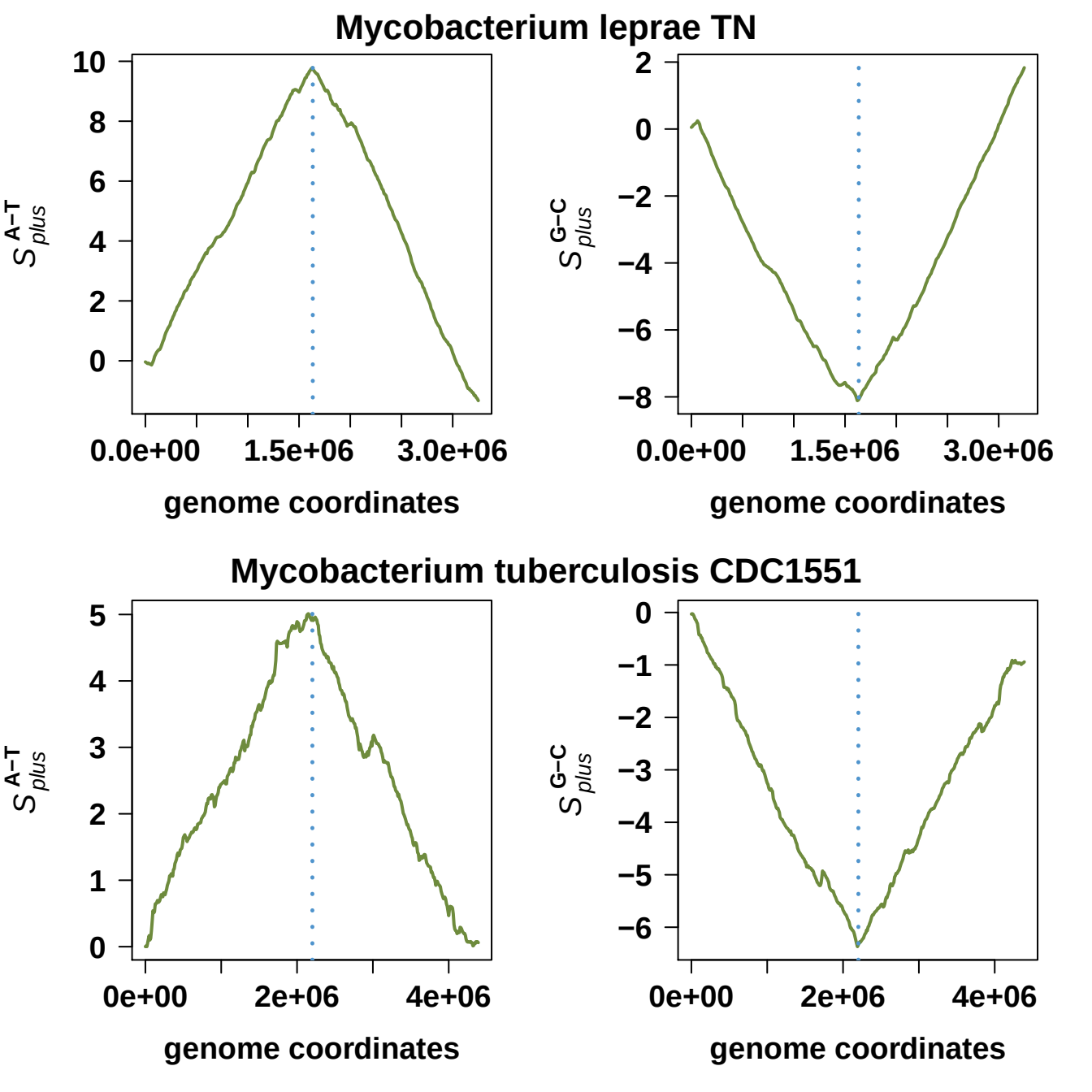
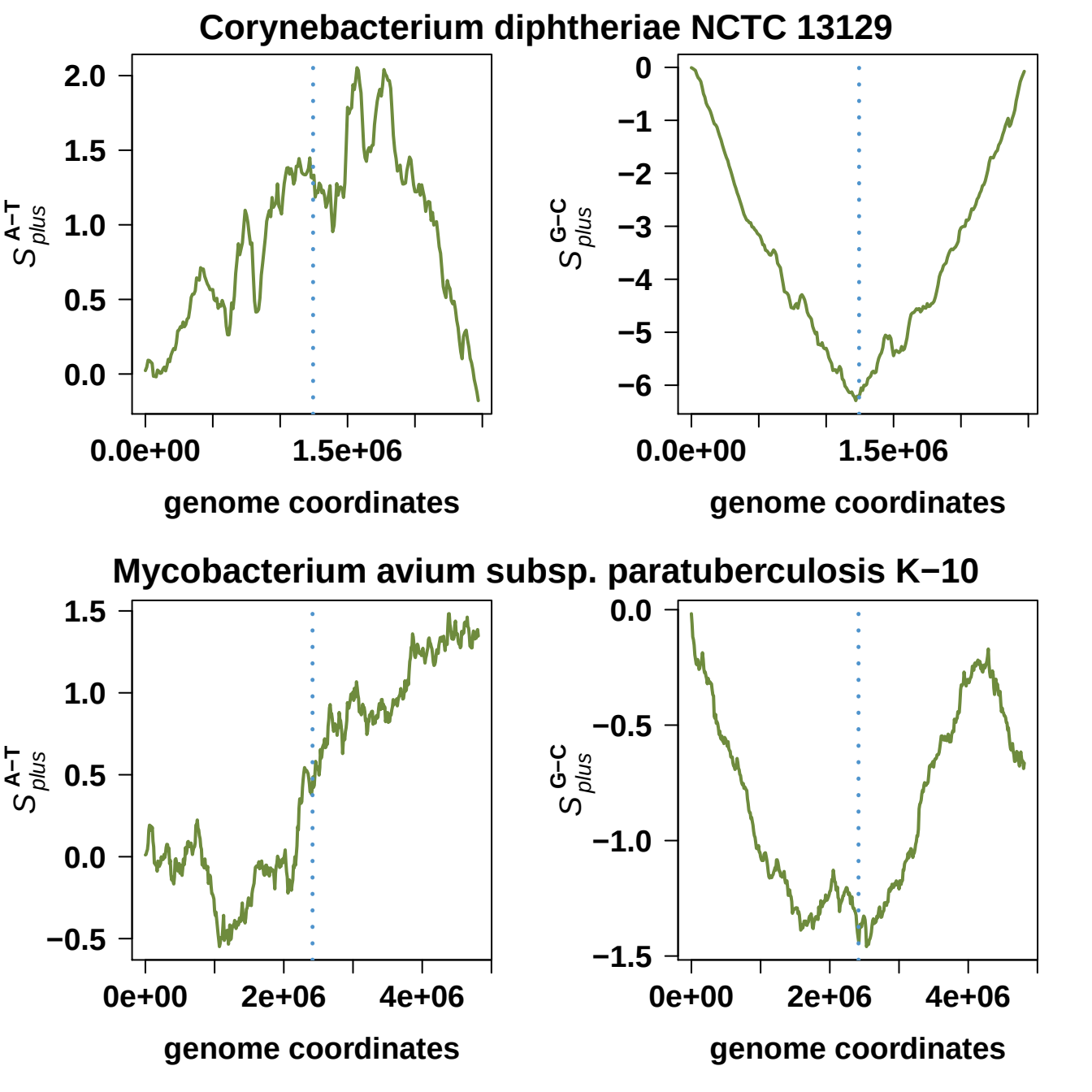
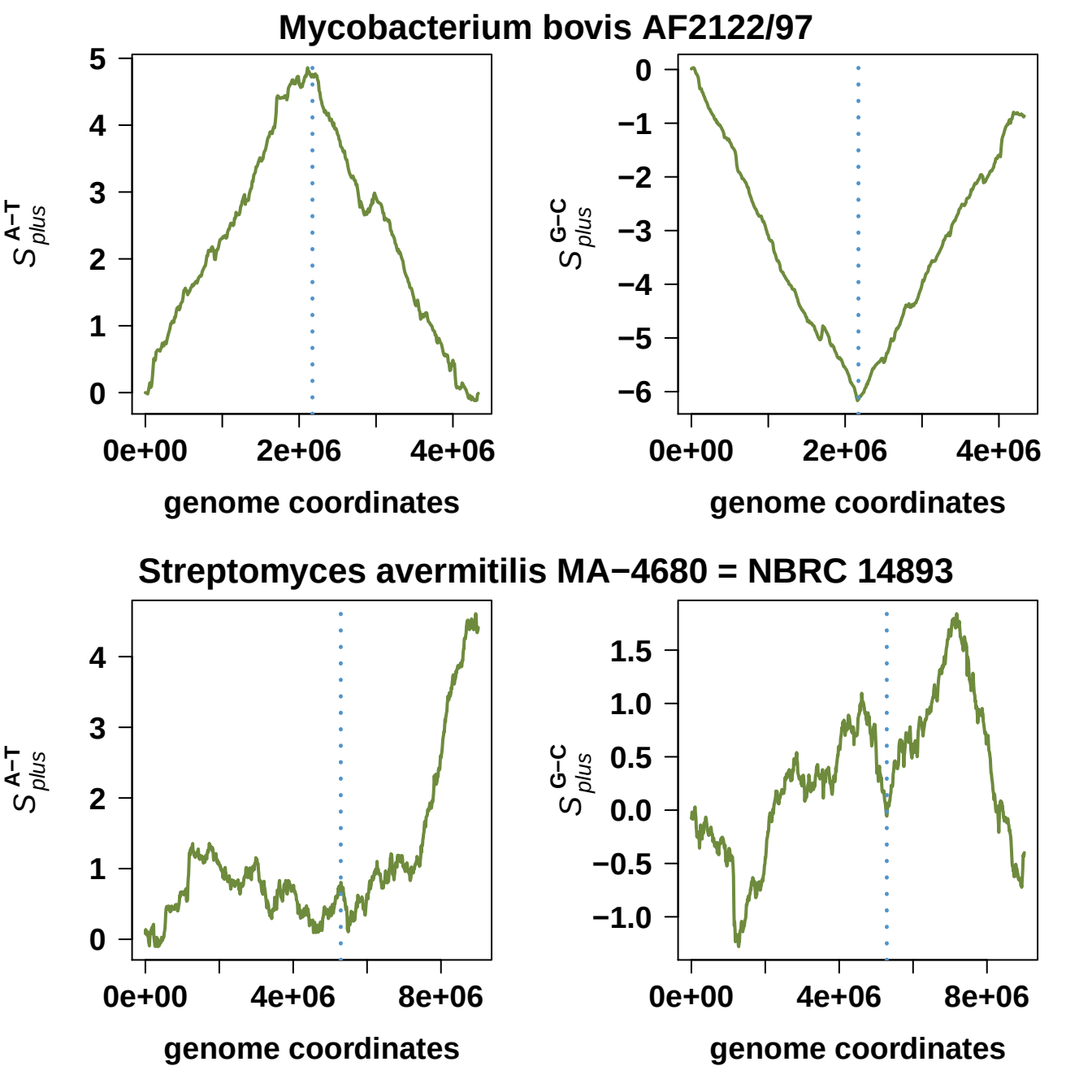
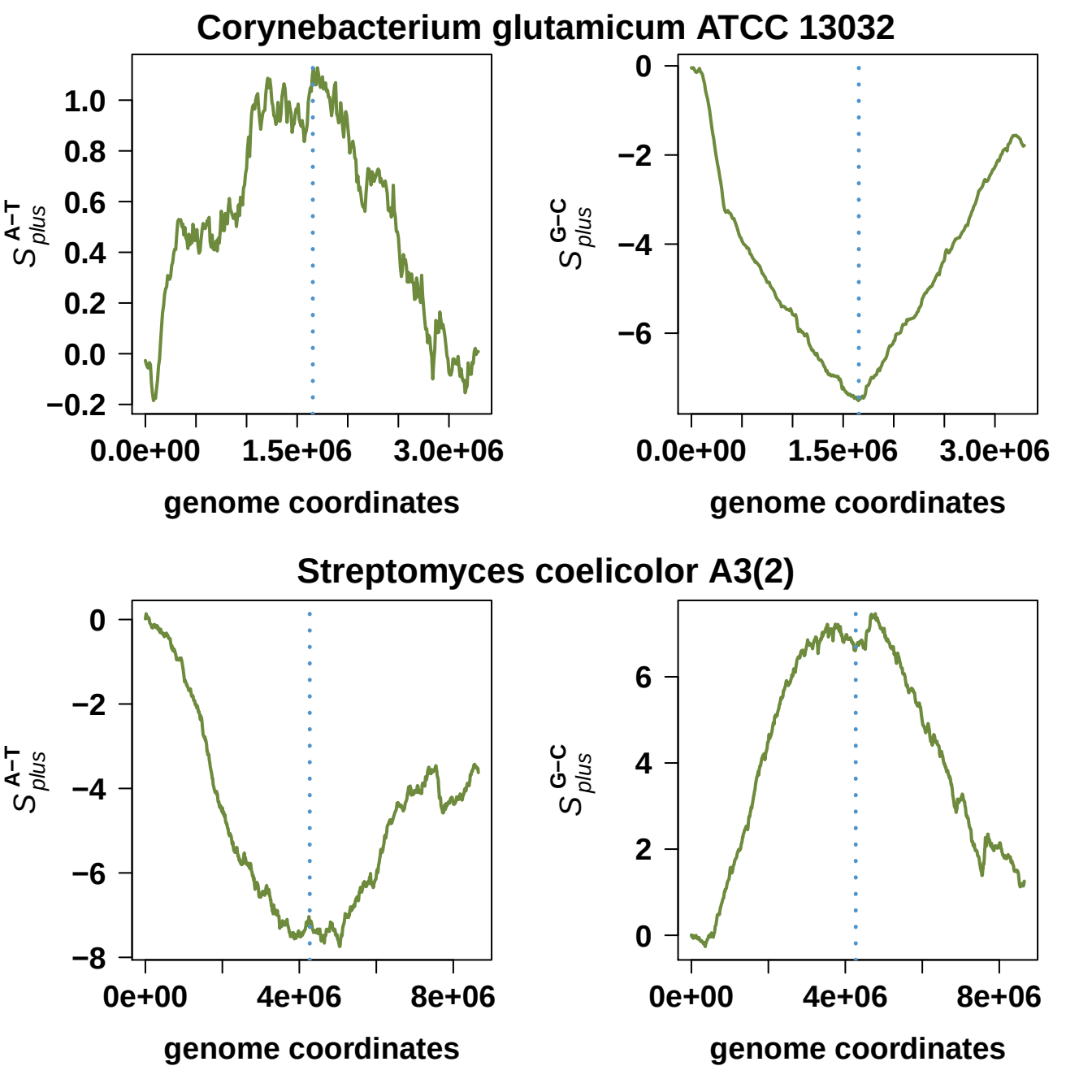
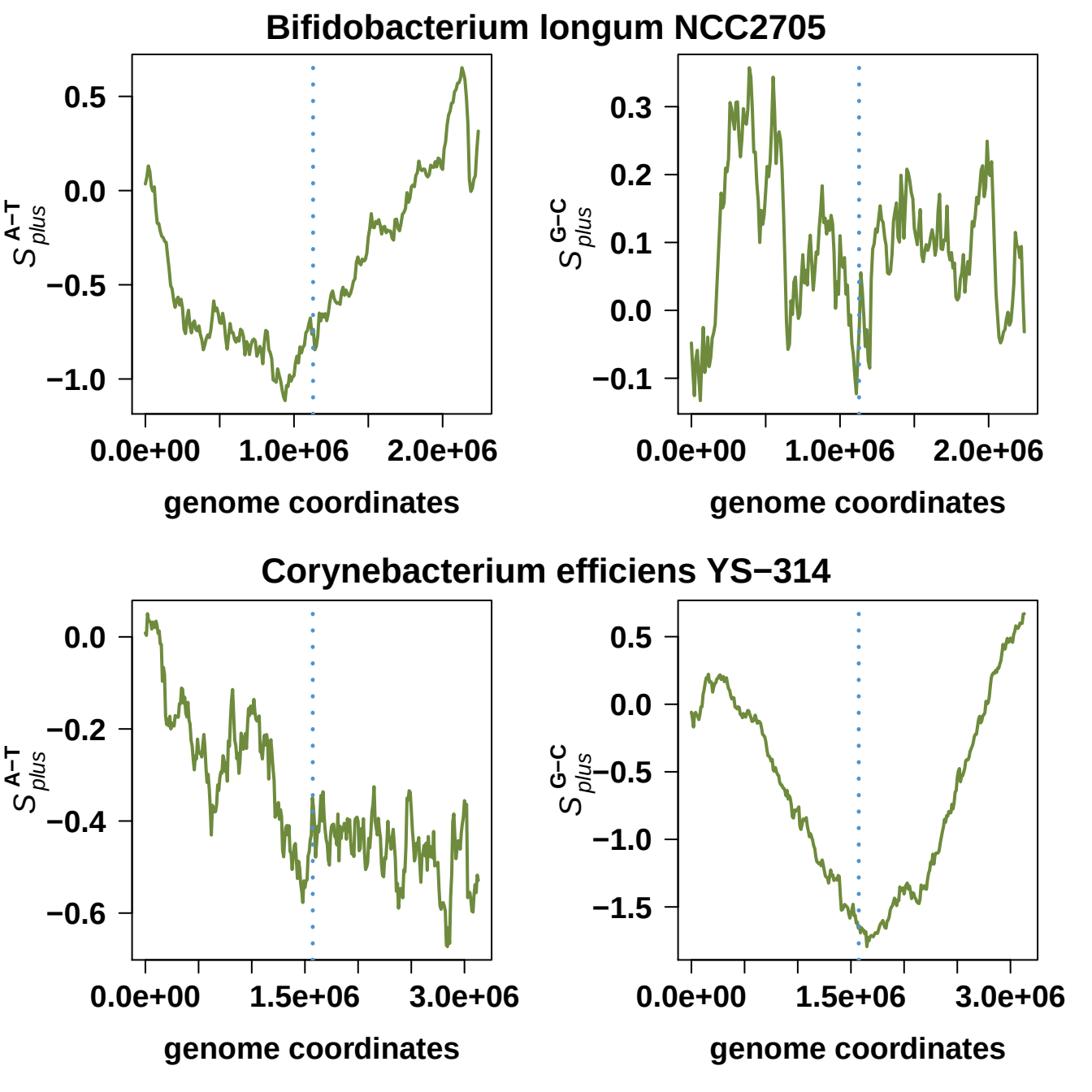
Cumulative diagrams of mononucleotide skews (S_{plus}^{A-T} and S_{plus}^{G-C}) along the plus (published) strand of all bacteria chromosomes in our collection. The vertical dotted blue line indicates the origin of replication (*ori*). The coordinates of all circular chromosomes are shifted so that the *ori* is placed at the middle of their published sequence.

