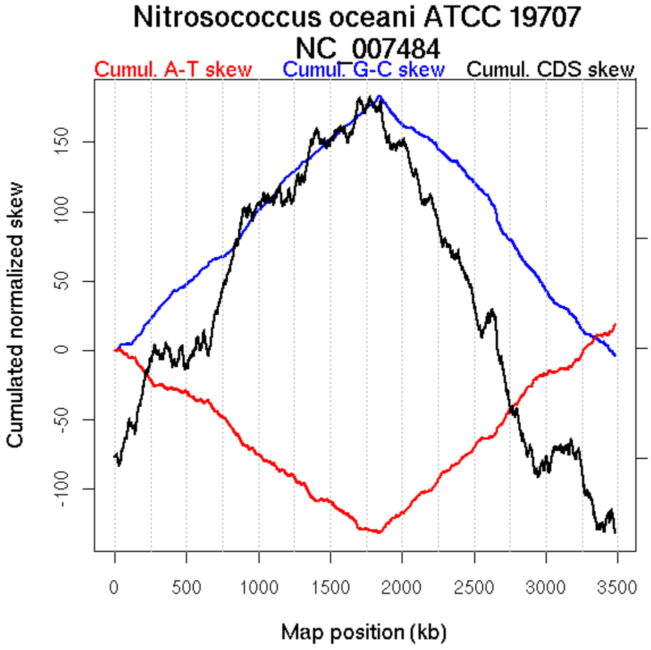
Segments:

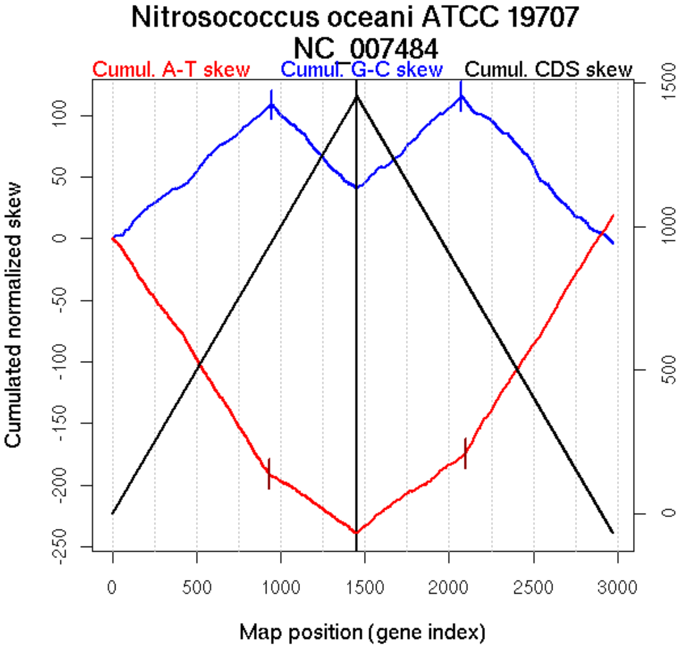
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	511 (1053.24 kb)	leading	-0.026
	512(1054.308 kb)	822 (1622.242 kb)	leading	0.007
	823(1625.363 kb)	1519 (3401.218 kb)	lagging	-0.105
GC-skew reverse	1520 (0 kb)	2162 (1601.9545 kb)	leading	0.103
	2163(1603.578 kb)	2937 (3021.5985 kb)	lagging	0.014
	2938(3026.647 kb)	3122 (3401.218 kb)	lagging	0.052
AT-skew forward	1 (0 kb)	163 (329.152 kb)	leading	-0.209
	164(330.2655 kb)	918 (1923.5765 kb)	leading	-0.287
	919(1925.218 kb)	1519 (3401.218 kb)	lagging	-0.131
AT-skew reverse	1520 (0 kb)	1629 (297.4475 kb)	leading	0.243
	1630(300.5415 kb)	2052(1292.04 kb)	leading	0.142
	2053(1308.042 kb)	2341(1903.2155 kb)	NA	0.175
	2342(1905.0565 kb)	3122(3401.218 kb)	lagging	0.288

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

224 Nitrosococcus oceani ATCC 19707

Bacteria; Proteobacteria; Gammaproteobacteria; Chromatiales; Chromatiaceae; Nitrosococcus.
Accession number: NC_007484; **Genome size (bp)**: 3481691.
Number of genes: 2974.
Oriloc predictions: Origin 0 kb Terminus 1834 kb
Worning et al., 2006: Origin 12 kb Terminus 1834 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1.553 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.85 kb, 1294.97 kb
Consensus predictions: Origin 0 kb Terminus 1834 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	944	0	1846
GC-skew reverse	2073	0	1836
AT-skew forward	933	0	1827
AT-skew reverse	2096	0	1869

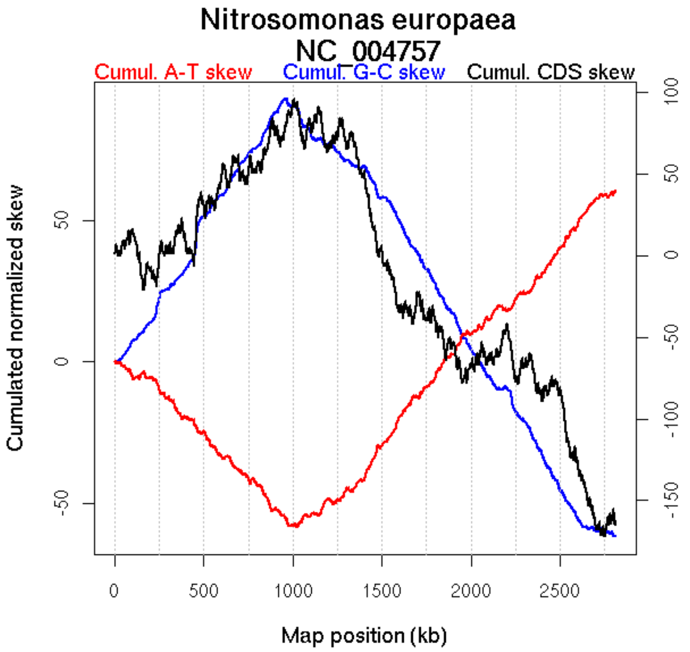
Segments:

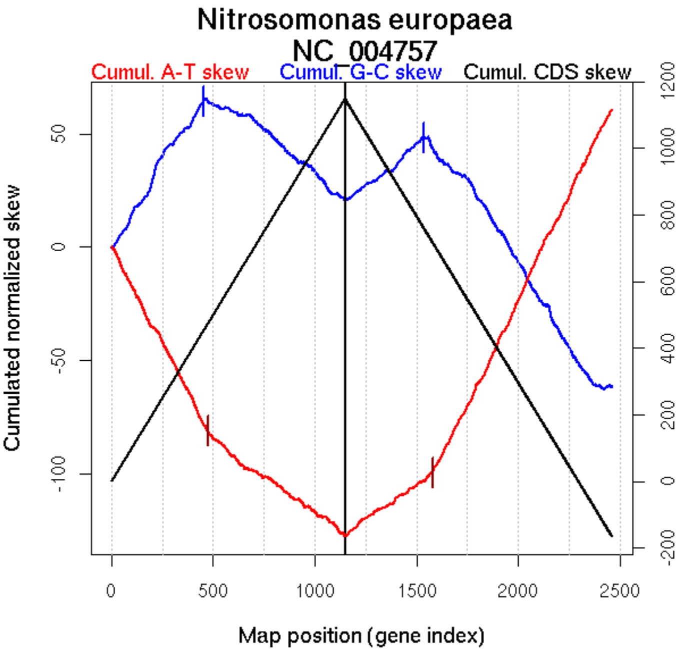
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	944 (1845.506 kb)	leading	0.117
	945(1846.842 kb)	1453 (3481.573 kb)	lagging	-0.14
GC-skew reverse	1454 (0 kb)	2073 (1835.6425 kb)	leading	0.122
	2074(1838.719 kb)	2974 (3481.573 kb)	lagging	-0.14
AT-skew forward	1 (0 kb)	933 (1826.995 kb)	leading	-0.207
	934(1827.771 kb)	1453 (3481.573 kb)	lagging	-0.093
AT-skew reverse	1454 (0 kb)	2096 (1869.154 kb)	leading	0.096
	2097(1870.527 kb)	2974(3481.573 kb)	lagging	0.219

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

225 Nitrosomonas europaea

Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales; Nitrosomonadaceae; Nitrosomonas.
Accession number: NC_004757; **Genome size (bp)**: 2812094.
Number of genes: 2461.
Oriloc predictions: Origin 0 kb Terminus 966 kb
Worning et al., 2006: Origin 24 kb Terminus 965 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1271.883 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.9 kb
Consensus predictions: Origin 0 kb Terminus 966 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	453	0	940
GC-skew reverse	1537	0	971
AT-skew forward	473	0	970
AT-skew reverse	1578	0	1049

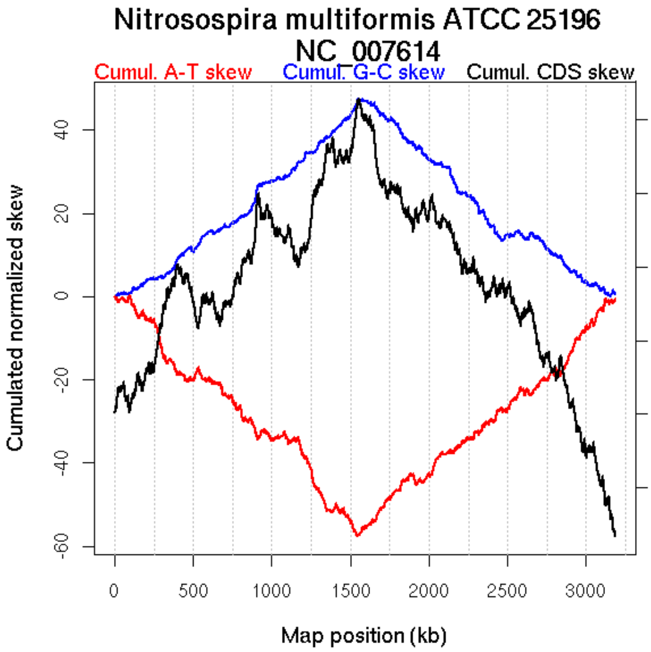
Segments:

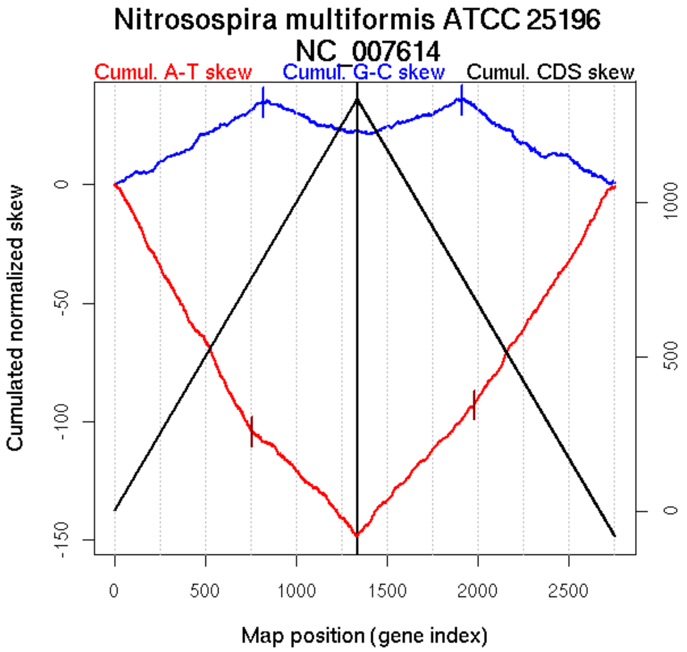
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	453 (940.105 kb)	leading	0.147
	454(942.472 kb)	1148 (2811.935 kb)	lagging	-0.067
GC-skew reverse	1149 (0 kb)	1537 (970.925 kb)	leading	0.072
	1538(975.0985 kb)	2461 (2811.935 kb)	lagging	-0.134
AT-skew forward	1 (0 kb)	473 (970.0765 kb)	leading	-0.17
	474(970.511 kb)	1148 (2811.935 kb)	lagging	-0.063
AT-skew reverse	1149 (0 kb)	1578 (1049.1565 kb)	leading	0.061
	1579(1051.2415 kb)	2461(2811.935 kb)	lagging	0.185

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

226 Nitrosospira multiformis ATCC 25196

Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales; Nitrosomonadaceae; Nitrosospira.
Accession number: NC_007614; **Genome size (bp)**: 3184243.
Number of genes: 2757.
Oriloc predictions: Origin 3154 kb Terminus 1562 kb
Worning et al., 2006: Origin 3 kb Terminus 1551 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1191.179 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.78 kb
Consensus predictions: Origin 3154 kb Terminus 1562 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	817	0	1693
GC-skew reverse	1911	0	1554
AT-skew forward	758	0	1524
AT-skew reverse	1980	0.00667	1671

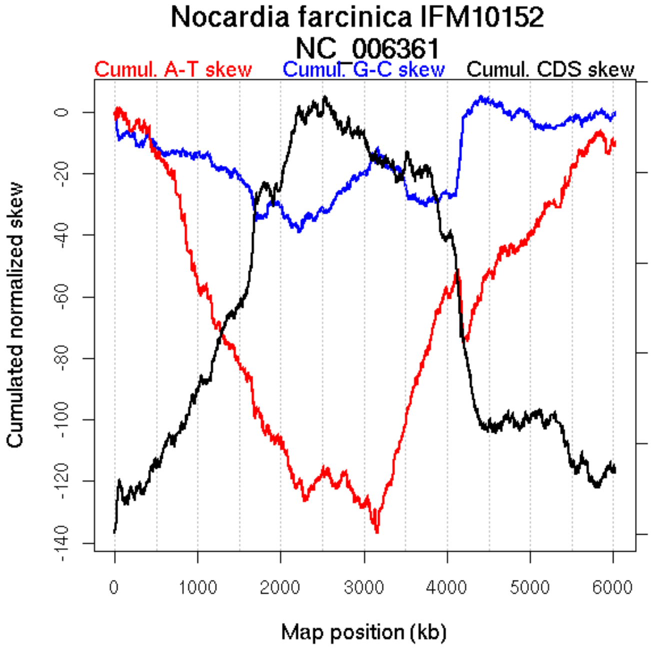
Segments:

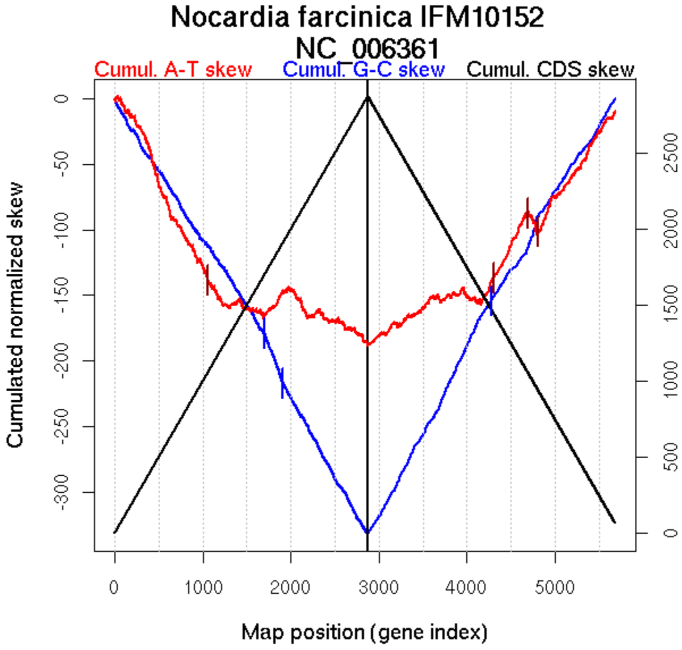
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	817 (1693.044 kb)	leading	0.043
	818(1694.5805 kb)	1337 (3184.135 kb)	lagging	-0.028
GC-skew reverse	1338 (0 kb)	1911 (1554.345 kb)	leading	0.025
	1912(1557.0355 kb)	2757 (3184.135 kb)	lagging	-0.041
AT-skew forward	1 (0 kb)	758 (1523.56 kb)	leading	-0.139
	759(1524.0505 kb)	1337 (3184.135 kb)	lagging	-0.076
AT-skew reverse	1338 (0 kb)	1980 (1670.7045 kb)	leading	0.084
	1981(1671.624 kb)	2757(3184.135 kb)	lagging	0.12

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

227 Nocardia farcinica IFM10152

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Nocardiaceae; Nocardia.
Accession number: NC_006361; **Genome size (bp)**: 6021225.
Number of genes: 5683.
Oriloc predictions: Origin NA Terminus NA
Worning et al., 2006: Origin 5845 kb Terminus 2527 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 113.434 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1 kb
Consensus predictions: Origin NA Terminus NA





Significant breakpoints (p-value <0.05):

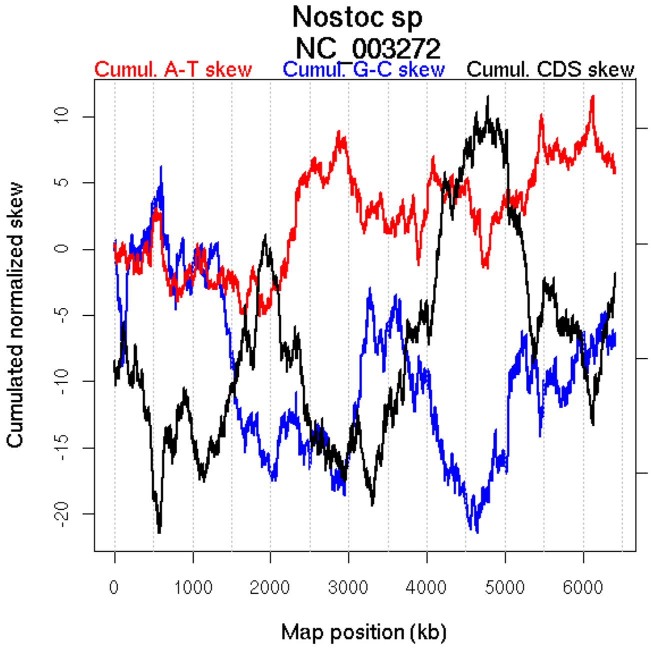
	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1704	0.00333	3176
	1908	0.02333	3622
GC-skew reverse	4277	0.04	3385
AT-skew forward	1059	0	1898
AT-skew reverse	4306	0.04	3453
	4698	0	4128
	4813	0.00444	4218

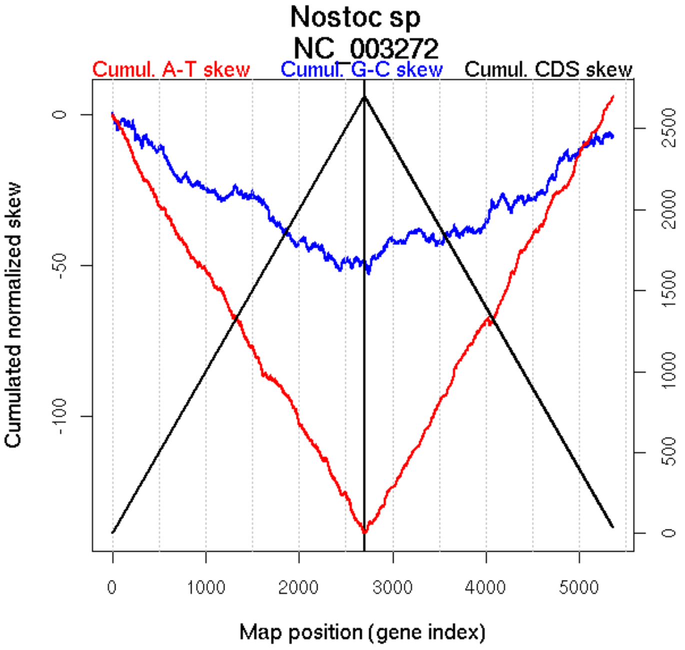
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1704 (3175.923 kb)	NA	-0.103
	1705(3176.5625 kb)	1908 (3621.567 kb)	NA	-0.179
	1909(3622.7295 kb)	2875 (6020.623 kb)	NA	-0.12
GC-skew reverse	2876 (0 kb)	4277 (3385.3735 kb)	NA	0.13
	4278(3386.7075 kb)	5683 (6020.623 kb)	NA	0.111
AT-skew forward	1 (0 kb)	1059 (1898.3745 kb)	NA	-0.144
	1060(1906.6205 kb)	2875 (6020.623 kb)	NA	-0.015
AT-skew reverse	2876 (0 kb)	4306 (3453.0505 kb)	NA	0.028
	4307(3454.2405 kb)	4698(4127.6695 kb)	NA	0.136
	4699(4128.3755 kb)	4813(4218.3725 kb)	NA	-0.151
	4814(4220.406 kb)	5683(6020.623 kb)	NA	0.103

228 Nostoc sp

Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
Accession number: NC_003272; **Genome size (bp)**: 6413771.
Number of genes: 5364.
Oriloc predictions: Origin NA Terminus NA
Worning et al., 2006: Origin 576 kb Terminus 4635 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 2404.588 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 2403.71 kb
Consensus predictions: Origin 2404 kb Terminus 5654 kb

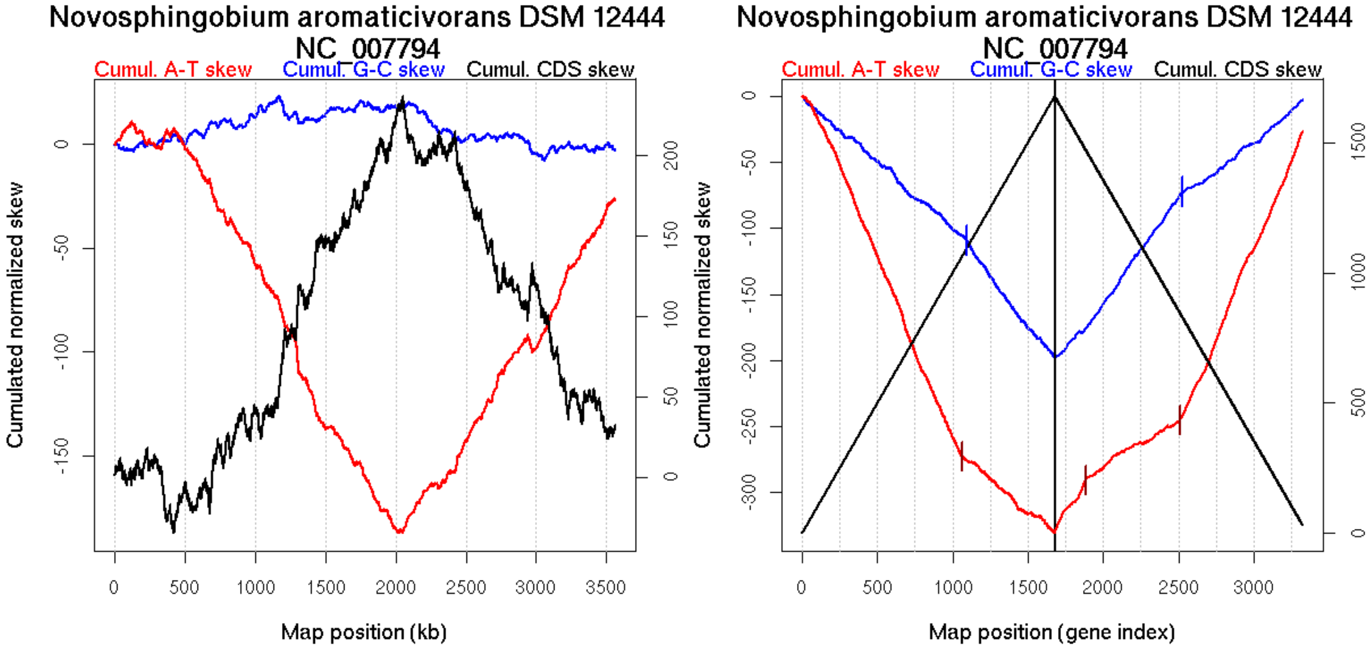




No significant breakpoints.

229 Novosphingobium aromaticivorans DSM 12444

Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Novosphingobium.
Accession number: NC_007794; **Genome size (bp)**: 3561584.
Number of genes: 3324.
Oriloc predictions: Origin 119 kb Terminus 2033 kb
Worning et al., 2006: Origin 120 kb Terminus 2023 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 118.317 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.77 kb
Consensus predictions: Origin 119 kb Terminus 2033 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1093	0	2106
GC-skew reverse	2526	0	2055
AT-skew forward	1064	0	2020
AT-skew reverse	1883	0.03667	417
	2510	0.00667	2016

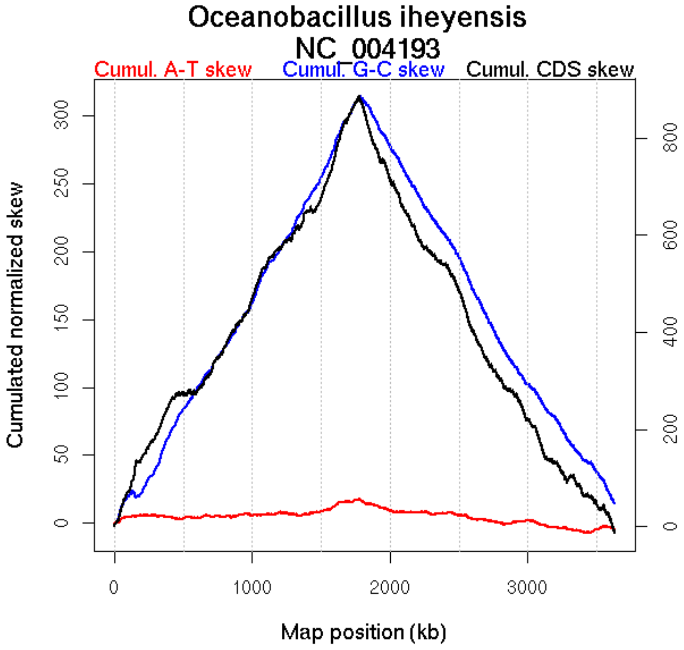
Segments:

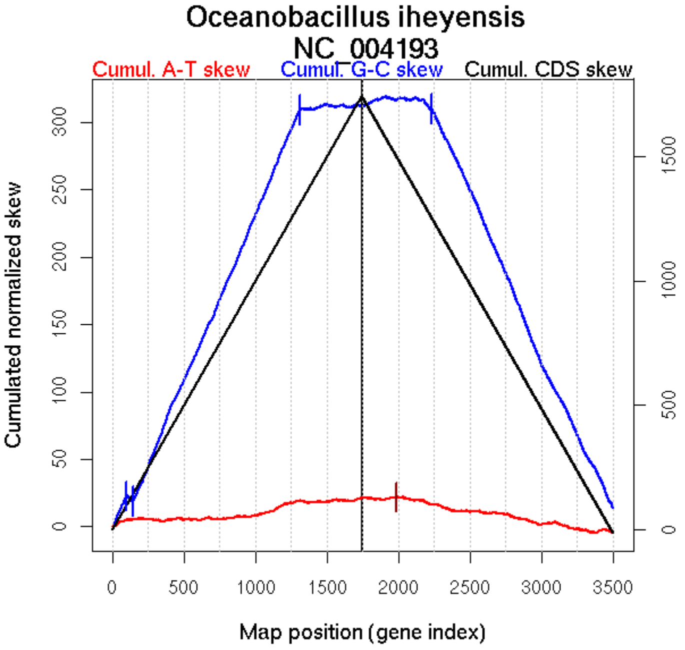
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1093 (2105.6135 kb)	leading	-0.099
	1094(2106.0215 kb)	1678 (3561.082 kb)	lagging	-0.149
GC-skew reverse	1679 (0 kb)	2526 (2055.2755 kb)	leading	0.153
	2527(2056.3885 kb)	3324 (3561.082 kb)	lagging	0.088
AT-skew forward	1 (0 kb)	1064 (2020.0765 kb)	leading	-0.271
	1065(2021.4565 kb)	1678 (3561.082 kb)	lagging	-0.095
AT-skew reverse	1679 (0 kb)	1883 (416.7905 kb)	NA	0.162
	1884(417.6275 kb)	2510(2015.8165 kb)	leading	0.069
	2511(2019.0955 kb)	3324(3561.082 kb)	lagging	0.269

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

230 Oceanobacillus iheyensis

Bacteria; Firmicutes; Bacillales; Bacillaceae; Oceanobacillus.
Accession number: NC_004193; **Genome size (bp)**: 3630528.
Number of genes: 3500.
Oriloc predictions: Origin 0 kb Terminus 1785 kb
Worning et al., 2006: Origin 3630 kb Terminus 1722 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 3627.341 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.97 kb, 1797.38 kb, 2190.32 kb
Consensus predictions: Origin 0 kb Terminus 1785 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	98	0	125
	140	0	158
	1313	0	1790
GC-skew reverse	2230	0	1838
AT-skew reverse	1988	0.03333	1034

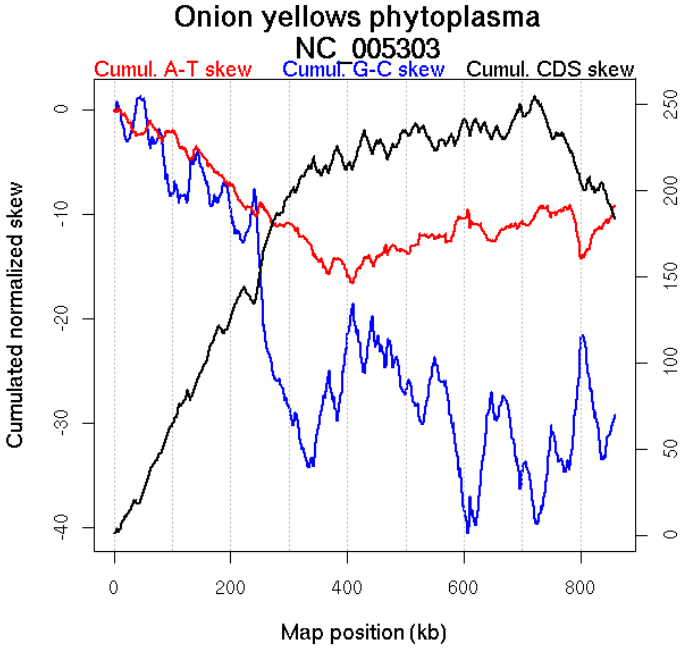
Segments:

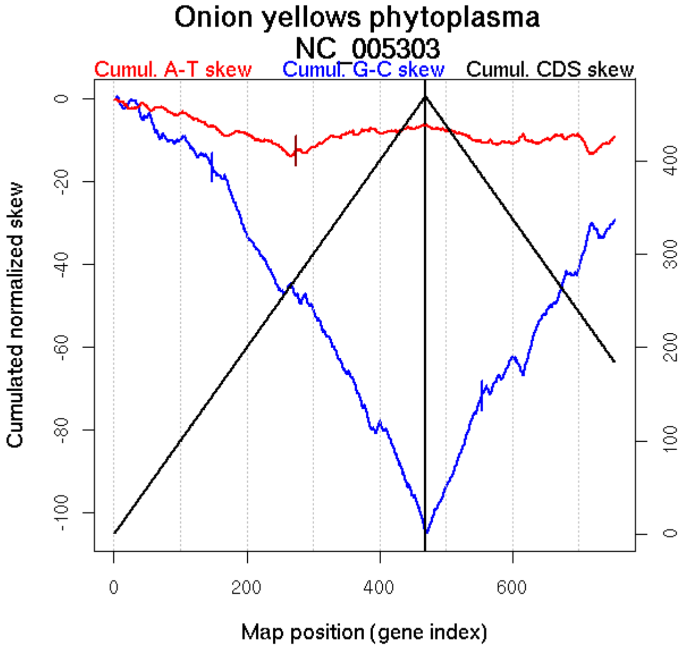
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	98 (125.168 kb)	leading	0.244
	99(125.767 kb)	140 (158.017 kb)	leading	-0.129
	141(158.8245 kb)	1313 (1789.5135 kb)	leading	0.248
	1314(1793.543 kb)	1743 (3630.057 kb)	lagging	0.006
GC-skew reverse	1744 (0 kb)	2230 (1838.074 kb)	leading	0
	2231(1839.262 kb)	3500 (3630.057 kb)	lagging	-0.238
AT-skew reverse	1744 (0 kb)	1988 (1034.004 kb)	leading	0
	1989(1035.038 kb)	3500(3630.057 kb)	lagging	-0.018

More A than T on the leading strand for replication - for reverse encoded genes.
More G than C on the leading strand for replication.

231 Onion yellows phytoplasma

Bacteria; Firmicutes; Mollicutes; Acholeplasmatales; Acholeplasmataceae; Candidatus Phytoplasma; Candidatus Phytoplasma asteris.
Accession number: NC_005303; **Genome size (bp)**: 860631.
Number of genes: 754.
Oriloc predictions: Origin NA Terminus NA
Worning et al., 2006: Origin 860 kb Terminus 335 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 234.659 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.76 kb, 772.01 kb
Consensus predictions: Origin 6 kb Terminus 406 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	148	0.01333	201
GC-skew reverse	554	0.04667	441
AT-skew forward	274	0.02	376

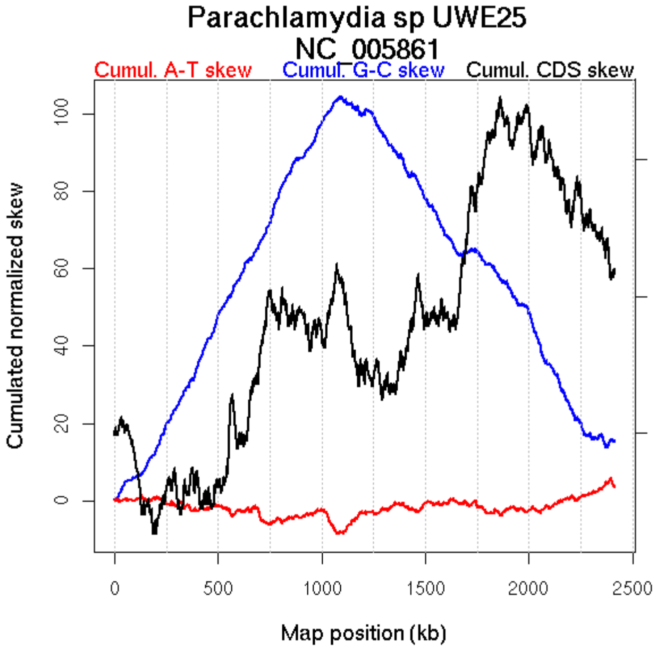
Segments:

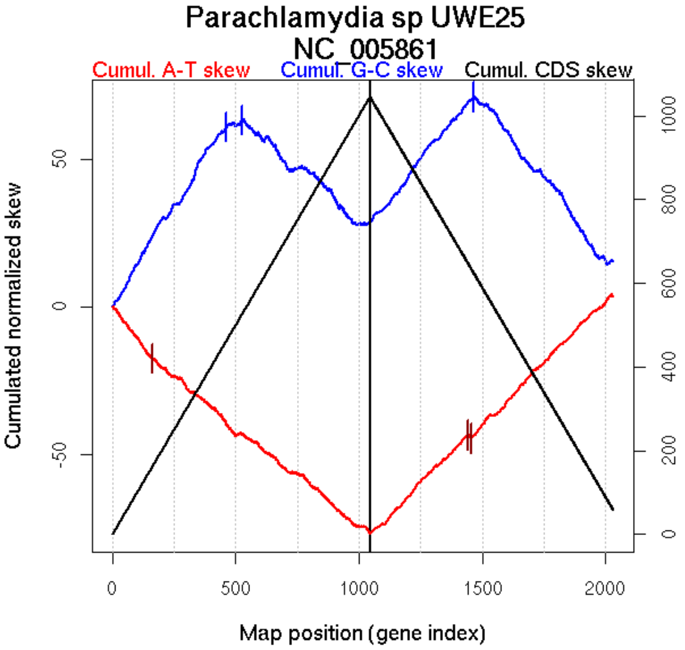
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	148 (200.8415 kb)	leading	-0.11
	149(201.886 kb)	469 (859.601 kb)	NA	-0.253
GC-skew reverse	470 (0 kb)	554 (441.0875 kb)	NA	0.397
	555(441.6905 kb)	754 (859.601 kb)	lagging	0.236
AT-skew forward	1 (0 kb)	274 (375.788 kb)	leading	-0.047
	275(376.885 kb)	469 (859.601 kb)	lagging	0.029

More T than A on the leading strand for replication - for forward encoded genes.

232 Parachlamydia sp UWE25

Bacteria; Chlamydiae; Chlamydiales; Parachlamydiaceae; Candidatus Protochlamydia.
Accession number: NC_005861; **Genome size (bp)**: 2414465.
Number of genes: 2031.
Oriloc predictions: Origin 0 kb Terminus 1092 kb
Worning et al., 2006: Origin 2401 kb Terminus 1092 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 636.887 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 424.97 kb, 1296.12 kb
Consensus predictions: Origin 0 kb Terminus 1092 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	463	0.02	1058
	527	0.03333	1216
GC-skew reverse	1465	0	1087
AT-skew forward	160	0.00667	472
AT-skew reverse	1442	0.00667	1013
	1454	0.00667	1050

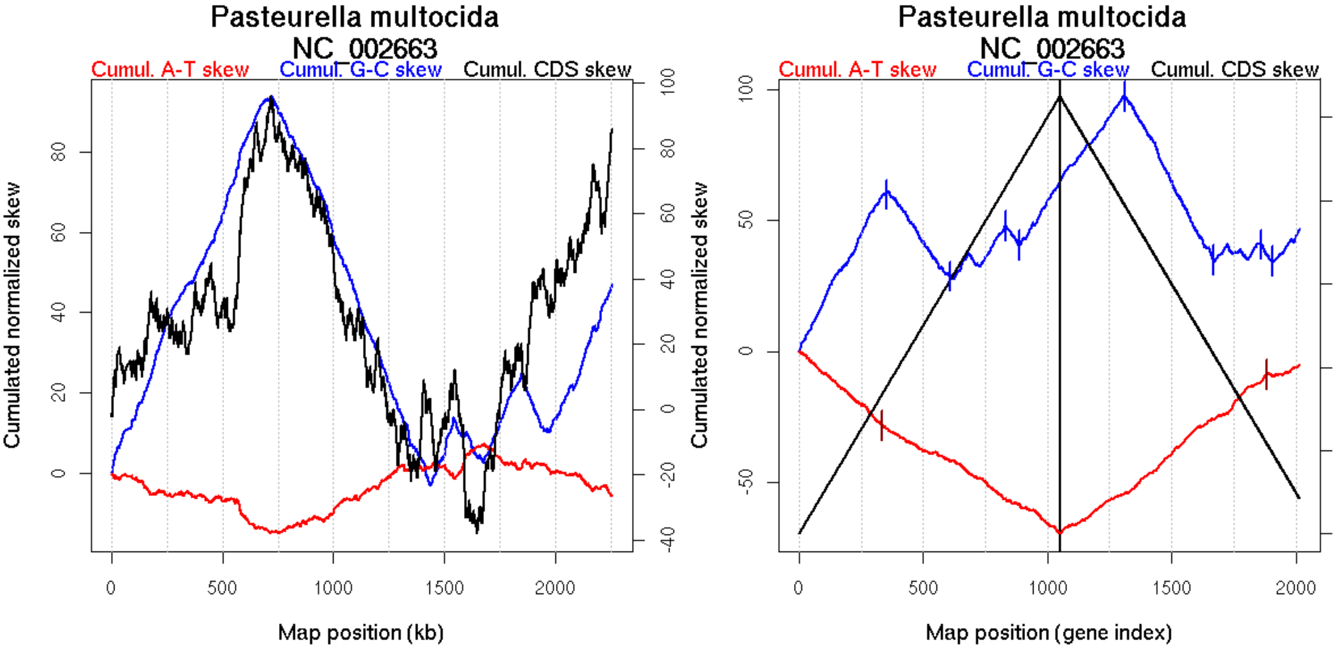
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	463 (1058.05 kb)	leading	0.133
	464(1060.165 kb)	527 (1216.14 kb)	NA	0.017
	528(1221.702 kb)	1045 (2414.389 kb)	lagging	-0.072
GC-skew reverse	1046 (0 kb)	1465 (1086.8535 kb)	leading	0.104
	1466(1089.291 kb)	2031 (2414.389 kb)	lagging	-0.107
AT-skew forward	1 (0 kb)	160 (472.4325 kb)	leading	-0.111
	161(475.734 kb)	1045 (2414.389 kb)	NA	-0.067
AT-skew reverse	1046 (0 kb)	1442 (1012.8655 kb)	leading	0.086
	1443(1015.5 kb)	1454(1049.5725 kb)	leading	-0.103
	1455(1051.295 kb)	2031(2414.389 kb)	lagging	0.085

More A than T on the leading strand for replication - for reverse encoded genes.
More G than C on the leading strand for replication.

233 Pasteurella multocida

Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales; Pasteurellaceae; Pasteurella.
Accession number: NC_002663; **Genome size (bp)**: 2257487.
Number of genes: 2015.
Oriloc predictions: Origin NA Terminus NA
Worning et al., 2006: Origin 1671 kb Terminus 715 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 933.707 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1357.68 kb
Consensus predictions: Origin 0 kb Terminus 715 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	352	0	714
	610	0.00333	1408
	832	0.005	1864
	889	0	1967
GC-skew reverse	1310	0	717
	1666	0.00667	1426
	1862	0.02167	1851
	1907	0	1968
AT-skew forward	335	0.04667	684
AT-skew reverse	1885	0.00667	1913

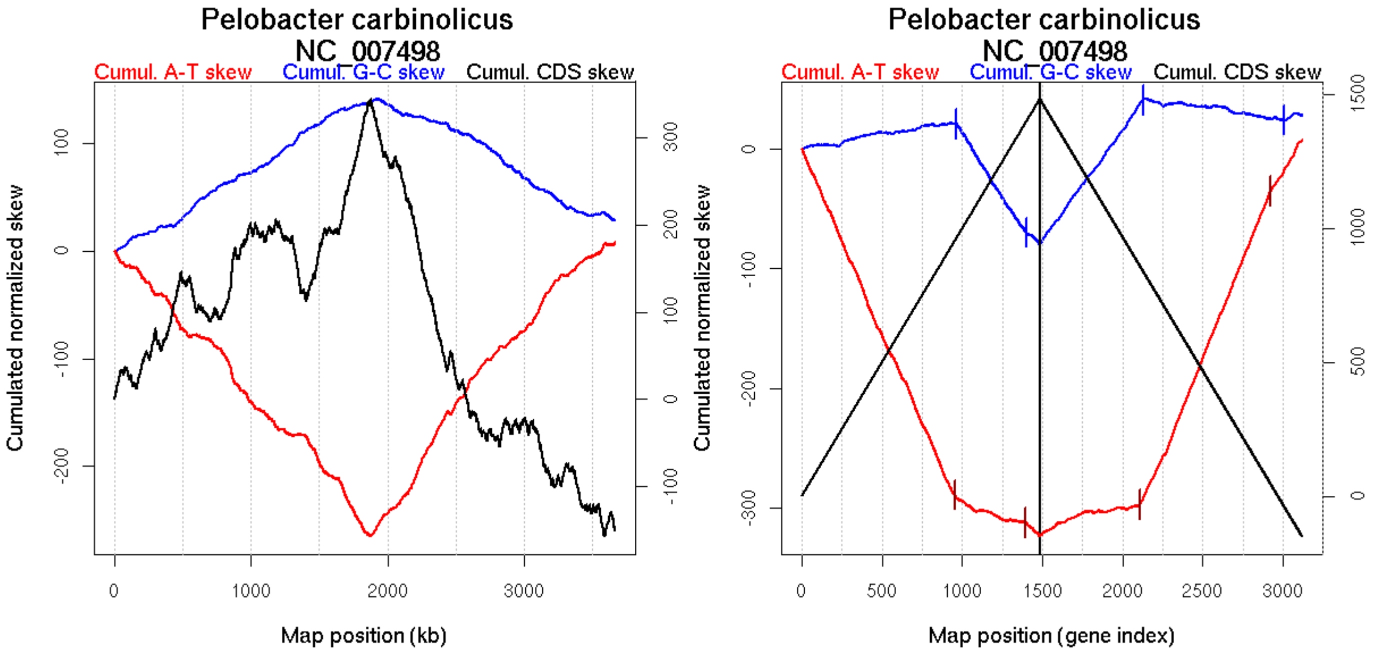
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	352 (713.9615 kb)	leading	0.174
	353(714.737 kb)	610 (1407.6845 kb)	lagging	-0.138
	611(1408.2155 kb)	832 (1863.9755 kb)	lagging	0.075
	833(1866.3625 kb)	889 (1967.129 kb)	lagging	-0.136
	890(1972.4515 kb)	1050 (2257.487 kb)	lagging	0.152
GC-skew reverse	1051 (0 kb)	1310 (717.3185 kb)	leading	0.122
	1311(719.255 kb)	1666 (1425.853 kb)	lagging	-0.182
	1667(1428.7425 kb)	1862 (1850.552 kb)	lagging	0.014
	1863(1851.7345 kb)	1907 (1967.724 kb)	lagging	-0.149
	1908(1969.5985 kb)	2015 (2257.487 kb)	lagging	0.11
AT-skew forward	1 (0 kb)	335 (683.782 kb)	leading	-0.083
	336(686.396 kb)	1050 (2257.487 kb)	lagging	-0.056
AT-skew reverse	1051 (0 kb)	1885 (1912.779 kb)	NA	0.074
	1886(1916.314 kb)	2015(2257.487 kb)	lagging	0.029

More T than A on the leading strand for replication - for forward encoded genes.
More G than C on the leading strand for replication.

234 Pelobacter carbinolicus

Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales; Pelobacteraceae; Pelobacter.
Accession number: NC_007498; **Genome size (bp)**: 3665893.
Number of genes: 3119.
Oriloc predictions: Origin 2 kb Terminus 1888 kb
Worning et al., 2006: Origin 2 kb Terminus 1882 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1823.666 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.75 kb
Consensus predictions: Origin 2 kb Terminus 1888 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	963	0	1873
	1398	0	3455
GC-skew reverse	2130	0	1909
	3008	0.03667	3458
AT-skew forward	952	0	1854
	1393	0.04333	3438
AT-skew reverse	2107	0	1874
	2921	0.01667	3272

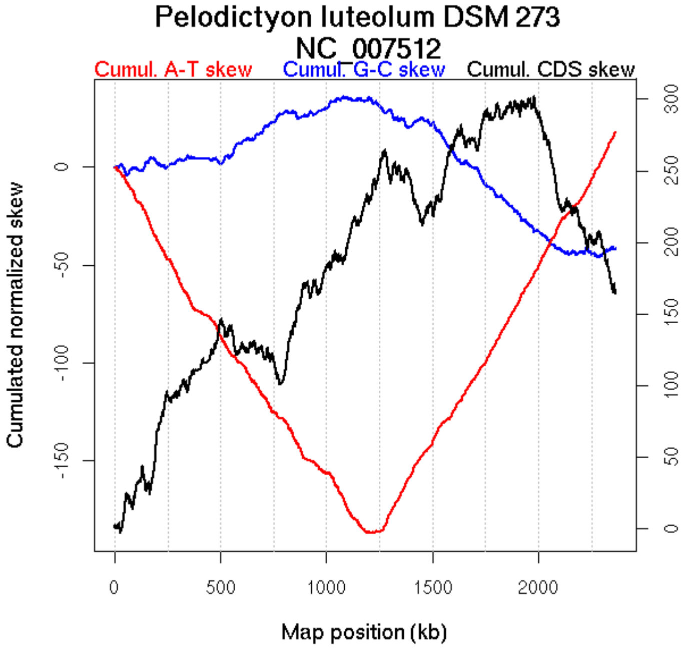
Segments:

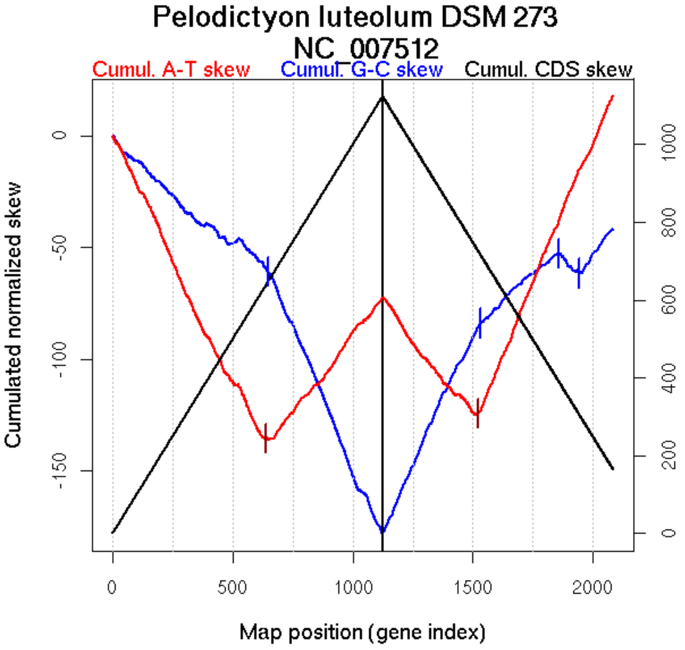
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	963 (1873.202 kb)	leading	0.023
	964(1874.681 kb)	1398 (3454.651 kb)	lagging	-0.213
	1399(3454.966 kb)	1484 (3665.632 kb)	lagging	-0.102
GC-skew reverse	1485 (0 kb)	2130 (1908.619 kb)	leading	0.185
	2131(1909.9865 kb)	3008 (3458.1925 kb)	lagging	-0.019
	3009(3459.9825 kb)	3119 (3665.632 kb)	lagging	0.051
AT-skew forward	1 (0 kb)	952 (1853.9505 kb)	leading	-0.304
	953(1854.575 kb)	1393 (3437.91 kb)	lagging	-0.047
	1394(3439.7075 kb)	1484 (3665.632 kb)	lagging	-0.121
AT-skew reverse	1485 (0 kb)	2107 (1873.5285 kb)	leading	0.035
	2108(1880.507 kb)	2921(3271.565 kb)	lagging	0.327
	2922(3273.391 kb)	3119(3665.632 kb)	lagging	0.225

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

235 Pelodictyon luteolum DSM 273

Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae; Chlorobium/Pelodictyon group; Pelodictyon.
Accession number: NC_007512; **Genome size (bp)**: 2364842.
Number of genes: 2083.
Oriloc predictions: Origin 0 kb Terminus 1190 kb
Worning et al., 2006: Origin 2 kb Terminus 1207 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 2363.17 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 2364.11 kb
Consensus predictions: Origin 0 kb Terminus 1190 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	648	0	1235
GC-skew reverse	1533	0.02667	1260
	1855	0.00667	1999
	1944	0	2134
AT-skew forward	636	0	1216
AT-skew reverse	1522	0	1208

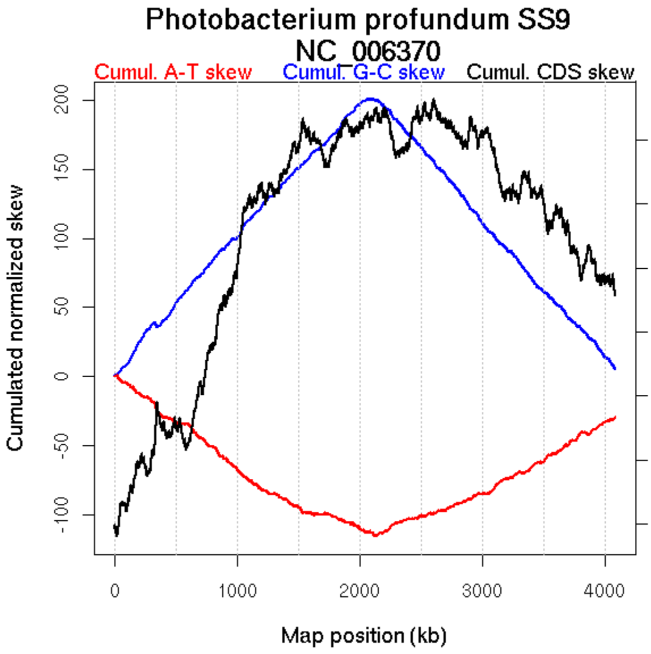
Segments:

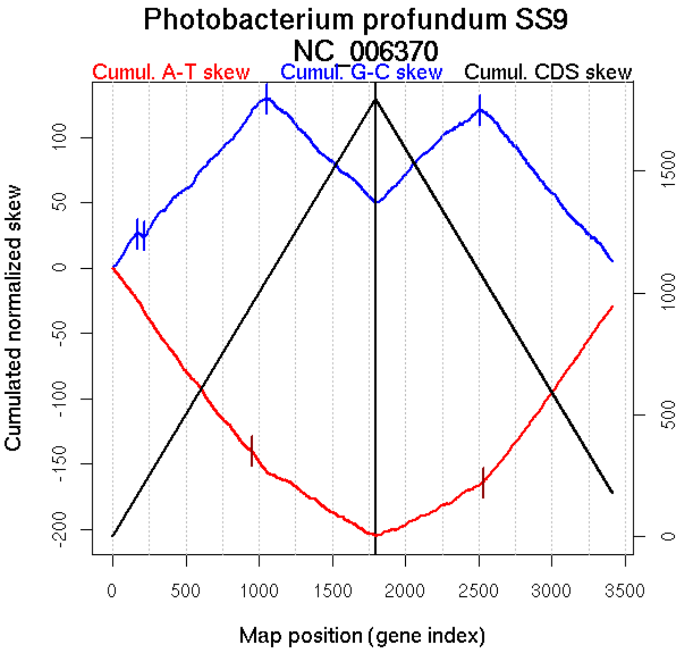
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	648 (1235.4635 kb)	leading	-0.088
	649(1236.6485 kb)	1124 (2364.839 kb)	lagging	-0.254
GC-skew reverse	1125 (0 kb)	1533 (1260.383 kb)	leading	0.234
	1534(1265.4005 kb)	1855 (1998.5085 kb)	lagging	0.098
	1856(2001.1965 kb)	1944 (2134.0925 kb)	lagging	-0.111
	1945(2135.8005 kb)	2083 (2364.839 kb)	lagging	0.155
AT-skew forward	1 (0 kb)	636 (1216.317 kb)	leading	-0.22
	637(1217.007 kb)	1124 (2364.839 kb)	lagging	0.136
AT-skew reverse	1125 (0 kb)	1522 (1207.687 kb)	leading	-0.134
	1523(1209.6035 kb)	2083(2364.839 kb)	lagging	0.256

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

236 Photobacterium profundum SS9

Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Photobacterium.
Accession number: NC_006370; **Genome size (bp)**: 4085304.
Number of genes: 3414.
Oriloc predictions: Origin 0 kb Terminus 2123 kb
Worning et al., 2006: Origin 4085 kb Terminus 2066 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 3808.111 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 8.08 kb, 2591.74 kb
Consensus predictions: Origin 0 kb Terminus 2123 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	167	0	311
	217	0.00222	383
	1053	0	2121
GC-skew reverse	2509	0	2069
AT-skew forward	949	0	1864
AT-skew reverse	2530	0	2129

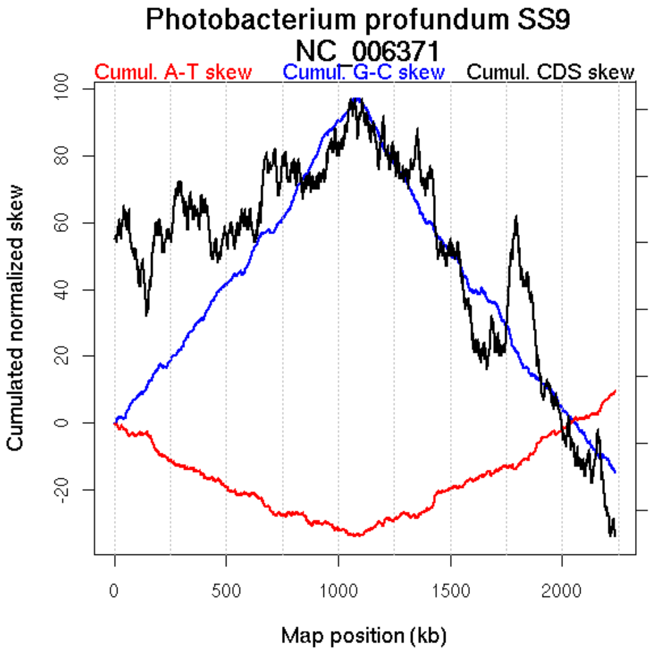
Segments:

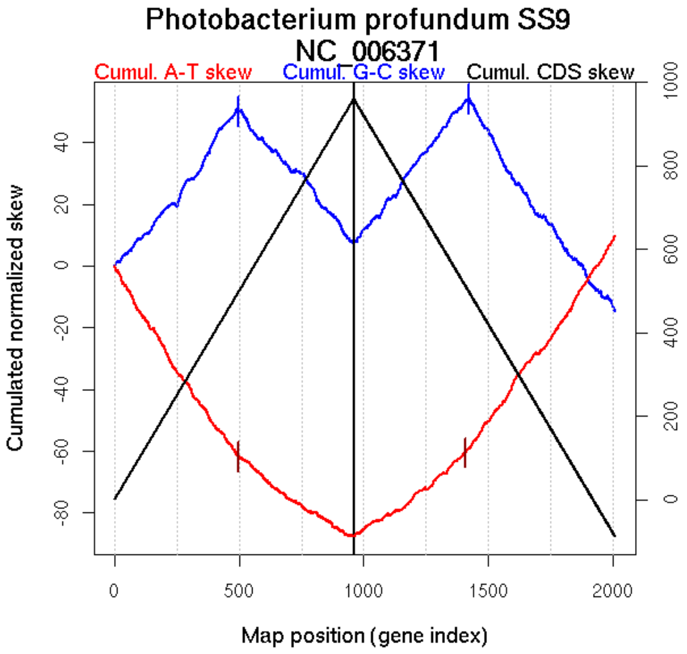
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	167 (310.7515 kb)	leading	0.174
	168(313.818 kb)	217 (383.2045 kb)	leading	-0.08
	218(384.813 kb)	1053 (2120.645 kb)	leading	0.124
	1054(2121.5165 kb)	1796 (4085.021 kb)	lagging	-0.109
GC-skew reverse	1797 (0 kb)	2509 (2068.9 kb)	leading	0.104
	2510(2070.3435 kb)	3414 (4085.021 kb)	lagging	-0.132
AT-skew forward	1 (0 kb)	949 (1863.6085 kb)	leading	-0.152
	950(1864.1425 kb)	1796 (4085.021 kb)	lagging	-0.072
AT-skew reverse	1797 (0 kb)	2530 (2128.7995 kb)	leading	0.057
	2531(2130.4195 kb)	3414(4085.021 kb)	lagging	0.155

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

237 Photobacterium profundum SS9

Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Photobacterium.
Accession number: NC_006371; **Genome size (bp)**: 2237943.
Number of genes: 2008.
Oriloc predictions: Origin 0 kb Terminus 1095 kb
Worning et al., 2006: Origin 0 kb Terminus 1070 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1531.278 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): NA
Consensus predictions: Origin 0 kb Terminus 1095 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	497	0	1089
GC-skew reverse	1419	0	1083
AT-skew forward	499	0.00667	1090
AT-skew reverse	1406	0	1064

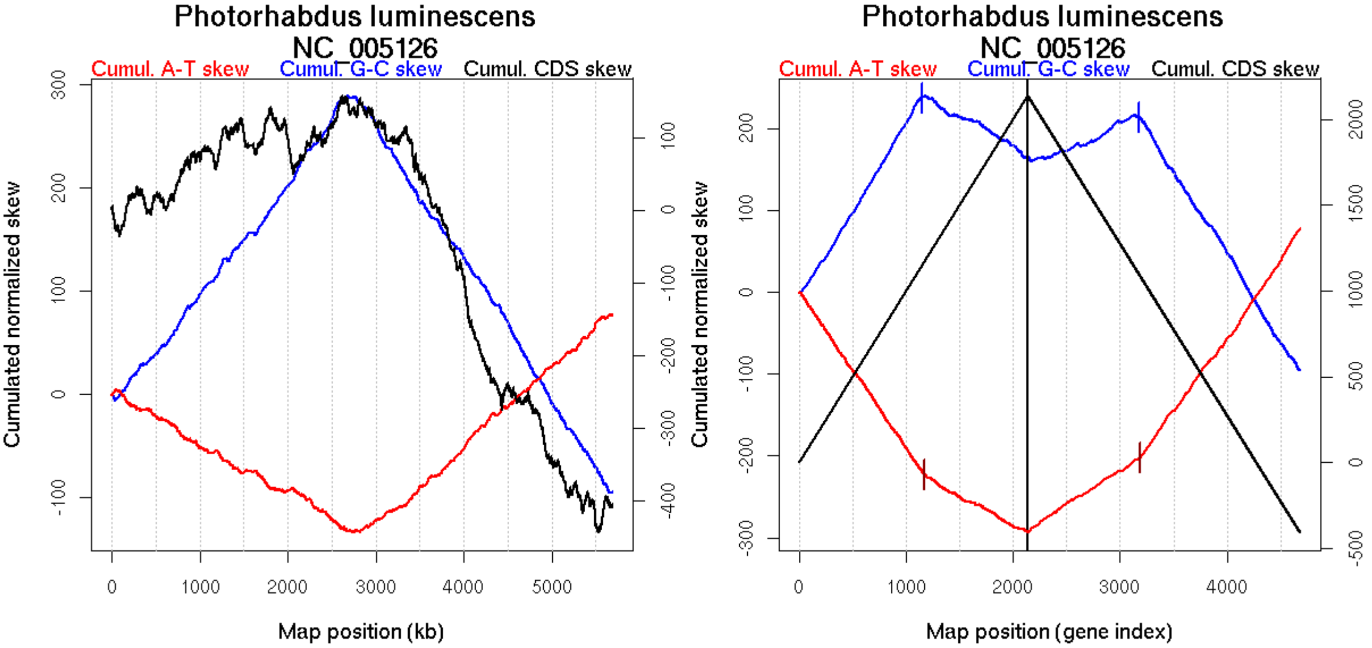
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	497 (1088.746 kb)	leading	0.104
	498(1089.249 kb)	960 (2237.067 kb)	lagging	-0.09
GC-skew reverse	961 (0 kb)	1419 (1083.096 kb)	leading	0.105
	1420(1084.173 kb)	2008 (2237.067 kb)	lagging	-0.114
AT-skew forward	1 (0 kb)	499 (1089.9885 kb)	leading	-0.123
	500(1090.629 kb)	960 (2237.067 kb)	lagging	-0.057
AT-skew reverse	961 (0 kb)	1406 (1064.4335 kb)	leading	0.059
	1407(1066.287 kb)	2008(2237.067 kb)	lagging	0.115

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

238 Photorhabdus luminescens

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Photorhabdus.
Accession number: NC_005126; **Genome size (bp)**: 5688987.
Number of genes: 4683.
Oriloc predictions: Origin 0 kb Terminus 2747 kb
Worning et al., 2006: Origin 43 kb Terminus 2633 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 5056.118 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.93 kb, 3263.81 kb
Consensus predictions: Origin 0 kb Terminus 2747 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1147	0	2651
GC-skew reverse	3174	0	2759
AT-skew forward	1168	0	2739
AT-skew reverse	3186	0	2783

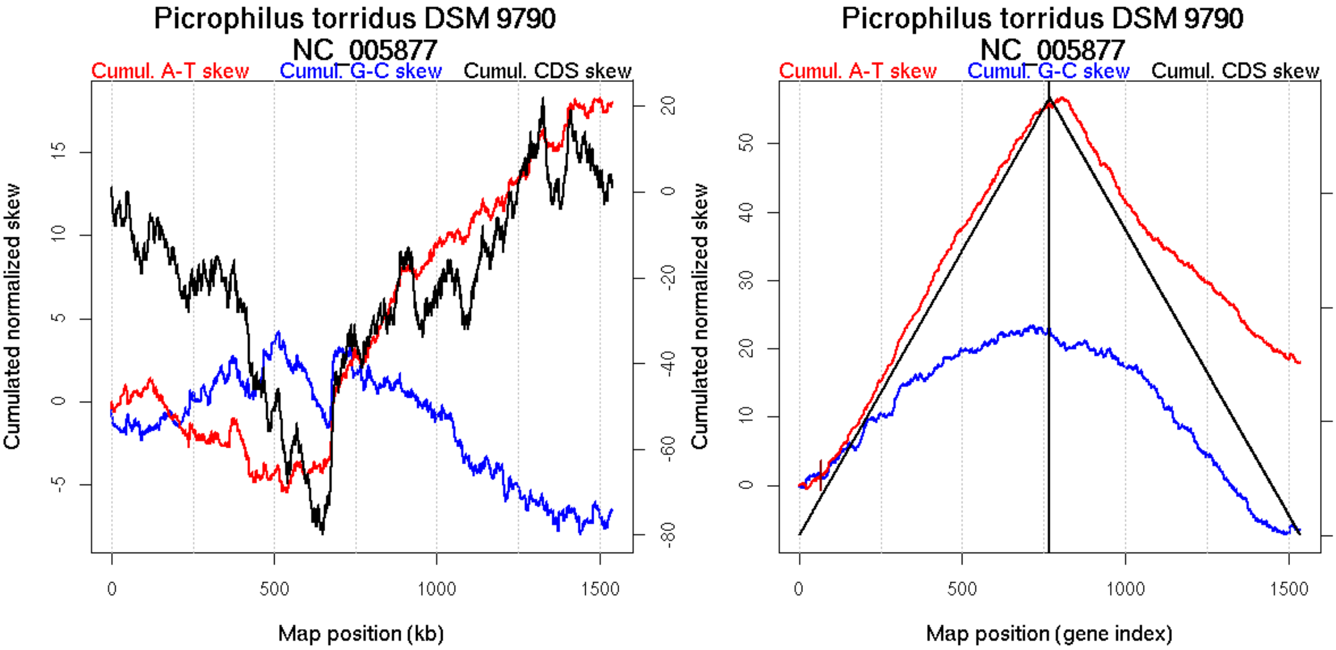
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1147 (2650.793 kb)	leading	0.214
	1148(2658.724 kb)	2137 (5688.532 kb)	lagging	-0.073
GC-skew reverse	2138 (0 kb)	3174 (2758.6765 kb)	leading	0.058
	3175(2760.8015 kb)	4683 (5688.532 kb)	lagging	-0.207
AT-skew forward	1 (0 kb)	1168 (2739.267 kb)	leading	-0.191
	1169(2740.0565 kb)	2137 (5688.532 kb)	lagging	-0.071
AT-skew reverse	2138 (0 kb)	3186 (2783.4815 kb)	leading	0.084
	3187(2783.9585 kb)	4683(5688.532 kb)	lagging	0.184

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

239 Picrophilus torridus DSM 9790

Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales; Picrophilaceae; Picrophilus.
Accession number: NC_005877; **Genome size (bp)**: 1545895.
Number of genes: 1535.
Oriloc predictions: Origin NA Terminus NA
Worning et al., 2006: Origin 650 kb Terminus 1414 kb
Position(s) of the ORC/Cdc6 gene(s): 1218.35 kb, 1265.92 kb
Consensus predictions: Origin NA Terminus NA



Significant breakpoints (p-value <0.05):

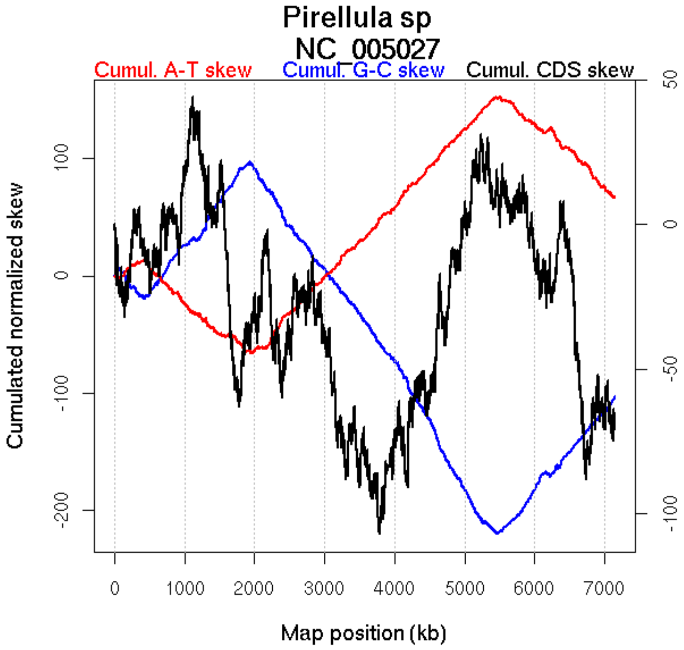
	Breakpoints	P-value	Chromosome coordinate (kb)
AT-skew forward	67	0	167

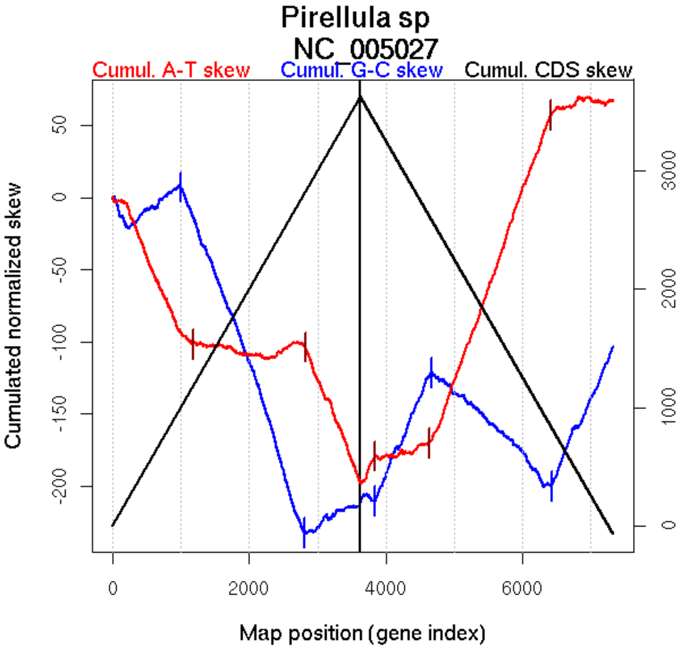
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
AT-skew forward	1 (0 kb)	67 (167.399 kb)	NA	0.022
	68(169.5565 kb)	768 (1540.068 kb)	NA	0.082

240 Pirellula sp

Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales; Planctomycetaceae; Rhodopi
Accession number: NC_005027; **Genome size (bp)**: 7145576.
Number of genes: 7325.
Oriloc predictions: Origin 5465 kb Terminus 1935 kb
Worning et al., 2006: Origin 5254 kb Terminus 1935 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 424.182 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 890.75 kb, 6247.2 kb
Consensus predictions: Origin 5465 kb Terminus 1935 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	996	0	1935
	2805	0	5462
GC-skew reverse	3838	0	421
	4666	0	1937
	6428	0	5477
AT-skew forward	1172	0	2222
	2816	0	5502
AT-skew reverse	3839	0	422
	4635	0	1899
	6414	0	5452

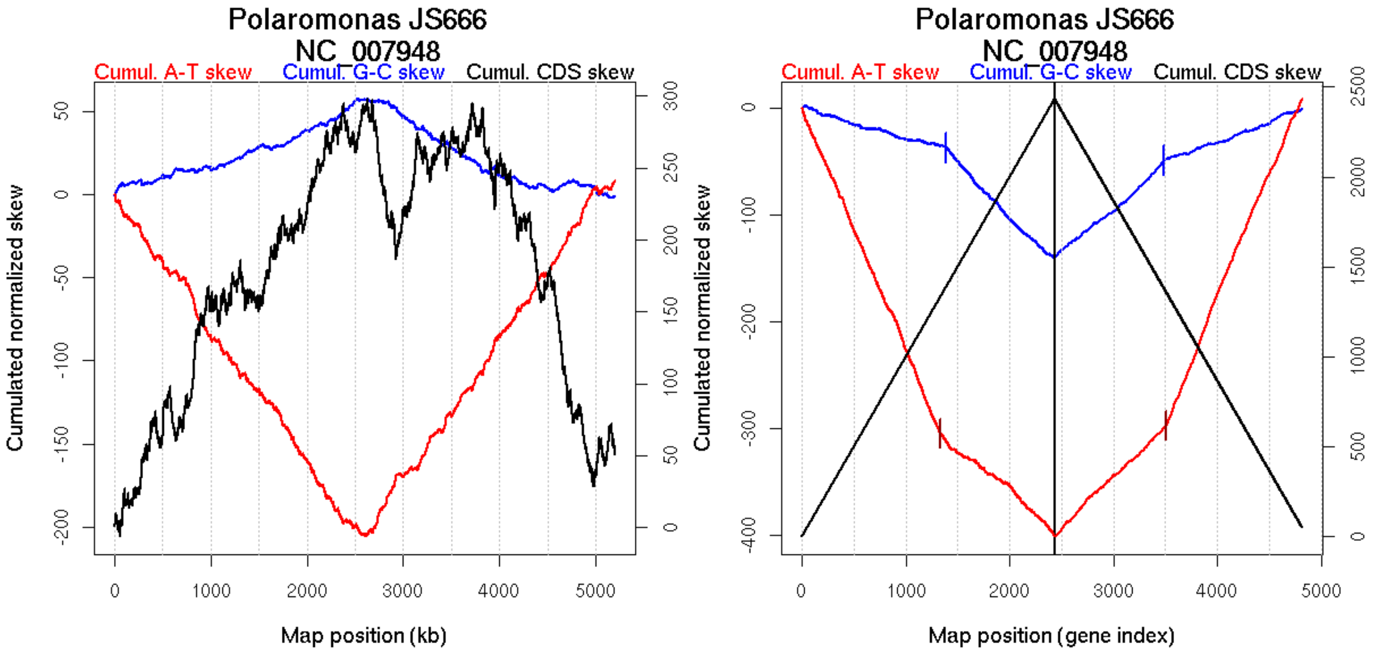
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	996 (1934.844 kb)	leading	0.021
	997(1937.932 kb)	2805 (5461.92 kb)	lagging	-0.133
	2806(5463.6515 kb)	3627 (7145.536 kb)	leading	0.027
GC-skew reverse	3628 (0 kb)	3838 (420.821 kb)	leading	-0.013
	3839(421.8245 kb)	4666 (1936.8815 kb)	leading	0.108
	4667(1938.2045 kb)	6428 (5477.159 kb)	lagging	-0.045
	6429(5482.1825 kb)	7325 (7145.536 kb)	leading	0.102
AT-skew forward	1 (0 kb)	1172 (2222.04 kb)	leading	-0.101
	1173(2226.737 kb)	2816 (5502.394 kb)	lagging	-0.002
	2817(5502.5805 kb)	3627 (7145.536 kb)	leading	-0.113
AT-skew reverse	3628 (0 kb)	3839 (421.8245 kb)	leading	0.1
	3840(422.535 kb)	4635(1899.32 kb)	leading	0.013
	4636(1900.516 kb)	6414(5451.5615 kb)	lagging	0.131
	6415(5457.225 kb)	7325(7145.536 kb)	leading	0.008

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

241 Polaromonas JS666

Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales; Comamonadaceae; Polaromonas.
Accession number: NC_007948; **Genome size (bp)**: 5200264.
Number of genes: 4817.
Oriloc predictions: Origin 4 kb Terminus 2592 kb
Worning et al., 2006: Origin 5182 kb Terminus 2594 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 3840.786 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.74 kb, 3764.01 kb
Consensus predictions: Origin 4 kb Terminus 2592 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1387	0	2665
GC-skew reverse	3490	0	2538
AT-skew forward	1337	0	2549
AT-skew reverse	3509	0	2609

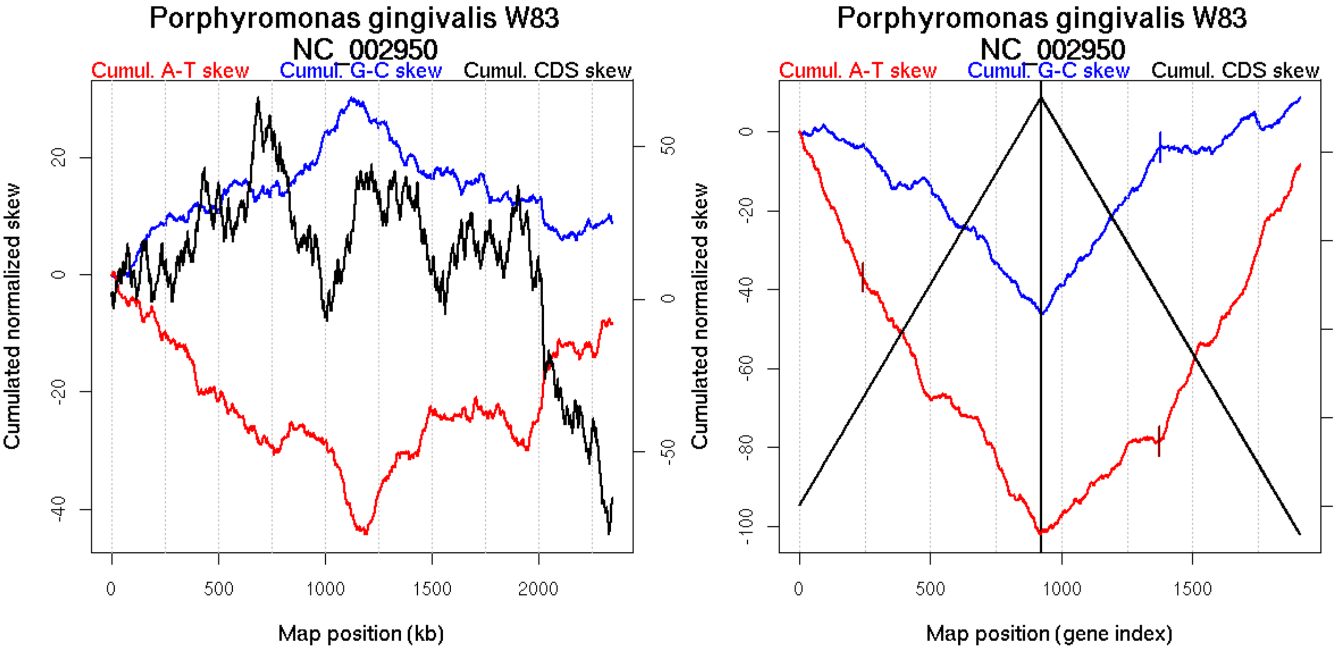
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1387 (2665.2485 kb)	leading	-0.028
	1388(2666.8615 kb)	2434 (5199.868 kb)	lagging	-0.1
GC-skew reverse	2435 (0 kb)	3490 (2537.688 kb)	leading	0.082
	3491(2538.9555 kb)	4817 (5199.868 kb)	lagging	0.037
AT-skew forward	1 (0 kb)	1337 (2549.1135 kb)	leading	-0.227
	1338(2549.4045 kb)	2434 (5199.868 kb)	lagging	-0.08
AT-skew reverse	2435 (0 kb)	3509 (2609.474 kb)	leading	0.094
	3510(2612.0485 kb)	4817(5199.868 kb)	lagging	0.235

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

242 Porphyromonas gingivalis W83

Bacteria; Bacteroidetes; Bacteroidetes (class); Bacteroidales; Porphyromonadaceae; Porphyromonas.
Accession number: NC_002950; **Genome size (bp)**: 2343476.
Number of genes: 1909.
Oriloc predictions: Origin 13 kb Terminus 1186 kb
Worning et al., 2006: Origin 2329 kb Terminus 1168 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 2098.396 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.71 kb
Consensus predictions: Origin 13 kb Terminus 1186 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew reverse	1379	0	1169
AT-skew forward	243	0	575
AT-skew reverse	1374	0	1154

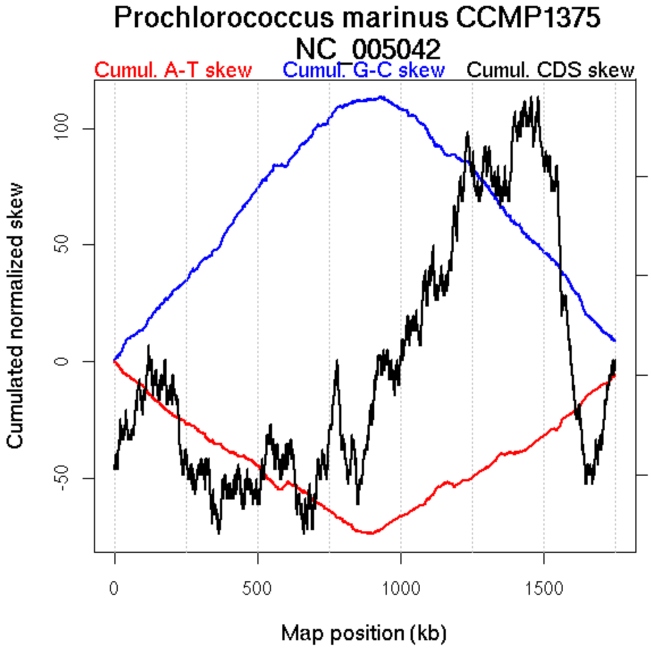
Segments:

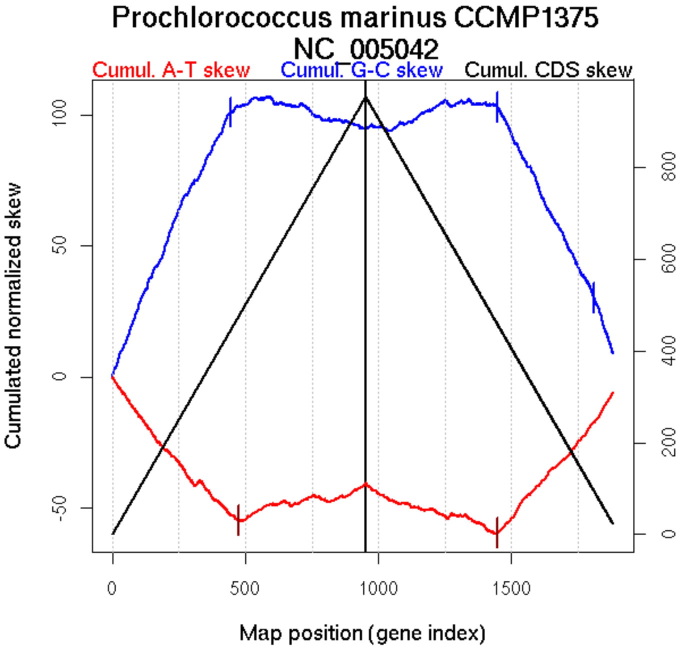
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew reverse	923 (0 kb)	1379 (1169.4065 kb)	leading	0.091
	1380(1171.4145 kb)	1909 (2342.801 kb)	lagging	0.024
AT-skew forward	1 (0 kb)	243 (574.7585 kb)	leading	-0.151
	244(575.858 kb)	922 (2342.801 kb)	NA	-0.09
AT-skew reverse	923 (0 kb)	1374 (1153.7455 kb)	leading	0.06
	1375(1155.6425 kb)	1909(2342.801 kb)	lagging	0.126

More T than A on the leading strand for replication - for reverse encoded genes.
More G than C on the leading strand for replication - for reverse encoded genes.

243 Prochlorococcus marinus CCMP1375

Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae; Prochlorococcus.
Accession number: NC_005042; **Genome size (bp)**: 1751080.
Number of genes: 1883.
Oriloc predictions: Origin 0 kb Terminus 886 kb
Worning et al., 2006: Origin 0 kb Terminus 867 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1360.24 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 538.65 kb
Consensus predictions: Origin 0 kb Terminus 886 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	445	0	806
GC-skew reverse	1449	0	933
	1811	0.04	1596
AT-skew forward	476	0	870
AT-skew reverse	1448	0	932

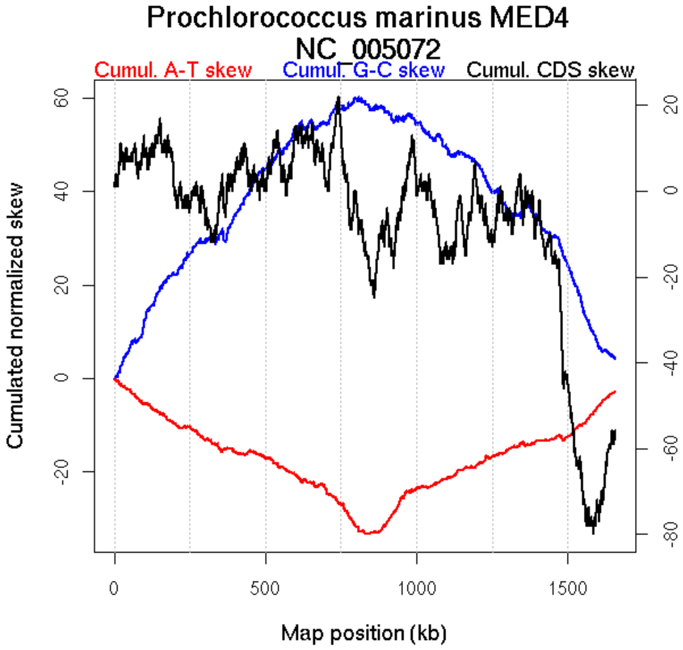
Segments:

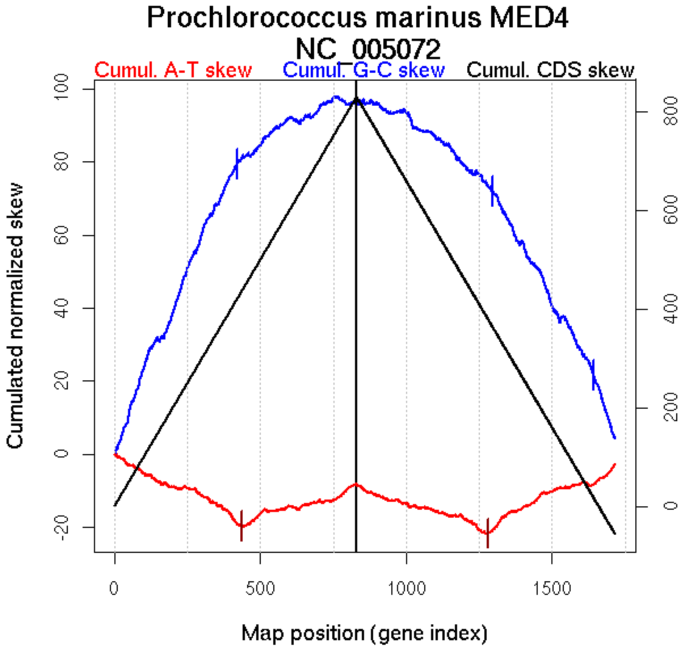
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	445 (806.331 kb)	leading	0.224
	446(808.0985 kb)	953 (1750.901 kb)	lagging	-0.021
GC-skew reverse	954 (0 kb)	1449 (933.328 kb)	leading	0.025
	1450(934.1545 kb)	1811 (1595.5925 kb)	lagging	-0.2
	1812(1596.9995 kb)	1883 (1750.901 kb)	lagging	-0.303
AT-skew forward	1 (0 kb)	476 (869.5775 kb)	leading	-0.113
	477(870.341 kb)	953 (1750.901 kb)	lagging	0.021
AT-skew reverse	954 (0 kb)	1448 (932.324 kb)	leading	-0.031
	1449(933.328 kb)	1883(1750.901 kb)	lagging	0.118

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

244 Prochlorococcus marinus MED4

Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae; Prochlorococcus.
Accession number: NC_005072; **Genome size (bp)**: 1657990.
Number of genes: 1716.
Oriloc predictions: Origin 0 kb Terminus 843 kb
Worning et al., 2006: Origin 1 kb Terminus 856 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 617.359 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 532.41 kb
Consensus predictions: Origin 0 kb Terminus 843 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	420	NA	810
GC-skew reverse	1295	NA	885
	1643	NA	1508
AT-skew forward	438	NA	864
AT-skew reverse	1280	NA	845

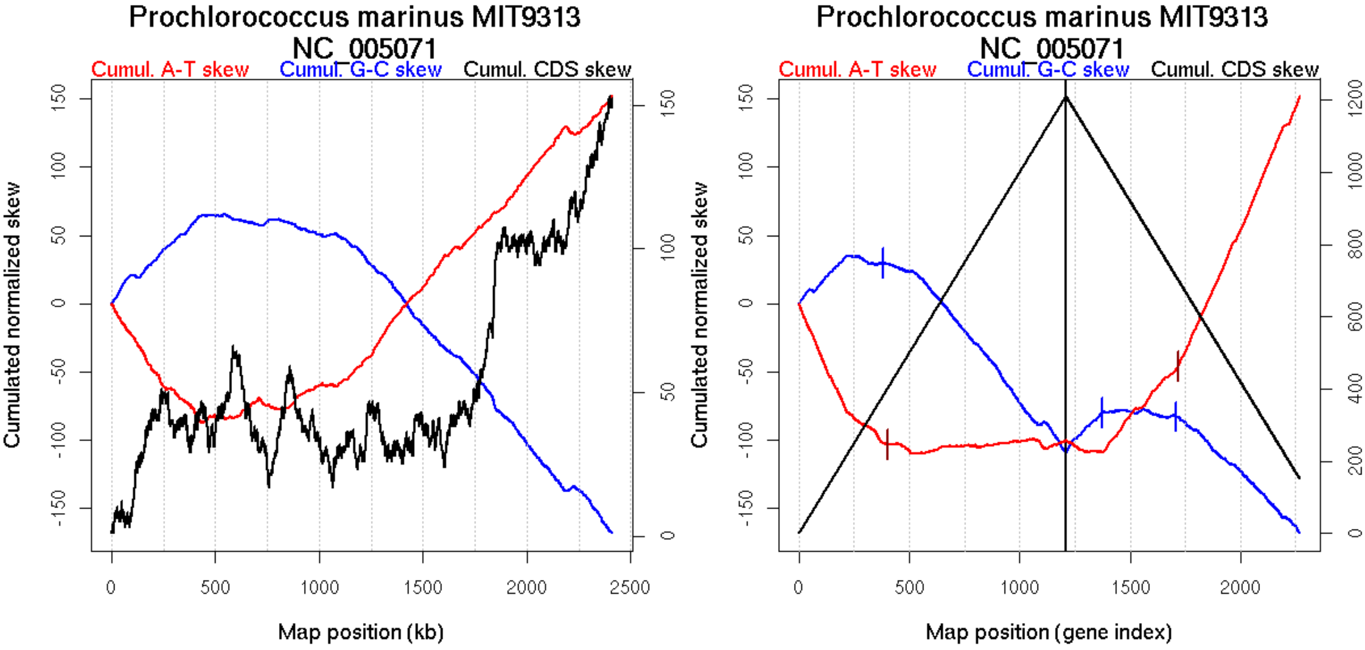
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	420 (809.7075 kb)	leading	0.189
	421(810.1935 kb)	830 (1657.814 kb)	lagging	0.043
GC-skew reverse	831 (0 kb)	1295 (884.831 kb)	leading	-0.054
	1296(886.9085 kb)	1643 (1507.8825 kb)	lagging	-0.143
	1644(1509.4125 kb)	1716 (1657.814 kb)	lagging	-0.246
AT-skew forward	1 (0 kb)	438 (863.7555 kb)	leading	-0.039
	439(865.7545 kb)	830 (1657.814 kb)	lagging	0.023
AT-skew reverse	831 (0 kb)	1280 (845.193 kb)	leading	-0.025
	1281(846.159 kb)	1716(1657.814 kb)	lagging	0.035

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

245 Prochlorococcus marinus MIT9313

Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae; Prochlorococcus.
Accession number: NC_005071; **Genome size (bp)**: 2410873.
Number of genes: 2268.
Oriloc predictions: Origin NA Terminus NA
Worning et al., 2006: Origin 0 kb Terminus 793 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1528.128 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1277.96 kb
Consensus predictions: Origin 0 kb Terminus 793 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	382	NA	798
GC-skew reverse	1376	NA	420
	1708	NA	1102
AT-skew forward	402	NA	832
AT-skew reverse	1717	NA	1123

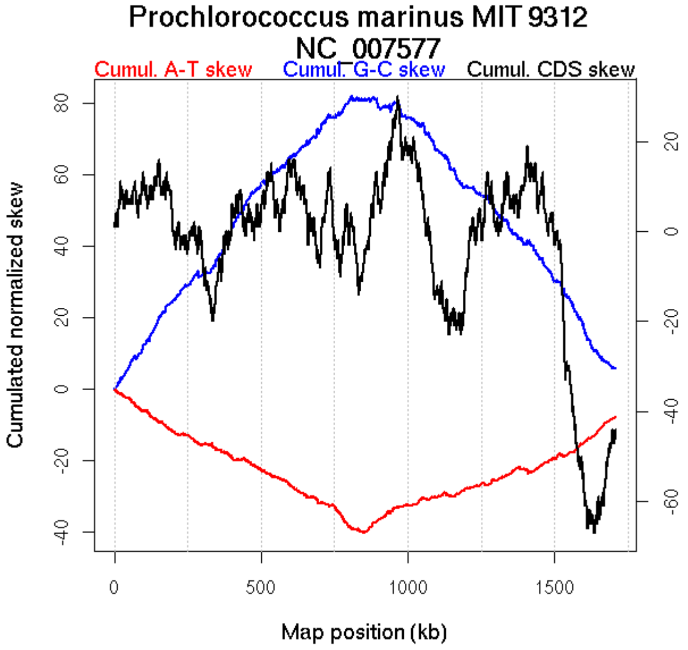
Segments:

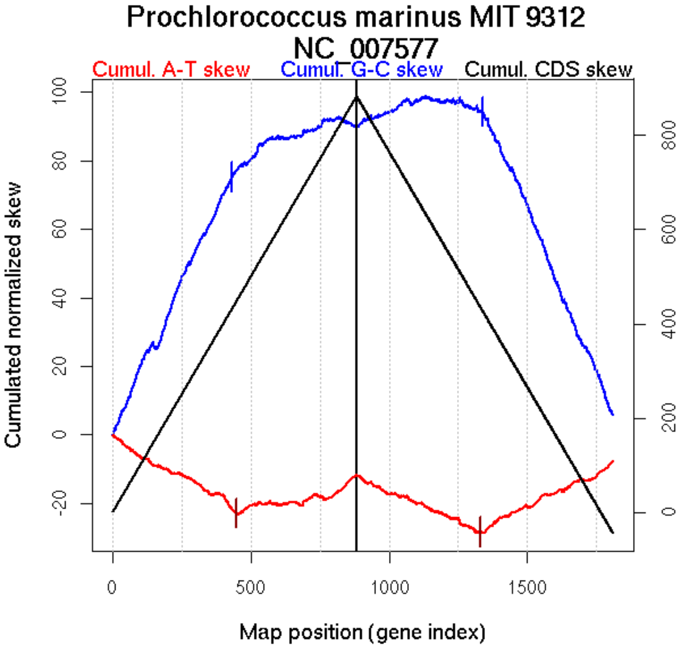
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	382 (798.0265 kb)	leading	0.079
	383(798.343 kb)	1210 (2410.634 kb)	lagging	-0.183
GC-skew reverse	1211 (0 kb)	1376 (420.115 kb)	leading	0.166
	1377(424.6345 kb)	1708 (1102.3615 kb)	NA	-0.014
	1709(1104.129 kb)	2268 (2410.634 kb)	lagging	-0.153
AT-skew forward	1 (0 kb)	402 (832.281 kb)	leading	-0.256
	403(833.744 kb)	1210 (2410.634 kb)	lagging	0.007
AT-skew reverse	1211 (0 kb)	1717 (1123.2375 kb)	NA	0.134
	1718(1130.5775 kb)	2268(2410.634 kb)	lagging	0.363

More T than A on the leading strand for replication - for forward encoded genes.
More G than C on the leading strand for replication - for forward encoded genes.