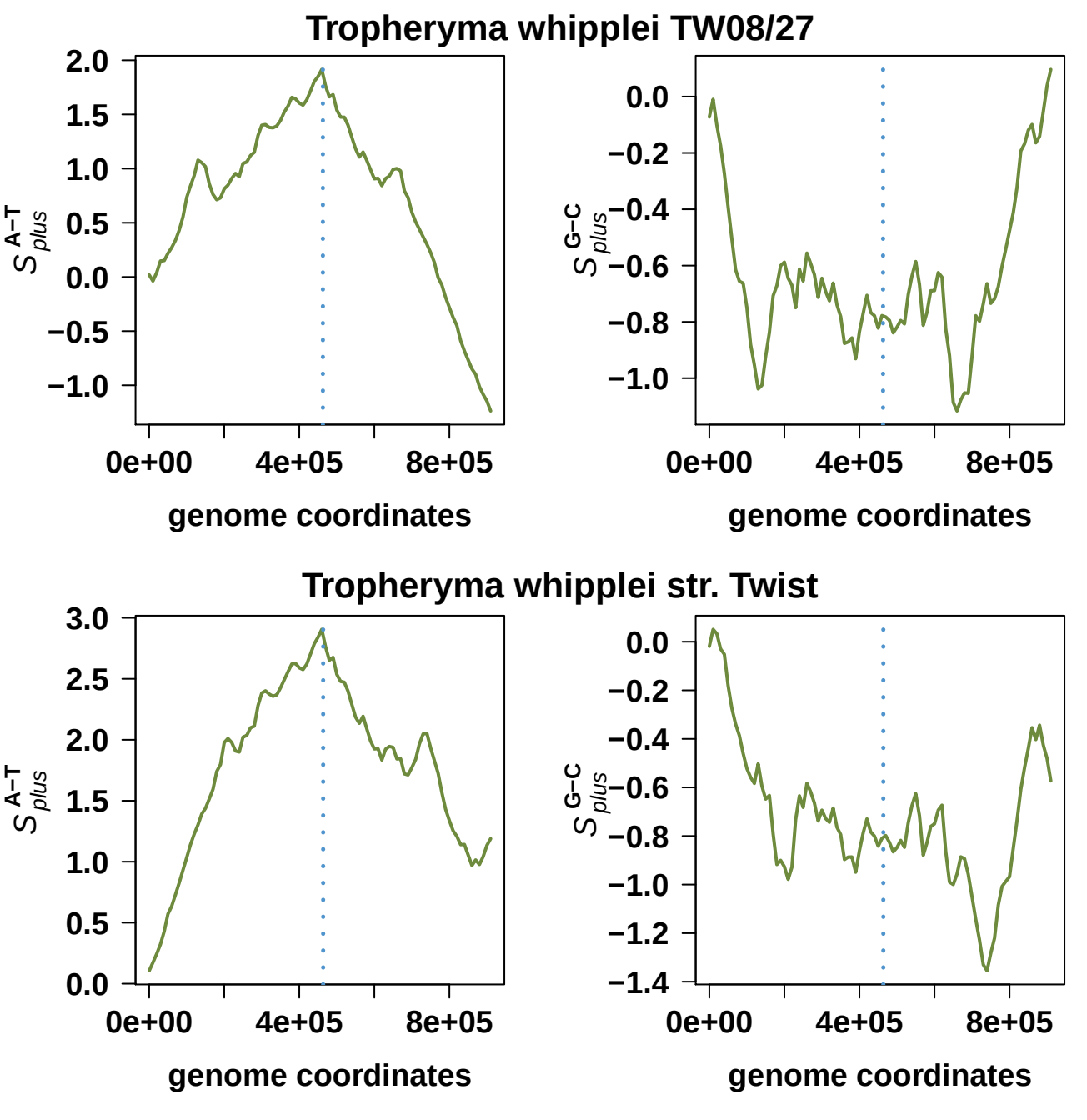

Mycobacterium leprae TN
S^{A-T}_{plus}
10
8
6
4
2
0
0.0e+00
1.5e+06
3.0e+06
genome coordinates
S^{G-C}_{plus}
2
0
−2
−4
−6
−8
0.0e+00
1.5e+06
3.0e+06
genome coordinates
Mycobacterium tuberculosis CDC1551
S^{A-T}_{plus}
5
4
3
2
1
0
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
−4
−5
−6
0e+00
2e+06
4e+06
genome coordinates

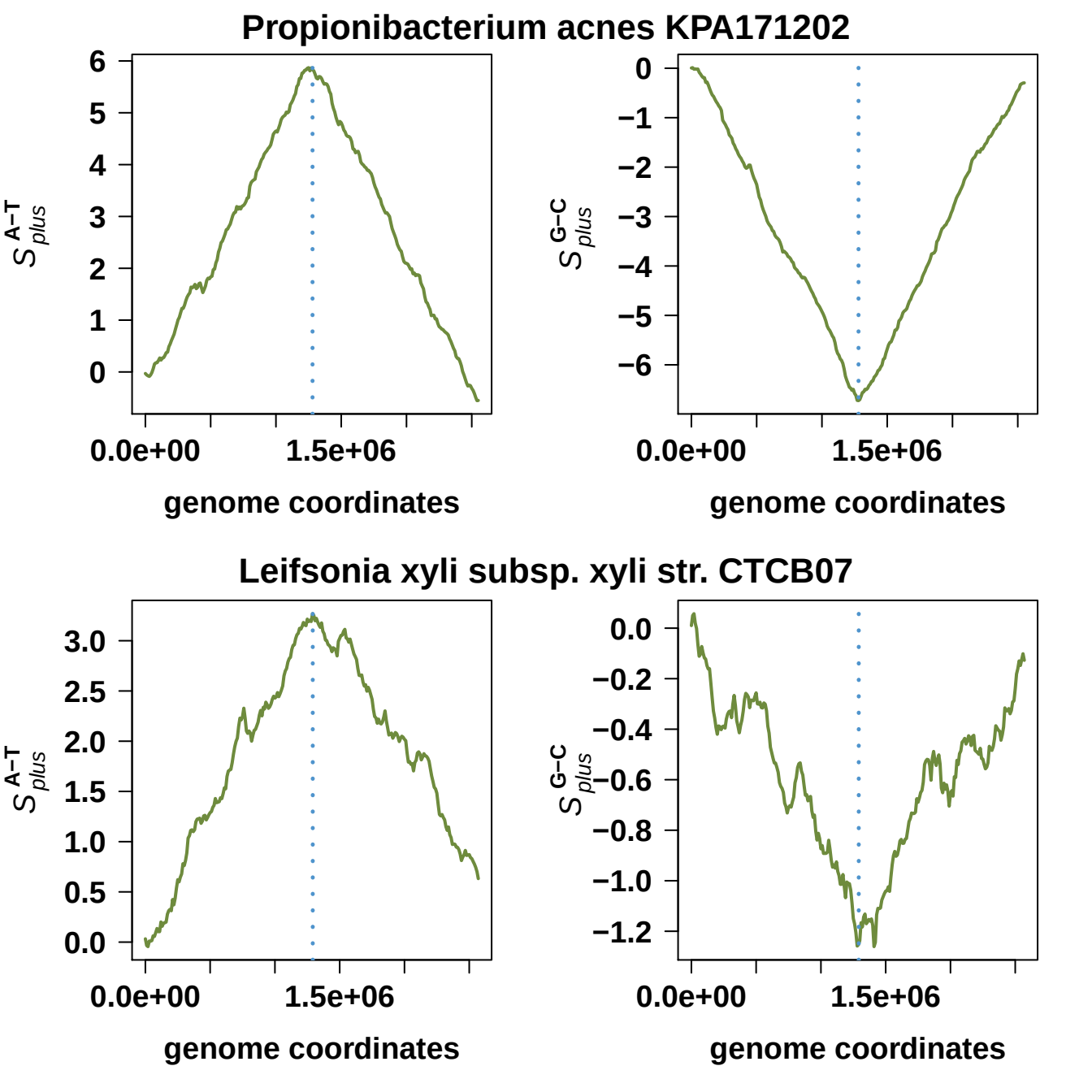

Corynebacterium diphtheriae NCTC 13129
S^{A-T}_{plus}
2.0
1.5
1.0
0.5
0.0
0.0e+00
1.5e+06
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
−4
−5
−6
0.0e+00
1.5e+06
genome coordinates
Mycobacterium avium subsp. paratuberculosis K−10
S^{A-T}_{plus}
1.5
1.0
0.5
0.0
−0.5
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
0.0
−0.5
−1.0
−1.5
0e+00
2e+06
4e+06
genome coordinates