246 Prochlorococcus marinus MIT 9312

Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae; Prochlorococcus.
Accession number: NC_007577; **Genome size (bp)**: 1709204.
Number of genes: 1810.
Oriloc predictions: Origin 0 kb Terminus 848 kb
Worning et al., 2006: Origin 1708 kb Terminus 858 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1220.397 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 527.02 kb
Consensus predictions: Origin 0 kb Terminus 848 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	433	NA	802
GC-skew reverse	1340	NA	833
AT-skew forward	449	NA	841
AT-skew reverse	1332	NA	825

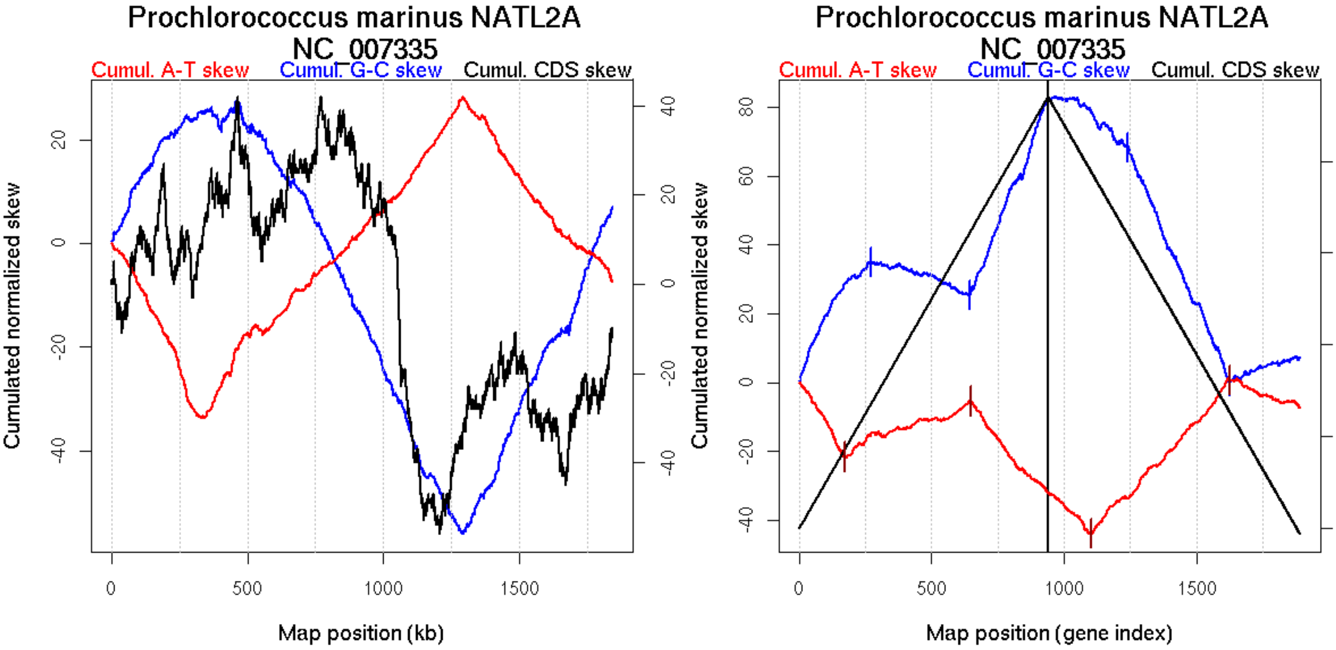
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	433 (802.4565 kb)	leading	0.174
	434(802.8615 kb)	883 (1709.066 kb)	lagging	0.032
GC-skew reverse	884 (0 kb)	1340 (832.5895 kb)	leading	0.01
	1341(835.954 kb)	1810 (1709.066 kb)	lagging	-0.191
AT-skew forward	1 (0 kb)	449 (840.6295 kb)	leading	-0.044
	450(843.96 kb)	883 (1709.066 kb)	lagging	0.018
AT-skew reverse	884 (0 kb)	1332 (825.346 kb)	leading	-0.035
	1333(827.3305 kb)	1810(1709.066 kb)	lagging	0.039

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

247 Prochlorococcus marinus NATL2A

Bacteria; Cyanobacteria; Prochlorales; Prochlorococcaceae; Prochlorococcus.
Accession number: NC_007335; **Genome size (bp)**: 1842899.
Number of genes: 1892.
Oriloc predictions: Origin 1291 kb Terminus 339 kb
Worning et al., 2006: Origin 1293 kb Terminus 333 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1292.44 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.79 kb
Consensus predictions: Origin 1291 kb Terminus 339 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	271	NA	477
	644	NA	1291
GC-skew reverse	1240	NA	549
	1626	NA	1317
AT-skew forward	173	NA	334
	648	NA	1297
AT-skew reverse	1103	NA	330
	1625	NA	1316

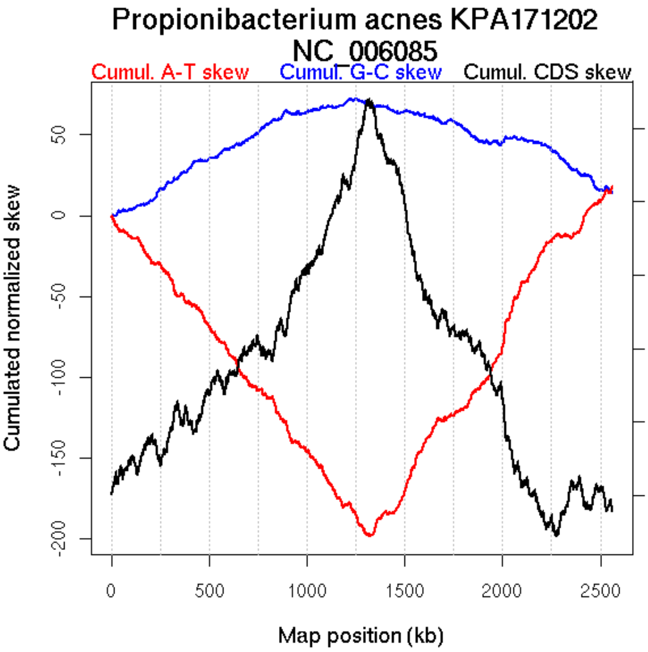
Segments:

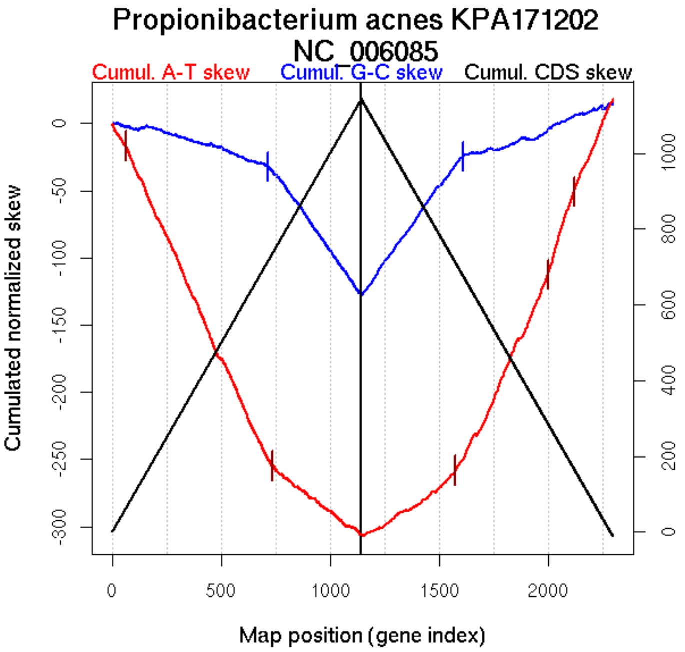
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	271 (477.0515 kb)	NA	0.122
	272(478.5085 kb)	644 (1291.189 kb)	lagging	-0.026
	645(1292.4965 kb)	940 (1842.768 kb)	leading	0.192
GC-skew reverse	941 (0 kb)	1240 (549.146 kb)	NA	-0.054
	1241(550.54 kb)	1626 (1317.42 kb)	lagging	-0.173
	1627(1319.3005 kb)	1892 (1842.768 kb)	leading	0.026
AT-skew forward	1 (0 kb)	173 (333.7655 kb)	leading	-0.131
	174(335.6275 kb)	648 (1297.0635 kb)	lagging	0.027
	649(1300.835 kb)	940 (1842.768 kb)	leading	-0.091
AT-skew reverse	941 (0 kb)	1103 (330.0025 kb)	leading	-0.076
	1104(333.008 kb)	1625(1315.895 kb)	lagging	0.082
	1626(1317.42 kb)	1892(1842.768 kb)	leading	-0.03

More T than A on the leading strand for replication.

248 Propionibacterium acnes KPA171202

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Propionibacterineae; Propionibacteriaceae; Propionibacterium.
Accession number: NC_006085; **Genome size (bp)**: 2560265.
Number of genes: 2297.
Oriloc predictions: Origin 0 kb Terminus 1310 kb
Worning et al., 2006: Origin 2 kb Terminus 1320 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 2427.345 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1 kb
Consensus predictions: Origin 0 kb Terminus 1310 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	715	0	1296
GC-skew reverse	1610	0	1324
AT-skew forward	61	0.03333	135
	733	0	1326
AT-skew reverse	1575	0.00444	1190
	1999	0.00889	1995
	2119	0.03333	2173

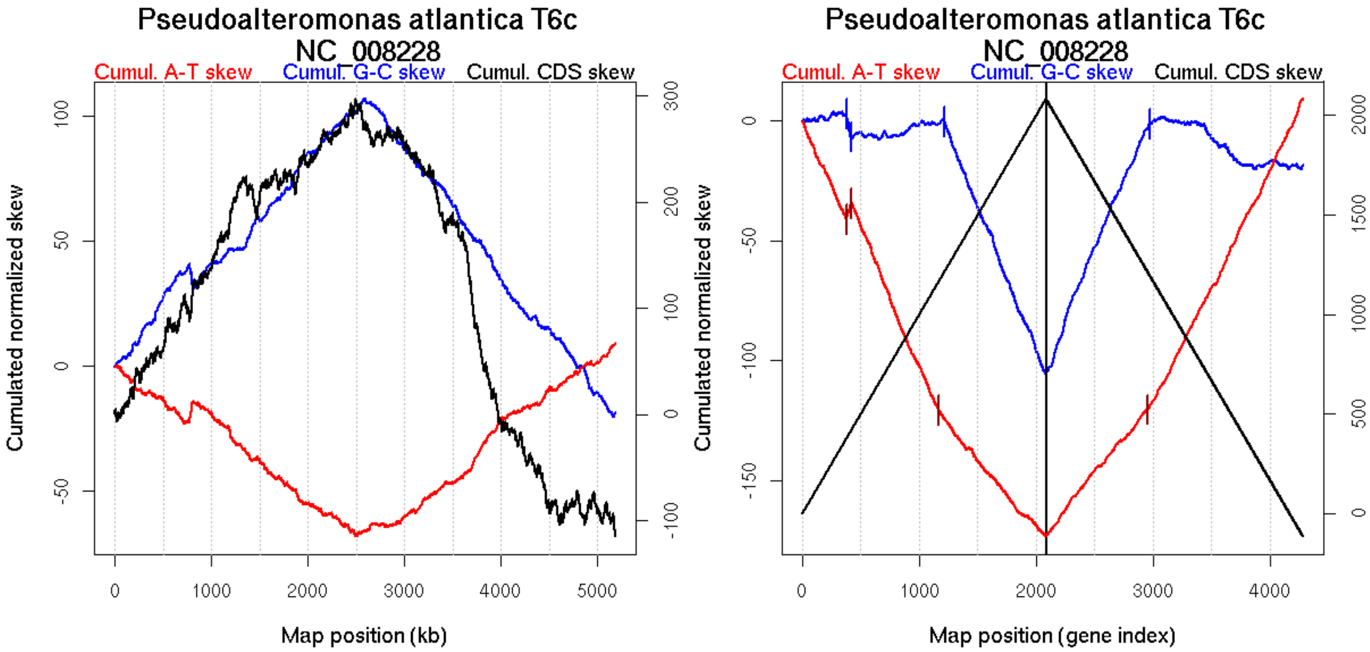
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	715 (1295.8895 kb)	leading	-0.046
	716(1296.285 kb)	1143 (2560.15 kb)	lagging	-0.229
GC-skew reverse	1144 (0 kb)	1610 (1324.0575 kb)	leading	0.226
	1611(1325.467 kb)	2297 (2560.15 kb)	lagging	0.061
AT-skew forward	1 (0 kb)	61 (135.021 kb)	leading	-0.256
	62(136.4535 kb)	733 (1326.4735 kb)	leading	-0.358
	734(1328.367 kb)	1143 (2560.15 kb)	lagging	-0.123
AT-skew reverse	1144 (0 kb)	1575 (1189.9535 kb)	leading	0.108
	1576(1190.582 kb)	1999(1995.038 kb)	lagging	0.349
	2000(1995.883 kb)	2119(2172.794 kb)	lagging	0.524
	2120(2173.585 kb)	2297(2560.15 kb)	lagging	0.383

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

249 Pseudoalteromonas atlantica T6c

Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales; Pseudoalteromonadaceae; Pseudoalteromonas.
Accession number: NC_008228; **Genome size (bp)**: 5187005.
Number of genes: 4281.
Oriloc predictions: Origin 0 kb Terminus 2588 kb
Worning et al., 2006: Origin NA kb Terminus NA kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 4309.437 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.81 kb, 3018.87 kb
Consensus predictions: Origin 0 kb Terminus 2588 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	376	0	763
	414	0	811
	1212	0	2616
GC-skew reverse	2974	0	2531
AT-skew forward	377	0	765
	420	0	816
	1167	0.02	2506
AT-skew reverse	2952	0	2493

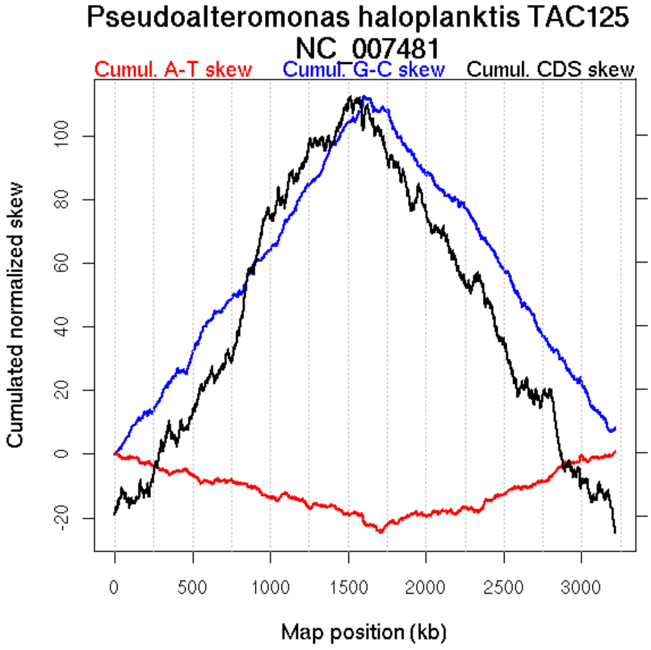
Segments:

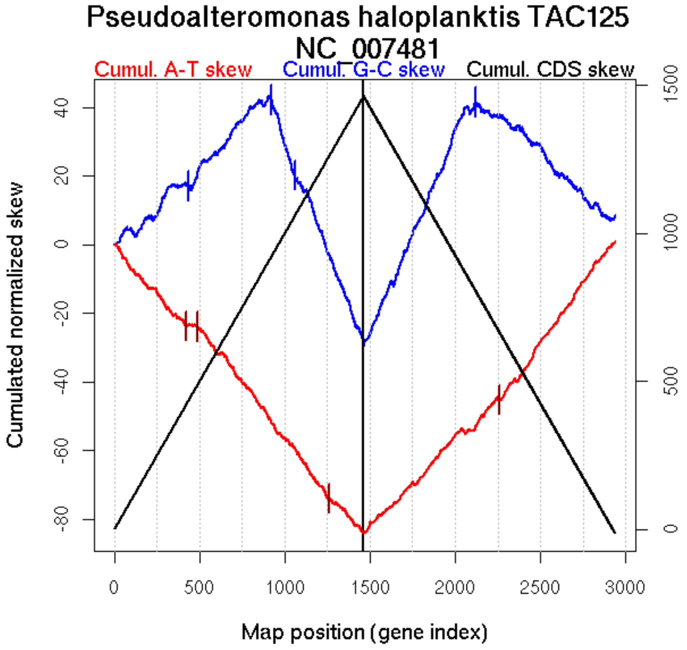
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	376 (762.631 kb)	leading	0.01
	377(764.6725 kb)	414 (810.706 kb)	leading	-0.261
	415(811.9105 kb)	1212 (2615.5155 kb)	leading	0.009
	1213(2619.9565 kb)	2083 (5186.593 kb)	lagging	-0.12
GC-skew reverse	2084 (0 kb)	2974 (2530.8285 kb)	leading	0.118
	2975(2533.1345 kb)	4281 (5186.593 kb)	lagging	-0.02
AT-skew forward	1 (0 kb)	377 (764.6725 kb)	leading	-0.107
	378(765.0995 kb)	420 (815.722 kb)	leading	0.166
	421(818.7025 kb)	1167 (2505.66 kb)	leading	-0.118
	1168(2506.3425 kb)	2083 (5186.593 kb)	lagging	-0.057
AT-skew reverse	2084 (0 kb)	2952 (2493.254 kb)	leading	0.06
	2953(2496.9205 kb)	4281(5186.593 kb)	lagging	0.098

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

250 Pseudoalteromonas haloplanktis TAC125

Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales; Pseudoalteromonadaceae; Pseudoalteromonas.
Accession number: NC_007481; **Genome size (bp)**: 3214944.
Number of genes: 2939.
Oriloc predictions: Origin 3179 kb Terminus 1611 kb
Worning et al., 2006: Origin 0 kb Terminus 1623 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 779.835 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): NA
Consensus predictions: Origin 3179 kb Terminus 1611 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	437	NA	798
	921	NA	1631
	1057	NA	2050
GC-skew reverse	2120	NA	1723
AT-skew forward	422	NA	777
	488	NA	854
	1259	NA	2637
AT-skew reverse	2257	NA	1981

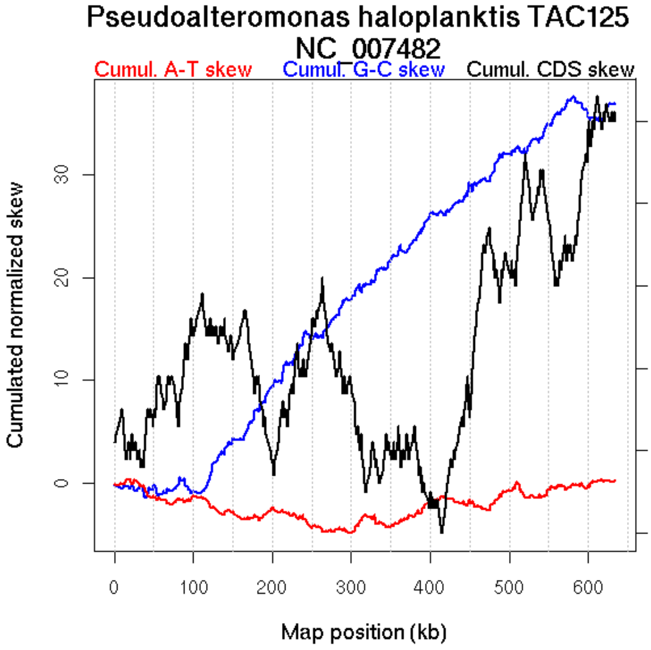
Segments:

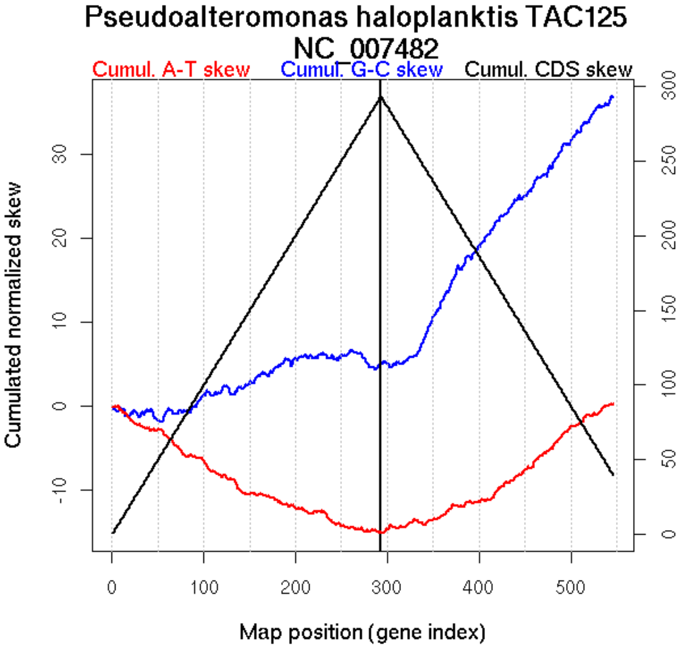
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	437 (797.523 kb)	leading	0.046
	438(799.511 kb)	921 (1630.574 kb)	leading	0.056
	922(1638.0575 kb)	1057 (2050.1615 kb)	lagging	-0.168
	1058(2052.996 kb)	1463 (3214.586 kb)	lagging	-0.126
GC-skew reverse	1464 (0 kb)	2120 (1723.3805 kb)	leading	0.114
	2121(1725.665 kb)	2939 (3214.586 kb)	lagging	-0.045
AT-skew forward	1 (0 kb)	422 (777.1425 kb)	leading	-0.055
	423(779.2505 kb)	488 (854.3135 kb)	leading	0.001
	489(855.053 kb)	1259 (2637.3115 kb)	NA	-0.065
	1260(2638.8125 kb)	1463 (3214.586 kb)	lagging	-0.051
AT-skew reverse	1464 (0 kb)	2257 (1981.3625 kb)	NA	0.05
	2258(1983.238 kb)	2939(3214.586 kb)	lagging	0.07

More G than C on the leading strand for replication.

251 Pseudoalteromonas haloplanktis TAC125

Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales; Pseudoalteromonadaceae; Pseudoalteromonas.
Accession number: NC_007482; **Genome size (bp)**: 635328.
Number of genes: 546.
Oriloc predictions: Origin NA Terminus NA
Worning et al., 2006: Origin 111 kb Terminus 321 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 116.001 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): NA
Consensus predictions: Origin NA Terminus NA

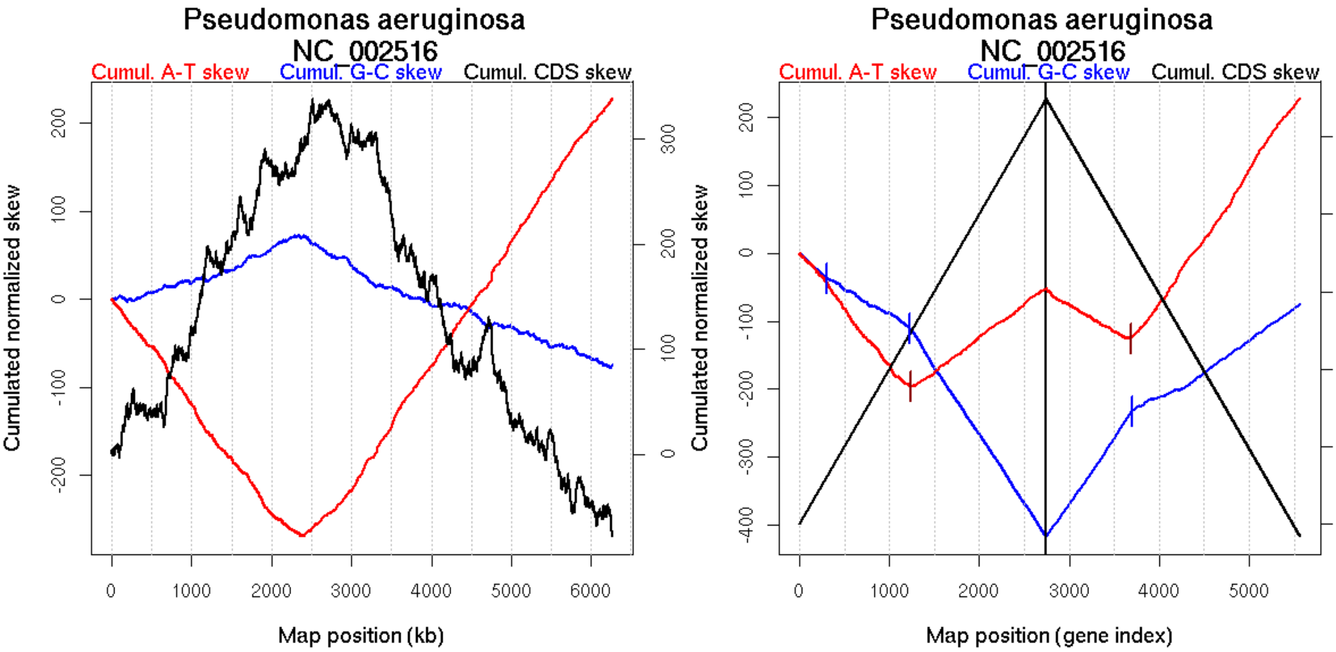




No significant breakpoints.

252 Pseudomonas aeruginosa

Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas.
Accession number: NC_002516; **Genome size (bp)**: 6264404.
Number of genes: 5566.
Oriloc predictions: Origin 0 kb Terminus 2333 kb
Worning et al., 2006: Origin 6256 kb Terminus 2443 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 6259.524 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1.25 kb
Consensus predictions: Origin 0 kb Terminus 2333 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	308	0.02333	631
	1227	0	2382
GC-skew reverse	3693	0	2410
AT-skew forward	1231	0	2393
AT-skew reverse	3686	0	2399

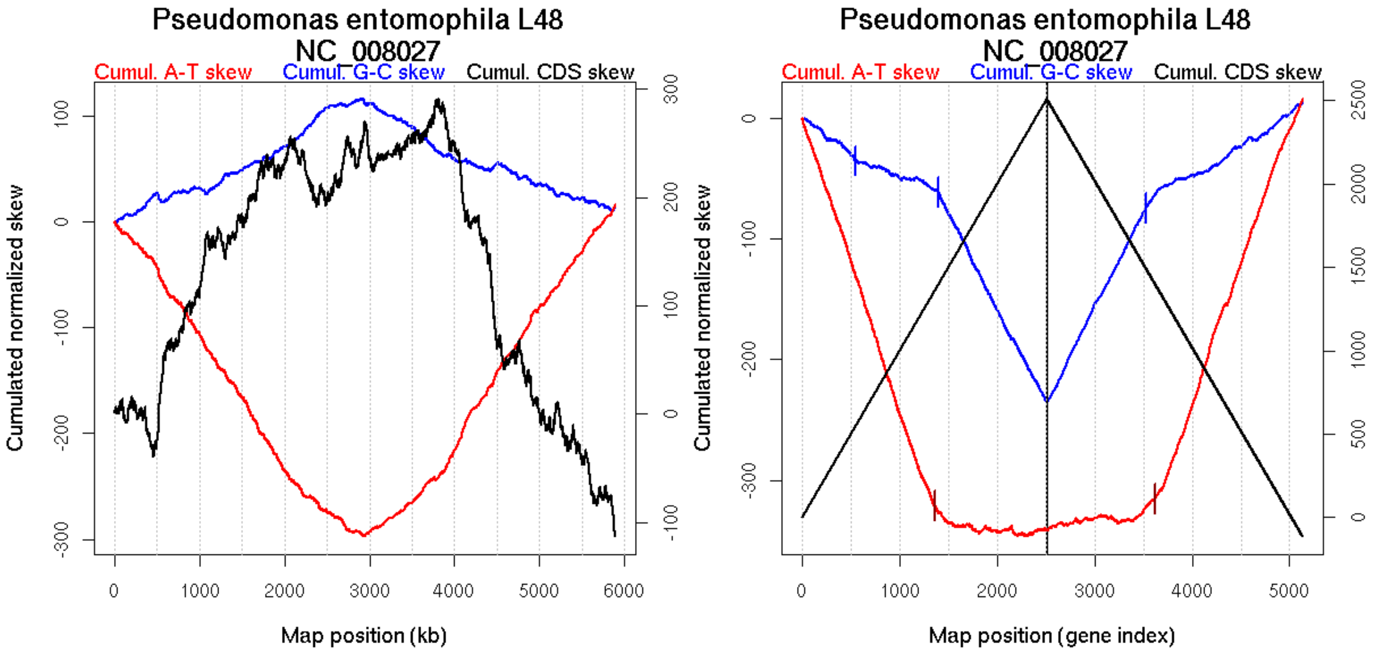
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	308 (631.0985 kb)	leading	-0.121
	309(640.7055 kb)	1227 (2381.93 kb)	leading	-0.077
	1228(2390.783 kb)	2744 (6264.361 kb)	lagging	-0.202
GC-skew reverse	2745 (0 kb)	3693 (2409.582 kb)	leading	0.194
	3694(2416.1835 kb)	5566 (6264.361 kb)	lagging	0.086
AT-skew forward	1 (0 kb)	1231 (2393.409 kb)	leading	-0.169
	1232(2393.669 kb)	2744 (6264.361 kb)	lagging	0.099
AT-skew reverse	2745 (0 kb)	3686 (2398.5895 kb)	leading	-0.077
	3687(2400.64 kb)	5566(6264.361 kb)	lagging	0.195

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

253 Pseudomonas entomophila L48

Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas.
Accession number: NC_008027; **Genome size (bp)**: 5888780.
Number of genes: 5133.
Oriloc predictions: Origin 9 kb Terminus 2905 kb
Worning et al., 2006: Origin 5887 kb Terminus 2910 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 5813.716 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1.31 kb
Consensus predictions: Origin 9 kb Terminus 2905 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	545	NA	1076
	1398	NA	2920
GC-skew reverse	3527	NA	2536
AT-skew forward	1357	NA	2852
AT-skew reverse	3616	NA	2809

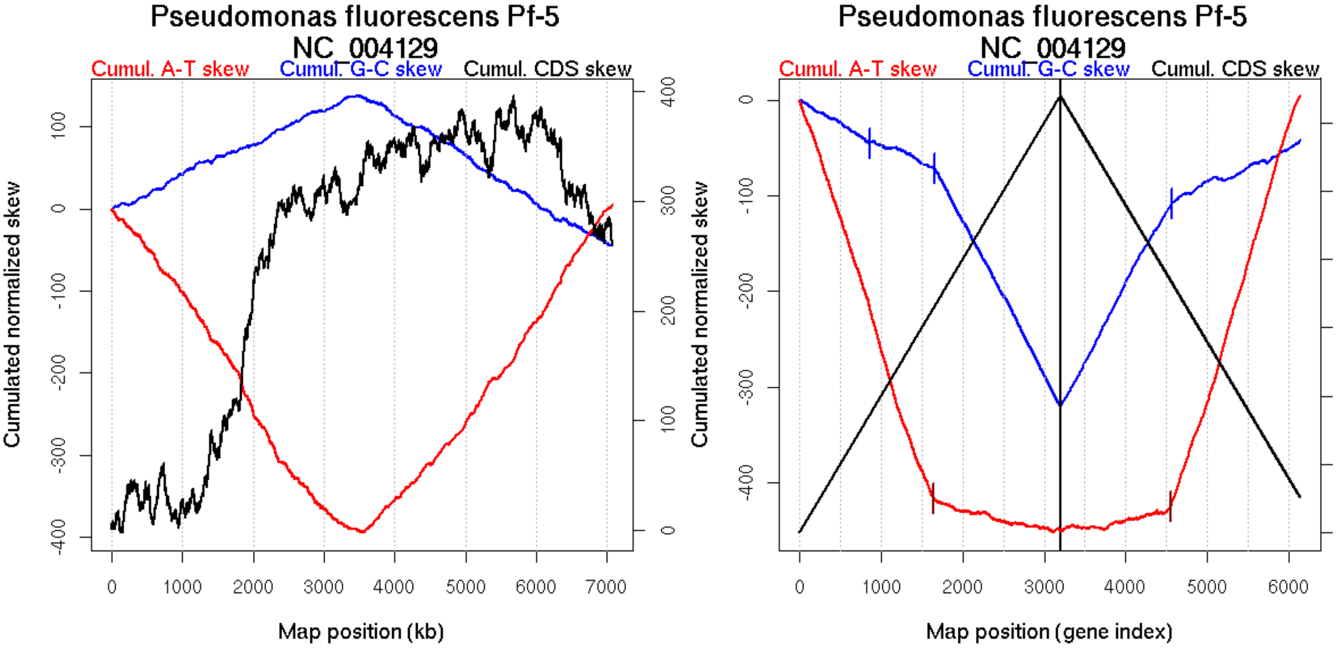
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	545 (1076.2455 kb)	leading	-0.06
	546(1077.4725 kb)	1398 (2920.2455 kb)	leading	-0.028
	1399(2922.388 kb)	2510 (5888.749 kb)	lagging	-0.157
GC-skew reverse	2511 (0 kb)	3527 (2536.2545 kb)	leading	0.159
	3528(2545.412 kb)	5133 (5888.749 kb)	lagging	0.049
AT-skew forward	1 (0 kb)	1357 (2852.214 kb)	leading	-0.243
	1358(2856.3275 kb)	2510 (5888.749 kb)	lagging	-0.011
AT-skew reverse	2511 (0 kb)	3616 (2809.3445 kb)	leading	0.013
	3617(2810.8415 kb)	5133(5888.749 kb)	lagging	0.229

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

254 Pseudomonas fluorescens Pf-5

Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas.
Accession number: NC_004129; **Genome size (bp)**: 7074893.
Number of genes: 6136.
Oriloc predictions: Origin 0 kb Terminus 3482 kb
Worning et al., 2006: Origin 7047 kb Terminus 3474 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 6983.667 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.87 kb
Consensus predictions: Origin 0 kb Terminus 3482 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	857	NA	1825
	1654	NA	3507
GC-skew reverse	4562	NA	3585
AT-skew forward	1642	NA	3486
AT-skew reverse	4551	NA	3536

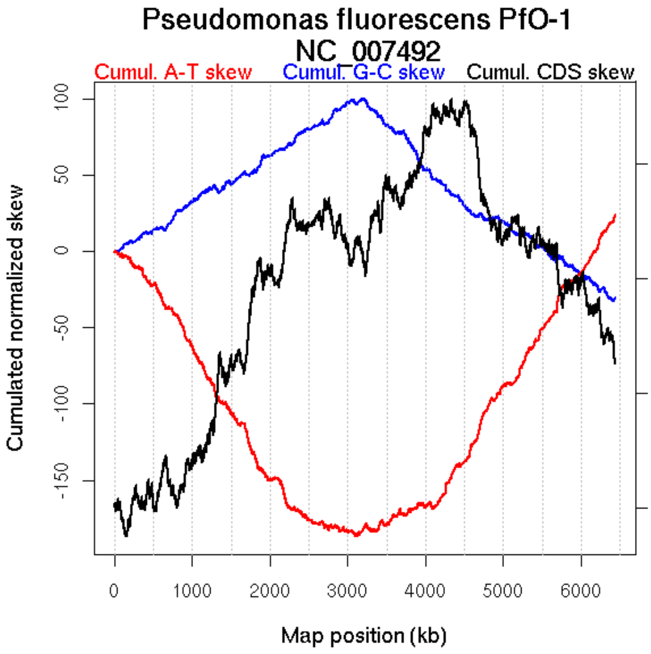
Segments:

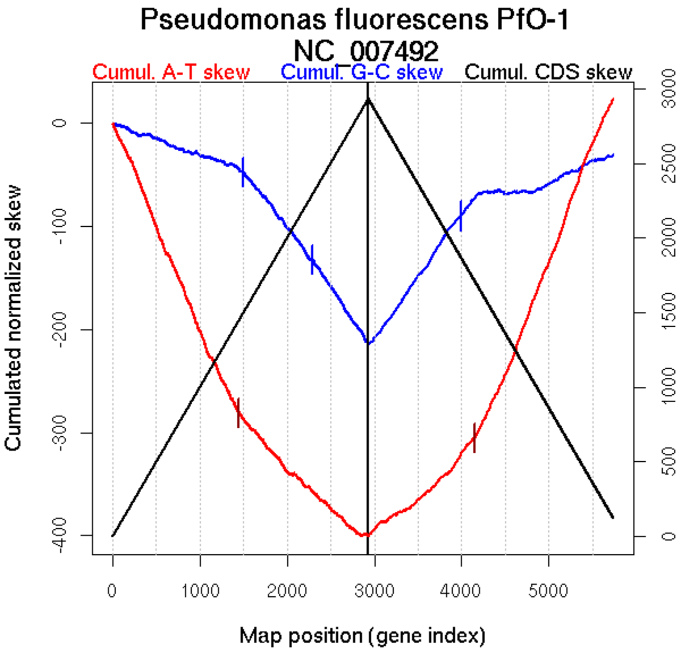
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	857 (1824.546 kb)	leading	-0.051
	858(1825.817 kb)	1654 (3507.2595 kb)	leading	-0.036
	1655(3508.2245 kb)	3198 (7074.427 kb)	lagging	-0.161
GC-skew reverse	3199 (0 kb)	4562 (3585.164 kb)	leading	0.16
	4563(3590.266 kb)	6136 (7074.427 kb)	lagging	0.037
AT-skew forward	1 (0 kb)	1642 (3486.311 kb)	leading	-0.265
	1643(3486.8745 kb)	3198 (7074.427 kb)	lagging	-0.02
AT-skew reverse	3199 (0 kb)	4551 (3536.177 kb)	leading	0.016
	4552(3542.212 kb)	6136(7074.427 kb)	lagging	0.281

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

255 Pseudomonas fluorescens PfO-1

Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas.
Accession number: NC_007492; **Genome size (bp)**: 6438405.
Number of genes: 5736.
Oriloc predictions: Origin 0 kb Terminus 3057 kb
Worning et al., 2006: Origin 6433 kb Terminus 3157 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 6309.819 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1.33 kb
Consensus predictions: Origin 0 kb Terminus 3057 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1502	NA	3231
	2295	NA	4904
GC-skew reverse	3989	NA	2739
AT-skew forward	1449	NA	3080
AT-skew reverse	4153	NA	3051

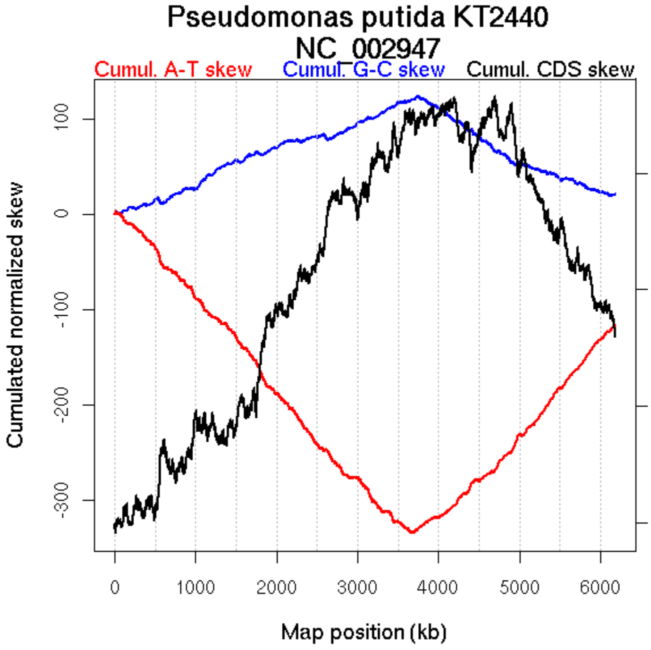
Segments:

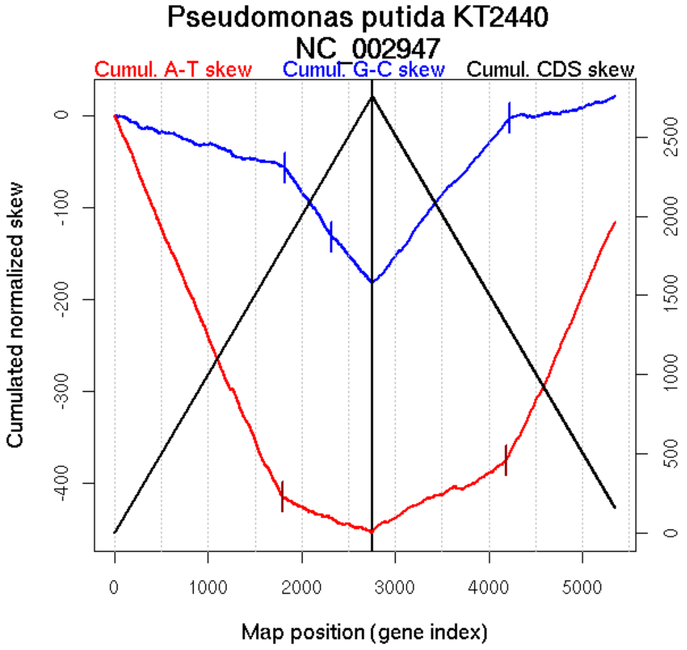
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1502 (3231.3365 kb)	leading	-0.03
	1503(3233.397 kb)	2295 (4903.6085 kb)	lagging	-0.109
	2296(4907.0355 kb)	2931 (6438.25 kb)	lagging	-0.128
GC-skew reverse	2932 (0 kb)	3989 (2738.6165 kb)	leading	0.123
	3990(2742.267 kb)	5736 (6438.25 kb)	lagging	0.027
AT-skew forward	1 (0 kb)	1449 (3079.818 kb)	leading	-0.2
	1450(3080.356 kb)	2931 (6438.25 kb)	lagging	-0.082
AT-skew reverse	2932 (0 kb)	4153 (3050.6685 kb)	leading	0.074
	4154(3057.05 kb)	5736(6438.25 kb)	lagging	0.217

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

256 Pseudomonas putida KT2440

Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas.
Accession number: NC_002947; **Genome size (bp)**: 6181863.
Number of genes: 5350.
Oriloc predictions: Origin 1 kb Terminus 3730 kb
Worning et al., 2006: Origin 8 kb Terminus 3731 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 9.322 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 10.3 kb
Consensus predictions: Origin 1 kb Terminus 3730 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1818	NA	3759
	2321	NA	4990
GC-skew reverse	4224	NA	3748
AT-skew forward	1794	NA	3702
AT-skew reverse	4188	NA	3678

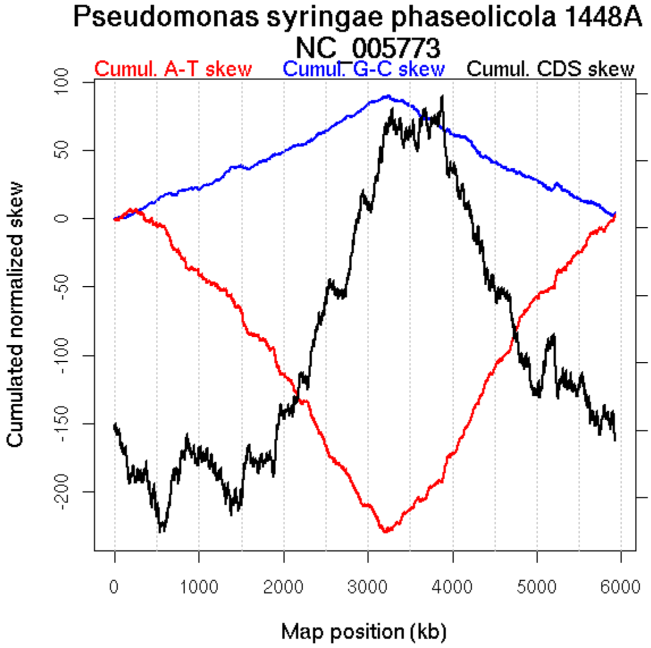
Segments:

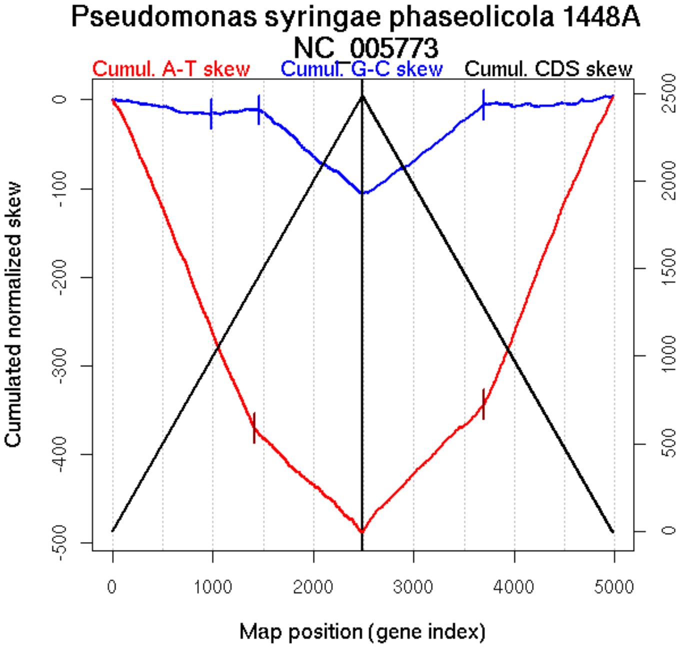
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1818 (3758.708 kb)	leading	-0.03
	1819(3759.353 kb)	2321 (4990.1835 kb)	lagging	-0.147
	2322(4993.293 kb)	2755 (6181.86 kb)	lagging	-0.121
GC-skew reverse	2756 (0 kb)	4224 (3748.178 kb)	leading	0.123
	4225(3749.404 kb)	5350 (6181.86 kb)	lagging	0.019
AT-skew forward	1 (0 kb)	1794 (3702.4565 kb)	leading	-0.234
	1795(3711.375 kb)	2755 (6181.86 kb)	lagging	-0.039
AT-skew reverse	2756 (0 kb)	4188 (3677.73 kb)	leading	0.048
	4189(3679.2275 kb)	5350(6181.86 kb)	lagging	0.229

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

257 Pseudomonas syringae phaseolicola 1448A

Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas.
Accession number: NC_005773; **Genome size (bp)**: 5928787.
Number of genes: 4982.
Oriloc predictions: Origin 108 kb Terminus 3197 kb
Worning et al., 2006: Origin 5896 kb Terminus 3255 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1692.574 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1.01 kb, 4253.97 kb
Consensus predictions: Origin 108 kb Terminus 3197 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	988	NA	2352
	1455	NA	3253
GC-skew reverse	3699	NA	3214
AT-skew forward	1413	NA	3177
AT-skew reverse	3700	NA	3217

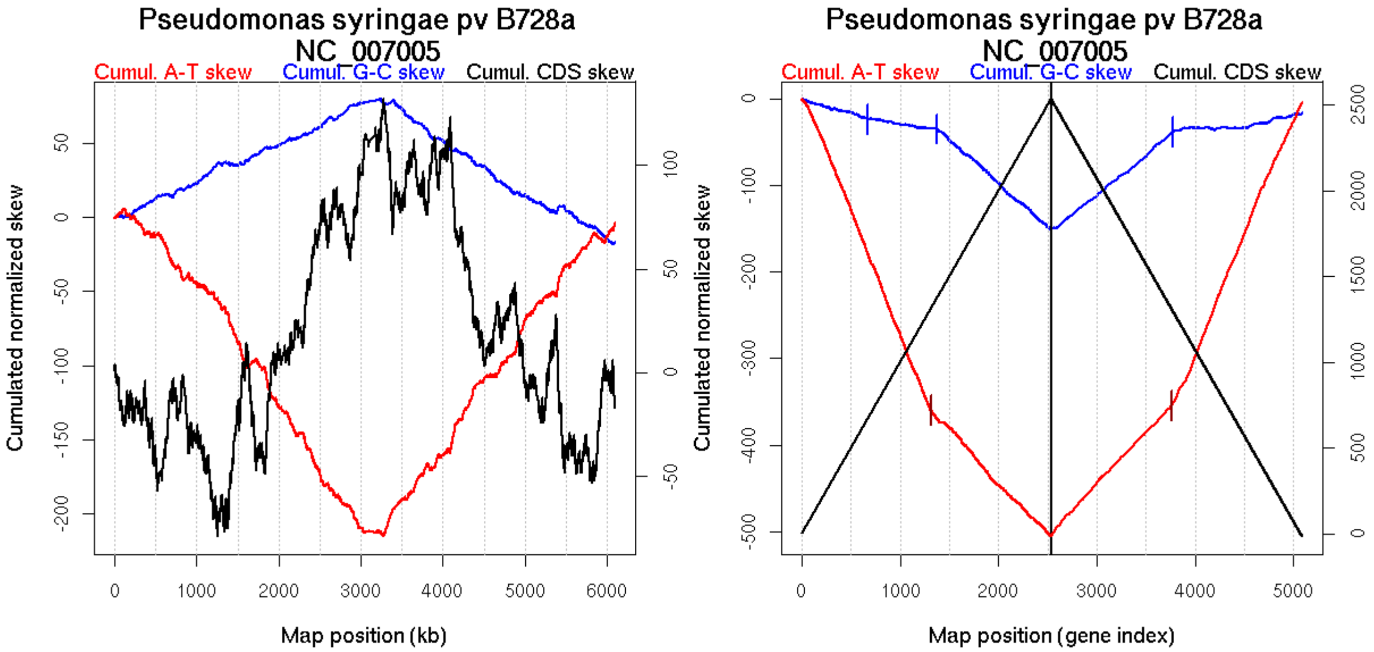
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	988 (2352.121 kb)	leading	-0.019
	989(2354.582 kb)	1455 (3253.1735 kb)	leading	0.012
	1456(3253.5845 kb)	2487 (5928.611 kb)	lagging	-0.093
GC-skew reverse	2488 (0 kb)	3699 (3213.7455 kb)	leading	0.085
	3700(3217.4635 kb)	4982 (5928.611 kb)	lagging	0.006
AT-skew forward	1 (0 kb)	1413 (3177.3095 kb)	leading	-0.272
	1414(3178.151 kb)	2487 (5928.611 kb)	lagging	-0.106
AT-skew reverse	2488 (0 kb)	3700 (3217.4635 kb)	leading	0.114
	3701(3220.4015 kb)	4982(5928.611 kb)	lagging	0.278

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

258 Pseudomonas syringae pv B728a

Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas.
Accession number: NC_007005; **Genome size (bp)**: 6093698.
Number of genes: 5089.
Oriloc predictions: Origin 0 kb Terminus 3241 kb
Worning et al., 2006: Origin 203 kb Terminus 3261 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 5999.825 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.77 kb
Consensus predictions: Origin 0 kb Terminus 3241 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	670	NA	1553
	1372	NA	3241
GC-skew reverse	3769	NA	3135
AT-skew forward	1313	NA	2978
AT-skew reverse	3760	NA	3036

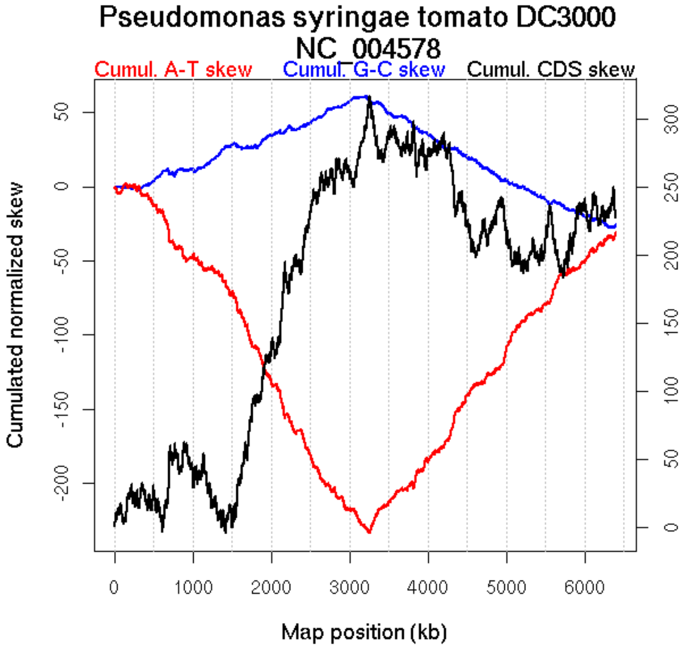
Segments:

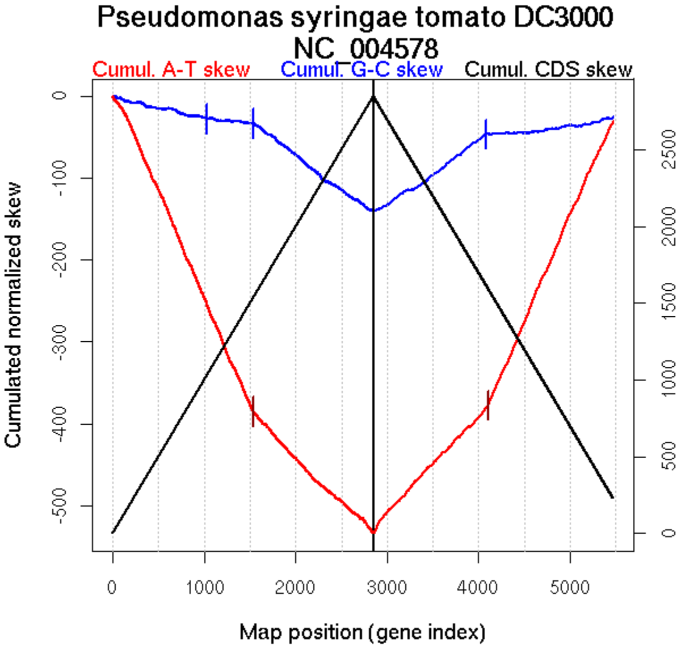
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	670 (1552.5515 kb)	leading	-0.032
	671(1553.05 kb)	1372 (3240.5735 kb)	leading	-0.018
	1373(3241.4125 kb)	2536 (6093.114 kb)	lagging	-0.101
GC-skew reverse	2537 (0 kb)	3769 (3135.389 kb)	leading	0.092
	3770(3179.9975 kb)	5089 (6093.114 kb)	lagging	0.014
AT-skew forward	1 (0 kb)	1313 (2978.12 kb)	leading	-0.283
	1314(2982.736 kb)	2536 (6093.114 kb)	lagging	-0.121
AT-skew reverse	2537 (0 kb)	3760 (3036.365 kb)	leading	0.12
	3761(3053.0205 kb)	5089(6093.114 kb)	lagging	0.273

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

259 Pseudomonas syringae tomato DC3000

Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Pseudomonas.
Accession number: NC_004578; **Genome size (bp)**: 6397126.
Number of genes: 5470.
Oriloc predictions: Origin 318 kb Terminus 3213 kb
Worning et al., 2006: Origin 229 kb Terminus 3208 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 6271.36 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1.11 kb
Consensus predictions: Origin 318 kb Terminus 3213 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1036	NA	2139
	1540	NA	3196
GC-skew reverse	4082	NA	3115
AT-skew forward	1541	NA	3198
AT-skew reverse	4104	NA	3246

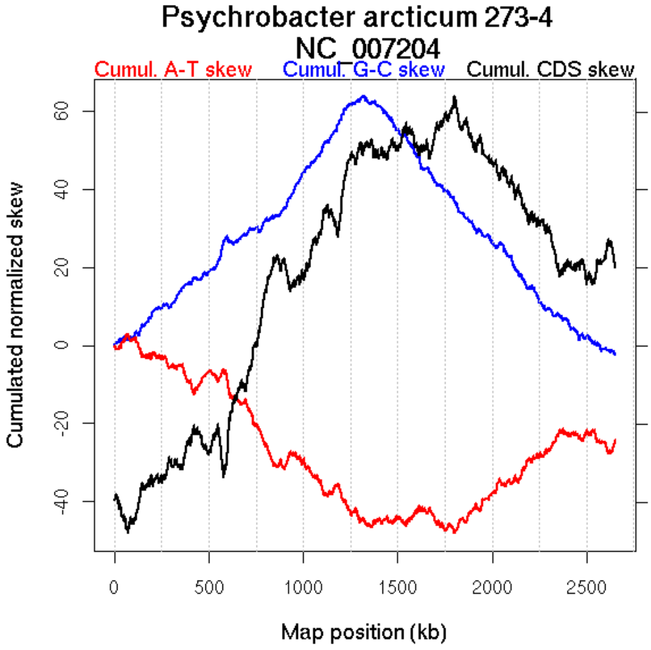
Segments:

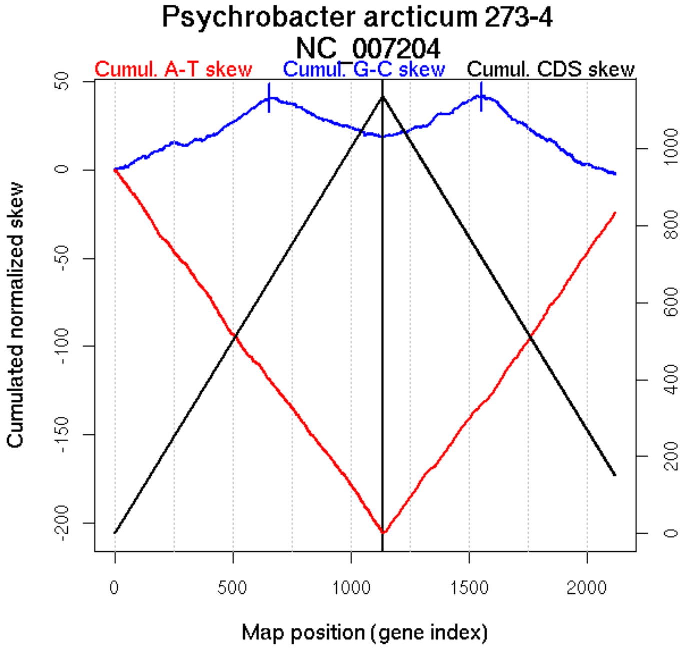
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1036 (2138.9175 kb)	leading	-0.025
	1037(2139.3825 kb)	1540 (3196.191 kb)	leading	-0.011
	1541(3198.443 kb)	2849 (6396.881 kb)	lagging	-0.084
GC-skew reverse	2850 (0 kb)	4082 (3114.8885 kb)	leading	0.078
	4083(3121.764 kb)	5470 (6396.881 kb)	lagging	0.014
AT-skew forward	1 (0 kb)	1541 (3198.443 kb)	leading	-0.259
	1542(3201.299 kb)	2849 (6396.881 kb)	lagging	-0.109
AT-skew reverse	2850 (0 kb)	4104 (3246.0015 kb)	leading	0.118
	4105(3247.286 kb)	5470(6396.881 kb)	lagging	0.256

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

260 Psychrobacter arcticum 273-4

Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Moraxellaceae; Psychrobacter.
Accession number: NC_007204; **Genome size (bp)**: 2650701.
Number of genes: 2120.
Oriloc predictions: Origin 0 kb Terminus 1336 kb
Worning et al., 2006: Origin 1 kb Terminus 1336 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 0.312 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 2004.65 kb
Consensus predictions: Origin 0 kb Terminus 1336 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	655	0	1320
GC-skew reverse	1555	0	1304

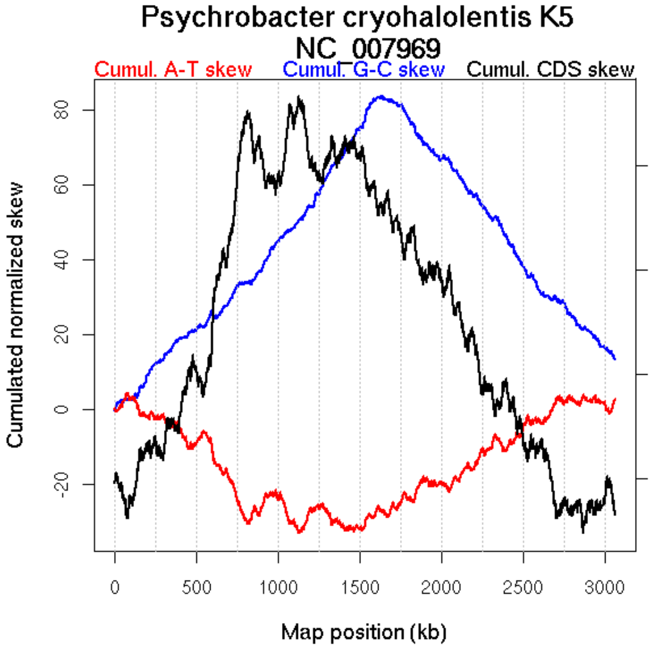
Segments:

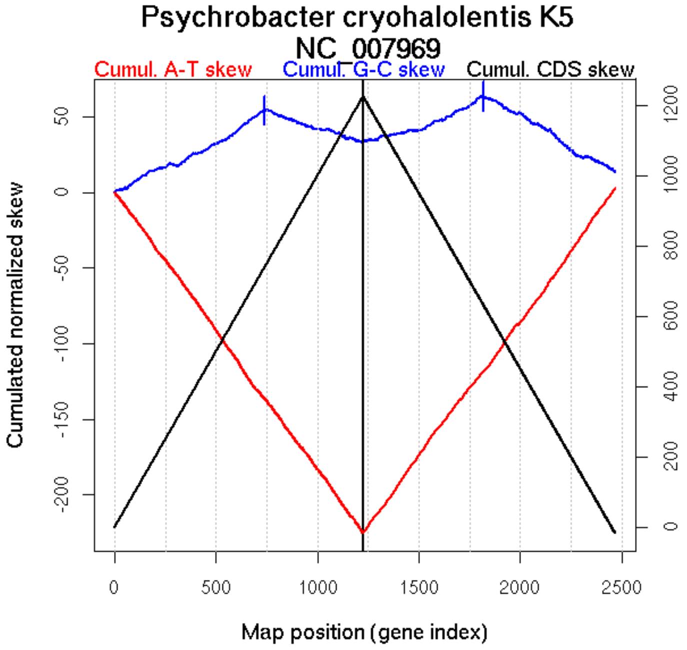
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	655 (1319.9835 kb)	leading	0.058
	656(1321.5995 kb)	1135 (2650.552 kb)	lagging	-0.049
GC-skew reverse	1136 (0 kb)	1555 (1303.784 kb)	leading	0.06
	1556(1306.285 kb)	2120 (2650.552 kb)	lagging	-0.083

More G than C on the leading strand for replication.

261 Psychrobacter cryohalolentis K5

Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Moraxellaceae; Psychrobacter.
Accession number: NC_007969; **Genome size (bp)**: 3059876.
Number of genes: 2467.
Oriloc predictions: Origin 0 kb Terminus 1670 kb
Worning et al., 2006: Origin 1 kb Terminus 1690 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1.169 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 2.09 kb, 2288.85 kb
Consensus predictions: Origin 0 kb Terminus 1670 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	741	NA	1655
GC-skew reverse	1816	NA	1607

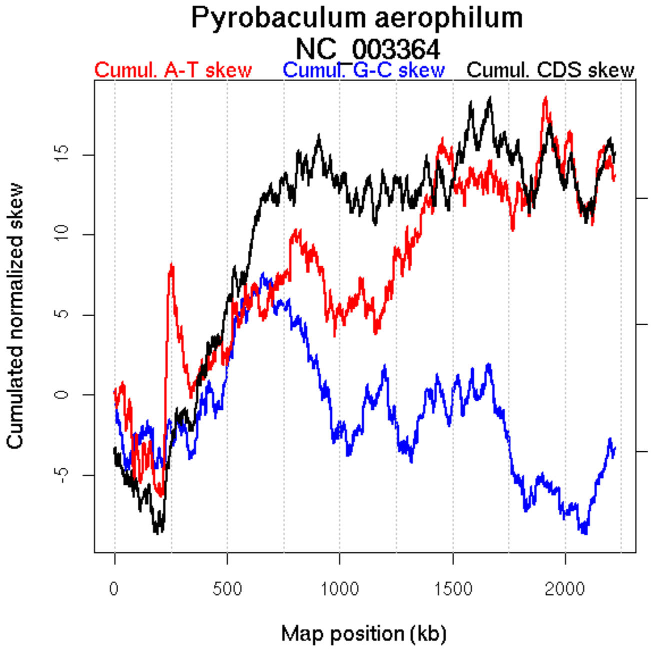
Segments:

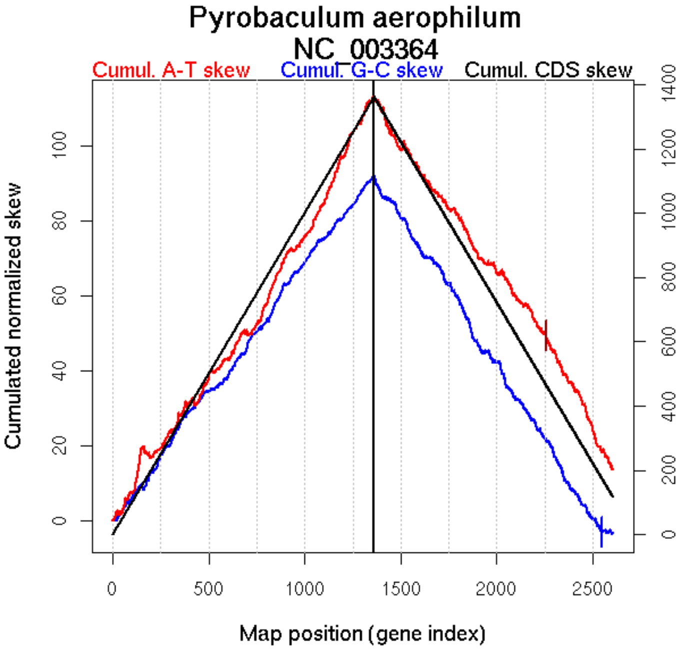
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	741 (1655.0605 kb)	leading	0.069
	742(1657.2385 kb)	1225 (3059.876 kb)	lagging	-0.043
GC-skew reverse	1226 (0 kb)	1816 (1607.261 kb)	leading	0.048
	1817(1608.022 kb)	2467 (3059.876 kb)	lagging	-0.08

More G than C on the leading strand for replication.

262 Pyrobaculum aerophilum

Archaea; Crenarchaeota; Thermoprotei; Thermoproteales; Thermoproteaceae; Pyrobaculum.
Accession number: NC_003364; **Genome size (bp)**: 2222430.
Number of genes: 2605.
Oriloc predictions: Origin NA Terminus NA
Worning et al., 2006: Origin 115 kb Terminus 818 kb
Position(s) of the ORC/Cdc6 gene(s): 383.23 kb, 410.68 kb, 1890.54 kb
Consensus predictions: Origin NA Terminus NA





Significant breakpoints (p-value <0.05):

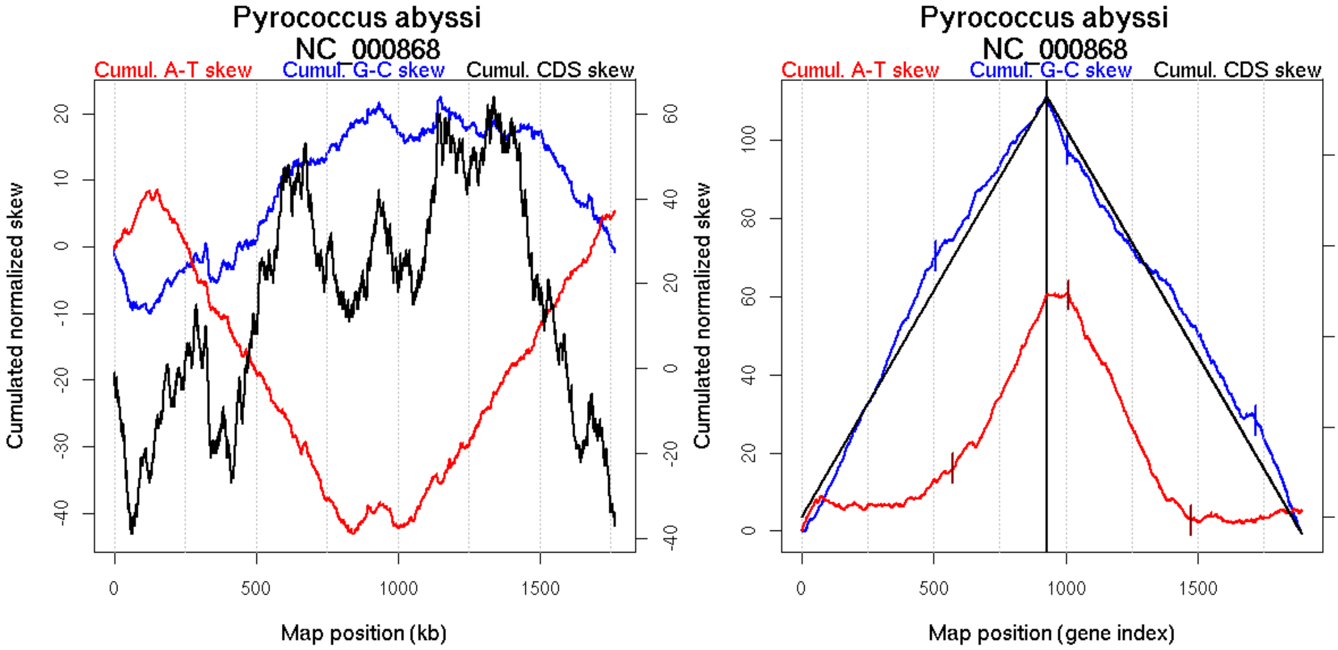
	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew reverse	2548	0	2100
AT-skew reverse	2257	0.02	1633

Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew reverse	1362 (0 kb)	2548 (2099.864 kb)	NA	-0.08
	2549(2100.848 kb)	2605 (2222.244 kb)	NA	-0.007
AT-skew reverse	1362 (0 kb)	2257 (1633.3875 kb)	NA	-0.068
	2258(1635.415 kb)	2605(2222.244 kb)	NA	-0.103

263 Pyrococcus abyssi

Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae; Pyrococcus.
Accession number: NC_000868; **Genome size (bp)**: 1765118.
Number of genes: 1895.
Oriloc predictions: Origin 122 kb Terminus 920 kb
Worning et al., 2006: Origin 123 kb Terminus 1316 kb
Position(s) of the ORC/Cdc6 gene(s): 122.05 kb, 384.8 kb, 817.96 kb, 1394.99 kb
Consensus predictions: Origin 122 kb Terminus 920 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	509	0.04	909
GC-skew reverse	1004	0.04	114
	1719	0.04333	1473
AT-skew forward	574	0	1030
AT-skew reverse	1011	0.00333	129
	1474	0.00333	1022

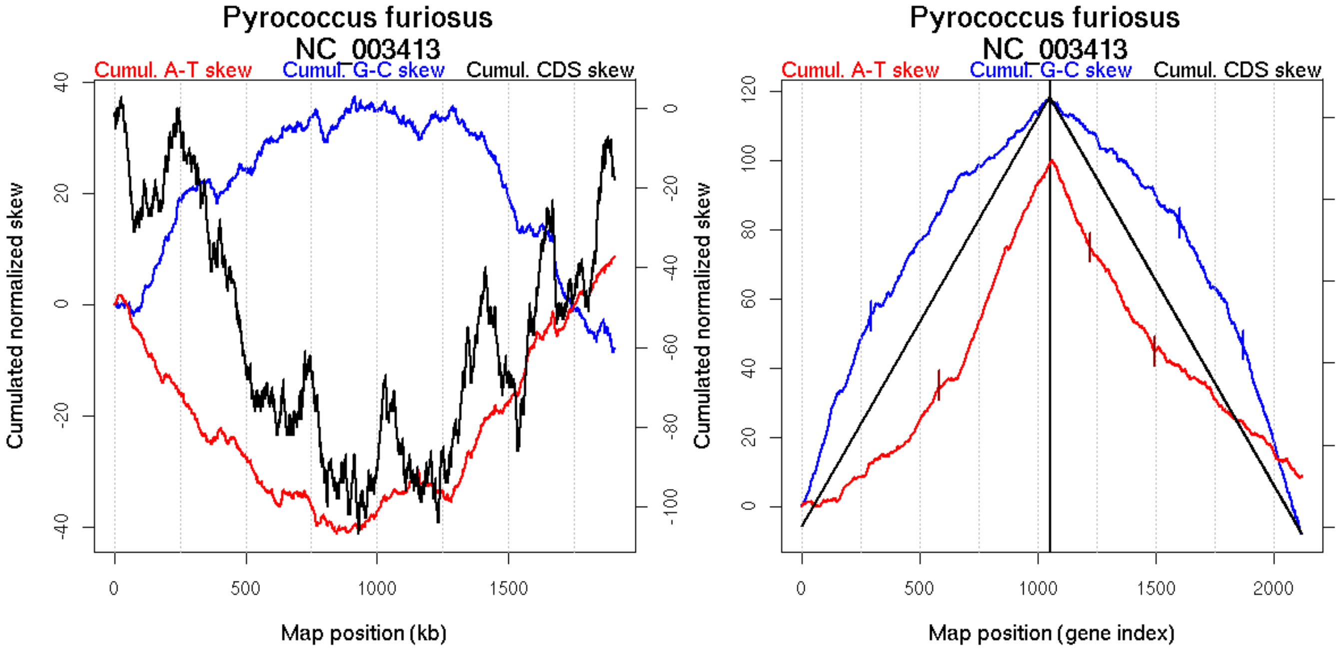
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	509 (908.9725 kb)	leading	0.146
	510(910.3845 kb)	929 (1764.508 kb)	lagging	0.099
GC-skew reverse	930 (0 kb)	1004 (114.3735 kb)	lagging	-0.171
	1005(116.976 kb)	1719 (1473.489 kb)	NA	-0.098
	1720(1474.1415 kb)	1895 (1764.508 kb)	lagging	-0.171
AT-skew forward	1 (0 kb)	574 (1030.3385 kb)	NA	0.014
	575(1034.789 kb)	929 (1764.508 kb)	lagging	0.127
AT-skew reverse	930 (0 kb)	1011 (128.517 kb)	lagging	0.001
	1012(133.1905 kb)	1474(1022.3855 kb)	leading	-0.132
	1475(1025.8025 kb)	1895(1764.508 kb)	lagging	0.006

More T than A on the leading strand for replication - for reverse encoded genes.
More G than C on the leading strand for replication - for forward encoded genes.

264 Pyrococcus furiosus

Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae; Pyrococcus.
Accession number: NC_003413; **Genome size (bp)**: 1908256.
Number of genes: 2120.
Oriloc predictions: Origin 0 kb Terminus 934 kb
Worning et al., 2006: Origin 24 kb Terminus 830 kb
Position(s) of the ORC/Cdc6 gene(s): 16.87 kb, 499.55 kb, 923.29 kb, 1735.13 kb
Consensus predictions: Origin 0 kb Terminus 934 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	293	NA	667
GC-skew reverse	1603	NA	929
	1870	NA	1442
AT-skew forward	584	NA	1161
AT-skew reverse	1222	NA	329
	1495	NA	776

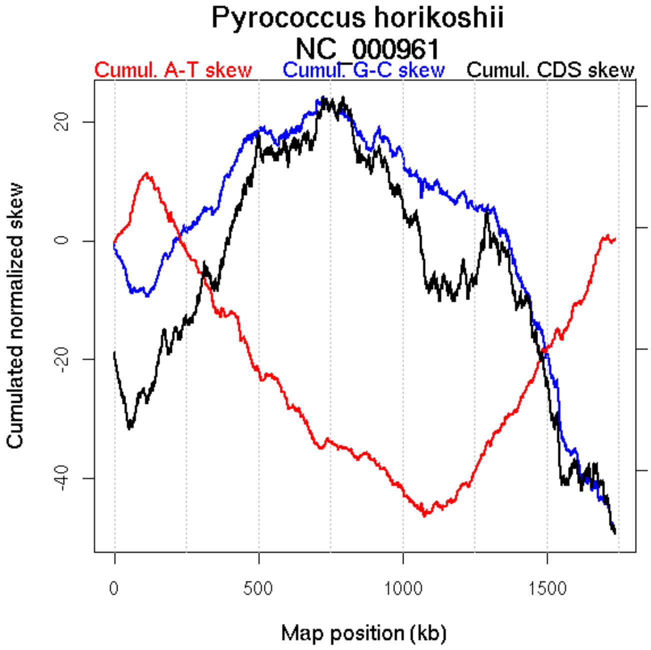
Segments:

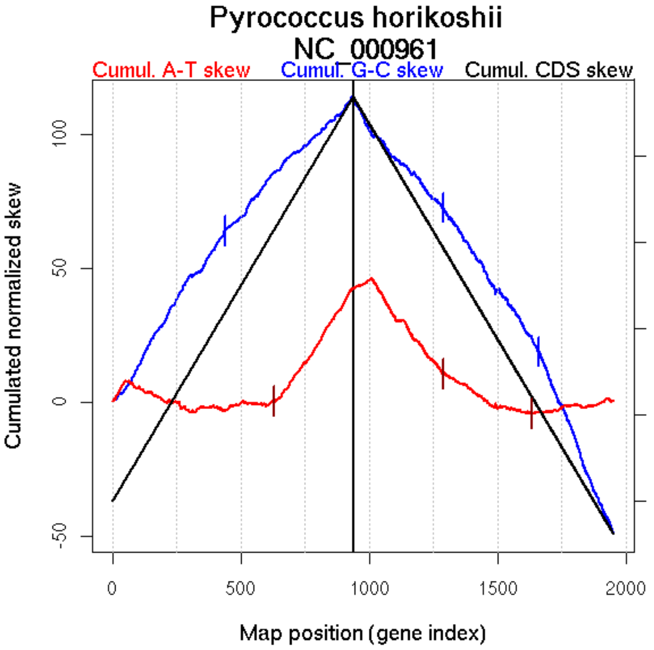
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	293 (666.6485 kb)	leading	0.192
	294(667.122 kb)	1051 (1908.185 kb)	NA	0.082
GC-skew reverse	1052 (0 kb)	1603 (929.011 kb)	leading	-0.064
	1604(929.6465 kb)	1870 (1442.22 kb)	lagging	-0.127
	1871(1443.859 kb)	2120 (1908.185 kb)	lagging	-0.221
AT-skew forward	1 (0 kb)	584 (1161.2355 kb)	NA	0.056
	585(1162.38 kb)	1051 (1908.185 kb)	lagging	0.155
AT-skew reverse	1052 (0 kb)	1222 (329.425 kb)	leading	-0.158
	1223(329.834 kb)	1495(775.814 kb)	leading	-0.11
	1496(776.613 kb)	2120(1908.185 kb)	NA	-0.061

More G than C on the leading strand for replication - for reverse encoded genes.

265 Pyrococcus horikoshii

Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae; Pyrococcus.
Accession number: NC_000961; **Genome size (bp)**: 1738505.
Number of genes: 1952.
Oriloc predictions: Origin 115 kb Terminus 1074 kb
Worning et al., 2006: Origin 111 kb Terminus 706 kb
Position(s) of the ORC/Cdc6 gene(s): 110.13 kb, 546.77 kb, 611.37 kb
Consensus predictions: Origin 115 kb Terminus 1074 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	438	NA	706
GC-skew reverse	1287	NA	726
	1660	NA	1355
AT-skew forward	630	NA	1134
AT-skew reverse	1289	NA	730
	1634	NA	1318

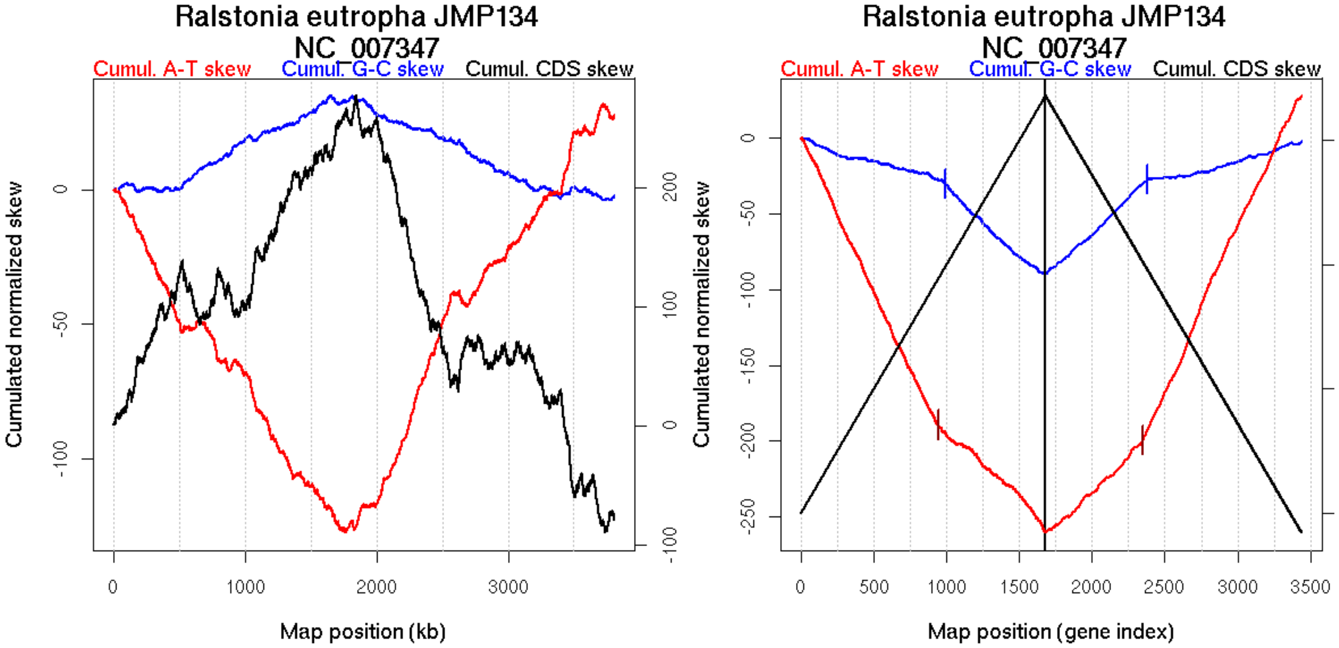
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	438 (706.4125 kb)	leading	0.151
	439(710.6125 kb)	938 (1737.901 kb)	NA	0.099
GC-skew reverse	939 (0 kb)	1287 (726.283 kb)	NA	-0.108
	1288(728.179 kb)	1660 (1354.784 kb)	NA	-0.142
	1661(1356.0775 kb)	1952 (1737.901 kb)	lagging	-0.237
AT-skew forward	1 (0 kb)	630 (1134.2525 kb)	leading	-0.011
	631(1136.7195 kb)	938 (1737.901 kb)	lagging	0.143
AT-skew reverse	939 (0 kb)	1289 (730.1955 kb)	NA	-0.109
	1290(732.902 kb)	1634(1318.0045 kb)	NA	-0.046
	1635(1318.568 kb)	1952(1737.901 kb)	lagging	0.015

More T than A on the leading strand for replication - for forward encoded genes.

266 Ralstonia eutropha JMP134

Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Cupriavidus.
Accession number: NC_007347; **Genome size (bp)**: 3806533.
Number of genes: 3439.
Oriloc predictions: Origin 3723 kb Terminus 1820 kb
Worning et al., 2006: Origin 3740 kb Terminus 1845 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 3757.762 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1.1 kb
Consensus predictions: Origin 3723 kb Terminus 1820 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	990	0	1907
GC-skew reverse	2382	0	1807
AT-skew forward	941	0.00667	1763
AT-skew reverse	2350	0	1734

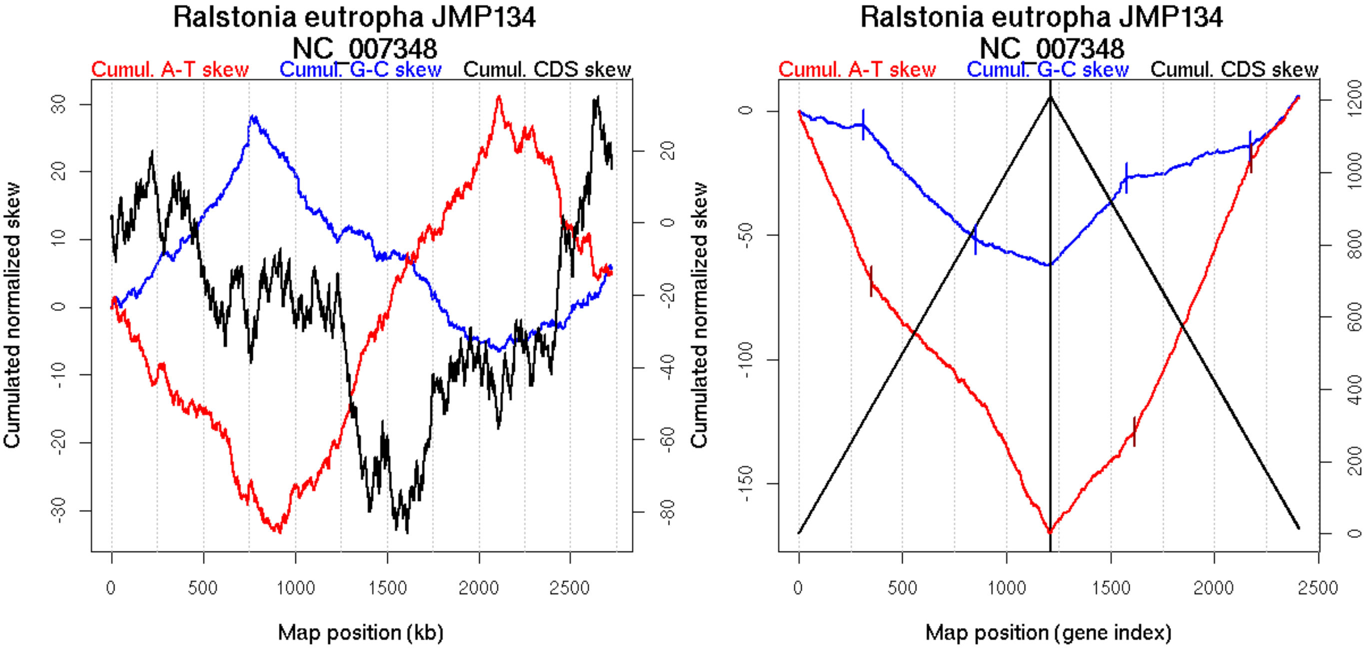
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	990 (1907.0155 kb)	leading	-0.026
	991(1909.8265 kb)	1680 (3805.995 kb)	lagging	-0.088
GC-skew reverse	1681 (0 kb)	2382 (1806.5985 kb)	leading	0.09
	2383(1809.431 kb)	3439 (3805.995 kb)	lagging	0.025
AT-skew forward	1 (0 kb)	941 (1762.848 kb)	leading	-0.205
	942(1764.5095 kb)	1680 (3805.995 kb)	lagging	-0.088
AT-skew reverse	1681 (0 kb)	2350 (1733.9905 kb)	leading	0.092
	2351(1735.4905 kb)	3439(3805.995 kb)	lagging	0.213

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

267 Ralstonia eutropha JMP134

Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Cupriavidus.
Accession number: NC_007348; **Genome size (bp)**: 2726152.
Number of genes: 2407.
Oriloc predictions: Origin 2107 kb Terminus 788 kb
Worning et al., 2006: Origin 2121 kb Terminus 767 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 262.041 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): NA
Consensus predictions: Origin 2107 kb Terminus 788 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	311	0.02	766
	853	0.02667	1961
GC-skew reverse	1580	0.00667	836
	2174	0.00667	2145
AT-skew forward	351	0	829
AT-skew reverse	1614	0.00333	923
	2178	0.01667	2152

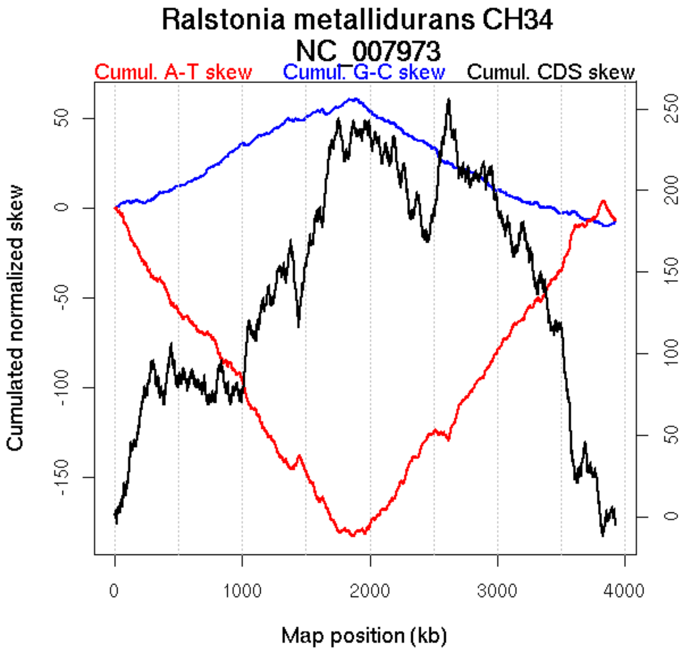
Segments:

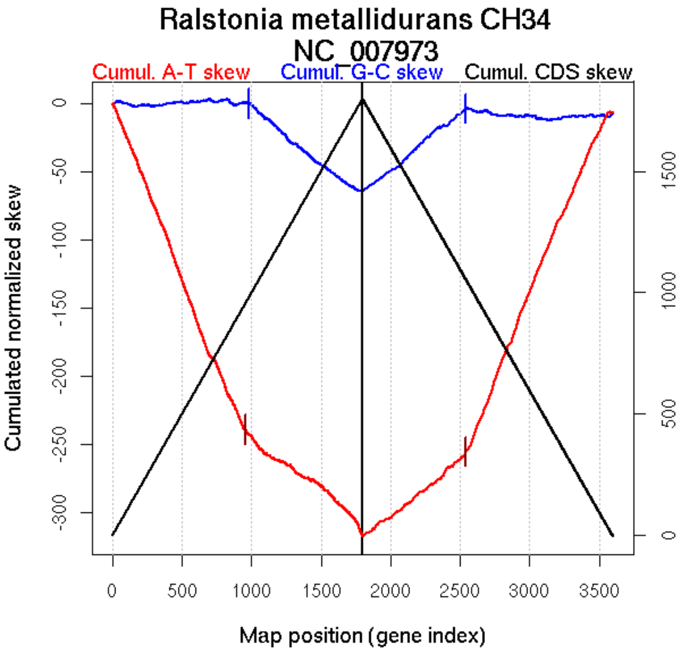
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	311 (766.199 kb)	leading	-0.019
	312(767.05 kb)	853 (1961.2345 kb)	lagging	-0.085
	854(1966.261 kb)	1211 (2725.616 kb)	leading	-0.029
GC-skew reverse	1212 (0 kb)	1580 (836.1595 kb)	leading	0.093
	1581(837.1095 kb)	2174 (2145.165 kb)	lagging	0.025
	2175(2147.6375 kb)	2407 (2725.616 kb)	leading	0.086
AT-skew forward	1 (0 kb)	351 (828.8445 kb)	leading	-0.194
	352(829.4665 kb)	1211 (2725.616 kb)	NA	-0.112
AT-skew reverse	1212 (0 kb)	1614 (922.603 kb)	leading	0.097
	1615(922.996 kb)	2178(2151.5915 kb)	lagging	0.197
	2179(2154.0095 kb)	2407(2725.616 kb)	leading	0.105

More T than A on the leading strand for replication - for reverse encoded genes.
More G than C on the leading strand for replication.