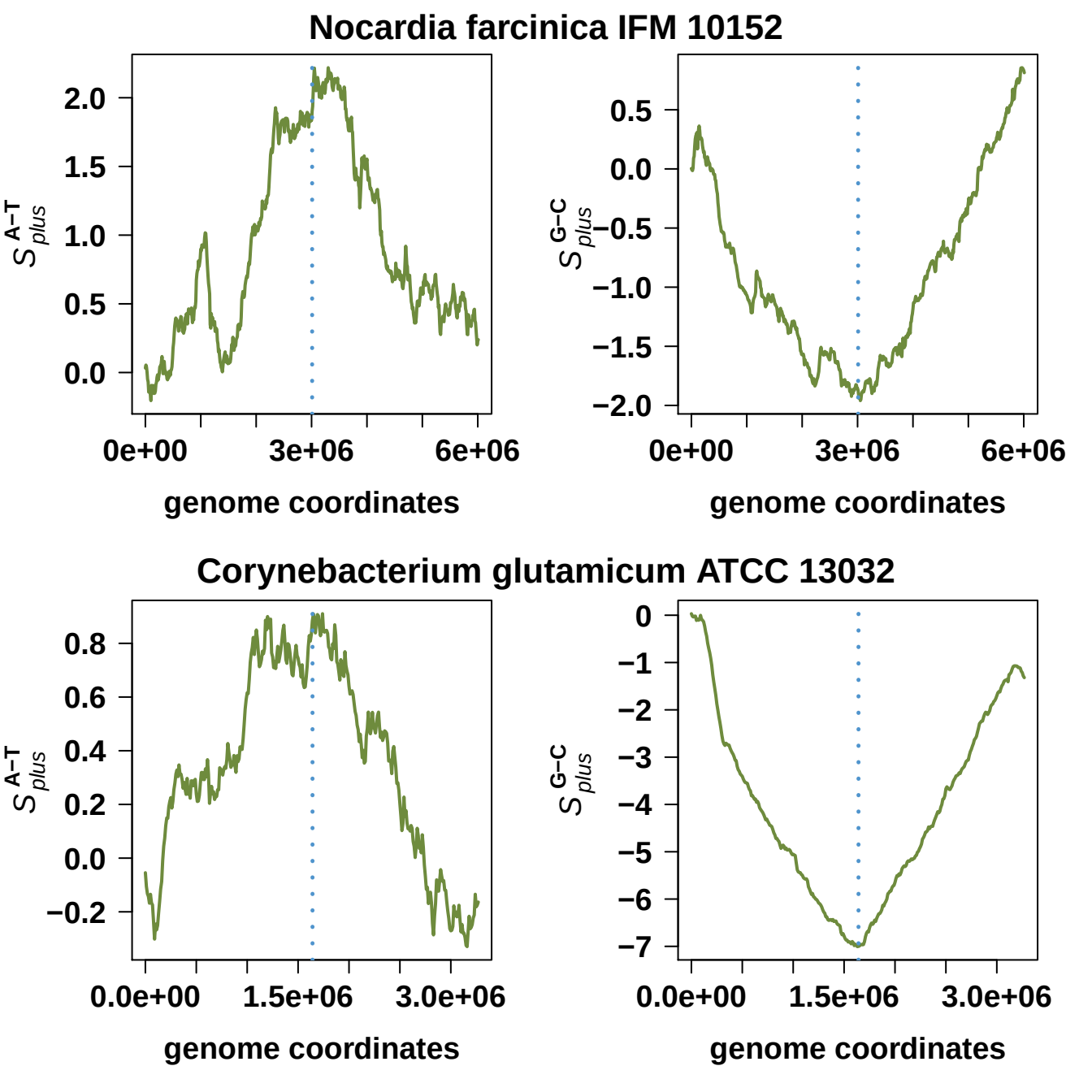

Mycobacterium bovis AF2122/97
S^{A-T}_{plus}
5
4
3
2
1
0
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
−4
−5
−6
0e+00
2e+06
4e+06
genome coordinates
Streptomyces avermitilis MA−4680 = NBRC 14893
S^{A-T}_{plus}
4
3
2
1
0
0e+00
4e+06
8e+06
genome coordinates
S^{G-C}_{plus}
1.5
1.0
0.5
0.0
−0.5
−1.0
0e+00
4e+06
8e+06
genome coordinates

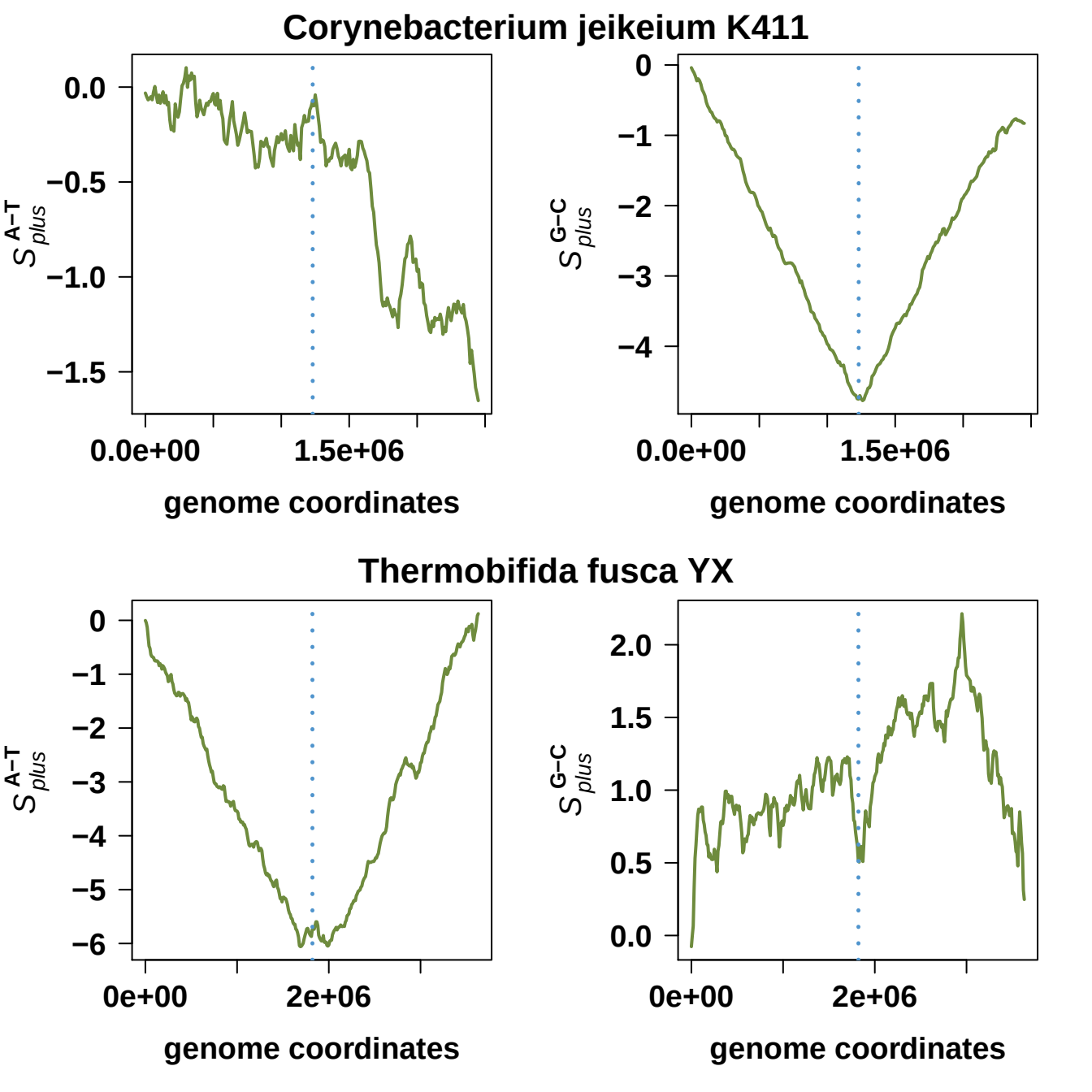

Corynebacterium glutamicum ATCC 13032
S^{A-T}_{plus}
1.0
0.8
0.6
0.4
0.2
0.0
−0.2
0.0e+00
1.5e+06
3.0e+06
genome coordinates
S^{G-C}_{plus}
0
−2
−4
−6
0.0e+00
1.5e+06
3.0e+06
genome coordinates
Streptomyces coelicolor A3(2)
S^{A-T}_{plus}
0
−2
−4
−6
−8
0e+00
4e+06
8e+06
genome coordinates
S^{G-C}_{plus}
6
4
2
0
0e+00
4e+06
8e+06
genome coordinates

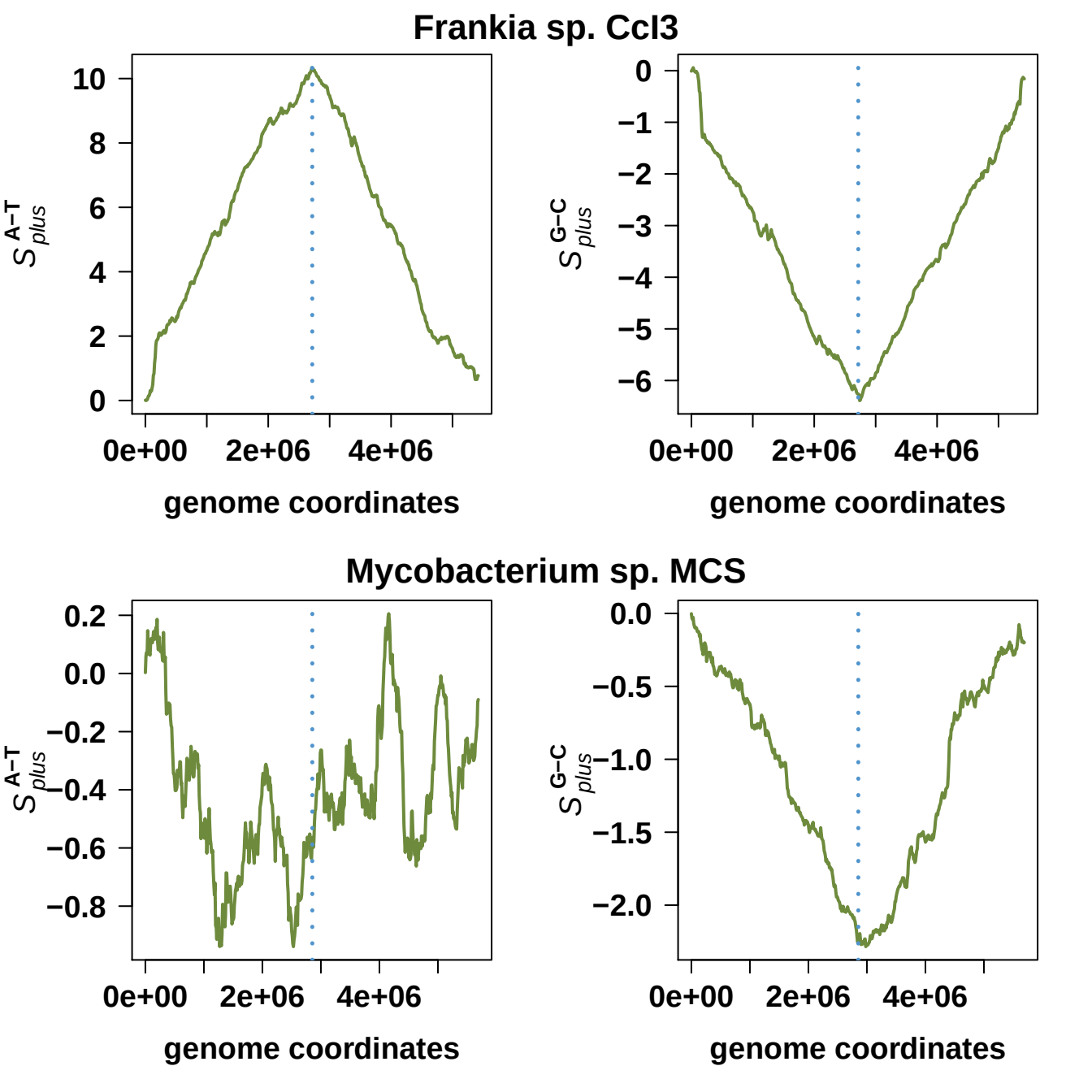

Bifidobacterium longum NCC2705
0.5
0.0
−0.5
−1.0
S^{A-T}_{plus}
0.0e+00
1.0e+06
2.0e+06
genome coordinates
0.3
0.2
0.1
0.0
−0.1
S^{G-C}_{plus}
0.0e+00
1.0e+06
2.0e+06
genome coordinates
Corynebacterium efficiens YS−314
0.0
−0.2
−0.4
−0.6
S^{A-T}_{plus}
0.0e+00
1.5e+06
3.0e+06
genome coordinates
0.5
0.0
−0.5
−1.0
−1.5
S^{G-C}_{plus}
0.0e+00
1.5e+06
3.0e+06
genome coordinates

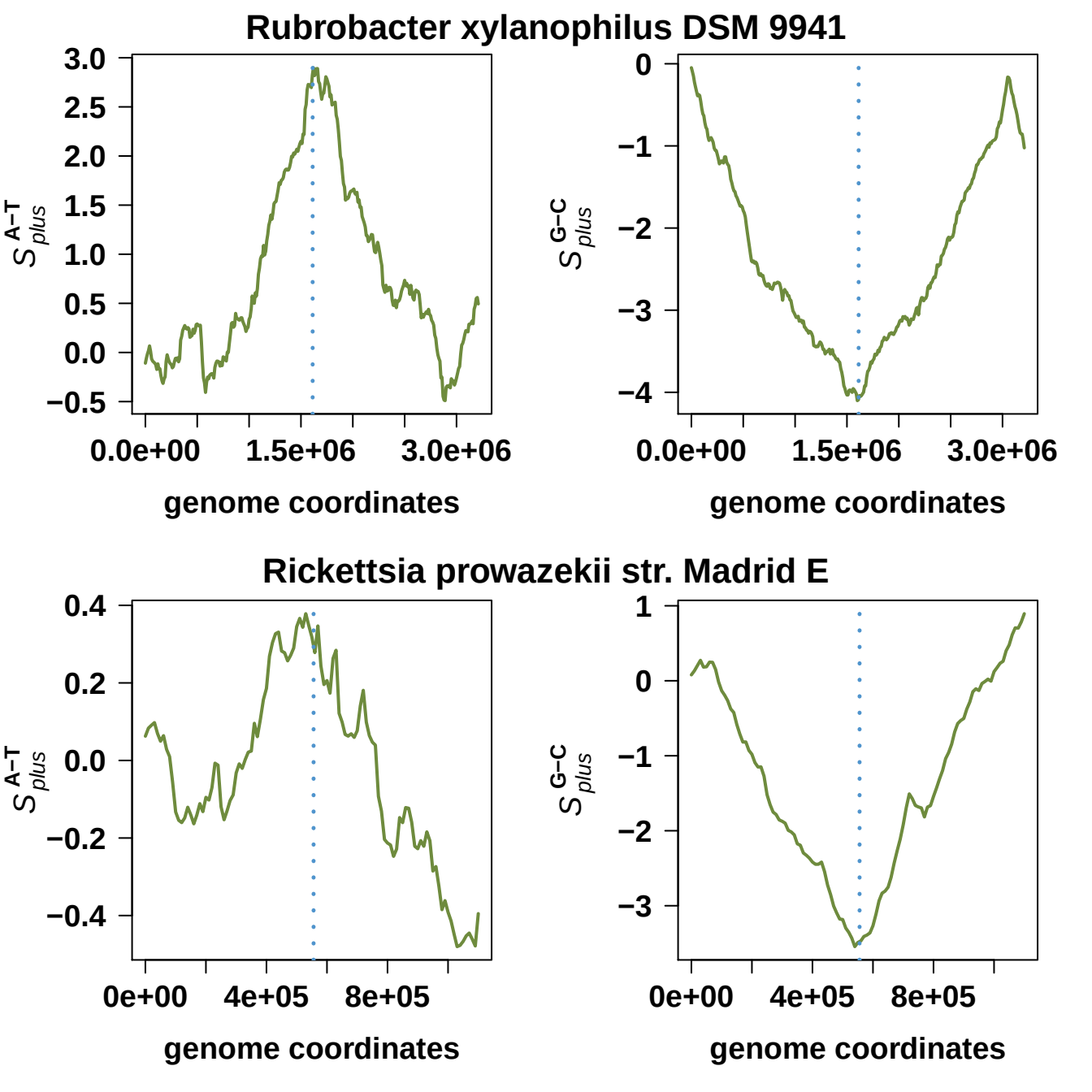

Tropheryma whipplei TW08/27
S^{A-T}_{plus}
2.0
1.5
1.0
0.5
0.0
−0.5
−1.0
0e+00
4e+05
8e+05
genome coordinates
S^{G-C}_{plus}
0.0
−0.2
−0.4
−0.6
−0.8
−1.0
0e+00
4e+05
8e+05
genome coordinates
Tropheryma whipplei str. Twist
S^{A-T}_{plus}
3.0
2.5
2.0
1.5
1.0
0.5
0.0
0e+00
4e+05
8e+05
genome coordinates
S^{G-C}_{plus}
0.0
−0.2
−0.4
−0.6
−0.8
−1.0
−1.2
−1.4
0e+00
4e+05
8e+05
genome coordinates

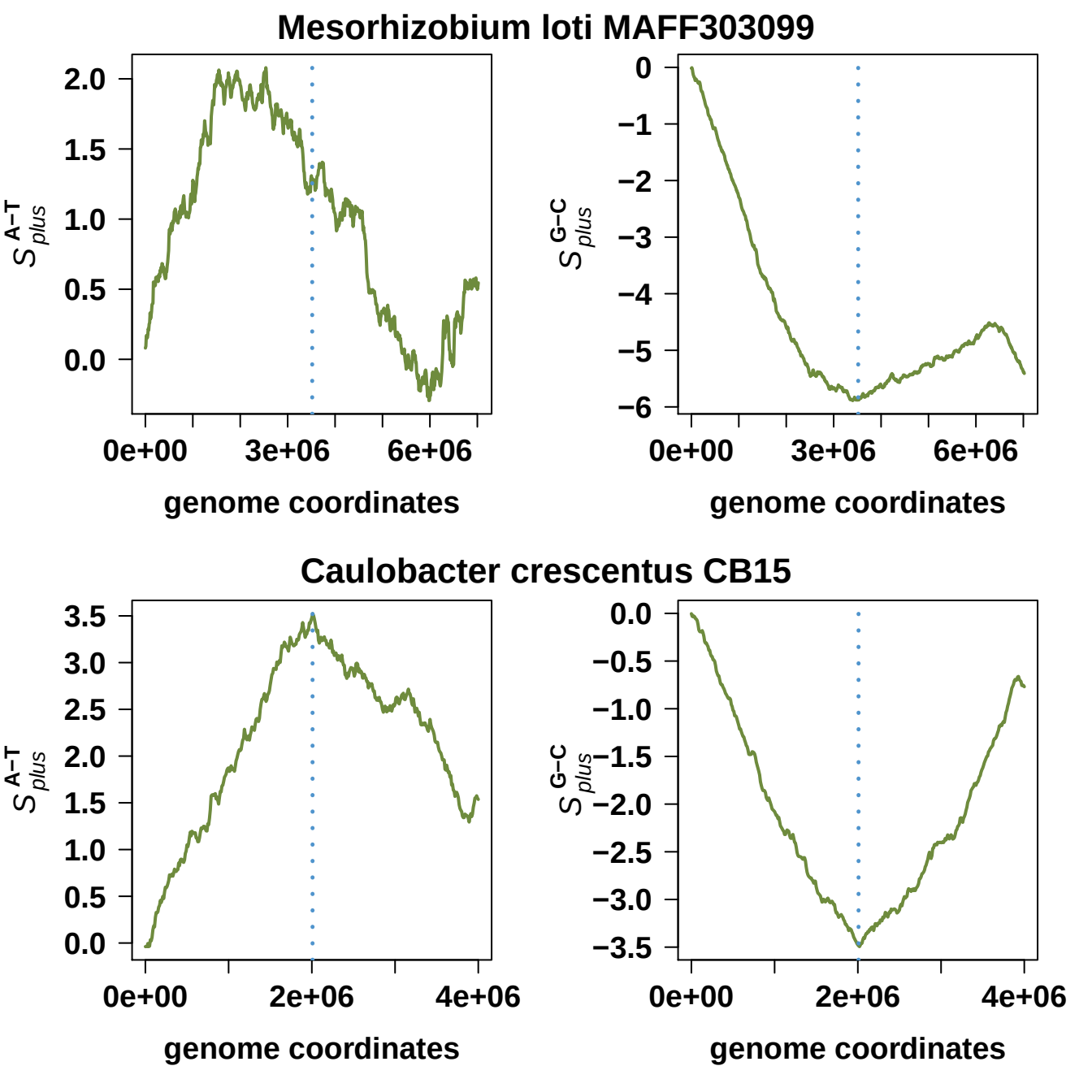

Propionibacterium acnes KPA171202
S^{A-T}_{plus}
6
5
4
3
2
1
0
0.0e+00
1.5e+06
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
−4
−5
−6
0.0e+00
1.5e+06
genome coordinates
Leifsonia xyli subsp. xyli str. CTCB07
S^{A-T}_{plus}
3.0
2.5
2.0
1.5
1.0
0.5
0.0
0.0e+00
1.5e+06
genome coordinates
S^{G-C}_{plus}
0.0
−0.2
−0.4
−0.6
−0.8
−1.0
−1.2
0.0e+00
1.5e+06
genome coordinates

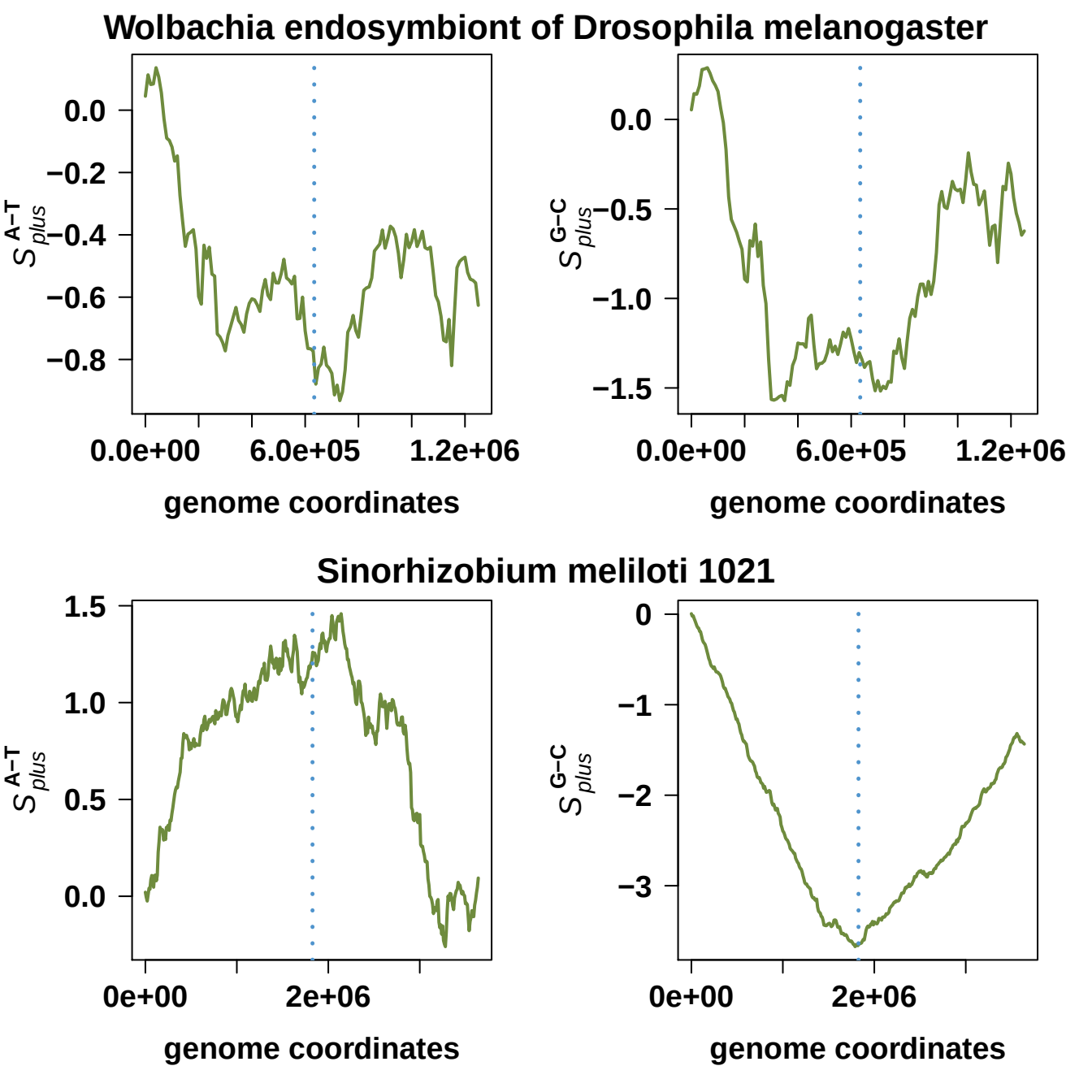

Nocardia farcinica IFM 10152
S^{A-T}_{plus}
2.0
1.5
1.0
0.5
0.0
0e+00
3e+06
6e+06
genome coordinates
S^{G-C}_{plus}
0.5
0.0
−0.5
−1.0
−1.5
−2.0
0e+00
3e+06
6e+06
genome coordinates
Corynebacterium glutamicum ATCC 13032
S^{A-T}_{plus}
0.8
0.6
0.4
0.2
0.0
−0.2
0.0e+00
1.5e+06
3.0e+06
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
−4
−5
−6
−7
0.0e+00
1.5e+06
3.0e+06
genome coordinates

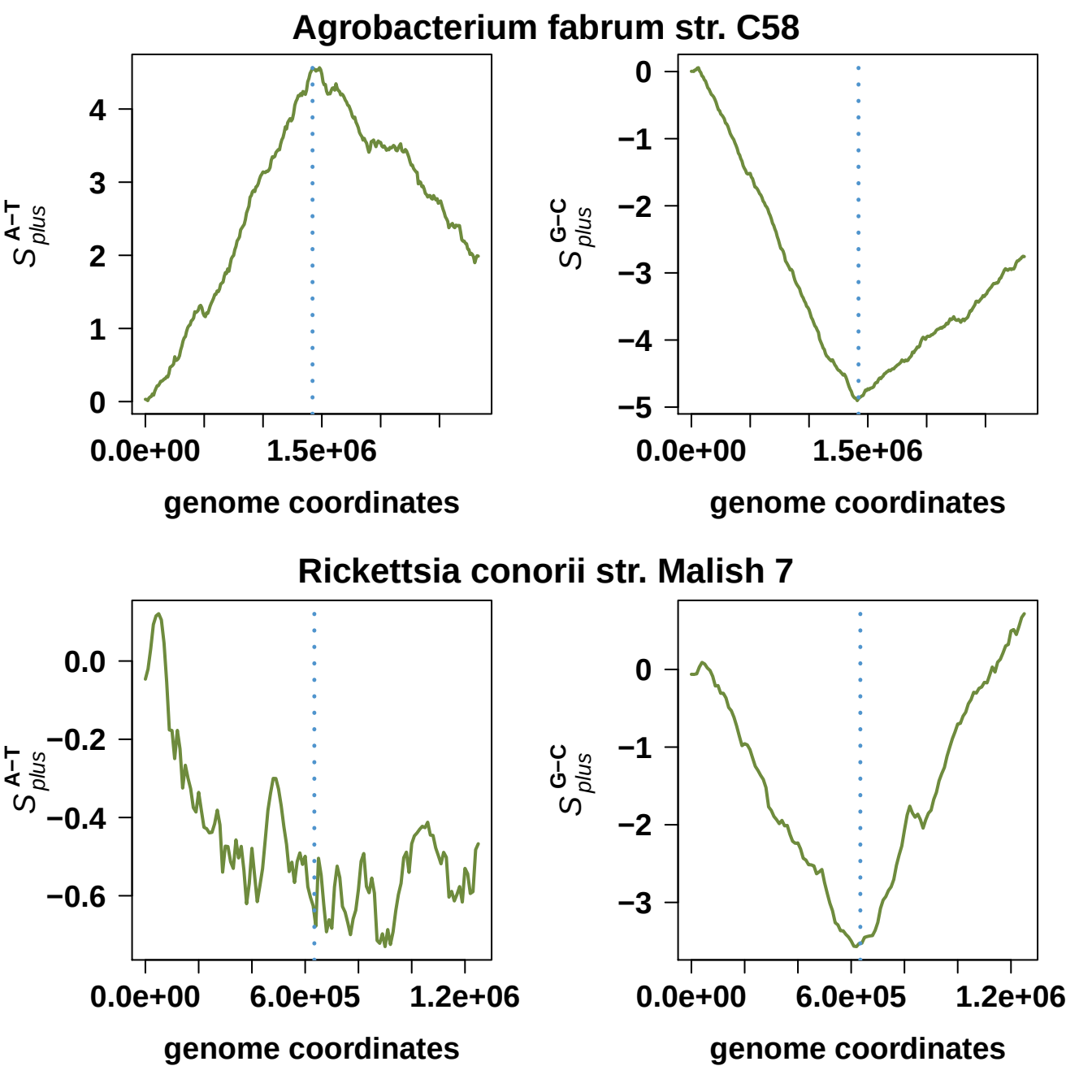

Corynebacterium jeikeium K411
0.0
−0.5
−1.0
−1.5
S^{A-T}_{plus}
0.0e+00
1.5e+06
genome coordinates
0
−1
−2
−3
−4
S^{G-C}_{plus}
0.0e+00
1.5e+06
genome coordinates
Thermobifida fusca YX
0
−1
−2
−3
−4
−5
−6
S^{A-T}_{plus}
0e+00
2e+06
genome coordinates
2.0
1.5
1.0
0.5
0.0
S^{G-C}_{plus}
0e+00
2e+06
genome coordinates