268 Ralstonia metallidurans CH34

Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Cupriavidus.
Accession number: NC_007973; **Genome size (bp)**: 3928089.
Number of genes: 3601.
Oriloc predictions: Origin 3832 kb Terminus 1885 kb
Worning et al., 2006: Origin 3849 kb Terminus 1877 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 3707.605 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.97 kb, 3166.98 kb
Consensus predictions: Origin 3832 kb Terminus 1885 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	984	NA	1885
GC-skew reverse	2544	NA	1883
AT-skew forward	954	NA	1834
AT-skew reverse	2544	NA	1883

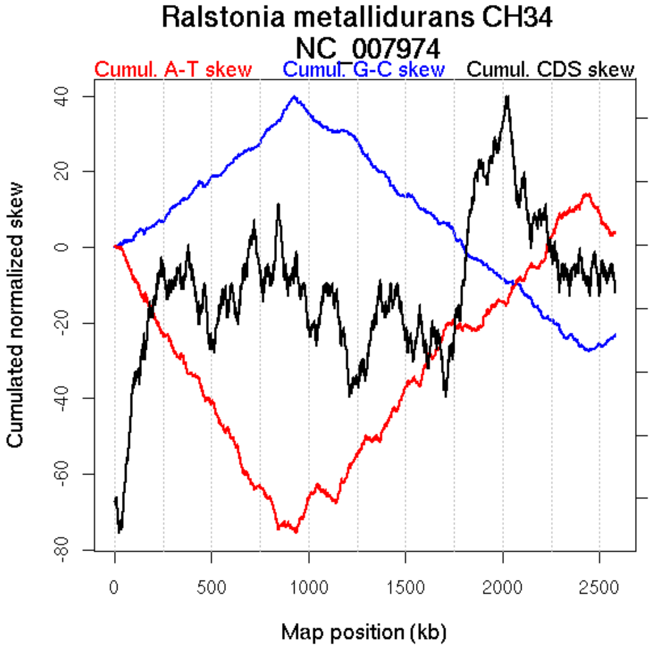
Segments:

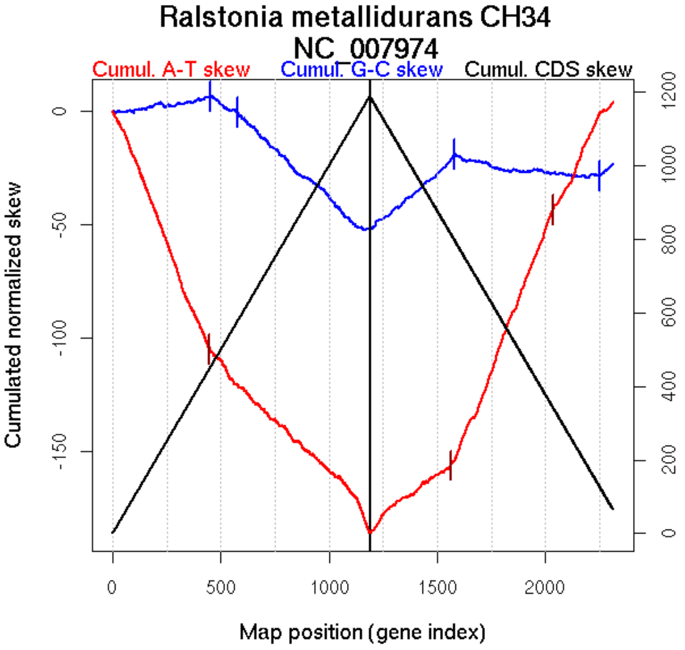
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	984 (1885.0875 kb)	leading	0.002
	985(1888.968 kb)	1798 (3927.779 kb)	lagging	-0.082
GC-skew reverse	1799 (0 kb)	2544 (1883.464 kb)	leading	0.084
	2545(1884.8975 kb)	3601 (3927.779 kb)	lagging	-0.004
AT-skew forward	1 (0 kb)	954 (1834.3095 kb)	leading	-0.259
	955(1837.886 kb)	1798 (3927.779 kb)	lagging	-0.077
AT-skew reverse	1799 (0 kb)	2544 (1883.464 kb)	leading	0.081
	2545(1884.8975 kb)	3601(3927.779 kb)	lagging	0.246

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

269 Ralstonia metallidurans CH34

Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Cupriavidus.
Accession number: NC_007974; **Genome size (bp)**: 2580084.
Number of genes: 2313.
Oriloc predictions: Origin 2444 kb Terminus 923 kb
Worning et al., 2006: Origin 2440 kb Terminus 937 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 558.31 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): NA
Consensus predictions: Origin 2444 kb Terminus 923 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	454	NA	912
	575	NA	1238
GC-skew reverse	1580	NA	929
	2252	NA	2444
AT-skew forward	448	NA	900
AT-skew reverse	1561	NA	887
	2036	NA	2044

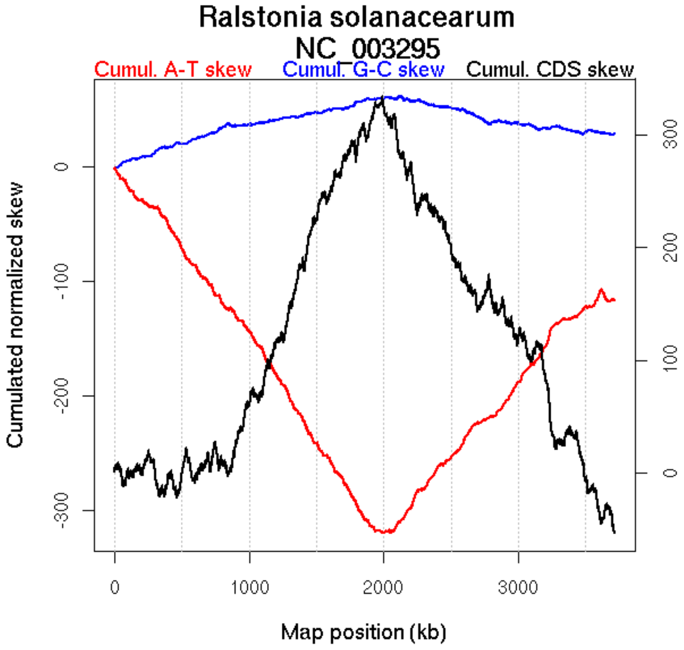
Segments:

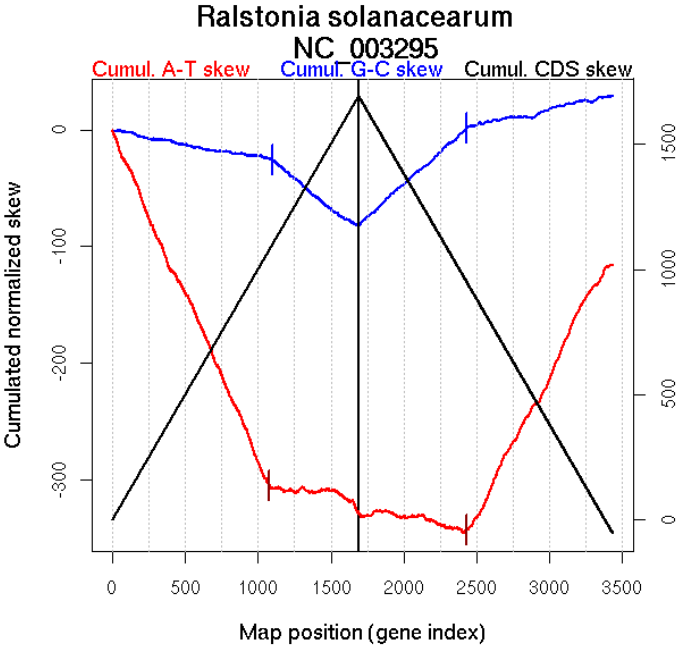
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	454 (912.1325 kb)	leading	0.014
	455(912.817 kb)	575 (1237.5465 kb)	lagging	-0.061
	576(1238.5885 kb)	1189 (2580.08 kb)	lagging	-0.088
GC-skew reverse	1190 (0 kb)	1580 (929.396 kb)	leading	0.081
	1581(936.93 kb)	2252 (2444.036 kb)	lagging	-0.012
	2253(2444.959 kb)	2313 (2580.08 kb)	leading	0.083
AT-skew forward	1 (0 kb)	448 (899.7585 kb)	leading	-0.244
	449(901.051 kb)	1189 (2580.08 kb)	lagging	-0.096
AT-skew reverse	1190 (0 kb)	1561 (886.6535 kb)	leading	0.074
	1562(888.172 kb)	2036(2043.6485 kb)	lagging	0.244
	2037(2044.312 kb)	2313(2580.08 kb)	NA	0.19

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

270 Ralstonia solanacearum

Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Ralstonia.
Accession number: NC_003295; **Genome size (bp)**: 3716413.
Number of genes: 3435.
Oriloc predictions: Origin 3 kb Terminus 2010 kb
Worning et al., 2006: Origin 340 kb Terminus 1967 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 0.025 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 2809.6 kb, 3715.49 kb
Consensus predictions: Origin 3 kb Terminus 2010 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1098	NA	2069
GC-skew reverse	2434	NA	1991
AT-skew forward	1078	NA	2020
AT-skew reverse	2429	NA	1944

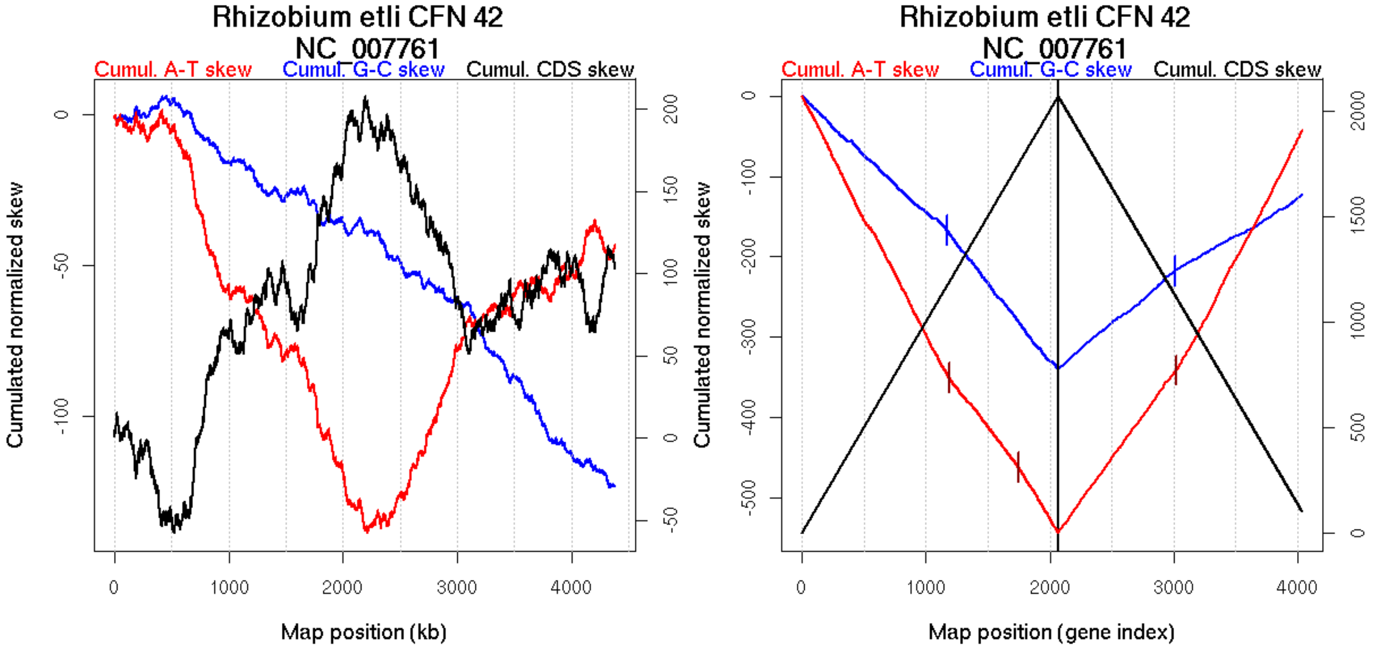
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1098 (2068.864 kb)	leading	-0.023
	1099(2069.8825 kb)	1691 (3716.276 kb)	lagging	-0.099
GC-skew reverse	1692 (0 kb)	2434 (1990.8585 kb)	leading	0.111
	2435(1991.6405 kb)	3435 (3716.276 kb)	lagging	0.027
AT-skew forward	1 (0 kb)	1078 (2020.4355 kb)	leading	-0.279
	1079(2026.753 kb)	1691 (3716.276 kb)	lagging	-0.019
AT-skew reverse	1692 (0 kb)	2429 (1943.7695 kb)	leading	-0.022
	2430(1951.5285 kb)	3435(3716.276 kb)	lagging	0.242

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

271 Rhizobium etli CFN 42

Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Rhizobium/Agroba group; Rhizobium.
Accession number: NC_007761; **Genome size (bp)**: 4381608.
Number of genes: 4035.
Oriloc predictions: Origin 511 kb Terminus 2257 kb
Worning et al., 2006: Origin 4180 kb Terminus 2204 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 2031.64 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 371.27 kb, 1562.45 kb
Consensus predictions: Origin NA Terminus NA



Significant breakpoints (p-value <0.05):

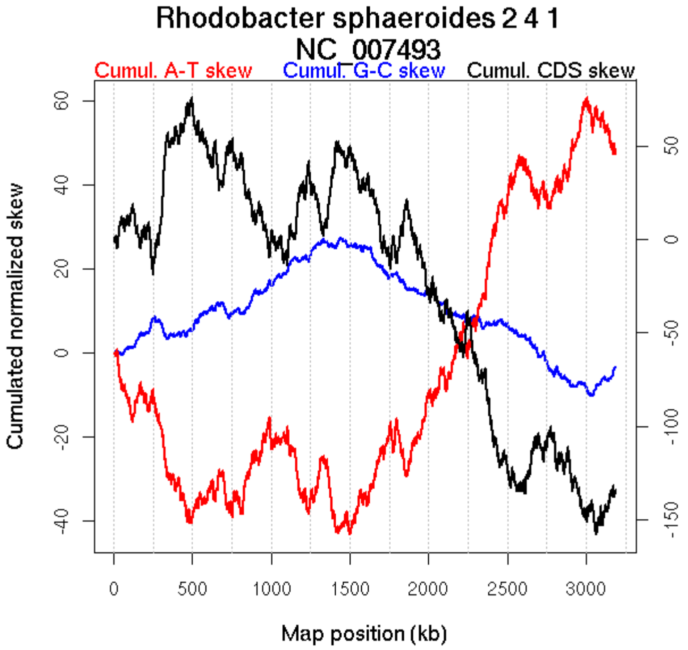
	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1174	0.00667	2324
GC-skew reverse	3008	0.00667	2226
AT-skew forward	1186	0.00667	2342
	1747	0.04333	3668
AT-skew reverse	3024	0	2257

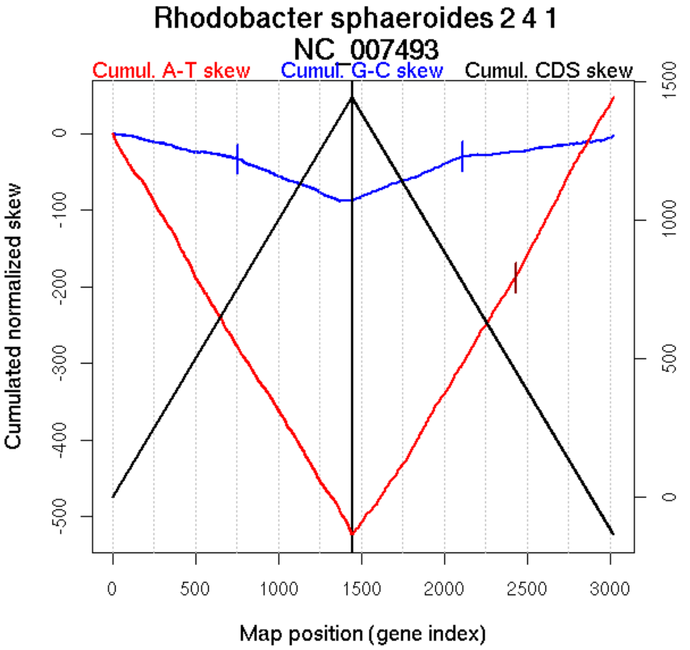
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1174 (2324.196 kb)	NA	-0.143
	1175(2324.8915 kb)	2069 (4381.608 kb)	NA	-0.195
GC-skew reverse	2070 (0 kb)	3008 (2225.8945 kb)	NA	0.126
	3009(2227.6095 kb)	4035 (4381.608 kb)	NA	0.089
AT-skew forward	1 (0 kb)	1186 (2342.205 kb)	NA	-0.296
	1187(2342.5785 kb)	1747 (3668.3385 kb)	NA	-0.197
	1748(3673.232 kb)	2069 (4381.608 kb)	NA	-0.255
AT-skew reverse	2070 (0 kb)	3024 (2257.4205 kb)	NA	0.213
	3025(2259.0875 kb)	4035(4381.608 kb)	NA	0.295

272 Rhodobacter sphaeroides 2 4 1

Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Rhodobacter.
Accession number: NC_007493; **Genome size (bp)**: 3188609.
Number of genes: 3022.
Oriloc predictions: Origin 3028 kb Terminus 1434 kb
Worning et al., 2006: Origin 3005 kb Terminus 1429 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 3004.996 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 3111.46 kb
Consensus predictions: Origin 3028 kb Terminus 1434 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	753	0.00667	1555
GC-skew reverse	2113	0	1446
AT-skew reverse	2431	0.04	2062

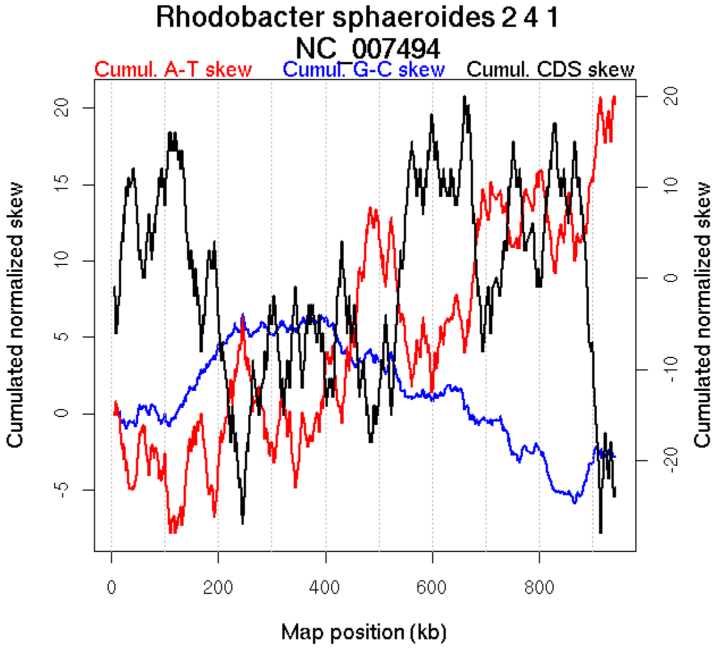
Segments:

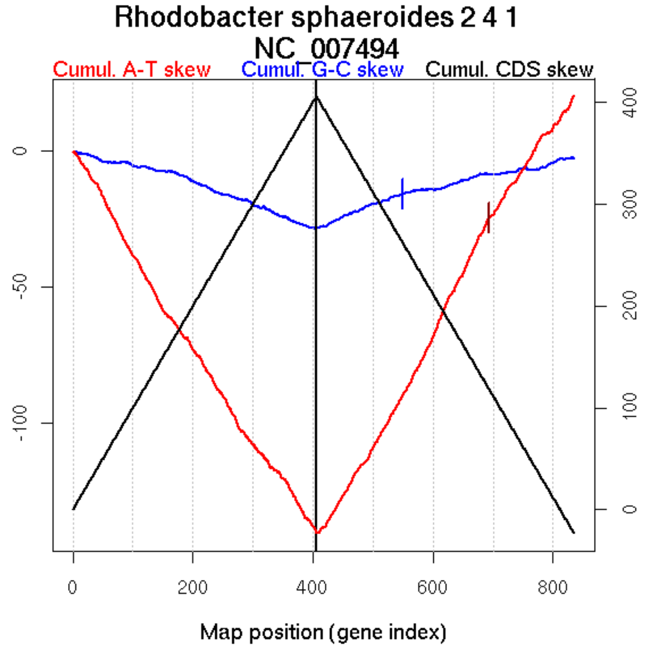
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	753 (1555.3225 kb)	leading	-0.045
	754(1567.0265 kb)	1444 (3188.117 kb)	lagging	-0.085
GC-skew reverse	1445 (0 kb)	2113 (1446.353 kb)	leading	0.084
	2114(1448.488 kb)	3022 (3188.117 kb)	lagging	0.027
AT-skew reverse	1445 (0 kb)	2431 (2061.721 kb)	NA	0.35
	2432(2063.162 kb)	3022(3188.117 kb)	lagging	0.4

More G than C on the leading strand for replication.

273 Rhodobacter sphaeroides 2 4 1

Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Rhodobacter.
Accession number: NC_007494; **Genome size (bp)**: 943016.
Number of genes: 835.
Oriloc predictions: Origin NA Terminus NA
Worning et al., 2006: Origin 867 kb Terminus 282 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 753.077 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 941.86 kb
Consensus predictions: Origin NA Terminus NA





Significant breakpoints (p-value <0.05):

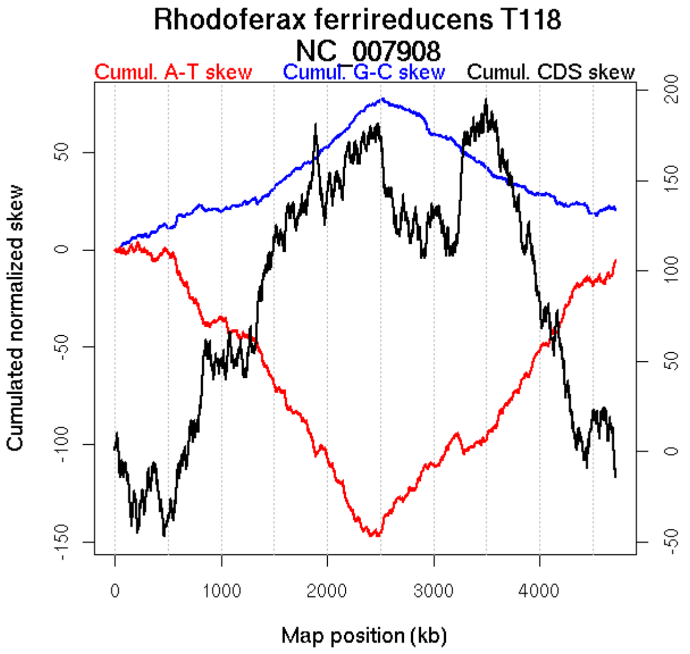
	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew reverse	549	0.04667	316
AT-skew reverse	694	0.02	674

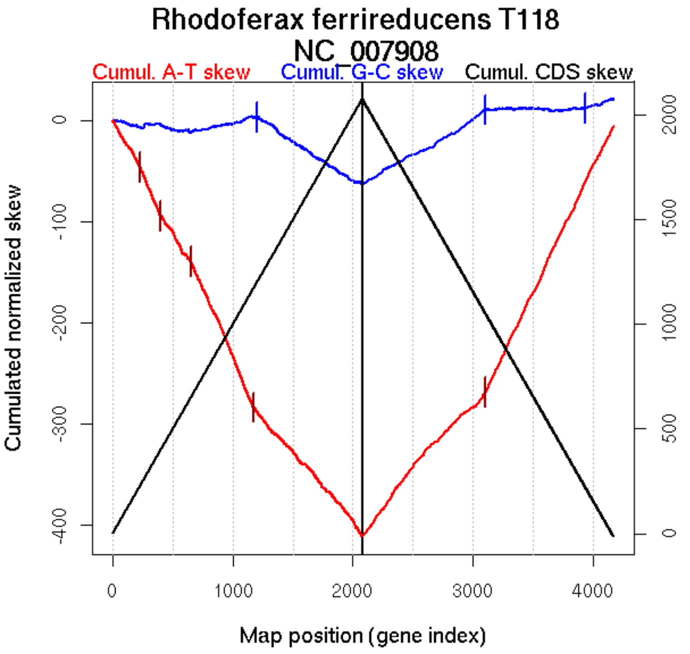
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew reverse	407 (0 kb)	549 (316.1965 kb)	NA	0.091
	550(317.158 kb)	835 (942.518 kb)	NA	0.046
AT-skew reverse	407 (0 kb)	694 (673.674 kb)	NA	0.413
	695(674.0555 kb)	835(942.518 kb)	NA	0.315

274 Rhodoferax ferrireducens T118

Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales; Comamonadaceae; Rhodoferax.
Accession number: NC_007908; **Genome size (bp)**: 4712337.
Number of genes: 4170.
Oriloc predictions: Origin 34 kb Terminus 2506 kb
Worning et al., 2006: Origin 280 kb Terminus 2506 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1876.056 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.71 kb, 2773.77 kb
Consensus predictions: Origin 34 kb Terminus 2506 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1206	0	2510
GC-skew reverse	3104	0.00333	2489
	3935	0.02333	4255
AT-skew forward	226	0.02167	517
	400	0.01667	818
	650	0.02333	1346
	1172	0.00167	2410
AT-skew reverse	3105	0	2492

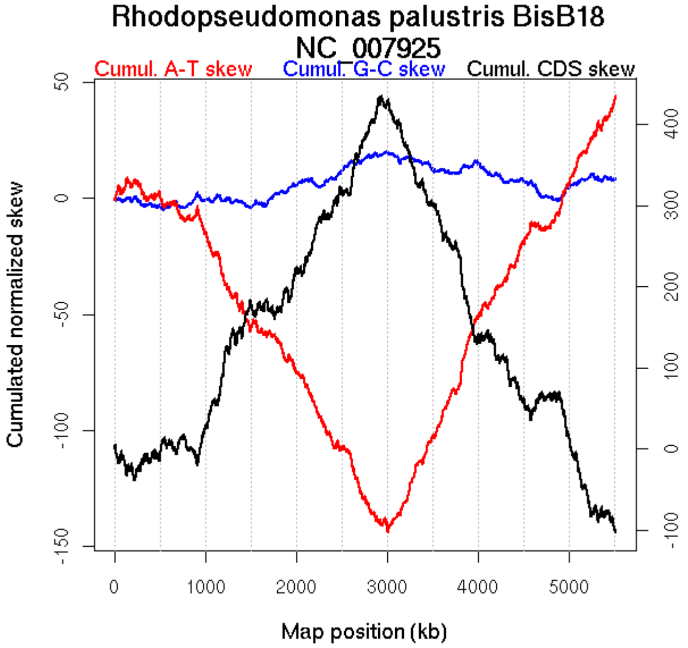
Segments:

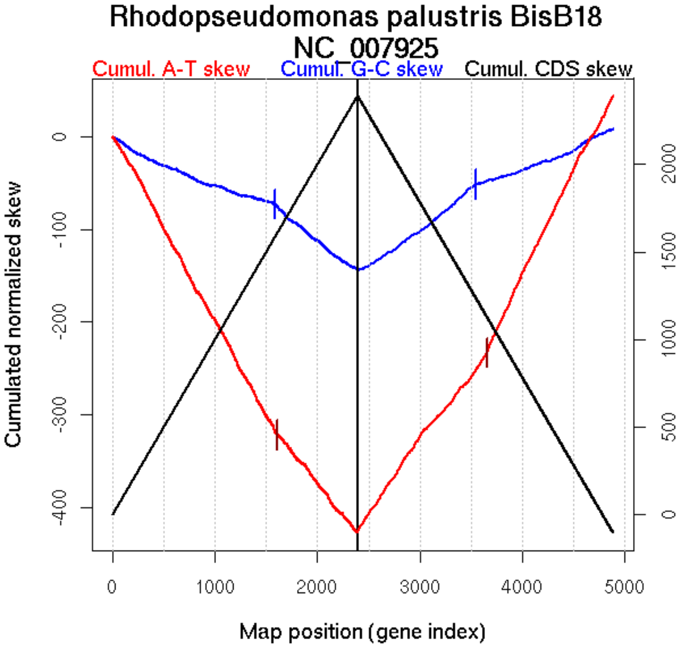
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1206 (2509.776 kb)	leading	0.002
	1207(2515.5245 kb)	2078 (4712.068 kb)	lagging	-0.078
GC-skew reverse	2079 (0 kb)	3104 (2489.429 kb)	leading	0.068
	3105(2491.515 kb)	3935 (4254.546 kb)	lagging	0
	3936(4256.9775 kb)	4170 (4712.068 kb)	lagging	0.04
AT-skew forward	1 (0 kb)	226 (517.3305 kb)	leading	-0.195
	227(517.91 kb)	400 (817.793 kb)	leading	-0.284
	401(819.6145 kb)	650 (1346.02 kb)	leading	-0.191
	651(1346.4515 kb)	1172 (2410.008 kb)	leading	-0.277
	1173(2416.271 kb)	2078 (4712.068 kb)	lagging	-0.134
AT-skew reverse	2079 (0 kb)	3105 (2491.515 kb)	leading	0.137
	3106(2492.338 kb)	4170(4712.068 kb)	lagging	0.248

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

275 Rhodopseudomonas palustris BisB18

Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae; Rhodopseudomonas.
Accession number: NC_007925; **Genome size (bp)**: 5513844.
Number of genes: 4886.
Oriloc predictions: Origin 0 kb Terminus 2943 kb
Worning et al., 2006: Origin 914 kb Terminus 2936 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 3033.628 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1.47 kb, 1929.94 kb, 2529.84 kb
Consensus predictions: Origin 0 kb Terminus 2943 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1582	0	3007
GC-skew reverse	3545	0.01333	3003
AT-skew forward	1608	0	3089
AT-skew reverse	3652	0.00667	3206

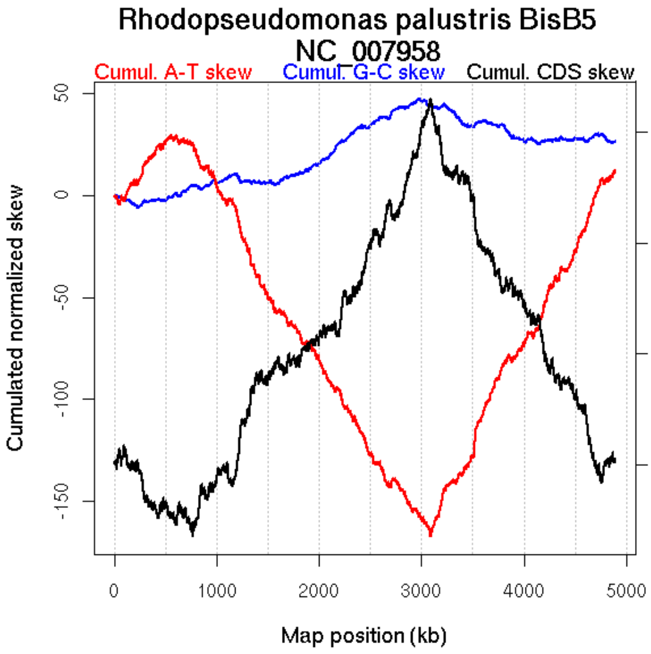
Segments:

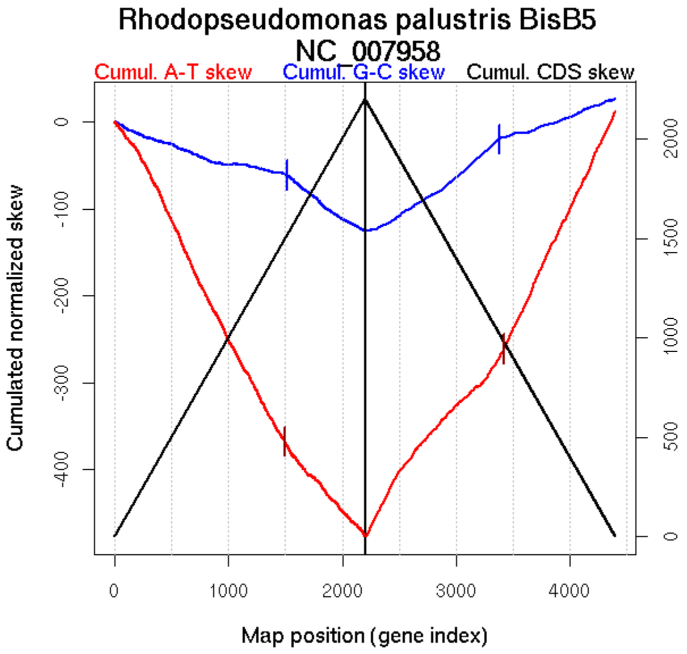
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1582 (3006.539 kb)	leading	-0.044
	1583(3007.502 kb)	2392 (5513.389 kb)	lagging	-0.088
GC-skew reverse	2393 (0 kb)	3545 (3003.399 kb)	leading	0.082
	3546(3006.95 kb)	4886 (5513.389 kb)	lagging	0.045
AT-skew forward	1 (0 kb)	1608 (3089.206 kb)	leading	-0.203
	1609(3093.2475 kb)	2392 (5513.389 kb)	lagging	-0.139
AT-skew reverse	2393 (0 kb)	3652 (3205.9805 kb)	leading	0.148
	3653(3206.553 kb)	4886(5513.389 kb)	lagging	0.223

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

276 Rhodopseudomonas palustris BisB5

Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae; Rhodopseudomonas.
Accession number: NC_007958; **Genome size (bp)**: 4892717.
Number of genes: 4397.
Oriloc predictions: Origin 234 kb Terminus 2963 kb
Worning et al., 2006: Origin 542 kb Terminus 3092 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 3747.063 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1.36 kb
Consensus predictions: Origin 234 kb Terminus 2963 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1514	NA	3047
GC-skew reverse	3376	NA	2962
AT-skew forward	1497	NA	3016
AT-skew reverse	3421	NA	3098

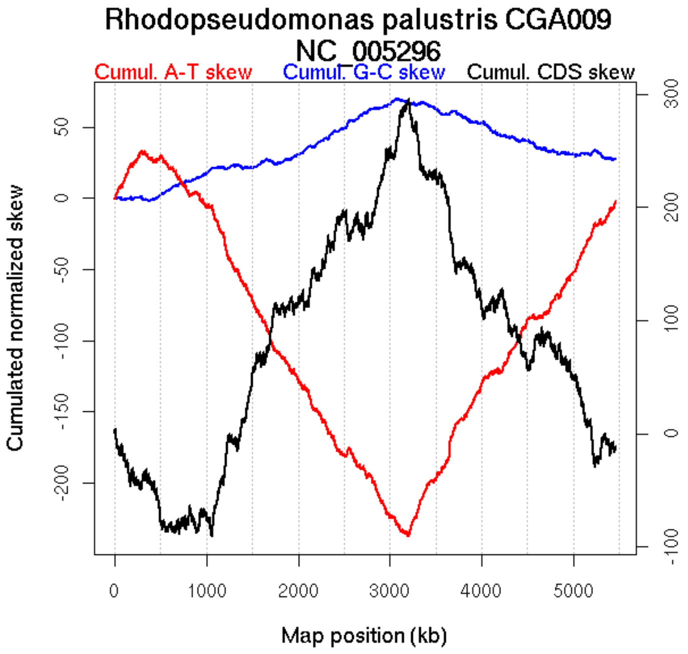
Segments:

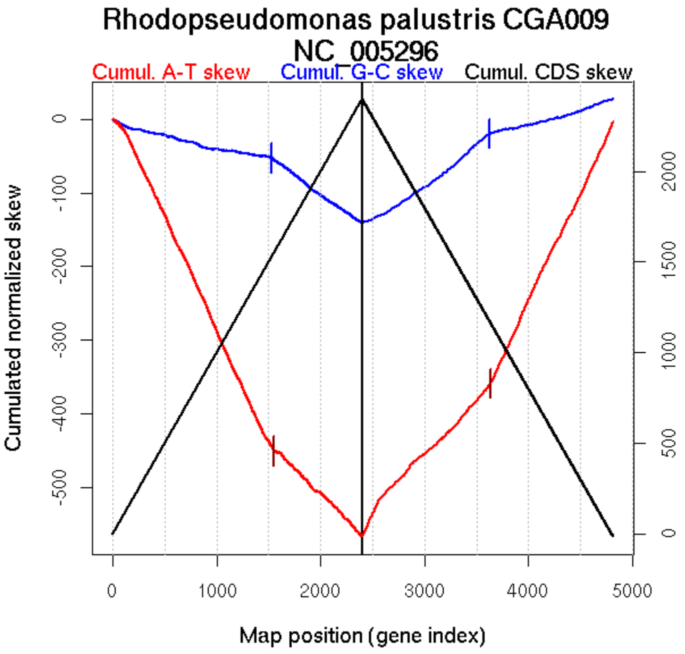
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1514 (3046.773 kb)	leading	-0.039
	1515(3048.847 kb)	2200 (4892.034 kb)	lagging	-0.096
GC-skew reverse	2201 (0 kb)	3376 (2961.934 kb)	leading	0.092
	3377(2967.832 kb)	4397 (4892.034 kb)	lagging	0.047
AT-skew forward	1 (0 kb)	1497 (3015.7655 kb)	leading	-0.259
	1498(3017.6825 kb)	2200 (4892.034 kb)	lagging	-0.146
AT-skew reverse	2201 (0 kb)	3421 (3098.4135 kb)	leading	0.162
	3422(3100.591 kb)	4397(4892.034 kb)	lagging	0.278

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

277 Rhodopseudomonas palustris CGA009

Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae; Rhodopseudomonas.
Accession number: NC_005296; **Genome size (bp)**: 5459213.
Number of genes: 4812.
Oriloc predictions: Origin 366 kb Terminus 3093 kb
Worning et al., 2006: Origin 519 kb Terminus 3169 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 3968.681 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1.39 kb
Consensus predictions: Origin 366 kb Terminus 3093 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1526	NA	3151
GC-skew reverse	3622	NA	3114
AT-skew forward	1555	NA	3208
AT-skew reverse	3631	NA	3136

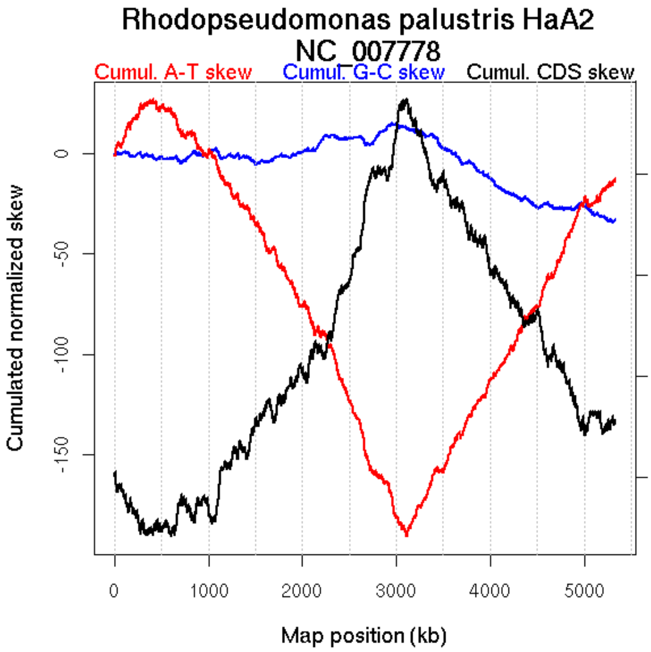
Segments:

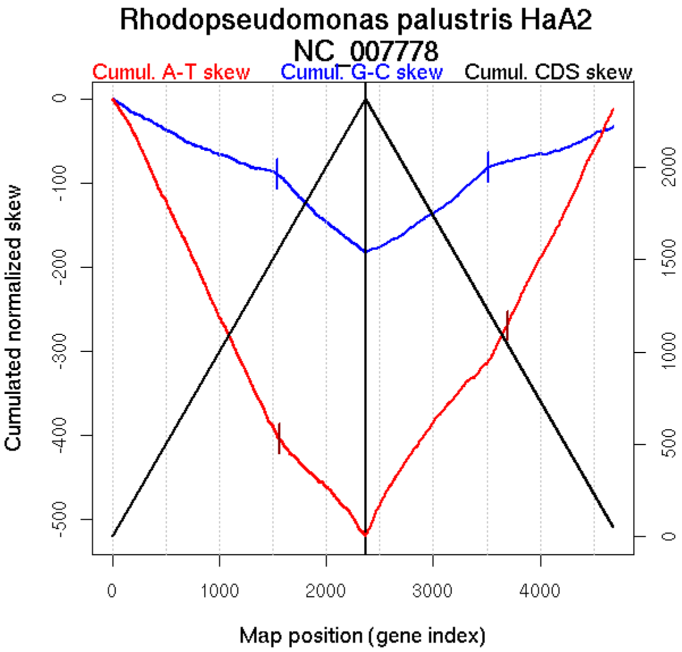
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1526 (3150.7445 kb)	leading	-0.032
	1527(3154.5955 kb)	2399 (5458.655 kb)	lagging	-0.103
GC-skew reverse	2400 (0 kb)	3622 (3113.5015 kb)	NA	0.101
	3623(3120.062 kb)	4812 (5458.655 kb)	lagging	0.039
AT-skew forward	1 (0 kb)	1555 (3208.134 kb)	leading	-0.306
	1556(3210.7595 kb)	2399 (5458.655 kb)	lagging	-0.138
AT-skew reverse	2400 (0 kb)	3631 (3135.7515 kb)	NA	0.15
	3632(3136.391 kb)	4812(5458.655 kb)	lagging	0.297

More T than A on the leading strand for replication - for forward encoded genes.
More G than C on the leading strand for replication - for forward encoded genes.

278 Rhodopseudomonas palustris HaA2

Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae; Rhodopseudomonas.
Accession number: NC_007778; **Genome size (bp)**: 5331656.
Number of genes: 4683.
Oriloc predictions: Origin 336 kb Terminus 3095 kb
Worning et al., 2006: Origin 411 kb Terminus 3113 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 2291.361 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1.38 kb
Consensus predictions: Origin 336 kb Terminus 3095 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1543	NA	3109
GC-skew reverse	3517	NA	3058
AT-skew forward	1560	NA	3165
AT-skew reverse	3694	NA	3373

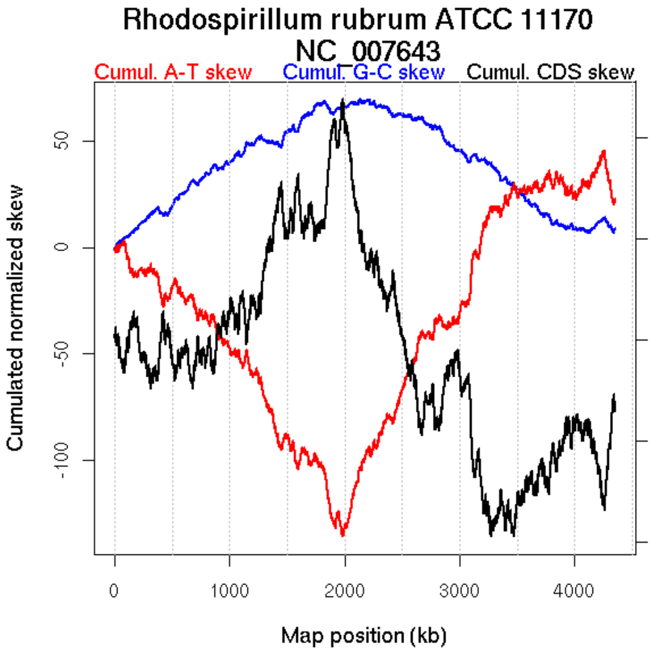
Segments:

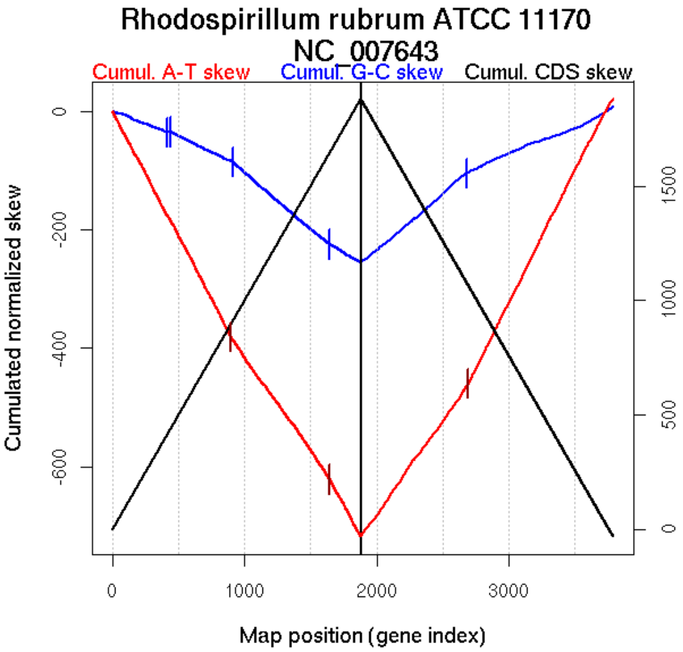
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1543 (3109.323 kb)	leading	-0.058
	1544(3110.981 kb)	2368 (5330.976 kb)	lagging	-0.113
GC-skew reverse	2369 (0 kb)	3517 (3057.9965 kb)	NA	0.089
	3518(3063.351 kb)	4683 (5330.976 kb)	lagging	0.039
AT-skew forward	1 (0 kb)	1560 (3165.2045 kb)	leading	-0.268
	1561(3167.5595 kb)	2368 (5330.976 kb)	lagging	-0.135
AT-skew reverse	2369 (0 kb)	3694 (3372.6935 kb)	NA	0.173
	3695(3374.151 kb)	4683(5330.976 kb)	lagging	0.256

More T than A on the leading strand for replication - for forward encoded genes.
More G than C on the leading strand for replication - for forward encoded genes.

279 Rhodospirillum rubrum ATCC 11170

Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales; Rhodospirillaceae; Rhodospirillum.
Accession number: NC_007643; **Genome size (bp)**: 4352825.
Number of genes: 3791.
Oriloc predictions: Origin 4134 kb Terminus 1823 kb
Worning et al., 2006: Origin 4155 kb Terminus 1986 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 4154.414 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.99 kb
Consensus predictions: Origin 4134 kb Terminus 1823 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	417	0.00333	984
	439	0	1042
	910	0.01	2014
	1644	0.04833	3866
GC-skew reverse	2679	0	2003
AT-skew forward	897	0.00667	1977
	1643	0.01	3865
AT-skew reverse	2695	0	2030

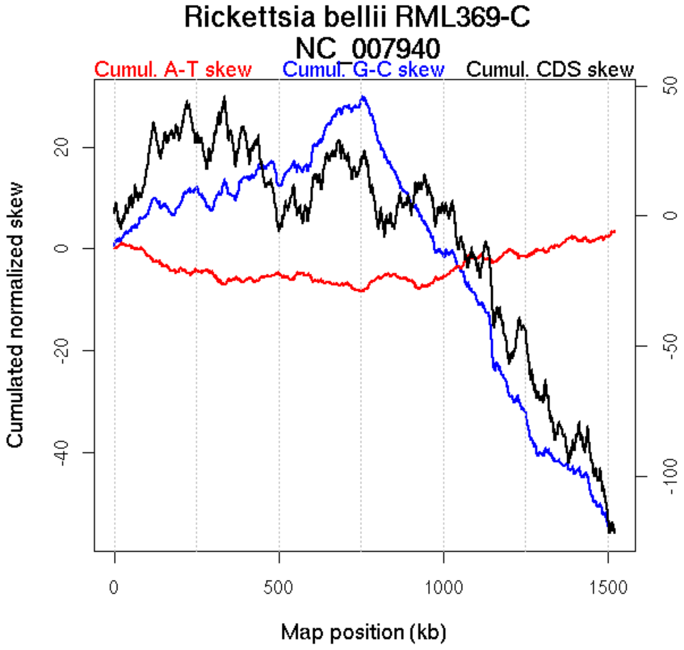
Segments:

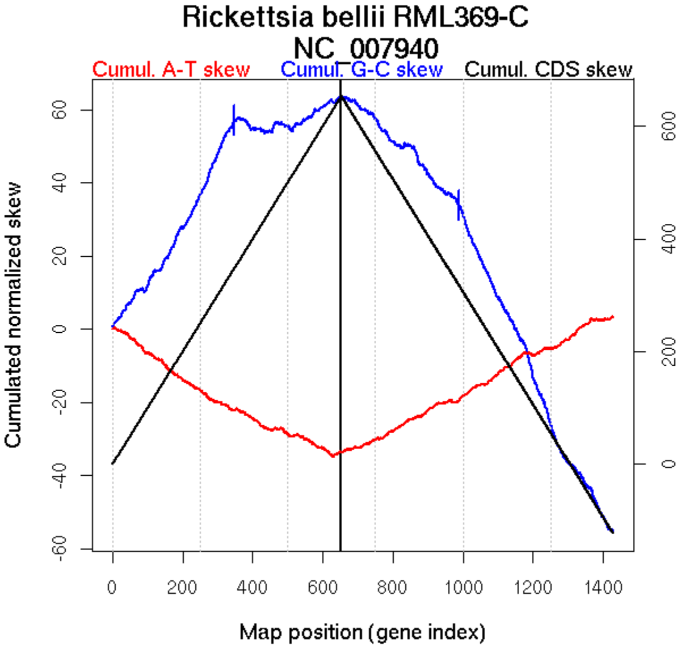
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	417 (984.363 kb)	leading	-0.087
	418(986.183 kb)	439 (1041.88 kb)	leading	0.034
	440(1049.738 kb)	910 (2014.297 kb)	NA	-0.109
	911(2014.8955 kb)	1644 (3865.7675 kb)	lagging	-0.19
	1645(3866.604 kb)	1880 (4352.278 kb)	NA	-0.136
GC-skew reverse	1881 (0 kb)	2679 (2003.18 kb)	leading	0.192
	2680(2004.5125 kb)	3791 (4352.278 kb)	lagging	0.093
AT-skew forward	1 (0 kb)	897 (1976.6665 kb)	leading	-0.422
	898(1978.284 kb)	1643 (3864.838 kb)	lagging	-0.315
	1644(3865.7675 kb)	1880 (4352.278 kb)	NA	-0.409
AT-skew reverse	1881 (0 kb)	2695 (2029.884 kb)	leading	0.316
	2696(2030.875 kb)	3791(4352.278 kb)	lagging	0.444

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

280 Rickettsia bellii RML369-C

Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales; Rickettsiaceae; Rickettsieae; Rickettsia.
Accession number: NC_007940; **Genome size (bp)**: 1522076.
Number of genes: 1428.
Oriloc predictions: Origin 0 kb Terminus 752 kb
Worning et al., 2006: Origin 1504 kb Terminus 762 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1521.93 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 598.19 kb, 933.5 kb, 1139.07 kb
Consensus predictions: Origin 0 kb Terminus 752 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	347	0	753
GC-skew reverse	987	0	770

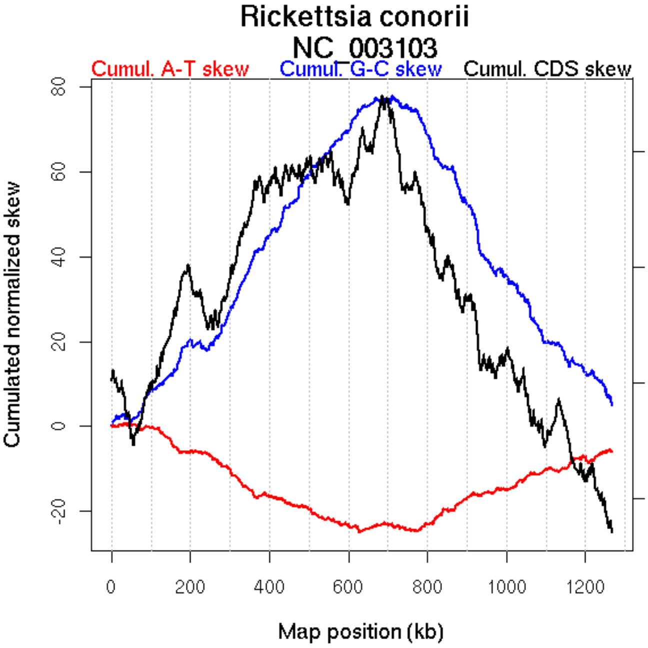
Segments:

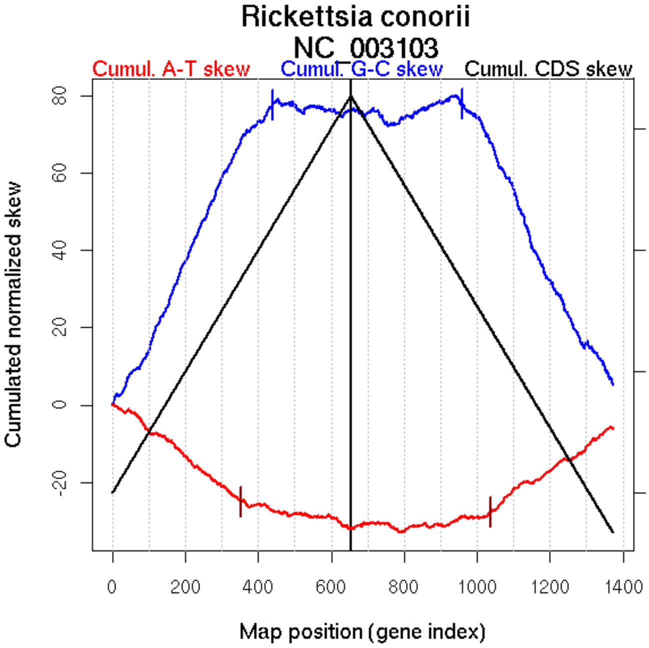
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	347 (752.9595 kb)	leading	0.162
	348(754.2005 kb)	653 (1521.685 kb)	lagging	0.023
GC-skew reverse	654 (0 kb)	987 (769.7505 kb)	leading	-0.092
	988(771.5635 kb)	1428 (1521.685 kb)	lagging	-0.209

More G than C on the leading strand for replication.

281 Rickettsia conorii

Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales; Rickettsiaceae; Rickettsieae; Rickettsia; spotted fever group.
Accession number: NC_003103; **Genome size (bp)**: 1268755.
Number of genes: 1373.
Oriloc predictions: Origin 0 kb Terminus 630 kb
Worning et al., 2006: Origin 1259 kb Terminus 682 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1268.609 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 863.61 kb
Consensus predictions: Origin 0 kb Terminus 630 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	440	NA	752
GC-skew reverse	960	NA	704
AT-skew forward	354	NA	607
AT-skew reverse	1038	NA	794

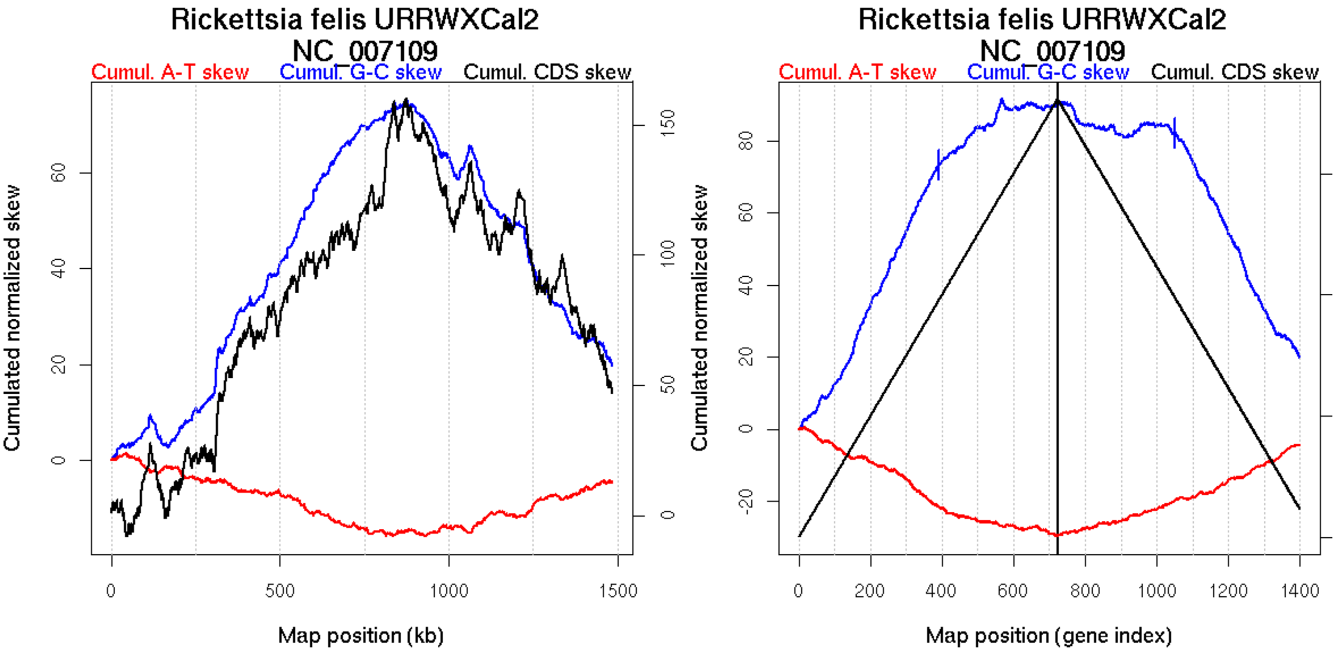
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	440 (751.84 kb)	leading	0.193
	441(755.1895 kb)	654 (1268.36 kb)	lagging	-0.013
GC-skew reverse	655 (0 kb)	960 (704.1815 kb)	leading	0.015
	961(705.0905 kb)	1373 (1268.36 kb)	lagging	-0.19
AT-skew forward	1 (0 kb)	354 (607.4135 kb)	leading	-0.074
	355(609.4305 kb)	654 (1268.36 kb)	lagging	-0.019
AT-skew reverse	655 (0 kb)	1038 (793.5185 kb)	NA	0.007
	1039(793.9295 kb)	1373(1268.36 kb)	lagging	0.062

More T than A on the leading strand for replication - for forward encoded genes.
More G than C on the leading strand for replication.

282 Rickettsia felis URRWXCal2

Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales; Rickettsiaceae; Rickettsieae; Rickettsia; spotted fever group.
Accession number: NC_007109; **Genome size (bp)**: 1485148.
Number of genes: 1399.
Oriloc predictions: Origin 40 kb Terminus 905 kb
Worning et al., 2006: Origin 168 kb Terminus 871 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1485.001 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 383.38 kb
Consensus predictions: Origin 40 kb Terminus 905 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	391	NA	725
GC-skew reverse	1052	NA	859

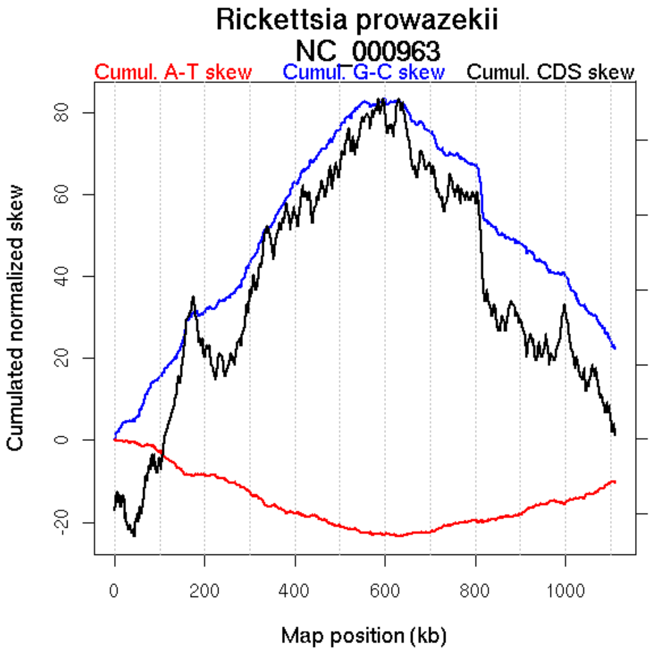
Segments:

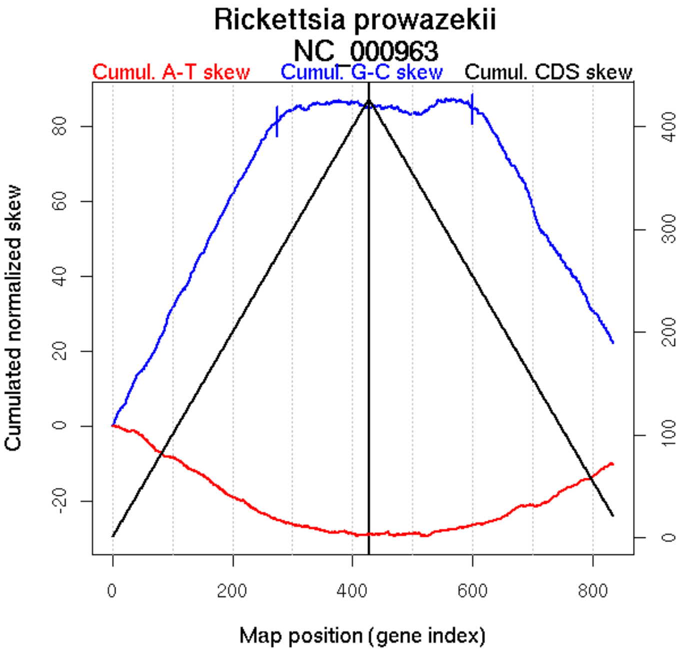
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	391 (725.2485 kb)	leading	0.199
	392(726.584 kb)	723 (1484.752 kb)	NA	0.051
GC-skew reverse	724 (0 kb)	1052 (858.626 kb)	leading	-0.016
	1053(863.944 kb)	1399 (1484.752 kb)	lagging	-0.192

More G than C on the leading strand for replication - for reverse encoded genes.

283 Rickettsia prowazekii

Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales; Rickettsiaceae; Rickettsieae; Rickettsia; typhus group.
Accession number: NC_000963; **Genome size (bp)**: 1111523.
Number of genes: 833.
Oriloc predictions: Origin 0 kb Terminus 627 kb
Worning et al., 2006: Origin 1105 kb Terminus 581 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1111.377 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 757.56 kb
Consensus predictions: Origin 0 kb Terminus 627 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	275	NA	572
GC-skew reverse	600	NA	587

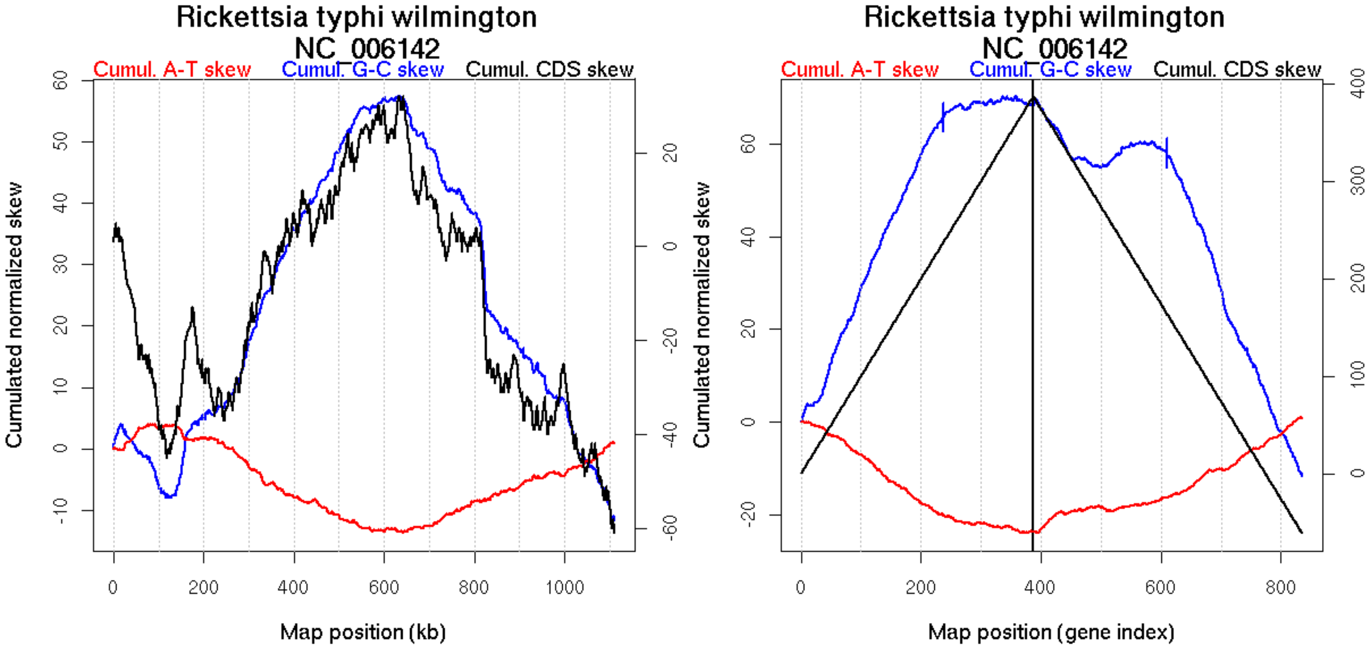
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	275 (572.383 kb)	leading	0.306
	276(573.8875 kb)	427 (1111.139 kb)	lagging	0.018
GC-skew reverse	428 (0 kb)	600 (587.19 kb)	leading	0.013
	601(588.3675 kb)	833 (1111.139 kb)	lagging	-0.284

More G than C on the leading strand for replication.

284 Rickettsia typhi wilmington

Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales; Rickettsiaceae; Rickettsieae; Rickettsia; typhus group.
Accession number: NC_006142; **Genome size (bp)**: 1111496.
Number of genes: 835.
Oriloc predictions: Origin 122 kb Terminus 634 kb
Worning et al., 2006: Origin 124 kb Terminus 599 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1111.35 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 763.36 kb
Consensus predictions: Origin 122 kb Terminus 634 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	237	NA	595
GC-skew reverse	610	NA	636

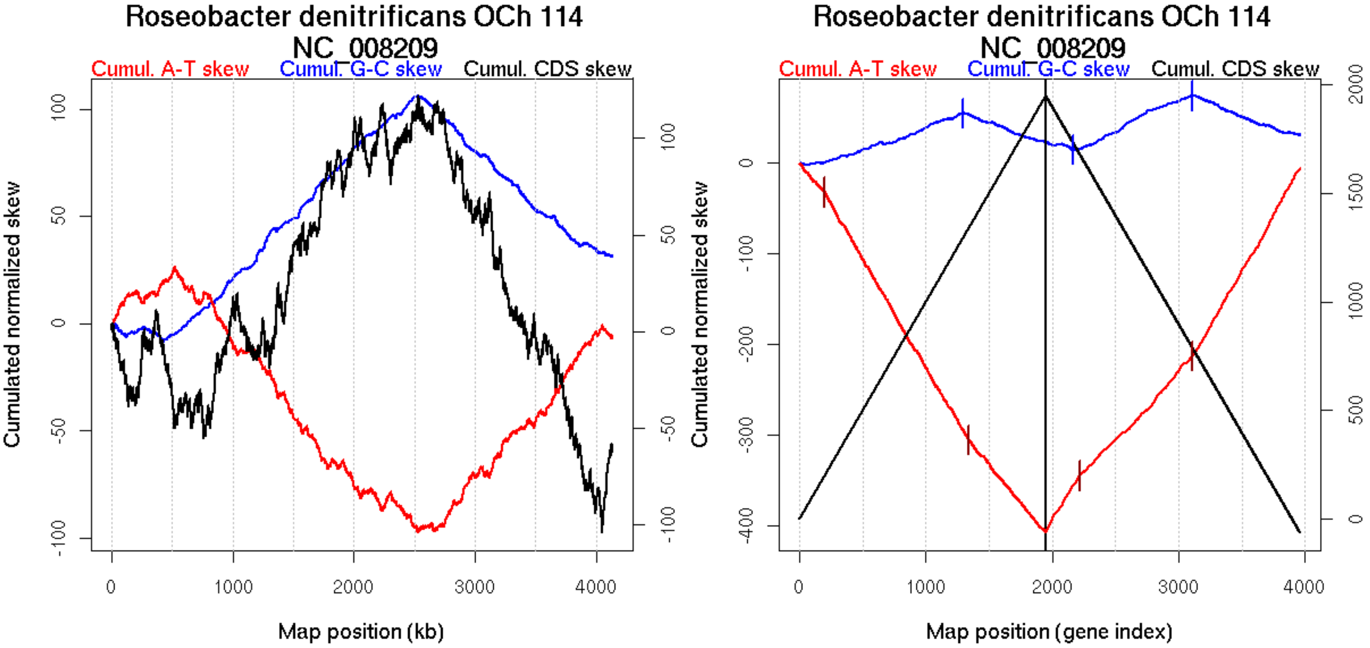
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	237 (594.724 kb)	leading	0.294
	238(596.3275 kb)	387 (1111.113 kb)	lagging	0.015
GC-skew reverse	388 (0 kb)	610 (635.5125 kb)	NA	-0.027
	611(637.971 kb)	835 (1111.113 kb)	lagging	-0.32

More G than C on the leading strand for replication - for forward encoded genes.

285 Roseobacter denitrificans OCh 114

Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Roseobacter.
Accession number: NC_008209; **Genome size (bp)**: 4133097.
Number of genes: 3960.
Oriloc predictions: Origin 426 kb Terminus 2532 kb
Worning et al., 2006: Origin NA kb Terminus NA kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 3042.122 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 205.64 kb
Consensus predictions: Origin 426 kb Terminus 2532 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1292	0	2529
GC-skew reverse	2168	0	443
	3110	0	2498
AT-skew forward	202	0	429
	1342	0.01	2653
AT-skew reverse	2217	0.04	515
	3108	0.00667	2494

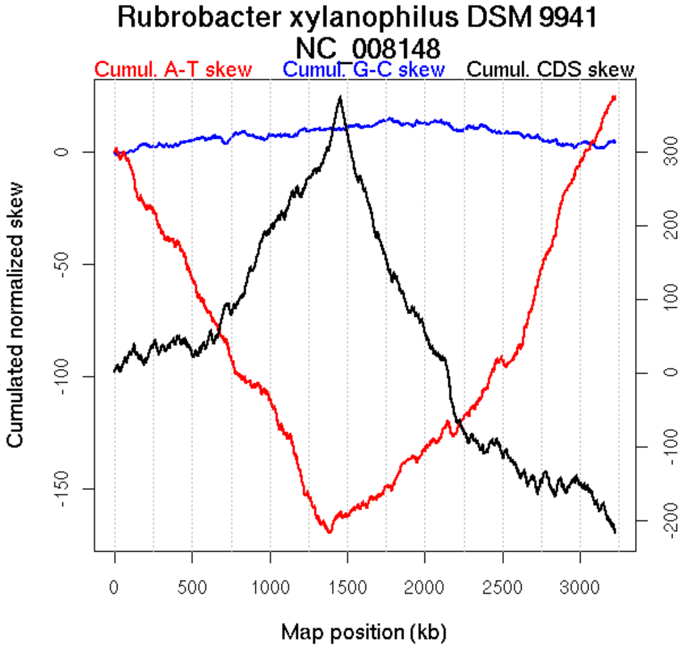
Segments:

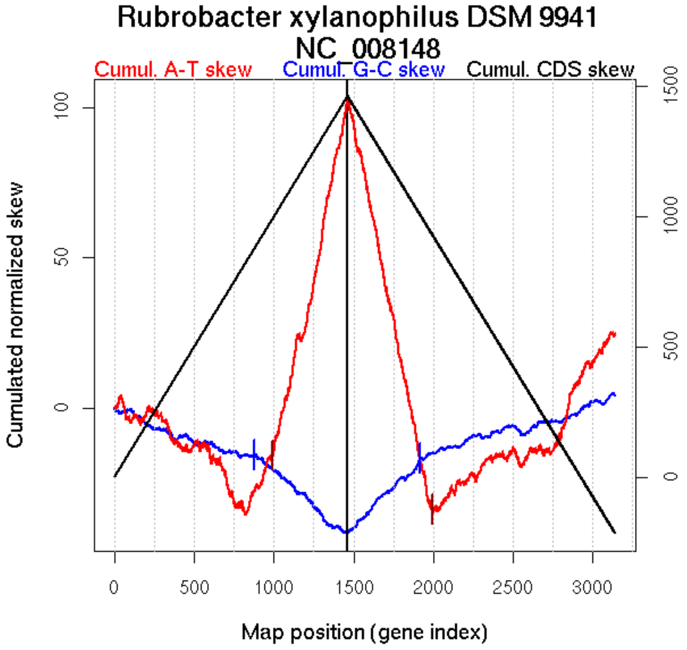
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1292 (2529.004 kb)	NA	0.046
	1293(2530.6275 kb)	1949 (4132.819 kb)	lagging	-0.052
GC-skew reverse	1950 (0 kb)	2168 (442.623 kb)	lagging	-0.027
	2169(444.6 kb)	3110 (2497.807 kb)	leading	0.07
	3111(2499.7815 kb)	3960 (4132.819 kb)	lagging	-0.055
AT-skew forward	1 (0 kb)	202 (429.459 kb)	lagging	-0.157
	203(430.718 kb)	1342 (2652.509 kb)	leading	-0.239
	1343(2652.612 kb)	1949 (4132.819 kb)	lagging	-0.168
AT-skew reverse	1950 (0 kb)	2217 (514.6925 kb)	NA	0.228
	2218(516.029 kb)	3108(2494.388 kb)	leading	0.147
	3109(2495.665 kb)	3960(4132.819 kb)	lagging	0.246

More T than A on the leading strand for replication.
More G than C on the leading strand for replication - for reverse encoded genes.

286 Rubrobacter xylanophilus DSM 9941

Bacteria; Actinobacteria; Rubrobacteridae; Rubrobacterales; Rubrobacterineae; Rubrobacteraceae; Rubrobacter.
Accession number: NC_008148; **Genome size (bp)**: 3225748.
Number of genes: 3140.
Oriloc predictions: Origin 59 kb Terminus 1538 kb
Worning et al., 2006: Origin 43 kb Terminus 1455 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1.624 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.68 kb
Consensus predictions: Origin 59 kb Terminus 1538 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	879	0.01333	1438
GC-skew reverse	1918	0.01333	1195
AT-skew forward	993	0	1973
AT-skew reverse	1992	0	1465

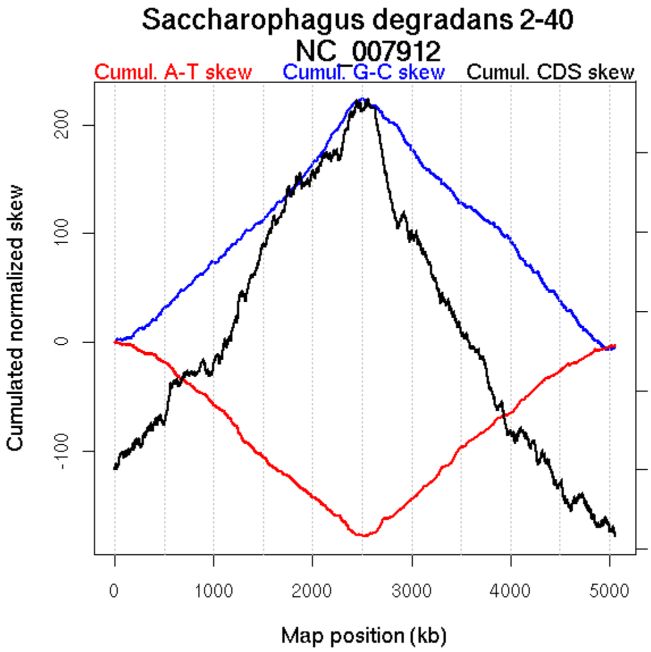
Segments:

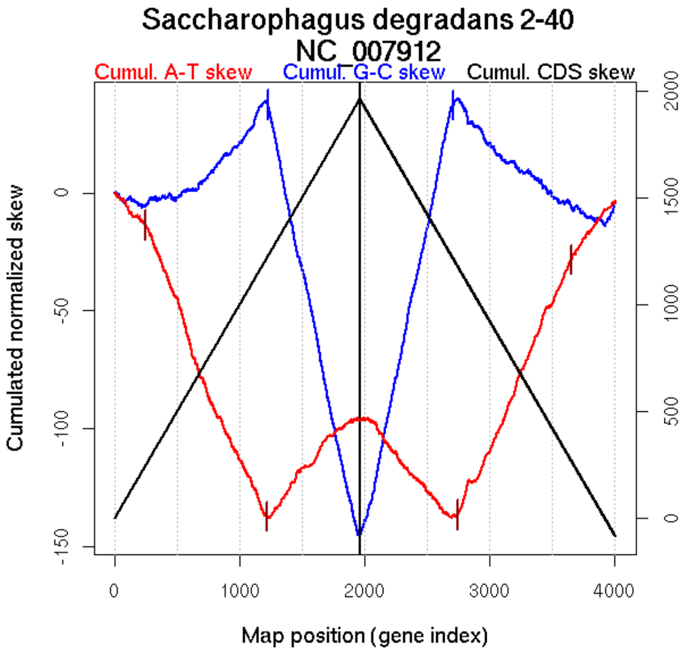
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	879 (1437.7175 kb)	leading	-0.019
	880(1438.046 kb)	1462 (3225.74 kb)	lagging	-0.048
GC-skew reverse	1463 (0 kb)	1918 (1195.302 kb)	leading	0.051
	1919(1198.7525 kb)	3140 (3225.74 kb)	lagging	0.015
AT-skew forward	1 (0 kb)	993 (1972.914 kb)	leading	-0.034
	994(1973.708 kb)	1462 (3225.74 kb)	lagging	0.251
AT-skew reverse	1463 (0 kb)	1992 (1465.4695 kb)	leading	-0.266
	1993(1466.175 kb)	3140(3225.74 kb)	lagging	0.046

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

287 Saccharophagus degradans 2-40

Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales; Alteromonadaceae; Saccharophagus.
Accession number: NC_007912; **Genome size (bp)**: 5057531.
Number of genes: 4008.
Oriloc predictions: Origin 5 kb Terminus 2507 kb
Worning et al., 2006: Origin 5019 kb Terminus 2456 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 4045.075 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 5018.86 kb
Consensus predictions: Origin 5 kb Terminus 2507 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1225	0	2518
GC-skew reverse	2706	0	2460
AT-skew forward	244	0.01333	521
	1216	0	2490
AT-skew reverse	2746	0	2566
	3653	0.04667	4346

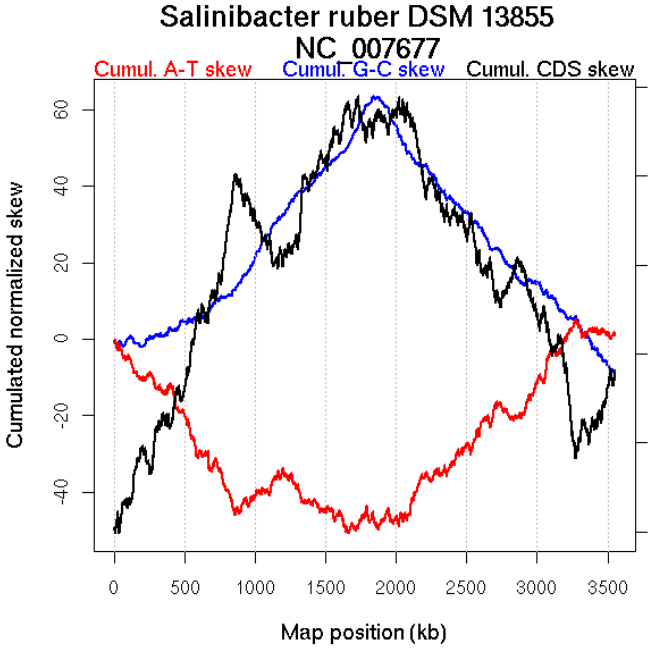
Segments:

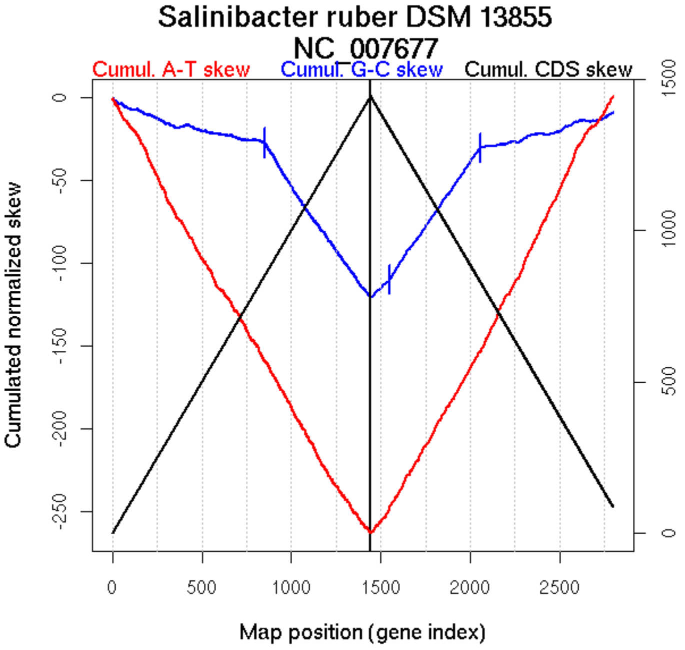
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1225 (2517.9665 kb)	leading	0.033
	1226(2519.29 kb)	1962 (5057.2 kb)	lagging	-0.255
GC-skew reverse	1963 (0 kb)	2706 (2459.675 kb)	leading	0.257
	2707(2460.6975 kb)	4008 (5057.2 kb)	lagging	-0.04
AT-skew forward	1 (0 kb)	244 (520.5385 kb)	leading	-0.056
	245(521.029 kb)	1216 (2489.525 kb)	leading	-0.131
	1217(2495.997 kb)	1962 (5057.2 kb)	lagging	0.062
AT-skew reverse	1963 (0 kb)	2746 (2566.09 kb)	leading	-0.061
	2747(2567.2485 kb)	3653(4345.6065 kb)	lagging	0.122
	3654(4346.057 kb)	4008(5057.2 kb)	lagging	0.07

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

288 Salinibacter ruber DSM 13855

Bacteria; Bacteroidetes; Sphingobacteria; Sphingobacteriales; Sphingobacteriales genera incertae sedis; Salinibacter.
Accession number: NC_007677; **Genome size (bp)**: 3551823.
Number of genes: 2800.
Oriloc predictions: Origin 0 kb Terminus 1834 kb
Worning et al., 2006: Origin 38 kb Terminus 1867 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 12.688 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.79 kb, 1718.88 kb
Consensus predictions: Origin 0 kb Terminus 1834 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	850	0	1869
GC-skew reverse	1550	0.02	383
	2057	0	1864

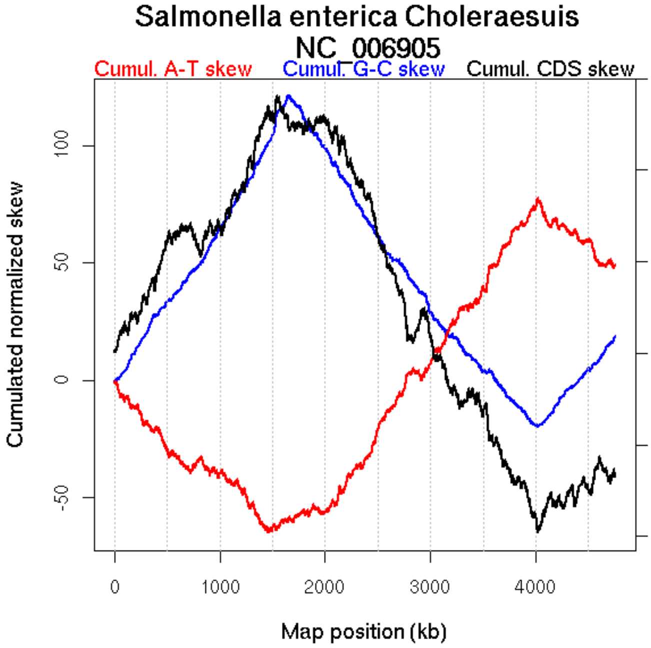
Segments:

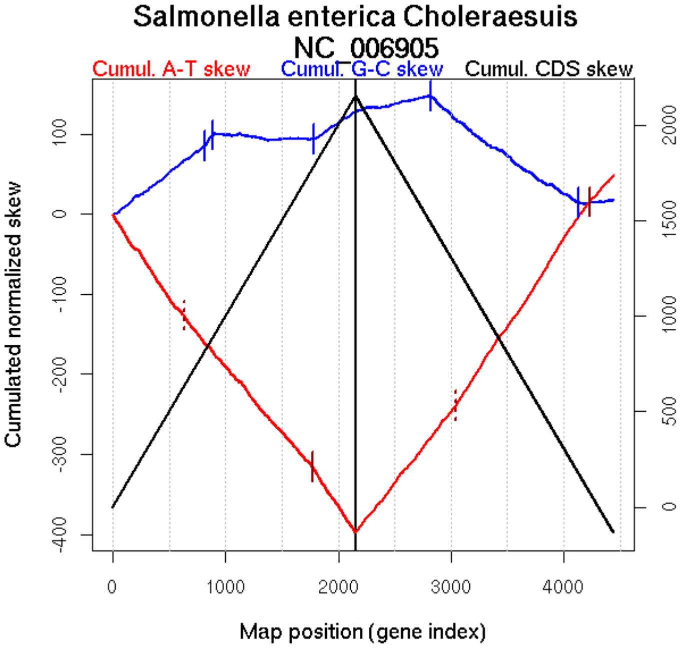
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	850 (1869.0535 kb)	leading	-0.029
	851(1872.309 kb)	1444 (3551.351 kb)	lagging	-0.157
GC-skew reverse	1445 (0 kb)	1550 (383.241 kb)	leading	0.1
	1551(386.381 kb)	2057 (1863.6105 kb)	leading	0.156
	2058(1867.5445 kb)	2800 (3551.351 kb)	lagging	0.028

More G than C on the leading strand for replication.