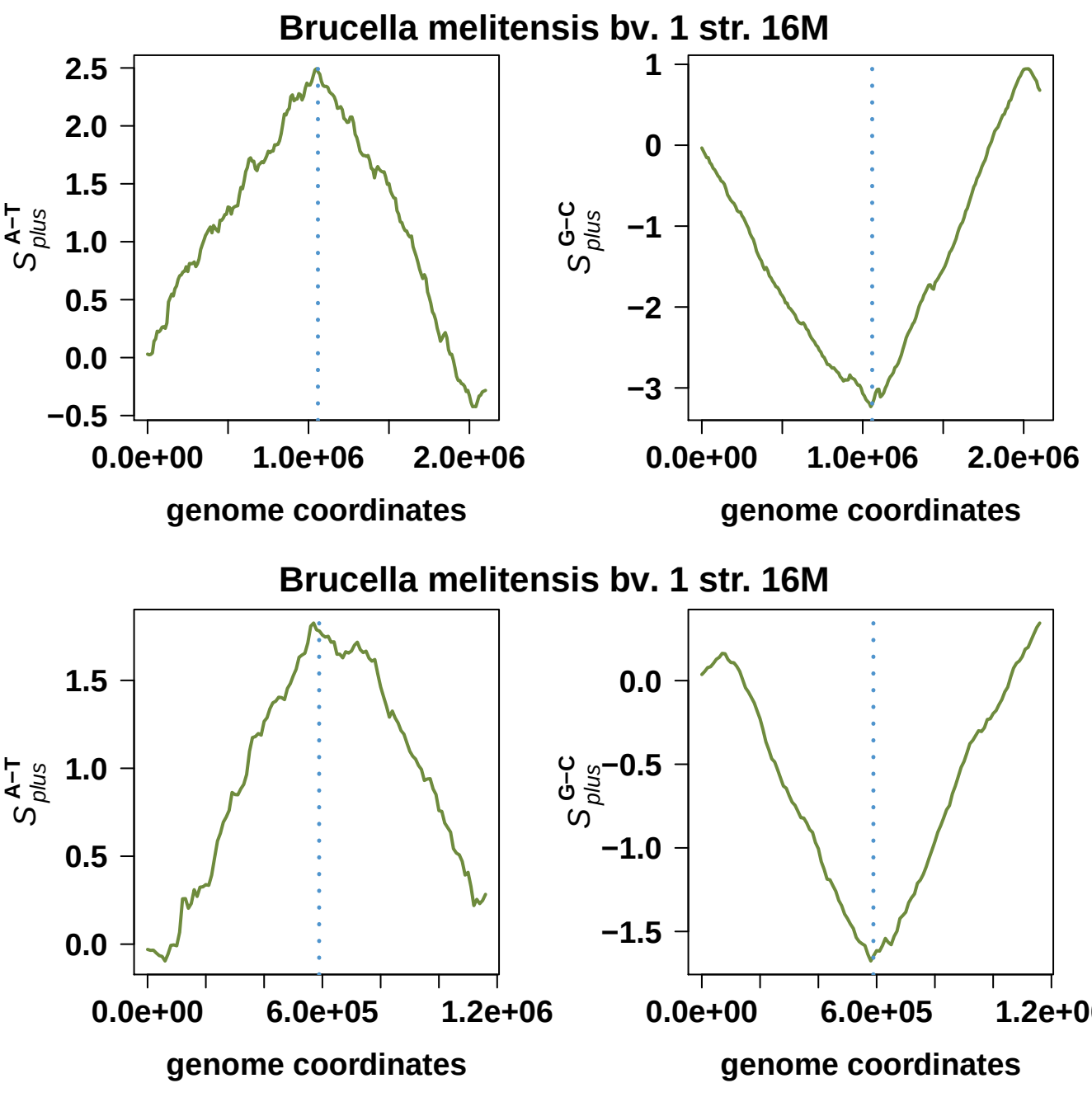

Frankia sp. CcI3
S^{A-T}_{plus}
10
8
6
4
2
0
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
−4
−5
−6
0e+00
2e+06
4e+06
genome coordinates
Mycobacterium sp. MCS
S^{A-T}_{plus}
0.2
0.0
−0.2
−0.4
−0.6
−0.8
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
0.0
−0.5
−1.0
−1.5
−2.0
0e+00
2e+06
4e+06
genome coordinates

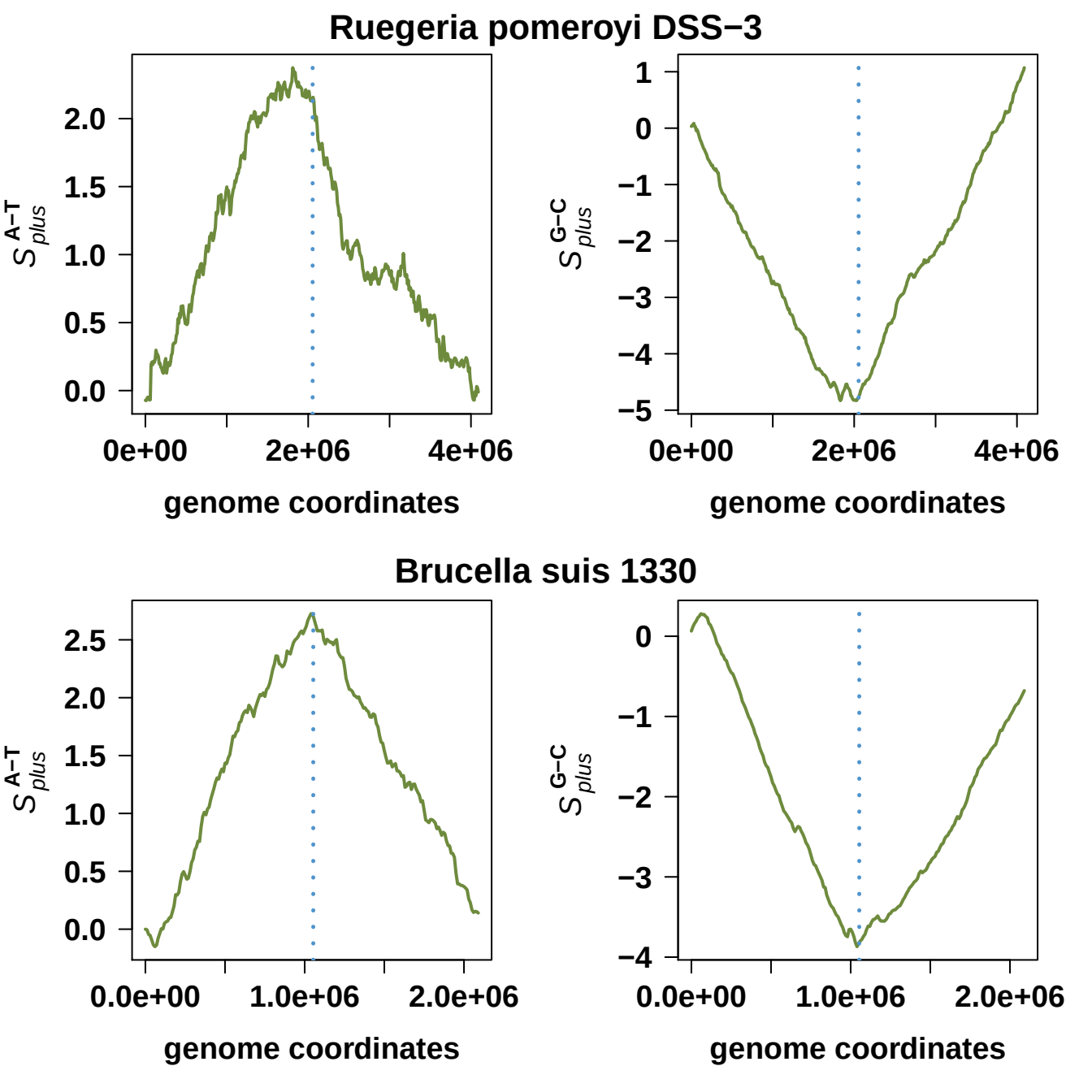

Rubrobacter xylanophilus DSM 9941
S^{A-T}_{plus}
3.0
2.5
2.0
1.5
1.0
0.5
0.0
−0.5
0.0e+00
1.5e+06
3.0e+06
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
−4
0.0e+00
1.5e+06
3.0e+06
genome coordinates
Rickettsia prowazekii str. Madrid E
S^{A-T}_{plus}
0.4
0.2
0.0
−0.2
−0.4
0e+00
4e+05
8e+05
genome coordinates
S^{G-C}_{plus}
1
0
−1
−2
−3
0e+00
4e+05
8e+05
genome coordinates

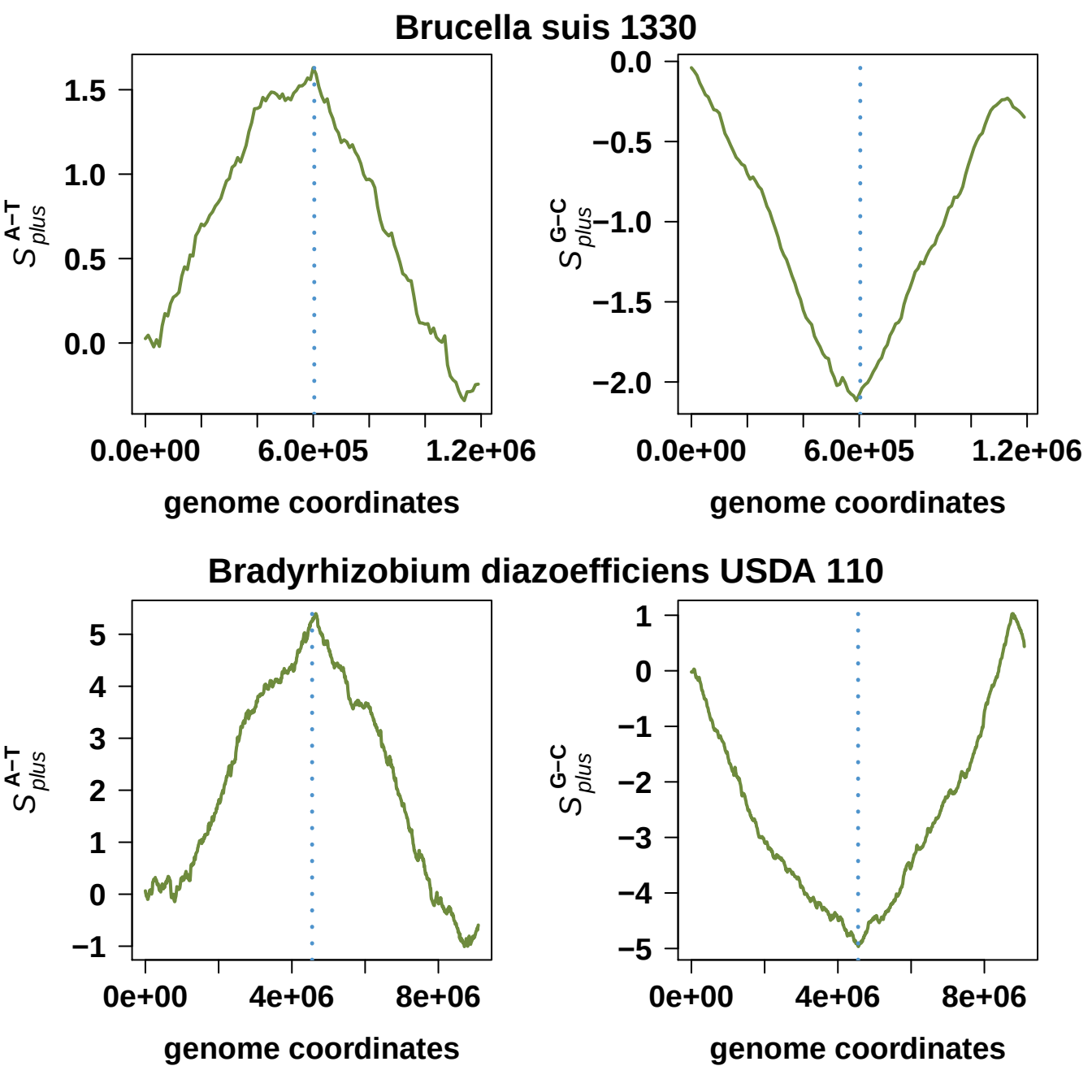

Mesorhizobium loti MAFF303099
S^{A-T}_{plus}
2.0
1.5
1.0
0.5
0.0
0e+00
3e+06
6e+06
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
−4
−5
−6
0e+00
3e+06
6e+06
genome coordinates
Caulobacter crescentus CB15
S^{A-T}_{plus}
3.5
3.0
2.5
2.0
1.5
1.0
0.5
0.0
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
0.0
−0.5
−1.0
−1.5
−2.0
−2.5
−3.0
−3.5
0e+00
2e+06
4e+06
genome coordinates