289 Salmonella enterica Choleraesuis

SC-B67 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Salmonella.
Accession number: NC_006905; **Genome size (bp)**: 4755700.
Number of genes: 4441.
Oriloc predictions: Origin 4017 kb Terminus 1645 kb
Worning et al., 2006: Origin 4019 kb Terminus 1647 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 4531.682 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): NA
Consensus predictions: Origin 4017 kb Terminus 1645 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	819	0.00444	1478
	888	0	1619
	1788	0.00444	3985
GC-skew reverse	2816	0	1663
	4128	0	4004
AT-skew forward	630	0.06667	1202
	1774	0.04667	3927
AT-skew reverse	3046	0.06	2119
	4227	0.01	4239

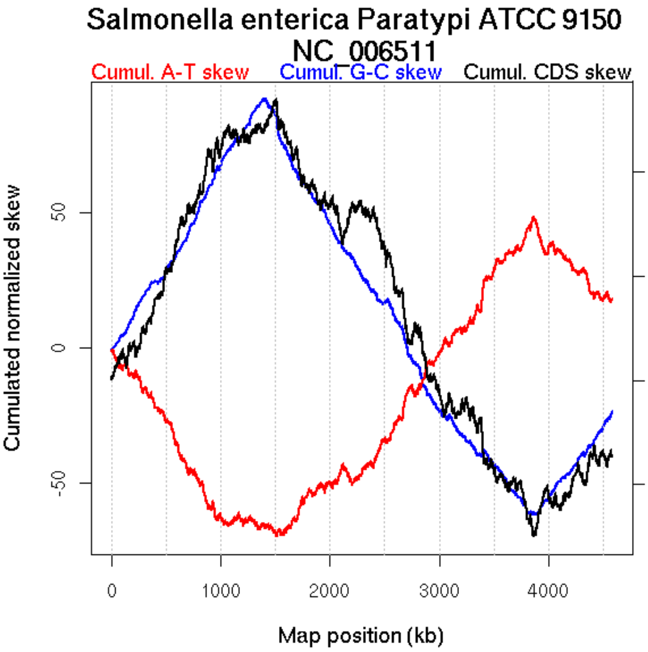
Segments:

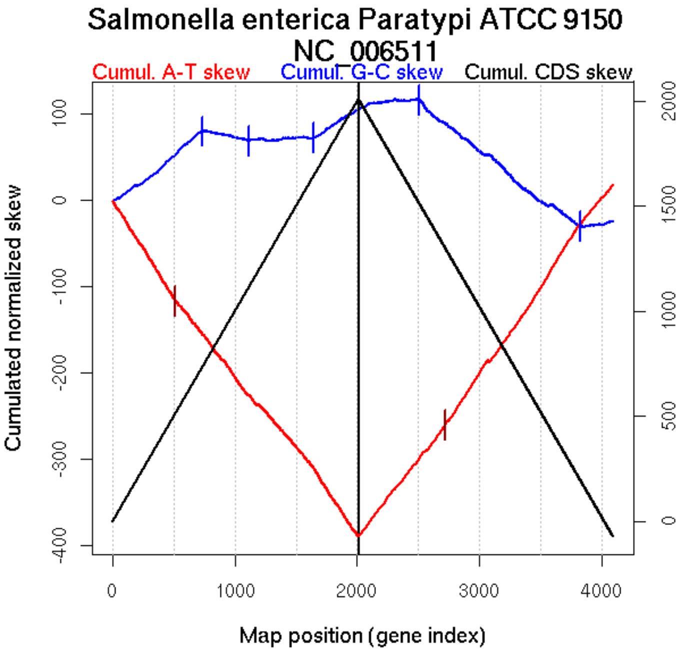
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	819 (1478.3285 kb)	leading	0.108
	820(1486.979 kb)	888 (1619.373 kb)	leading	0.21
	889(1620.3445 kb)	1788 (3985.349 kb)	lagging	-0.009
	1789(3987.1325 kb)	2154 (4755.673 kb)	leading	0.095
GC-skew reverse	2155 (0 kb)	2816 (1663.485 kb)	leading	0.028
	2817(1667.743 kb)	4128 (4003.5985 kb)	lagging	-0.1
	4129(4005.7885 kb)	4441 (4755.673 kb)	leading	0.013
AT-skew forward	1 (0 kb)	630 (1202.1115 kb)	leading	-0.203
	631(1204.9115 kb)	1774 (3926.6775 kb)	NA	-0.164
	1775(3936.686 kb)	2154 (4755.673 kb)	leading	-0.213
AT-skew reverse	2155 (0 kb)	3046 (2119.09 kb)	NA	0.179
	3047(2119.9635 kb)	4227(4238.741 kb)	lagging	0.216
	4228(4241.724 kb)	4441(4755.673 kb)	leading	0.155

More G than C on the leading strand for replication.

290 Salmonella enterica Paratypi ATCC 9150

9150 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Salmonella.
Accession number: NC_006511; **Genome size (bp)**: 4585229.
Number of genes: 4092.
Oriloc predictions: Origin 3857 kb Terminus 1409 kb
Worning et al., 2006: Origin 3859 kb Terminus 1363 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 3859.119 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 437.14 kb, 3826.28 kb
Consensus predictions: Origin 3857 kb Terminus 1409 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	730	NA	1394
	1113	NA	2308
	1644	NA	3793
GC-skew reverse	2510	NA	1424
	3826	NA	3893
AT-skew forward	512	NA	949
AT-skew reverse	2716	NA	1774

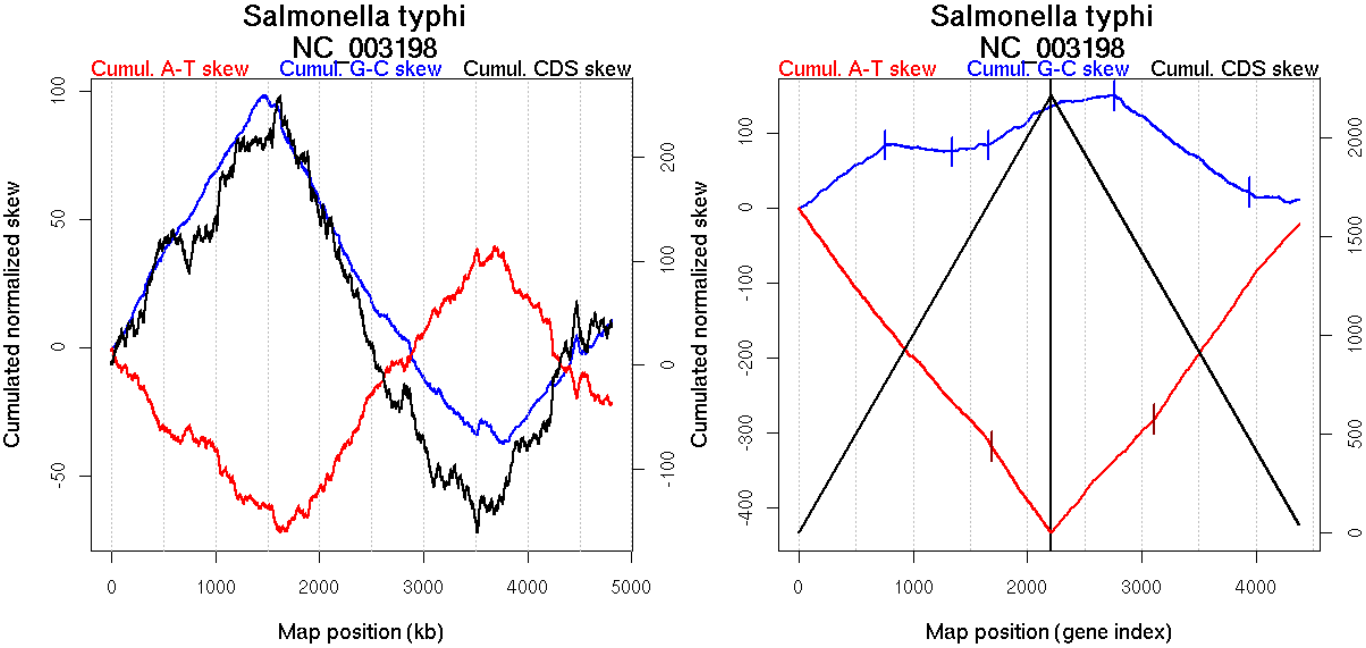
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	730 (1394.284 kb)	leading	0.115
	731(1399.1945 kb)	1113 (2308.3445 kb)	lagging	-0.03
	1114(2310.4335 kb)	1644 (3792.6025 kb)	lagging	0.006
	1645(3796.363 kb)	2010 (4585.202 kb)	leading	0.094
GC-skew reverse	2011 (0 kb)	2510 (1423.845 kb)	leading	0.017
	2511(1425.917 kb)	3826 (3893.4235 kb)	lagging	-0.11
	3827(3897.7285 kb)	4092 (4585.202 kb)	leading	0.022
AT-skew forward	1 (0 kb)	512 (948.5575 kb)	leading	-0.225
	513(949.551 kb)	2010 (4585.202 kb)	NA	-0.178
AT-skew reverse	2011 (0 kb)	2716 (1774.1325 kb)	NA	0.179
	2717(1775.486 kb)	4092(4585.202 kb)	NA	0.208

More G than C on the leading strand for replication.

291 Salmonella typhi

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Salmonella.
Accession number: NC_003198; **Genome size (bp)**: 4809037.
Number of genes: 4381.
Oriloc predictions: Origin 3764 kb Terminus 1486 kb
Worning et al., 2006: Origin 3761 kb Terminus 1488 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 3765.123 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 2573.94 kb, 3805.83 kb
Consensus predictions: Origin 3764 kb Terminus 1486 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	760	NA	1452
	1346	NA	2993
	1658	NA	3765
GC-skew reverse	2767	NA	1470
	3947	NA	3644
AT-skew forward	1685	NA	3808
AT-skew reverse	3112	NA	2050

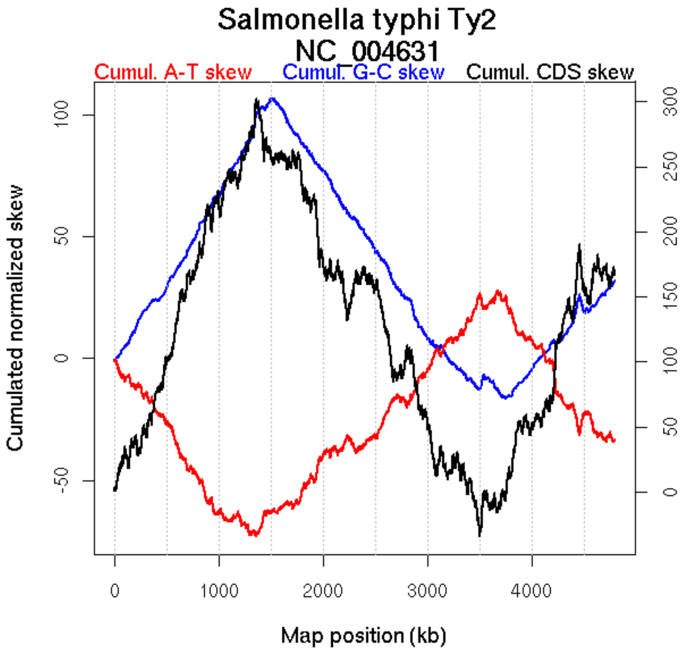
Segments:

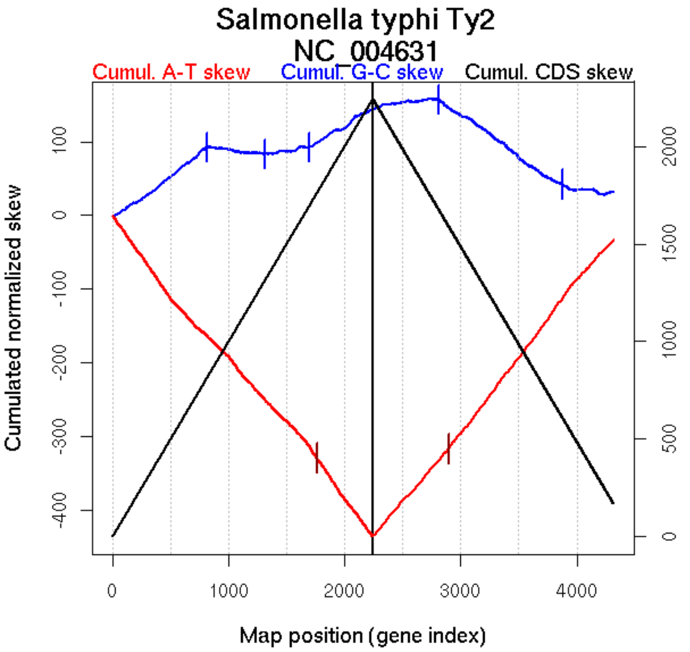
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	760 (1451.615 kb)	leading	0.112
	761(1456.216 kb)	1346 (2993.277 kb)	lagging	-0.018
	1347(2996.3525 kb)	1658 (3765.245 kb)	lagging	0.031
	1659(3767.375 kb)	2210 (4809.01 kb)	leading	0.097
GC-skew reverse	2211 (0 kb)	2767 (1470.295 kb)	leading	0.023
	2768(1474.614 kb)	3947 (3643.8785 kb)	lagging	-0.112
	3948(3650.833 kb)	4381 (4809.01 kb)	leading	-0.02
AT-skew forward	1 (0 kb)	1685 (3807.7295 kb)	NA	-0.184
	1686(3808.916 kb)	2210 (4809.01 kb)	leading	-0.221
AT-skew reverse	2211 (0 kb)	3112 (2050.242 kb)	NA	0.167
	3113(2051.4805 kb)	4381(4809.01 kb)	NA	0.209

More G than C on the leading strand for replication.

292 Salmonella typhi Ty2

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Salmonella.
Accession number: NC_004631; **Genome size (bp)**: 4791961.
Number of genes: 4317.
Oriloc predictions: Origin 3750 kb Terminus 1493 kb
Worning et al., 2006: Origin 3751 kb Terminus 1517 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 3750.614 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 430.91 kb, 3791.32 kb
Consensus predictions: Origin 3750 kb Terminus 1493 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	811	NA	1503
	1309	NA	2786
	1694	NA	3753
GC-skew reverse	2808	NA	1531
	3877	NA	3594
AT-skew forward	1758	NA	3849
AT-skew reverse	2897	NA	1731

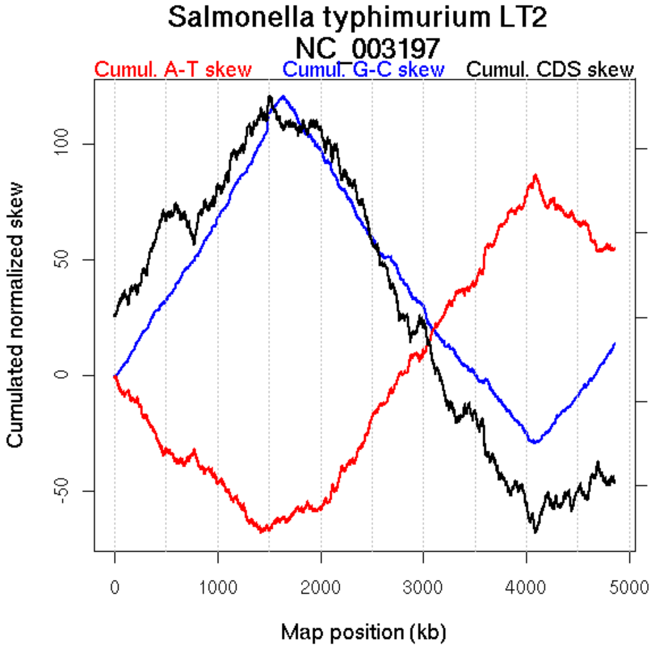
Segments:

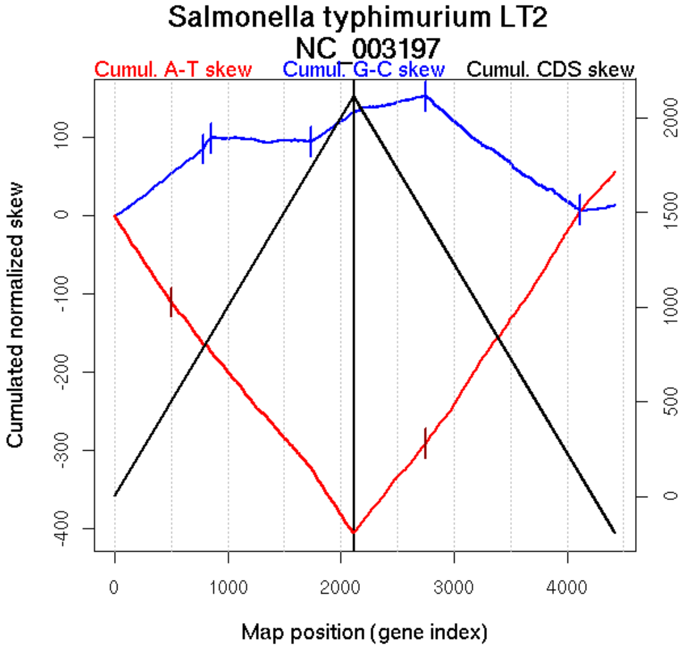
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	811 (1503.3555 kb)	leading	0.118
	812(1507.4625 kb)	1309 (2786.4815 kb)	lagging	-0.021
	1310(2787.799 kb)	1694 (3752.866 kb)	lagging	0.028
	1695(3753.8475 kb)	2243 (4791.934 kb)	leading	0.097
GC-skew reverse	2244 (0 kb)	2808 (1530.838 kb)	leading	0.021
	2809(1539.024 kb)	3877 (3594.154 kb)	lagging	-0.113
	3878(3595.2 kb)	4317 (4791.934 kb)	leading	-0.021
AT-skew forward	1 (0 kb)	1758 (3848.926 kb)	NA	-0.179
	1759(3849.8545 kb)	2243 (4791.934 kb)	leading	-0.22
AT-skew reverse	2244 (0 kb)	2897 (1731.135 kb)	NA	0.181
	2898(1732.2395 kb)	4317(4791.934 kb)	NA	0.204

More G than C on the leading strand for replication.

293 Salmonella typhimurium LT2

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Salmonella.
Accession number: NC_003197; **Genome size (bp)**: 4857432.
Number of genes: 4425.
Oriloc predictions: Origin 4082 kb Terminus 1635 kb
Worning et al., 2006: Origin 4081 kb Terminus 1604 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 4084.1 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 2610.22 kb, 4044.32 kb
Consensus predictions: Origin 4082 kb Terminus 1635 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	782	NA	1454
	852	NA	1597
	1739	NA	4050
GC-skew reverse	2752	NA	1627
	4119	NA	4093
AT-skew forward	499	NA	972
AT-skew reverse	2754	NA	1634

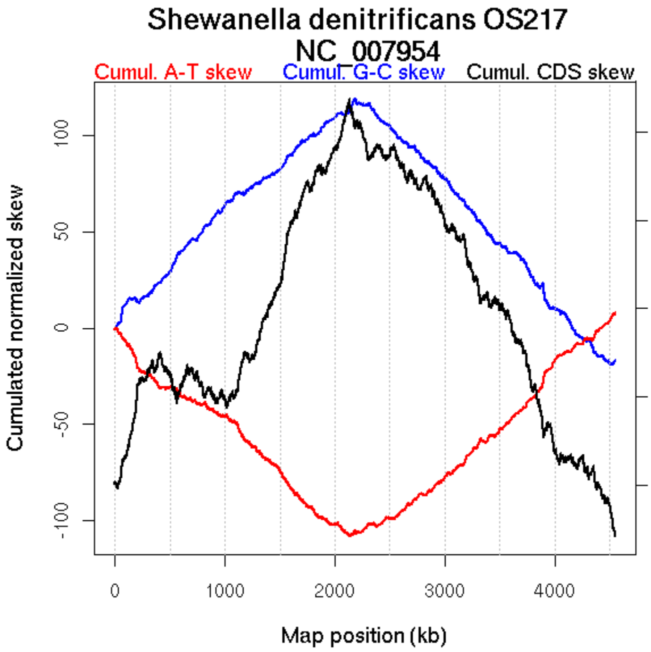
Segments:

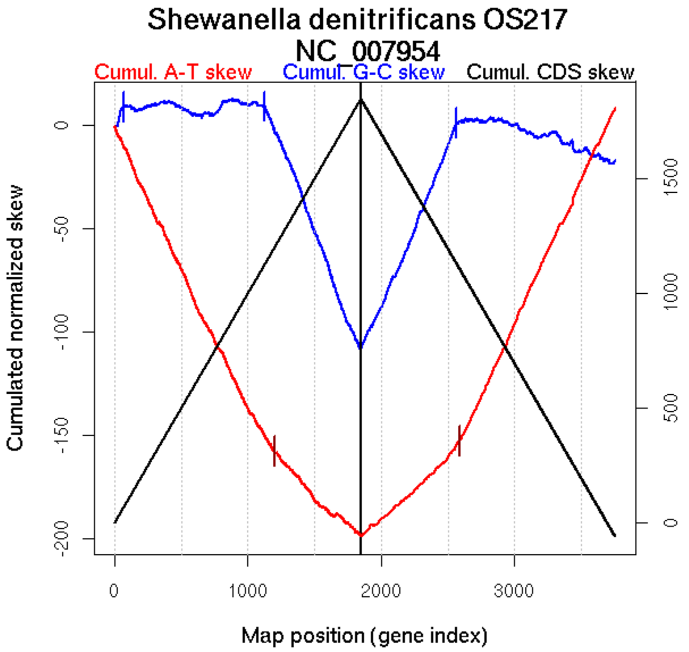
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	782 (1454.186 kb)	leading	0.112
	783(1454.928 kb)	852 (1597.459 kb)	leading	0.204
	853(1600.0175 kb)	1739 (4050.476 kb)	lagging	-0.006
	1740(4052.3385 kb)	2115 (4857.405 kb)	leading	0.1
GC-skew reverse	2116 (0 kb)	2752 (1626.8275 kb)	leading	0.03
	2753(1629.3565 kb)	4119 (4093.344 kb)	lagging	-0.105
	4120(4098.581 kb)	4425 (4857.405 kb)	leading	0.022
AT-skew forward	1 (0 kb)	499 (971.579 kb)	leading	-0.221
	500(972.5455 kb)	2115 (4857.405 kb)	NA	-0.177
AT-skew reverse	2116 (0 kb)	2754 (1634.2715 kb)	leading	0.179
	2755(1638.3915 kb)	4425(4857.405 kb)	NA	0.213

More G than C on the leading strand for replication.

294 Shewanella denitrificans OS217

Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales; Shewanellaceae; Shewanella.
Accession number: NC_007954; **Genome size (bp)**: 4545906.
Number of genes: 3754.
Oriloc predictions: Origin 0 kb Terminus 2168 kb
Worning et al., 2006: Origin 4531 kb Terminus 2171 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 3324.546 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.7 kb, 1908.35 kb
Consensus predictions: Origin 0 kb Terminus 2168 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	68	0	116
	1128	0	2192
GC-skew reverse	2565	0	2181
AT-skew forward	1199	0	2411
AT-skew reverse	2589	0	2236

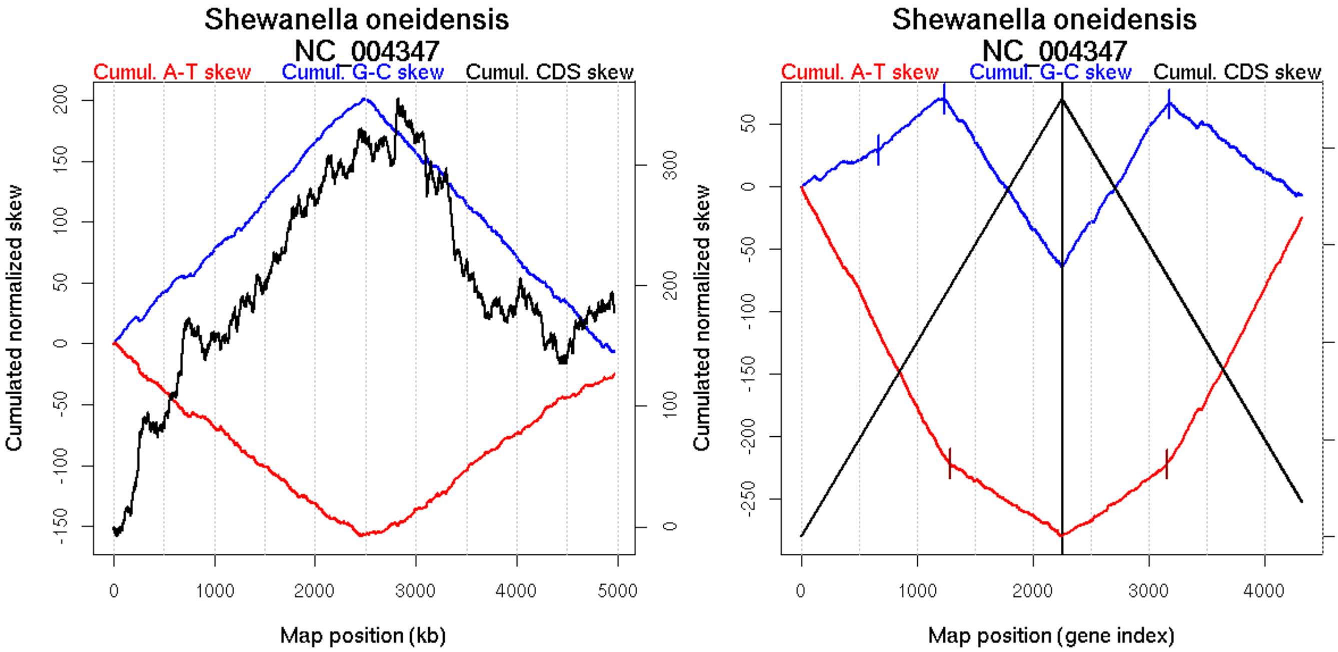
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	68 (115.748 kb)	leading	0.184
	69(116.2885 kb)	1128 (2192.0895 kb)	leading	0.001
	1129(2192.7045 kb)	1848 (4545.451 kb)	lagging	-0.17
GC-skew reverse	1849 (0 kb)	2565 (2181.352 kb)	leading	0.153
	2566(2184.312 kb)	3754 (4545.451 kb)	lagging	-0.019
AT-skew forward	1 (0 kb)	1199 (2410.766 kb)	leading	-0.133
	1200(2412.729 kb)	1848 (4545.451 kb)	lagging	-0.063
AT-skew reverse	1849 (0 kb)	2589 (2236.39 kb)	leading	0.06
	2590(2237.0955 kb)	3754(4545.451 kb)	lagging	0.139

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

295 Shewanella oneidensis

Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales; Shewanellaceae; Shewanella.
Accession number: NC_004347; **Genome size (bp)**: 4969803.
Number of genes: 4324.
Oriloc predictions: Origin 0 kb Terminus 2488 kb
Worning et al., 2006: Origin 0 kb Terminus 2494 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1388.423 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 7.56 kb, 2997.81 kb
Consensus predictions: Origin 0 kb Terminus 2488 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	672	NA	1304
	1237	NA	2481
GC-skew reverse	3181	NA	2511
AT-skew forward	1282	NA	2603
AT-skew reverse	3158	NA	2468

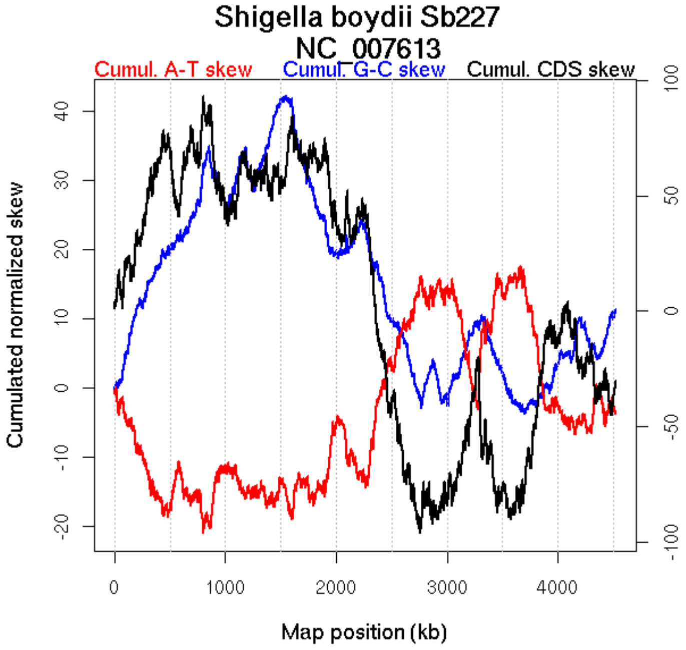
Segments:

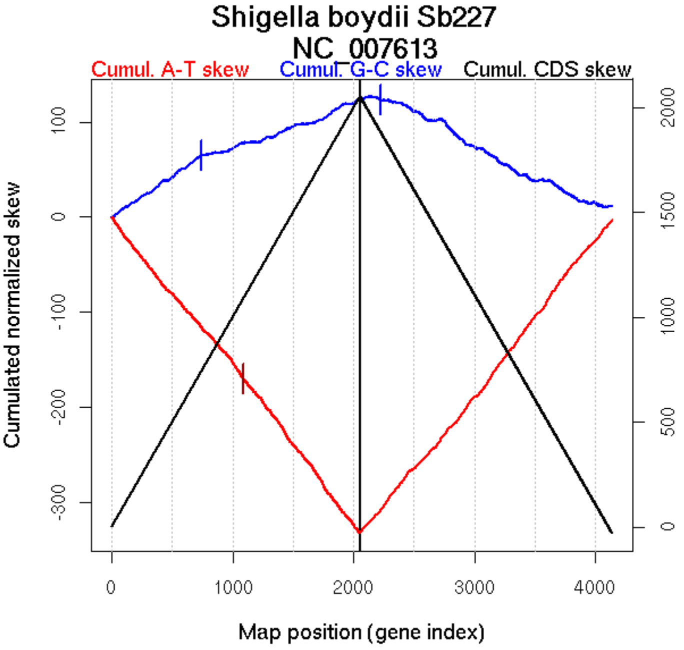
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	672 (1304.285 kb)	leading	0.042
	673(1306.8395 kb)	1237 (2480.975 kb)	leading	0.076
	1238(2481.403 kb)	2251 (4969.696 kb)	lagging	-0.136
GC-skew reverse	2252 (0 kb)	3181 (2511.0705 kb)	leading	0.144
	3182(2514.632 kb)	4324 (4969.696 kb)	lagging	-0.066
AT-skew forward	1 (0 kb)	1282 (2603.2745 kb)	leading	-0.176
	1283(2605.7675 kb)	2251 (4969.696 kb)	lagging	-0.058
AT-skew reverse	2252 (0 kb)	3158 (2468.4555 kb)	leading	0.064
	3159(2468.8385 kb)	4324(4969.696 kb)	lagging	0.171

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

296 Shigella boydii Sb227

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Shigella.
Accession number: NC_007613; **Genome size (bp)**: 4519823.
Number of genes: 4136.
Oriloc predictions: Origin NA Terminus NA
Worning et al., 2006: Origin 3567 kb Terminus 1440 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 360.318 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 3689.89 kb
Consensus predictions: Origin 3667 kb Terminus 1597 kb





Significant breakpoints (p-value <0.05):

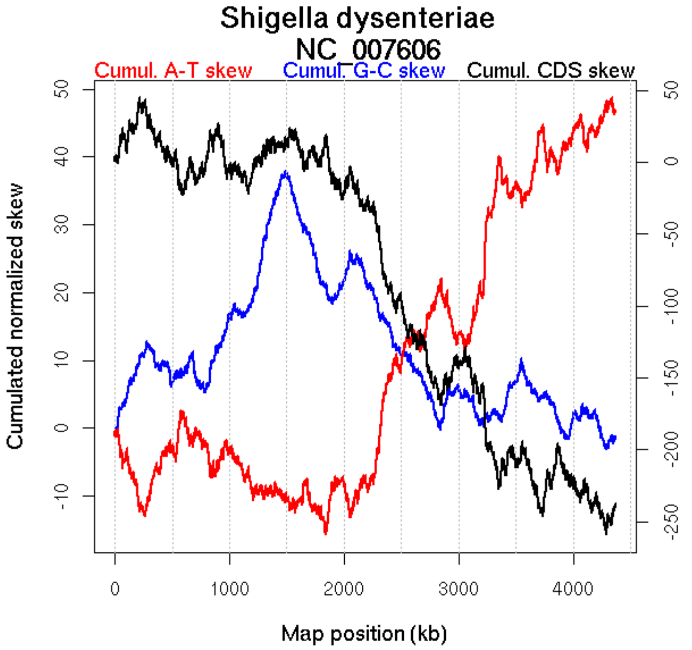
	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	742	0.00667	1536
GC-skew reverse	2221	0	456
AT-skew forward	1088	0.04667	2325

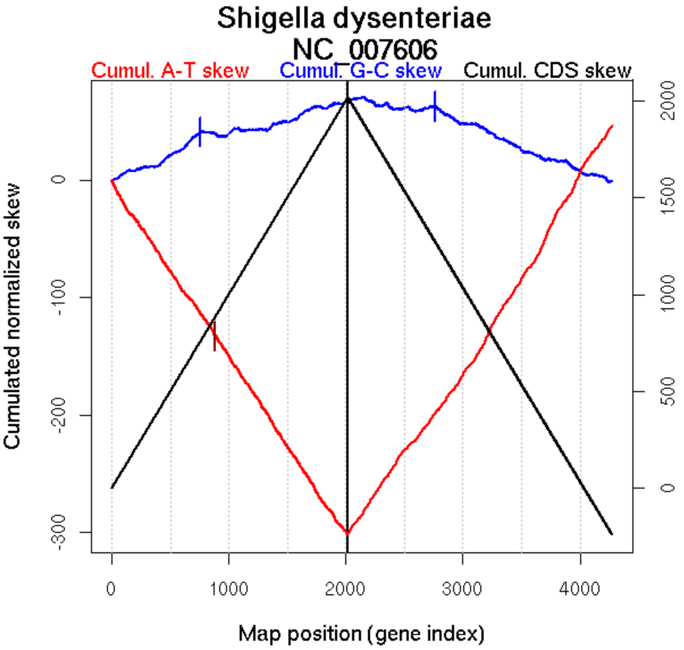
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	742 (1536.2135 kb)	leading	0.087
	743(1539.238 kb)	2053 (4519.796 kb)	NA	0.046
GC-skew reverse	2054 (0 kb)	2221 (456.4965 kb)	leading	0.001
	2222(457.3315 kb)	4136 (4519.796 kb)	NA	-0.066
AT-skew forward	1 (0 kb)	1088 (2325.104 kb)	NA	-0.149
	1089(2327.7335 kb)	2053 (4519.796 kb)	NA	-0.172

297 Shigella dysenteriae

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Shigella.
Accession number: NC_007606; **Genome size (bp)**: 4369232.
Number of genes: 4274.
Oriloc predictions: Origin NA Terminus NA
Worning et al., 2006: Origin 3735 kb Terminus 1487 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 3740.648 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 3918.91 kb
Consensus predictions: Origin 4335 kb Terminus 1485 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	761	NA	1484
GC-skew reverse	2759	NA	1464
AT-skew forward	886	NA	1728

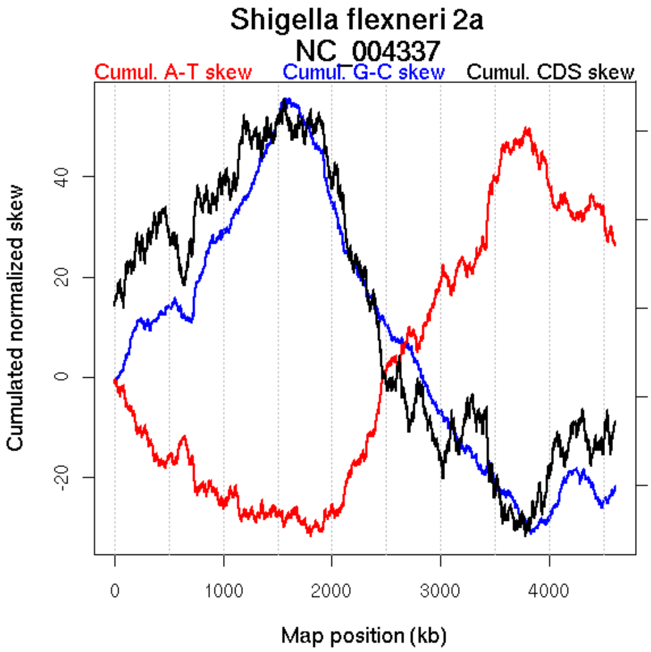
Segments:

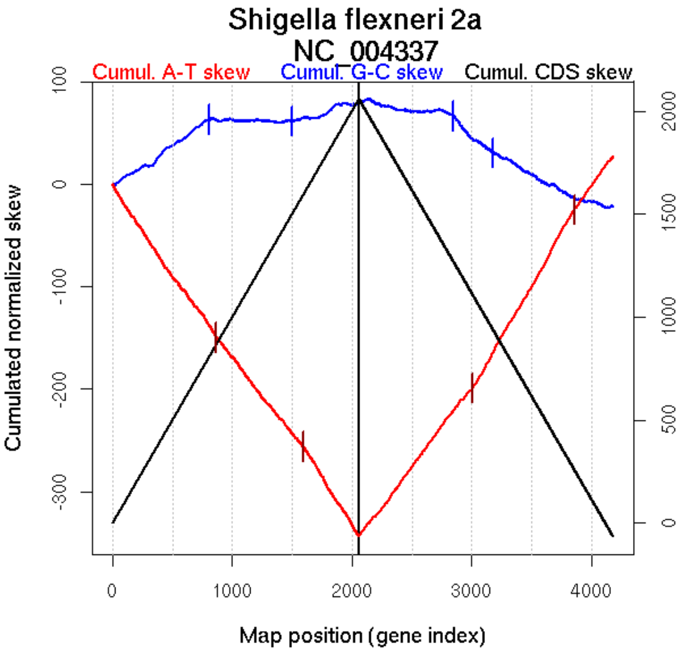
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	761 (1483.5335 kb)	leading	0.049
	762(1484.1155 kb)	2018 (4369.205 kb)	lagging	0.025
GC-skew reverse	2019 (0 kb)	2759 (1463.928 kb)	leading	-0.014
	2760(1466.938 kb)	4274 (4369.205 kb)	lagging	-0.041
AT-skew forward	1 (0 kb)	886 (1727.6915 kb)	leading	-0.145
	887(1732.2625 kb)	2018 (4369.205 kb)	lagging	-0.152

More A than T on the leading strand for replication - for forward encoded genes.
More G than C on the leading strand for replication.

298 Shigella flexneri 2a

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Shigella.
Accession number: NC_004337; **Genome size (bp)**: 4607203.
Number of genes: 4182.
Oriloc predictions: Origin 3820 kb Terminus 1619 kb
Worning et al., 2006: Origin 3814 kb Terminus 1563 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 2011.079 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 3869.71 kb
Consensus predictions: Origin 3820 kb Terminus 1619 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	809	NA	1626
	1503	NA	3366
GC-skew reverse	2849	NA	1820
	3181	NA	2435
AT-skew forward	868	NA	1767
	1596	NA	3608
AT-skew reverse	3009	NA	2107
	3857	NA	3795

Segments:

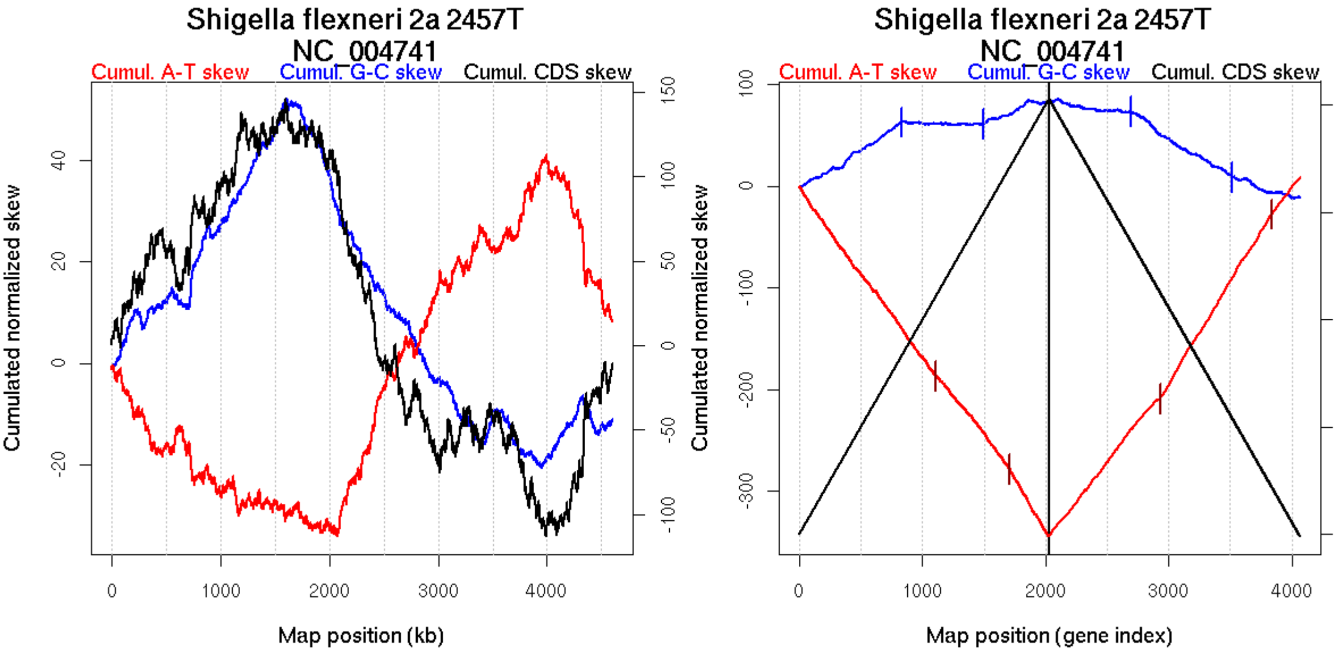
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	809 (1625.642 kb)	leading	0.082
	810(1630.4005 kb)	1503 (3366.085 kb)	lagging	-0.003
	1504(3368.5165 kb)	2059 (4607.176 kb)	NA	0.038
GC-skew reverse	2060 (0 kb)	2849 (1819.695 kb)	leading	-0.016
	2850(1820.8555 kb)	3181 (2435.006 kb)	lagging	-0.105
	3182(2435.931 kb)	4182 (4607.176 kb)	NA	-0.057
AT-skew forward	1 (0 kb)	868 (1766.6965 kb)	leading	-0.167
	869(1769.0685 kb)	1596 (3608.3975 kb)	lagging	-0.148
	1597(3610.3015 kb)	2059 (4607.176 kb)	NA	-0.189
AT-skew reverse	2060 (0 kb)	3009 (2107.4545 kb)	NA	0.156
	3010(2108.74 kb)	3857(3795.098 kb)	lagging	0.205
	3858(3801.181 kb)	4182(4607.176 kb)	leading	0.163

More T than A on the leading strand for replication - for forward encoded genes.

299 Shigella flexneri 2a 2457T

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Shigella.

Accession number: NC_004741; **Genome size (bp)**: 4599354.
Number of genes: 4067.
Oriloc predictions: Origin 3953 kb Terminus 1659 kb
Worning et al., 2006: Origin 3980 kb Terminus 1601 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1987.731 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 2584.77 kb, 3904.86 kb
Consensus predictions: Origin 3953 kb Terminus 1659 kb



Significant breakpoints (p-value <0.05):

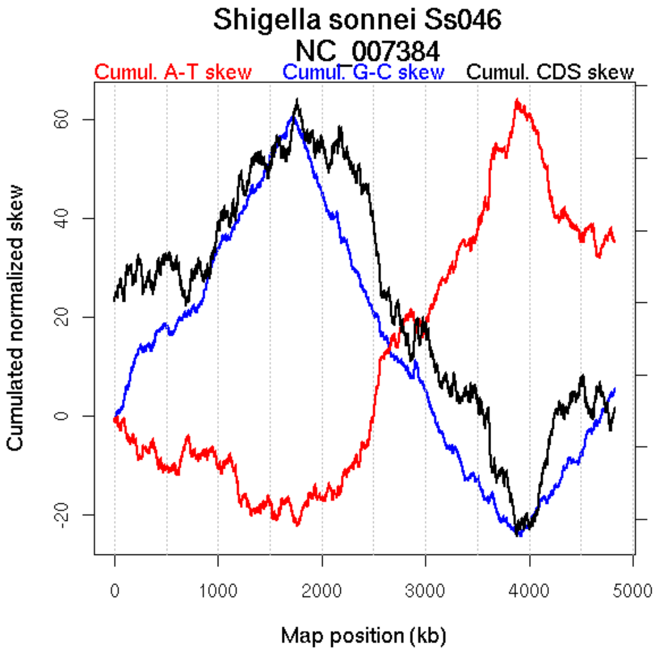
	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	831	NA	1686
	1499	NA	3422
GC-skew reverse	2694	NA	1612
	3516	NA	3296
AT-skew forward	1106	NA	2493
	1711	NA	4002
AT-skew reverse	2931	NA	2090
	3835	NA	3985

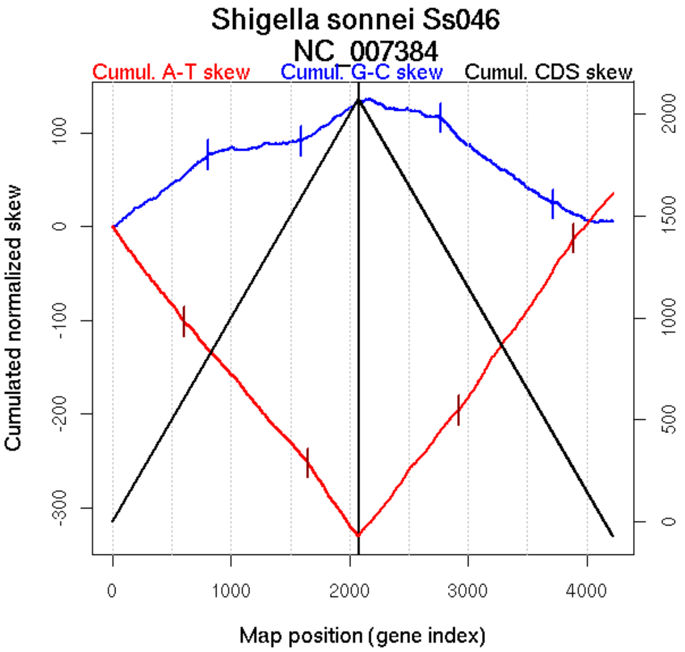
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	831 (1686.0965 kb)	leading	0.078
	832(1687.621 kb)	1499 (3421.966 kb)	lagging	-0.003
	1500(3425.6975 kb)	2028 (4599.327 kb)	NA	0.044
GC-skew reverse	2029 (0 kb)	2694 (1611.7795 kb)	leading	-0.019
	2695(1614.5655 kb)	3516 (3295.83 kb)	lagging	-0.077
	3517(3297.708 kb)	4067 (4599.327 kb)	NA	-0.04
AT-skew forward	1 (0 kb)	1106 (2493.201 kb)	NA	-0.165
	1107(2496.3 kb)	1711 (4002.355 kb)	lagging	-0.153
	1712(4003.385 kb)	2028 (4599.327 kb)	leading	-0.21
AT-skew reverse	2029 (0 kb)	2931 (2090.0935 kb)	NA	0.155
	2932(2091.125 kb)	3835(3984.507 kb)	lagging	0.2
	3836(3986.3175 kb)	4067(4599.327 kb)	leading	0.159

300 Shigella sonnei Ss046

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Shigella.
Accession number: NC_007384; **Genome size (bp)**: 4825265.
Number of genes: 4223.
Oriloc predictions: Origin 3918 kb Terminus 1739 kb
Worning et al., 2006: Origin 3882 kb Terminus 1740 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1312.317 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 3823.94 kb
Consensus predictions: Origin 3918 kb Terminus 1739 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	809	NA	1696
	1592	NA	3709
GC-skew reverse	2770	NA	1678
	3714	NA	3614
AT-skew forward	600	NA	1279
	1650	NA	3888
AT-skew reverse	2923	NA	2028
	3893	NA	3915

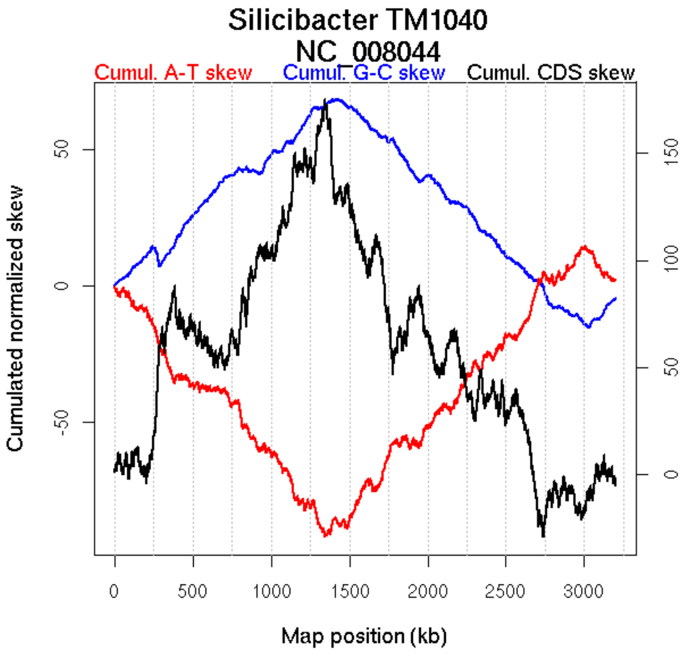
Segments:

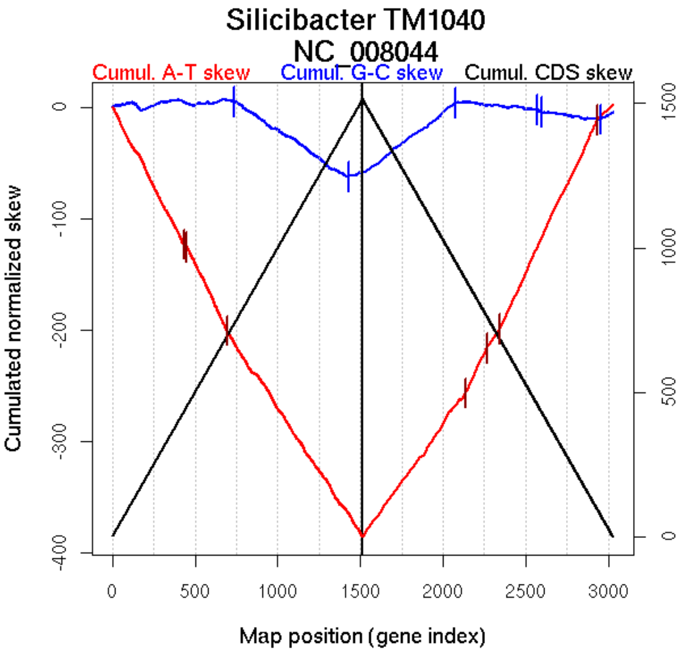
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	809 (1696.3625 kb)	leading	0.093
	810(1698.0415 kb)	1592 (3709.045 kb)	lagging	0.017
	1593(3709.83 kb)	2075 (4825.238 kb)	leading	0.087
GC-skew reverse	2076 (0 kb)	2770 (1678.14 kb)	leading	-0.028
	2771(1678.4605 kb)	3714 (3613.659 kb)	lagging	-0.093
	3715(3614.378 kb)	4223 (4825.238 kb)	NA	-0.043
AT-skew forward	1 (0 kb)	600 (1278.862 kb)	leading	-0.164
	601(1279.536 kb)	1650 (3888.4155 kb)	NA	-0.145
	1651(3890.209 kb)	2075 (4825.238 kb)	leading	-0.186
AT-skew reverse	2076 (0 kb)	2923 (2027.9685 kb)	NA	0.163
	2924(2030.5295 kb)	3893(3915.1345 kb)	lagging	0.187
	3894(3918.4695 kb)	4223(4825.238 kb)	leading	0.148

More G than C on the leading strand for replication - for forward encoded genes.

301 Silicibacter TM1040

Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Silicibacter.
Accession number: NC_008044; **Genome size (bp)**: 3200938.
Number of genes: 3030.
Oriloc predictions: Origin 3030 kb Terminus 1384 kb
Worning et al., 2006: Origin 3012 kb Terminus 1376 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 959.193 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.75 kb, 1957.88 kb
Consensus predictions: Origin 3030 kb Terminus 1384 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	737	0	1433
	1427	0	3034
GC-skew reverse	2076	0.005	1382
	2571	0.02667	2260
	2596	0.04	2302
	2952	0.01667	3039
AT-skew forward	431	0	843
	449	0	856
	692	0.03333	1313
AT-skew reverse	2135	0.01167	1464
	2265	0.02	1713
	2344	0.02167	1825
	2936	0.00167	2998

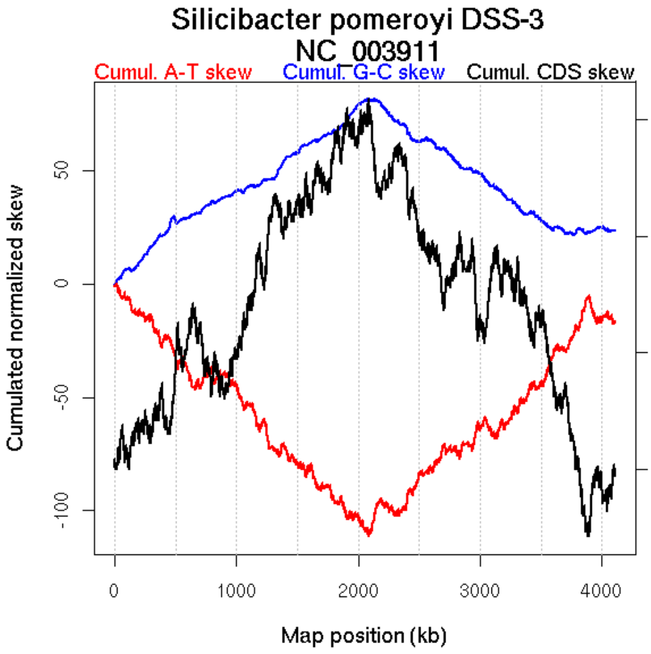
Segments:

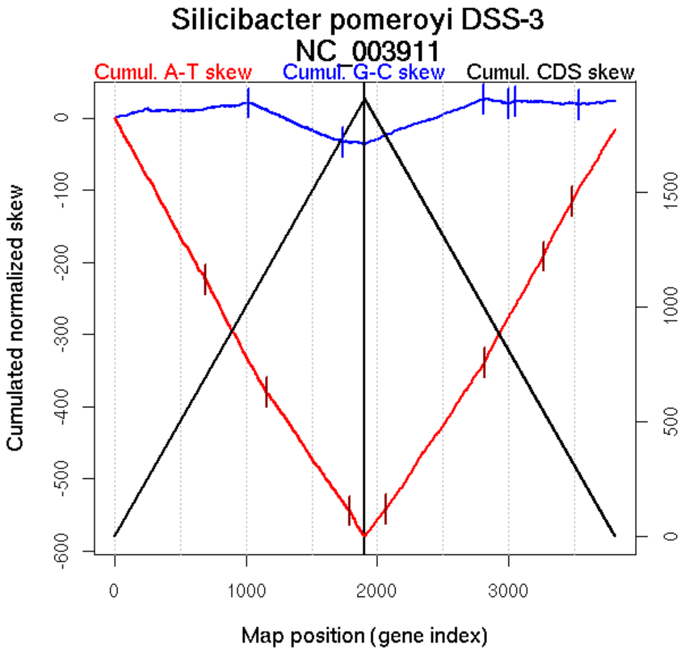
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	737 (1432.5035 kb)	leading	0.006
	738(1433.265 kb)	1427 (3034.0055 kb)	lagging	-0.1
	1428(3035.889 kb)	1514 (3200.382 kb)	leading	0.05
GC-skew reverse	1515 (0 kb)	2076 (1382.016 kb)	leading	0.113
	2077(1382.5055 kb)	2571 (2259.748 kb)	lagging	-0.014
	2572(2262.852 kb)	2596 (2301.6385 kb)	lagging	-0.093
	2597(2304.402 kb)	2952 (3039.458 kb)	lagging	-0.02
	2953(3040.3865 kb)	3030 (3200.382 kb)	leading	0.073
AT-skew forward	1 (0 kb)	431 (843.241 kb)	leading	-0.284
	432(843.762 kb)	449 (855.898 kb)	leading	-0.121
	450(856.4325 kb)	692 (1313.266 kb)	leading	-0.31
	693(1316.344 kb)	1514 (3200.382 kb)	lagging	-0.223
AT-skew reverse	1515 (0 kb)	2135 (1463.669 kb)	leading	0.208
	2136(1464.8365 kb)	2265(1713.4965 kb)	lagging	0.318
	2266(1714.12 kb)	2344(1825.3865 kb)	lagging	0.214
	2345(1826.4625 kb)	2936(2997.5475 kb)	lagging	0.316
	2937(3000.141 kb)	3030(3200.382 kb)	leading	0.132

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

302 Silicibacter pomeroyi DSS-3

Bacteria; Proteobacteria; Alphaproteobacteria; Rhodobacterales; Rhodobacteraceae; Silicibacter.
Accession number: NC_003911; **Genome size (bp)**: 4109442.
Number of genes: 3810.
Oriloc predictions: Origin 0 kb Terminus 2129 kb
Worning et al., 2006: Origin 3893 kb Terminus 2089 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 2549.983 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 165.03 kb
Consensus predictions: Origin 0 kb Terminus 2129 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1019	NA	2051
	1741	NA	3758
GC-skew reverse	2810	NA	2118
	2995	NA	2481
	3047	NA	2583
	3533	NA	3579
AT-skew forward	695	NA	1381
	1156	NA	2373
	1792	NA	3900
AT-skew reverse	2069	NA	390
	2815	NA	2126
	3264	NA	3037
	3486	NA	3502

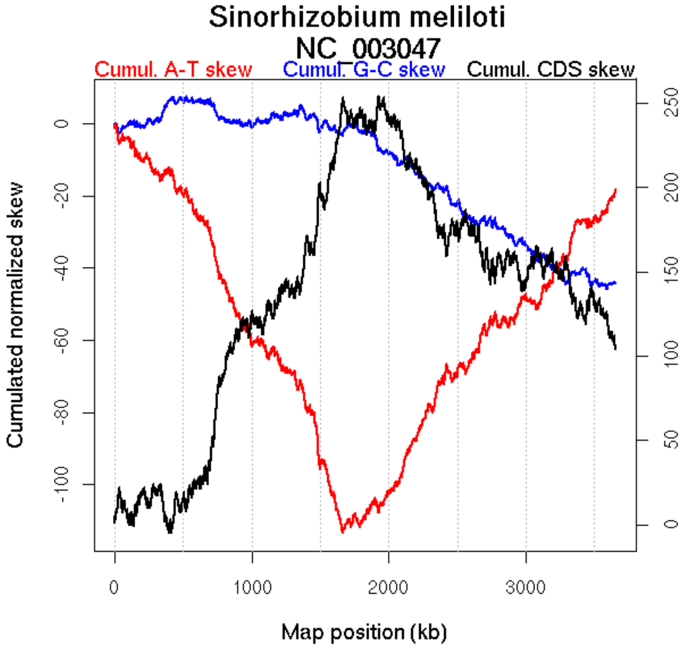
Segments:

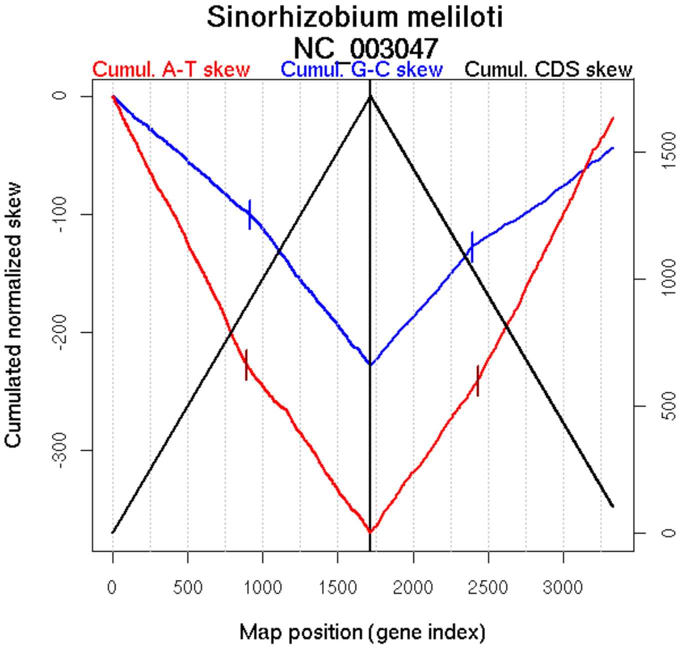
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1019 (2051.4305 kb)	leading	0.014
	1020(2057.945 kb)	1741 (3757.546 kb)	lagging	-0.078
	1742(3759.258 kb)	1905 (4109.427 kb)	lagging	-0.017
GC-skew reverse	1906 (0 kb)	2810 (2117.6135 kb)	leading	0.067
	2811(2118.4545 kb)	2995 (2480.679 kb)	lagging	-0.036
	2996(2482.0195 kb)	3047 (2582.9855 kb)	lagging	0.065
	3048(2584.551 kb)	3533 (3578.6715 kb)	lagging	-0.009
	3534(3580.764 kb)	3810 (4109.427 kb)	lagging	0.018
AT-skew forward	1 (0 kb)	695 (1380.7005 kb)	leading	-0.326
	696(1383.08 kb)	1156 (2372.624 kb)	NA	-0.339
	1157(2373.4705 kb)	1792 (3900.396 kb)	lagging	-0.265
	1793(3901.0945 kb)	1905 (4109.427 kb)	lagging	-0.321
AT-skew reverse	1906 (0 kb)	2069 (389.937 kb)	leading	0.241
	2070(390.8395 kb)	2815(2126.0475 kb)	leading	0.272
	2816(2127.8105 kb)	3264(3036.5775 kb)	lagging	0.323
	3265(3039.5255 kb)	3486(3501.737 kb)	lagging	0.34
	3487(3503.01 kb)	3810(4109.427 kb)	lagging	0.302

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

303 Sinorhizobium meliloti

Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
Accession number: NC_003047; **Genome size (bp)**: 3654135.
Number of genes: 3332.
Oriloc predictions: Origin 0 kb Terminus 1901 kb
Worning et al., 2006: Origin 0 kb Terminus 1738 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 0.346 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 400.09 kb
Consensus predictions: Origin 0 kb Terminus 1901 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	918	0	1742
GC-skew reverse	2393	0	1734
AT-skew forward	894	0	1664
AT-skew reverse	2430	0	1812

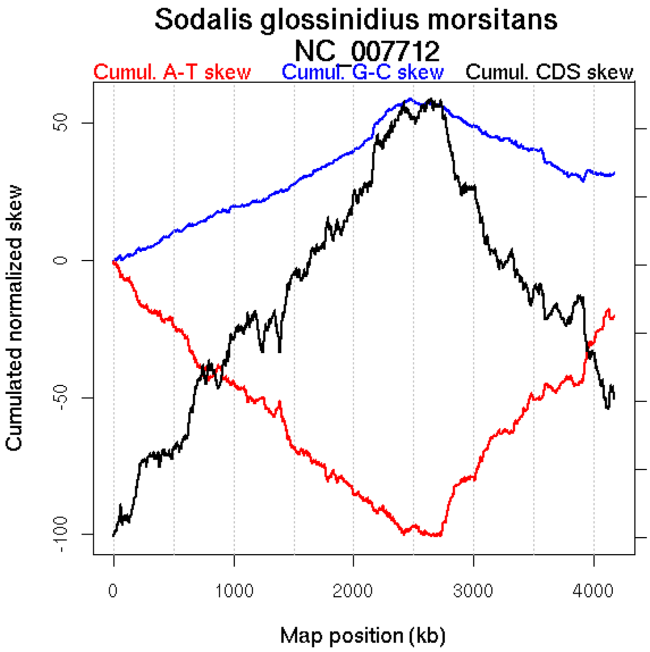
Segments:

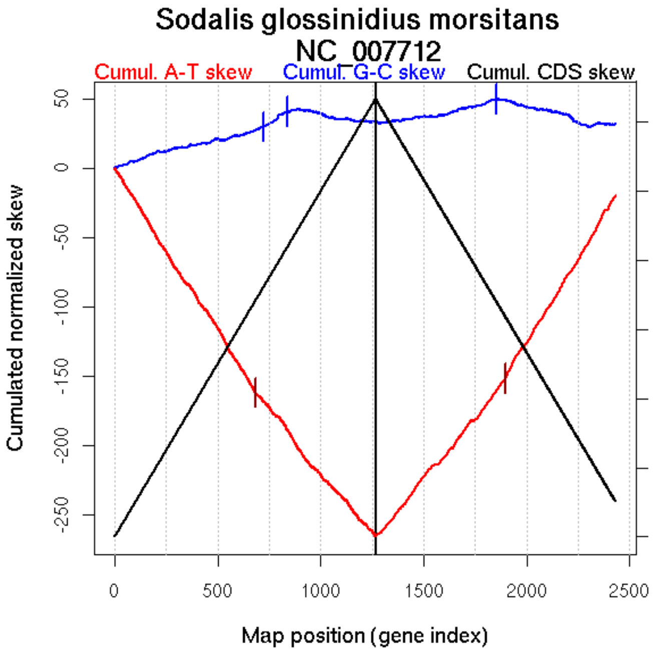
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	918 (1742.091 kb)	leading	-0.109
	919(1745.187 kb)	1718 (3654.135 kb)	lagging	-0.162
GC-skew reverse	1719 (0 kb)	2393 (1734.2625 kb)	leading	0.146
	2394(1735.9575 kb)	3332 (3654.135 kb)	lagging	0.089
AT-skew forward	1 (0 kb)	894 (1664.24 kb)	leading	-0.251
	895(1666.679 kb)	1718 (3654.135 kb)	lagging	-0.175
AT-skew reverse	1719 (0 kb)	2430 (1812.3565 kb)	leading	0.179
	2431(1813.4605 kb)	3332(3654.135 kb)	lagging	0.251

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

304 Sodalis glossinidius morsitans

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Sodalis.
Accession number: NC_007712; **Genome size (bp)**: 4171146.
Number of genes: 2432.
Oriloc predictions: Origin 0 kb Terminus 2461 kb
Worning et al., 2006: Origin 4128 kb Terminus 2463 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 4127.636 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.7 kb
Consensus predictions: Origin 0 kb Terminus 2461 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	725	0.02	2007
	839	0	2294
GC-skew reverse	1853	0	2475
AT-skew forward	684	0.01333	1904
AT-skew reverse	1898	0.00667	2710

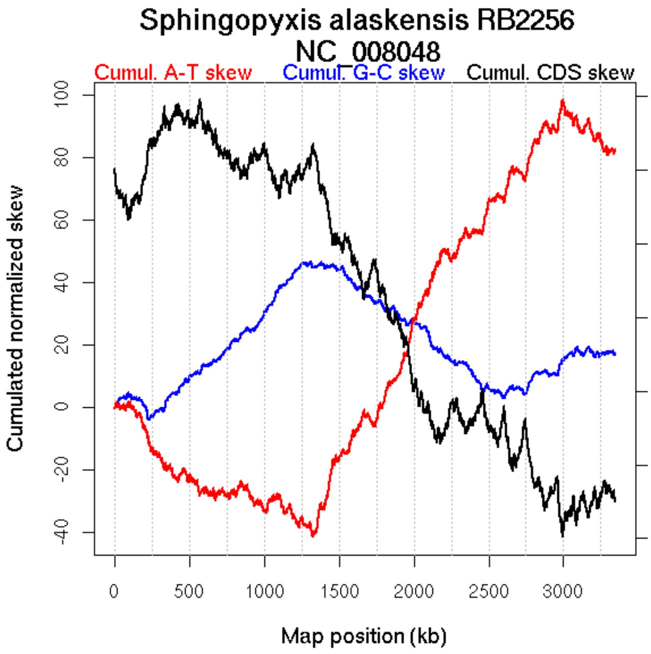
Segments:

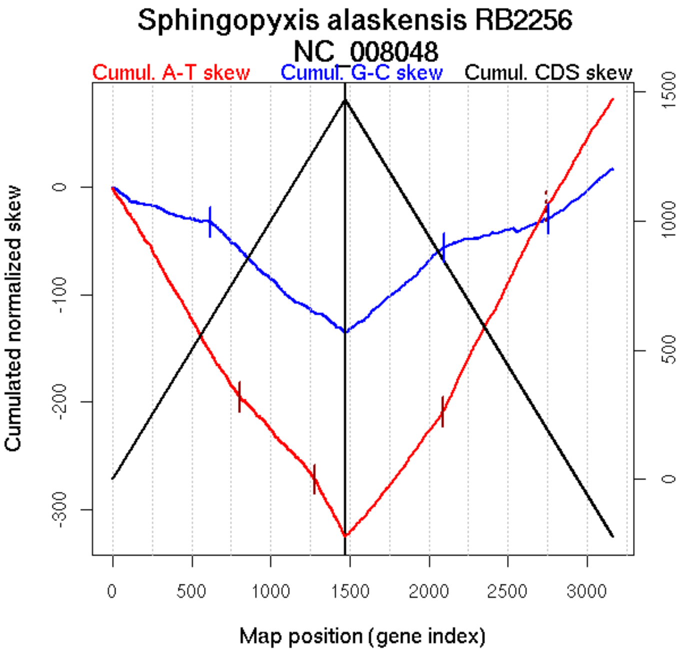
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	725 (2007.235 kb)	leading	0.037
	726(2009.1665 kb)	839 (2293.9915 kb)	leading	0.104
	840(2299.0505 kb)	1267 (4170.51 kb)	lagging	-0.025
GC-skew reverse	1268 (0 kb)	1853 (2474.602 kb)	leading	0.028
	1854(2476.211 kb)	2432 (4170.51 kb)	lagging	-0.037
AT-skew forward	1 (0 kb)	684 (1903.5435 kb)	leading	-0.233
	685(1906.2415 kb)	1267 (4170.51 kb)	NA	-0.18
AT-skew reverse	1268 (0 kb)	1898 (2709.9375 kb)	leading	0.179
	1899(2714.6985 kb)	2432(4170.51 kb)	lagging	0.243

More T than A on the leading strand for replication - for reverse encoded genes.
More G than C on the leading strand for replication.

305 Sphingopyxis alaskensis RB2256

Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Sphingopyxis.
Accession number: NC_008048; **Genome size (bp)**: 3345170.
Number of genes: 3165.
Oriloc predictions: Origin 2655 kb Terminus 1380 kb
Worning et al., 2006: Origin 2563 kb Terminus 1343 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1.56 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.85 kb
Consensus predictions: Origin 2655 kb Terminus 1380 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	621	0.00667	1303
GC-skew reverse	2094	0.01	1331
	2755	0.01333	2544
AT-skew forward	806	0.03	1797
	1278	0.00667	2952
AT-skew reverse	2088	0.02	1302
	2742	0.19333	2515

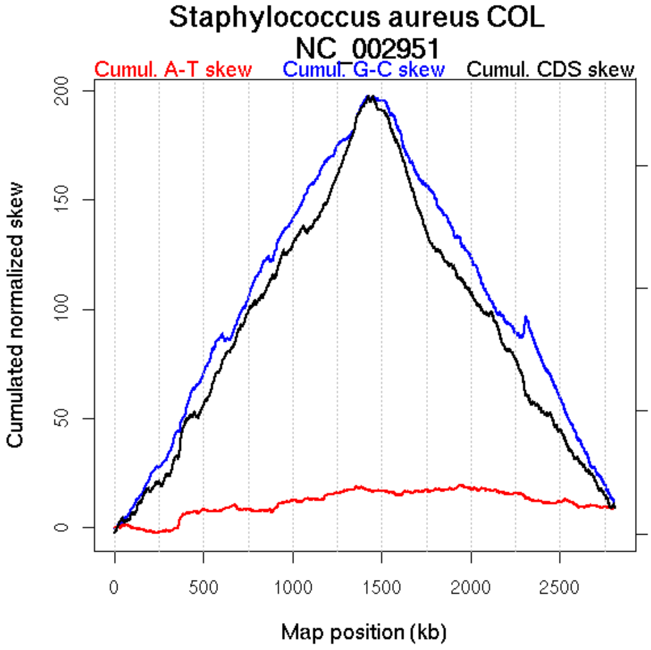
Segments:

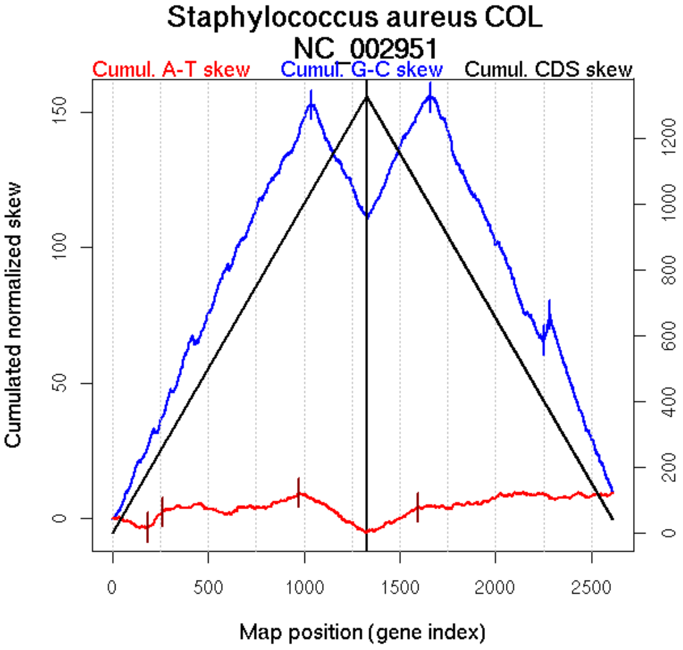
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	621 (1303.404 kb)	leading	-0.049
	622(1307.7945 kb)	1471 (3344.839 kb)	NA	-0.121
GC-skew reverse	1472 (0 kb)	2094 (1330.5195 kb)	leading	0.129
	2095(1331.943 kb)	2755 (2544.049 kb)	lagging	0.035
	2756(2545.773 kb)	3165 (3344.839 kb)	NA	0.118
AT-skew forward	1 (0 kb)	806 (1797.4815 kb)	NA	-0.249
	807(1800.0655 kb)	1278 (2951.6355 kb)	NA	-0.16
	1279(2952.246 kb)	1471 (3344.839 kb)	leading	-0.276
AT-skew reverse	1472 (0 kb)	2088 (1301.837 kb)	leading	0.191
	2089(1303.6175 kb)	2742(2515.3615 kb)	lagging	0.29
	2743(2517.5575 kb)	3165(3344.839 kb)	NA	0.246

More T than A on the leading strand for replication - for reverse encoded genes.
More G than C on the leading strand for replication - for reverse encoded genes.

306 Staphylococcus aureus COL

Bacteria; Firmicutes; Bacillales; Staphylococcus.
Accession number: NC_002951; **Genome size (bp)**: 2809422.
Number of genes: 2613.
Oriloc predictions: Origin 0 kb Terminus 1420 kb
Worning et al., 2006: Origin 0 kb Terminus 1426 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 2096.123 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1.22 kb, 1619.4 kb, 1763.69 kb
Consensus predictions: Origin 0 kb Terminus 1420 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1037	0	1443
GC-skew reverse	1661	0	1450
	2254	0	2293
	2284	0	2310
AT-skew forward	186	0.00889	324
	263	0.00889	382
	973	0.04667	1353
AT-skew reverse	1596	0.02	1096

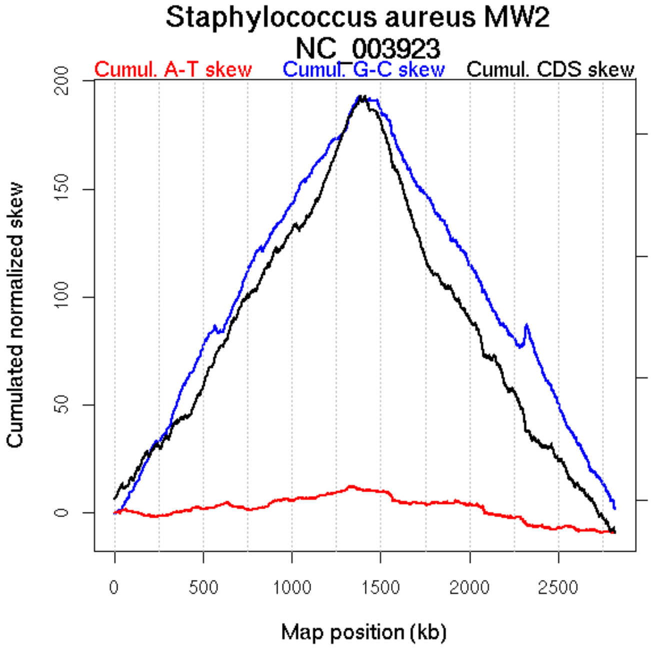
Segments:

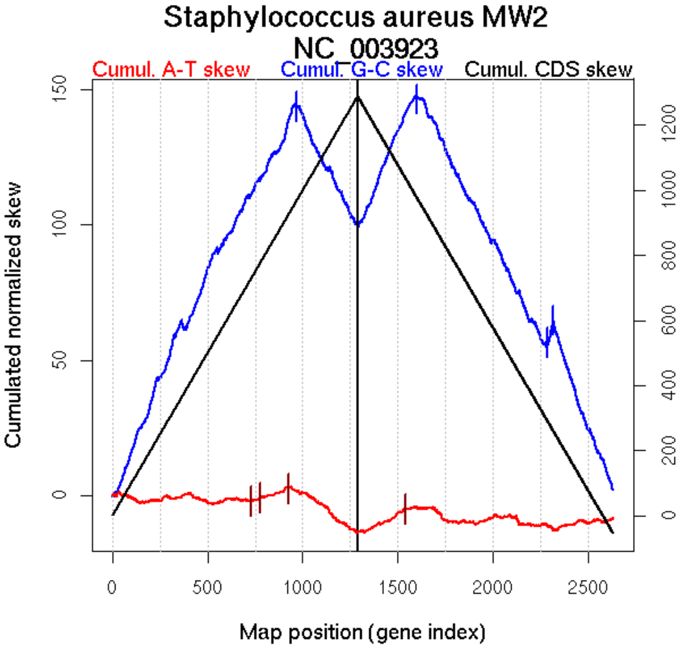
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1037 (1442.8585 kb)	leading	0.149
	1038(1443.745 kb)	1327 (2809.235 kb)	lagging	-0.145
GC-skew reverse	1328 (0 kb)	1661 (1450.031 kb)	leading	0.145
	1662(1451.6705 kb)	2254 (2293.083 kb)	lagging	-0.157
	2255(2294.237 kb)	2284 (2310.2165 kb)	lagging	0.326
	2285(2312.123 kb)	2613 (2809.235 kb)	lagging	-0.194
AT-skew forward	1 (0 kb)	186 (323.9315 kb)	leading	-0.024
	187(324.792 kb)	263 (381.8285 kb)	leading	0.084
	264(382.2285 kb)	973 (1352.546 kb)	leading	0.004
	974(1353.134 kb)	1327 (2809.235 kb)	NA	-0.044
AT-skew reverse	1328 (0 kb)	1596 (1095.522 kb)	leading	0.034
	1597(1096.2165 kb)	2613(2809.235 kb)	lagging	0.005

More A than T on the leading strand for replication - for reverse encoded genes.
More G than C on the leading strand for replication.

307 Staphylococcus aureus MW2

Bacteria; Firmicutes; Bacillales; Staphylococcus.
Accession number: NC_003923; **Genome size (bp)**: 2820462.
Number of genes: 2632.
Oriloc predictions: Origin 0 kb Terminus 1380 kb
Worning et al., 2006: Origin 1 kb Terminus 1410 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 0.194 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1.2 kb, 140.35 kb, 140.72 kb, 1757.01 kb
Consensus predictions: Origin 0 kb Terminus 1380 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	967	NA	1403
GC-skew reverse	1598	NA	1393
	2285	NA	2302
	2318	NA	2321
AT-skew forward	727	NA	1087
	775	NA	1153
	926	NA	1336
AT-skew reverse	1542	NA	1049

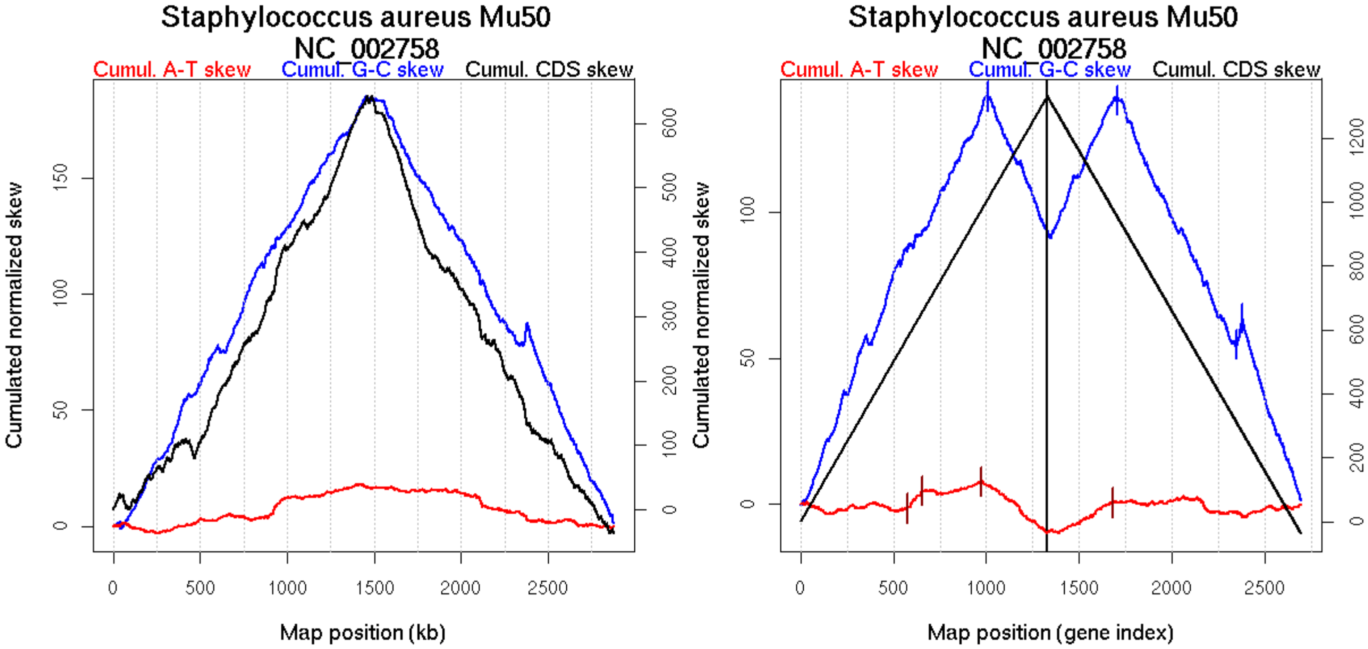
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	967 (1402.7245 kb)	leading	0.147
	968(1403.7465 kb)	1289 (2820.248 kb)	lagging	-0.14
GC-skew reverse	1290 (0 kb)	1598 (1393.182 kb)	leading	0.169
	1599(1393.988 kb)	2285 (2302.3875 kb)	lagging	-0.139
	2286(2303.1315 kb)	2318 (2321.029 kb)	lagging	0.293
	2319(2322.7755 kb)	2632 (2820.248 kb)	lagging	-0.192
AT-skew forward	1 (0 kb)	727 (1087.299 kb)	leading	-0.002
	728(1089.8355 kb)	775 (1152.566 kb)	leading	0.016
	776(1152.795 kb)	926 (1335.765 kb)	leading	0.024
	927(1336.1865 kb)	1289 (2820.248 kb)	lagging	-0.05
AT-skew reverse	1290 (0 kb)	1542 (1048.8695 kb)	leading	0.035
	1543(1055.846 kb)	2632(2820.248 kb)	lagging	-0.004

More A than T on the leading strand for replication.
More G than C on the leading strand for replication.

308 Staphylococcus aureus Mu50

Bacteria; Firmicutes; Bacillales; Staphylococcus.
Accession number: NC_002758; **Genome size (bp)**: 2878529.
Number of genes: 2697.
Oriloc predictions: Origin 0 kb Terminus 1454 kb
Worning et al., 2006: Origin 0 kb Terminus 1458 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 2168.866 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1.2 kb, 1794.39 kb
Consensus predictions: Origin 0 kb Terminus 1454 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1009	NA	1478
GC-skew reverse	1705	NA	1485
	2347	NA	2360
	2381	NA	2379
AT-skew forward	576	NA	903
	656	NA	967
	976	NA	1417
AT-skew reverse	1680	NA	1394

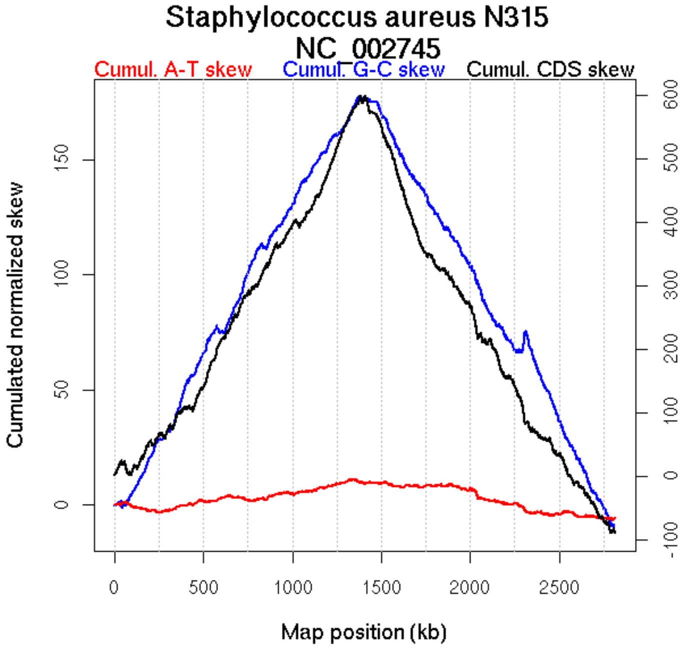
Segments:

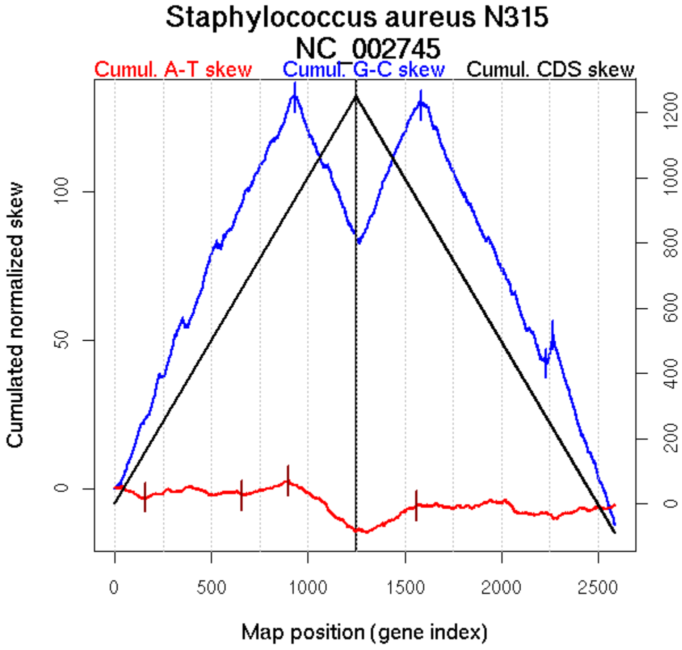
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1009 (1478.3295 kb)	leading	0.138
	1010(1479.216 kb)	1330 (2878.315 kb)	lagging	-0.143
GC-skew reverse	1331 (0 kb)	1705 (1484.9635 kb)	leading	0.137
	1706(1485.502 kb)	2347 (2359.755 kb)	lagging	-0.134
	2348(2360.4825 kb)	2381 (2379.124 kb)	lagging	0.286
	2382(2380.8705 kb)	2697 (2878.315 kb)	lagging	-0.189
AT-skew forward	1 (0 kb)	576 (903.42 kb)	leading	0
	577(904.1625 kb)	656 (967.136 kb)	leading	0.074
	657(968.5105 kb)	976 (1417.0815 kb)	leading	0.01
	977(1417.552 kb)	1330 (2878.315 kb)	lagging	-0.052
AT-skew reverse	1331 (0 kb)	1680 (1394.2145 kb)	leading	0.032
	1681(1398.36 kb)	2697(2878.315 kb)	lagging	-0.004

More A than T on the leading strand for replication.
More G than C on the leading strand for replication.

309 Staphylococcus aureus N315

Bacteria; Firmicutes; Bacillales; Staphylococcus.
Accession number: NC_002745; **Genome size (bp)**: 2814816.
Number of genes: 2588.
Oriloc predictions: Origin 0 kb Terminus 1378 kb
Worning et al., 2006: Origin 0 kb Terminus 1408 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 2092.433 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1.2 kb, 1717.99 kb
Consensus predictions: Origin 0 kb Terminus 1378 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	932	NA	1404
GC-skew reverse	1587	NA	1396
	2232	NA	2288
	2268	NA	2310
AT-skew forward	157	NA	293
	660	NA	1013
	897	NA	1341
AT-skew reverse	1563	NA	1309

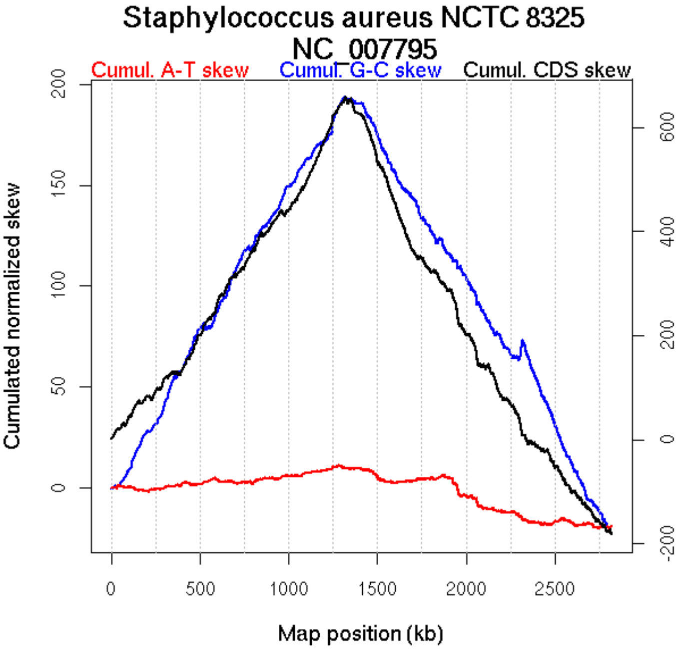
Segments:

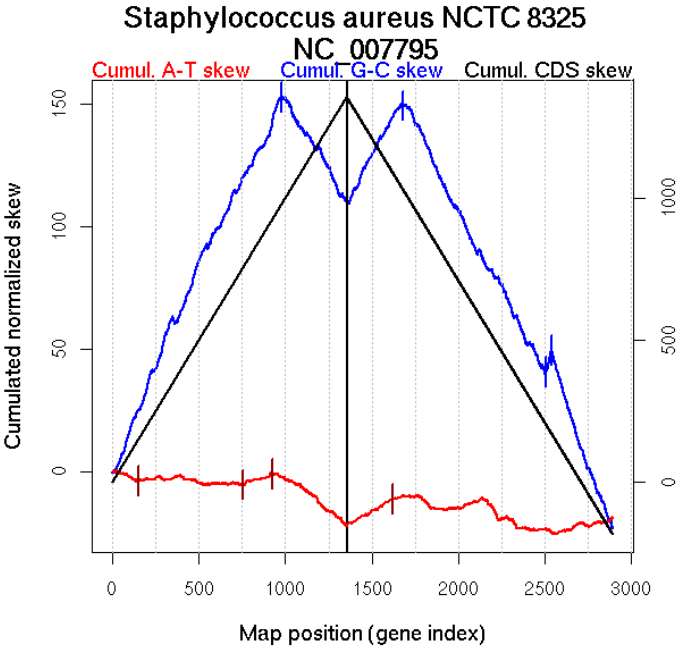
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	932 (1403.621 kb)	leading	0.143
	933(1404.425 kb)	1249 (2814.602 kb)	lagging	-0.148
GC-skew reverse	1250 (0 kb)	1587 (1395.5045 kb)	leading	0.156
	1588(1402.3345 kb)	2232 (2287.604 kb)	lagging	-0.138
	2233(2288.8785 kb)	2268 (2309.624 kb)	lagging	0.275
	2269(2311.3705 kb)	2588 (2814.602 kb)	lagging	-0.191
AT-skew forward	1 (0 kb)	157 (292.6525 kb)	leading	-0.027
	158(293.629 kb)	660 (1013.119 kb)	leading	0.001
	661(1014.5665 kb)	897 (1340.7525 kb)	leading	0.019
	898(1341.223 kb)	1249 (2814.602 kb)	lagging	-0.05
AT-skew reverse	1250 (0 kb)	1563 (1309.48 kb)	leading	0.031
	1564(1317.8855 kb)	2588(2814.602 kb)	lagging	-0.002

More A than T on the leading strand for replication.
More G than C on the leading strand for replication.

310 Staphylococcus aureus NCTC 8325

Bacteria; Firmicutes; Bacillales; Staphylococcus.
Accession number: NC_007795; **Genome size (bp)**: 2821361.
Number of genes: 2892.
Oriloc predictions: Origin 0 kb Terminus 1316 kb
Worning et al., 2006: Origin NA kb Terminus NA kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 2106.86 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1.2 kb
Consensus predictions: Origin 0 kb Terminus 1316 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	977	NA	1330
GC-skew reverse	1679	NA	1325
	2507	NA	2303
	2537	NA	2321
AT-skew forward	153	NA	249
	752	NA	1058
	928	NA	1256
AT-skew reverse	1623	NA	1007

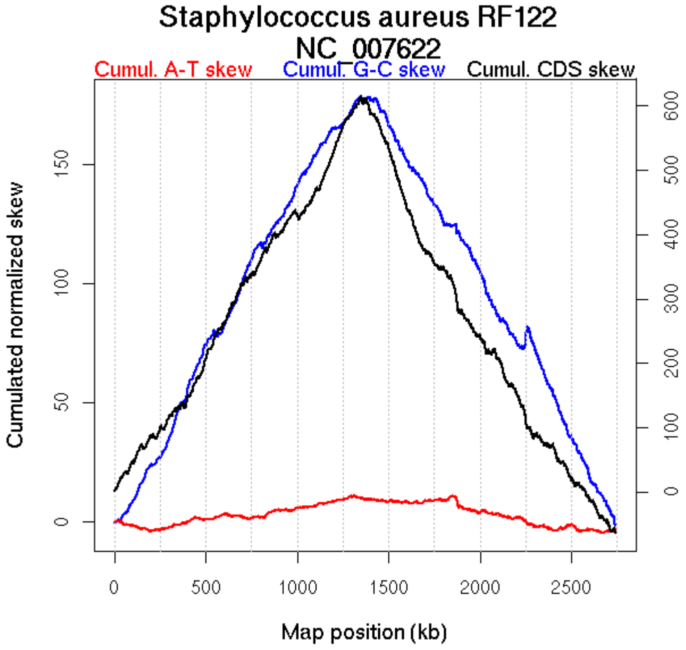
Segments:

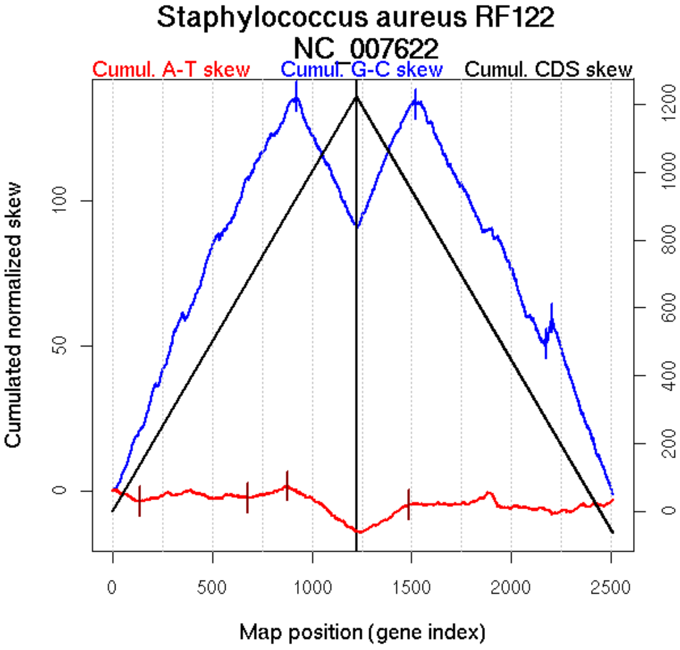
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	977 (1330.262 kb)	leading	0.155
	978(1333.773 kb)	1355 (2821.147 kb)	lagging	-0.116
GC-skew reverse	1356 (0 kb)	1679 (1325.385 kb)	leading	0.133
	1680(1326.8515 kb)	2507 (2302.8545 kb)	lagging	-0.135
	2508(2303.736 kb)	2537 (2320.8695 kb)	lagging	0.325
	2538(2321.6535 kb)	2892 (2821.147 kb)	lagging	-0.202
AT-skew forward	1 (0 kb)	153 (248.709 kb)	leading	-0.029
	154(250.5195 kb)	752 (1057.646 kb)	leading	-0.005
	753(1059.3995 kb)	928 (1255.525 kb)	leading	0.021
	929(1256.505 kb)	1355 (2821.147 kb)	lagging	-0.052
AT-skew reverse	1356 (0 kb)	1623 (1006.745 kb)	leading	0.04
	1624(1014.065 kb)	2892(2821.147 kb)	lagging	-0.012

More A than T on the leading strand for replication.
More G than C on the leading strand for replication.

311 Staphylococcus aureus RF122

Bacteria; Firmicutes; Bacillales; Staphylococcus.
Accession number: NC_007622; **Genome size (bp)**: 2742531.
Number of genes: 2510.
Oriloc predictions: Origin 3 kb Terminus 1344 kb
Worning et al., 2006: Origin 0 kb Terminus 1372 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 2058.578 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1443.84 kb, 1665.62 kb
Consensus predictions: Origin 3 kb Terminus 1344 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	922	NA	1437
GC-skew reverse	1522	NA	1361
	2174	NA	2243
	2203	NA	2260
AT-skew forward	136	NA	241
	680	NA	1041
	875	NA	1307
AT-skew reverse	1488	NA	1117

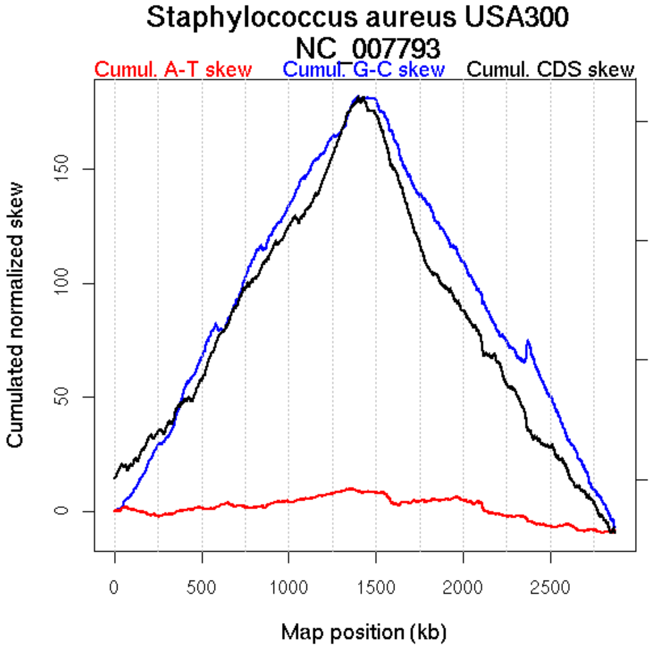
Segments:

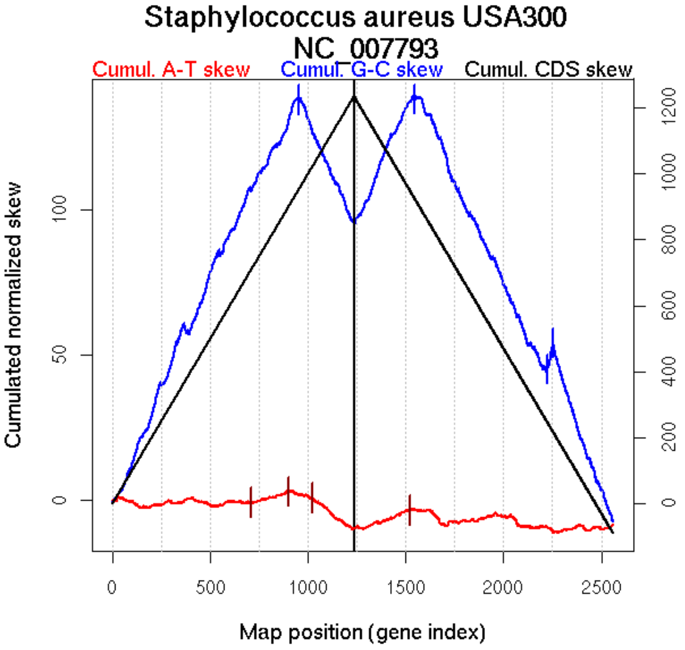
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	922 (1437.0975 kb)	leading	0.152
	923(1439.81 kb)	1223 (2742.317 kb)	lagging	-0.147
GC-skew reverse	1224 (0 kb)	1522 (1360.623 kb)	leading	0.157
	1523(1367.041 kb)	2174 (2243.381 kb)	lagging	-0.129
	2175(2244.2065 kb)	2203 (2259.5935 kb)	lagging	0.331
	2204(2262.5515 kb)	2510 (2742.317 kb)	lagging	-0.196
AT-skew forward	1 (0 kb)	136 (240.9435 kb)	leading	-0.031
	137(242.4645 kb)	680 (1040.8225 kb)	leading	0.001
	681(1041.847 kb)	875 (1306.7465 kb)	leading	0.019
	876(1307.217 kb)	1223 (2742.317 kb)	lagging	-0.047
AT-skew reverse	1224 (0 kb)	1488 (1117.463 kb)	leading	0.039
	1489(1119.3315 kb)	2510(2742.317 kb)	lagging	-0.002

More A than T on the leading strand for replication.
More G than C on the leading strand for replication.

312 Staphylococcus aureus USA300

Bacteria; Firmicutes; Bacillales; Staphylococcus.
Accession number: NC_007793; **Genome size (bp)**: 2872769.
Number of genes: 2560.
Oriloc predictions: Origin 0 kb Terminus 1396 kb
Worning et al., 2006: Origin 1 kb Terminus 1400 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 2159.927 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1.22 kb
Consensus predictions: Origin 0 kb Terminus 1396 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	952	NA	1423
GC-skew reverse	1545	NA	1409
	2223	NA	2356
	2253	NA	2372
AT-skew forward	709	NA	1094
	903	NA	1337
	1020	NA	1963
AT-skew reverse	1519	NA	1209

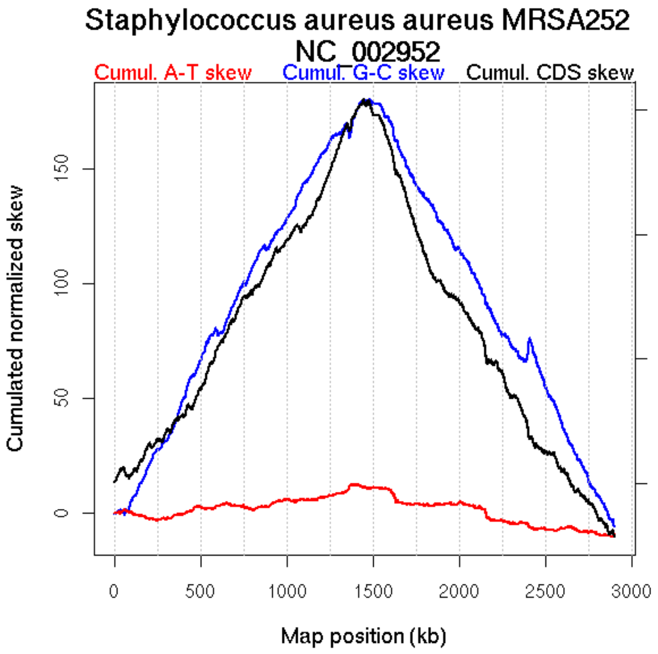
Segments:

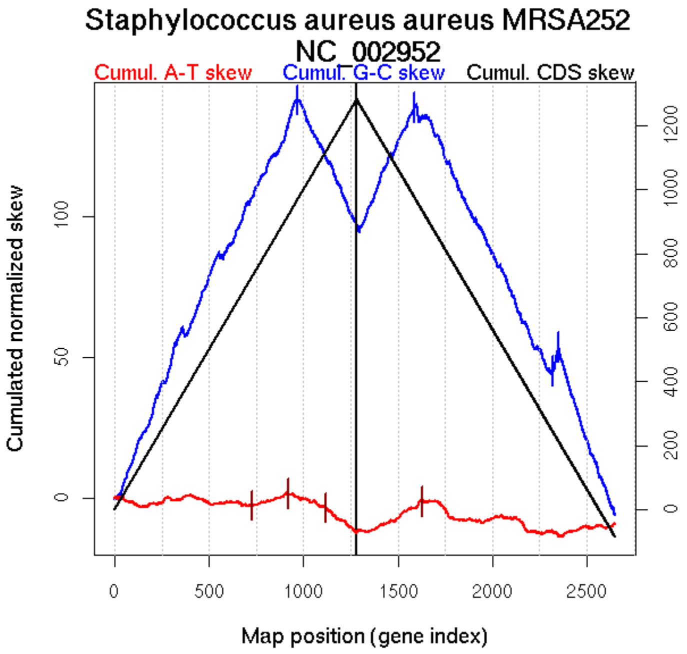
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	952 (1422.711 kb)	leading	0.148
	953(1423.7935 kb)	1235 (2872.582 kb)	lagging	-0.155
GC-skew reverse	1236 (0 kb)	1545 (1409.314 kb)	leading	0.154
	1546(1410.227 kb)	2223 (2356.0685 kb)	lagging	-0.147
	2224(2356.95 kb)	2253 (2372.2585 kb)	lagging	0.322
	2254(2374.0835 kb)	2560 (2872.582 kb)	lagging	-0.193
AT-skew forward	1 (0 kb)	709 (1093.5005 kb)	leading	0
	710(1093.9315 kb)	903 (1337.1935 kb)	leading	0.02
	904(1338.285 kb)	1020 (1962.822 kb)	NA	-0.02
	1021(1968.0245 kb)	1235 (2872.582 kb)	lagging	-0.052
AT-skew reverse	1236 (0 kb)	1519 (1209.0945 kb)	leading	0.024
	1520(1218.097 kb)	2560(2872.582 kb)	lagging	-0.006

More A than T on the leading strand for replication.
More G than C on the leading strand for replication.

313 Staphylococcus aureus aureus MRSA252

Bacteria; Firmicutes; Bacillales; Staphylococcus.
Accession number: NC_002952; **Genome size (bp)**: 2902619.
Number of genes: 2650.
Oriloc predictions: Origin 0 kb Terminus 1443 kb
Worning et al., 2006: Origin 0 kb Terminus 1476 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 2197.065 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1.2 kb, 745.9 kb, 1828.63 kb
Consensus predictions: Origin 0 kb Terminus 1443 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	966	NA	1463
GC-skew reverse	1589	NA	1185
	2319	NA	2390
	2350	NA	2409
AT-skew forward	728	NA	1142
	920	NA	1381
	1116	NA	2249
AT-skew reverse	1631	NA	1450

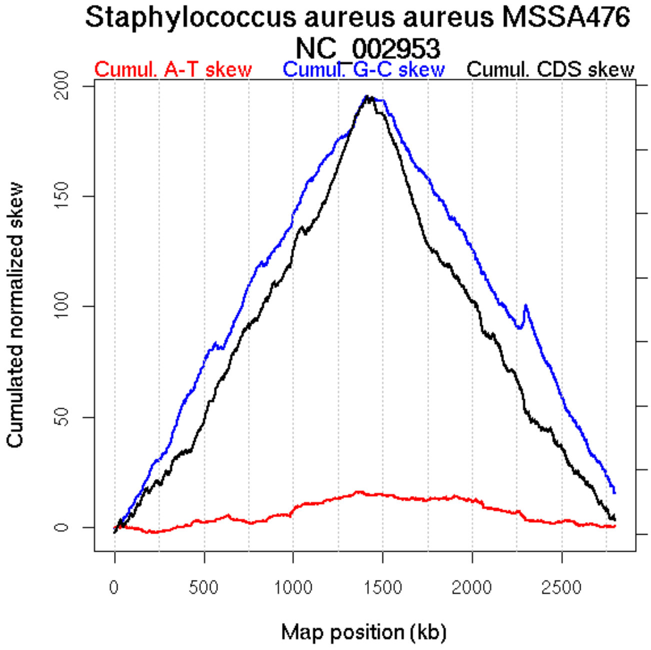
Segments:

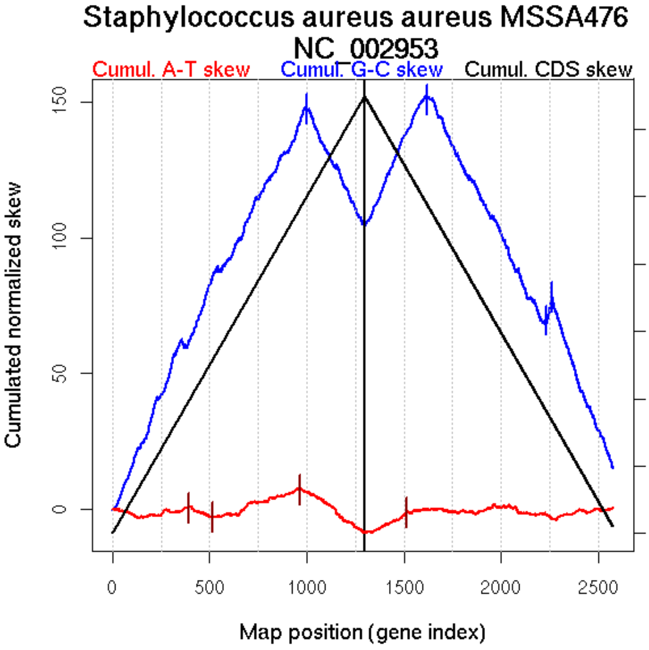
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	966 (1463.173 kb)	leading	0.144
	967(1464.8385 kb)	1282 (2902.405 kb)	lagging	-0.143
GC-skew reverse	1283 (0 kb)	1589 (1185.4935 kb)	leading	0.149
	1590(1186.3235 kb)	2319 (2389.8445 kb)	lagging	-0.138
	2320(2390.6455 kb)	2350 (2408.572 kb)	lagging	0.315
	2351(2410.3195 kb)	2650 (2902.405 kb)	lagging	-0.195
AT-skew forward	1 (0 kb)	728 (1142.223 kb)	leading	-0.001
	729(1143.3255 kb)	920 (1380.821 kb)	leading	0.021
	921(1381.5385 kb)	1116 (2248.7135 kb)	NA	-0.025
	1117(2251.7565 kb)	1282 (2902.405 kb)	lagging	-0.051
AT-skew reverse	1283 (0 kb)	1631 (1449.885 kb)	leading	0.033
	1632(1450.6405 kb)	2650(2902.405 kb)	lagging	-0.009

More A than T on the leading strand for replication - for reverse encoded genes.
More G than C on the leading strand for replication.

314 Staphylococcus aureus aureus MSSA476

Bacteria; Firmicutes; Bacillales; Staphylococcus.
Accession number: NC_002953; **Genome size (bp)**: 2799802.
Number of genes: 2576.
Oriloc predictions: Origin 2 kb Terminus 1409 kb
Worning et al., 2006: Origin 0 kb Terminus 1414 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 2100.163 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1.2 kb, 1736.66 kb
Consensus predictions: Origin 2 kb Terminus 1409 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	999	NA	1433
GC-skew reverse	1618	NA	1423
	2230	NA	2281
	2263	NA	2300
AT-skew forward	390	NA	619
	515	NA	784
	964	NA	1368
AT-skew reverse	1516	NA	919

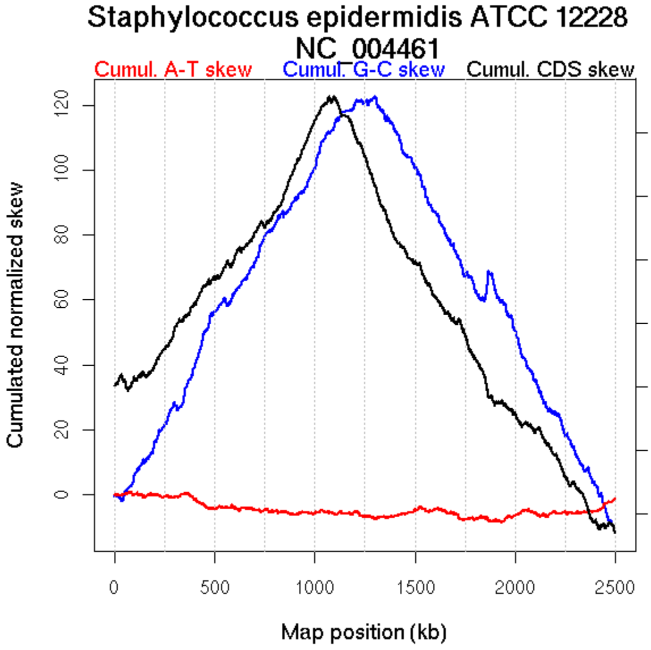
Segments:

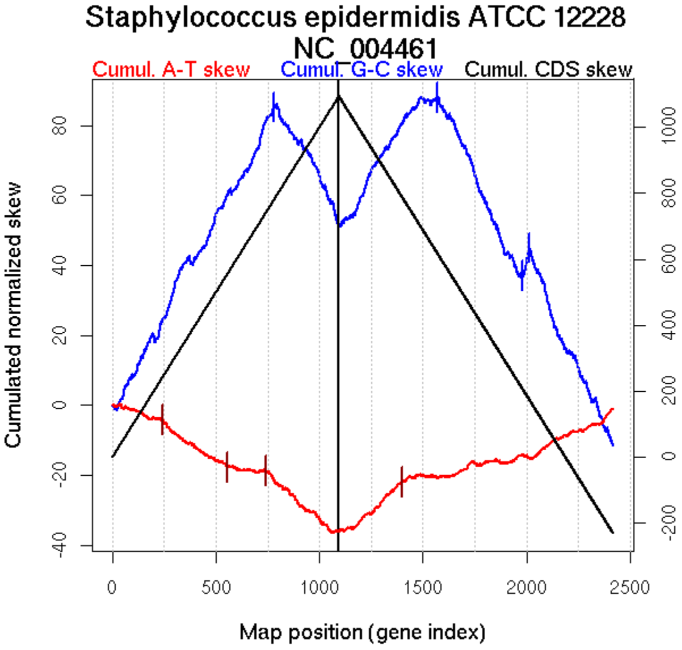
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	999 (1433.187 kb)	leading	0.146
	1000(1433.921 kb)	1298 (2799.588 kb)	lagging	-0.146
GC-skew reverse	1299 (0 kb)	1618 (1423.455 kb)	leading	0.16
	1619(1424.5015 kb)	2230 (2281.4925 kb)	lagging	-0.141
	2231(2282.2365 kb)	2263 (2300.134 kb)	lagging	0.299
	2264(2301.8805 kb)	2576 (2799.588 kb)	lagging	-0.192
AT-skew forward	1 (0 kb)	390 (619.337 kb)	leading	0.002
	391(620.552 kb)	515 (783.922 kb)	leading	-0.031
	516(786.178 kb)	964 (1367.922 kb)	leading	0.025
	965(1368.7975 kb)	1298 (2799.588 kb)	lagging	-0.052
AT-skew reverse	1299 (0 kb)	1516 (918.981 kb)	leading	0.034
	1517(926.4965 kb)	2576(2799.588 kb)	lagging	-0.001

More A than T on the leading strand for replication.
More G than C on the leading strand for replication.

315 Staphylococcus epidermidis ATCC 12228

Bacteria; Firmicutes; Bacillales; Staphylococcus.
Accession number: NC_004461; **Genome size (bp)**: 2499279.
Number of genes: 2419.
Oriloc predictions: Origin 0 kb Terminus 1297 kb
Worning et al., 2006: Origin 0 kb Terminus 1103 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 0.038 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1.04 kb, 107.17 kb, 1179.54 kb, 1390.85 kb, 1553.1 kb
Consensus predictions: Origin 0 kb Terminus 1297 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	780	NA	1207
GC-skew reverse	1567	NA	1297
	1981	NA	1849
	2015	NA	1868
AT-skew forward	241	NA	367
	556	NA	823
	741	NA	1049
AT-skew reverse	1397	NA	1073

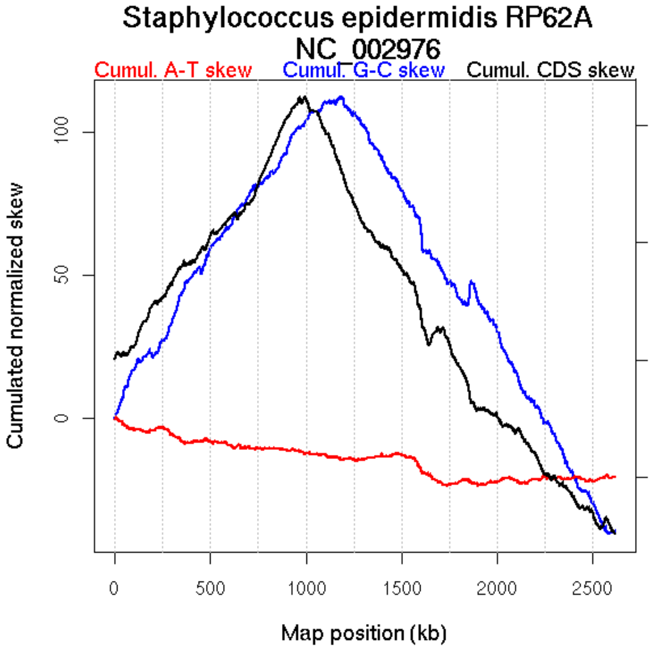
Segments:

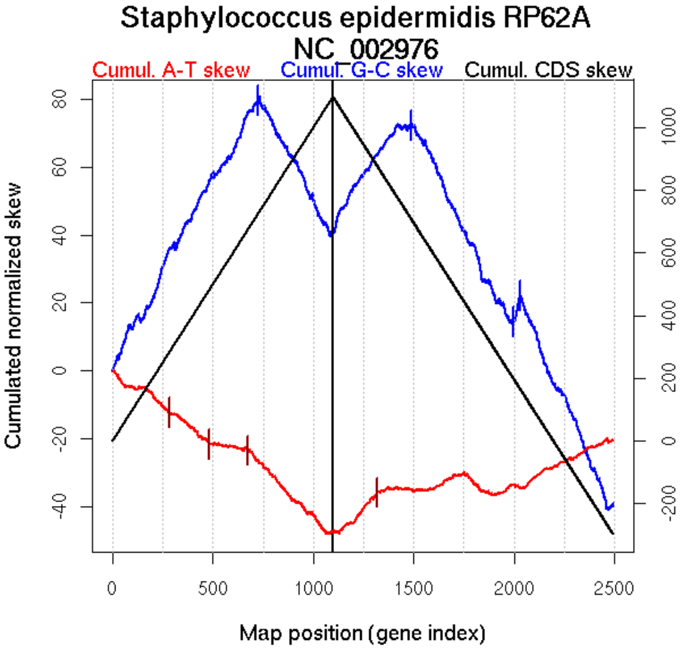
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	780 (1207.469 kb)	leading	0.109
	781(1213.49 kb)	1094 (2498.917 kb)	lagging	-0.102
GC-skew reverse	1095 (0 kb)	1567 (1296.711 kb)	leading	0.089
	1568(1297.688 kb)	1981 (1849.19 kb)	lagging	-0.135
	1982(1849.928 kb)	2015 (1868.31 kb)	lagging	0.253
	2016(1869.9935 kb)	2419 (2498.917 kb)	lagging	-0.133
AT-skew forward	1 (0 kb)	241 (367.2205 kb)	leading	-0.02
	242(368.593 kb)	556 (823.3355 kb)	leading	-0.039
	557(824.5775 kb)	741 (1049.043 kb)	leading	-0.008
	742(1050.0555 kb)	1094 (2498.917 kb)	lagging	-0.052
AT-skew reverse	1095 (0 kb)	1397 (1073.496 kb)	leading	0.05
	1398(1074.37 kb)	2419(2498.917 kb)	NA	0.018

More A than T on the leading strand for replication - for forward encoded genes.
More G than C on the leading strand for replication.

316 Staphylococcus epidermidis RP62A

Bacteria; Firmicutes; Bacillales; Staphylococcus.
Accession number: NC_002976; **Genome size (bp)**: 2616530.
Number of genes: 2493.
Oriloc predictions: Origin 0 kb Terminus 1185 kb
Worning et al., 2006: Origin 0 kb Terminus 995 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 0.125 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1285.49 kb, 2615.65 kb
Consensus predictions: Origin 0 kb Terminus 1185 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	727	NA	1243
GC-skew reverse	1488	NA	1176
	1997	NA	1844
	2032	NA	1864
AT-skew forward	286	NA	413
	483	NA	710
	676	NA	956
AT-skew reverse	1320	NA	839

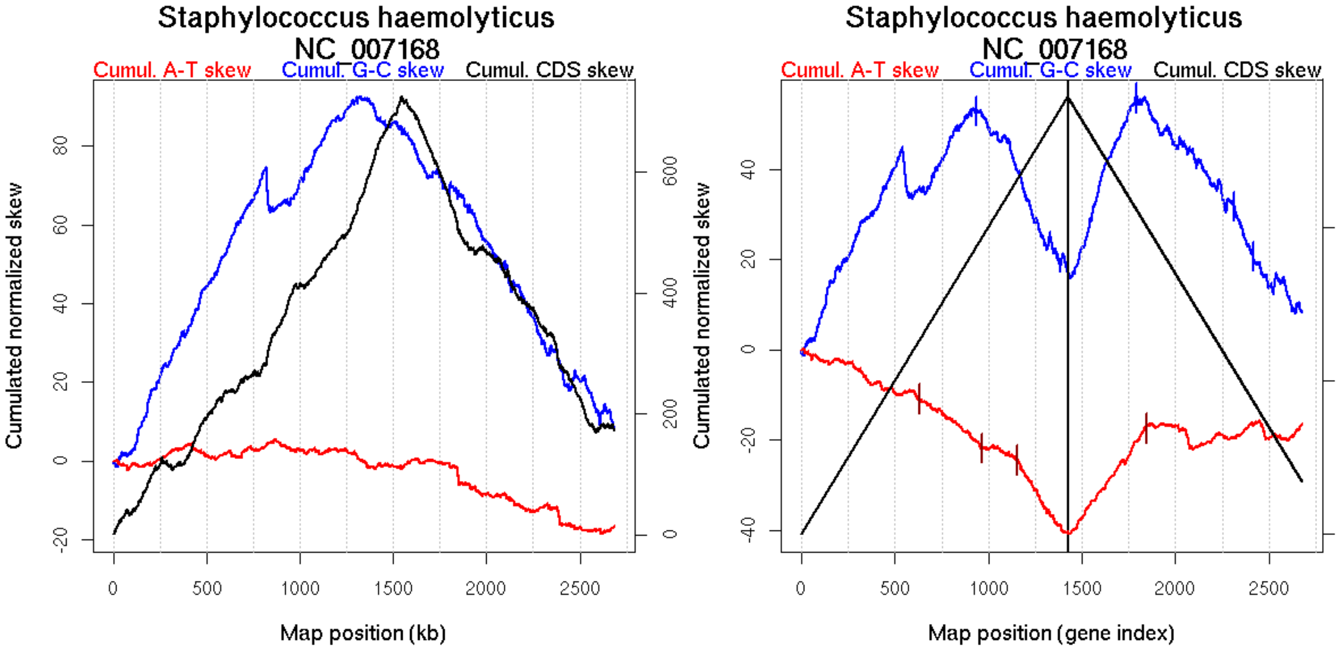
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	727 (1243.462 kb)	leading	0.108
	728(1252.361 kb)	1098 (2616.331 kb)	lagging	-0.112
GC-skew reverse	1099 (0 kb)	1488 (1176.3275 kb)	leading	0.082
	1489(1177.4465 kb)	1997 (1844.217 kb)	lagging	-0.123
	1998(1844.955 kb)	2032 (1863.56 kb)	lagging	0.257
	2033(1865.0235 kb)	2493 (2616.331 kb)	lagging	-0.136
AT-skew forward	1 (0 kb)	286 (412.8055 kb)	leading	-0.036
	287(416.424 kb)	483 (710.2325 kb)	leading	-0.048
	484(711.5505 kb)	676 (956.053 kb)	leading	-0.009
	677(957.0515 kb)	1098 (2616.331 kb)	lagging	-0.061
AT-skew reverse	1099 (0 kb)	1320 (838.5435 kb)	leading	0.057
	1321(876.3645 kb)	2493(2616.331 kb)	NA	0.011

More A than T on the leading strand for replication - for forward encoded genes.
More G than C on the leading strand for replication.

317 Staphylococcus haemolyticus

Bacteria; Firmicutes; Bacillales; Staphylococcus.
Accession number: NC_007168; **Genome size (bp)**: 2685015.
Number of genes: 2676.
Oriloc predictions: Origin 24 kb Terminus 1323 kb
Worning et al., 2006: Origin 2586 kb Terminus 1571 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 29.095 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1.19 kb, 1276.36 kb, 2329.02 kb
Consensus predictions: Origin 24 kb Terminus 1323 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	934	NA	1341
GC-skew reverse	1789	NA	1294
	2314	NA	2202
	2414	NA	2341
AT-skew forward	629	NA	909
	963	NA	1368
	1151	NA	1852
AT-skew reverse	1844	NA	1587

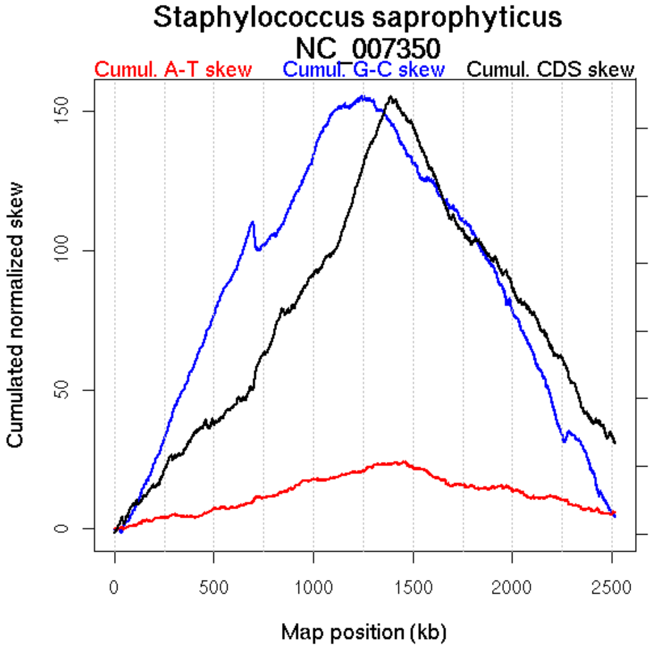
Segments:

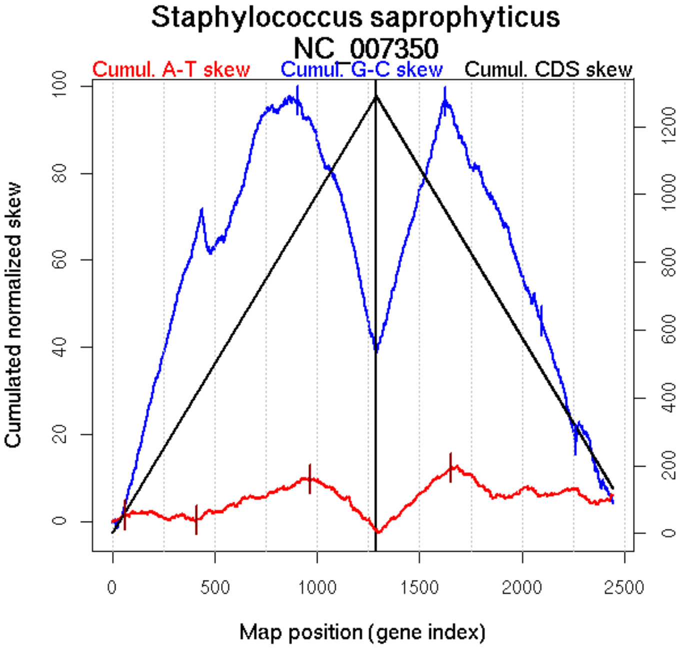
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	934 (1341.354 kb)	leading	0.052
	935(1341.8755 kb)	1424 (2684.844 kb)	lagging	-0.081
GC-skew reverse	1425 (0 kb)	1789 (1293.8315 kb)	leading	0.12
	1790(1301.414 kb)	2314 (2202.295 kb)	lagging	-0.046
	2315(2203.46 kb)	2414 (2341.317 kb)	lagging	-0.107
	2415(2341.6155 kb)	2676 (2684.844 kb)	lagging	-0.042
AT-skew forward	1 (0 kb)	629 (908.541 kb)	leading	-0.018
	630(910.122 kb)	963 (1368.3975 kb)	leading	-0.031
	964(1369.4415 kb)	1151 (1852.2305 kb)	lagging	-0.014
	1152(1853.2965 kb)	1424 (2684.844 kb)	lagging	-0.063
AT-skew reverse	1425 (0 kb)	1844 (1587.1575 kb)	leading	0.057
	1845(1589.6275 kb)	2676(2684.844 kb)	lagging	-0.001

More A than T on the leading strand for replication.
More G than C on the leading strand for replication.

318 Staphylococcus saprophyticus

Bacteria; Firmicutes; Bacillales; Staphylococcus.
Accession number: NC_007350; **Genome size (bp)**: 2516575.
Number of genes: 2445.
Oriloc predictions: Origin 33 kb Terminus 1279 kb
Worning et al., 2006: Origin 0 kb Terminus 1389 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 0.419 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1.19 kb, 1127.1 kb, 1336.22 kb, 1705.65 kb
Consensus predictions: Origin 33 kb Terminus 1279 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	902	NA	1277
GC-skew reverse	1625	NA	1296
	2094	NA	2023
	2262	NA	2259
AT-skew forward	62	NA	100
	412	NA	662
	967	NA	1358
AT-skew reverse	1653	NA	1416

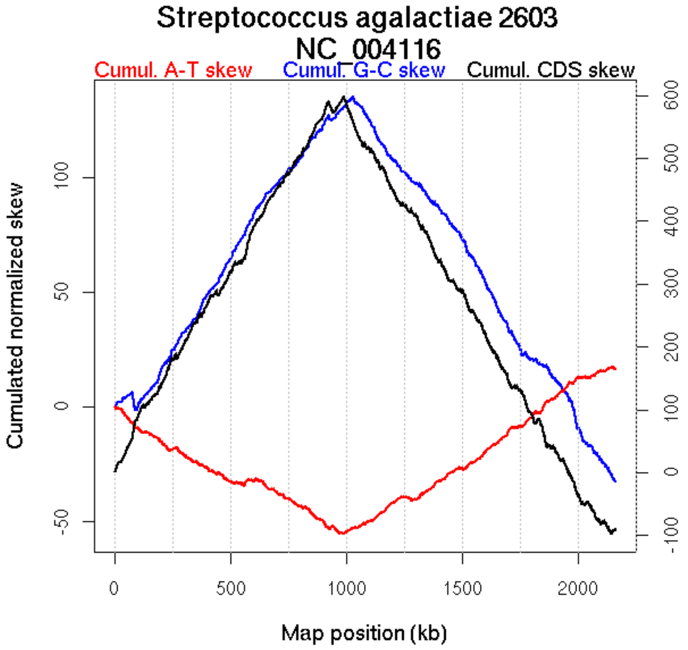
Segments:

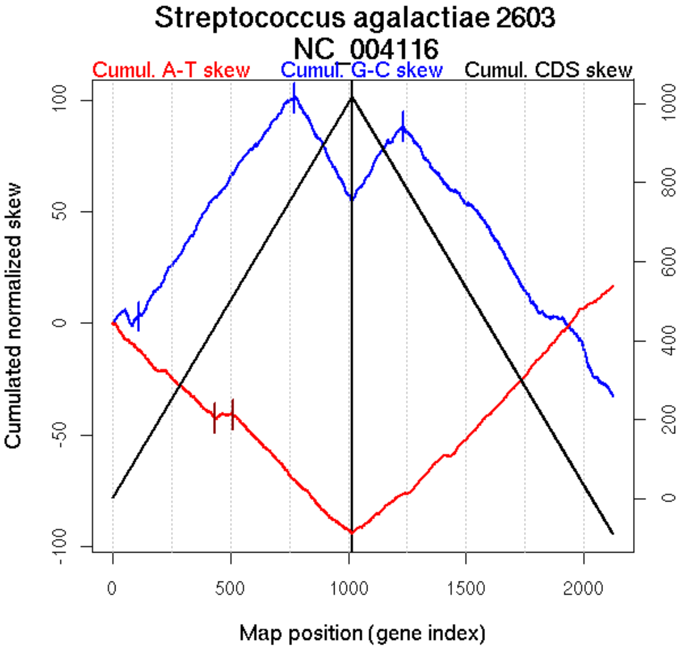
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	902 (1277.121 kb)	leading	0.114
	903(1279.071 kb)	1289 (2516.352 kb)	lagging	-0.149
GC-skew reverse	1290 (0 kb)	1625 (1295.5225 kb)	leading	0.173
	1626(1297.8165 kb)	2094 (2023.1695 kb)	lagging	-0.106
	2095(2024.3765 kb)	2262 (2259.4425 kb)	lagging	-0.16
	2263(2260.183 kb)	2445 (2516.352 kb)	lagging	-0.11
AT-skew forward	1 (0 kb)	62 (99.839 kb)	NA	0.029
	63(100.5815 kb)	412 (662.47 kb)	leading	-0.004
	413(663.082 kb)	967 (1357.682 kb)	leading	0.016
	968(1358.22 kb)	1289 (2516.352 kb)	lagging	-0.037
AT-skew reverse	1290 (0 kb)	1653 (1416.098 kb)	leading	0.042
	1654(1417.2505 kb)	2445(2516.352 kb)	lagging	-0.007

More A than T on the leading strand for replication.
More G than C on the leading strand for replication.

319 Streptococcus agalactiae 2603

Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.
Accession number: NC_004116; **Genome size (bp)**: 2160267.
Number of genes: 2124.
Oriloc predictions: Origin 0 kb Terminus 987 kb
Worning et al., 2006: Origin 2143 kb Terminus 989 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1327.93 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.78 kb, 236.27 kb
Consensus predictions: Origin 0 kb Terminus 987 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	111	0	127
	772	0	982
GC-skew reverse	1233	0	1028
AT-skew forward	433	0.00667	553
	510	0.00667	621

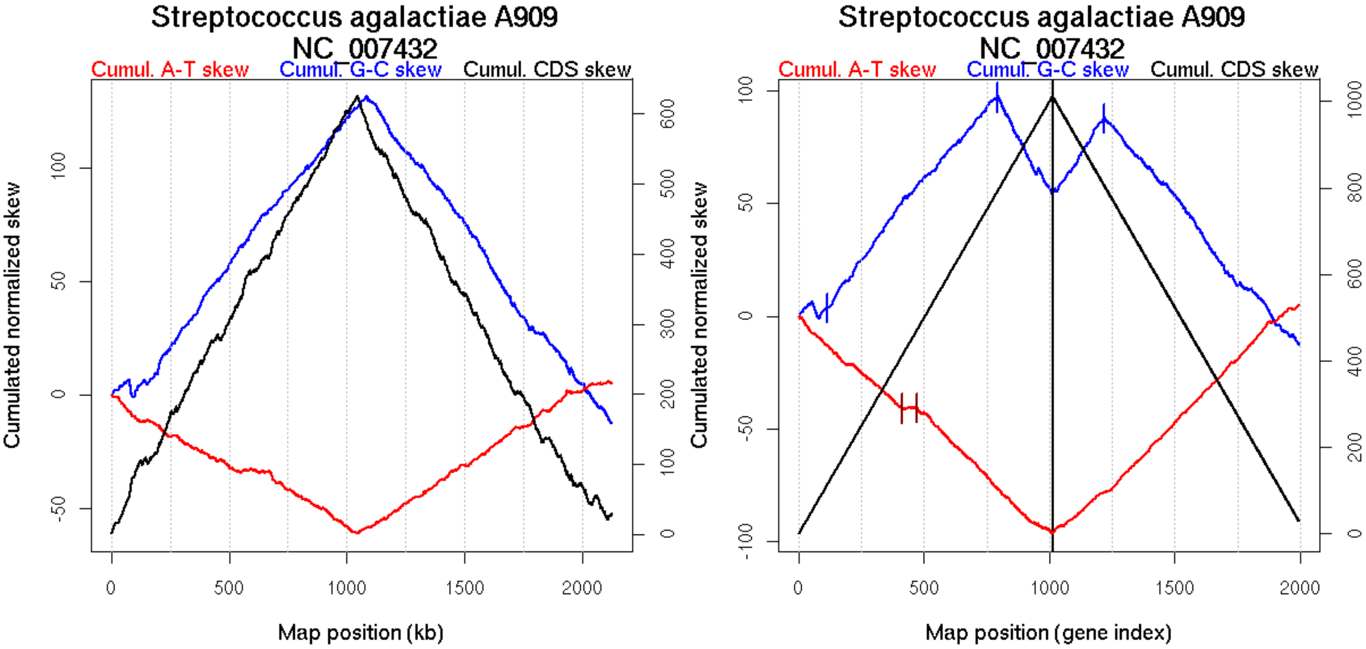
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	111 (127.465 kb)	leading	-0.013
	112(131.5245 kb)	772 (981.8665 kb)	leading	0.152
	773(983.8775 kb)	1017 (2160.167 kb)	lagging	-0.195
GC-skew reverse	1018 (0 kb)	1233 (1028.019 kb)	NA	0.158
	1234(1029.4775 kb)	2124 (2160.167 kb)	lagging	-0.134
AT-skew forward	1 (0 kb)	433 (552.905 kb)	leading	-0.094
	434(554.798 kb)	510 (621.314 kb)	leading	0.023
	511(621.851 kb)	1017 (2160.167 kb)	NA	-0.109

More G than C on the leading strand for replication - for forward encoded genes.

320 Streptococcus agalactiae A909

Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.
Accession number: NC_007432; **Genome size (bp)**: 2127839.
Number of genes: 1995.
Oriloc predictions: Origin 0 kb Terminus 1046 kb
Worning et al., 2006: Origin 2111 kb Terminus 1048 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 2127.83 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.78 kb, 244.17 kb, 245.71 kb, 1627.69 kb, 1942.93 kb
Consensus predictions: Origin 0 kb Terminus 1046 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	116	NA	140
	791	NA	1039
GC-skew reverse	1217	NA	1082
AT-skew forward	413	NA	539
	471	NA	598

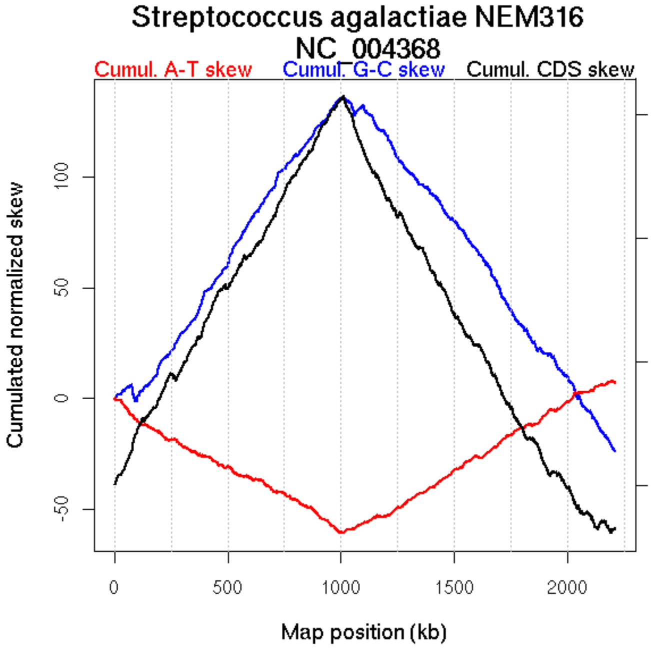
Segments:

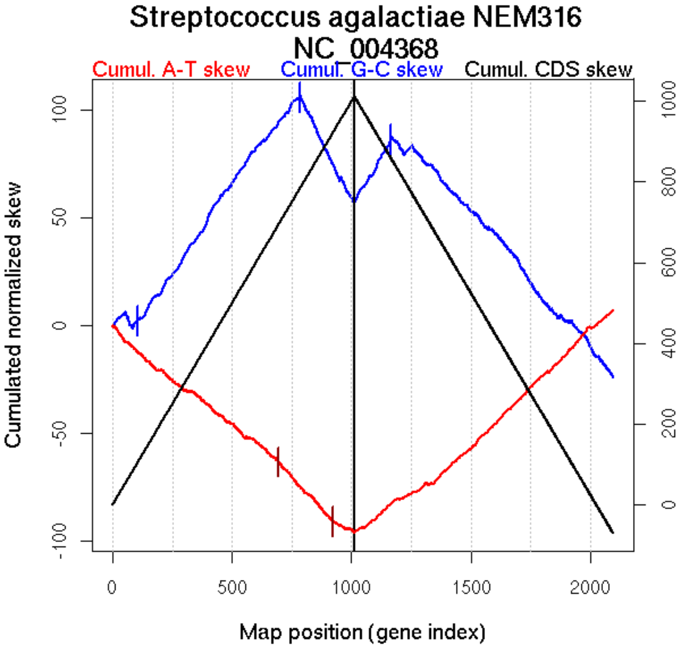
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	116 (140.4875 kb)	leading	-0.004
	117(140.935 kb)	791 (1039.2865 kb)	leading	0.137
	792(1040.0525 kb)	1012 (2127.728 kb)	lagging	-0.198
GC-skew reverse	1013 (0 kb)	1217 (1081.57 kb)	NA	0.171
	1218(1082.976 kb)	1995 (2127.728 kb)	lagging	-0.133
AT-skew forward	1 (0 kb)	413 (538.901 kb)	leading	-0.094
	414(539.823 kb)	471 (597.759 kb)	leading	0.013
	472(600.2635 kb)	1012 (2127.728 kb)	NA	-0.109

More G than C on the leading strand for replication - for forward encoded genes.

321 Streptococcus agalactiae NEM316

Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.
Accession number: NC_004368; **Genome size (bp)**: 2211485.
Number of genes: 2094.
Oriloc predictions: Origin 0 kb Terminus 1010 kb
Worning et al., 2006: Origin NA kb Terminus NA kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1440.072 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.86 kb
Consensus predictions: Origin 0 kb Terminus 1010 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	103	NA	116
	783	NA	1005
GC-skew reverse	1164	NA	985
AT-skew forward	696	NA	884
	924	NA	1931

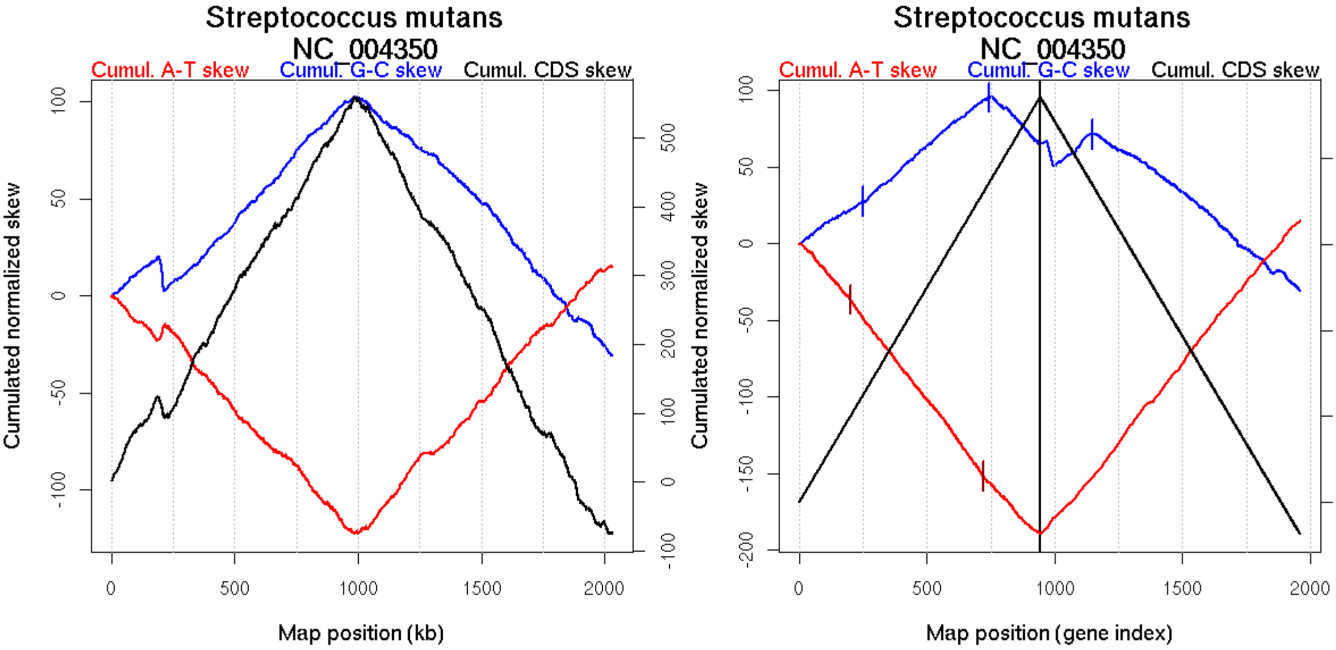
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	103 (115.814 kb)	leading	-0.018
	104(117.609 kb)	783 (1004.6445 kb)	leading	0.159
	784(1006.6555 kb)	1012 (2211.459 kb)	lagging	-0.222
GC-skew reverse	1013 (0 kb)	1164 (985.1335 kb)	leading	0.182
	1165(992.642 kb)	2094 (2211.459 kb)	lagging	-0.123
AT-skew forward	1 (0 kb)	696 (884.1345 kb)	leading	-0.087
	697(884.9125 kb)	924 (1930.7765 kb)	NA	-0.119
	925(1931.806 kb)	1012 (2211.459 kb)	lagging	-0.05

More G than C on the leading strand for replication.

322 Streptococcus mutans

Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.
Accession number: NC_004350; **Genome size (bp)**: 2030921.
Number of genes: 1960.
Oriloc predictions: Origin 0 kb Terminus 1001 kb
Worning et al., 2006: Origin 2022 kb Terminus 1000 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 0.092 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.87 kb
Consensus predictions: Origin 0 kb Terminus 1001 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	251	NA	335
	745	NA	980
GC-skew reverse	1145	NA	1002
AT-skew forward	199	NA	283
	719	NA	944

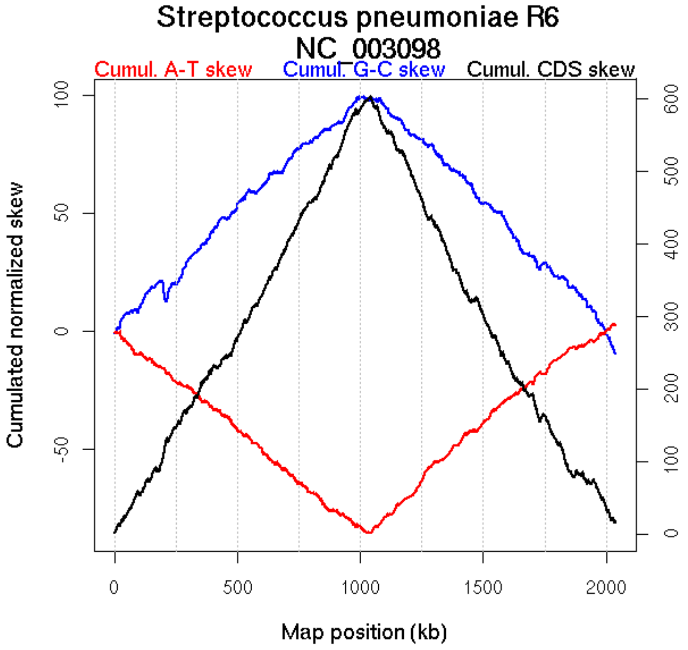
Segments:

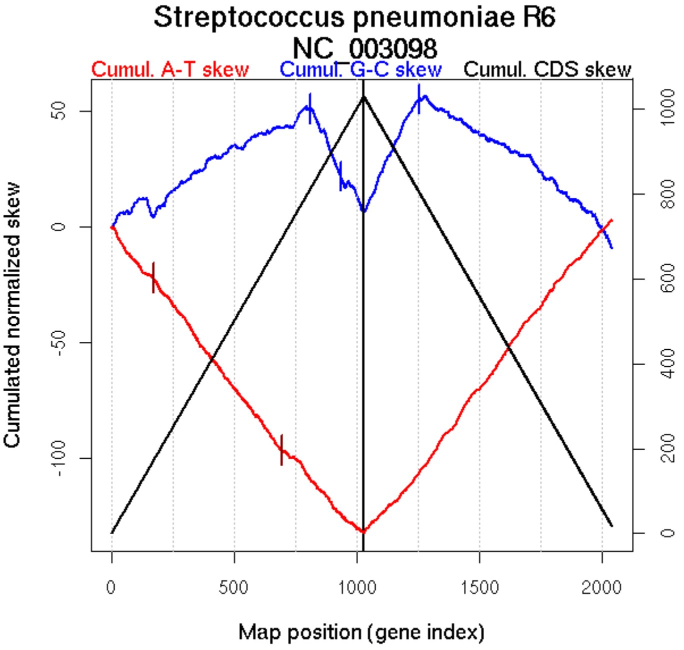
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	251 (334.5155 kb)	leading	0.108
	252(335.079 kb)	745 (979.7765 kb)	leading	0.142
	746(980.4345 kb)	943 (2030.91 kb)	lagging	-0.164
GC-skew reverse	944 (0 kb)	1145 (1001.8985 kb)	leading	0.048
	1146(1002.5775 kb)	1960 (2030.91 kb)	lagging	-0.13
AT-skew forward	1 (0 kb)	199 (282.9585 kb)	leading	-0.19
	200(284.021 kb)	719 (943.522 kb)	leading	-0.216
	720(944.3475 kb)	943 (2030.91 kb)	NA	-0.177

More G than C on the leading strand for replication.

323 Streptococcus pneumoniae R6

Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.
Accession number: NC_003098; **Genome size (bp)**: 2038615.
Number of genes: 2043.
Oriloc predictions: Origin 0 kb Terminus 1040 kb
Worning et al., 2006: Origin 2037 kb Terminus 1041 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 2038.503 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.68 kb, 1537.67 kb
Consensus predictions: Origin 0 kb Terminus 1040 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	809	NA	1008
	936	NA	1635
GC-skew reverse	1255	NA	1046
AT-skew forward	170	NA	209
	694	NA	873

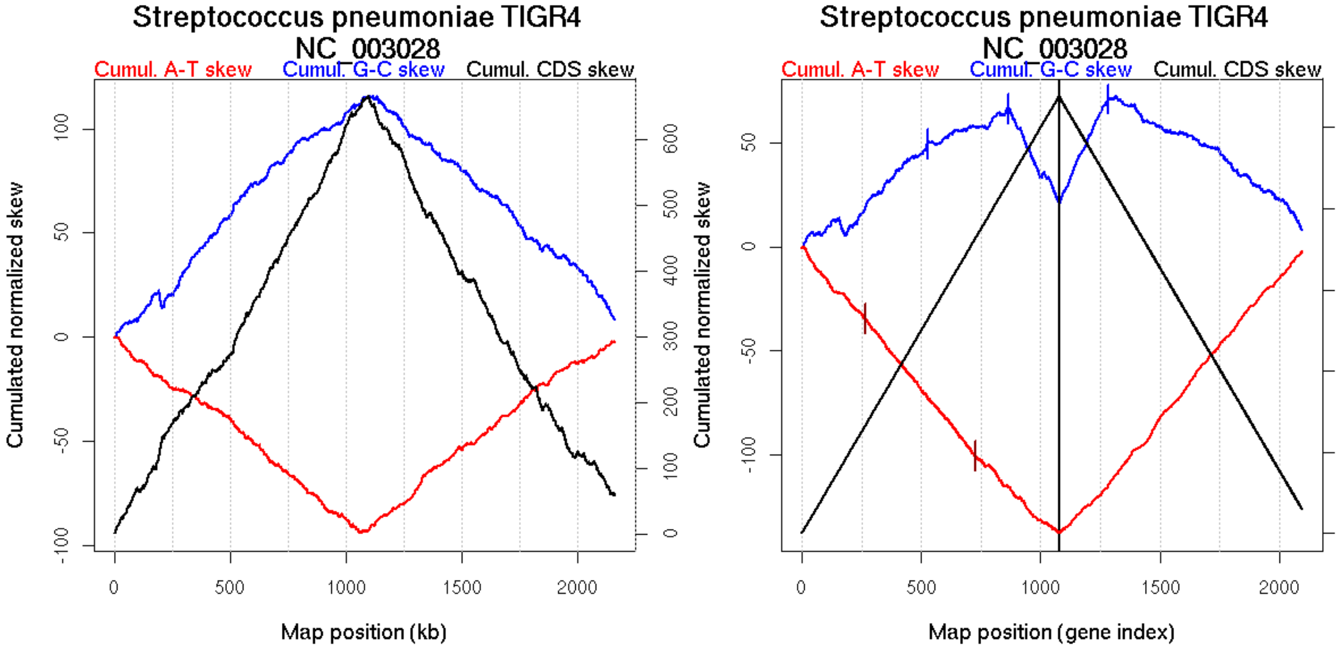
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	809 (1008.2115 kb)	leading	0.062
	810(1010.034 kb)	936 (1634.8795 kb)	lagging	-0.241
	937(1635.8995 kb)	1030 (2038.4 kb)	lagging	-0.144
GC-skew reverse	1031 (0 kb)	1255 (1046.2735 kb)	leading	0.226
	1256(1047.535 kb)	2043 (2038.4 kb)	lagging	-0.075
AT-skew forward	1 (0 kb)	170 (208.5745 kb)	leading	-0.135
	171(208.988 kb)	694 (872.628 kb)	leading	-0.141
	695(874.4405 kb)	1030 (2038.4 kb)	NA	-0.117

More G than C on the leading strand for replication.

324 Streptococcus pneumoniae TIGR4

Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.
Accession number: NC_003028; **Genome size (bp)**: 2160837.
Number of genes: 2094.
Oriloc predictions: Origin 0 kb Terminus 1080 kb
Worning et al., 2006: Origin 2159 kb Terminus 1095 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 2061.437 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.88 kb
Consensus predictions: Origin 0 kb Terminus 1080 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	528	NA	671
	866	NA	1090
GC-skew reverse	1284	NA	1098
AT-skew forward	266	NA	327
	726	NA	917

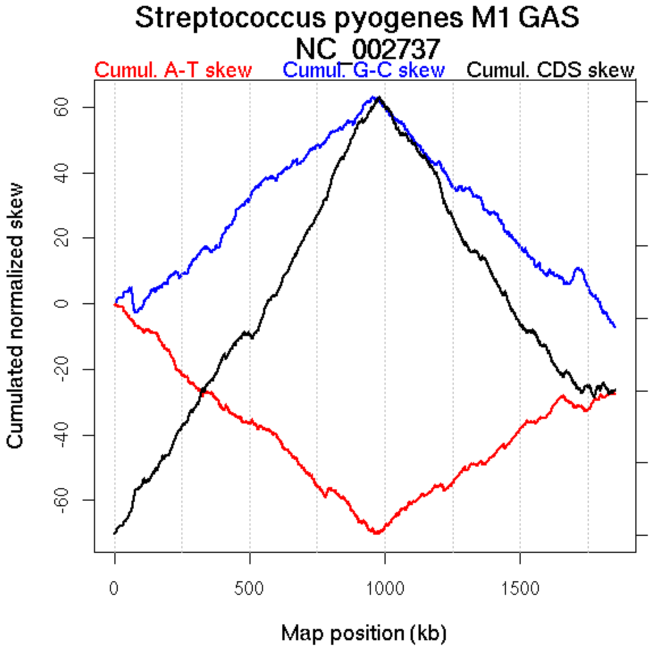
Segments:

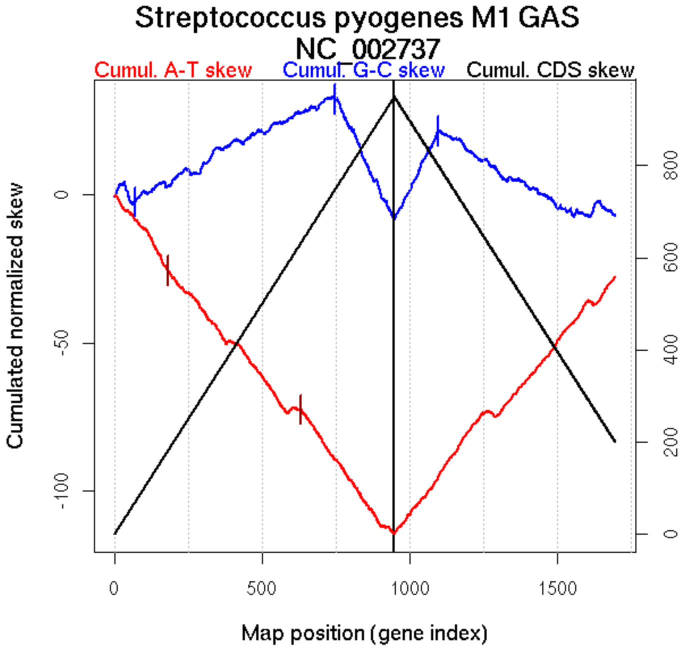
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	528 (670.942 kb)	leading	0.092
	529(671.7215 kb)	866 (1090.114 kb)	leading	0.046
	867(1091.182 kb)	1077 (2160.818 kb)	lagging	-0.207
GC-skew reverse	1078 (0 kb)	1284 (1097.6915 kb)	leading	0.248
	1285(1099.171 kb)	2094 (2160.818 kb)	lagging	-0.072
AT-skew forward	1 (0 kb)	266 (326.938 kb)	leading	-0.126
	267(328.053 kb)	726 (916.658 kb)	leading	-0.141
	727(917.5065 kb)	1077 (2160.818 kb)	NA	-0.112

More G than C on the leading strand for replication.

325 Streptococcus pyogenes M1 GAS

Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.
Accession number: NC_002737; **Genome size (bp)**: 1852441.
Number of genes: 1697.
Oriloc predictions: Origin 0 kb Terminus 967 kb
Worning et al., 2006: Origin NA kb Terminus NA kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1757.8 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.91 kb
Consensus predictions: Origin 0 kb Terminus 967 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	69	NA	97
	749	NA	966
GC-skew reverse	1098	NA	961
AT-skew forward	182	NA	252
	633	NA	817

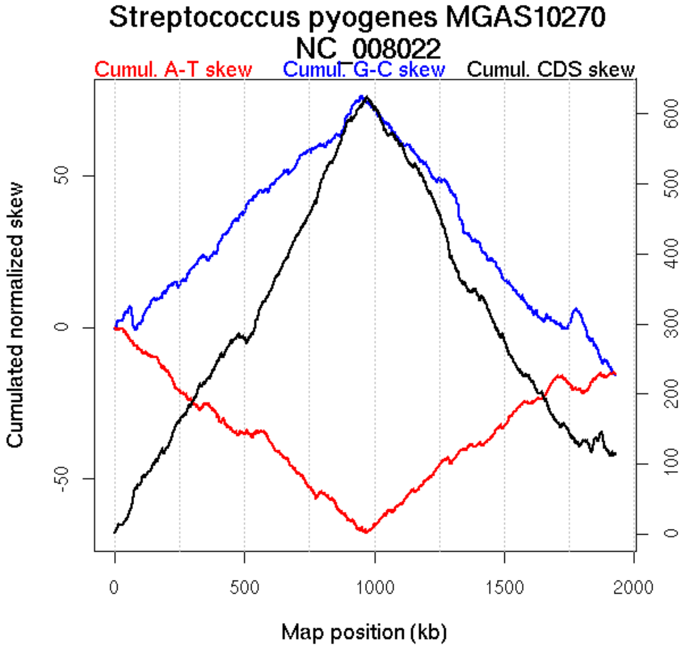
Segments:

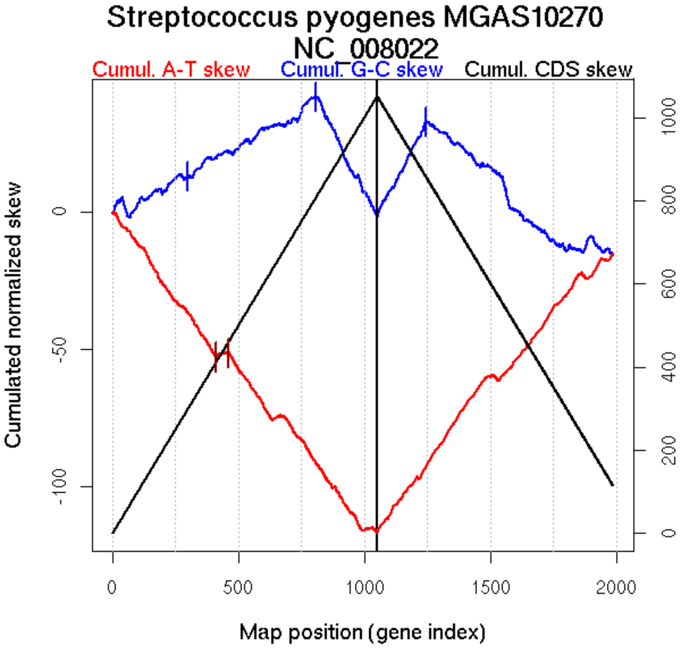
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	69 (97.196 kb)	leading	-0.079
	70(100.9585 kb)	749 (966.2665 kb)	leading	0.052
	750(966.6215 kb)	949 (1852.437 kb)	lagging	-0.211
GC-skew reverse	950 (0 kb)	1098 (961.137 kb)	leading	0.2
	1099(968.7455 kb)	1697 (1852.437 kb)	lagging	-0.05
AT-skew forward	1 (0 kb)	182 (251.957 kb)	leading	-0.135
	183(252.426 kb)	633 (817.4295 kb)	leading	-0.112
	634(819.0475 kb)	949 (1852.437 kb)	NA	-0.139

More G than C on the leading strand for replication.

326 Streptococcus pyogenes MGAS10270

Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.
Accession number: NC_008022; **Genome size (bp)**: 1928252.
Number of genes: 1987.
Oriloc predictions: Origin 0 kb Terminus 960 kb
Worning et al., 2006: Origin 1924 kb Terminus 972 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1818.736 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.88 kb
Consensus predictions: Origin 0 kb Terminus 960 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	299	NA	374
	805	NA	950
GC-skew reverse	1246	NA	953
AT-skew forward	409	NA	527
	458	NA	566

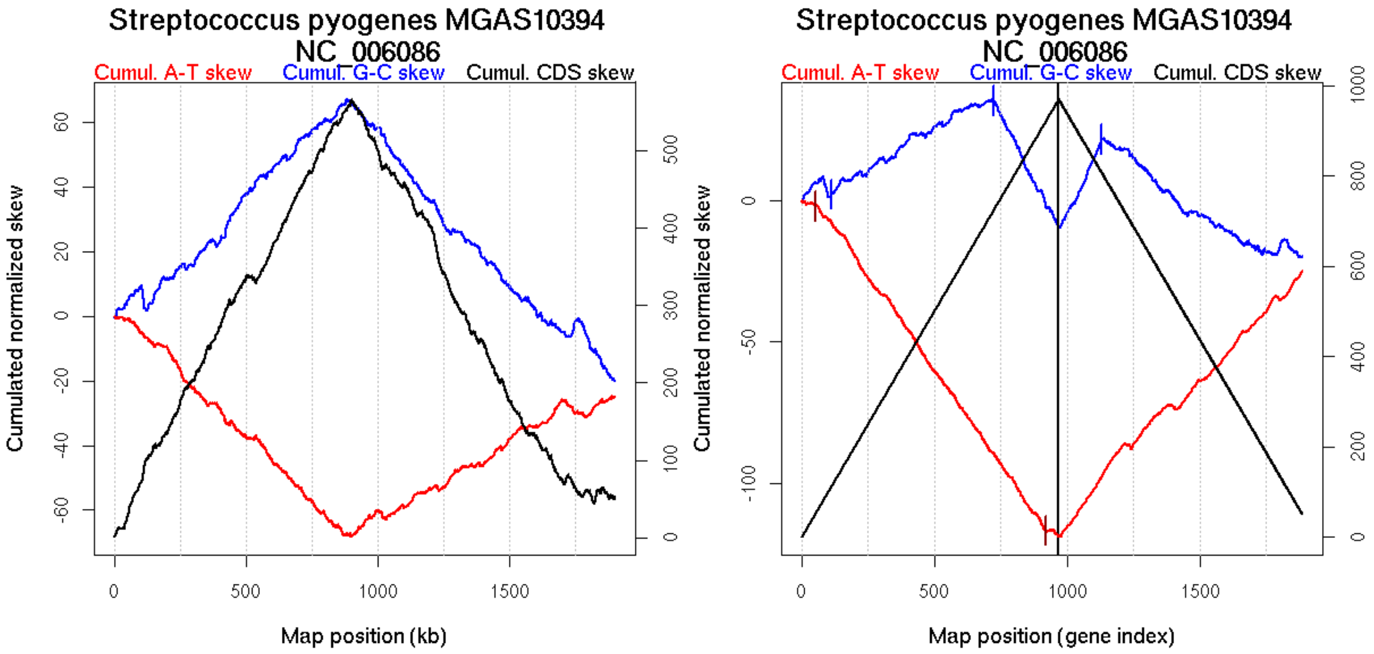
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	299 (374.234 kb)	leading	0.046
	300(375.096 kb)	805 (949.9785 kb)	leading	0.051
	806(952.595 kb)	1051 (1928.218 kb)	lagging	-0.181
GC-skew reverse	1052 (0 kb)	1246 (952.848 kb)	leading	0.171
	1247(957.4895 kb)	1987 (1928.218 kb)	lagging	-0.074
AT-skew forward	1 (0 kb)	409 (526.57 kb)	leading	-0.128
	410(527.544 kb)	458 (565.878 kb)	leading	0.029
	459(567.7765 kb)	1051 (1928.218 kb)	NA	-0.114

More G than C on the leading strand for replication.

327 Streptococcus pyogenes MGAS10394

Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.
Accession number: NC_006086; **Genome size (bp)**: 1899877.
Number of genes: 1886.
Oriloc predictions: Origin 0 kb Terminus 890 kb
Worning et al., 2006: Origin 1898 kb Terminus 891 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1804.414 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.88 kb
Consensus predictions: Origin 0 kb Terminus 890 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	114	NA	129
	723	NA	893
GC-skew reverse	1131	NA	880
AT-skew forward	53	NA	68
	920	NA	1794

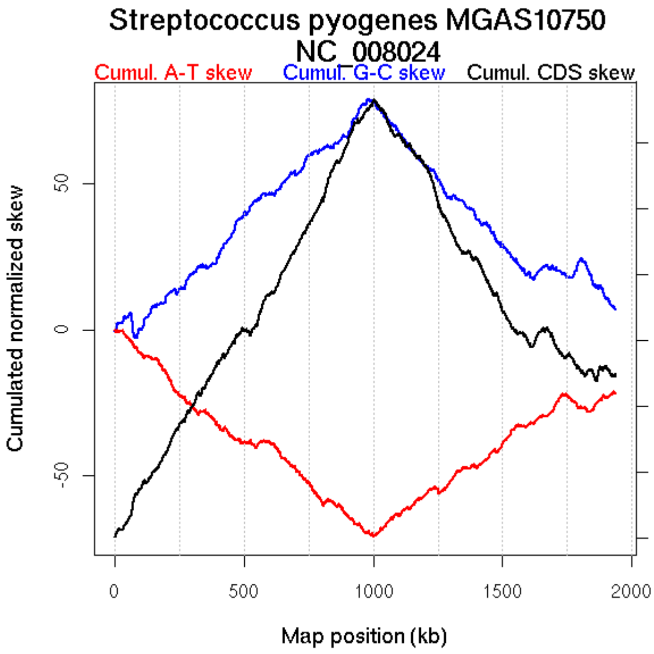
Segments:

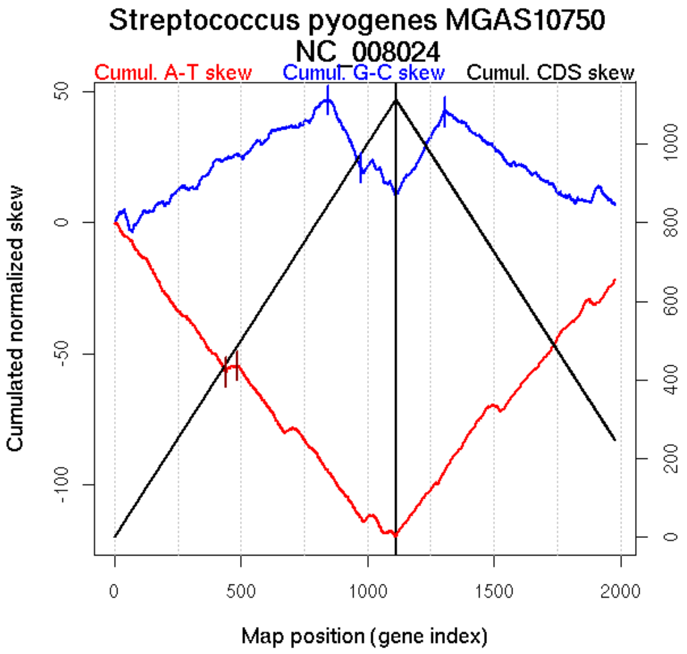
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	114 (128.5735 kb)	leading	0.016
	115(129.0735 kb)	723 (892.5765 kb)	leading	0.056
	724(894.7505 kb)	969 (1899.873 kb)	lagging	-0.184
GC-skew reverse	970 (0 kb)	1131 (880.307 kb)	leading	0.194
	1132(886.109 kb)	1886 (1899.873 kb)	lagging	-0.059
AT-skew forward	1 (0 kb)	53 (68.0715 kb)	leading	-0.02
	54(69.9895 kb)	920 (1793.8815 kb)	NA	-0.134
	921(1798.136 kb)	969 (1899.873 kb)	lagging	-0.036

More G than C on the leading strand for replication.

328 Streptococcus pyogenes MGAS10750

Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.
Accession number: NC_008024; **Genome size (bp)**: 1937111.
Number of genes: 1979.
Oriloc predictions: Origin 0 kb Terminus 991 kb
Worning et al., 2006: Origin 1927 kb Terminus 1006 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1847.203 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.88 kb
Consensus predictions: Origin 0 kb Terminus 991 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	844	NA	985
	974	NA	1577
GC-skew reverse	1306	NA	984
AT-skew forward	442	NA	550
	487	NA	580

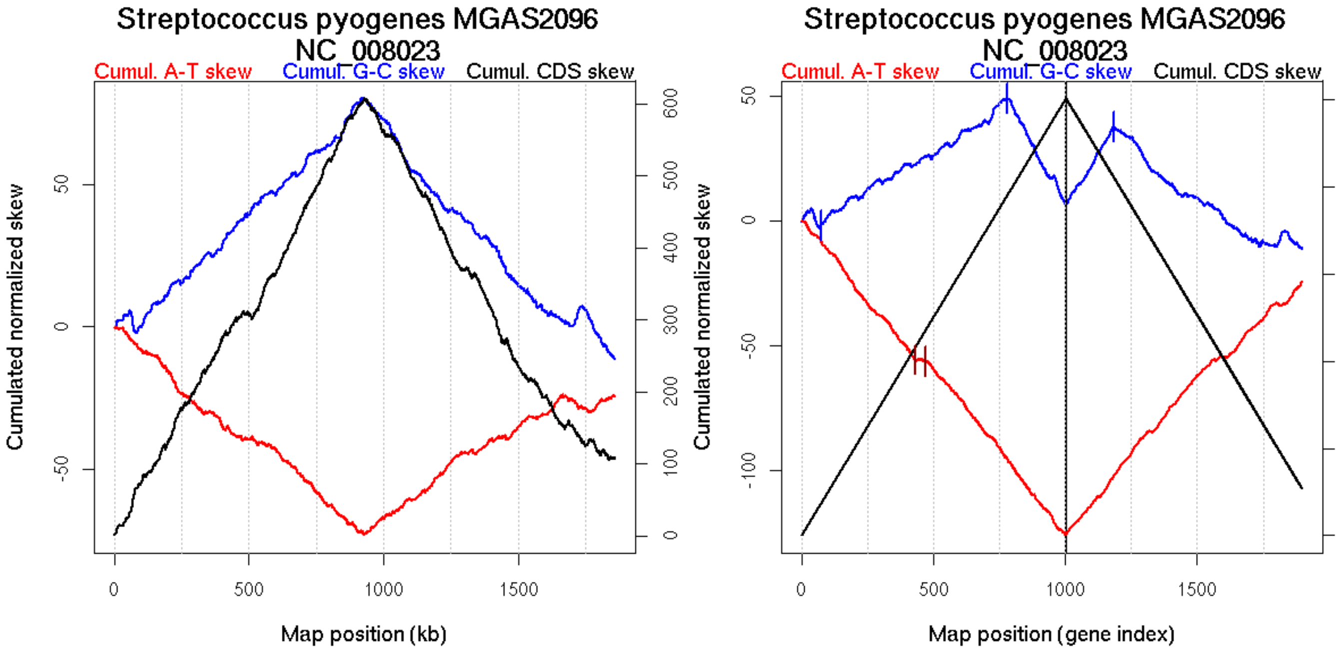
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	844 (984.7625 kb)	leading	0.057
	845(985.816 kb)	974 (1577.242 kb)	lagging	-0.205
	975(1578.5745 kb)	1113 (1937.077 kb)	lagging	-0.075
GC-skew reverse	1114 (0 kb)	1306 (983.995 kb)	leading	0.163
	1307(988.6445 kb)	1979 (1937.077 kb)	lagging	-0.054
AT-skew forward	1 (0 kb)	442 (549.874 kb)	leading	-0.13
	443(550.4995 kb)	487 (579.899 kb)	leading	0.029
	488(582.04 kb)	1113 (1937.077 kb)	NA	-0.107

More G than C on the leading strand for replication.

329 Streptococcus pyogenes MGAS2096

Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.
Accession number: NC_008023; **Genome size (bp)**: 1860355.
Number of genes: 1898.
Oriloc predictions: Origin 0 kb Terminus 927 kb
Worning et al., 2006: Origin 1840 kb Terminus 929 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1780.619 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.88 kb
Consensus predictions: Origin 0 kb Terminus 927 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	73	NA	87
	779	NA	919
GC-skew reverse	1182	NA	922
AT-skew forward	430	NA	527
	470	NA	562

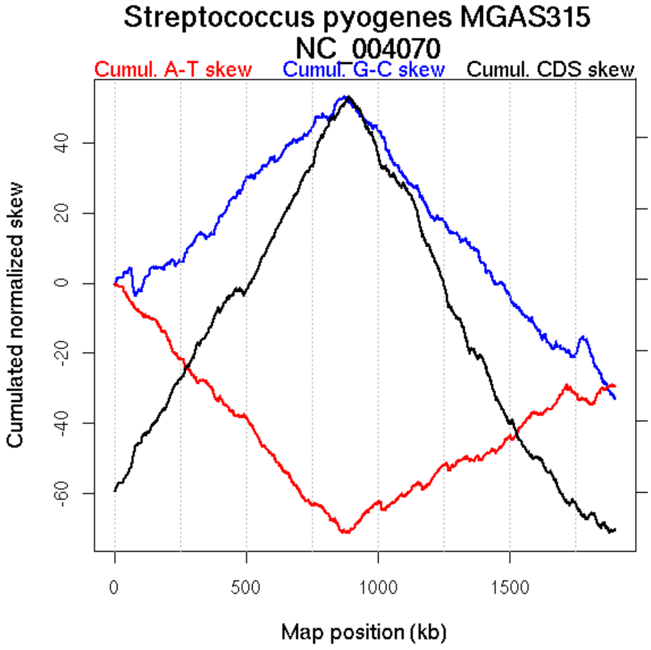
Segments:

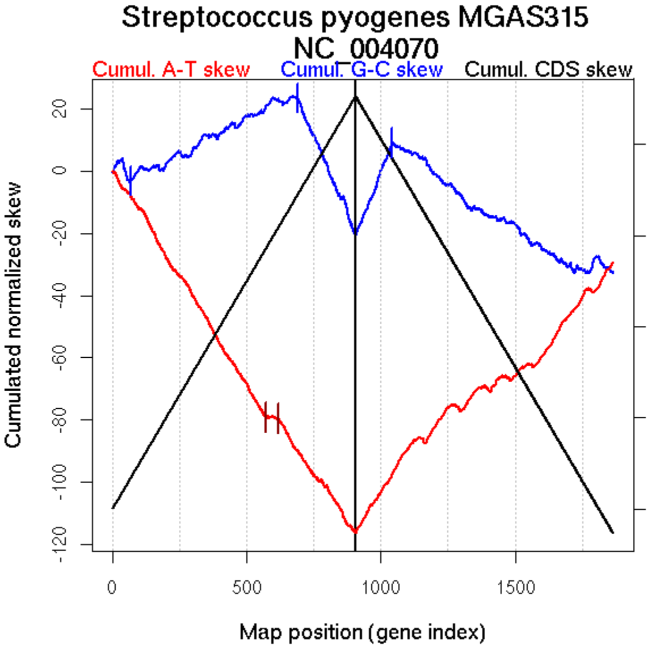
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	73 (87.1985 kb)	leading	-0.064
	74(87.5005 kb)	779 (918.902 kb)	leading	0.065
	780(919.824 kb)	1003 (1860.321 kb)	lagging	-0.192
GC-skew reverse	1004 (0 kb)	1182 (922.39 kb)	leading	0.171
	1183(926.426 kb)	1898 (1860.321 kb)	lagging	-0.069
AT-skew forward	1 (0 kb)	430 (526.785 kb)	leading	-0.13
	431(528.349 kb)	470 (562.443 kb)	leading	-0.002
	471(564.587 kb)	1003 (1860.321 kb)	NA	-0.134

More G than C on the leading strand for replication.

330 Streptococcus pyogenes MGAS315

Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.
Accession number: NC_004070; **Genome size (bp)**: 1900521.
Number of genes: 1865.
Oriloc predictions: Origin 0 kb Terminus 878 kb
Worning et al., 2006: Origin 1890 kb Terminus 893 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1820.566 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.91 kb, 287.11 kb
Consensus predictions: Origin 0 kb Terminus 878 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	67	NA	87
	688	NA	878
GC-skew reverse	1041	NA	869
AT-skew forward	570	NA	748
	618	NA	789

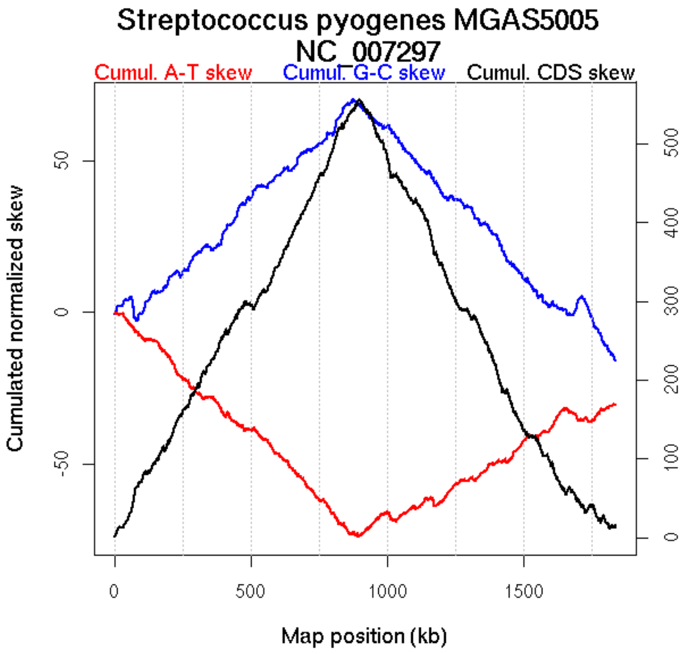
Segments:

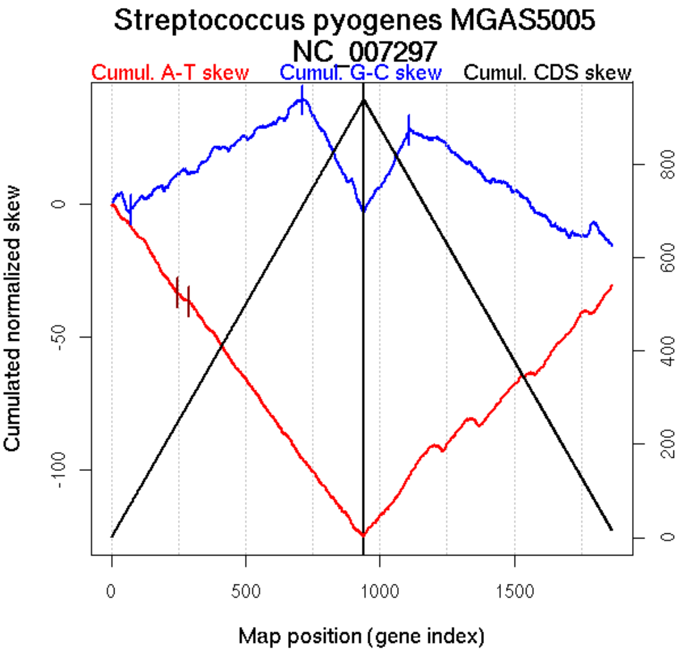
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	67 (87.312 kb)	leading	-0.076
	68(88.4185 kb)	688 (878.4185 kb)	leading	0.045
	689(881.4105 kb)	906 (1900.517 kb)	lagging	-0.198
GC-skew reverse	907 (0 kb)	1041 (869.142 kb)	leading	0.217
	1042(874.9435 kb)	1865 (1900.517 kb)	lagging	-0.054
AT-skew forward	1 (0 kb)	570 (748.3465 kb)	leading	-0.14
	571(750.754 kb)	618 (788.7415 kb)	leading	-0.012
	619(791.234 kb)	906 (1900.517 kb)	NA	-0.124

More G than C on the leading strand for replication.