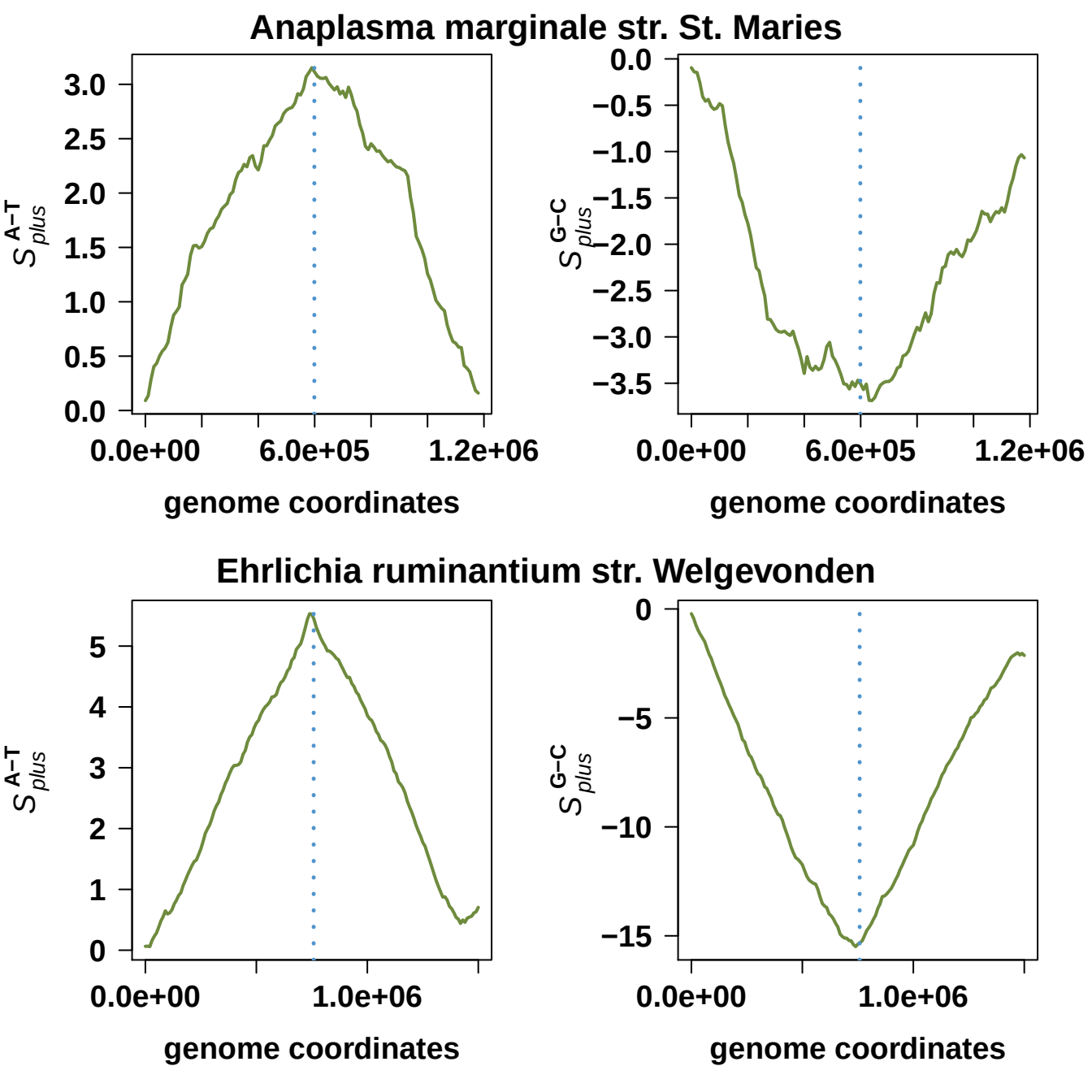

Wolbachia endosymbiont of Drosophila melanogaster
0.0
−0.2
−0.4
−0.6
−0.8
S^{A-T}_{plus}
0.0e+00
6.0e+05
1.2e+06
genome coordinates
0.0
−0.5
−1.0
−1.5
S^{G-C}_{plus}
0.0e+00
6.0e+05
1.2e+06
genome coordinates
Sinorhizobium meliloti 1021
1.5
1.0
0.5
0.0
S^{A-T}_{plus}
0e+00
2e+06
genome coordinates
0
−1
−2
−3
S^{G-C}_{plus}
0e+00
2e+06
genome coordinates

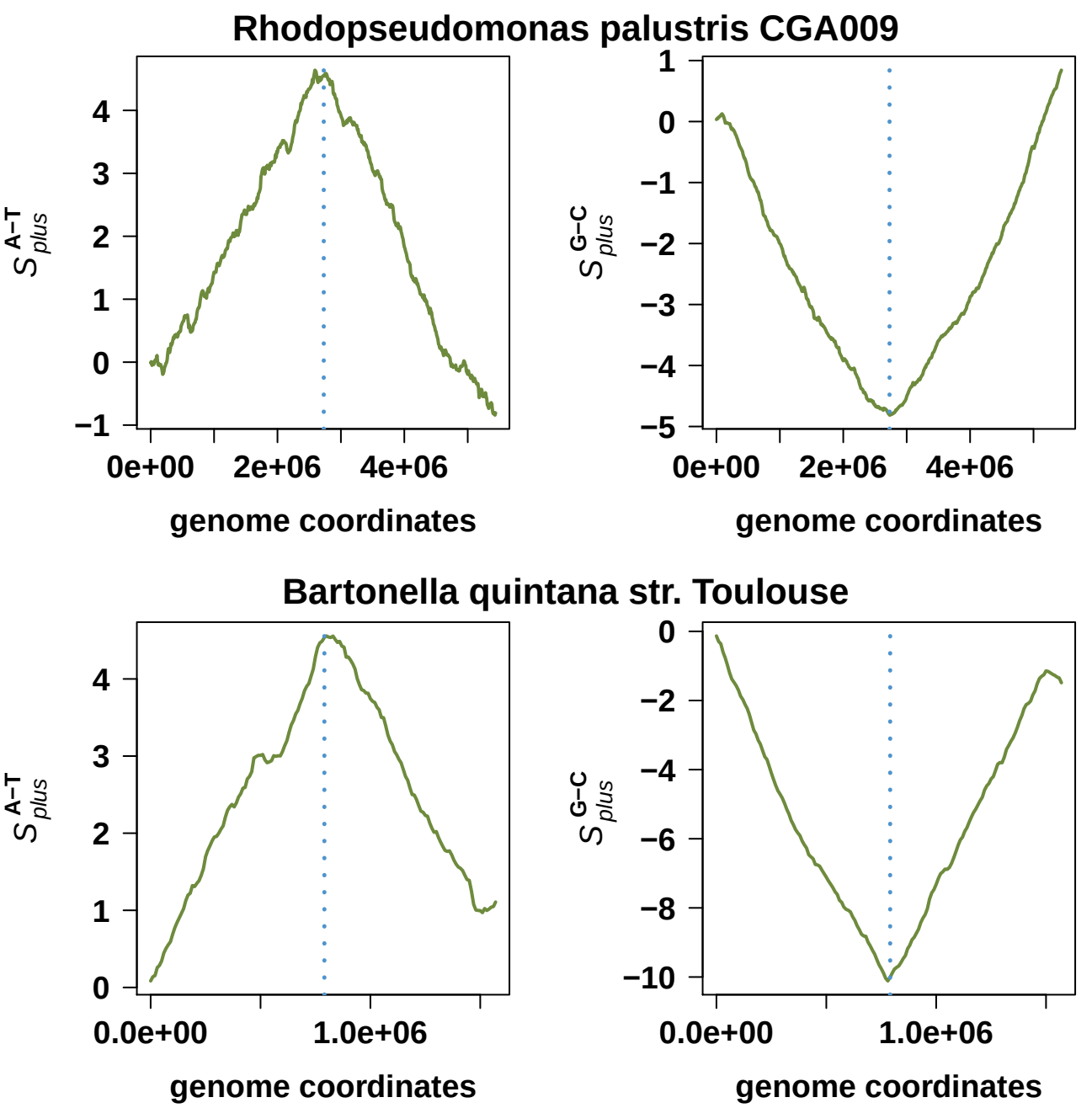

Agrobacterium fabrum str. C58
S^{A-T}_{plus}
4
3
2
1
0
0.0e+00
1.5e+06
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
−4
−5
0.0e+00
1.5e+06
genome coordinates
Rickettsia conorii str. Malish 7
S^{A-T}_{plus}
0.0
−0.2
−0.4
−0.6
0.0e+00
6.0e+05
1.2e+06
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
0.0e+00
6.0e+05
1.2e+06
genome coordinates

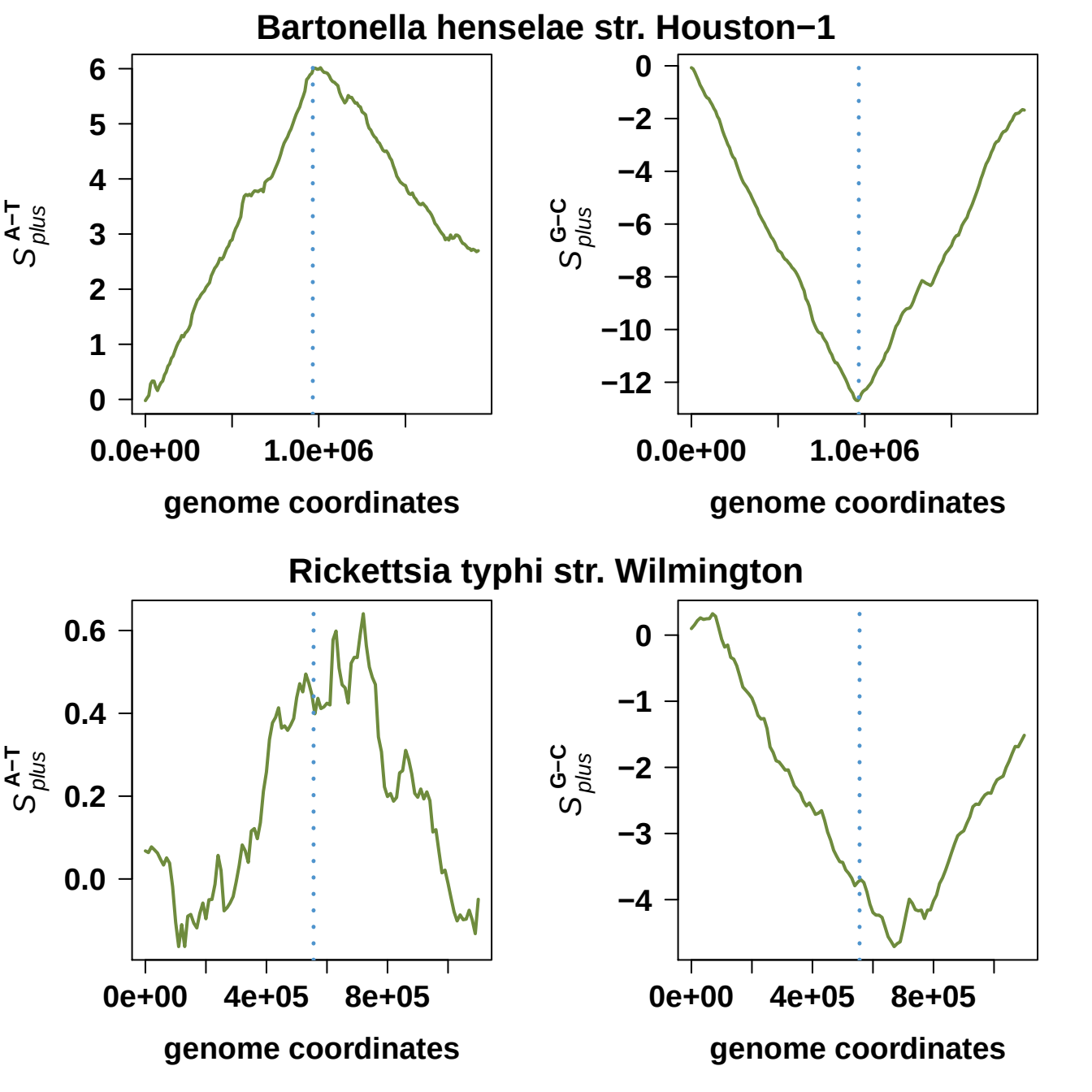

Brucella melitensis bv. 1 str. 16M
S^{A-T}_{plus}
2.5
2.0
1.5
1.0
0.5
0.0
−0.5
0.0e+00
1.0e+06
2.0e+06
genome coordinates
S^{G-C}_{plus}
1
0
−1
−2
−3
0.0e+00
1.0e+06
2.0e+06
genome coordinates
Brucella melitensis bv. 1 str. 16M
S^{A-T}_{plus}
1.5
1.0
0.5
0.0
0.0e+00
6.0e+05
1.2e+06
genome coordinates
S^{G-C}_{plus}
0.0
−0.5
−1.0
−1.5
0.0e+00
6.0e+05
1.2e+06
genome coordinates