331 Streptococcus pyogenes MGAS5005

Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.
Accession number: NC_007297; **Genome size (bp)**: 1838554.
Number of genes: 1865.
Oriloc predictions: Origin 0 kb Terminus 885 kb
Worning et al., 2006: Origin 1836 kb Terminus 897 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1757.412 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.88 kb
Consensus predictions: Origin 0 kb Terminus 885 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	71	NA	87
	713	NA	875
GC-skew reverse	1108	NA	871
AT-skew forward	245	NA	311
	287	NA	358

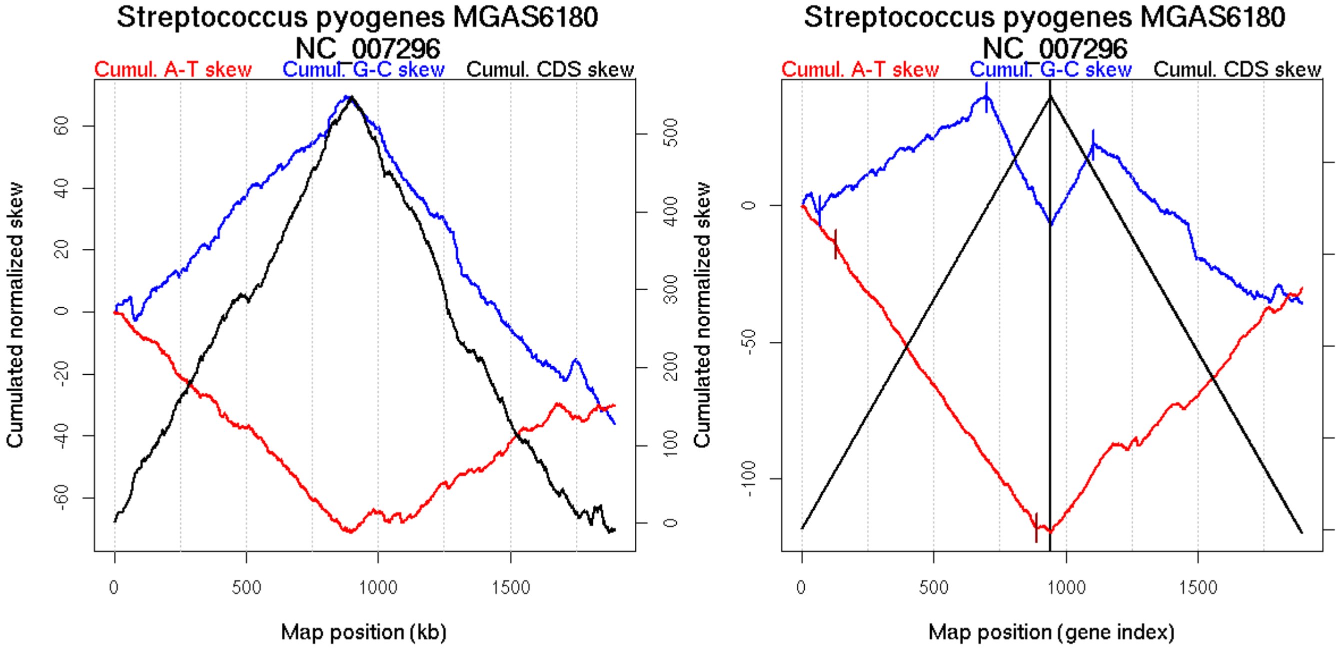
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	71 (87.4445 kb)	leading	-0.069
	72(87.7135 kb)	713 (875.064 kb)	leading	0.06
	714(877.7315 kb)	940 (1838.52 kb)	lagging	-0.188
GC-skew reverse	941 (0 kb)	1108 (870.9885 kb)	leading	0.175
	1109(871.721 kb)	1865 (1838.52 kb)	lagging	-0.062
AT-skew forward	1 (0 kb)	245 (311.29 kb)	leading	-0.139
	246(311.817 kb)	287 (357.509 kb)	leading	-0.074
	288(358.325 kb)	940 (1838.52 kb)	NA	-0.138

More G than C on the leading strand for replication.

332 Streptococcus pyogenes MGAS6180

Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.
Accession number: NC_007296; **Genome size (bp)**: 1897573.
Number of genes: 1894.
Oriloc predictions: Origin 0 kb Terminus 888 kb
Worning et al., 2006: Origin 1877 kb Terminus 904 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1791.627 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.88 kb
Consensus predictions: Origin 0 kb Terminus 888 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	69	NA	87
	700	NA	884
GC-skew reverse	1106	NA	885
AT-skew forward	129	NA	170
	888	NA	1785

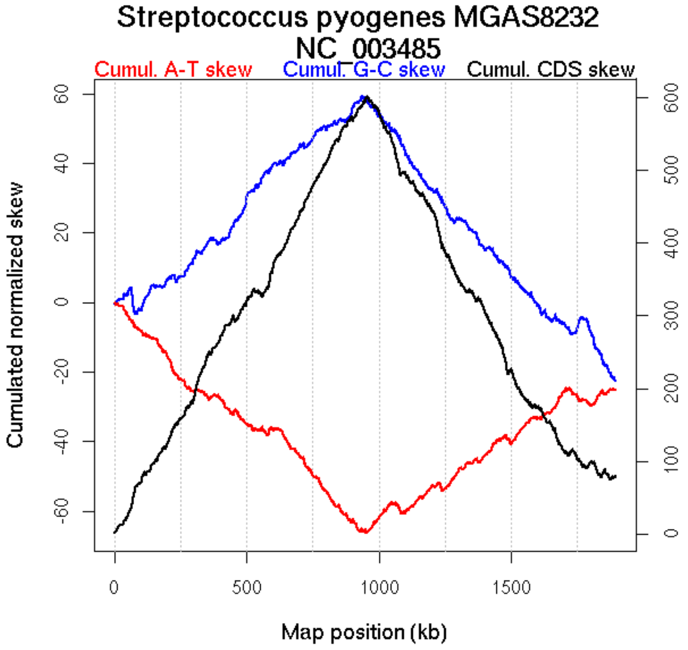
Segments:

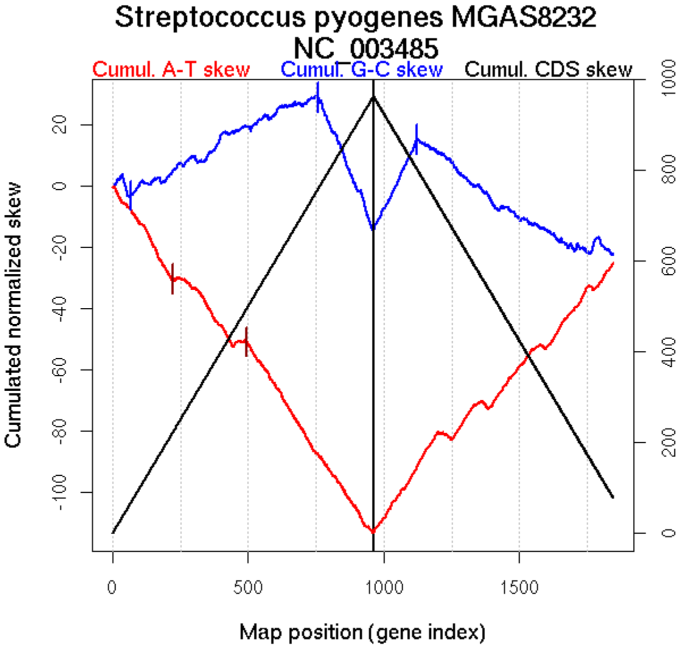
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	69 (86.8995 kb)	leading	-0.069
	70(87.2015 kb)	700 (883.7255 kb)	leading	0.061
	701(885.245 kb)	943 (1897.539 kb)	lagging	-0.2
GC-skew reverse	944 (0 kb)	1106 (884.9515 kb)	leading	0.179
	1107(889.5645 kb)	1894 (1897.539 kb)	lagging	-0.082
AT-skew forward	1 (0 kb)	129 (170.1245 kb)	leading	-0.112
	130(170.36 kb)	888 (1785.3275 kb)	NA	-0.135
	889(1789.542 kb)	943 (1897.539 kb)	lagging	-0.026

More G than C on the leading strand for replication.

333 Streptococcus pyogenes MGAS8232

Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.
Accession number: NC_003485; **Genome size (bp)**: 1895017.
Number of genes: 1845.
Oriloc predictions: Origin 0 kb Terminus 943 kb
Worning et al., 2006: Origin 1875 kb Terminus 959 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1814.237 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.88 kb
Consensus predictions: Origin 0 kb Terminus 943 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	68	NA	87
	757	NA	948
GC-skew reverse	1123	NA	946
AT-skew forward	221	NA	298
	494	NA	616

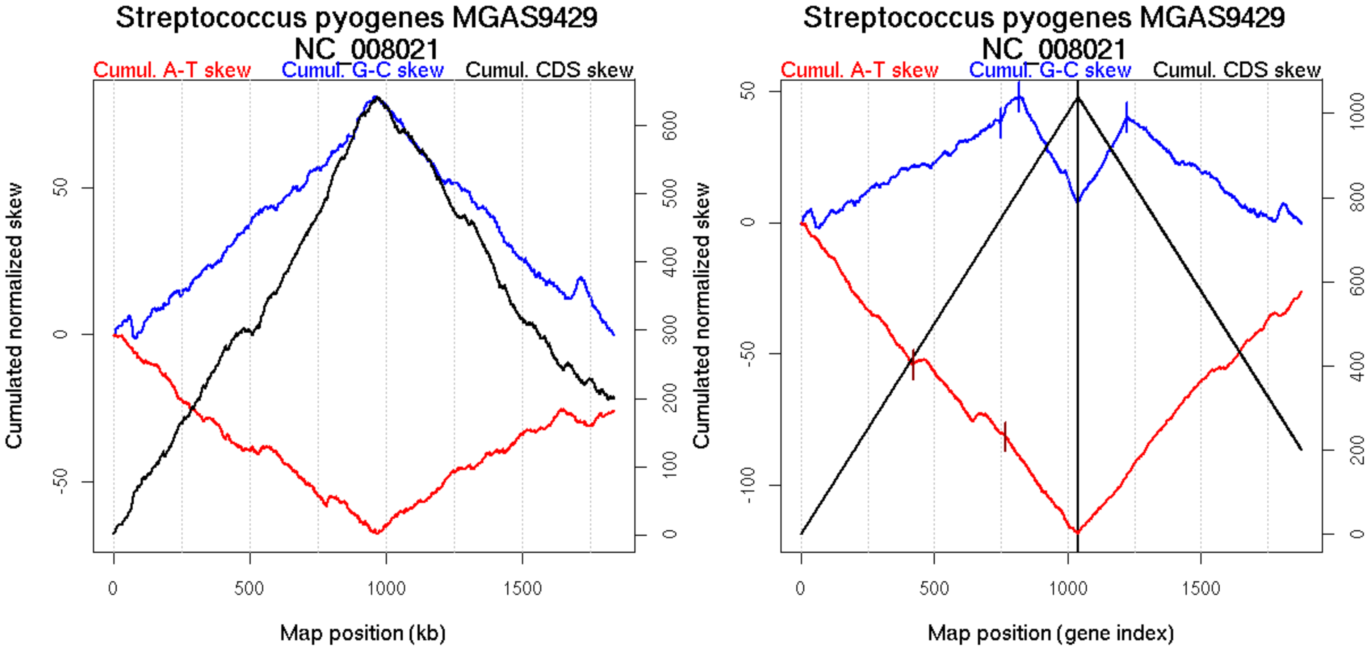
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	68 (87.204 kb)	leading	-0.066
	69(88.3105 kb)	757 (948.168 kb)	leading	0.048
	758(949.3205 kb)	962 (1895.013 kb)	lagging	-0.211
GC-skew reverse	963 (0 kb)	1123 (945.8655 kb)	leading	0.182
	1124(950.4765 kb)	1845 (1895.013 kb)	lagging	-0.054
AT-skew forward	1 (0 kb)	221 (298.2395 kb)	leading	-0.139
	222(299.3015 kb)	494 (615.573 kb)	leading	-0.1
	495(615.8565 kb)	962 (1895.013 kb)	NA	-0.135

More G than C on the leading strand for replication.

334 Streptococcus pyogenes MGAS9429

Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.
Accession number: NC_008021; **Genome size (bp)**: 1836467.
Number of genes: 1877.
Oriloc predictions: Origin 0 kb Terminus 966 kb
Worning et al., 2006: Origin 1816 kb Terminus 968 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1756.74 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.88 kb
Consensus predictions: Origin 0 kb Terminus 966 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	748	NA	881
	817	NA	957
GC-skew reverse	1224	NA	969
AT-skew forward	420	NA	533
	768	NA	896

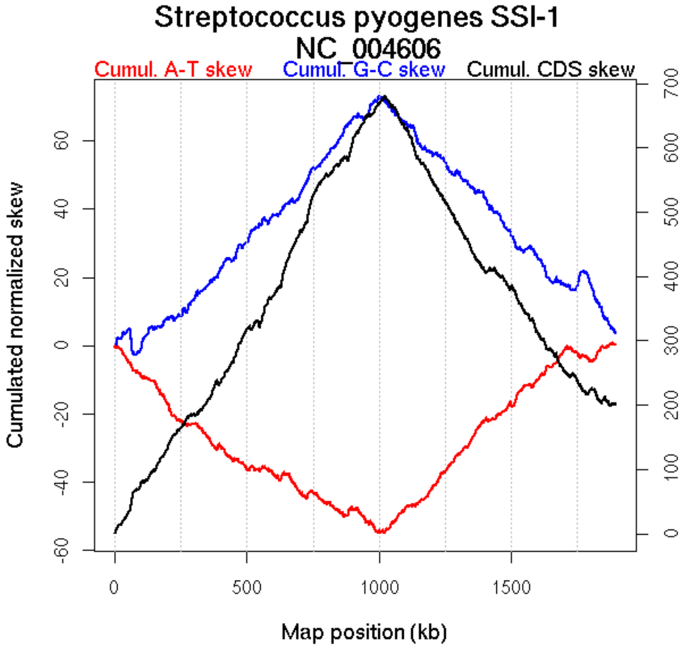
Segments:

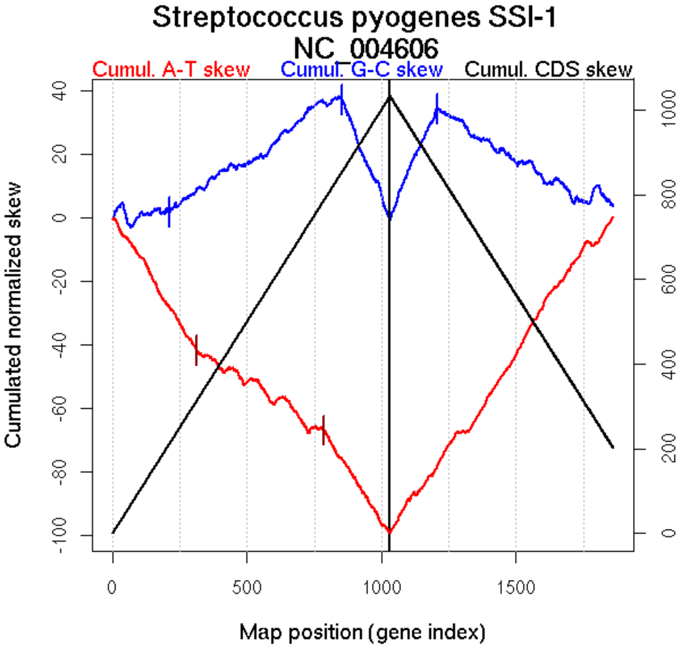
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	748 (881.23 kb)	leading	0.053
	749(881.346 kb)	817 (957.3145 kb)	leading	0.132
	818(958.133 kb)	1039 (1836.433 kb)	lagging	-0.18
GC-skew reverse	1040 (0 kb)	1224 (969.27 kb)	leading	0.173
	1225(970.7405 kb)	1877 (1836.433 kb)	lagging	-0.063
AT-skew forward	1 (0 kb)	420 (533.439 kb)	leading	-0.13
	421(534.5475 kb)	768 (895.723 kb)	leading	-0.091
	769(896.193 kb)	1039 (1836.433 kb)	NA	-0.138

More G than C on the leading strand for replication.

335 Streptococcus pyogenes SSI-1

Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.
Accession number: NC_004606; **Genome size (bp)**: 1894275.
Number of genes: 1861.
Oriloc predictions: Origin 0 kb Terminus 1005 kb
Worning et al., 2006: Origin 1874 kb Terminus 1021 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1814.352 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.91 kb
Consensus predictions: Origin 0 kb Terminus 1005 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	213	NA	274
	854	NA	1016
GC-skew reverse	1208	NA	1011
AT-skew forward	315	NA	417
	786	NA	926

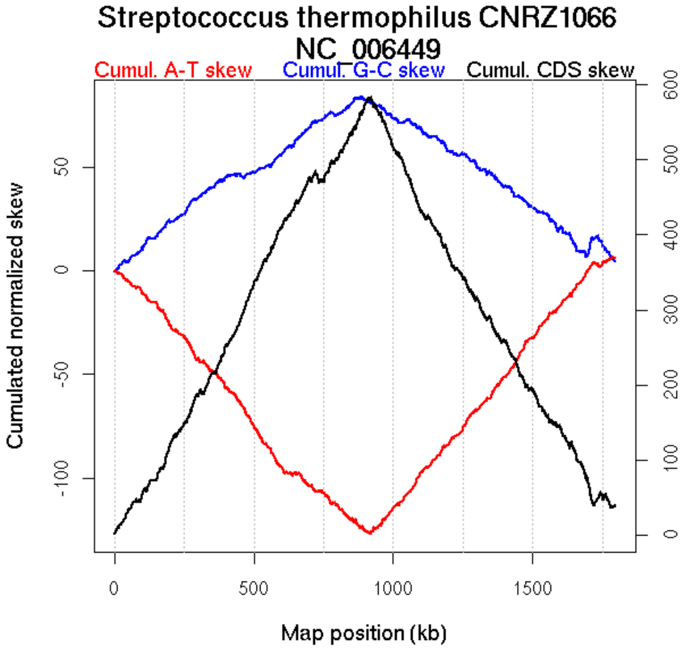
Segments:

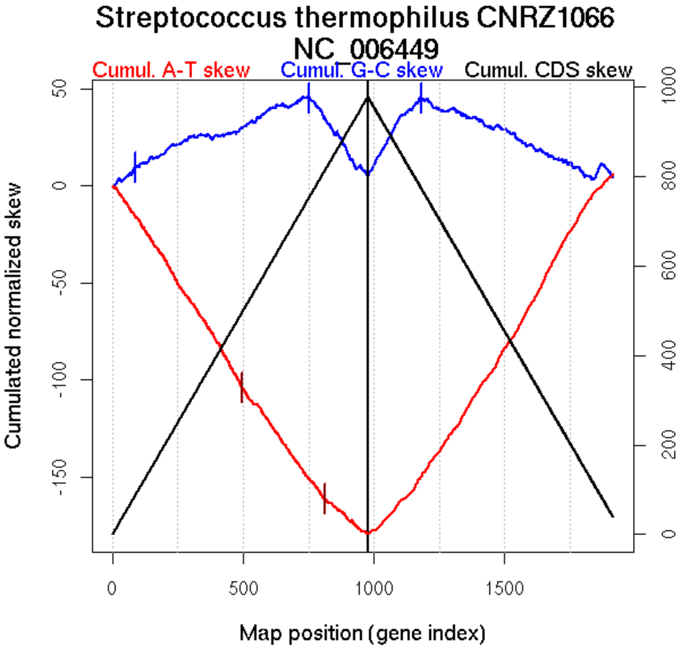
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	213 (273.8165 kb)	leading	0.004
	214(276.3945 kb)	854 (1016.2185 kb)	leading	0.058
	855(1017.101 kb)	1032 (1894.271 kb)	lagging	-0.207
GC-skew reverse	1033 (0 kb)	1208 (1011.0635 kb)	leading	0.192
	1209(1012.284 kb)	1861 (1894.271 kb)	lagging	-0.047
AT-skew forward	1 (0 kb)	315 (417.457 kb)	leading	-0.136
	316(417.9845 kb)	786 (926.466 kb)	leading	-0.055
	787(927.282 kb)	1032 (1894.271 kb)	NA	-0.133

More G than C on the leading strand for replication.

336 Streptococcus thermophilus CNRZ1066

Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.
Accession number: NC_006449; **Genome size (bp)**: 1796226.
Number of genes: 1915.
Oriloc predictions: Origin 0 kb Terminus 907 kb
Worning et al., 2006: Origin 1794 kb Terminus 909 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 0.058 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.87 kb, 304.04 kb, 1732.93 kb
Consensus predictions: Origin 0 kb Terminus 907 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	86	NA	119
	753	NA	888
GC-skew reverse	1180	NA	925
AT-skew forward	495	NA	581
	811	NA	1123

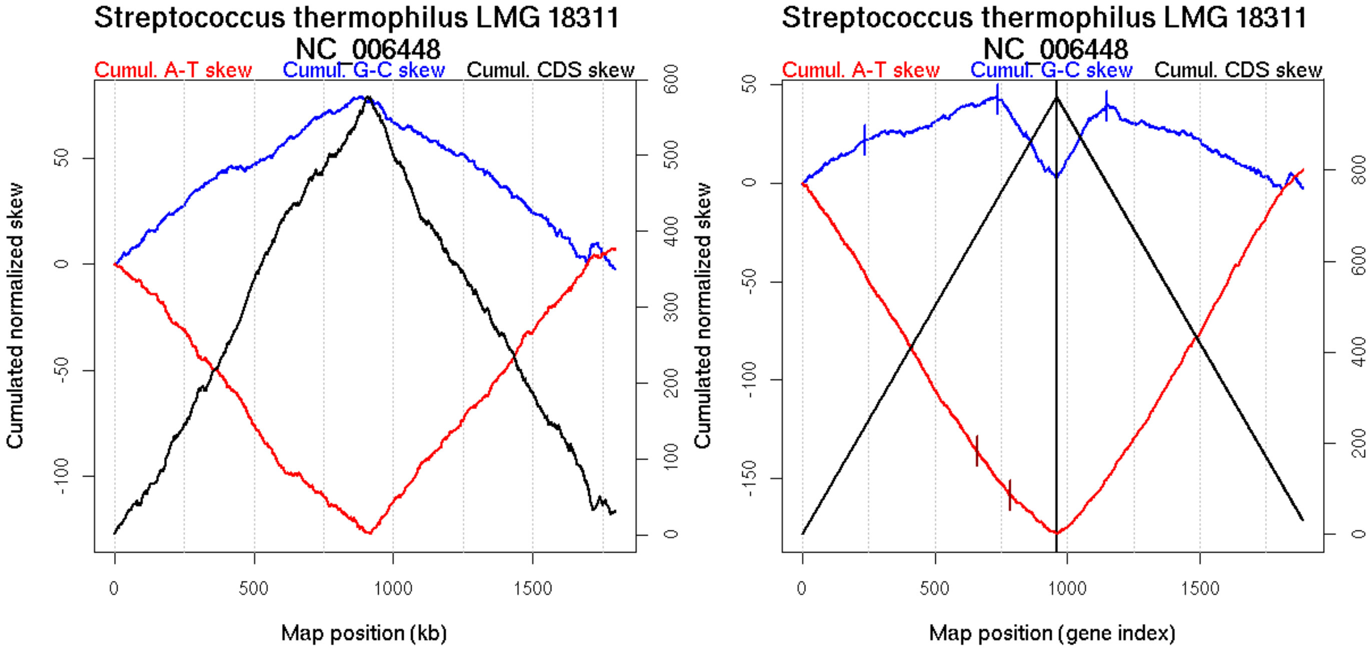
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	86 (119.14 kb)	leading	0.095
	87(119.896 kb)	753 (888.3155 kb)	leading	0.051
	754(890.7625 kb)	977 (1796.169 kb)	lagging	-0.191
GC-skew reverse	978 (0 kb)	1180 (925.295 kb)	leading	0.2
	1181(926.3155 kb)	1915 (1796.169 kb)	lagging	-0.058
AT-skew forward	1 (0 kb)	495 (581.11 kb)	leading	-0.209
	496(581.514 kb)	811 (1123.3905 kb)	leading	-0.184
	812(1123.9145 kb)	977 (1796.169 kb)	lagging	-0.115

More T than A on the leading strand for replication - for forward encoded genes.
More G than C on the leading strand for replication.

337 Streptococcus thermophilus LMG 18311

Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Streptococcus.
Accession number: NC_006448; **Genome size (bp)**: 1796846.
Number of genes: 1889.
Oriloc predictions: Origin 0 kb Terminus 904 kb
Worning et al., 2006: Origin 1788 kb Terminus 906 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 0.058 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.87 kb, 311.49 kb, 1731.06 kb
Consensus predictions: Origin 0 kb Terminus 904 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	237	NA	296
	739	NA	891
GC-skew reverse	1148	NA	920
AT-skew forward	659	NA	799
	786	NA	1096

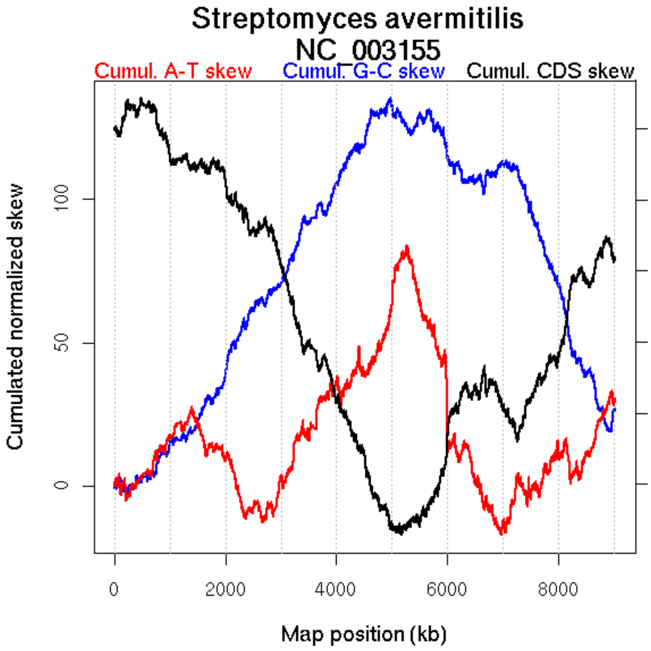
Segments:

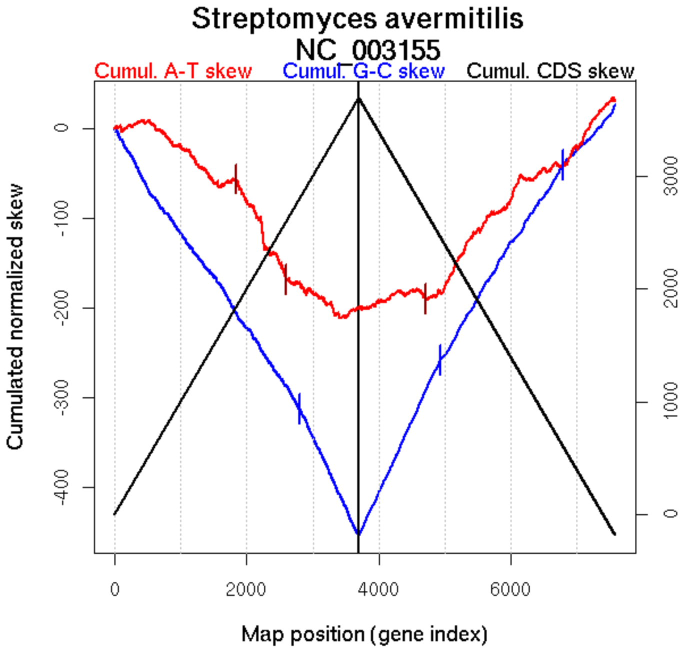
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	237 (295.7045 kb)	leading	0.089
	238(296.458 kb)	739 (890.846 kb)	leading	0.045
	740(891.434 kb)	960 (1796.789 kb)	lagging	-0.197
GC-skew reverse	961 (0 kb)	1148 (919.7045 kb)	leading	0.205
	1149(920.9525 kb)	1889 (1796.789 kb)	lagging	-0.056
AT-skew forward	1 (0 kb)	659 (799.267 kb)	leading	-0.213
	660(800.356 kb)	786 (1096.1 kb)	NA	-0.178
	787(1103.4155 kb)	960 (1796.789 kb)	lagging	-0.116

More T than A on the leading strand for replication - for forward encoded genes.
More G than C on the leading strand for replication.

338 Streptomyces avermitilis

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
Accession number: NC_003155; **Genome size (bp)**: 9025608.
Number of genes: 7577.
Oriloc predictions: Origin 4982 kb Terminus 0 kb
Worning et al., 2006: Origin NA kb Terminus NA kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 5308.401 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 3685.51 kb, 4616.8 kb, 4908.87 kb, 5286.95 kb
Consensus predictions: Origin 5308 kb Terminus 0 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	2804	0	7274
GC-skew reverse	4934	0.02333	2839
	6781	0.04333	6983
AT-skew forward	1836	0.02667	5194
	2602	0.01667	6741
AT-skew reverse	4717	0.02667	2333

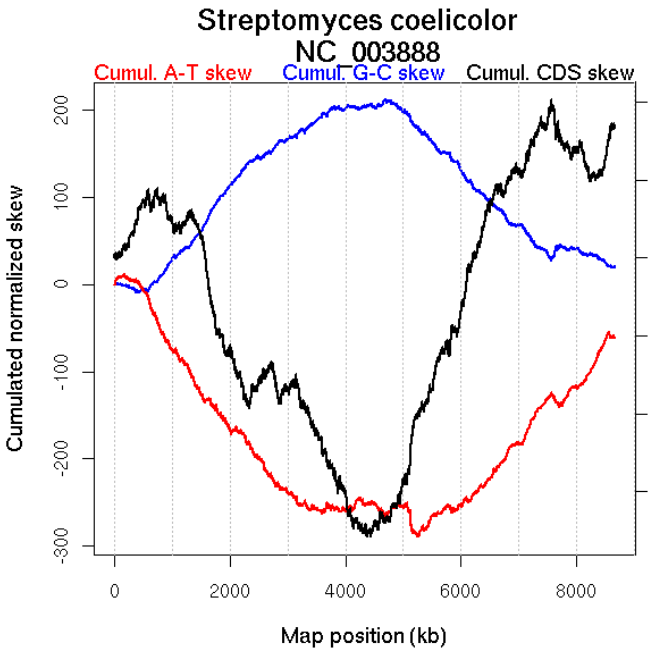
Segments:

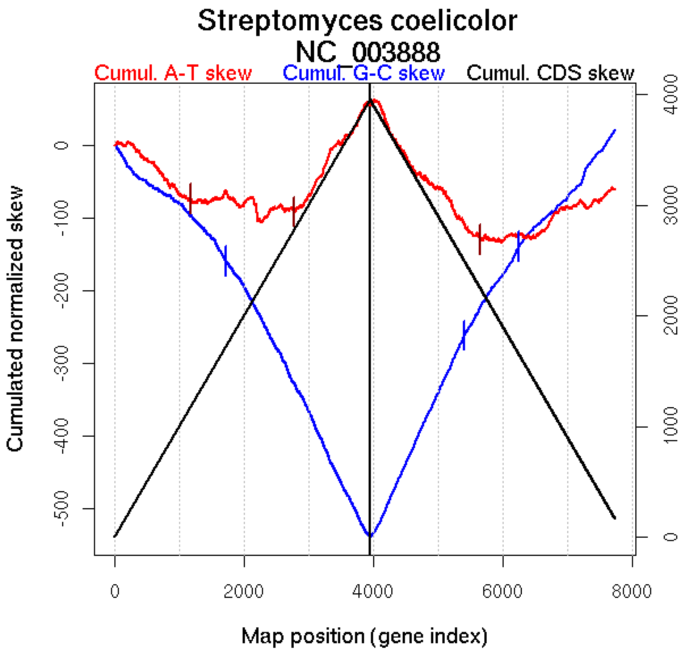
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	2804 (7274.0665 kb)	NA	-0.108
	2805(7276.519 kb)	3697 (9024.537 kb)	leading	-0.16
GC-skew reverse	3698 (0 kb)	4934 (2838.684 kb)	lagging	0.16
	4935(2843.069 kb)	6781 (6982.5085 kb)	NA	0.117
	6782(6983.572 kb)	7577 (9024.537 kb)	leading	0.078
AT-skew forward	1 (0 kb)	1836 (5193.527 kb)	lagging	-0.046
	1837(5197.487 kb)	2602 (6740.525 kb)	leading	-0.144
	2603(6741.757 kb)	3697 (9024.537 kb)	leading	-0.041
AT-skew reverse	3698 (0 kb)	4717 (2332.79 kb)	lagging	0.021
	4718(2341.106 kb)	7577(9024.537 kb)	NA	0.076

More A than T on the leading strand for replication - for forward encoded genes.

339 Streptomyces coelicolor

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
Accession number: NC_003888; **Genome size (bp)**: 8667507.
Number of genes: 7742.
Oriloc predictions: Origin 4685 kb Terminus 373 kb
Worning et al., 2006: Origin NA kb Terminus NA kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 4239.649 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 3604.8 kb, 4271.76 kb, 4331.34 kb, 4390.39 kb, 5815.73 kb
Consensus predictions: Origin 4270 kb Terminus 373 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1718	NA	4227
GC-skew reverse	5411	NA	3054
	6258	NA	4752
AT-skew forward	1182	NA	2744
	2782	NA	6148
AT-skew reverse	5661	NA	3591

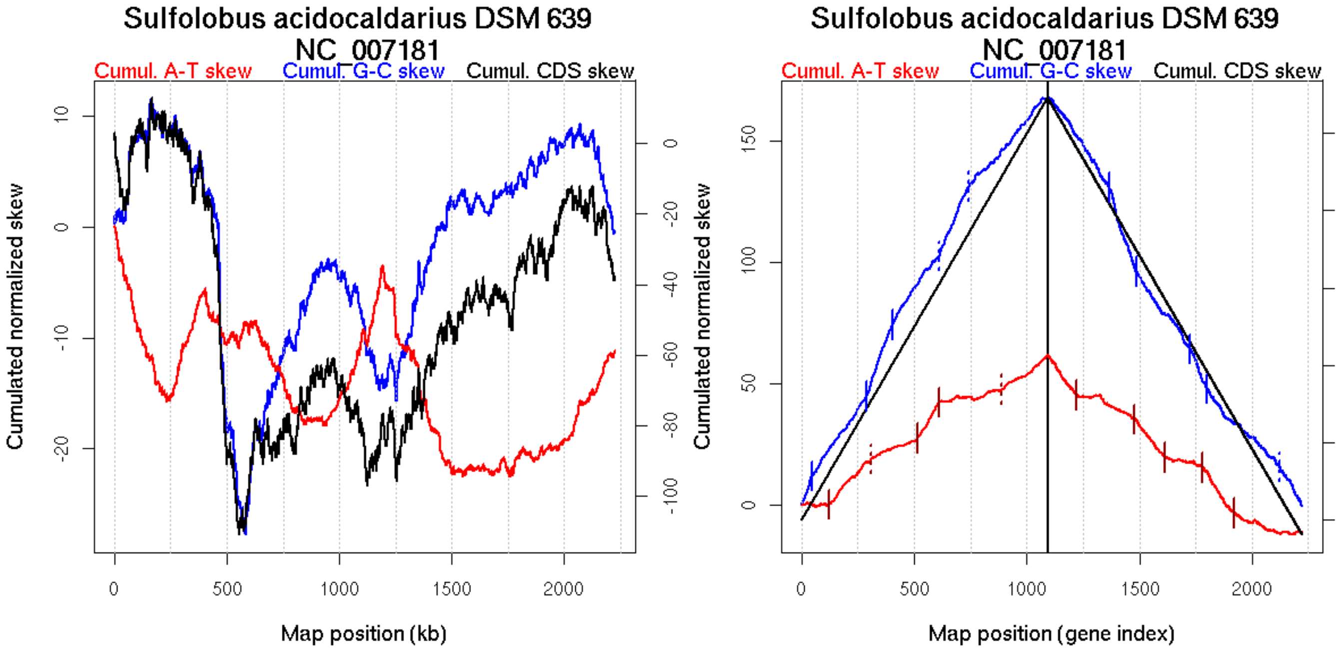
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1718 (4227.0225 kb)	lagging	-0.08
	1719(4228.25 kb)	3954 (8667.062 kb)	leading	-0.177
GC-skew reverse	3955 (0 kb)	5411 (3053.7465 kb)	lagging	0.195
	5412(3057.7065 kb)	6258 (4752.391 kb)	NA	0.139
	6259(4755.536 kb)	7742 (8667.062 kb)	leading	0.105
AT-skew forward	1 (0 kb)	1182 (2743.5445 kb)	NA	-0.078
	1183(2748.2675 kb)	2782 (6148.188 kb)	NA	-0.012
	2783(6152.5645 kb)	3954 (8667.062 kb)	leading	0.135
AT-skew reverse	3955 (0 kb)	5661 (3591.1655 kb)	lagging	-0.113
	5662(3592.1025 kb)	7742(8667.062 kb)	NA	0.037

More C than G on the leading strand for replication.

340 Sulfolobus acidocaldarius DSM 639

Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae; Sulfolobus.
Accession number: NC_007181; **Genome size (bp)**: 2225959.
Number of genes: 2222.
Oriloc predictions: Origin NA Terminus NA
Worning et al., 2006: Origin 1666 kb Terminus 165 kb
Position(s) of the ORC/Cdc6 gene(s): 0.68 kb, 578.76 kb, 724.91 kb
Consensus predictions: Origin NA Terminus NA



Significant breakpoints (p-value <0.05):

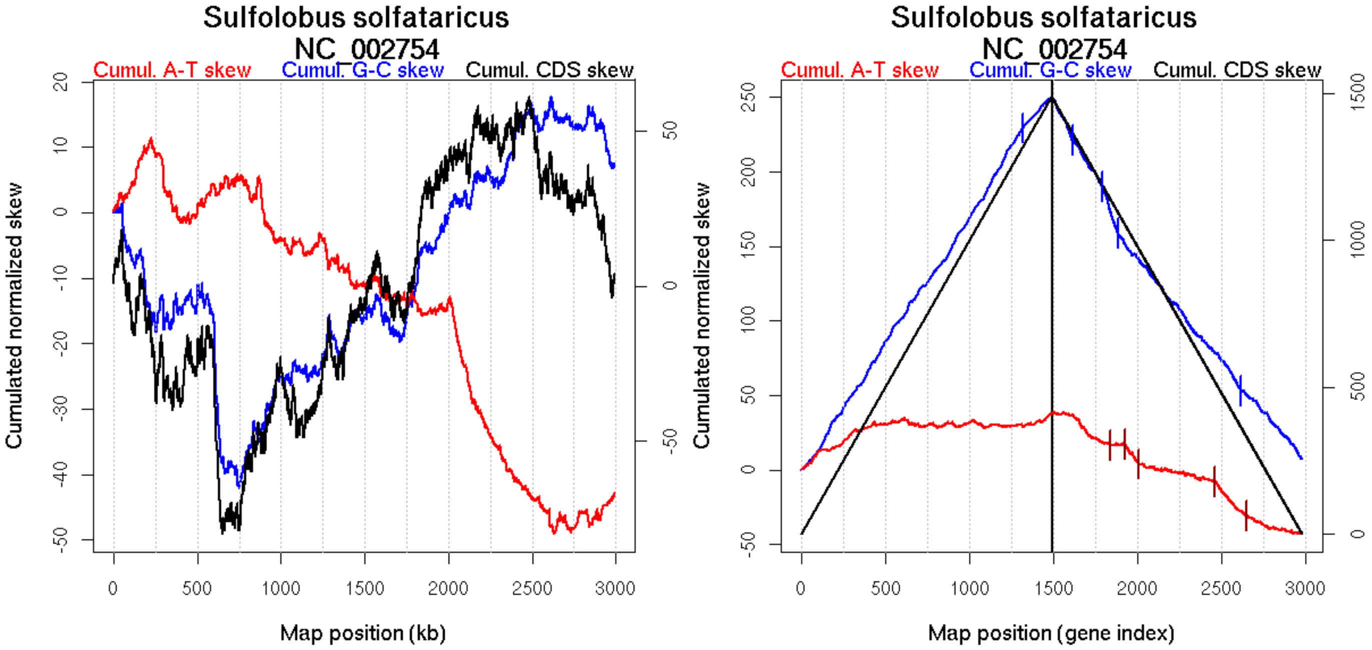
	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	45	0.03467	73
	287	0.04533	586
	404	0.048	764
	609	0.15733	1193
	743	0.07067	1429
GC-skew reverse	1364	0.008	447
	1486	0.00533	596
	1726	0.04667	1088
	1800	0.00933	1237
	2124	0.25333	2035
AT-skew forward	123	0.024	213
	310	0.08667	612
	513	0.01467	996
	608	0.00533	1191
	889	0.20933	1770
AT-skew reverse	1222	0.02933	234
	1479	0.048	575
	1615	0.01867	846
	1781	0.00267	1195
	1918	0.00267	1488

Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	45 (72.54 kb)	NA	0.27
	46(74.706 kb)	287 (586.3565 kb)	NA	0.132
	288(587.1 kb)	404 (764.333 kb)	NA	0.262
	405(767.156 kb)	609 (1192.5145 kb)	NA	0.135
	610(1193.0685 kb)	743 (1428.519 kb)	NA	0.219
	744(1429.042 kb)	1092 (2225.625 kb)	NA	0.109
GC-skew reverse	1093 (0 kb)	1364 (446.8155 kb)	NA	-0.14
	1365(448.9095 kb)	1486 (595.6655 kb)	NA	-0.288
	1487(596.5075 kb)	1726 (1087.991 kb)	NA	-0.125
	1727(1088.568 kb)	1800 (1237.3085 kb)	NA	-0.238
	1801(1237.6585 kb)	2124 (2035.385 kb)	NA	-0.091
	2125(2036.768 kb)	2222 (2225.625 kb)	NA	-0.161
AT-skew forward	1 (0 kb)	123 (212.637 kb)	NA	-0.003
	124(215.373 kb)	310 (611.998 kb)	NA	0.101
	311(614.046 kb)	513 (995.8855 kb)	NA	0.036
	514(998.912 kb)	608 (1190.9515 kb)	NA	0.159
	609(1192.5145 kb)	889 (1770.12 kb)	NA	0.017
	890(1770.8105 kb)	1092 (2225.625 kb)	NA	0.064
AT-skew reverse	1093 (0 kb)	1222 (233.58 kb)	NA	-0.131
	1223(235.0805 kb)	1479(575.05 kb)	NA	-0.04
	1480(576.4995 kb)	1615(846.006 kb)	NA	-0.12
	1616(847.904 kb)	1781(1195.3185 kb)	NA	-0.019
	1782(1196.7385 kb)	1918(1487.6655 kb)	NA	-0.146
	1919(1489.5275 kb)	2222(2225.625 kb)	NA	-0.027

341 Sulfolobus solfataricus

Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae; Sulfolobus.
Accession number: NC_002754; **Genome size (bp)**: 2992245.
Number of genes: 2976.
Oriloc predictions: Origin NA Terminus NA
Worning et al., 2006: Origin 639 kb Terminus 2011 kb
Position(s) of the ORC/Cdc6 gene(s): 221.67 kb, 2009.98 kb, 221.67 kb, 2009.98 kb, 221.67 kb, 656.6 kb, 2009.98 kb
Consensus predictions: Origin NA Terminus NA



Significant breakpoints (p-value <0.05):

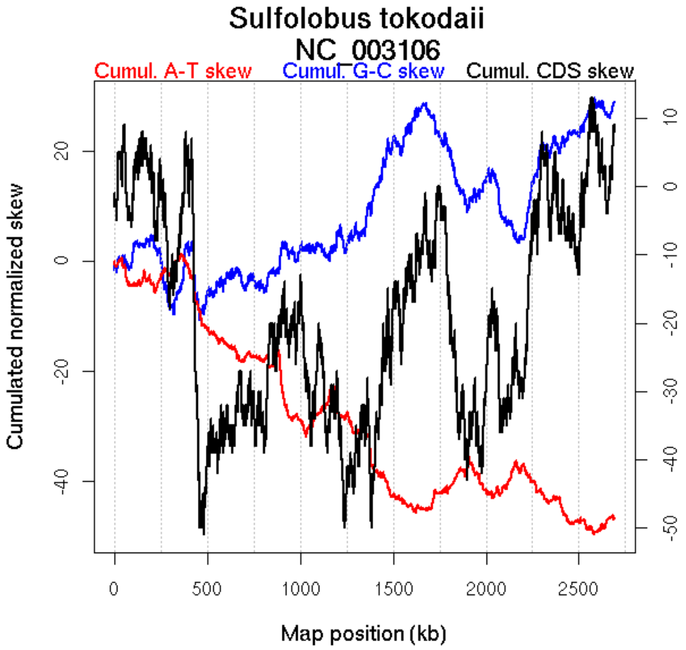
	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1315	NA	2606
GC-skew reverse	1612	NA	225
	1787	NA	551
	1881	NA	661
	2615	NA	2304
AT-skew reverse	1837	NA	611
	1921	NA	742
	2008	NA	962
	2459	NA	1993
	2648	NA	2381

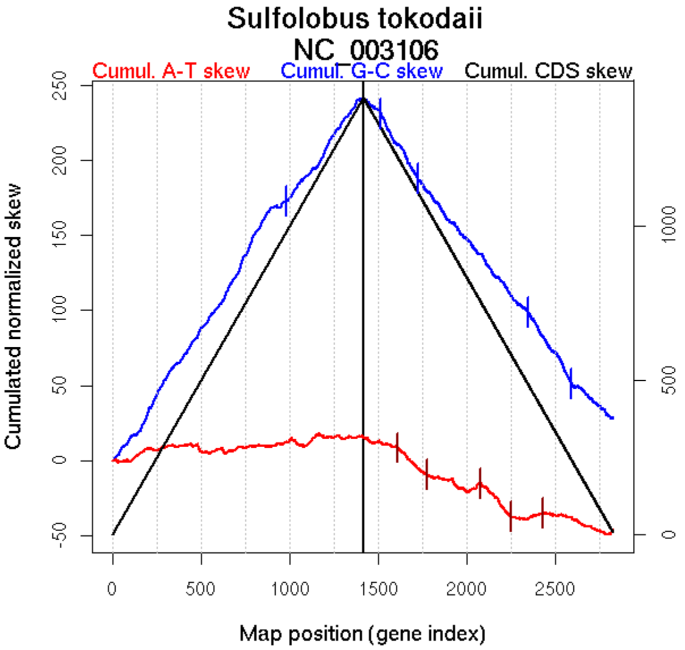
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1315 (2606.347 kb)	NA	0.174
	1316(2609.16 kb)	1489 (2991.218 kb)	NA	0.122
GC-skew reverse	1490 (0 kb)	1612 (225.077 kb)	NA	-0.233
	1613(225.7645 kb)	1787 (551.459 kb)	NA	-0.178
	1788(561.0495 kb)	1881 (661.4725 kb)	NA	-0.35
	1882(662.986 kb)	2615 (2303.6075 kb)	NA	-0.139
	2616(2306.2395 kb)	2976 (2991.218 kb)	NA	-0.127
AT-skew reverse	1490 (0 kb)	1837 (611.1495 kb)	NA	-0.077
	1838(611.804 kb)	1921(742.1445 kb)	NA	0.011
	1922(743.7635 kb)	2008(962.4095 kb)	NA	-0.155
	2009(965.536 kb)	2459(1992.592 kb)	NA	-0.024
	2460(1994.561 kb)	2648(2380.9365 kb)	NA	-0.123
	2649(2381.867 kb)	2976(2991.218 kb)	NA	-0.035

342 Sulfolobus tokodaii

Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae; Sulfolobus.
Accession number: NC_003106; **Genome size (bp)**: 2694756.
Number of genes: 2825.
Oriloc predictions: Origin NA Terminus NA
Worning et al., 2006: Origin 31 kb Terminus 1910 kb
Position(s) of the ORC/Cdc6 gene(s): 322.84 kb, 473.68 kb, 1216.64 kb, 1712.8 kb, 2602.52 kb
Consensus predictions: Origin NA Terminus NA





Significant breakpoints (p-value <0.05):

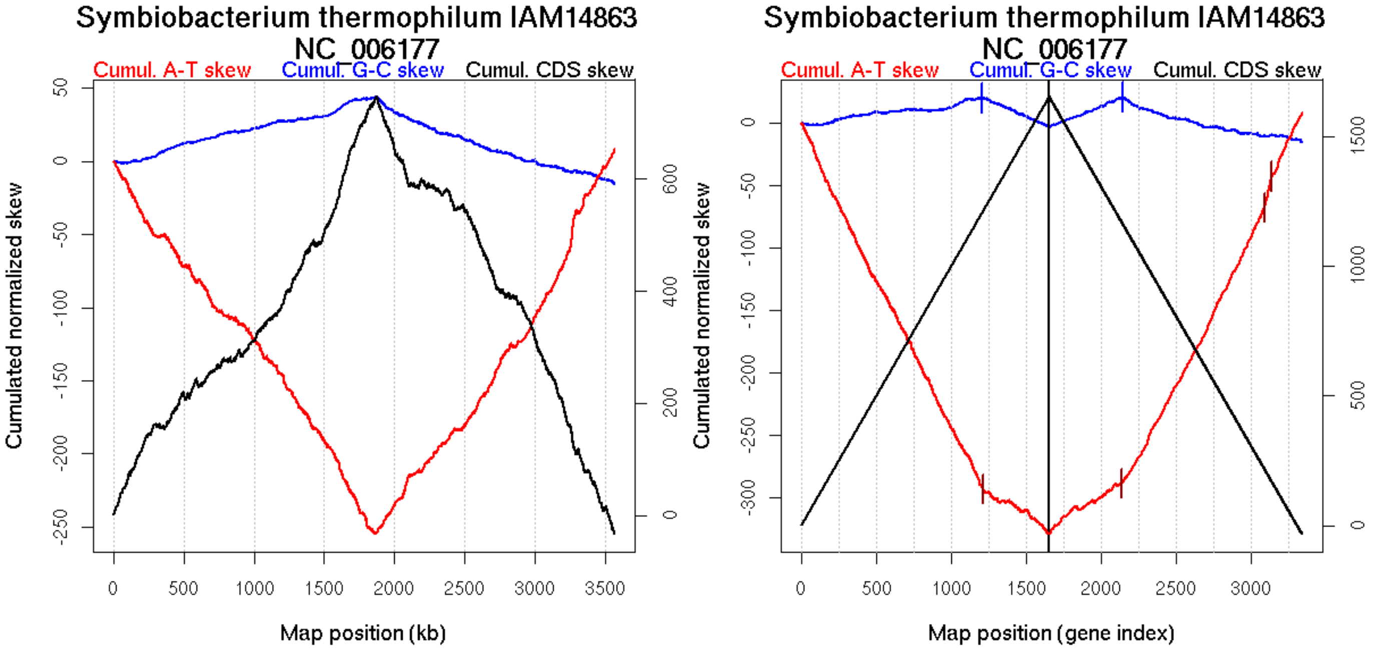
	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	983	NA	1864
GC-skew reverse	1511	NA	201
	1723	NA	521
	2345	NA	1706
	2590	NA	2160
AT-skew reverse	1610	NA	368
	1773	NA	607
	2079	NA	1200
	2247	NA	1512
	2430	NA	1855

Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	983 (1863.5835 kb)	NA	0.188
	984(1865.028 kb)	1417 (2692.28 kb)	NA	0.168
GC-skew reverse	1418 (0 kb)	1511 (200.8325 kb)	NA	-0.095
	1512(201.305 kb)	1723 (520.9875 kb)	NA	-0.199
	1724(521.8935 kb)	2345 (1706.1145 kb)	NA	-0.144
	2346(1707.7665 kb)	2590 (2160.2555 kb)	NA	-0.185
	2591(2160.6245 kb)	2825 (2692.28 kb)	NA	-0.105
AT-skew reverse	1418 (0 kb)	1610 (367.8645 kb)	NA	-0.03
	1611(370.079 kb)	1773(607.396 kb)	NA	-0.114
	1774(610.4245 kb)	2079(1200.4885 kb)	NA	-0.034
	2080(1201.764 kb)	2247(1511.9815 kb)	NA	-0.134
	2248(1513.204 kb)	2430(1854.937 kb)	NA	0.017
	2431(1857.37 kb)	2825(2692.28 kb)	NA	-0.041

343 Symbiobacterium thermophilum IAM14863

Bacteria; Firmicutes; Lactobacillales; Symbiobacterium.
Accession number: NC_006177; **Genome size (bp)**: 3566135.
Number of genes: 3337.
Oriloc predictions: Origin 0 kb Terminus 1873 kb
Worning et al., 2006: Origin 3566 kb Terminus 1875 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1.483 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.69 kb, 3480.95 kb
Consensus predictions: Origin 0 kb Terminus 1873 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1207	0	1831
GC-skew reverse	2143	0	1877
AT-skew forward	1212	0	1842
AT-skew reverse	2133	0.02	1839
	3086	0	3249
	3137	0	3290

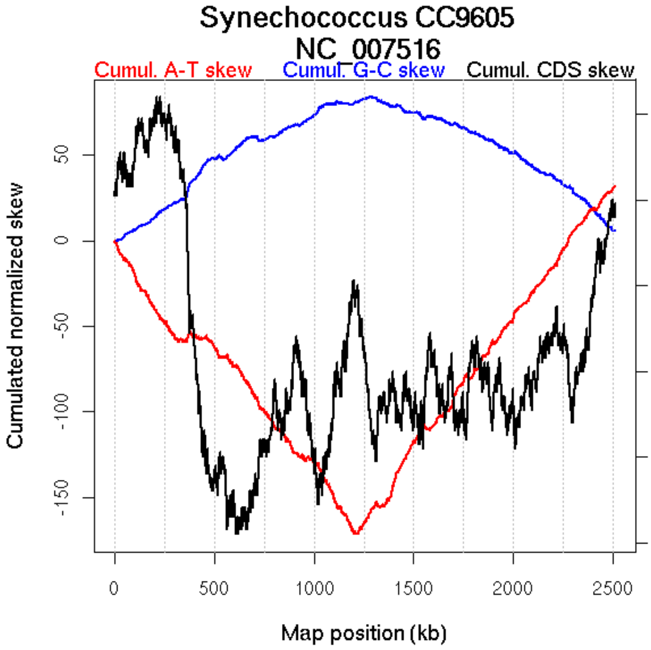
Segments:

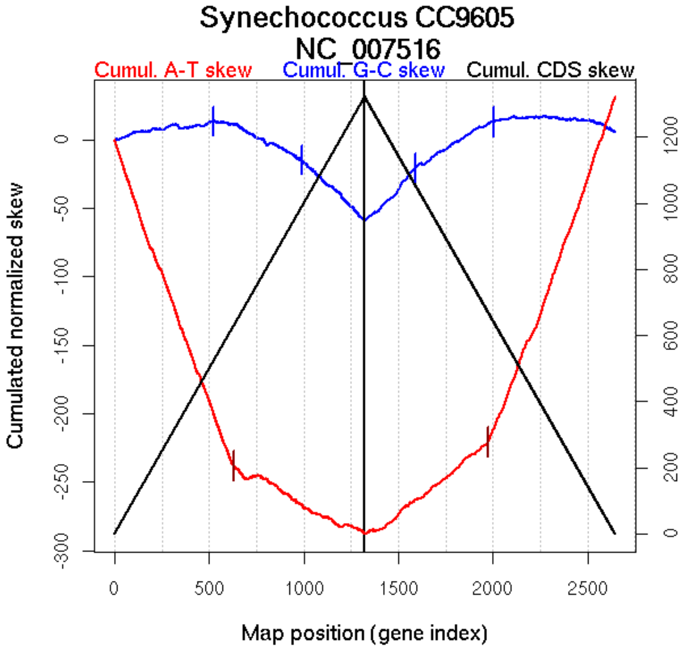
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1207 (1830.6575 kb)	leading	0.016
	1208(1832.13 kb)	1652 (3565.7 kb)	lagging	-0.053
GC-skew reverse	1653 (0 kb)	2143 (1876.673 kb)	leading	0.048
	2144(1877.5345 kb)	3337 (3565.7 kb)	lagging	-0.026
AT-skew forward	1 (0 kb)	1212 (1842.058 kb)	leading	-0.238
	1213(1843.338 kb)	1652 (3565.7 kb)	lagging	-0.071
AT-skew reverse	1653 (0 kb)	2133 (1839.3385 kb)	leading	0.075
	2134(1840.835 kb)	3086(3248.921 kb)	lagging	0.234
	3087(3250.864 kb)	3137(3290.228 kb)	lagging	0.506
	3138(3291.069 kb)	3337(3565.7 kb)	lagging	0.261

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

344 Synechococcus CC9605

Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
Accession number: NC_007516; **Genome size (bp)**: 2510659.
Number of genes: 2645.
Oriloc predictions: Origin 0 kb Terminus 1203 kb
Worning et al., 2006: Origin 1 kb Terminus 1240 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 517.486 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 928.44 kb
Consensus predictions: Origin 0 kb Terminus 1203 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	521	0.02	1059
	988	0.03333	1873
GC-skew reverse	1587	0.04667	464
	2003	0.03	1262
AT-skew forward	629	0	1220
AT-skew reverse	1973	0	1222

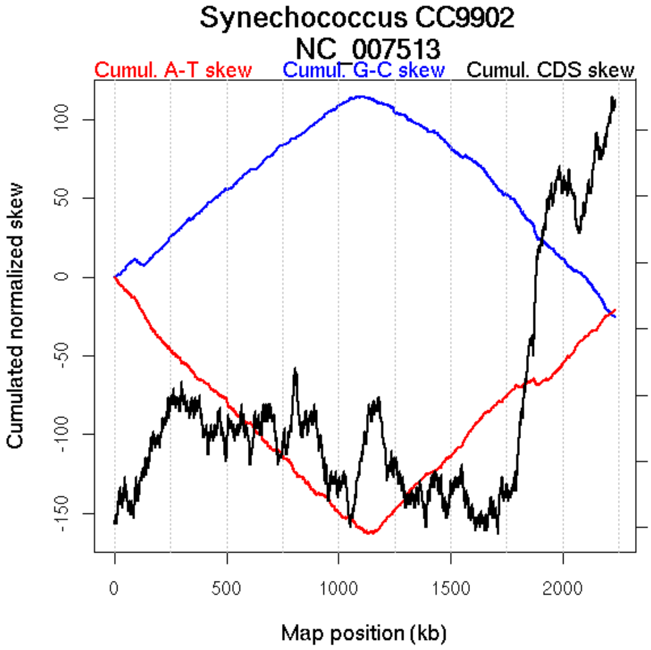
Segments:

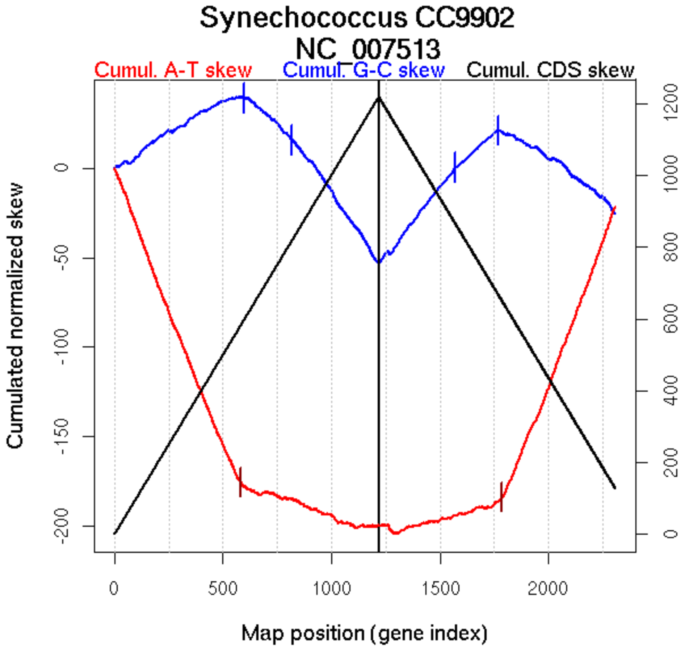
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	521 (1058.612 kb)	leading	0.02
	522(1062.5965 kb)	988 (1873.152 kb)	NA	-0.064
	989(1875.07 kb)	1322 (2510.454 kb)	lagging	-0.13
GC-skew reverse	1323 (0 kb)	1587 (463.7185 kb)	leading	0.146
	1588(466.006 kb)	2003 (1261.969 kb)	leading	0.085
	2004(1262.572 kb)	2645 (2510.454 kb)	lagging	-0.009
AT-skew forward	1 (0 kb)	629 (1219.9745 kb)	leading	-0.376
	630(1226.698 kb)	1322 (2510.454 kb)	lagging	-0.073
AT-skew reverse	1323 (0 kb)	1973 (1221.826 kb)	leading	0.108
	1974(1223.04 kb)	2645(2510.454 kb)	lagging	0.376

More T than A on the leading strand for replication.
More G than C on the leading strand for replication - for reverse encoded genes.

345 Synechococcus CC9902

Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
Accession number: NC_007513; **Genome size (bp)**: 2234828.
Number of genes: 2307.
Oriloc predictions: Origin 0 kb Terminus 1134 kb
Worning et al., 2006: Origin 1 kb Terminus 1119 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 62.754 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 882.38 kb
Consensus predictions: Origin 0 kb Terminus 1134 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	596	NA	1132
	819	NA	1595
GC-skew reverse	1571	NA	752
	1768	NA	1087
AT-skew forward	583	NA	1114
AT-skew reverse	1787	NA	1147

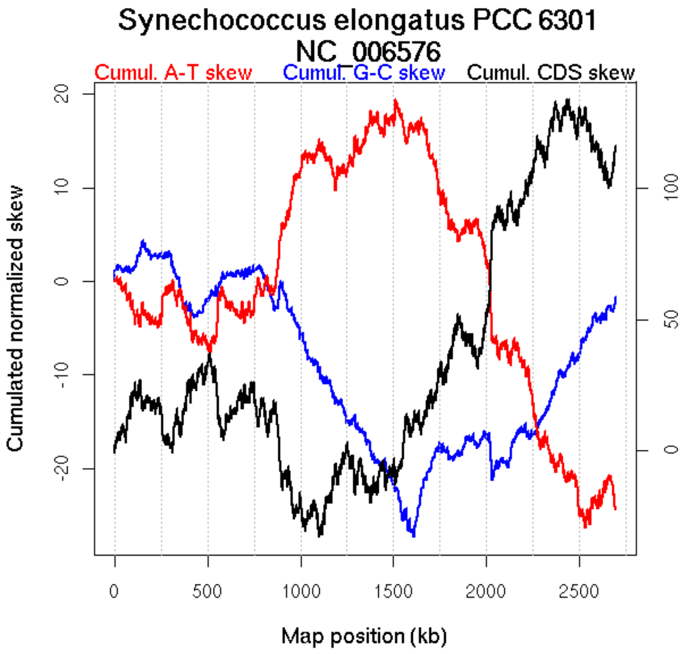
Segments:

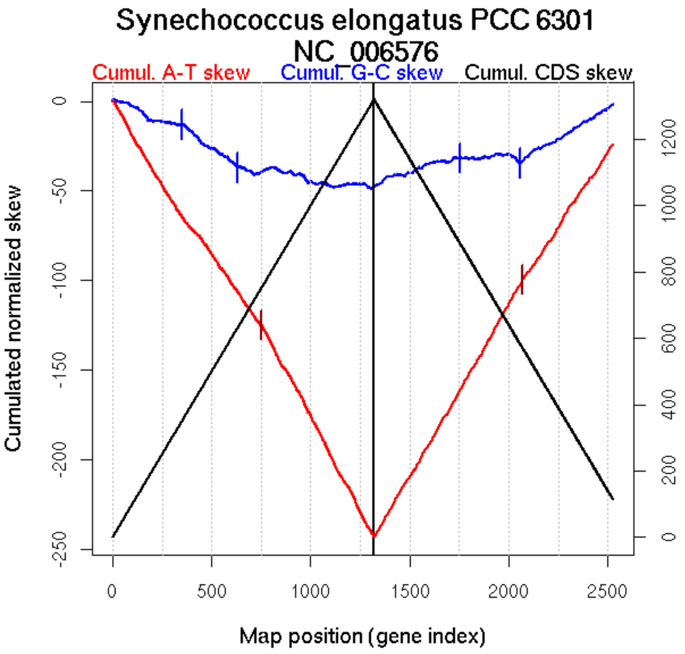
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	596 (1132.0265 kb)	leading	0.073
	597(1133.458 kb)	819 (1594.7765 kb)	lagging	-0.109
	820(1595.6505 kb)	1218 (2234.629 kb)	lagging	-0.176
GC-skew reverse	1219 (0 kb)	1571 (751.879 kb)	leading	0.155
	1572(755.642 kb)	1768 (1086.961 kb)	leading	0.111
	1769(1091.9545 kb)	2307 (2234.629 kb)	lagging	-0.084
AT-skew forward	1 (0 kb)	583 (1113.88 kb)	leading	-0.307
	584(1114.4155 kb)	1218 (2234.629 kb)	lagging	-0.041
AT-skew reverse	1219 (0 kb)	1787 (1146.694 kb)	leading	0.03
	1788(1147.507 kb)	2307(2234.629 kb)	lagging	0.315

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

346 Synechococcus elongatus PCC 6301

Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
Accession number: NC_006576; **Genome size (bp)**: 2696255.
Number of genes: 2526.
Oriloc predictions: Origin 1594 kb Terminus 0 kb
Worning et al., 2006: Origin 1595 kb Terminus 206 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1620.985 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 502.98 kb
Consensus predictions: Origin 1620 kb Terminus 0 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	352	NA	779
	630	NA	1387
GC-skew reverse	1753	NA	949
	2056	NA	1603
AT-skew forward	752	NA	1613
AT-skew reverse	2070	NA	1637

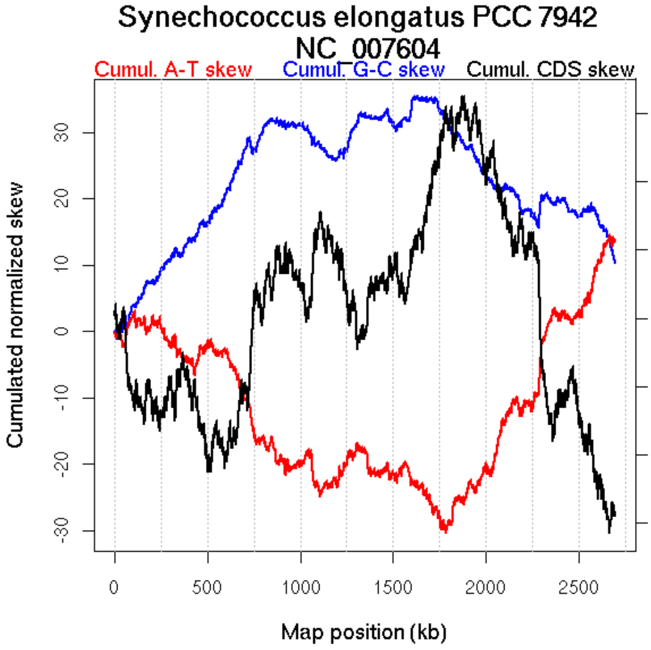
Segments:

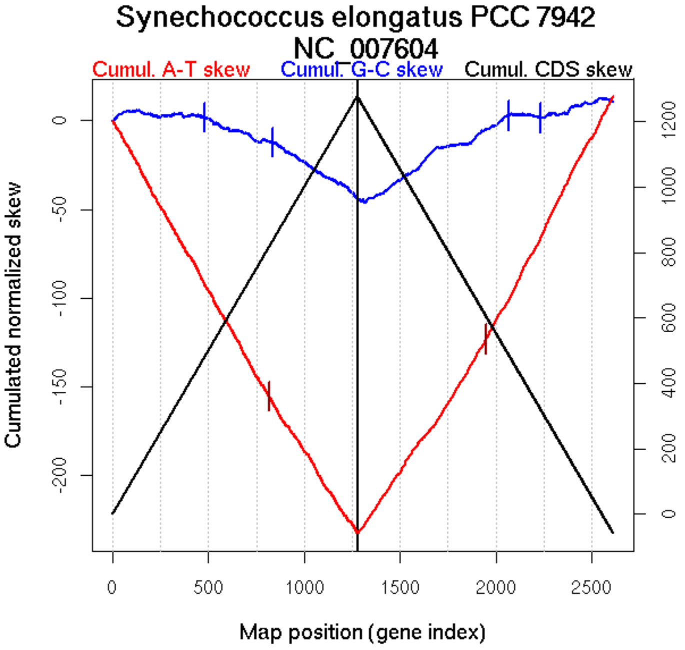
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	352 (778.5815 kb)	lagging	-0.047
	353(779.765 kb)	630 (1386.556 kb)	lagging	-0.082
	631(1387.7405 kb)	1320 (2695.791 kb)	NA	-0.018
GC-skew reverse	1321 (0 kb)	1753 (948.722 kb)	lagging	0.035
	1754(950.177 kb)	2056 (1603.13 kb)	lagging	0.004
	2057(1606.922 kb)	2526 (2695.791 kb)	leading	0.066
AT-skew forward	1 (0 kb)	752 (1612.691 kb)	lagging	-0.164
	753(1613.139 kb)	1320 (2695.791 kb)	leading	-0.21
AT-skew reverse	1321 (0 kb)	2070 (1637.151 kb)	lagging	0.192
	2071(1638.138 kb)	2526(2695.791 kb)	leading	0.168

More T than A on the leading strand for replication.
More G than C on the leading strand for replication - for reverse encoded genes.

347 Synechococcus elongatus PCC 7942

Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
Accession number: NC_007604; **Genome size (bp)**: 2695903.
Number of genes: 2612.
Oriloc predictions: Origin 24 kb Terminus 1715 kb
Worning et al., 2006: Origin 25 kb Terminus 1783 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 2695.801 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1117.83 kb
Consensus predictions: Origin 0 kb Terminus 1715 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	483	NA	965
	836	NA	1707
GC-skew reverse	2068	NA	1685
	2231	NA	2030
AT-skew forward	819	NA	1680
AT-skew reverse	1951	NA	1395

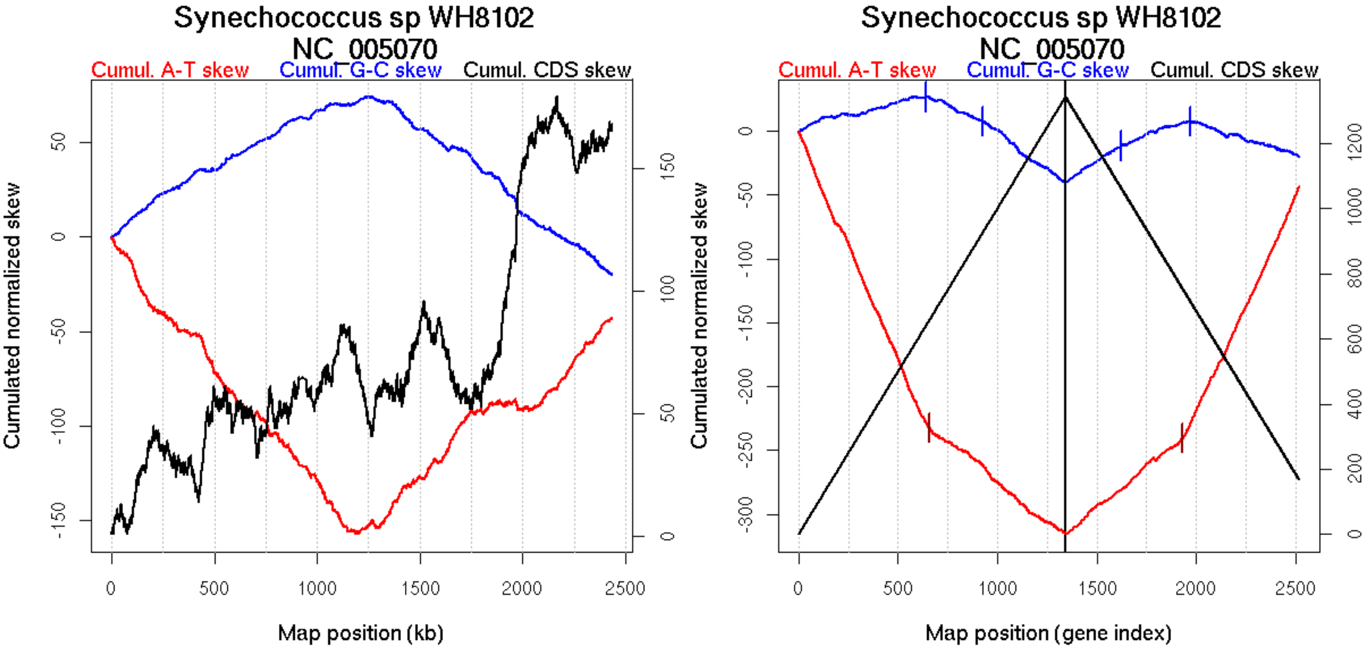
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	483 (965.0685 kb)	leading	-0.003
	484(966.6555 kb)	836 (1707.0415 kb)	leading	-0.04
	837(1707.827 kb)	1277 (2695.87 kb)	lagging	-0.068
GC-skew reverse	1278 (0 kb)	2068 (1684.917 kb)	leading	0.064
	2069(1690.653 kb)	2231 (2029.685 kb)	lagging	-0.008
	2232(2031.2305 kb)	2612 (2695.87 kb)	lagging	0.031
AT-skew forward	1 (0 kb)	819 (1680.454 kb)	leading	-0.191
	820(1682.6395 kb)	1277 (2695.87 kb)	lagging	-0.167
AT-skew reverse	1278 (0 kb)	1951 (1394.614 kb)	leading	0.16
	1952(1398.2945 kb)	2612(2695.87 kb)	NA	0.209

More T than A on the leading strand for replication - for forward encoded genes.
More G than C on the leading strand for replication.

348 Synechococcus sp WH8102

Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
Accession number: NC_005070; **Genome size (bp)**: 2434428.
Number of genes: 2518.
Oriloc predictions: Origin 0 kb Terminus 1237 kb
Worning et al., 2006: Origin 0 kb Terminus 1233 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 521.773 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1480.27 kb
Consensus predictions: Origin 0 kb Terminus 1237 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	641	NA	1216
	928	NA	1735
GC-skew reverse	1624	NA	597
	1971	NA	1314
AT-skew forward	656	NA	1272
AT-skew reverse	1933	NA	1235

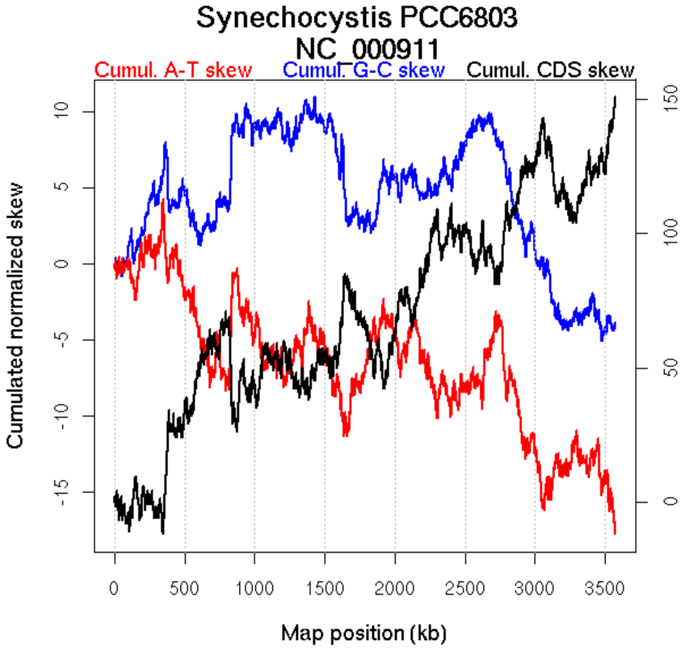
Segments:

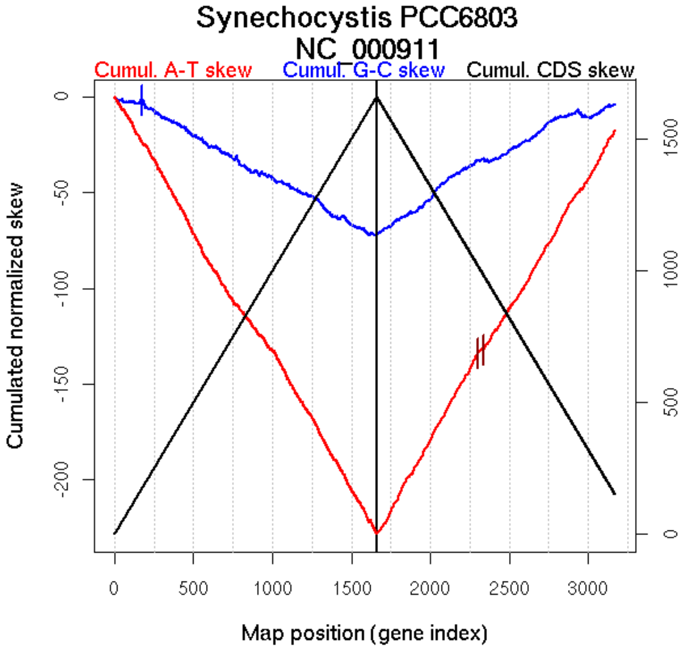
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	641 (1216.2305 kb)	leading	0.038
	642(1220.713 kb)	928 (1734.7115 kb)	lagging	-0.072
	929(1736.807 kb)	1343 (2434.164 kb)	lagging	-0.119
GC-skew reverse	1344 (0 kb)	1624 (596.685 kb)	leading	0.102
	1625(604.7675 kb)	1971 (1314.3465 kb)	leading	0.057
	1972(1318.91 kb)	2518 (2434.164 kb)	lagging	-0.048
AT-skew forward	1 (0 kb)	656 (1272.194 kb)	leading	-0.354
	657(1274.33 kb)	1343 (2434.164 kb)	lagging	-0.127
AT-skew reverse	1344 (0 kb)	1933 (1235.182 kb)	leading	0.128
	1934(1237.868 kb)	2518(2434.164 kb)	lagging	0.334

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

349 Synechocystis PCC6803

Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
Accession number: NC_000911; **Genome size (bp)**: 3573470.
Number of genes: 3171.
Oriloc predictions: Origin NA Terminus NA
Worning et al., 2006: Origin 665 kb Terminus 3117 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 560.361 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1350.91 kb
Consensus predictions: Origin 220 kb Terminus 3062 kb





Significant breakpoints (p-value <0.05):

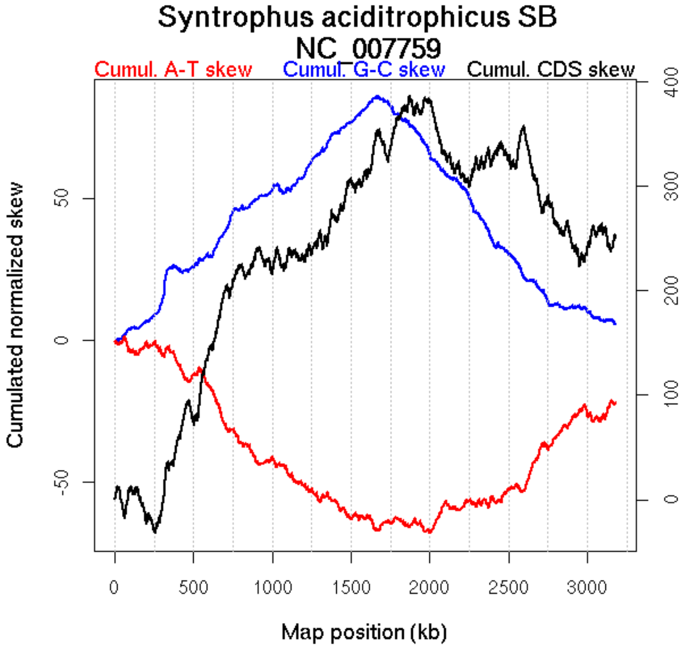
	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	174	0.01333	369
AT-skew reverse	2303	0.02333	1481
	2339	0.03	1557

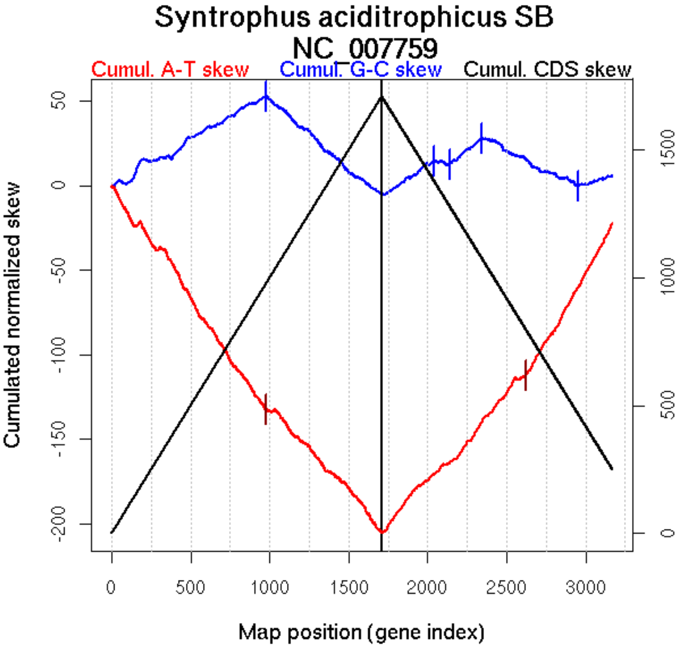
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	174 (369.028 kb)	NA	-0.009
	175(370.2505 kb)	1661 (3572.4 kb)	leading	-0.046
AT-skew reverse	1662 (0 kb)	2303 (1480.668 kb)	NA	0.148
	2304(1481.314 kb)	2339(1556.5955 kb)	leading	0.063
	2340(1557.5645 kb)	3171(3572.4 kb)	NA	0.138

350 Syntrophus aciditrophicus SB

Bacteria; Proteobacteria; Deltaproteobacteria; Syntrophobacterales; Syntrophaceae; Syntrophus.
Accession number: NC_007759; **Genome size (bp)**: 3179300.
Number of genes: 3168.
Oriloc predictions: Origin 0 kb Terminus 1665 kb
Worning et al., 2006: Origin 3149 kb Terminus 1798 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 859.145 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.84 kb
Consensus predictions: Origin 0 kb Terminus 1665 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	980	0	1660
GC-skew reverse	2043	0.03	936
	2141	0.02167	1123
	2343	0.00667	1668
	2956	0.04833	2782
AT-skew forward	975	0.01333	1656
AT-skew reverse	2622	0.00667	2205

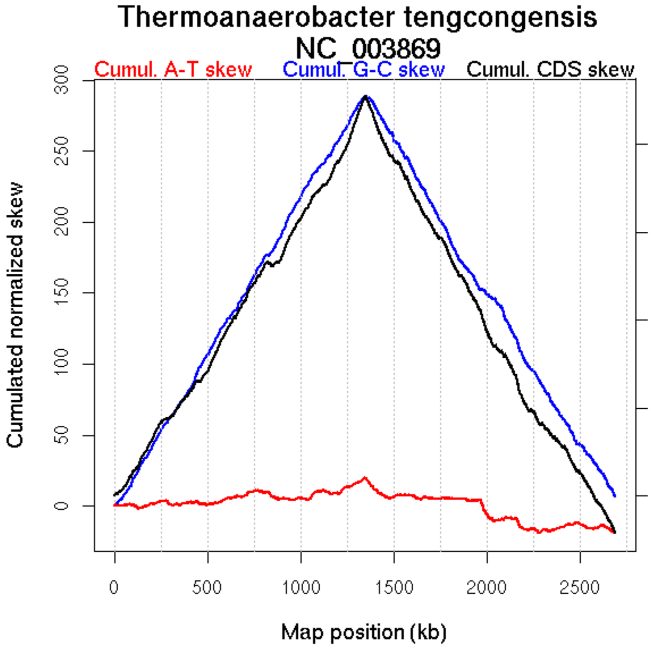
Segments:

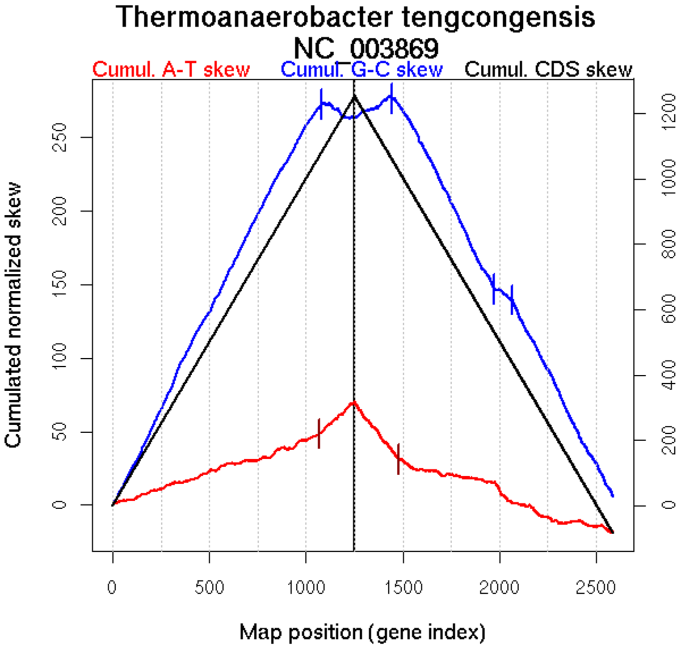
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	980 (1660.08 kb)	leading	0.055
	981(1661.6295 kb)	1710 (3178.51 kb)	lagging	-0.082
GC-skew reverse	1711 (0 kb)	2043 (936.269 kb)	leading	0.065
	2044(938.773 kb)	2141 (1122.8715 kb)	leading	-0.024
	2142(1124.362 kb)	2343 (1668.4735 kb)	leading	0.076
	2344(1669.327 kb)	2956 (2782.393 kb)	lagging	-0.048
	2957(2783.173 kb)	3168 (3178.51 kb)	lagging	0.029
AT-skew forward	1 (0 kb)	975 (1656.4535 kb)	leading	-0.136
	976(1657.2495 kb)	1710 (3178.51 kb)	lagging	-0.101
AT-skew reverse	1711 (0 kb)	2622 (2205.2075 kb)	NA	0.102
	2623(2205.943 kb)	3168(3178.51 kb)	lagging	0.163

More T than A on the leading strand for replication - for forward encoded genes.
More G than C on the leading strand for replication.

351 Thermoanaerobacter tengcongensis

Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales; Thermoanaerobacteriaceae; Thermoanaerobacter.
Accession number: NC_003869; **Genome size (bp)**: 2689445.
Number of genes: 2588.
Oriloc predictions: Origin 0 kb Terminus 1345 kb
Worning et al., 2006: Origin 0 kb Terminus 1346 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 519.651 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1.03 kb
Consensus predictions: Origin 0 kb Terminus 1345 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1082	0	1341
GC-skew reverse	1446	0	1363
	1975	0.00667	1960
	2064	0.00667	2037
AT-skew forward	1071	0	1330
AT-skew reverse	1480	0	1394

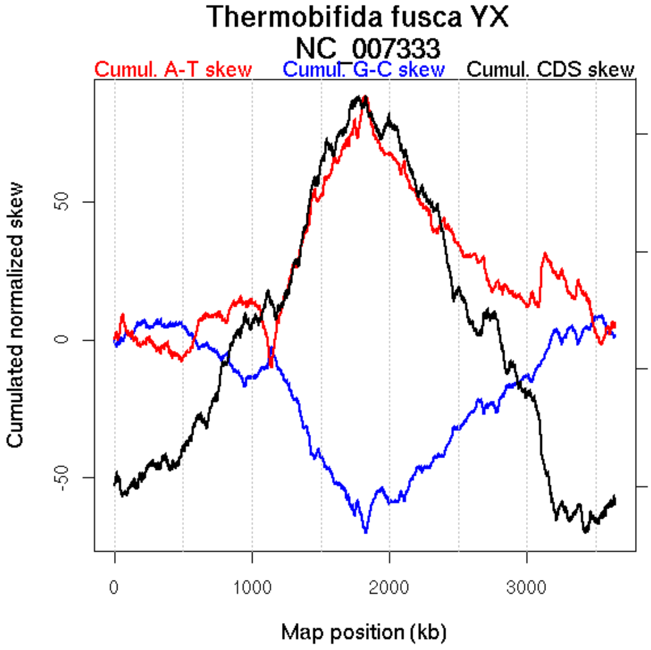
Segments:

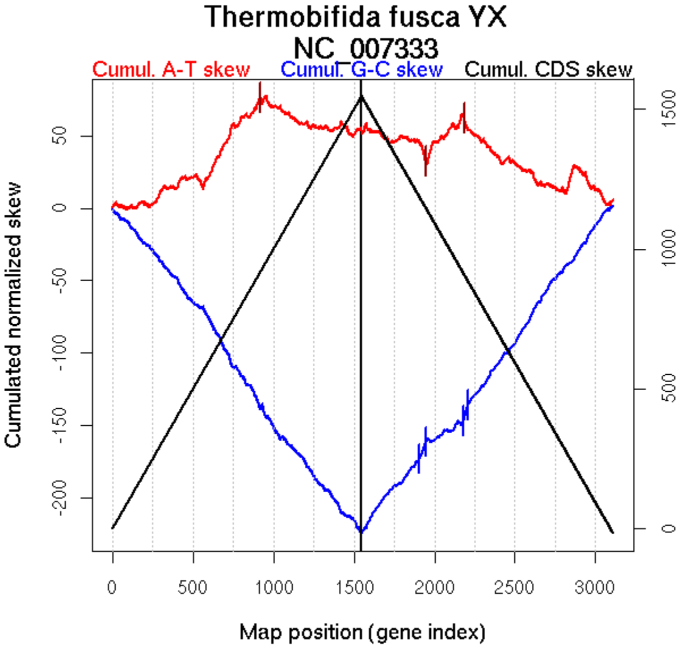
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1082 (1340.943 kb)	leading	0.259
	1083(1342.719 kb)	1252 (2689.325 kb)	lagging	-0.075
GC-skew reverse	1253 (0 kb)	1446 (1362.7245 kb)	leading	0.072
	1447(1363.977 kb)	1975 (1959.6505 kb)	lagging	-0.259
	1976(1960.7975 kb)	2064 (2037.0795 kb)	lagging	-0.09
	2065(2038.3285 kb)	2588 (2689.325 kb)	lagging	-0.257
AT-skew forward	1 (0 kb)	1071 (1330.136 kb)	leading	0.043
	1072(1331.3915 kb)	1252 (2689.325 kb)	lagging	0.12
AT-skew reverse	1253 (0 kb)	1480 (1393.87 kb)	NA	-0.164
	1481(1394.8155 kb)	2588(2689.325 kb)	lagging	-0.047

More T than A on the leading strand for replication - for forward encoded genes.
More G than C on the leading strand for replication.

352 Thermobifida fusca YX

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Streptosporangineae; Nocardiopsaceae; Thermobifida.
Accession number: NC_007333; **Genome size (bp)**: 3642249.
Number of genes: 3110.
Oriloc predictions: Origin 3497 kb Terminus 1828 kb
Worning et al., 2006: Origin 1829 kb Terminus 3507 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 2.227 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1.12 kb
Consensus predictions: Origin 3497 kb Terminus 1828 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew reverse	1905	0.025	1012
	1948	0.01	1133
	2182	0.00167	1841
	2209	0.00667	1903
AT-skew forward	917	0.00667	1744
AT-skew reverse	1946	0.04667	1128
	2186	0.04333	1847

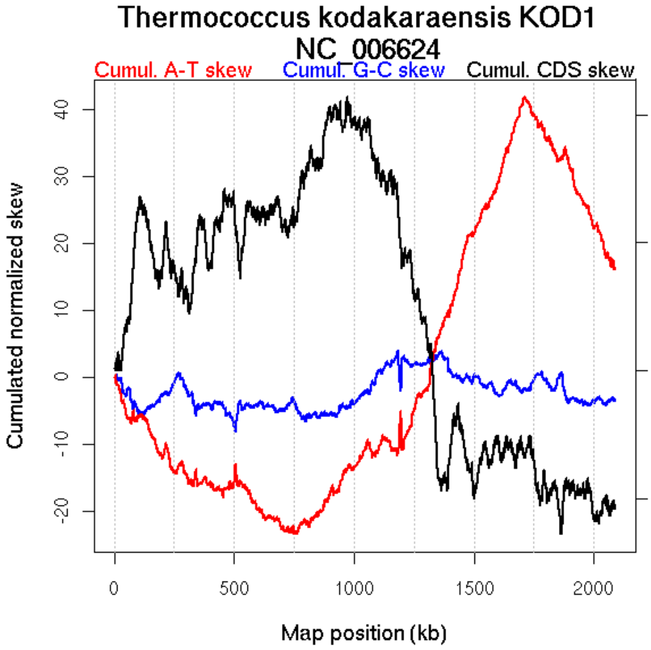
Segments:

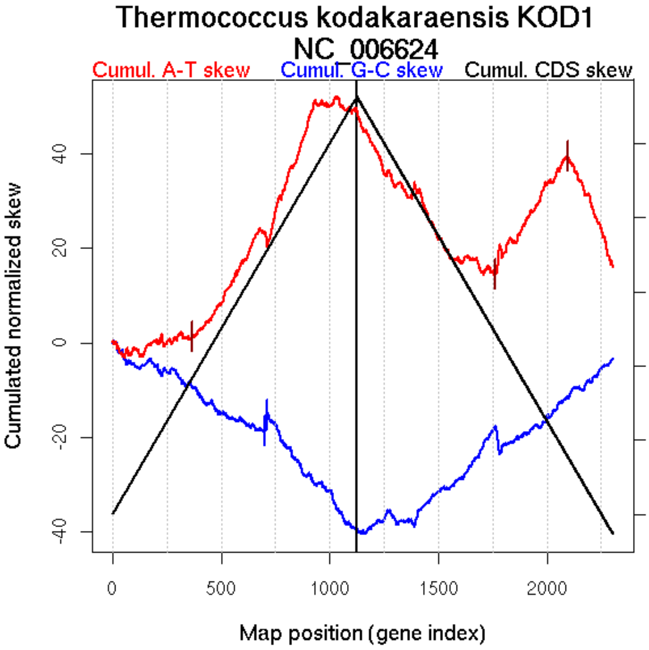
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew reverse	1548 (0 kb)	1905 (1012.204 kb)	leading	0.135
	1906(1014.24 kb)	1948 (1132.7905 kb)	leading	0.276
	1949(1133.404 kb)	2182 (1841.465 kb)	leading	0.063
	2183(1842.1525 kb)	2209 (1902.707 kb)	lagging	0.416
	2210(1905.343 kb)	3110 (3641.655 kb)	lagging	0.157
AT-skew forward	1 (0 kb)	917 (1744.0325 kb)	leading	0.081
	918(1747.9295 kb)	1547 (3641.655 kb)	NA	-0.035
AT-skew reverse	1548 (0 kb)	1946 (1128.164 kb)	leading	-0.031
	1947(1130.325 kb)	2186(1847.268 kb)	leading	0.118
	2187(1850.481 kb)	3110(3641.655 kb)	lagging	-0.047

More A than T on the leading strand for replication - for reverse encoded genes.
More C than G on the leading strand for replication - for reverse encoded genes.

353 Thermococcus kodakaraensis KOD1

Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae; Thermococcus.
Accession number: NC_006624; **Genome size (bp)**: 2088737.
Number of genes: 2305.
Oriloc predictions: Origin 1710 kb Terminus 741 kb
Worning et al., 2006: Origin 1722 kb Terminus 934 kb
Position(s) of the ORC/Cdc6 gene(s): 1712.78 kb
Consensus predictions: Origin 1710 kb Terminus 741 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	702	0	1178
	713	0	1208
AT-skew forward	367	0	579
AT-skew reverse	1760	0.01	1182
	2095	0	1728

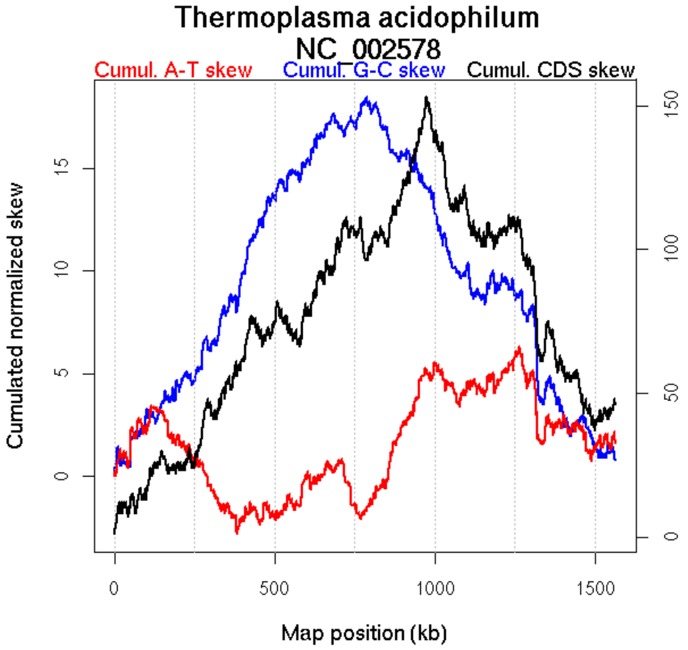
Segments:

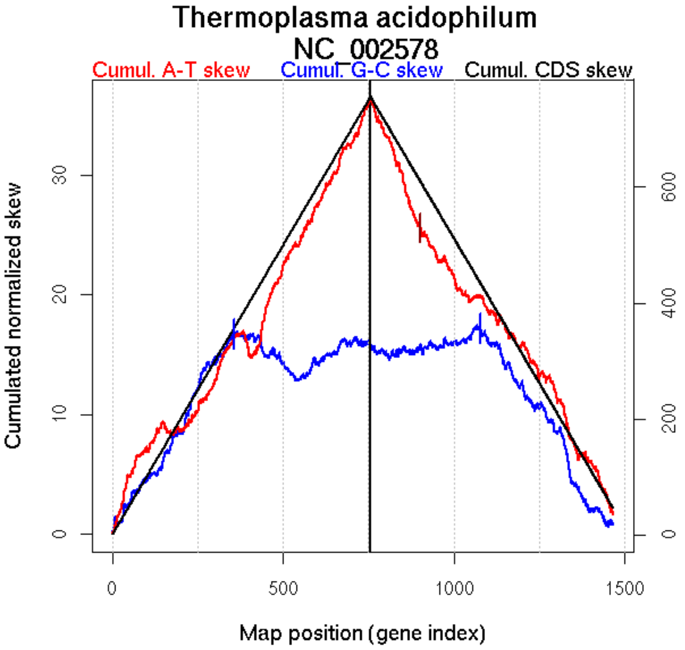
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	702 (1178.024 kb)	NA	-0.027
	703(1178.8205 kb)	713 (1208.4405 kb)	lagging	0.41
	714(1209.222 kb)	1126 (2088.278 kb)	NA	-0.058
AT-skew forward	1 (0 kb)	367 (578.5775 kb)	leading	0.01
	368(579.2805 kb)	1126 (2088.278 kb)	NA	0.078
AT-skew reverse	1127 (0 kb)	1760 (1181.5765 kb)	NA	-0.053
	1761(1181.9395 kb)	2095(1728.435 kb)	lagging	0.071
	2096(1731.83 kb)	2305(2088.278 kb)	leading	-0.111

More T than A on the leading strand for replication - for reverse-encoded genes.

354 Thermoplasma acidophilum

Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales; Thermoplasmataceae; Thermoplasma.
Accession number: NC_002578; **Genome size (bp)**: 1564906.
Number of genes: 1466.
Oriloc predictions: Origin 0 kb Terminus 787 kb
Worning et al., 2006: Origin 1500 kb Terminus 974 kb
Position(s) of the ORC/Cdc6 gene(s): 667.47 kb
Consensus predictions: Origin 0 kb Terminus 787 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	355	0.01333	659
GC-skew reverse	1077	0.00667	814
AT-skew reverse	903	0.04	377

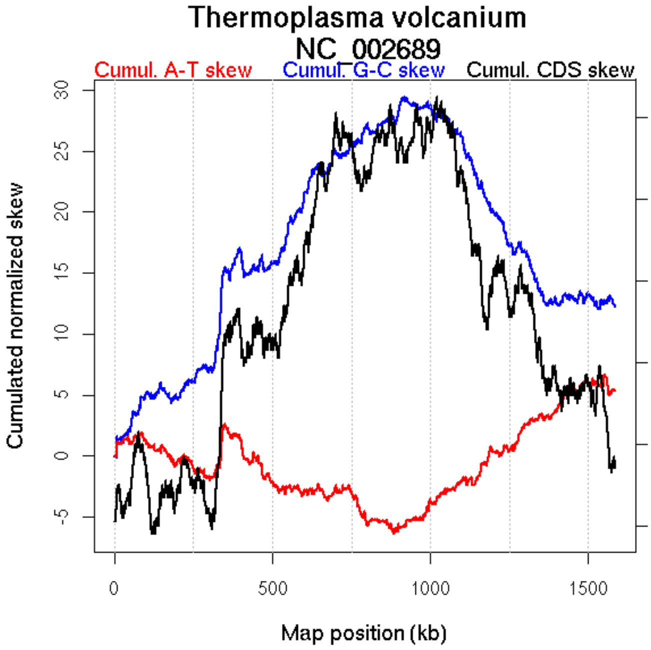
Segments:

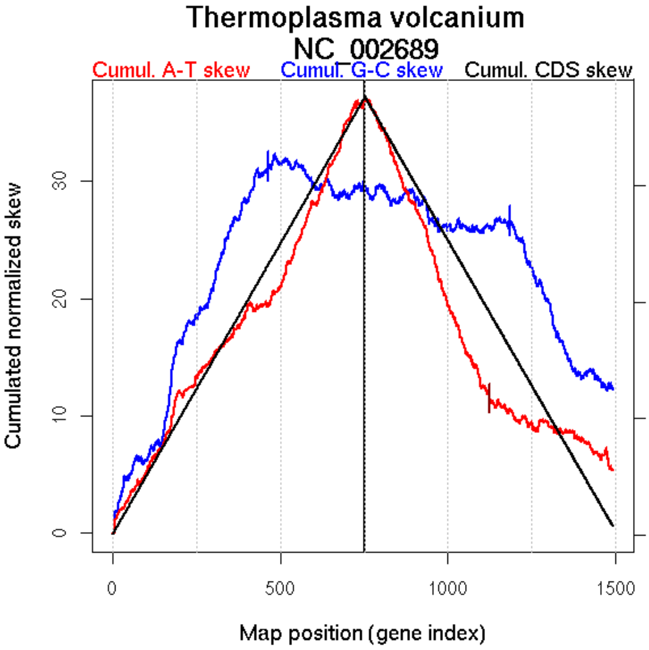
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	355 (658.852 kb)	leading	0.048
	356(660.029 kb)	756 (1564.68 kb)	lagging	-0.001
GC-skew reverse	757 (0 kb)	1077 (813.6245 kb)	leading	0.005
	1078(816.0535 kb)	1466 (1564.68 kb)	lagging	-0.046
AT-skew reverse	757 (0 kb)	903 (377.294 kb)	leading	-0.076
	904(379.068 kb)	1466(1564.68 kb)	NA	-0.039

More G than C on the leading strand for replication.

355 Thermoplasma volcanium

Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales; Thermoplasmataceae; Thermoplasma.
Accession number: NC_002689; **Genome size (bp)**: 1584804.
Number of genes: 1492.
Oriloc predictions: Origin 27 kb Terminus 914 kb
Worning et al., 2006: Origin 185 kb Terminus 952 kb
Position(s) of the ORC/Cdc6 gene(s): 772.43 kb
Consensus predictions: Origin 27 kb Terminus 914 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	465	NA	871
GC-skew reverse	1185	NA	1023
AT-skew reverse	1123	NA	879

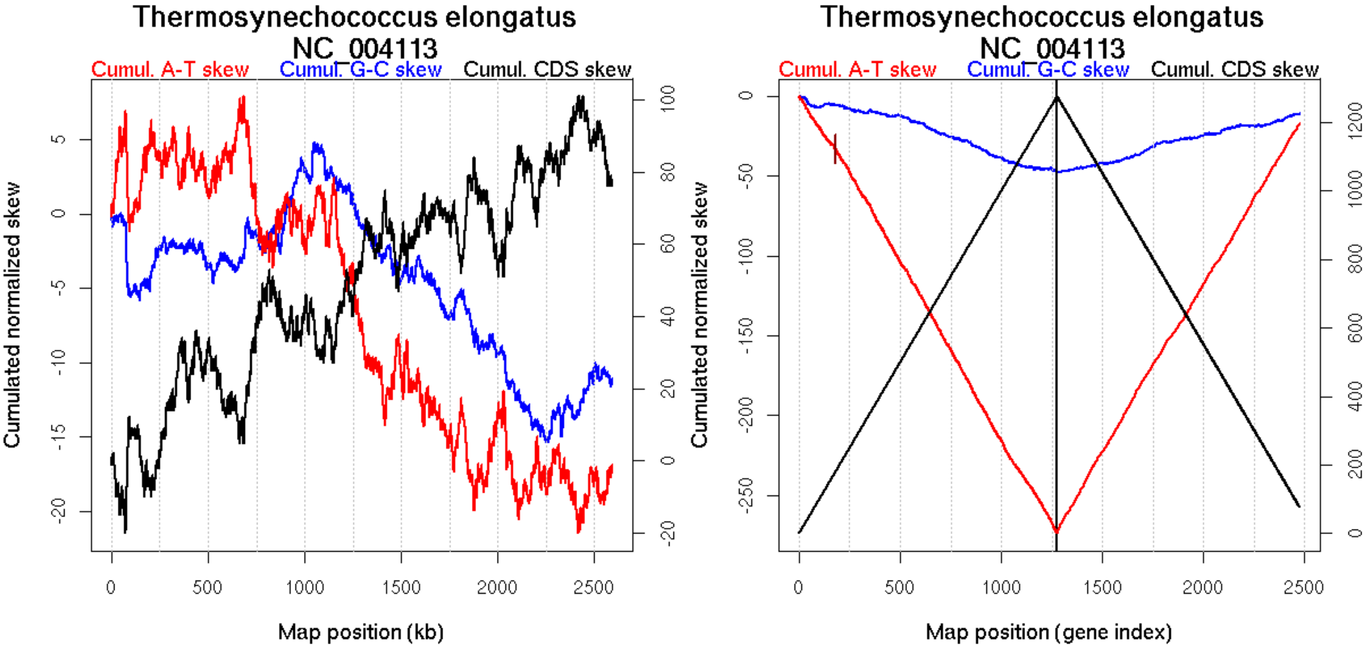
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	465 (870.804 kb)	leading	0.069
	466(871.9805 kb)	753 (1584.691 kb)	lagging	-0.012
GC-skew reverse	754 (0 kb)	1185 (1023.305 kb)	leading	-0.009
	1186(1025.164 kb)	1492 (1584.691 kb)	lagging	-0.05
AT-skew reverse	754 (0 kb)	1123 (878.703 kb)	leading	-0.073
	1124(879.2315 kb)	1492(1584.691 kb)	lagging	-0.013

More T than A on the leading strand for replication - for reverse encoded genes.
More G than C on the leading strand for replication.

356 Thermosynechococcus elongatus

Bacteria; Cyanobacteria; Chroococcales; Thermosynechococcus.
Accession number: NC_004113; **Genome size (bp)**: 2593857.
Number of genes: 2475.
Oriloc predictions: Origin NA Terminus NA
Worning et al., 2006: Origin 441 kb Terminus 1534 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 2339.219 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 610.67 kb
Consensus predictions: Origin 2339 kb Terminus 1125 kb



Significant breakpoints (p-value <0.05):

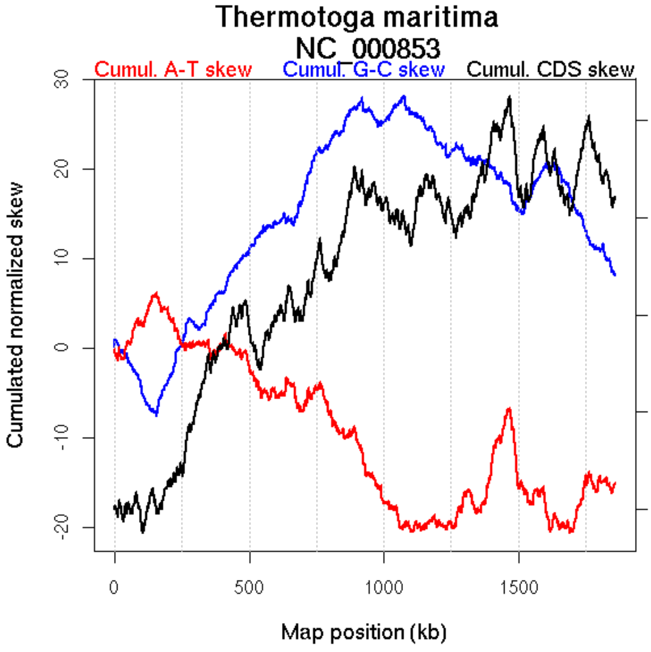
	Breakpoints	P-value	Chromosome coordinate (kb)
AT-skew forward	181	0.04667	334

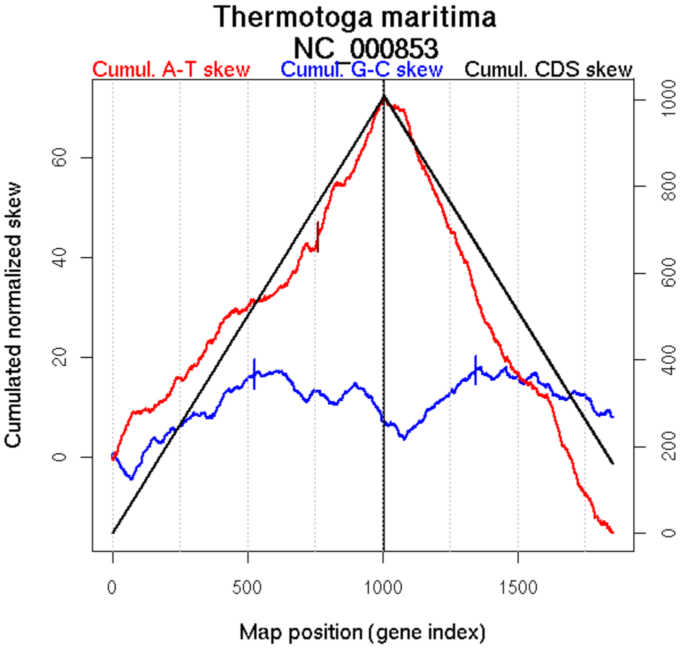
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
AT-skew forward	1 (0 kb)	181 (333.756 kb)	leading	-0.186
	182(334.583 kb)	1276 (2593.504 kb)	NA	-0.221

357 Thermotoga maritima

Bacteria; Thermotogae; Thermotogales; Thermotogaceae; Thermotoga.
Accession number: NC_000853; **Genome size (bp)**: 1860725.
Number of genes: 1854.
Oriloc predictions: Origin 156 kb Terminus 1076 kb
Worning et al., 2006: Origin 164 kb Terminus 892 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1798.282 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 944.91 kb
Consensus predictions: Origin 156 kb Terminus 1076 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	526	0.00667	916
GC-skew reverse	1344	0	852
AT-skew forward	762	0.01333	1385

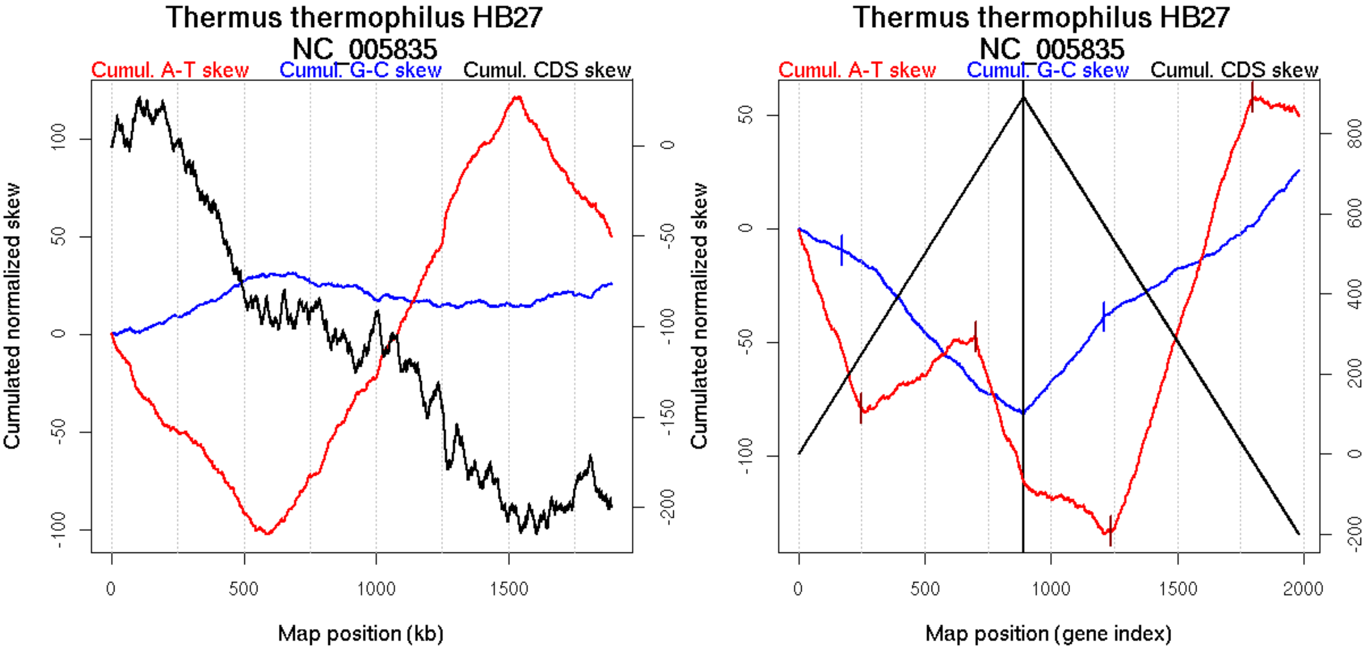
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	526 (916.348 kb)	leading	0.037
	527(916.979 kb)	1007 (1860.498 kb)	lagging	-0.013
GC-skew reverse	1008 (0 kb)	1344 (851.633 kb)	NA	0.039
	1345(863.6995 kb)	1854 (1860.498 kb)	NA	-0.018
AT-skew forward	1 (0 kb)	762 (1384.94 kb)	NA	0.053
	763(1385.536 kb)	1007 (1860.498 kb)	lagging	0.102

More G than C on the leading strand for replication - for forward encoded genes.

358 Thermus thermophilus HB27

Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae; Thermus.
Accession number: NC_005835; **Genome size (bp)**: 1894877.
Number of genes: 1982.
Oriloc predictions: Origin 1532 kb Terminus 609 kb
Worning et al., 2006: Origin 1543 kb Terminus 606 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1524.36 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1523.67 kb
Consensus predictions: Origin 1524 kb Terminus 609 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	173	0.01333	365
GC-skew reverse	1210	0.00667	538
AT-skew forward	247	0	573
	700	0	1524
AT-skew reverse	1238	0	591
	1799	0	1536

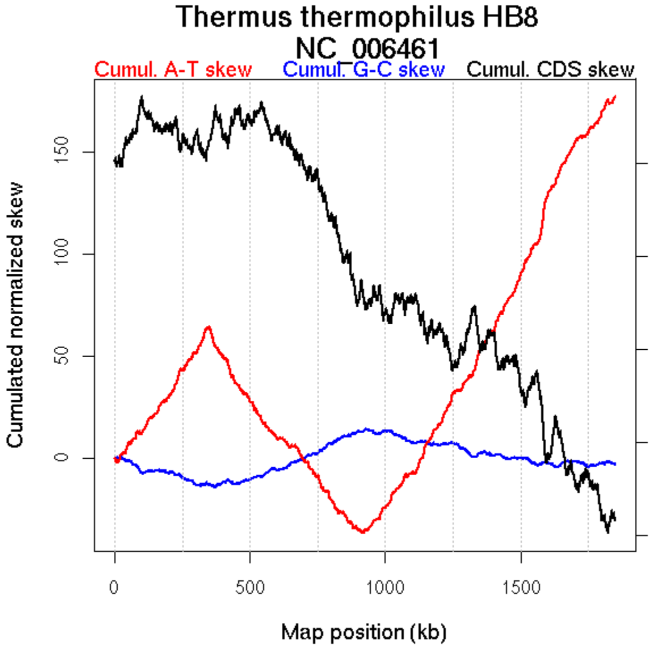
Segments:

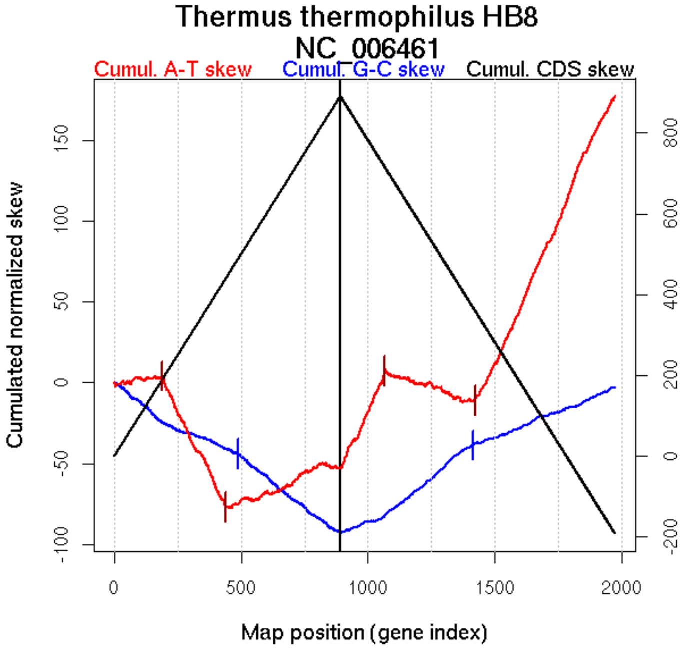
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	173 (365.194 kb)	leading	-0.053
	174(372.289 kb)	891 (1891.601 kb)	NA	-0.111
GC-skew reverse	892 (0 kb)	1210 (538.108 kb)	leading	0.13
	1211(542.6895 kb)	1982 (1891.601 kb)	NA	0.078
AT-skew forward	1 (0 kb)	247 (573.086 kb)	leading	-0.315
	248(574.73 kb)	700 (1524.4895 kb)	lagging	0.08
	701(1525.794 kb)	891 (1891.601 kb)	leading	-0.319
AT-skew reverse	892 (0 kb)	1238 (590.7325 kb)	leading	-0.058
	1239(591.3 kb)	1799(1535.845 kb)	lagging	0.358
	1800(1538.5205 kb)	1982(1891.601 kb)	leading	-0.033

More T than A on the leading strand for replication.

359 Thermus thermophilus HB8

Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae; Thermus.
Accession number: NC_006461; **Genome size (bp)**: 1849742.
Number of genes: 1973.
Oriloc predictions: Origin 372 kb Terminus 927 kb
Worning et al., 2006: Origin 372 kb Terminus 932 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1849.515 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1848.84 kb
Consensus predictions: Origin 372 kb Terminus 927 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	488	NA	1002
GC-skew reverse	1414	NA	919
AT-skew forward	189	NA	348
	440	NA	901
AT-skew reverse	1067	NA	337
	1422	NA	928

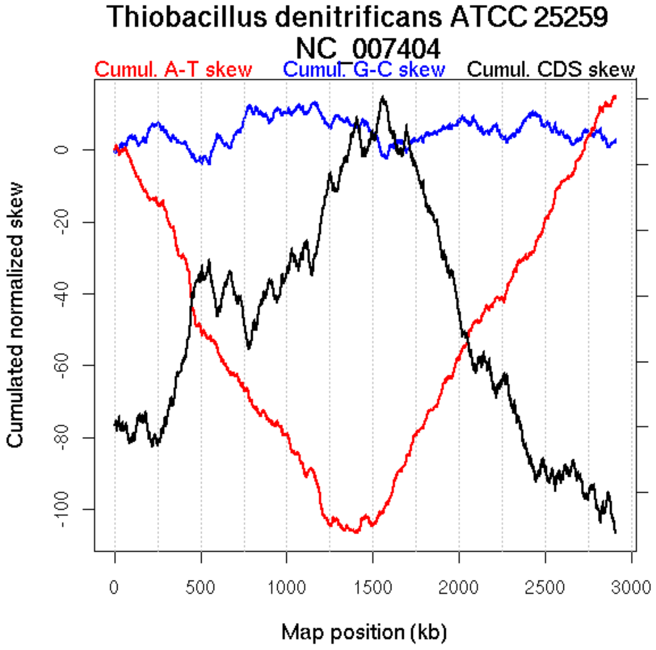
Segments:

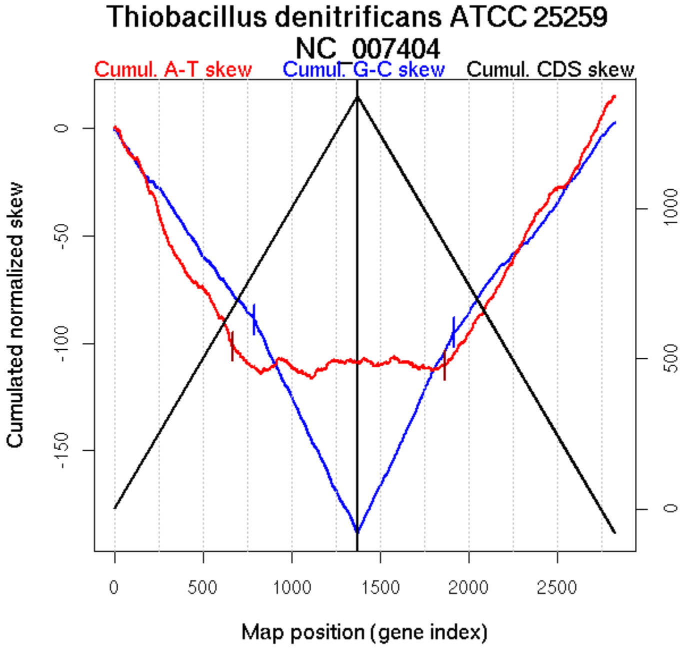
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	488 (1001.9755 kb)	NA	-0.088
	489(1002.524 kb)	891 (1849.492 kb)	lagging	-0.123
GC-skew reverse	892 (0 kb)	1414 (919.412 kb)	NA	0.112
	1415(920.361 kb)	1973 (1849.492 kb)	lagging	0.064
AT-skew forward	1 (0 kb)	189 (348.162 kb)	lagging	0.025
	190(350.4885 kb)	440 (900.803 kb)	leading	-0.31
	441(902.327 kb)	891 (1849.492 kb)	lagging	0.067
AT-skew reverse	892 (0 kb)	1067 (337.4085 kb)	lagging	0.331
	1068(337.979 kb)	1422(928.27 kb)	leading	-0.053
	1423(931.1855 kb)	1973(1849.492 kb)	lagging	0.358

More T than A on the leading strand for replication.

360 Thiobacillus denitrificans ATCC 25259

Bacteria; Proteobacteria; Betaproteobacteria; Hydrogenophilales; Hydrogenophilaceae; Thiobacillus.
Accession number: NC_007404; **Genome size (bp)**: 2909809.
Number of genes: 2827.
Oriloc predictions: Origin 0 kb Terminus 1442 kb
Worning et al., 2006: Origin 2908 kb Terminus 1407 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1.523 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.82 kb
Consensus predictions: Origin 0 kb Terminus 1442 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	791	0	1454
GC-skew reverse	1918	0	1405
AT-skew forward	668	0	1220
AT-skew reverse	1869	0	1214

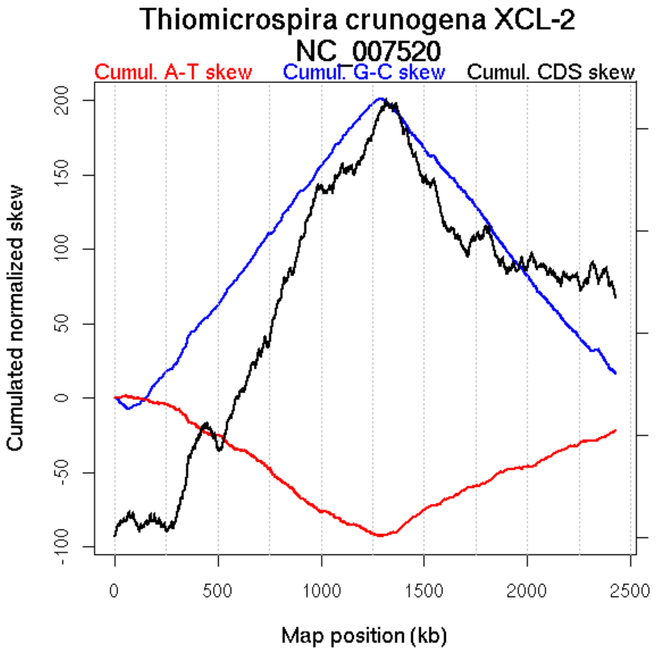
Segments:

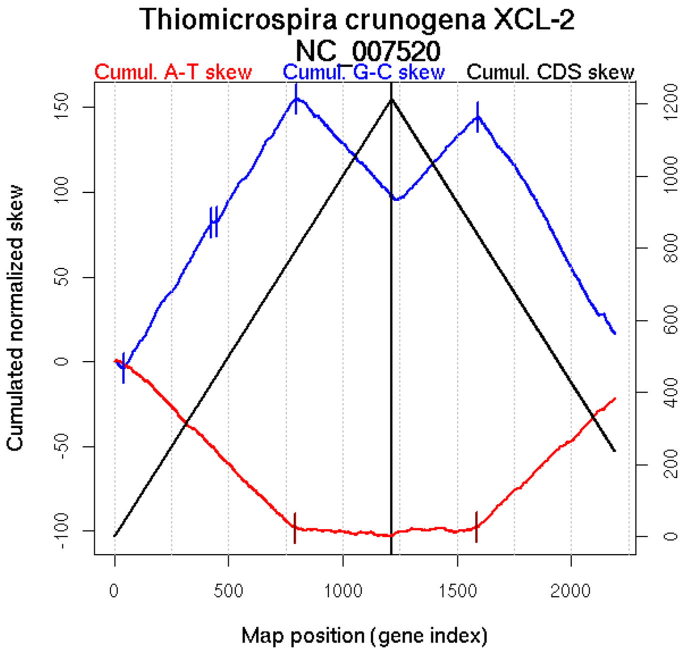
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	791 (1453.5595 kb)	leading	-0.113
	792(1453.9225 kb)	1373 (2909.751 kb)	lagging	-0.17
GC-skew reverse	1374 (0 kb)	1918 (1405.1915 kb)	leading	0.174
	1919(1409.4315 kb)	2827 (2909.751 kb)	lagging	0.106
AT-skew forward	1 (0 kb)	668 (1219.6705 kb)	leading	-0.153
	669(1220.054 kb)	1373 (2909.751 kb)	NA	-0.002
AT-skew reverse	1374 (0 kb)	1869 (1214.088 kb)	leading	-0.007
	1870(1219.3625 kb)	2827(2909.751 kb)	lagging	0.131

More T than A on the leading strand for replication - for reverse encoded genes.
More G than C on the leading strand for replication.

361 Thiomicrospira crunogena XCL-2

Bacteria; Proteobacteria; Gammaproteobacteria; Thiotrichales; Piscirickettsiaceae; Thiomicrospira.
Accession number: NC_007520; **Genome size (bp)**: 2427734.
Number of genes: 2192.
Oriloc predictions: Origin 65 kb Terminus 1293 kb
Worning et al., 2006: Origin 54 kb Terminus 1320 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 2427.486 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.7 kb, 1125.83 kb
Consensus predictions: Origin 65 kb Terminus 1293 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	38	0	66
	423	0.00667	729
	450	0.01	764
	796	0	1286
GC-skew reverse	1592	0	1272
AT-skew forward	791	0	1279
AT-skew reverse	1587	0	1231

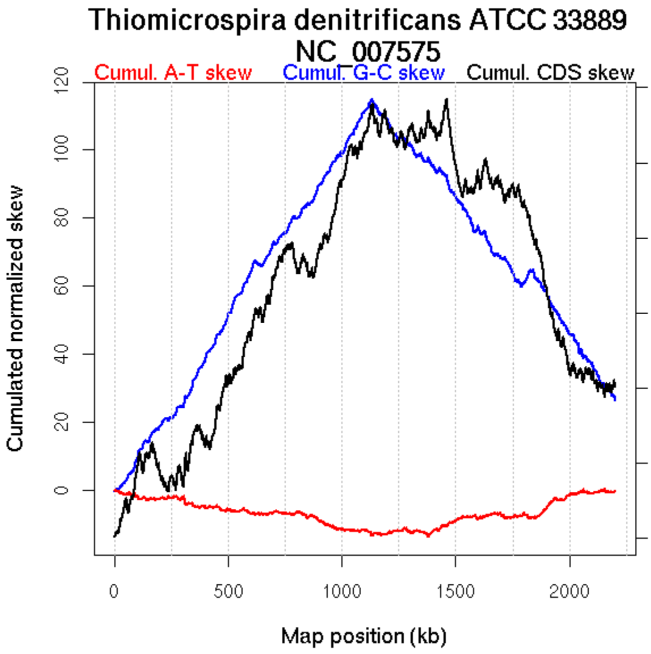
Segments:

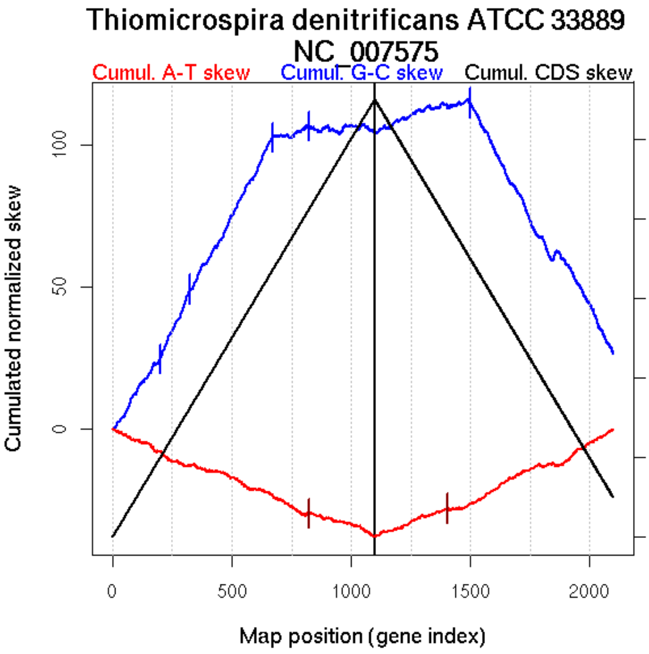
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	38 (66.3575 kb)	lagging	-0.124
	39(67.1255 kb)	423 (728.6795 kb)	leading	0.222
	424(734.7235 kb)	450 (763.987 kb)	leading	0.009
	451(764.5035 kb)	796 (1285.526 kb)	leading	0.211
	797(1288.1035 kb)	1214 (2427.452 kb)	lagging	-0.142
GC-skew reverse	1215 (0 kb)	1592 (1271.9675 kb)	leading	0.143
	1593(1276.181 kb)	2192 (2427.452 kb)	lagging	-0.225
AT-skew forward	1 (0 kb)	791 (1278.896 kb)	leading	-0.132
	792(1279.5865 kb)	1214 (2427.452 kb)	lagging	-0.01
AT-skew reverse	1215 (0 kb)	1587 (1231.1895 kb)	leading	0.003
	1588(1232.836 kb)	2192(2427.452 kb)	lagging	0.126

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

362 Thiomicrospira denitrificans ATCC 33889

Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae.
Accession number: NC_007575; **Genome size (bp)**: 2201561.
Number of genes: 2097.
Oriloc predictions: Origin 17 kb Terminus 1132 kb
Worning et al., 2006: Origin 2186 kb Terminus 1133 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 2073.631 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.67 kb
Consensus predictions: Origin 17 kb Terminus 1132 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	199	NA	336
	325	NA	542
	671	NA	1126
	824	NA	1445
GC-skew reverse	1497	NA	1141
AT-skew forward	823	NA	1445
AT-skew reverse	1403	NA	828

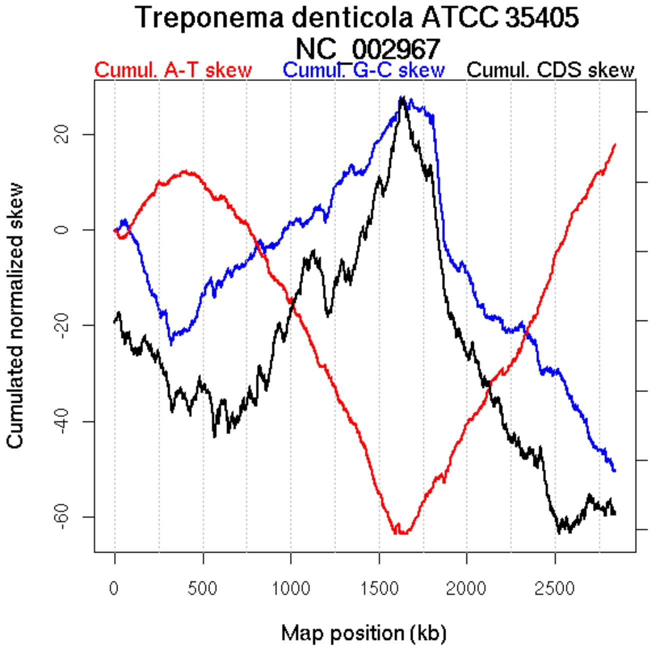
Segments:

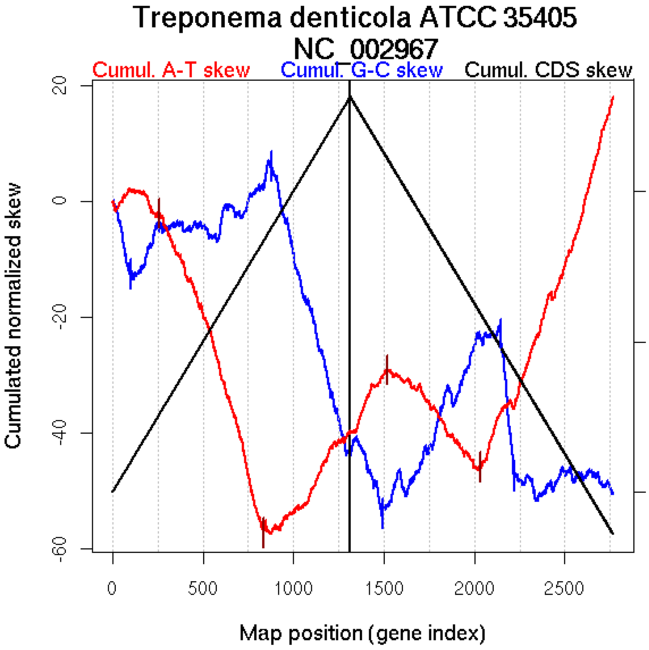
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	199 (335.598 kb)	leading	0.133
	200(336.4615 kb)	325 (541.914 kb)	leading	0.187
	326(543.411 kb)	671 (1126.308 kb)	leading	0.156
	672(1127.1445 kb)	824 (1445.4465 kb)	lagging	0.023
	825(1445.8985 kb)	1099 (2201.474 kb)	lagging	0.002
GC-skew reverse	1100 (0 kb)	1497 (1141.1595 kb)	leading	0.027
	1498(1142.0275 kb)	2097 (2201.474 kb)	lagging	-0.14
AT-skew forward	1 (0 kb)	823 (1444.694 kb)	NA	-0.035
	824(1445.4465 kb)	1099 (2201.474 kb)	lagging	-0.027
AT-skew reverse	1100 (0 kb)	1403 (828.2695 kb)	leading	0.033
	1404(831.2045 kb)	2097(2201.474 kb)	lagging	0.041

More T than A on the leading strand for replication - for reverse encoded genes.
More G than C on the leading strand for replication.

363 Treponema denticola ATCC 35405

Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
Accession number: NC_002967; **Genome size (bp)**: 2843201.
Number of genes: 2767.
Oriloc predictions: Origin 397 kb Terminus 1592 kb
Worning et al., 2006: Origin 325 kb Terminus 1641 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 256.83 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.87 kb
Consensus predictions: Origin 397 kb Terminus 1592 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	103	0	277
	877	0	1666
GC-skew reverse	1491	0.03778	325
	2145	0	1813
	2224	0	1880
AT-skew forward	257	0.02	608
	836	0.01333	1593
AT-skew reverse	1520	0.01333	404
	2034	0.00667	1654

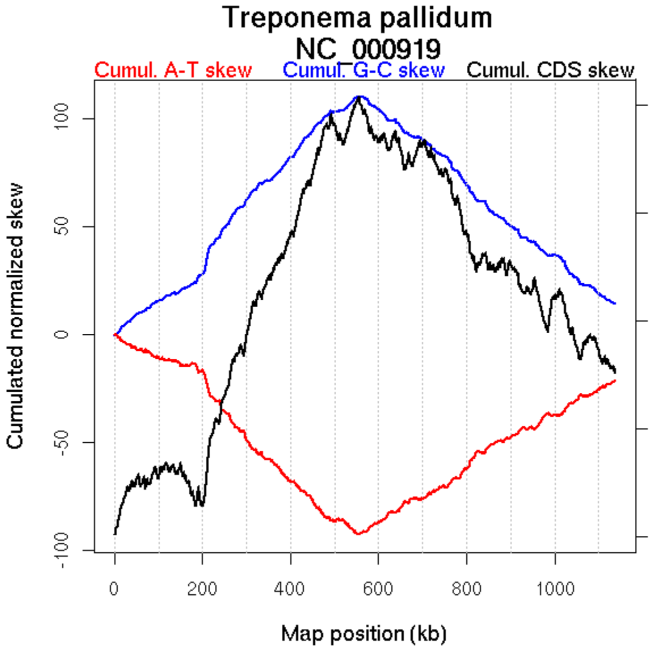
Segments:

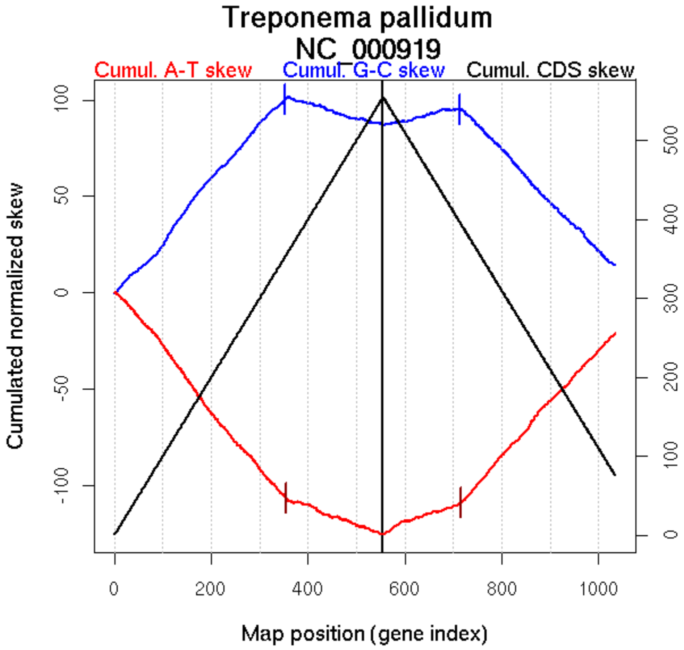
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	103 (277.024 kb)	lagging	-0.144
	104(282.626 kb)	877 (1666.271 kb)	leading	0.016
	878(1676.4335 kb)	1314 (2842.762 kb)	lagging	-0.117
GC-skew reverse	1315 (0 kb)	1491 (325.1615 kb)	lagging	-0.07
	1492(326.072 kb)	2145 (1813.0125 kb)	NA	0.054
	2146(1813.528 kb)	2224 (1879.7535 kb)	lagging	-0.328
	2225(1880.813 kb)	2767 (2842.762 kb)	lagging	0.002
AT-skew forward	1 (0 kb)	257 (607.776 kb)	NA	-0.005
	258(612.606 kb)	836 (1592.8755 kb)	leading	-0.096
	837(1595.2325 kb)	1314 (2842.762 kb)	lagging	0.041
AT-skew reverse	1315 (0 kb)	1520 (404.11 kb)	lagging	0.059
	1521(406.8645 kb)	2034(1654.093 kb)	leading	-0.036
	2035(1654.5635 kb)	2767(2842.762 kb)	lagging	0.085

More T than A on the leading strand for replication.
More G than C on the leading strand for replication - for forward encoded genes.

364 Treponema pallidum

Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
Accession number: NC_000919; **Genome size (bp)**: 1138011.
Number of genes: 1034.
Oriloc predictions: Origin 0 kb Terminus 554 kb
Worning et al., 2006: Origin 3 kb Terminus 553 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1.434 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.7 kb
Consensus predictions: Origin 0 kb Terminus 554 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	353	NA	544
GC-skew reverse	714	NA	561
AT-skew forward	354	NA	546
AT-skew reverse	716	NA	564

Segments:

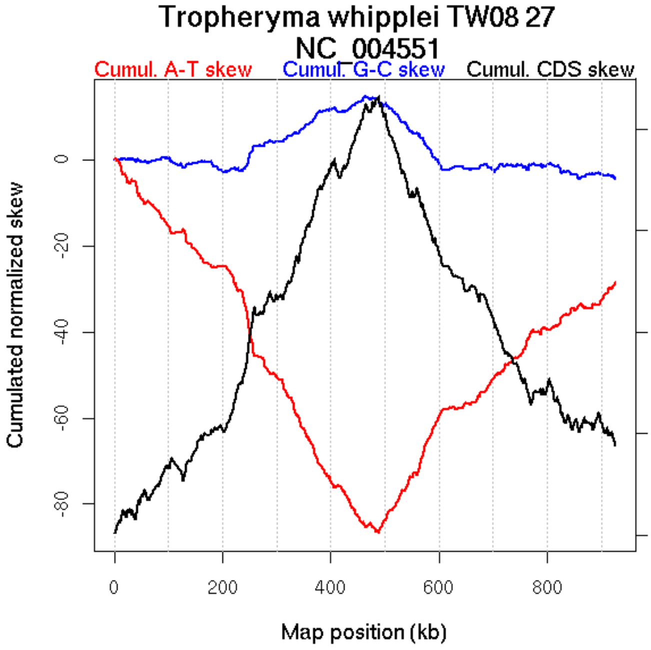
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	353 (544.344 kb)	leading	0.299
	354(545.979 kb)	555 (1137.932 kb)	lagging	-0.075
GC-skew reverse	556 (0 kb)	714 (561.0875 kb)	leading	0.06
	715(562.618 kb)	1034 (1137.932 kb)	lagging	-0.262
AT-skew forward	1 (0 kb)	354 (545.979 kb)	leading	-0.315
	355(547.648 kb)	555 (1137.932 kb)	lagging	-0.094
AT-skew reverse	556 (0 kb)	716 (563.8345 kb)	leading	0.09
	717(565.397 kb)	1034(1137.932 kb)	lagging	0.279

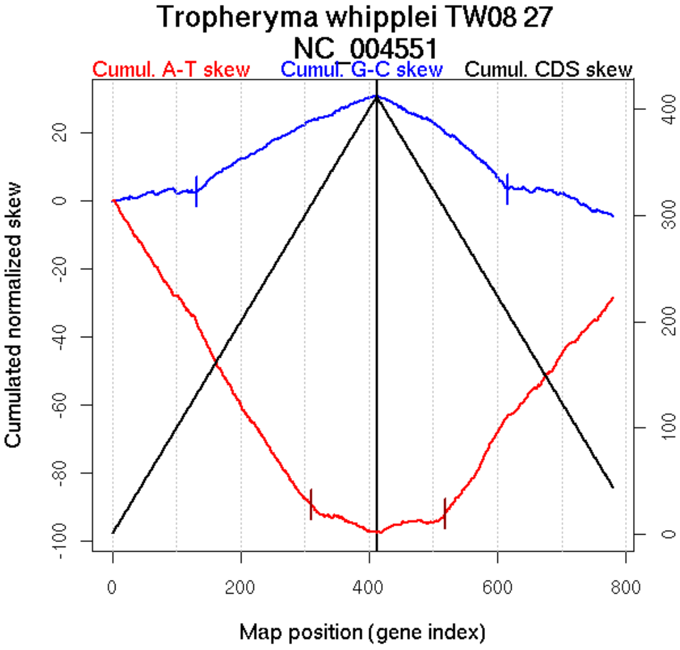
More T than A on the leading strand for replication.

More G than C on the leading strand for replication.

365 Tropheryma whipplei TW08 27

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Micrococcineae; Cellulomonadaceae; Tropheryma.
Accession number: NC_004551; **Genome size (bp)**: 925938.
Number of genes: 780.
Oriloc predictions: Origin 3 kb Terminus 484 kb
Worning et al., 2006: Origin 478 kb Terminus 4 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1.479 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.72 kb
Consensus predictions: Origin 3 kb Terminus 484 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	131	0.00667	239
GC-skew reverse	616	0.04	620
AT-skew forward	310	0	476
AT-skew reverse	518	0	491

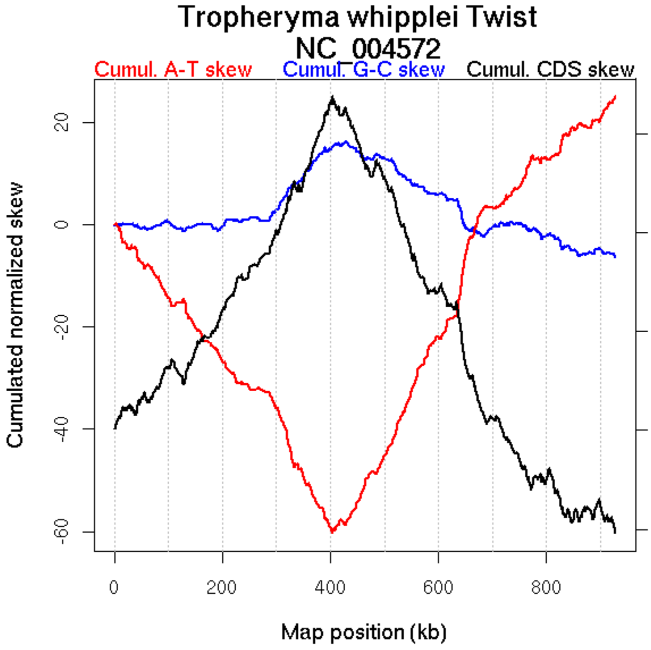
Segments:

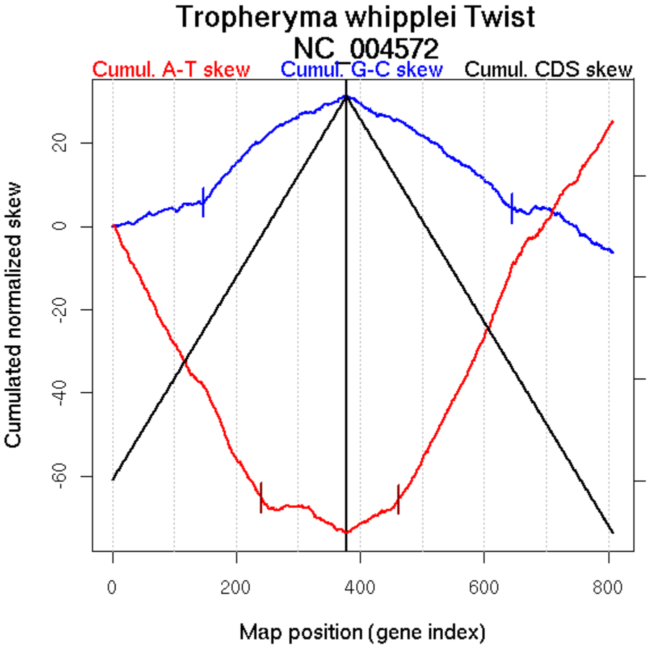
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	131 (239.1485 kb)	leading	0.024
	132(240.175 kb)	412 (925.735 kb)	NA	0.098
GC-skew reverse	413 (0 kb)	616 (619.615 kb)	NA	-0.129
	617(620.812 kb)	780 (925.735 kb)	lagging	-0.055
AT-skew forward	1 (0 kb)	310 (476.237 kb)	leading	-0.298
	311(476.6185 kb)	412 (925.735 kb)	lagging	-0.07
AT-skew reverse	413 (0 kb)	518 (490.7535 kb)	leading	0.033
	519(491.3895 kb)	780(925.735 kb)	lagging	0.241

More T than A on the leading strand for replication.

366 Tropheryma whipplei Twist

Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Micrococcineae; Cellulomonadaceae; Tropheryma.
Accession number: NC_004572; **Genome size (bp)**: 927303.
Number of genes: 808.
Oriloc predictions: Origin 0 kb Terminus 407 kb
Worning et al., 2006: Origin 410 kb Terminus 8 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1.479 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.72 kb
Consensus predictions: Origin 0 kb Terminus 407 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	148	NA	289
GC-skew reverse	646	NA	657
AT-skew forward	241	NA	401
AT-skew reverse	462	NA	414

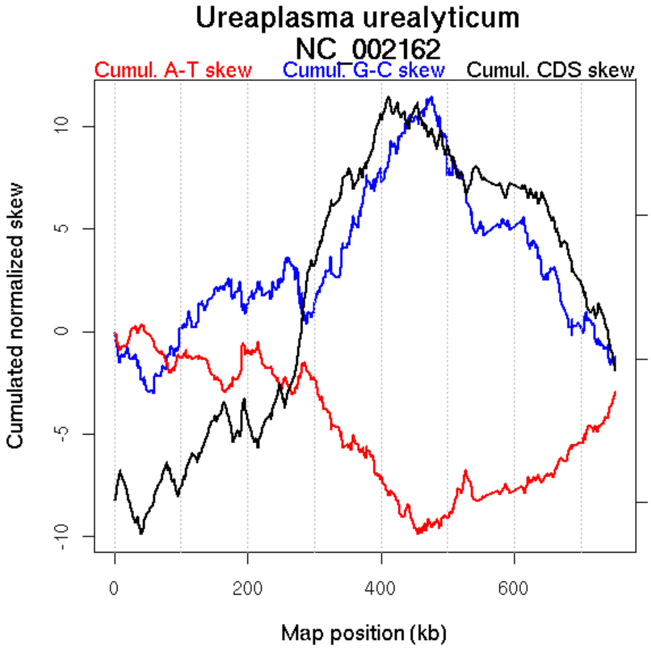
Segments:

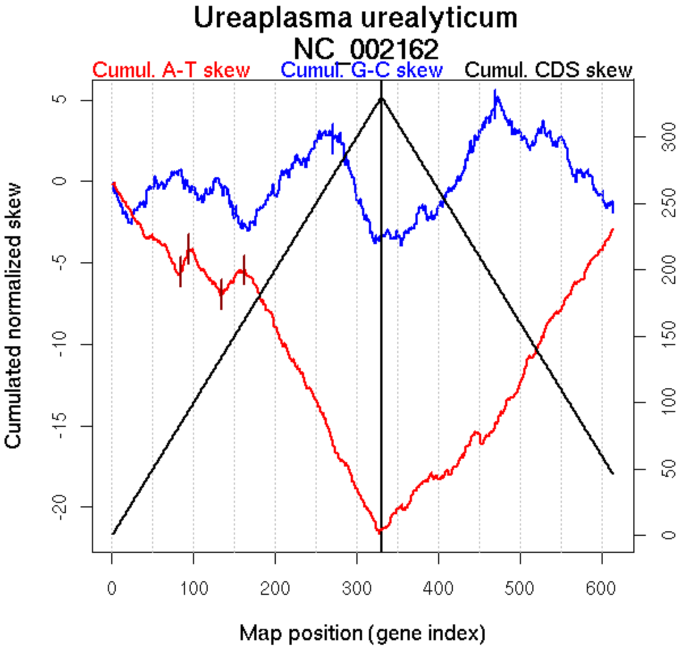
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	148 (288.537 kb)	leading	0.043
	149(288.861 kb)	378 (927.266 kb)	NA	0.104
GC-skew reverse	379 (0 kb)	646 (656.997 kb)	NA	-0.097
	647(659.044 kb)	808 (927.266 kb)	lagging	-0.073
AT-skew forward	1 (0 kb)	241 (400.5935 kb)	leading	-0.272
	242(402.0155 kb)	378 (927.266 kb)	lagging	-0.049
AT-skew reverse	379 (0 kb)	462 (413.783 kb)	leading	0.083
	463(416.0635 kb)	808(927.266 kb)	lagging	0.272

More T than A on the leading strand for replication.

367 Ureaplasma urealyticum

Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Ureaplasma.
Accession number: NC_002162; **Genome size (bp)**: 751719.
Number of genes: 614.
Oriloc predictions: Origin 30 kb Terminus 459 kb
Worning et al., 2006: Origin 41 kb Terminus 477 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 7.598 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.69 kb
Consensus predictions: Origin 0 kb Terminus 459 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	270	0	465
GC-skew reverse	470	0.04667	467
AT-skew forward	85	0.00333	190
	94	0.00167	193
	134	0.03833	268
	162	0.02167	286

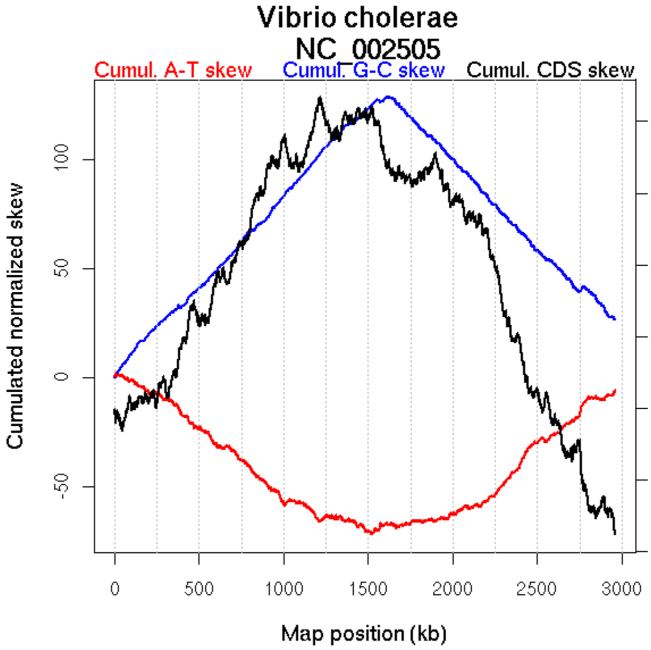
Segments:

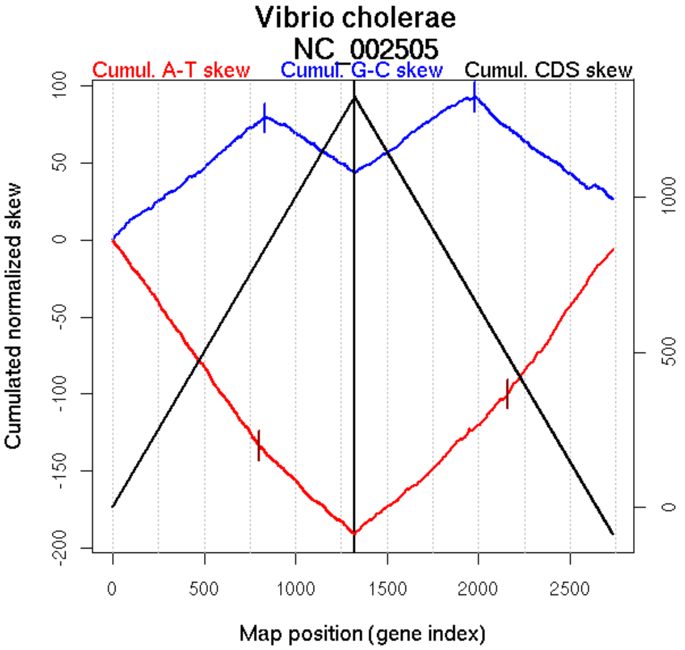
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	270 (465.478 kb)	leading	0.01
	271(469.4695 kb)	330 (751.549 kb)	lagging	-0.131
GC-skew reverse	331 (0 kb)	470 (467.002 kb)	leading	0.06
	471(468.704 kb)	614 (751.549 kb)	lagging	-0.04
AT-skew forward	1 (0 kb)	85 (189.7935 kb)	leading	-0.063
	86(190.4065 kb)	94 (192.8035 kb)	leading	0.165
	95(193.4825 kb)	134 (267.907 kb)	leading	-0.07
	135(270.4155 kb)	162 (285.616 kb)	leading	0.058
	163(287.062 kb)	330 (751.549 kb)	NA	-0.099

More G than C on the leading strand for replication.

368 Vibrio cholerae

Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio.
Accession number: NC_002505; **Genome size (bp)**: 2961149.
Number of genes: 2736.
Oriloc predictions: Origin 5 kb Terminus 1620 kb
Worning et al., 2006: Origin 7 kb Terminus 1564 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 0.219 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 8.11 kb
Consensus predictions: Origin 5 kb Terminus 1620 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	833	0	1641
GC-skew reverse	1982	0	1624
AT-skew forward	802	0.00667	1517
AT-skew reverse	2161	0	1987

Segments:

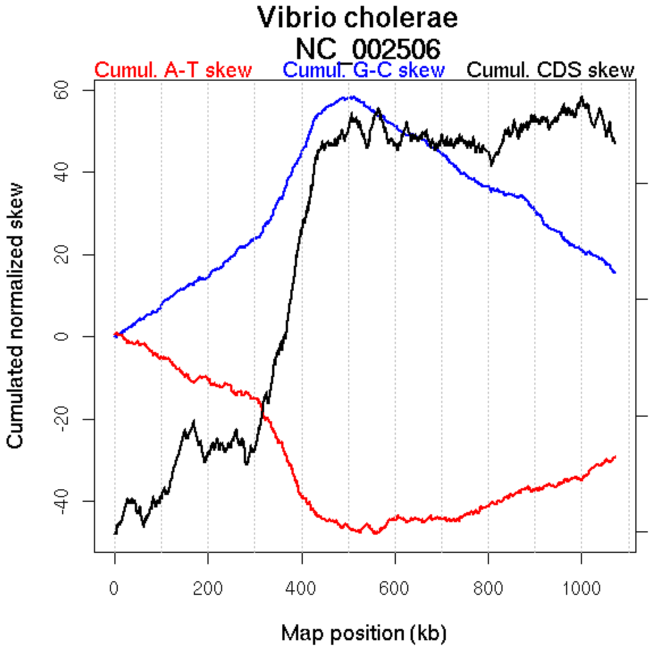
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	833 (1640.6995 kb)	leading	0.093
	834(1641.286 kb)	1324 (2961.046 kb)	lagging	-0.076
GC-skew reverse	1325 (0 kb)	1982 (1623.6115 kb)	leading	0.081
	1983(1624.1205 kb)	2736 (2961.046 kb)	lagging	-0.086
AT-skew forward	1 (0 kb)	802 (1516.533 kb)	leading	-0.168
	803(1517.347 kb)	1324 (2961.046 kb)	lagging	-0.11
AT-skew reverse	1325 (0 kb)	2161 (1986.5735 kb)	NA	0.108
	2162(1987.6625 kb)	2736(2961.046 kb)	lagging	0.168

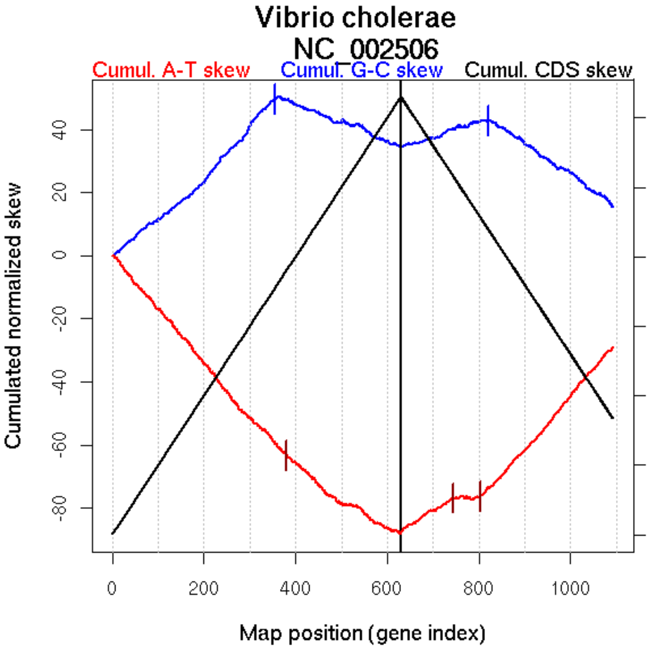
More T than A on the leading strand for replication - for forward encoded genes.

More G than C on the leading strand for replication.

369 Vibrio cholerae

Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio.
Accession number: NC_002506; **Genome size (bp)**: 1072315.
Number of genes: 1093.
Oriloc predictions: Origin 5 kb Terminus 512 kb
Worning et al., 2006: Origin 100 kb Terminus 514 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 723.731 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): NA
Consensus predictions: Origin 5 kb Terminus 512 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	354	0	486
GC-skew reverse	821	0	509
AT-skew forward	381	0.01333	545
AT-skew reverse	745	0.03333	281
	803	0	458

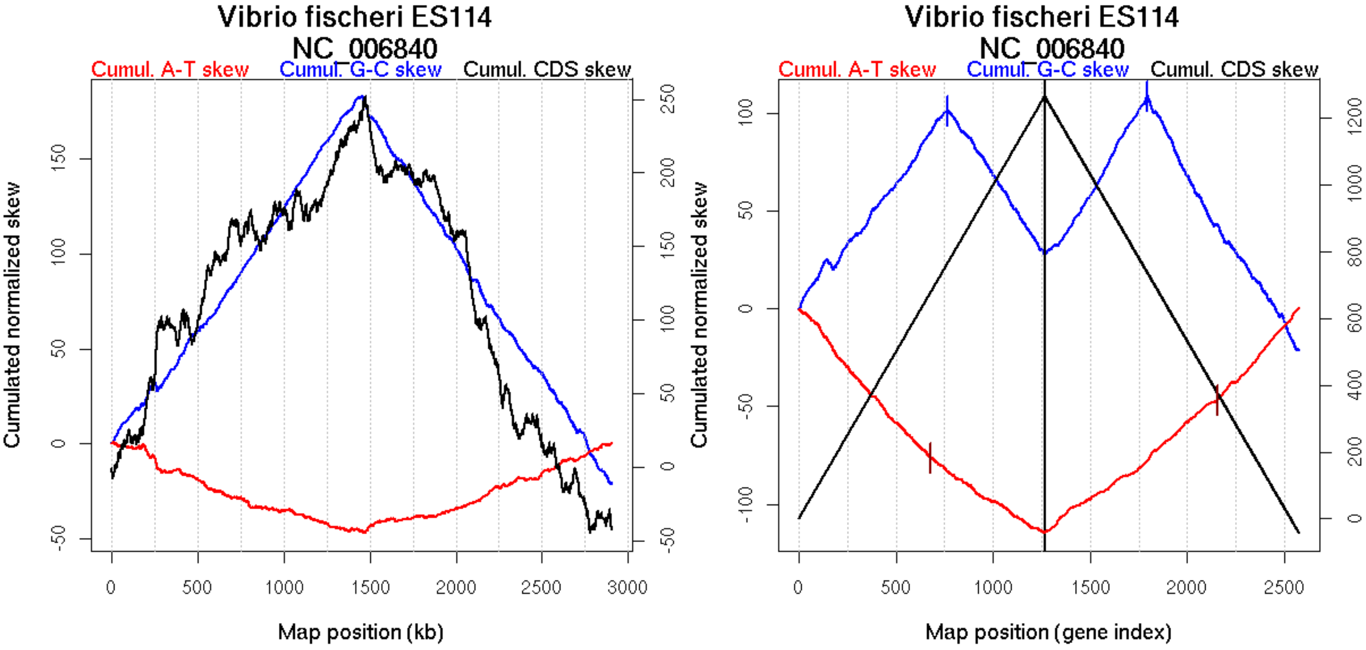
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	354 (485.741 kb)	leading	0.14
	355(486.27 kb)	630 (1072.22 kb)	lagging	-0.058
GC-skew reverse	631 (0 kb)	821 (509.385 kb)	leading	0.048
	822(510.0315 kb)	1093 (1072.22 kb)	lagging	-0.099
AT-skew forward	1 (0 kb)	381 (544.911 kb)	leading	-0.17
	382(545.865 kb)	630 (1072.22 kb)	lagging	-0.099
AT-skew reverse	631 (0 kb)	745 (281.249 kb)	leading	0.089
	746(282.224 kb)	803(458.1885 kb)	leading	0
	804(459.648 kb)	1093(1072.22 kb)	lagging	0.167

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

370 Vibrio fischeri ES114

Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio.
Accession number: NC_006840; **Genome size (bp)**: 2906179.
Number of genes: 2575.
Oriloc predictions: Origin 0 kb Terminus 1463 kb
Worning et al., 2006: Origin 6 kb Terminus 1448 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 2756.972 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 8.11 kb
Consensus predictions: Origin 0 kb Terminus 1463 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	764	NA	1443
GC-skew reverse	1792	NA	1447
AT-skew forward	680	NA	1289
AT-skew reverse	2153	NA	2116

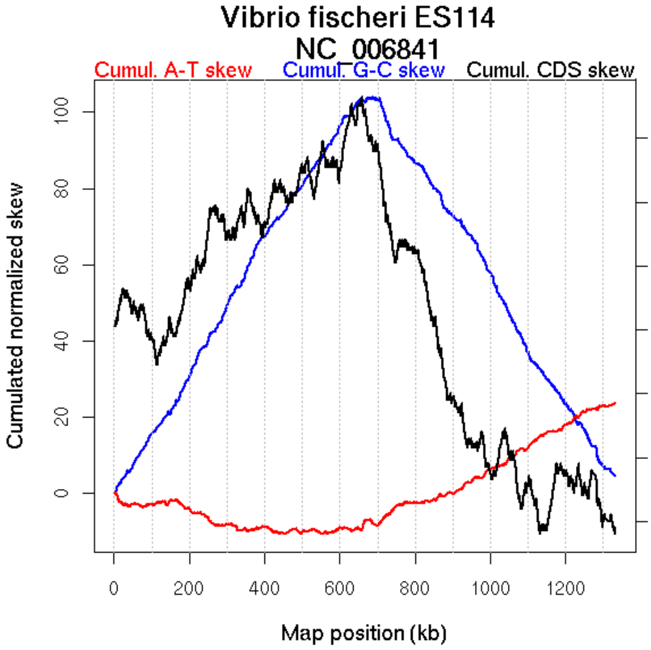
Segments:

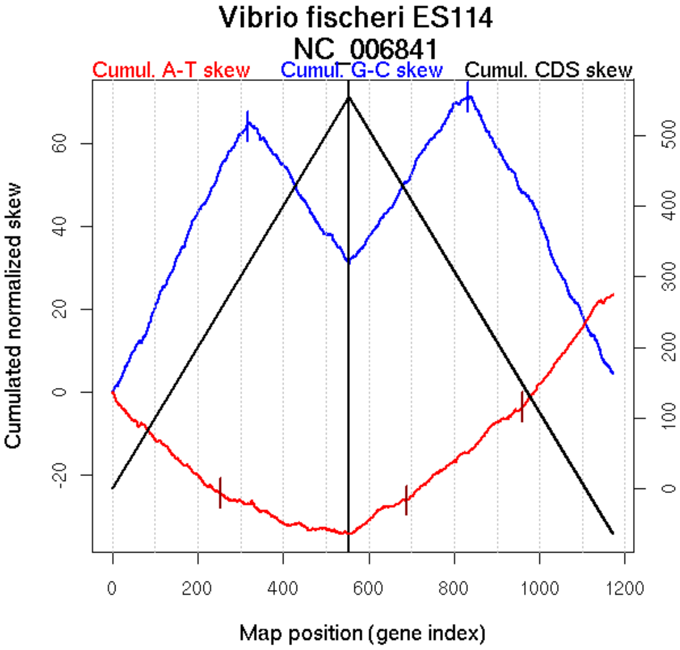
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	764 (1443.327 kb)	leading	0.129
	765(1445.069 kb)	1266 (2906.068 kb)	lagging	-0.151
GC-skew reverse	1267 (0 kb)	1792 (1446.6805 kb)	leading	0.163
	1793(1447.5885 kb)	2575 (2906.068 kb)	lagging	-0.16
AT-skew forward	1 (0 kb)	680 (1288.8275 kb)	leading	-0.116
	681(1290.281 kb)	1266 (2906.068 kb)	NA	-0.065
AT-skew reverse	1267 (0 kb)	2153 (2116.3535 kb)	NA	0.076
	2154(2116.9155 kb)	2575(2906.068 kb)	lagging	0.113

More G than C on the leading strand for replication.

371 Vibrio fischeri ES114

Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio.
Accession number: NC_006841; **Genome size (bp)**: 1332022.
Number of genes: 1172.
Oriloc predictions: Origin 0 kb Terminus 701 kb
Worning et al., 2006: Origin 0 kb Terminus 659 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 696.583 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): NA
Consensus predictions: Origin 0 kb Terminus 701 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	317	NA	649
GC-skew reverse	831	NA	692
AT-skew forward	252	NA	533
AT-skew reverse	690	NA	343
	961	NA	890

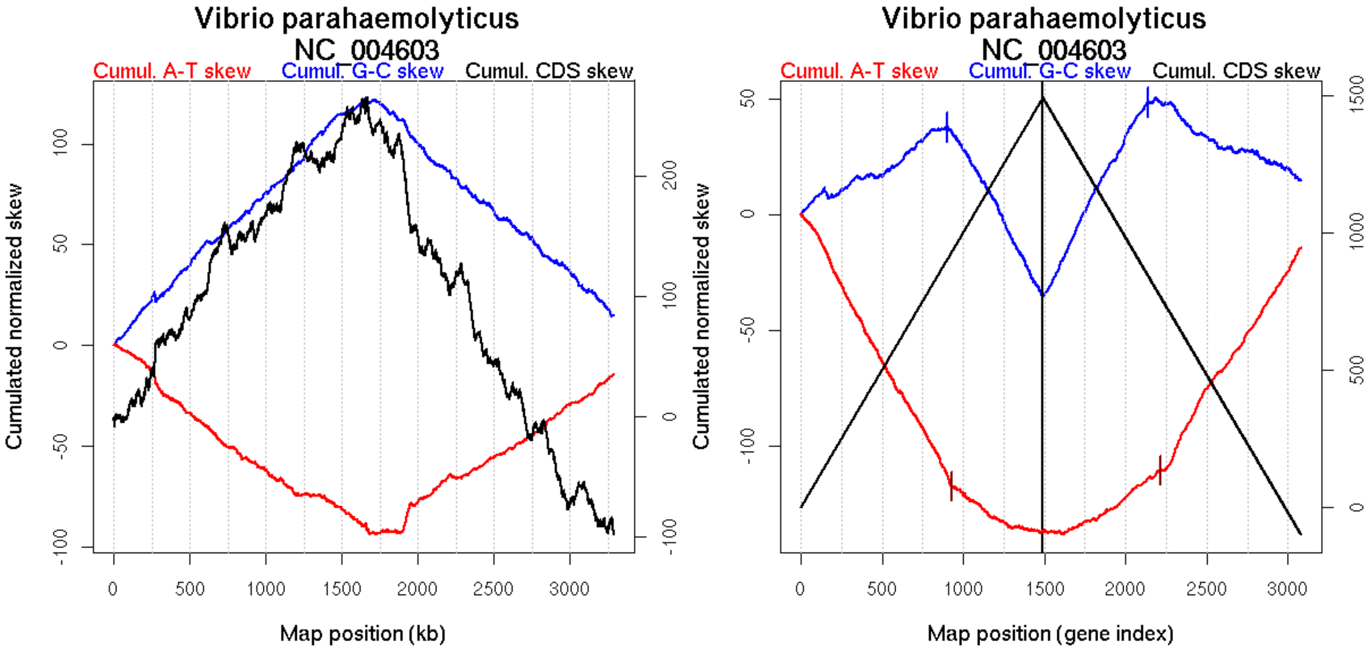
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	317 (649.016 kb)	leading	0.213
	318(649.878 kb)	554 (1332.014 kb)	lagging	-0.15
GC-skew reverse	555 (0 kb)	831 (692.004 kb)	leading	0.155
	832(695.4375 kb)	1172 (1332.014 kb)	lagging	-0.203
AT-skew forward	1 (0 kb)	252 (532.857 kb)	leading	-0.093
	253(533.5695 kb)	554 (1332.014 kb)	NA	-0.033
AT-skew reverse	555 (0 kb)	690 (342.858 kb)	leading	0.065
	691(344.1075 kb)	961(890.0645 kb)	NA	0.084
	962(892.748 kb)	1172(1332.014 kb)	lagging	0.136

More G than C on the leading strand for replication.

372 Vibrio parahaemolyticus

Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio.
Accession number: NC_004603; **Genome size (bp)**: 3288558.
Number of genes: 3080.
Oriloc predictions: Origin 0 kb Terminus 1707 kb
Worning et al., 2006: Origin 3287 kb Terminus 1667 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 0.219 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 8.38 kb, 1678.39 kb
Consensus predictions: Origin 0 kb Terminus 1707 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	905	NA	1661
GC-skew reverse	2135	NA	1653
AT-skew forward	927	NA	1717
AT-skew reverse	2213	NA	1796

Segments:

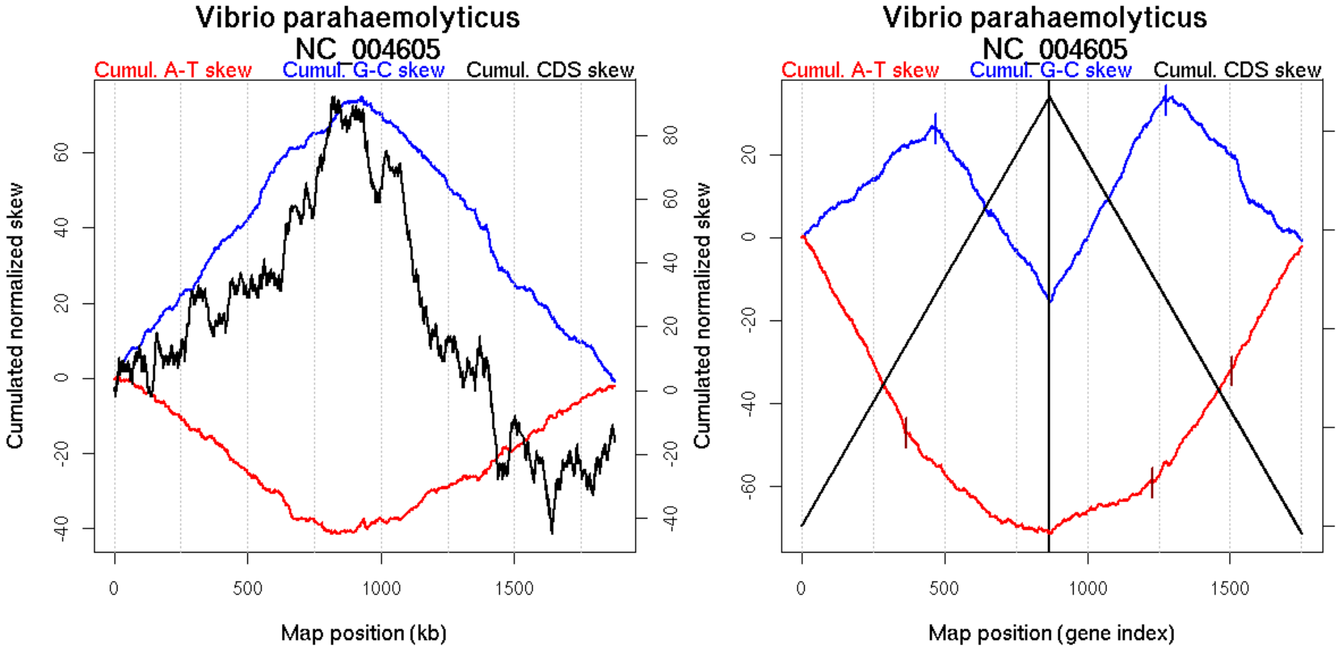
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	905 (1660.9875 kb)	leading	0.04
	906(1661.2225 kb)	1491 (3288.454 kb)	lagging	-0.129
GC-skew reverse	1492 (0 kb)	2135 (1653.116 kb)	leading	0.134
	2136(1653.9305 kb)	3080 (3288.454 kb)	lagging	-0.036
AT-skew forward	1 (0 kb)	927 (1717.393 kb)	leading	-0.127
	928(1718.648 kb)	1491 (3288.454 kb)	lagging	-0.037
AT-skew reverse	1492 (0 kb)	2213 (1796.4455 kb)	leading	0.04
	2214(1797.792 kb)	3080(3288.454 kb)	lagging	0.11

More T than A on the leading strand for replication.

More G than C on the leading strand for replication.

373 Vibrio parahaemolyticus

Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio.
Accession number: NC_004605; **Genome size (bp)**: 1877212.
Number of genes: 1752.
Oriloc predictions: Origin 0 kb Terminus 895 kb
Worning et al., 2006: Origin 0 kb Terminus 935 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 916.772 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 944.02 kb
Consensus predictions: Origin 0 kb Terminus 895 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	470	NA	890
GC-skew reverse	1277	NA	939
AT-skew forward	365	NA	699
AT-skew reverse	1230	NA	845
	1505	NA	1365

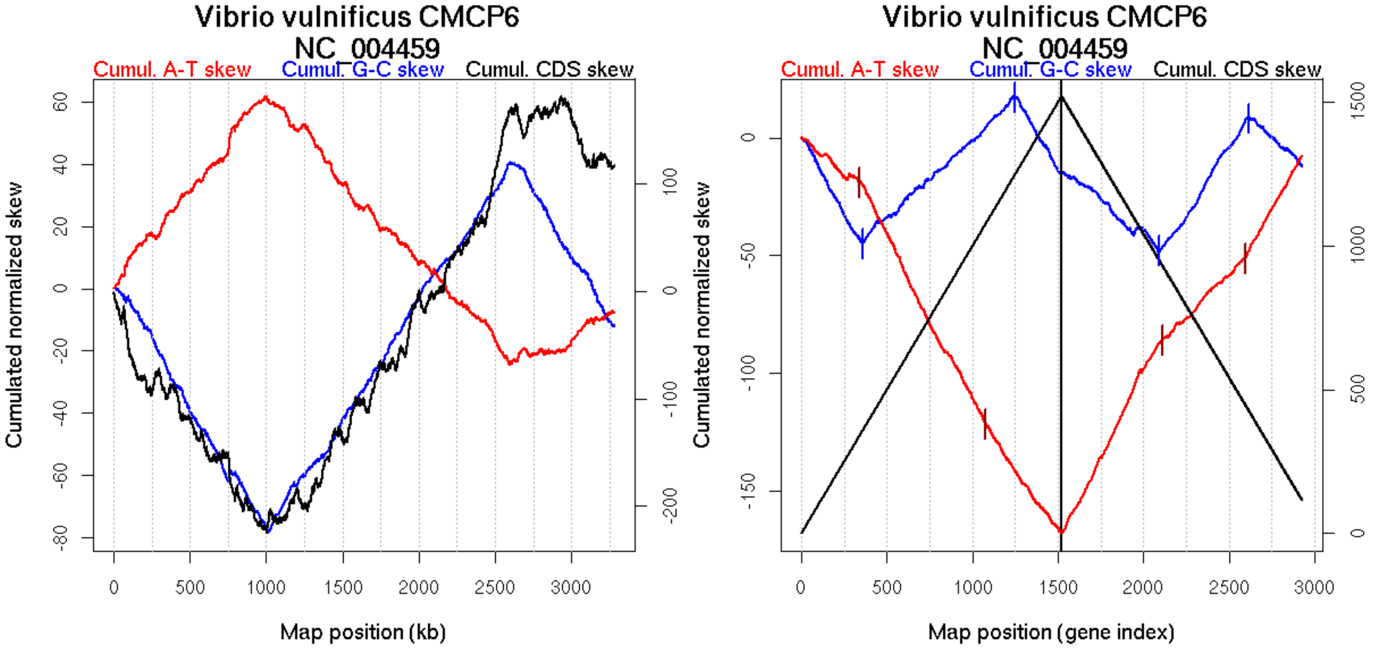
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	470 (890.2455 kb)	leading	0.057
	471(893.33 kb)	868 (1877.11 kb)	lagging	-0.104
GC-skew reverse	869 (0 kb)	1277 (939.4735 kb)	leading	0.125
	1278(940.0345 kb)	1752 (1877.11 kb)	lagging	-0.082
AT-skew forward	1 (0 kb)	365 (699.1065 kb)	leading	-0.128
	366(702.4925 kb)	868 (1877.11 kb)	NA	-0.049
AT-skew reverse	869 (0 kb)	1230 (845.1575 kb)	leading	0.028
	1231(846.814 kb)	1505(1365.345 kb)	lagging	0.099
	1506(1368.5195 kb)	1752(1877.11 kb)	lagging	0.123

More T than A on the leading strand for replication - for reverse encoded genes.
More G than C on the leading strand for replication.

374 Vibrio vulnificus CMCP6

Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio.
Accession number: NC_004459; **Genome size (bp)**: 3281945.
Number of genes: 2926.
Oriloc predictions: Origin 1013 kb Terminus 2596 kb
Worning et al., 2006: Origin 1006 kb Terminus 2640 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1012.476 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1004.52 kb
Consensus predictions: Origin 1013 kb Terminus 2596 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	357	NA	1015
	1250	NA	2611
GC-skew reverse	2090	NA	1001
	2613	NA	2636
AT-skew forward	341	NA	985
	1078	NA	2341
AT-skew reverse	2108	NA	1047
	2595	NA	2591

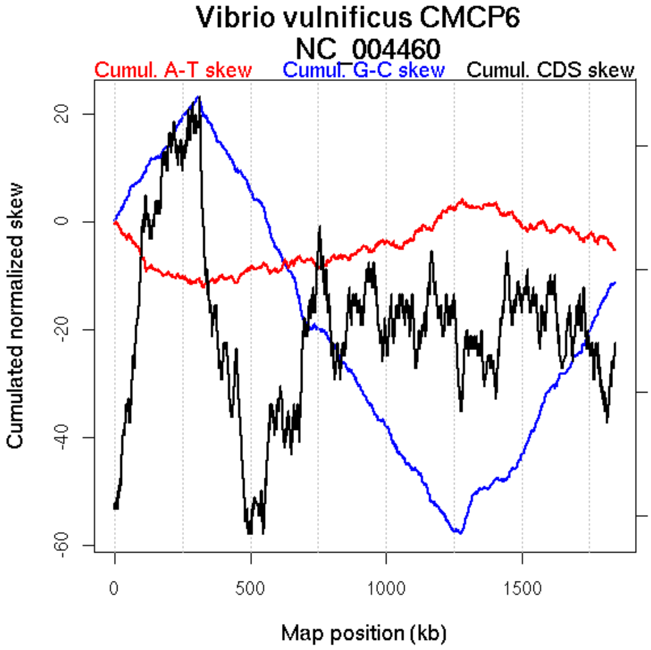
Segments:

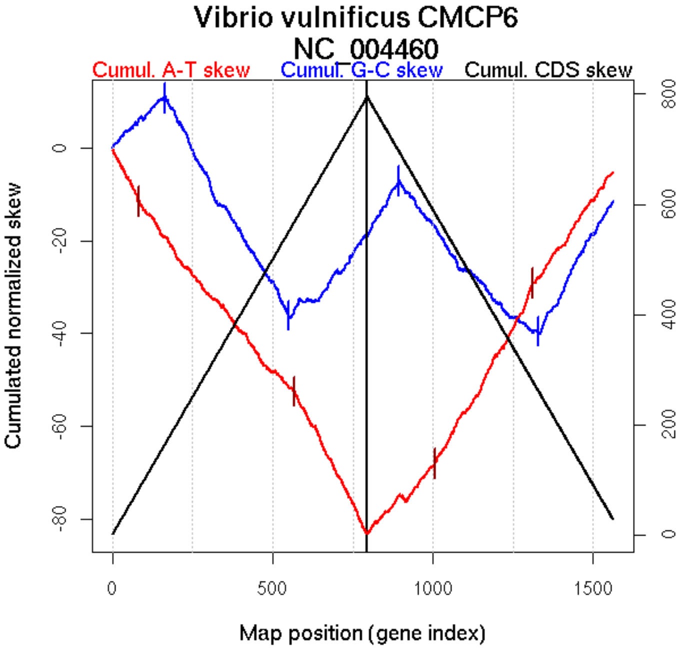
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	357 (1014.698 kb)	lagging	-0.134
	358(1015.337 kb)	1250 (2610.9615 kb)	leading	0.067
	1251(2615.102 kb)	1521 (3281.905 kb)	lagging	-0.126
GC-skew reverse	1522 (0 kb)	2090 (1000.904 kb)	lagging	-0.059
	2091(1002.677 kb)	2613 (2636.461 kb)	leading	0.113
	2614(2638.6655 kb)	2926 (3281.905 kb)	lagging	-0.065
AT-skew forward	1 (0 kb)	341 (985.466 kb)	lagging	-0.058
	342(986.716 kb)	1078 (2341.0775 kb)	leading	-0.141
	1079(2345.081 kb)	1521 (3281.905 kb)	NA	-0.104
AT-skew reverse	1522 (0 kb)	2108 (1047.394 kb)	lagging	0.146
	2109(1048.79 kb)	2595(2590.733 kb)	leading	0.073
	2596(2595.09 kb)	2926(3281.905 kb)	lagging	0.129

More T than A on the leading strand for replication - for reverse encoded genes.
More G than C on the leading strand for replication.