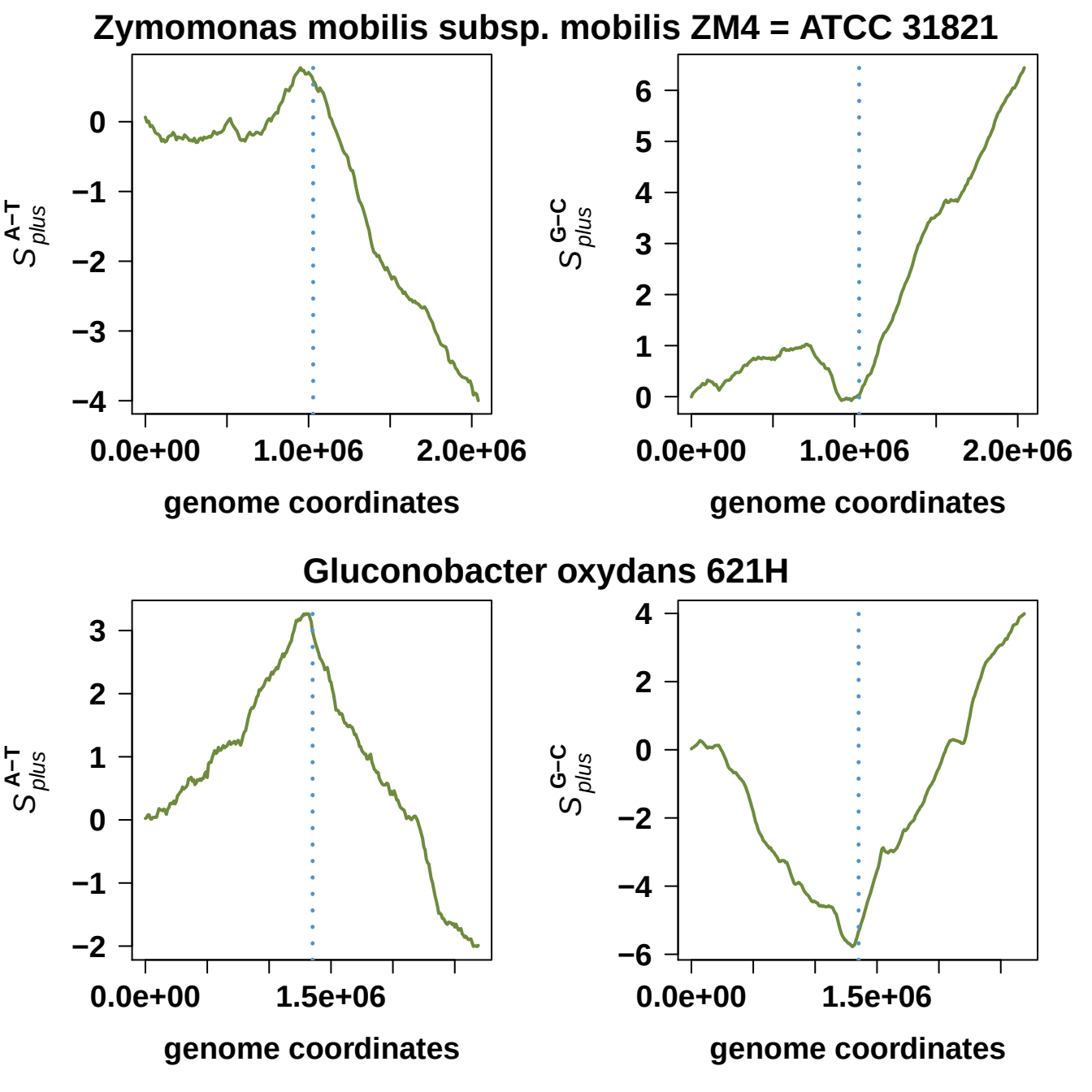

Ruegeria pomeroyi DSS−3
S^{A-T}_{plus}
2.0
1.5
1.0
0.5
0.0
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
1
0
−1
−2
−3
−4
−5
0e+00
2e+06
4e+06
genome coordinates
Brucella suis 1330
S^{A-T}_{plus}
2.5
2.0
1.5
1.0
0.5
0.0
0.0e+00
1.0e+06
2.0e+06
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
−4
0.0e+00
1.0e+06
2.0e+06
genome coordinates

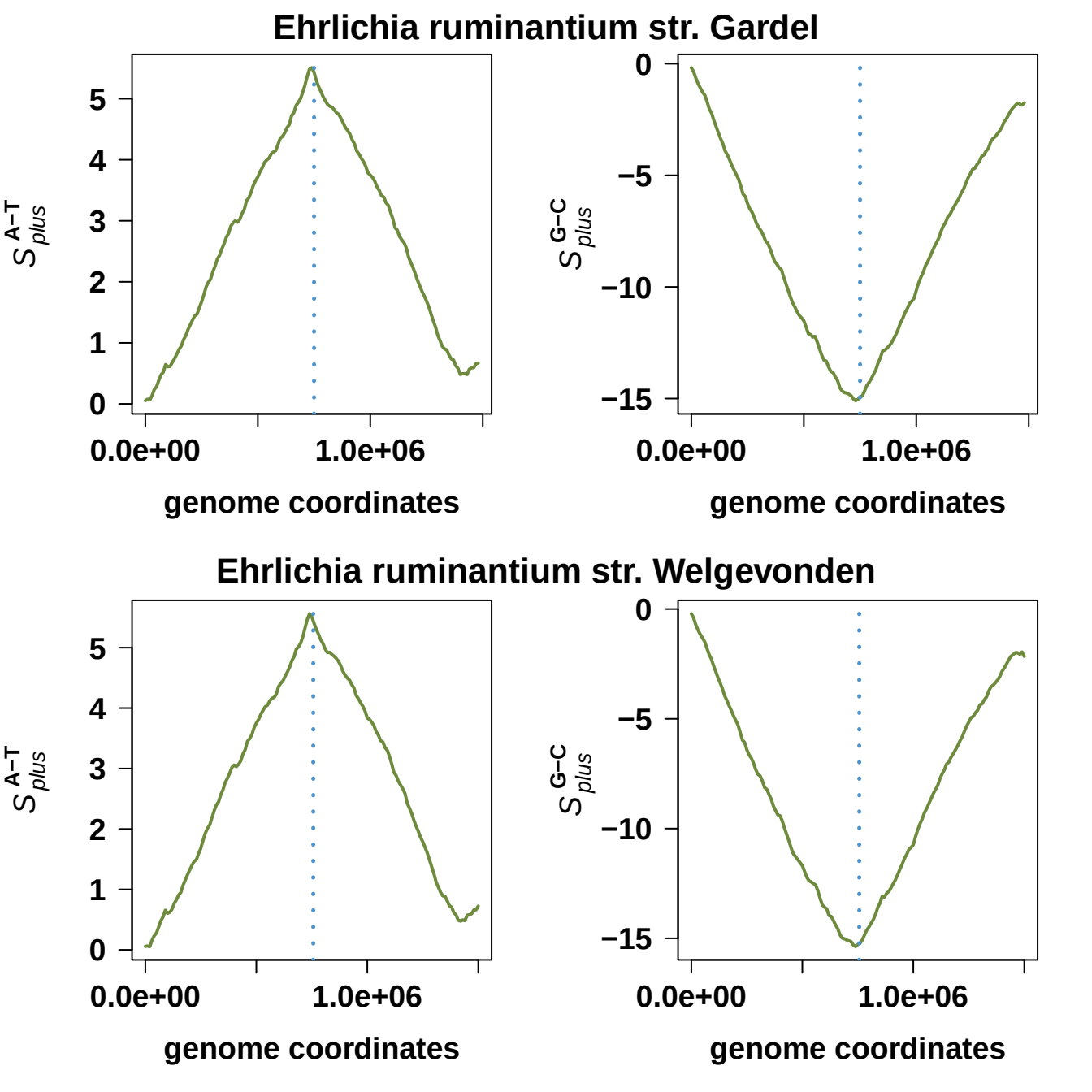

Brucella suis 1330
S^{A-T}_{plus}
1.5
1.0
0.5
0.0
0.0e+00
6.0e+05
1.2e+06
genome coordinates
S^{G-C}_{plus}
0.0
−0.5
−1.0
−1.5
−2.0
0.0e+00
6.0e+05
1.2e+06
genome coordinates
Bradyrhizobium diazoefficiens USDA 110
S^{A-T}_{plus}
5
4
3
2
1
0
−1
0e+00
4e+06
8e+06
genome coordinates
S^{G-C}_{plus}
1
0
−1
−2
−3
−4
−5
0e+00
4e+06
8e+06
genome coordinates

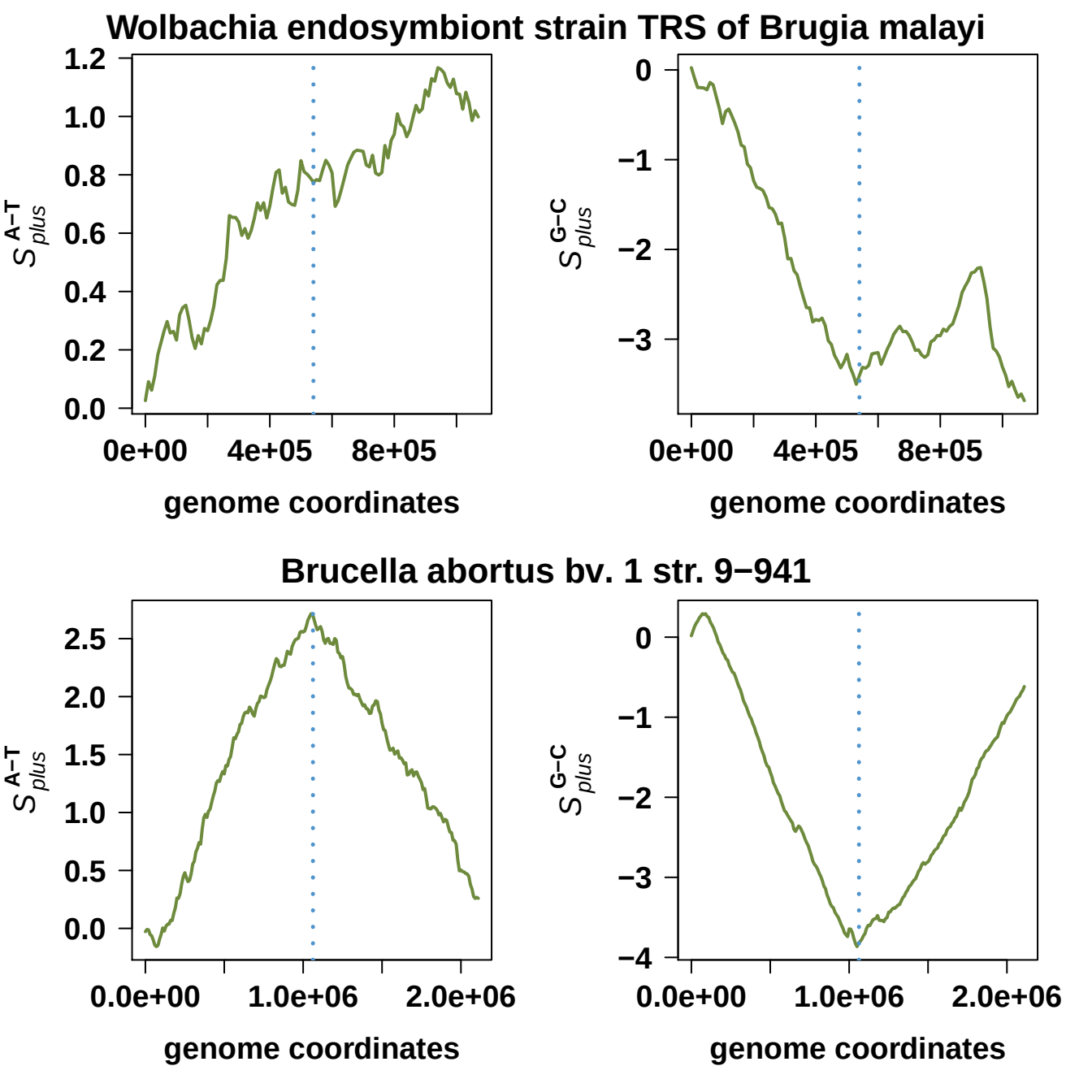

Anaplasma marginale str. St. Maries
S^{A-T}_{plus}
3.0
2.5
2.0
1.5
1.0
0.5
0.0
0.0e+00
6.0e+05
1.2e+06
genome coordinates
S^{G-C}_{plus}
0.0
−0.5
−1.0
−1.5
−2.0
−2.5
−3.0
−3.5
0.0e+00
6.0e+05
1.2e+06
genome coordinates
Ehrlichia ruminantium str. Welgevonden
S^{A-T}_{plus}
5
4
3
2
1
0
0.0e+00
1.0e+06
genome coordinates
S^{G-C}_{plus}
0
−5
−10
−15
0.0e+00
1.0e+06
genome coordinates

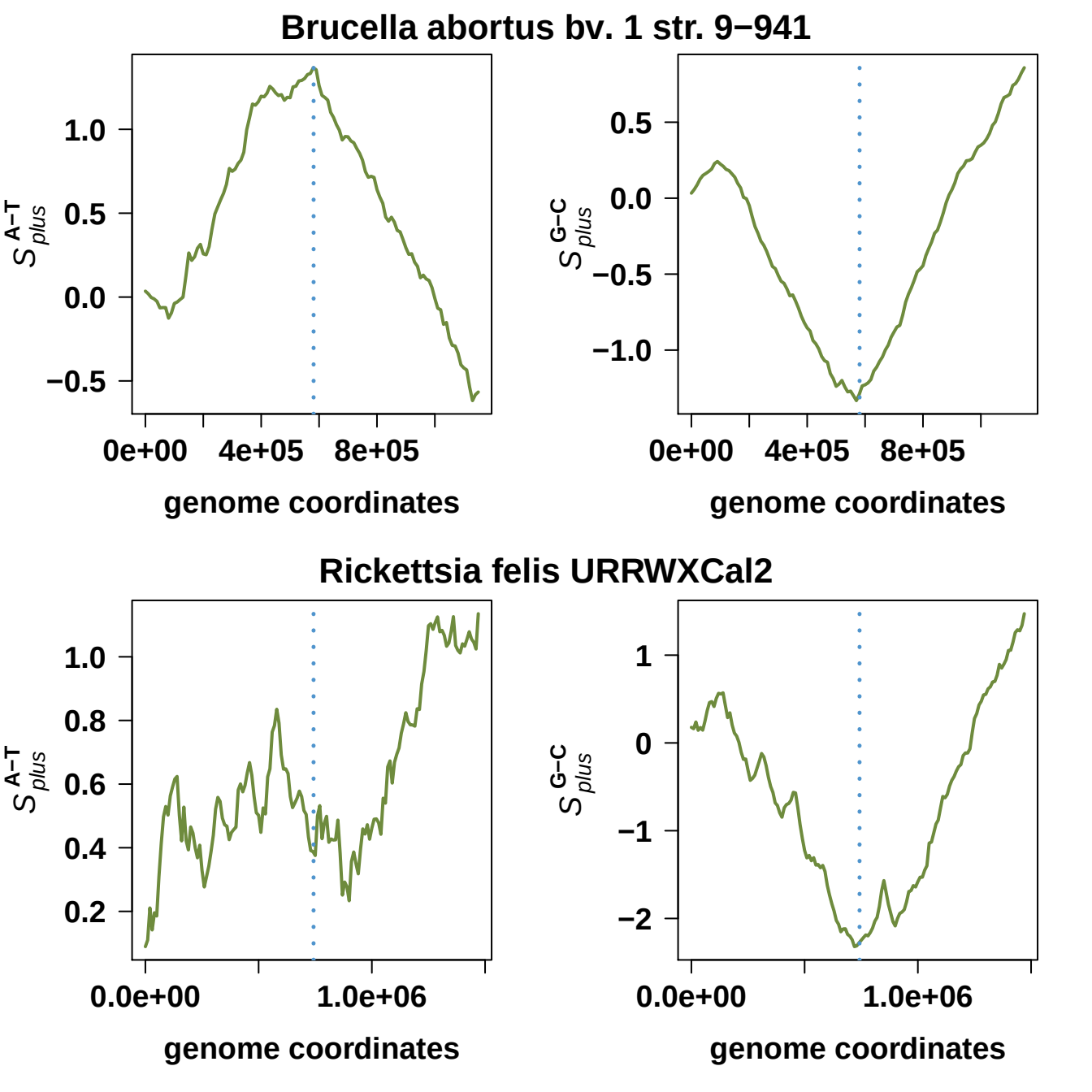

Rhodopseudomonas palustris CGA009
S^{A-T}_{plus}
4
3
2
1
0
−1
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
1
0
−1
−2
−3
−4
−5
0e+00
2e+06
4e+06
genome coordinates
Bartonella quintana str. Toulouse
S^{A-T}_{plus}
4
3
2
1
0
0.0e+00
1.0e+06
genome coordinates
S^{G-C}_{plus}
0
−2
−4
−6
−8
−10
0.0e+00
1.0e+06
genome coordinates