375 Vibrio vulnificus CMCP6

Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio.
Accession number: NC_004460; **Genome size (bp)**: 1844853.
Number of genes: 1562.
Oriloc predictions: Origin 1275 kb Terminus 305 kb
Worning et al., 2006: Origin 1276 kb Terminus 314 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 297.595 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): NA
Consensus predictions: Origin 1275 kb Terminus 305 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	165	NA	313
	549	NA	1241
GC-skew reverse	894	NA	308
	1327	NA	1267
AT-skew forward	82	NA	124
	567	NA	1290
AT-skew reverse	1006	NA	487
	1311	NA	1241

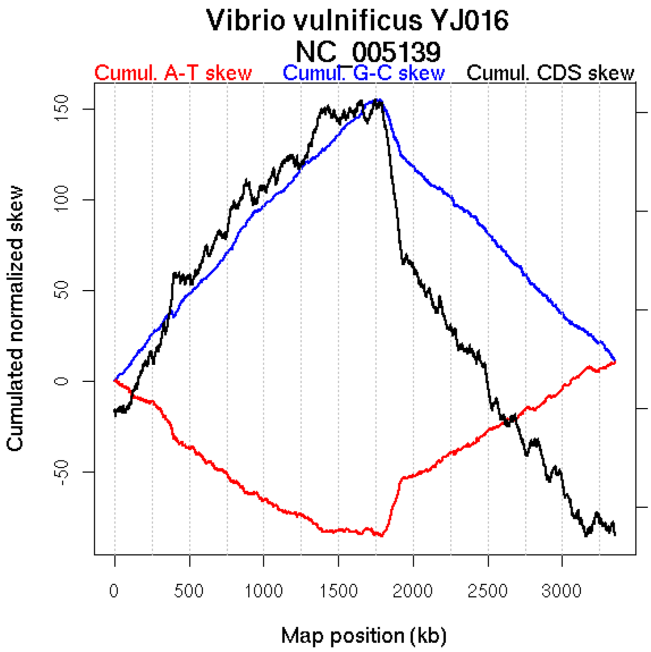
Segments:

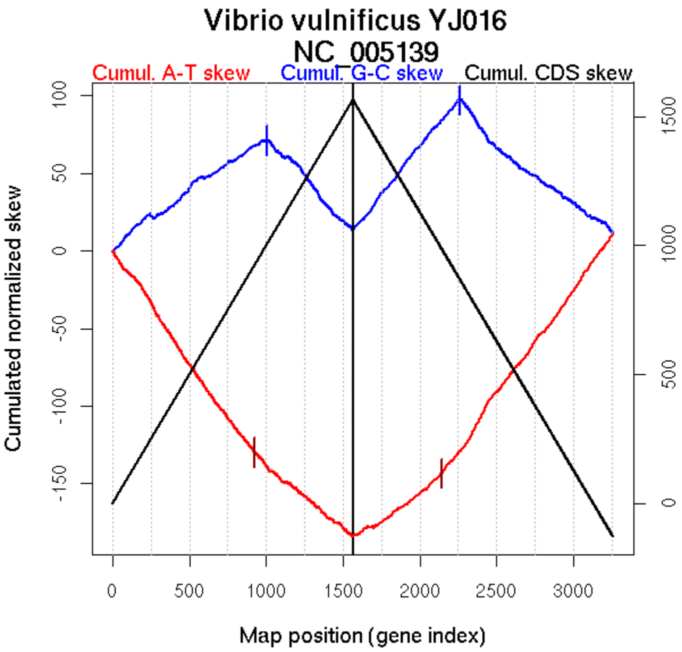
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	165 (312.806 kb)	leading	0.066
	166(313.33 kb)	549 (1240.7605 kb)	lagging	-0.119
	550(1244.8975 kb)	795 (1844.753 kb)	leading	0.071
GC-skew reverse	796 (0 kb)	894 (307.707 kb)	leading	0.119
	895(311.537 kb)	1327 (1266.558 kb)	lagging	-0.078
	1328(1267.9345 kb)	1562 (1844.753 kb)	leading	0.125
AT-skew forward	1 (0 kb)	82 (124.022 kb)	leading	-0.132
	83(129.4735 kb)	567 (1289.51 kb)	NA	-0.085
	568(1290.6135 kb)	795 (1844.753 kb)	leading	-0.135
AT-skew reverse	796 (0 kb)	1006 (487.371 kb)	NA	0.066
	1007(488.338 kb)	1311(1240.589 kb)	lagging	0.122
	1312(1242.925 kb)	1562(1844.753 kb)	leading	0.099

More G than C on the leading strand for replication.

376 Vibrio vulnificus YJ016

Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio.
Accession number: NC_005139; **Genome size (bp)**: 3354505.
Number of genes: 3259.
Oriloc predictions: Origin 0 kb Terminus 1777 kb
Worning et al., 2006: Origin 3353 kb Terminus 1743 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 0.211 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 8.15 kb
Consensus predictions: Origin 0 kb Terminus 1777 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1006	NA	1762
GC-skew reverse	2264	NA	1757
AT-skew forward	923	NA	1595
AT-skew reverse	2141	NA	1483

Segments:

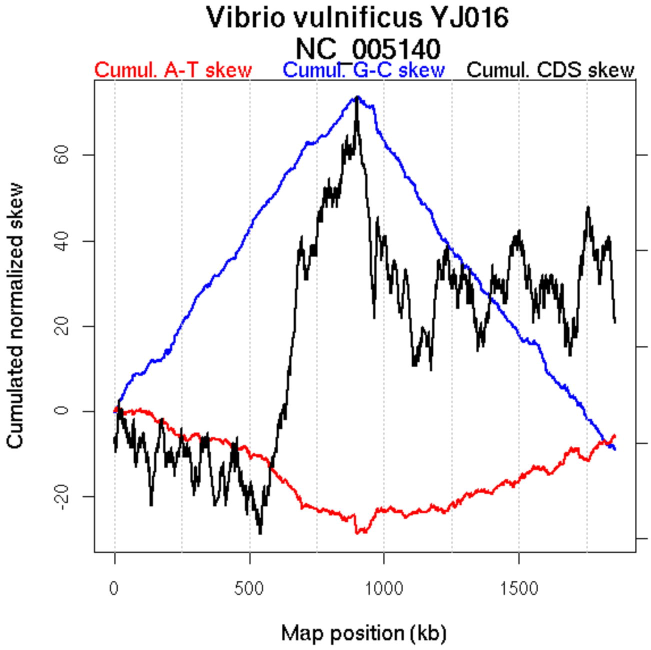
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1006 (1761.8195 kb)	leading	0.07
	1007(1765.1285 kb)	1565 (3354.389 kb)	lagging	-0.11
GC-skew reverse	1566 (0 kb)	2264 (1757.347 kb)	leading	0.123
	2265(1759.984 kb)	3259 (3354.389 kb)	lagging	-0.079
AT-skew forward	1 (0 kb)	923 (1595.1955 kb)	leading	-0.144
	924(1596.738 kb)	1565 (3354.389 kb)	lagging	-0.082
AT-skew reverse	1566 (0 kb)	2141 (1483.045 kb)	leading	0.07
	2142(1484.6765 kb)	3259(3354.389 kb)	lagging	0.138

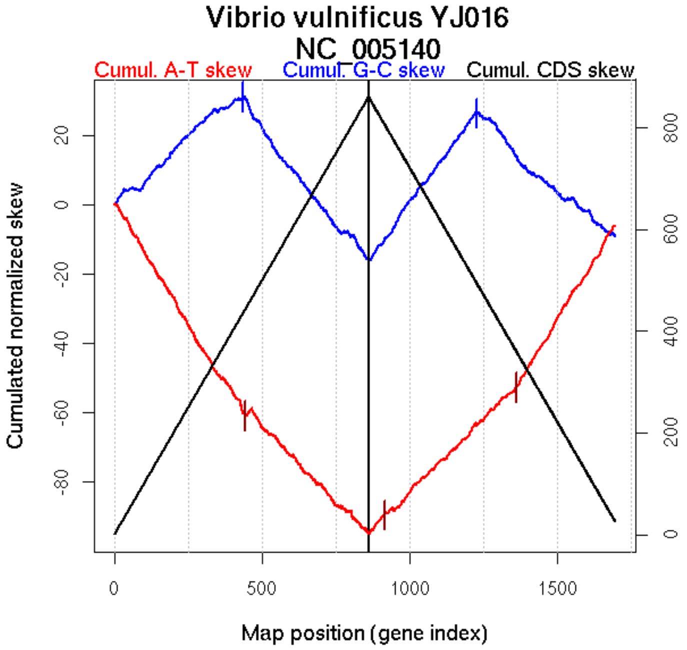
More T than A on the leading strand for replication.

More G than C on the leading strand for replication.

377 Vibrio vulnificus YJ016

Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales; Vibrionaceae; Vibrio.
Accession number: NC_005140; **Genome size (bp)**: 1857073.
Number of genes: 1696.
Oriloc predictions: Origin 0 kb Terminus 901 kb
Worning et al., 2006: Origin 1856 kb Terminus 899 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 873.435 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): NA
Consensus predictions: Origin 0 kb Terminus 901 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	437	NA	898
GC-skew reverse	1228	NA	900
AT-skew forward	444	NA	959
AT-skew reverse	915	NA	124
	1360	NA	1130

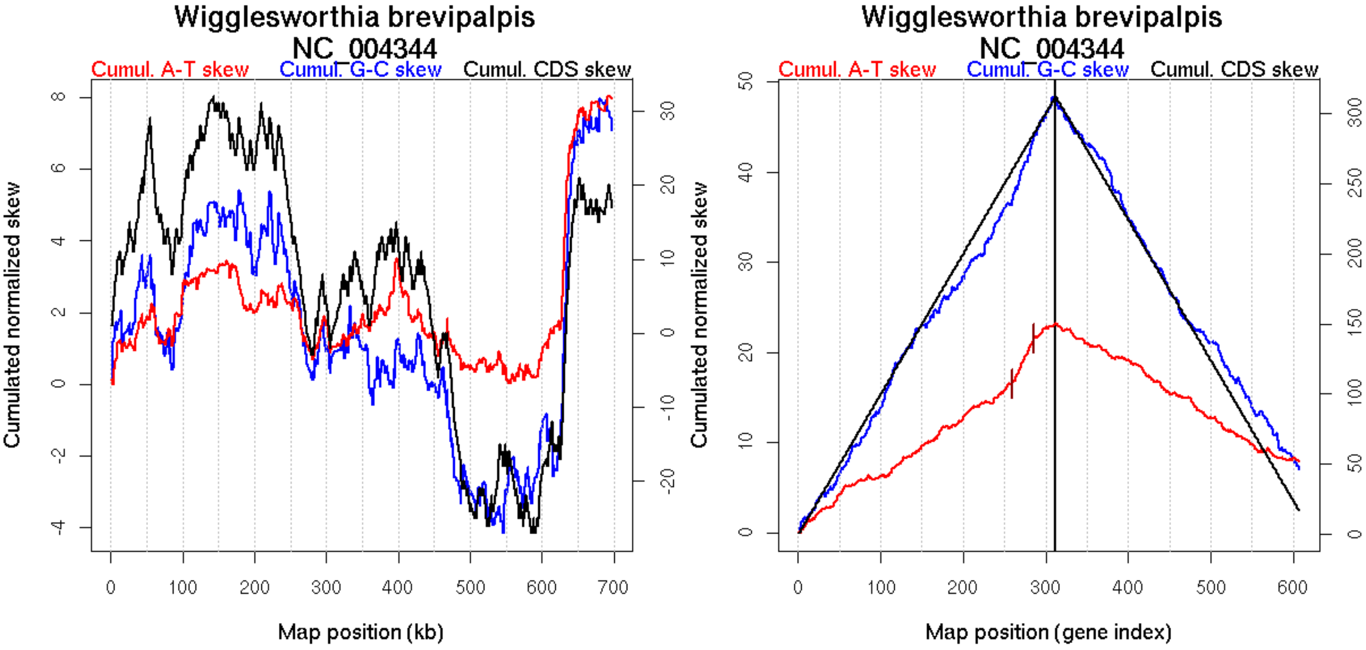
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	437 (898.4515 kb)	leading	0.076
	438(903.528 kb)	861 (1855.943 kb)	lagging	-0.107
GC-skew reverse	862 (0 kb)	1228 (900.251 kb)	leading	0.117
	1229(900.8235 kb)	1696 (1855.943 kb)	lagging	-0.077
AT-skew forward	1 (0 kb)	444 (958.9125 kb)	leading	-0.139
	445(962.156 kb)	861 (1855.943 kb)	lagging	-0.087
AT-skew reverse	862 (0 kb)	915 (124.0755 kb)	leading	0.106
	916(125.024 kb)	1360(1130.131 kb)	NA	0.085
	1361(1133.4665 kb)	1696(1855.943 kb)	lagging	0.139

More T than A on the leading strand for replication - for forward encoded genes.
More G than C on the leading strand for replication.

378 Wigglesworthia brevipalpis

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Wigglesworthia.
Accession number: NC_004344; **Genome size (bp)**: 697724.
Number of genes: 607.
Oriloc predictions: Origin NA Terminus NA
Worning et al., 2006: Origin 591 kb Terminus 136 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 438.94 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): NA
Consensus predictions: Origin NA Terminus NA



Significant breakpoints (p-value <0.05):

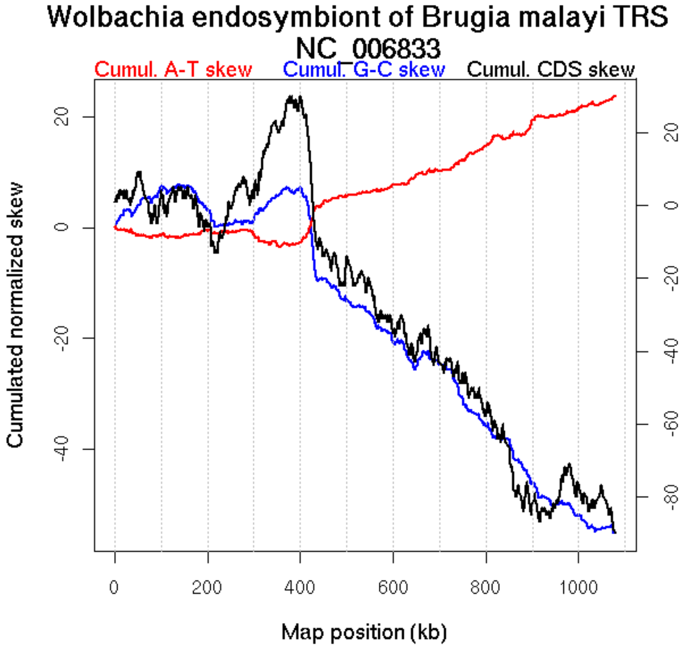
	Breakpoints	P-value	Chromosome coordinate (kb)
AT-skew forward	259	0.00667	622
	286	0.00667	638

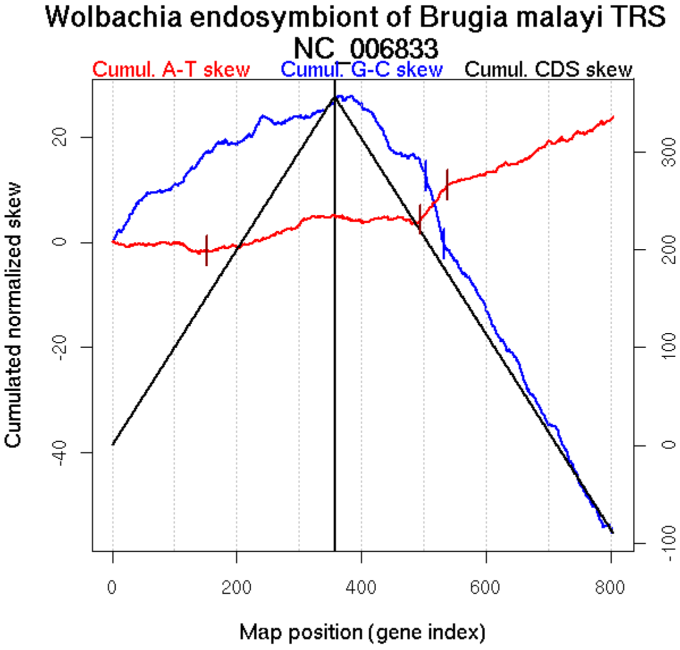
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
AT-skew forward	1 (0 kb)	259 (622.1515 kb)	NA	0.06
	260(624.4135 kb)	286 (637.9835 kb)	NA	0.194
	287(638.991 kb)	312 (697.375 kb)	NA	0.065

379 Wolbachia endosymbiont of Brugia malayi TRS

Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales; Rickettsiaceae; Wolbachieae; Wolbachia.
Accession number: NC_006833; **Genome size (bp)**: 1080084.
Number of genes: 804.
Oriloc predictions: Origin NA Terminus NA
Worning et al., 2006: Origin 0 kb Terminus 401 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 187.627 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 960.26 kb
Consensus predictions: Origin NA Terminus NA





Significant breakpoints (p-value <0.05):

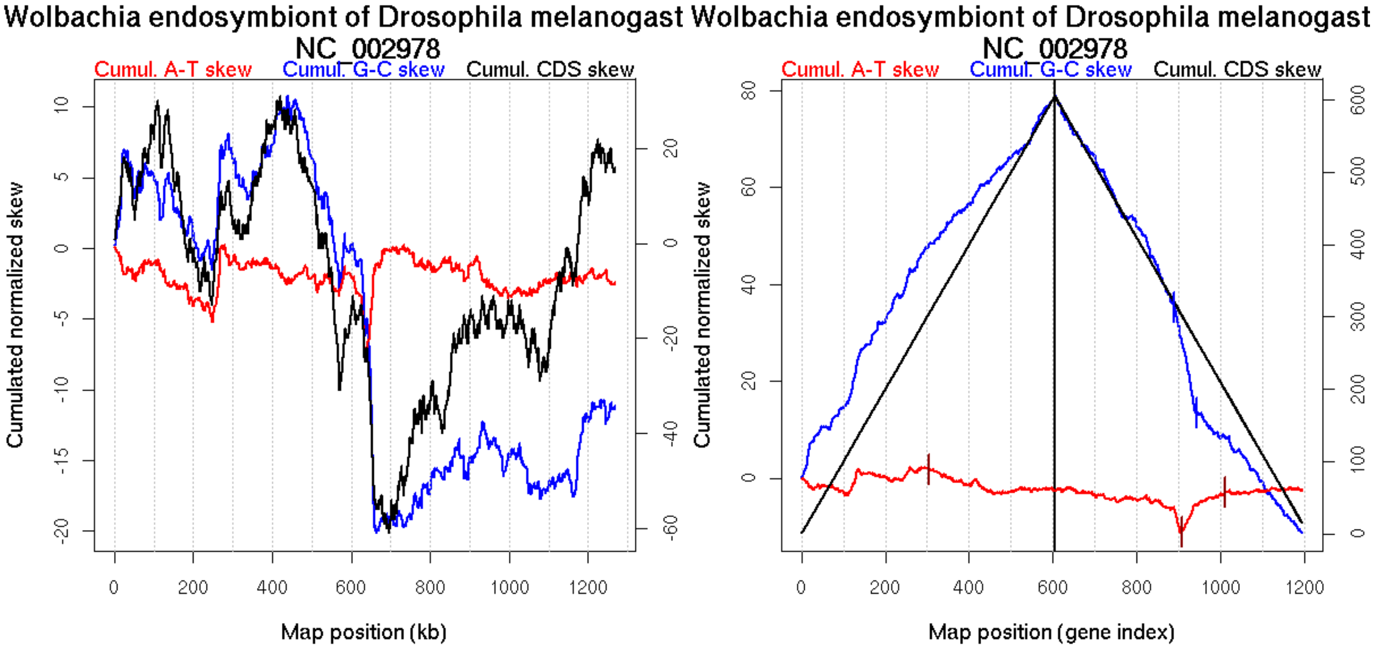
	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew reverse	503	0	417
	532	0.01333	435
AT-skew forward	152	0.03333	368
AT-skew reverse	495	0.00333	406
	538	0.03	448

Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew reverse	358 (0 kb)	503 (417.0695 kb)	NA	-0.112
	504(417.588 kb)	532 (434.5125 kb)	NA	-0.442
	533(435.9335 kb)	804 (1079.739 kb)	NA	-0.211
AT-skew forward	1 (0 kb)	152 (368.2655 kb)	NA	-0.008
	153(369.2805 kb)	357 (1079.739 kb)	NA	0.038
AT-skew reverse	358 (0 kb)	495 (405.946 kb)	NA	-0.003
	496(406.781 kb)	538(447.7035 kb)	NA	0.155
	539(448.2395 kb)	804(1079.739 kb)	NA	0.049

380 Wolbachia endosymbiont of Drosophila melanogaster

Bacteria; Proteobacteria; Alphaproteobacteria; Rickettsiales; Rickettsiaceae; Wolbachieae; Wolbachia.
Accession number: NC_002978; **Genome size (bp)**: 1267782.
Number of genes: 1195.
Oriloc predictions: Origin NA Terminus NA
Worning et al., 2006: Origin 668 kb Terminus 271 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 631.461 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.84 kb, 1097.43 kb
Consensus predictions: Origin NA Terminus NA



Significant breakpoints (p-value <0.05):

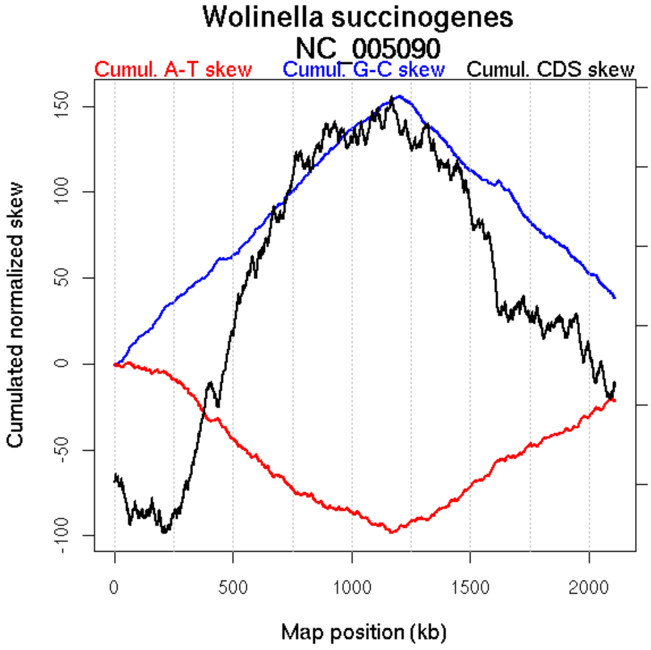
	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew reverse	890	NA	610
	944	NA	675
AT-skew forward	303	NA	716
AT-skew reverse	907	NA	641
	1011	NA	829

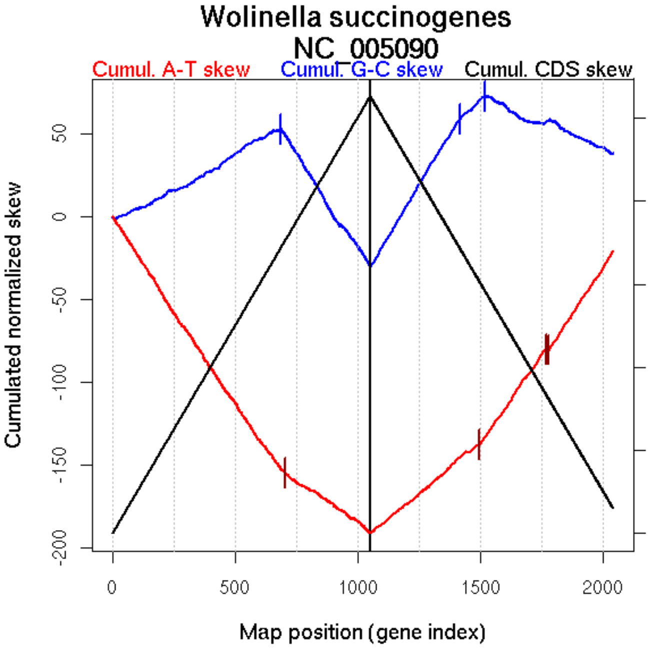
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew reverse	606 (0 kb)	890 (609.766 kb)	NA	-0.144
	891(611.415 kb)	944 (674.9975 kb)	NA	-0.431
	945(677.7365 kb)	1195 (1267.608 kb)	NA	-0.101
AT-skew forward	1 (0 kb)	303 (716.068 kb)	NA	0.013
	304(717.0945 kb)	605 (1267.608 kb)	NA	-0.013
AT-skew reverse	606 (0 kb)	907 (640.751 kb)	NA	-0.016
	908(641.6775 kb)	1011(829.254 kb)	NA	0.066
	1012(833.0705 kb)	1195(1267.608 kb)	NA	0.005

381 Wolinella succinogenes

Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales; Helicobacteraceae; Wolinella.
Accession number: NC_005090; **Genome size (bp)**: 2110355.
Number of genes: 2043.
Oriloc predictions: Origin 2 kb Terminus 1188 kb
Worning et al., 2006: Origin 3 kb Terminus 1187 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 577.98 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.66 kb
Consensus predictions: Origin 2 kb Terminus 1188 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	688	0	1186
GC-skew reverse	1420	0.04	987
	1521	0	1206
AT-skew forward	705	0	1241
AT-skew reverse	1498	0.04222	1173
	1769	0	1610
	1781	0	1616

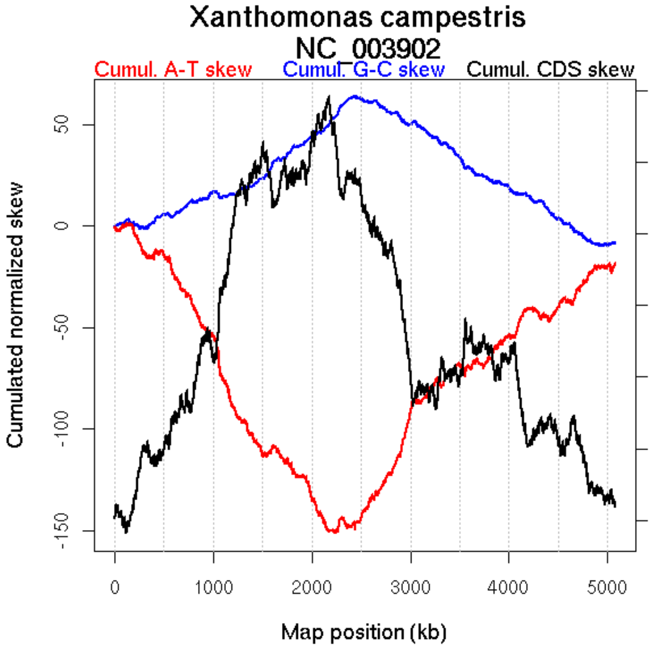
Segments:

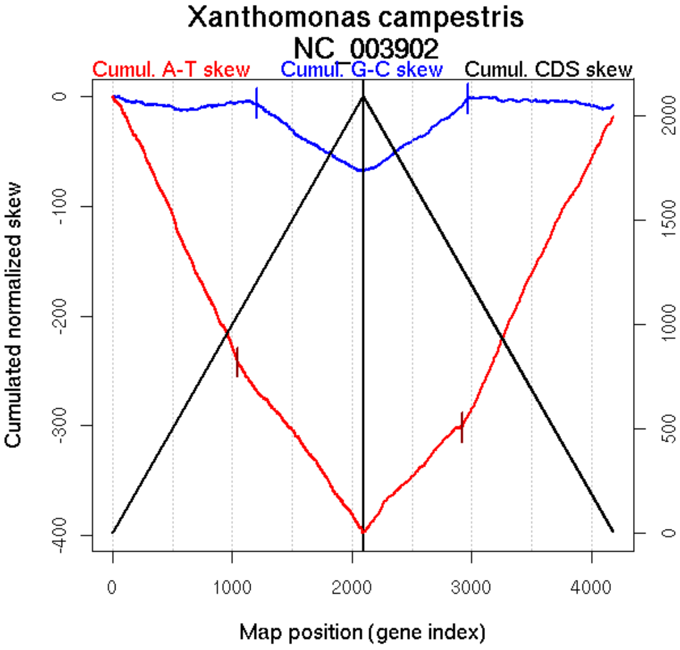
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	688 (1186.425 kb)	leading	0.084
	689(1197.7575 kb)	1052 (2110.227 kb)	lagging	-0.229
GC-skew reverse	1053 (0 kb)	1420 (986.7825 kb)	leading	0.247
	1421(989.3985 kb)	1521 (1206.2 kb)	leading	0.137
	1522(1209.098 kb)	2043 (2110.227 kb)	lagging	-0.062
AT-skew forward	1 (0 kb)	705 (1241.0945 kb)	leading	-0.223
	706(1247.355 kb)	1052 (2110.227 kb)	lagging	-0.099
AT-skew reverse	1053 (0 kb)	1498 (1173.144 kb)	leading	0.124
	1499(1173.95 kb)	1769(1610.395 kb)	lagging	0.215
	1770(1611.039 kb)	1781(1616.155 kb)	lagging	-0.031
	1782(1618.301 kb)	2043(2110.227 kb)	lagging	0.225

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

382 Xanthomonas campestris

Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Xanthomonas.
Accession number: NC_003902; **Genome size (bp)**: 5076188.
Number of genes: 4181.
Oriloc predictions: Origin 4944 kb Terminus 2371 kb
Worning et al., 2006: Origin 5 kb Terminus 2441 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1726.68 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.71 kb, 2436.89 kb, 2446.65 kb
Consensus predictions: Origin 4944 kb Terminus 2371 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1207	0.00667	2654
GC-skew reverse	2971	0	2381
AT-skew forward	1048	0	2142
AT-skew reverse	2918	0	2261

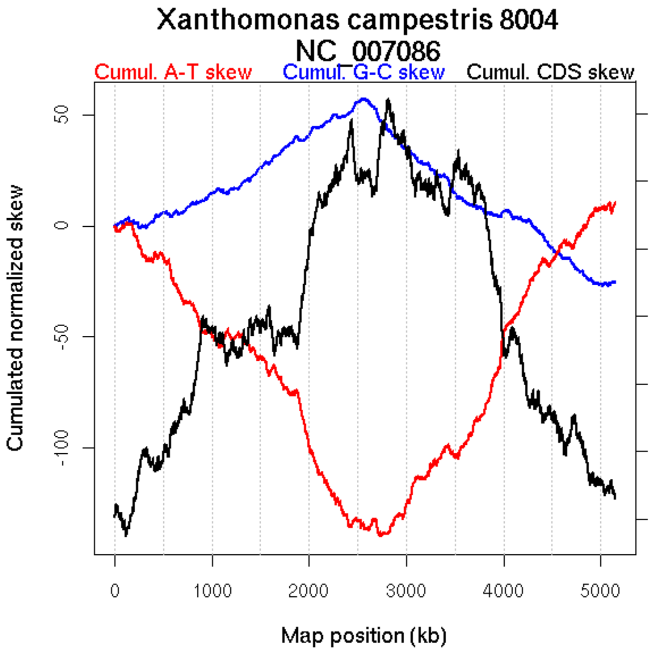
Segments:

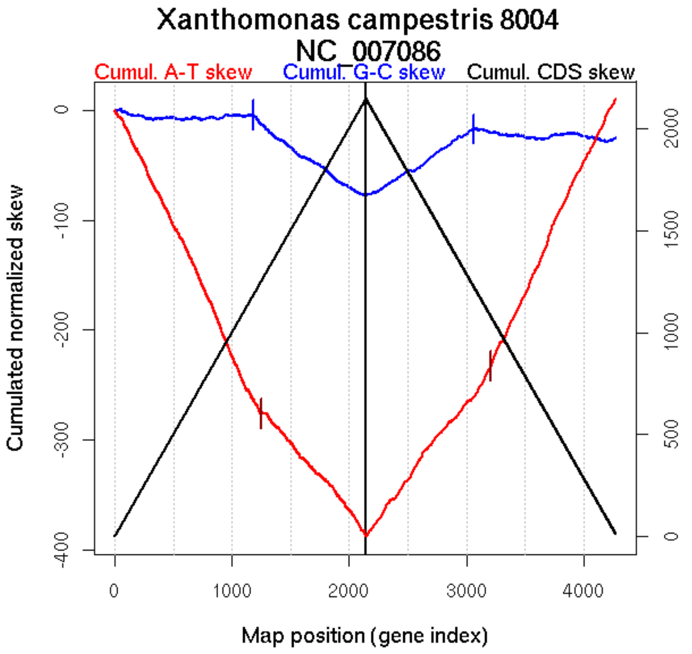
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1207 (2653.757 kb)	leading	-0.002
	1208(2655.307 kb)	2095 (5075.986 kb)	lagging	-0.071
GC-skew reverse	2096 (0 kb)	2971 (2380.9105 kb)	leading	0.075
	2972(2389.1925 kb)	4181 (5075.986 kb)	lagging	-0.007
AT-skew forward	1 (0 kb)	1048 (2142.1395 kb)	leading	-0.237
	1049(2143.3865 kb)	2095 (5075.986 kb)	lagging	-0.144
AT-skew reverse	2096 (0 kb)	2918 (2261.2395 kb)	leading	0.119
	2919(2263.4075 kb)	4181(5075.986 kb)	lagging	0.227

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

383 Xanthomonas campestris 8004

Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Xanthomonas.
Accession number: NC_007086; **Genome size (bp)**: 5148708.
Number of genes: 4273.
Oriloc predictions: Origin 5018 kb Terminus 2606 kb
Worning et al., 2006: Origin 5061 kb Terminus 2537 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1564.534 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.71 kb, 2532.59 kb
Consensus predictions: Origin 5018 kb Terminus 2606 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1184	NA	2584
GC-skew reverse	3063	NA	2549
AT-skew forward	1247	NA	2724
AT-skew reverse	3210	NA	2979

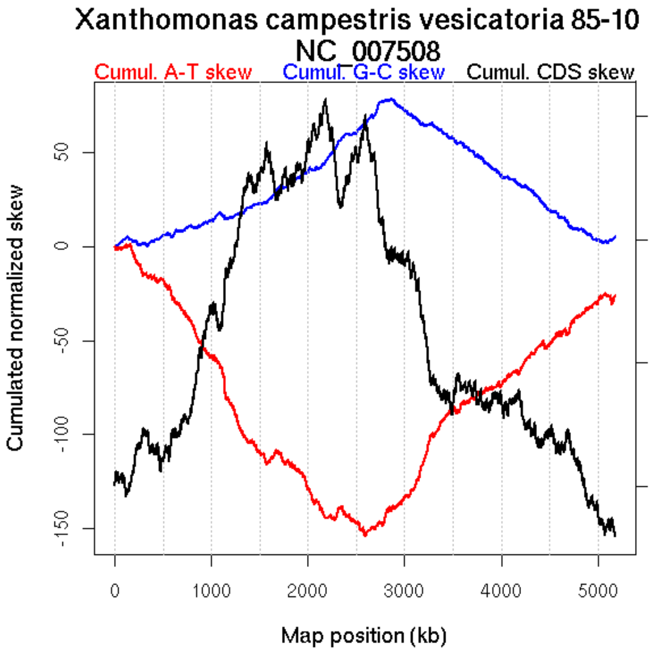
Segments:

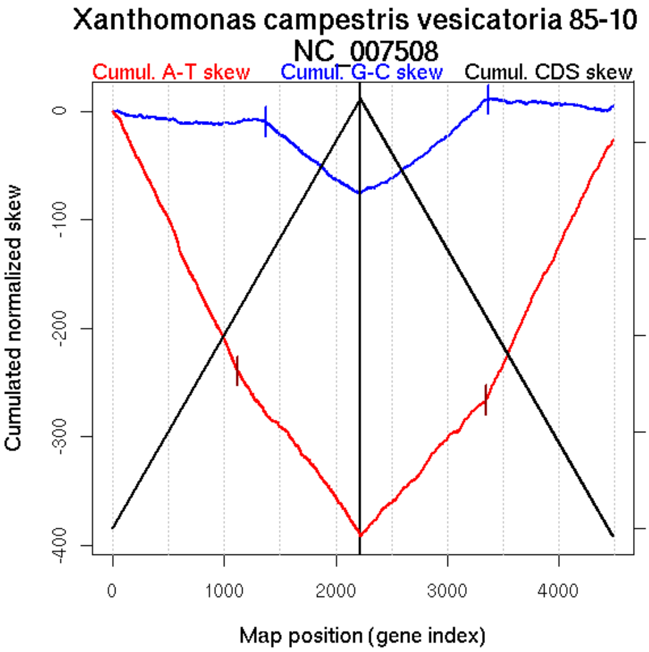
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1184 (2583.5915 kb)	leading	-0.002
	1185(2584.786 kb)	2144 (5148.507 kb)	lagging	-0.075
GC-skew reverse	2145 (0 kb)	3063 (2549.3225 kb)	leading	0.069
	3064(2550.2865 kb)	4273 (5148.507 kb)	lagging	-0.006
AT-skew forward	1 (0 kb)	1247 (2724.249 kb)	leading	-0.228
	1248(2724.866 kb)	2144 (5148.507 kb)	lagging	-0.123
AT-skew reverse	2145 (0 kb)	3210 (2979.41 kb)	leading	0.14
	3211(2981.987 kb)	4273(5148.507 kb)	lagging	0.232

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

384 Xanthomonas campestris vesicatoria 85-10

Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Xanthomonas.
Accession number: NC_007508; **Genome size (bp)**: 5178466.
Number of genes: 4487.
Oriloc predictions: Origin 5053 kb Terminus 2855 kb
Worning et al., 2006: Origin 46 kb Terminus 2764 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1768.544 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.66 kb, 2794.39 kb
Consensus predictions: Origin 5053 kb Terminus 2855 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1372	NA	2886
GC-skew reverse	3371	NA	2810
AT-skew forward	1122	NA	2241
AT-skew reverse	3347	NA	2787

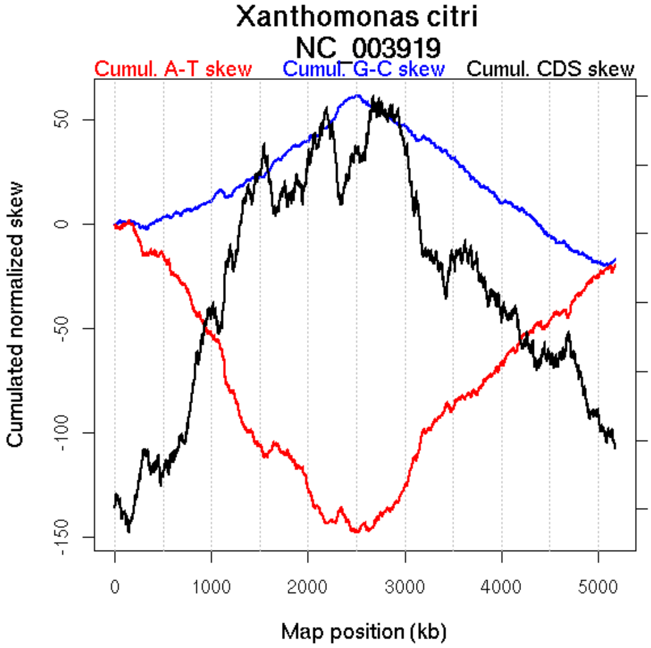
Segments:

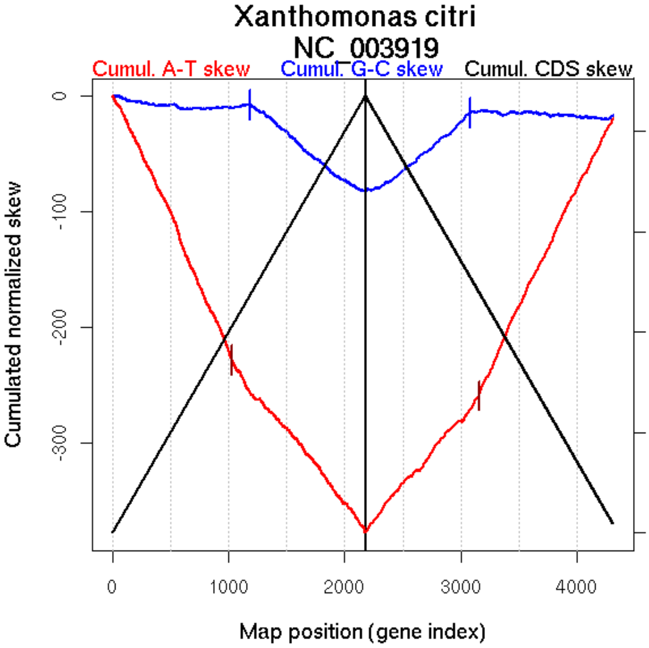
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1372 (2885.949 kb)	leading	-0.006
	1373(2887.2965 kb)	2223 (5178.224 kb)	lagging	-0.08
GC-skew reverse	2224 (0 kb)	3371 (2810.323 kb)	leading	0.078
	3372(2812.2885 kb)	4487 (5178.224 kb)	lagging	-0.009
AT-skew forward	1 (0 kb)	1122 (2240.5625 kb)	leading	-0.218
	1123(2240.794 kb)	2223 (5178.224 kb)	NA	-0.13
AT-skew reverse	2224 (0 kb)	3347 (2786.79 kb)	leading	0.113
	3348(2787.061 kb)	4487(5178.224 kb)	lagging	0.213

More T than A on the leading strand for replication - for reverse encoded genes.
More G than C on the leading strand for replication.

385 Xanthomonas citri

Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Xanthomonas.
Accession number: NC_003919; **Genome size (bp)**: 5175554.
Number of genes: 4312.
Oriloc predictions: Origin 5065 kb Terminus 2523 kb
Worning et al., 2006: Origin 0 kb Terminus 2493 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1760.988 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.71 kb
Consensus predictions: Origin 5065 kb Terminus 2523 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1179	NA	2491
GC-skew reverse	3078	NA	2427
AT-skew forward	1027	NA	2113
AT-skew reverse	3155	NA	2680

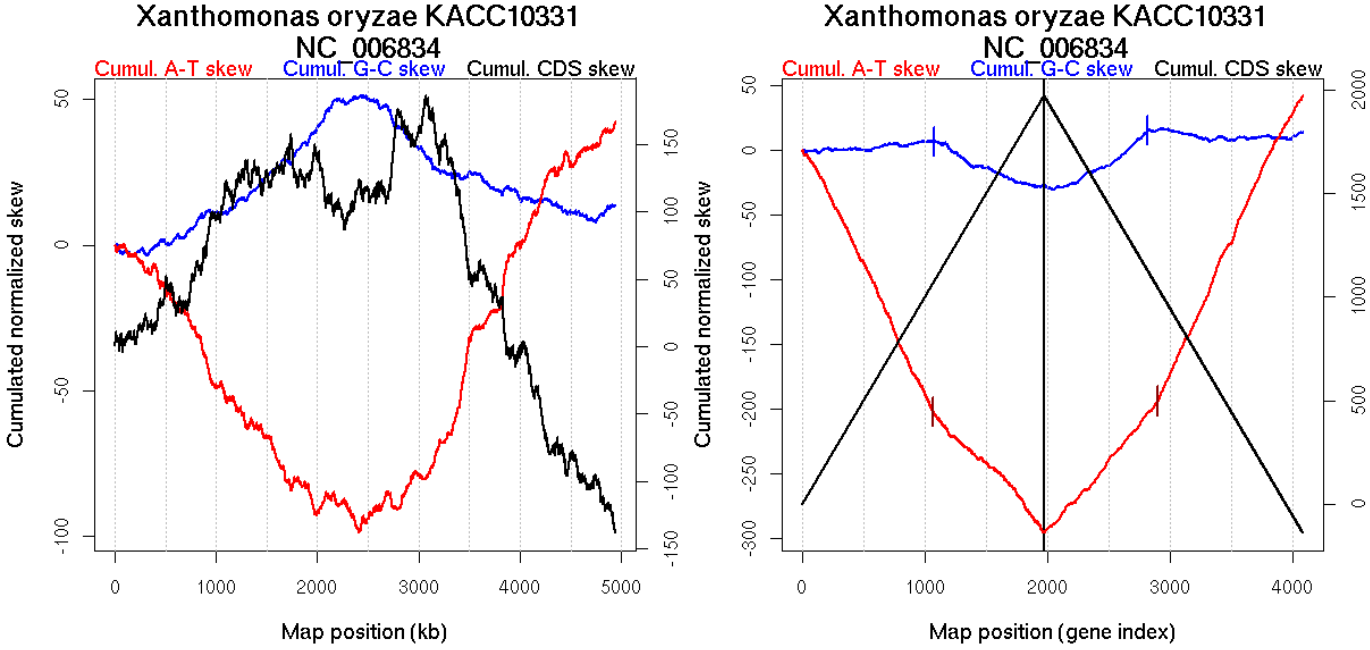
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1179 (2490.75 kb)	leading	-0.007
	1180(2492.963 kb)	2178 (5175.353 kb)	lagging	-0.081
GC-skew reverse	2179 (0 kb)	3078 (2426.863 kb)	leading	0.078
	3079(2443.4445 kb)	4312 (5175.353 kb)	lagging	-0.005
AT-skew forward	1 (0 kb)	1027 (2113.0395 kb)	leading	-0.225
	1028(2113.8735 kb)	2178 (5175.353 kb)	NA	-0.122
AT-skew reverse	2179 (0 kb)	3155 (2680.371 kb)	leading	0.116
	3156(2681.588 kb)	4312(5175.353 kb)	lagging	0.206

More T than A on the leading strand for replication - for reverse encoded genes.
More G than C on the leading strand for replication.

386 Xanthomonas oryzae KACC10331

Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Xanthomonas.
Accession number: NC_006834; **Genome size (bp)**: 4941439.
Number of genes: 4080.
Oriloc predictions: Origin 192 kb Terminus 2419 kb
Worning et al., 2006: Origin 4825 kb Terminus 2388 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 2135.949 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.71 kb
Consensus predictions: Origin 192 kb Terminus 2419 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1074	NA	2458
GC-skew reverse	2815	NA	2154
AT-skew forward	1066	NA	2440
AT-skew reverse	2896	NA	2348

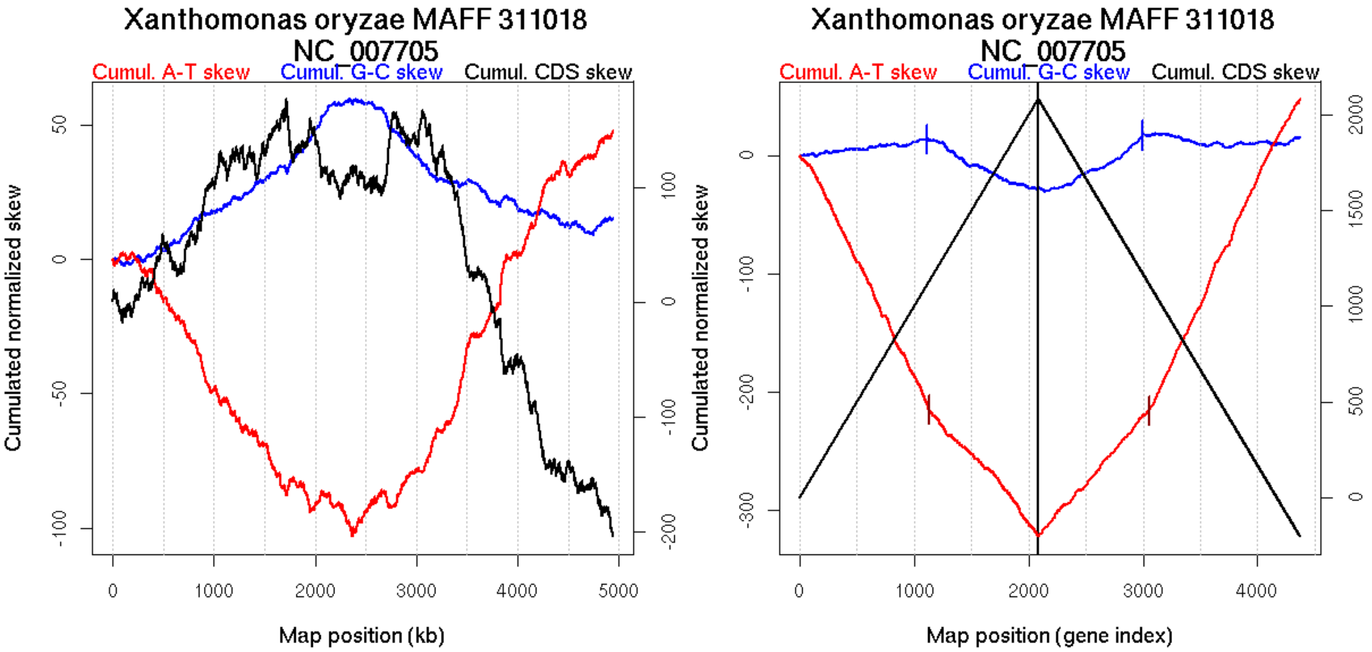
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1074 (2457.876 kb)	leading	0.008
	1075(2458.9565 kb)	1971 (4941.104 kb)	lagging	-0.042
GC-skew reverse	1972 (0 kb)	2815 (2153.6355 kb)	leading	0.053
	2816(2154.9405 kb)	4080 (4941.104 kb)	lagging	-0.004
AT-skew forward	1 (0 kb)	1066 (2439.577 kb)	leading	-0.197
	1067(2445.0285 kb)	1971 (4941.104 kb)	lagging	-0.094
AT-skew reverse	1972 (0 kb)	2896 (2348.1695 kb)	leading	0.111
	2897(2348.6795 kb)	4080(4941.104 kb)	lagging	0.206

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

387 Xanthomonas oryzae MAFF 311018

Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Xanthomonas.
Accession number: NC_007705; **Genome size (bp)**: 4940217.
Number of genes: 4372.
Oriloc predictions: Origin 174 kb Terminus 2400 kb
Worning et al., 2006: Origin 4698 kb Terminus 2369 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 2116.049 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.7 kb, 2375.56 kb
Consensus predictions: Origin 174 kb Terminus 2400 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1109	NA	2337
GC-skew reverse	2995	NA	2134
AT-skew forward	1131	NA	2379
AT-skew reverse	3051	NA	2243

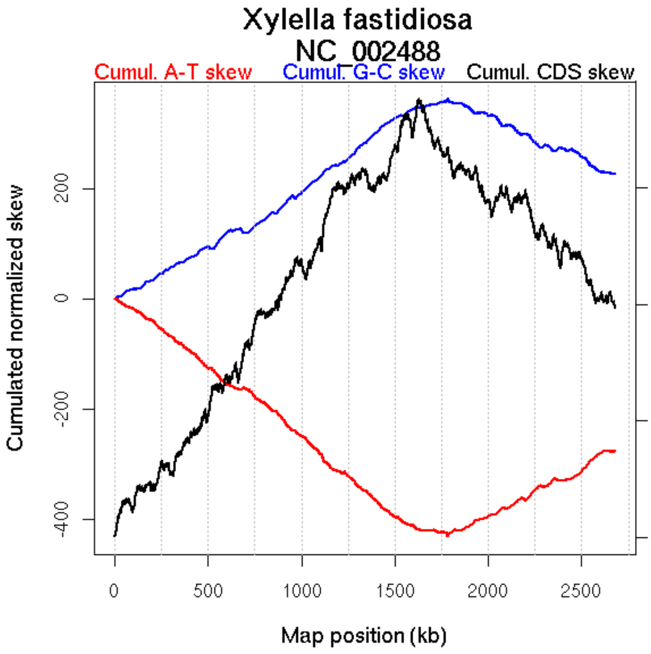
Segments:

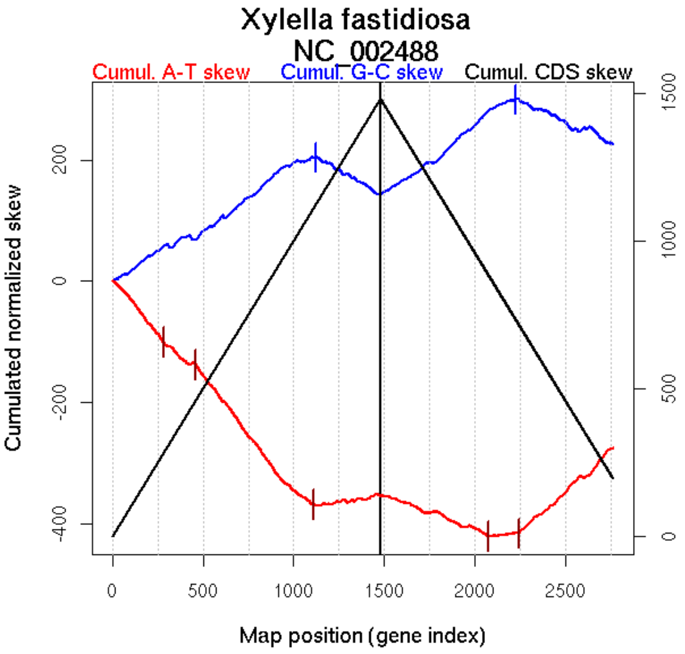
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1109 (2337.088 kb)	leading	0.011
	1110(2339.05 kb)	2084 (4940.015 kb)	lagging	-0.047
GC-skew reverse	2085 (0 kb)	2995 (2133.736 kb)	leading	0.05
	2996(2135.039 kb)	4372 (4940.015 kb)	lagging	-0.005
AT-skew forward	1 (0 kb)	1131 (2378.5945 kb)	leading	-0.195
	1132(2379.2775 kb)	2084 (4940.015 kb)	lagging	-0.106
AT-skew reverse	2085 (0 kb)	3051 (2243.1325 kb)	leading	0.11
	3052(2244.922 kb)	4372(4940.015 kb)	lagging	0.205

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

388 Xylella fastidiosa

Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Xylella.
Accession number: NC_002488; **Genome size (bp)**: 2679306.
Number of genes: 2765.
Oriloc predictions: Origin 0 kb Terminus 1784 kb
Worning et al., 2006: Origin 2656 kb Terminus 1785 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 2248.809 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.8 kb
Consensus predictions: Origin 0 kb Terminus 1784 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1124	0	1845
GC-skew reverse	2228	0	1752
AT-skew forward	282	0.03556	472
	459	0.03556	709
	1108	0	1821
AT-skew reverse	2077	0.03333	1455
	2247	0	1786

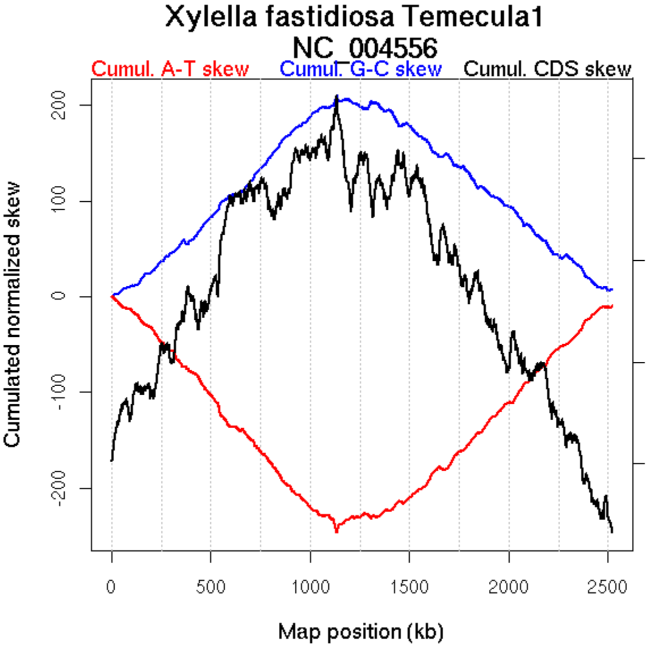
Segments:

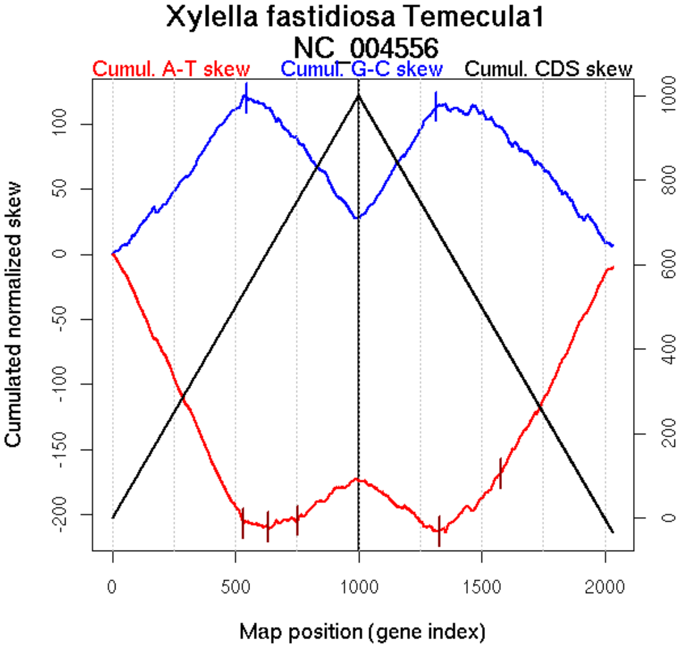
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1124 (1845.445 kb)	leading	0.191
	1125(1848.5435 kb)	1481 (2679.225 kb)	lagging	-0.176
GC-skew reverse	1482 (0 kb)	2228 (1751.6025 kb)	leading	0.23
	2229(1752.422 kb)	2765 (2679.225 kb)	lagging	-0.135
AT-skew forward	1 (0 kb)	282 (471.7725 kb)	leading	-0.369
	283(474.3305 kb)	459 (709.152 kb)	leading	-0.23
	460(710.744 kb)	1108 (1821.3865 kb)	leading	-0.372
	1109(1821.9925 kb)	1481 (2679.225 kb)	lagging	0.046
AT-skew reverse	1482 (0 kb)	2077 (1455.2565 kb)	leading	-0.113
	2078(1458.997 kb)	2247(1785.6935 kb)	leading	0.036
	2248(1786.54 kb)	2765(2679.225 kb)	lagging	0.266

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

389 Xylella fastidiosa Temecula1

Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales; Xanthomonadaceae; Xylella.
Accession number: NC_004556; **Genome size (bp)**: 2519802.
Number of genes: 2034.
Oriloc predictions: Origin 0 kb Terminus 1134 kb
Worning et al., 2006: Origin 2500 kb Terminus 1195 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 1622.748 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 0.81 kb
Consensus predictions: Origin 0 kb Terminus 1134 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	547	NA	1211
GC-skew reverse	1316	NA	1024
AT-skew forward	533	NA	1134
	631	NA	1389
	752	NA	1714
AT-skew reverse	1327	NA	1062
	1578	NA	1575

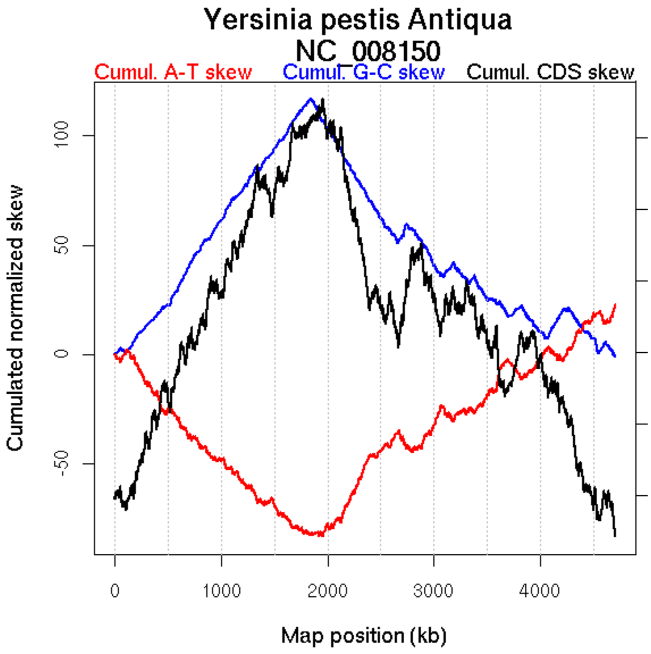
Segments:

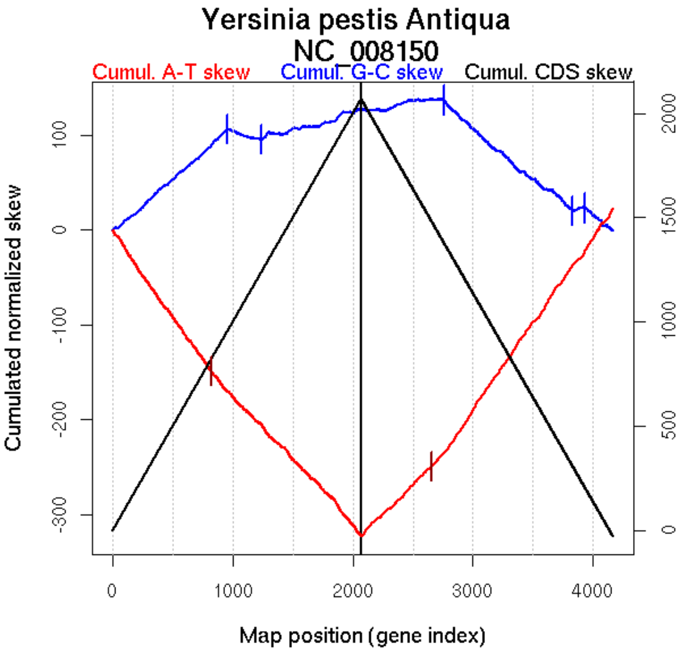
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	547 (1211.0005 kb)	leading	0.232
	548(1211.8495 kb)	1000 (2519.722 kb)	lagging	-0.221
GC-skew reverse	1001 (0 kb)	1316 (1024.099 kb)	leading	0.285
	1317(1026.3725 kb)	2034 (2519.722 kb)	lagging	-0.164
AT-skew forward	1 (0 kb)	533 (1134.281 kb)	leading	-0.4
	534(1138.761 kb)	631 (1389.473 kb)	lagging	-0.046
	632(1389.925 kb)	752 (1713.539 kb)	lagging	0.056
	753(1714.3595 kb)	1000 (2519.722 kb)	lagging	0.127
AT-skew reverse	1001 (0 kb)	1327 (1061.5505 kb)	leading	-0.131
	1328(1063.704 kb)	1578(1575.3635 kb)	lagging	0.171
	1579(1575.9775 kb)	2034(2519.722 kb)	lagging	0.362

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

390 Yersinia pestis Antiqua

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Yersinia.
Accession number: NC_008150; **Genome size (bp)**: 4702289.
Number of genes: 4167.
Oriloc predictions: Origin 112 kb Terminus 1842 kb
Worning et al., 2006: Origin 114 kb Terminus 1838 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 3640.496 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 4667.6 kb
Consensus predictions: Origin 112 kb Terminus 1842 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	953	0	1848
	1243	0.02667	2673
GC-skew reverse	2756	0.00667	1835
	3830	0.00222	4045
	3928	0.00222	4251
AT-skew forward	818	0	1593
AT-skew reverse	2658	0	1576

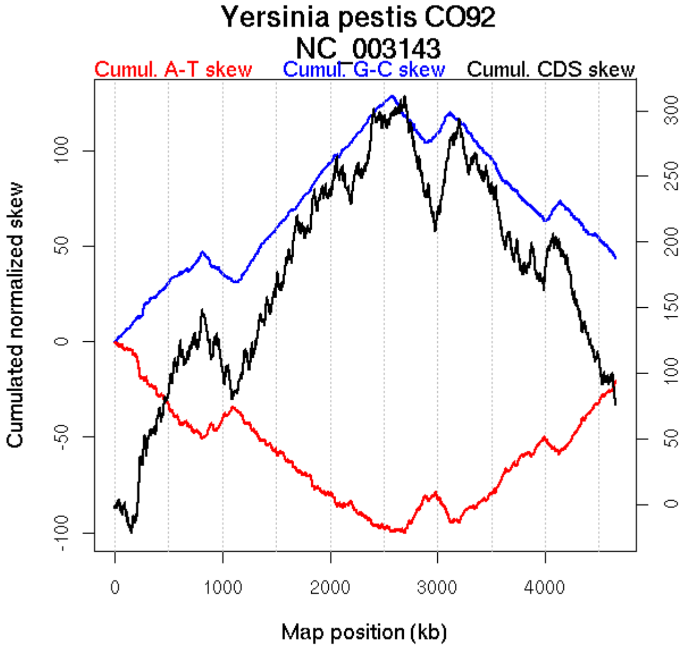
Segments:

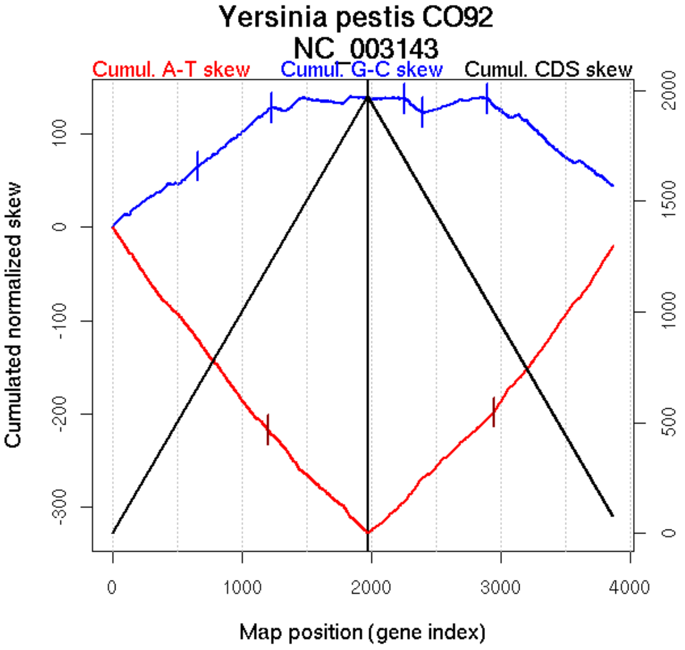
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	953 (1848.303 kb)	leading	0.112
	954(1849.159 kb)	1243 (2672.6375 kb)	lagging	-0.041
	1244(2674.032 kb)	2069 (4702.178 kb)	lagging	0.035
GC-skew reverse	2070 (0 kb)	2756 (1834.717 kb)	leading	0.023
	2757(1840.922 kb)	3830 (4044.832 kb)	lagging	-0.105
	3831(4045.8835 kb)	3928 (4250.703 kb)	lagging	0.044
	3929(4251.1275 kb)	4167 (4702.178 kb)	lagging	-0.107
AT-skew forward	1 (0 kb)	818 (1592.754 kb)	leading	-0.18
	819(1594.788 kb)	2069 (4702.178 kb)	lagging	-0.134
AT-skew reverse	2070 (0 kb)	2658 (1575.5305 kb)	leading	0.124
	2659(1579.2835 kb)	4167(4702.178 kb)	lagging	0.182

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

391 Yersinia pestis CO92

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Yersinia.
Accession number: NC_003143; **Genome size (bp)**: 4653728.
Number of genes: 3870.
Oriloc predictions: Origin 0 kb Terminus 2580 kb
Worning et al., 2006: Origin 0 kb Terminus 2547 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 185.682 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 3427.28 kb, 4619.03 kb
Consensus predictions: Origin 0 kb Terminus 2580 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	655	NA	1400
	1227	NA	2578
GC-skew reverse	2260	NA	816
	2400	NA	1102
	2897	NA	2559
AT-skew forward	1201	NA	2517
AT-skew reverse	2949	NA	2698

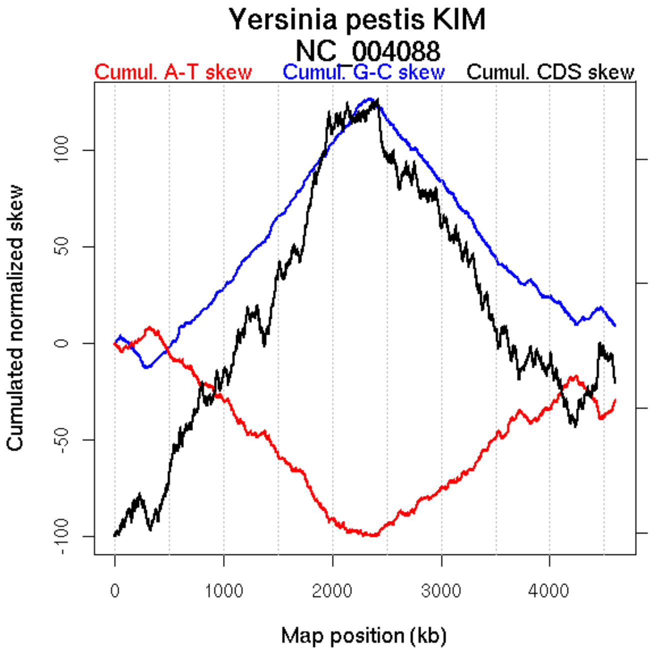
Segments:

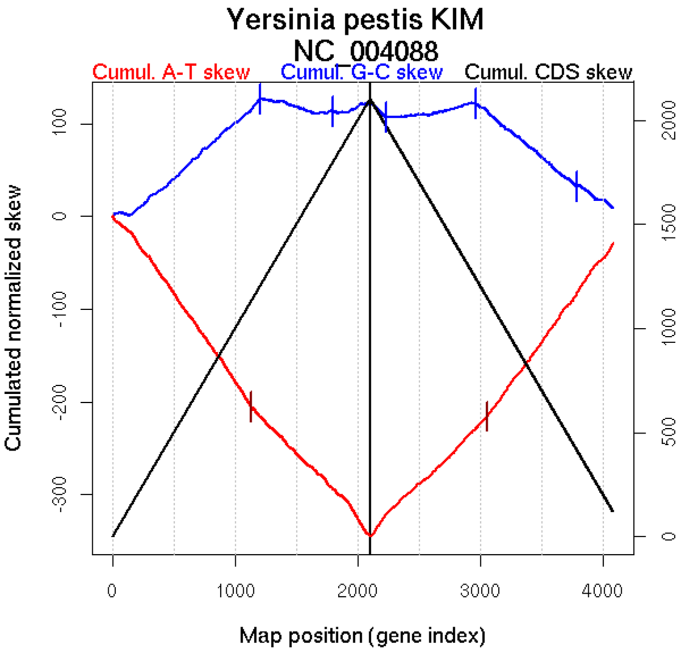
	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	655 (1399.768 kb)	leading	0.089
	656(1399.963 kb)	1227 (2577.6135 kb)	leading	0.113
	1228(2580.0645 kb)	1973 (4653.617 kb)	lagging	0.015
GC-skew reverse	1974 (0 kb)	2260 (815.995 kb)	leading	0.004
	2261(818.769 kb)	2400 (1101.7175 kb)	leading	-0.112
	2401(1108.6315 kb)	2897 (2559.184 kb)	leading	0.037
	2898(2563.7185 kb)	3870 (4653.617 kb)	lagging	-0.095
AT-skew forward	1 (0 kb)	1201 (2517.403 kb)	leading	-0.18
	1202(2523.9985 kb)	1973 (4653.617 kb)	lagging	-0.14
AT-skew reverse	1974 (0 kb)	2949 (2697.6315 kb)	leading	0.137
	2950(2698.6515 kb)	3870(4653.617 kb)	lagging	0.189

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

392 Yersinia pestis KIM

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Yersinia.
Accession number: NC_004088; **Genome size (bp)**: 4600755.
Number of genes: 4086.
Oriloc predictions: Origin 318 kb Terminus 2348 kb
Worning et al., 2006: Origin 333 kb Terminus 2324 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 4408.751 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1567.37 kb, 4565.82 kb
Consensus predictions: Origin 318 kb Terminus 2348 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1207	NA	2331
	1796	NA	3881
GC-skew reverse	2229	NA	293
	2963	NA	2300
	3787	NA	3934
AT-skew forward	1132	NA	2165
AT-skew reverse	3059	NA	2485

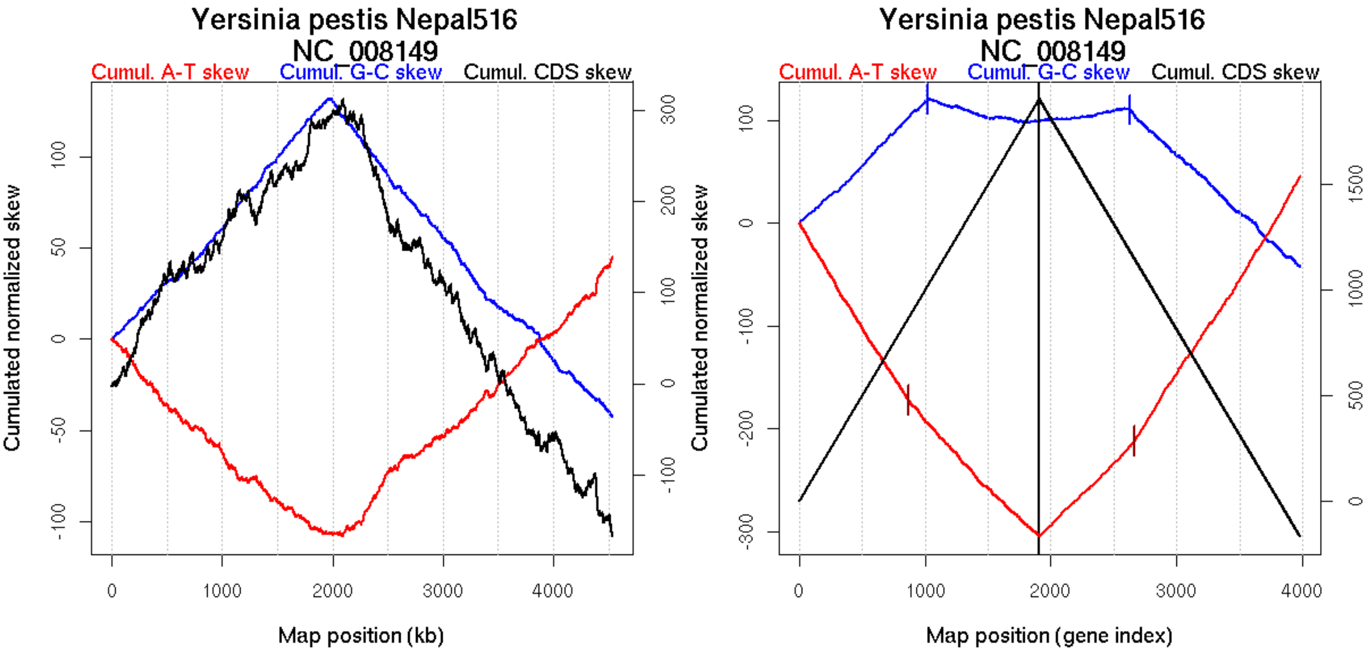
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1207 (2331.1835 kb)	leading	0.111
	1208(2334.4595 kb)	1796 (3881.068 kb)	lagging	-0.031
	1797(3883.126 kb)	2103 (4600.476 kb)	lagging	0.041
GC-skew reverse	2104 (0 kb)	2229 (293.0815 kb)	lagging	-0.124
	2230(294.723 kb)	2963 (2299.7165 kb)	leading	0.022
	2964(2300.1995 kb)	3787 (3934.19 kb)	lagging	-0.11
	3788(3935.0275 kb)	4086 (4600.476 kb)	lagging	-0.081
AT-skew forward	1 (0 kb)	1132 (2164.588 kb)	leading	-0.184
	1133(2164.978 kb)	2103 (4600.476 kb)	lagging	-0.137
AT-skew reverse	2104 (0 kb)	3059 (2484.838 kb)	NA	0.129
	3060(2485.4475 kb)	4086(4600.476 kb)	lagging	0.182

More T than A on the leading strand for replication - for forward encoded genes.
More G than C on the leading strand for replication.

393 Yersinia pestis Nepal516

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Yersinia.
Accession number: NC_008149; **Genome size (bp)**: 4534590.
Number of genes: 3981.
Oriloc predictions: Origin 0 kb Terminus 1981 kb
Worning et al., 2006: Origin NA kb Terminus NA kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 4432.612 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 4499.9 kb
Consensus predictions: Origin 0 kb Terminus 1981 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1023	NA	1985
GC-skew reverse	2628	NA	1956
AT-skew forward	868	NA	1703
AT-skew reverse	2666	NA	2062

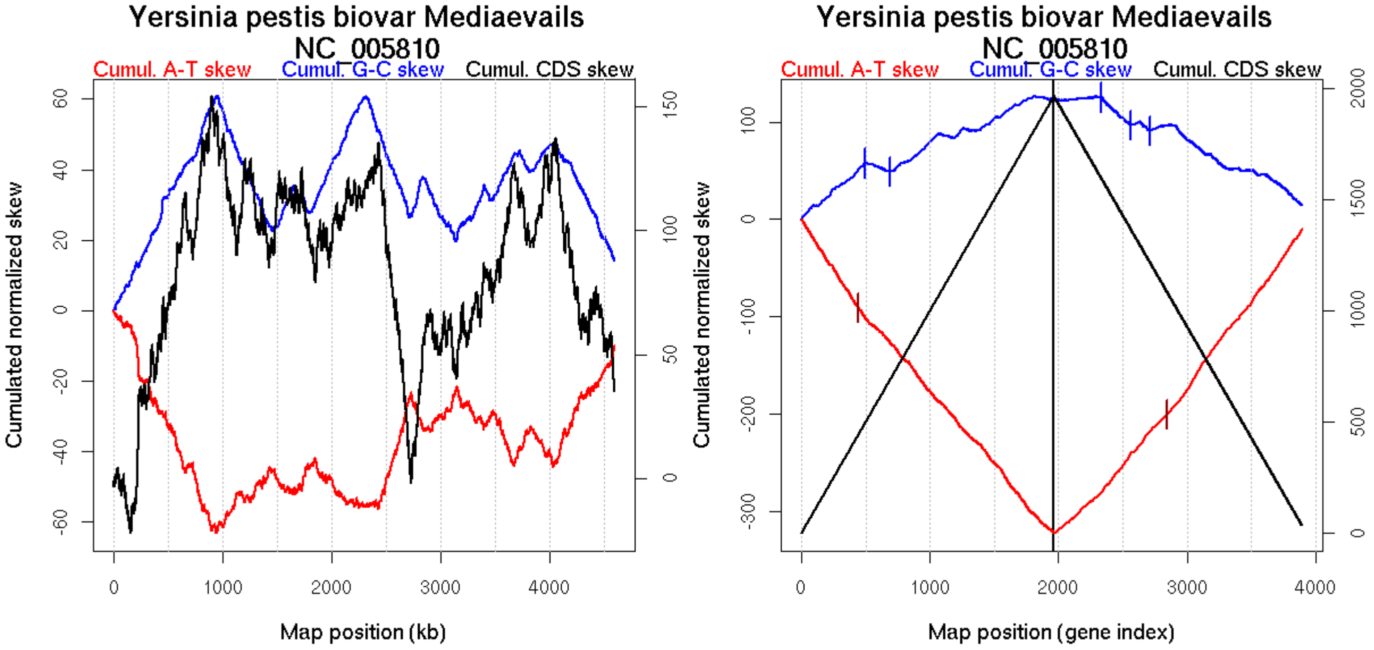
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1023 (1984.8975 kb)	leading	0.12
	1024(1988.202 kb)	1907 (4534.479 kb)	lagging	-0.026
GC-skew reverse	1908 (0 kb)	2628 (1955.8275 kb)	leading	0.018
	2629(1958.0275 kb)	3981 (4534.479 kb)	lagging	-0.112
AT-skew forward	1 (0 kb)	868 (1702.894 kb)	leading	-0.198
	869(1703.7495 kb)	1907 (4534.479 kb)	lagging	-0.127
AT-skew reverse	1908 (0 kb)	2666 (2062.139 kb)	leading	0.12
	2667(2063.0985 kb)	3981(4534.479 kb)	lagging	0.191

More T than A on the leading strand for replication.
More G than C on the leading strand for replication.

394 Yersinia pestis biovar Mediaevails

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Yersinia.
Accession number: NC_005810; **Genome size (bp)**: 4595065.
Number of genes: 3895.
Oriloc predictions: Origin NA Terminus NA
Worning et al., 2006: Origin 4592 kb Terminus 2733 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 186.372 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 2983.32 kb, 4560.13 kb
Consensus predictions: Origin NA Terminus NA



Significant breakpoints (p-value <0.05):

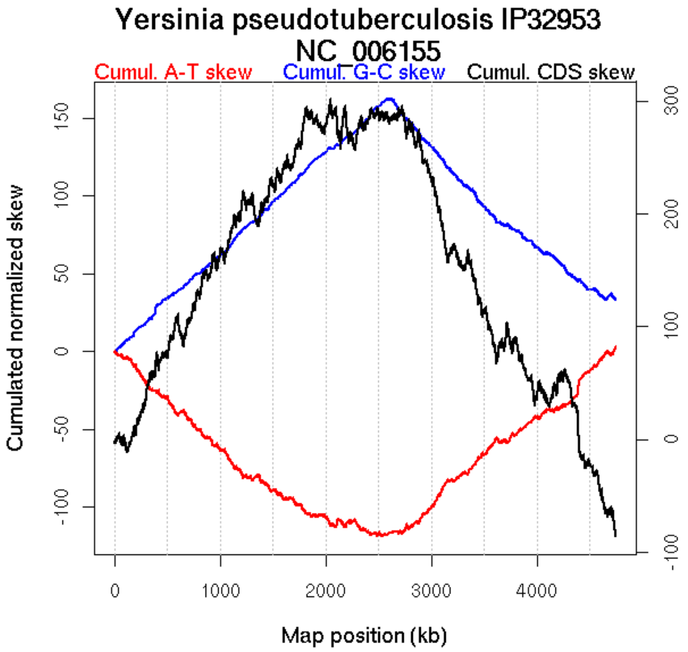
	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	496	NA	936
	689	NA	1449
GC-skew reverse	2328	NA	956
	2562	NA	1455
	2709	NA	1789
AT-skew forward	442	NA	833
AT-skew reverse	2848	NA	2162

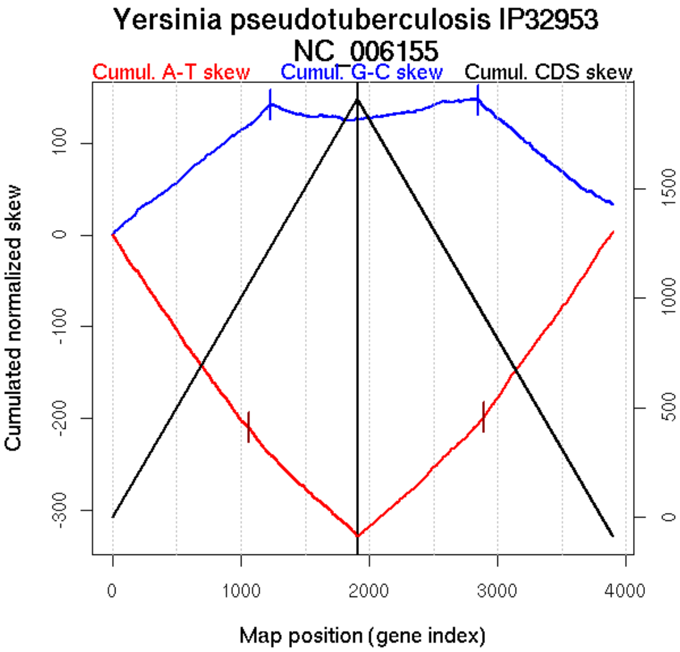
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	496 (935.95 kb)	NA	0.11
	497(937.7045 kb)	689 (1449.118 kb)	NA	-0.05
	690(1452.9205 kb)	1965 (4594.786 kb)	NA	0.061
GC-skew reverse	1966 (0 kb)	2328 (956.3415 kb)	NA	0.011
	2329(957.103 kb)	2562 (1455.038 kb)	NA	-0.123
	2563(1457.2995 kb)	2709 (1788.919 kb)	NA	-0.039
	2710(1794.8815 kb)	3895 (4594.786 kb)	NA	-0.068
AT-skew forward	1 (0 kb)	442 (832.539 kb)	NA	-0.204
	443(834.1105 kb)	1965 (4594.786 kb)	NA	-0.154
AT-skew reverse	1966 (0 kb)	2848 (2161.8335 kb)	NA	0.145
	2849(2164.7045 kb)	3895(4594.786 kb)	NA	0.18

395 Yersinia pseudotuberculosis IP32953

Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Yersinia.
Accession number: NC_006155; **Genome size (bp)**: 4744671.
Number of genes: 3900.
Oriloc predictions: Origin 0 kb Terminus 2581 kb
Worning et al., 2006: Origin 0 kb Terminus 2576 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 4430.825 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 3295.21 kb, 4709.95 kb
Consensus predictions: Origin 0 kb Terminus 2581 kb





Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	1229	NA	2605
GC-skew reverse	2845	NA	2586
AT-skew forward	1063	NA	2228
AT-skew reverse	2896	NA	2725

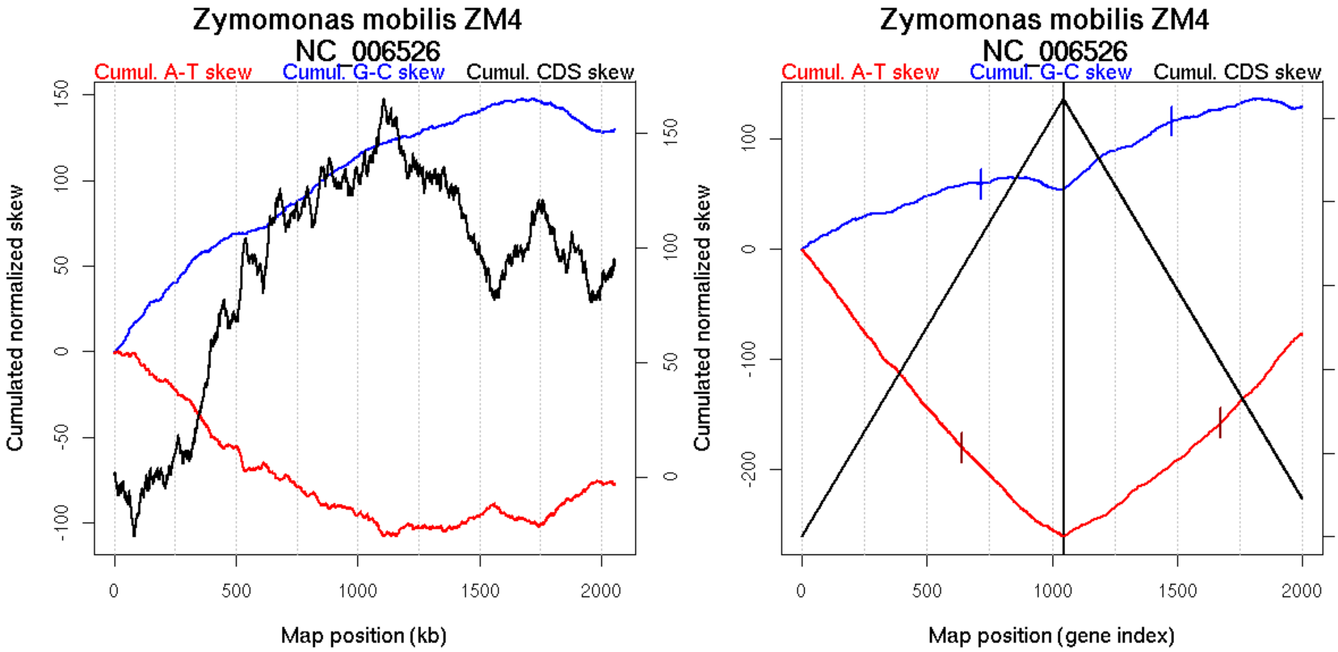
Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	1229 (2605.037 kb)	leading	0.112
	1230(2607.548 kb)	1907 (4744.56 kb)	lagging	-0.022
GC-skew reverse	1908 (0 kb)	2845 (2585.529 kb)	leading	0.027
	2846(2587.808 kb)	3900 (4744.56 kb)	lagging	-0.111
AT-skew forward	1 (0 kb)	1063 (2228.3695 kb)	leading	-0.2
	1064(2229.0835 kb)	1907 (4744.56 kb)	NA	-0.134
AT-skew reverse	1908 (0 kb)	2896 (2725.358 kb)	leading	0.132
	2897(2726.68 kb)	3900(4744.56 kb)	lagging	0.199

More T than A on the leading strand for replication - for reverse encoded genes.
More G than C on the leading strand for replication.

396 Zymomonas mobilis ZM4

Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales; Sphingomonadaceae; Zymomonas.
Accession number: NC_006526; **Genome size (bp)**: 2056416.
Number of genes: 1998.
Oriloc predictions: Origin 0 kb Terminus 1741 kb
Worning et al., 2006: Origin 2015 kb Terminus 1323 kb
Position of the first peak in DnaA box distribution (Mackiewicz et al., 2004): 2055.757 kb
Position(s) of the dnaA gene(s) (Mackiewicz et al., 2004): 1371.41 kb
Consensus predictions: Origin 0 kb Terminus 1741 kb



Significant breakpoints (p-value <0.05):

	Breakpoints	P-value	Chromosome coordinate (kb)
GC-skew forward	715	0	1314
GC-skew reverse	1478	0	1013
AT-skew forward	641	0	1146
AT-skew reverse	1674	0	1393

Segments:

	From (index/coord.)	To (index/coord.)	Strand	Slope
GC-skew forward	1 (0 kb)	715 (1313.5815 kb)	leading	0.083
	716(1315.65 kb)	1045 (2055.614 kb)	NA	-0.024
GC-skew reverse	1046 (0 kb)	1478 (1012.55 kb)	leading	0.134
	1479(1021.4075 kb)	1998 (2055.614 kb)	NA	0.031
AT-skew forward	1 (0 kb)	641 (1145.9105 kb)	leading	-0.284
	642(1146.431 kb)	1045 (2055.614 kb)	NA	-0.209
AT-skew reverse	1046 (0 kb)	1674 (1393.1455 kb)	leading	0.166
	1675(1397.461 kb)	1998(2055.614 kb)	NA	0.259