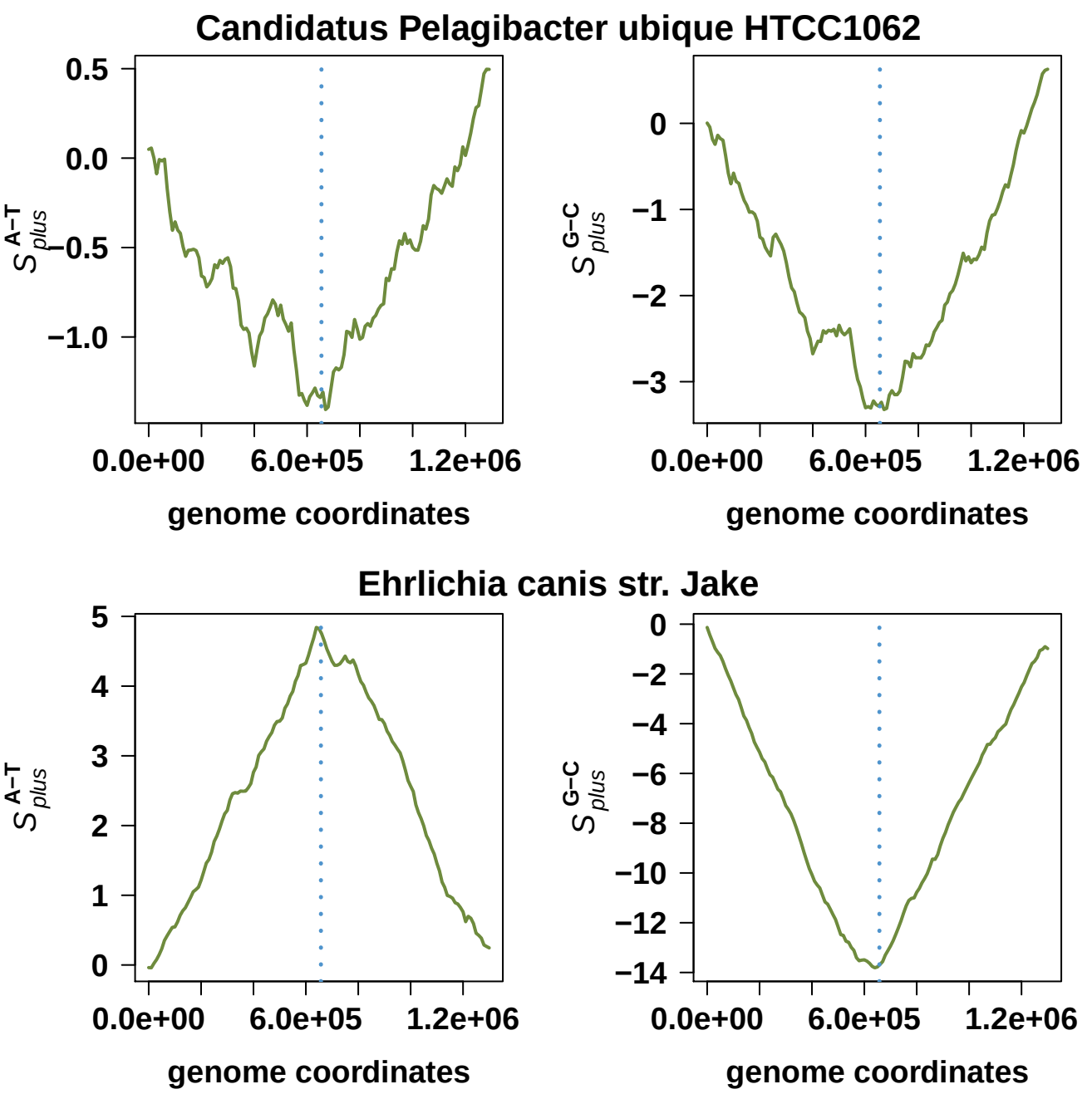

Bartonella henselae str. Houston−1
S^{A-T}_{plus}
6
5
4
3
2
1
0
0.0e+00
1.0e+06
genome coordinates
S^{G-C}_{plus}
0
−2
−4
−6
−8
−10
−12
0.0e+00
1.0e+06
genome coordinates
Rickettsia typhi str. Wilmington
S^{A-T}_{plus}
0.6
0.4
0.2
0.0
0e+00
4e+05
8e+05
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
−4
0e+00
4e+05
8e+05
genome coordinates

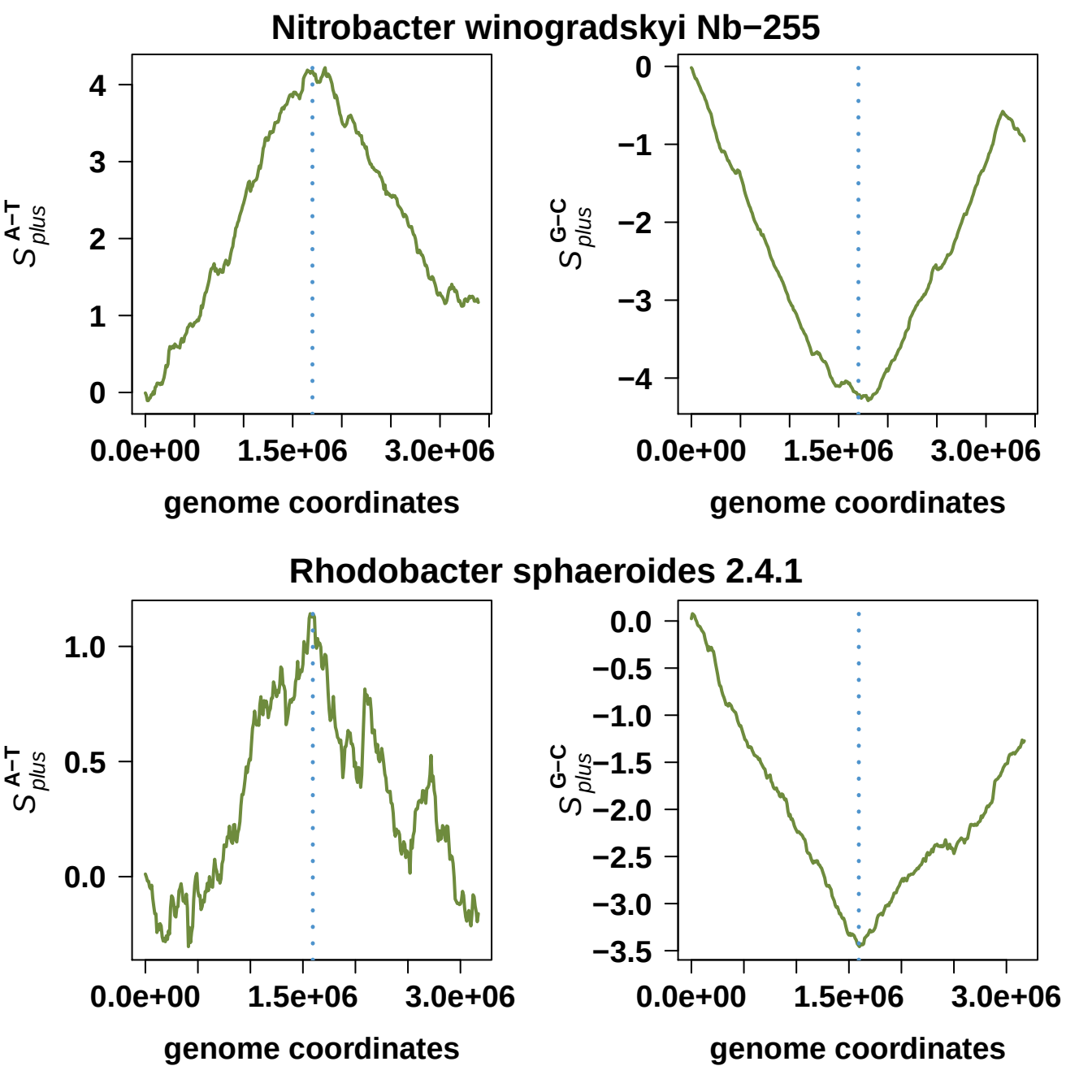

Zymomonas mobilis subsp. mobilis ZM4 = ATCC 31821
S^{A-T}_{plus}
0
−1
−2
−3
−4
0.0e+00
1.0e+06
2.0e+06
genome coordinates
S^{G-C}_{plus}
6
5
4
3
2
1
0
0.0e+00
1.0e+06
2.0e+06
genome coordinates
Gluconobacter oxydans 621H
S^{A-T}_{plus}
3
2
1
0
−1
−2
0.0e+00
1.5e+06
genome coordinates
S^{G-C}_{plus}
4
2
0
−2
−4
−6
0.0e+00
1.5e+06
genome coordinates

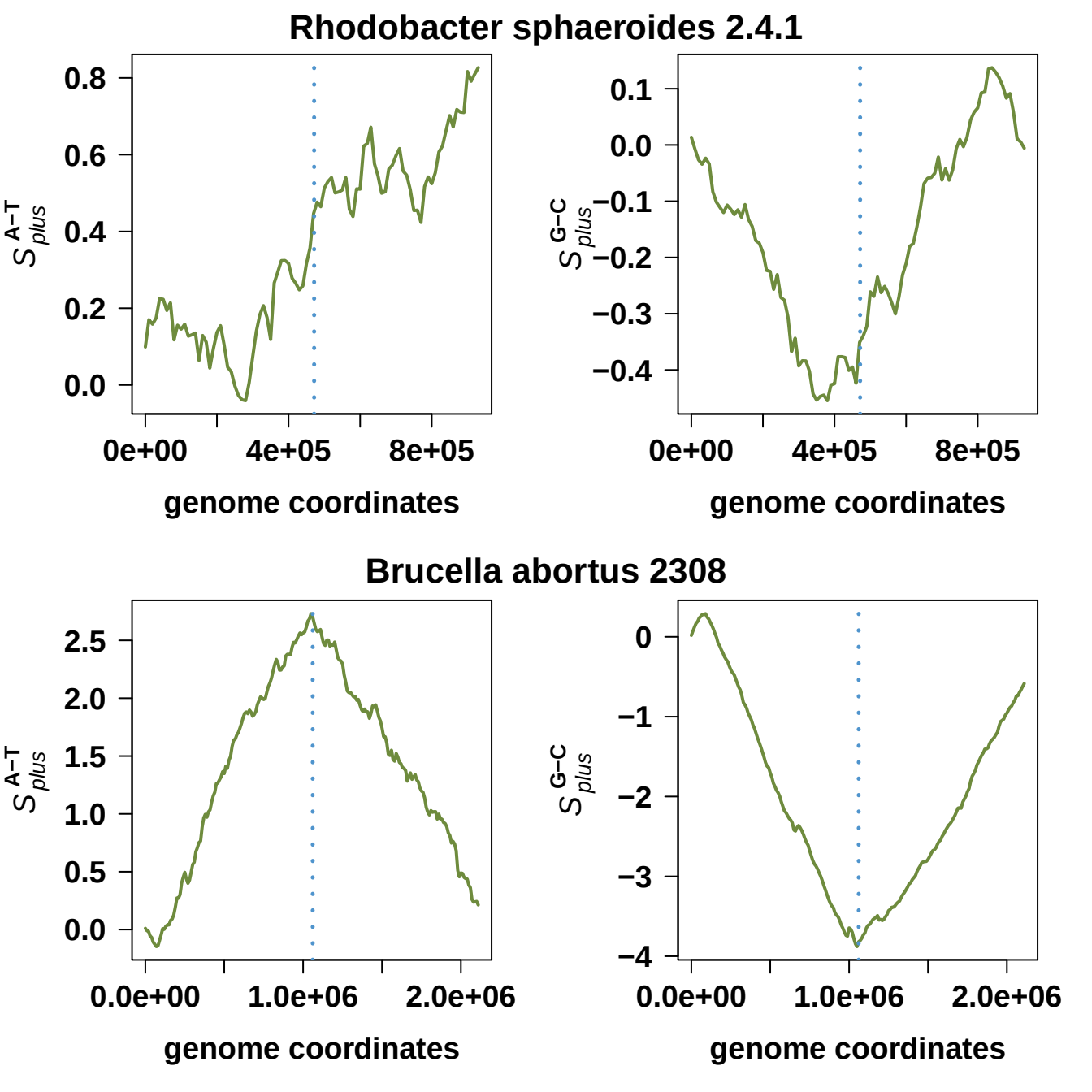

Ehrlichia ruminantium str. Gardel
S^{A-T}_{plus}
5
4
3
2
1
0
0.0e+00
1.0e+06
genome coordinates
S^{G-C}_{plus}
0
−5
−10
−15
0.0e+00
1.0e+06
genome coordinates
Ehrlichia ruminantium str. Welgevonden
S^{A-T}_{plus}
5
4
3
2
1
0
0.0e+00
1.0e+06
genome coordinates
S^{G-C}_{plus}
0
−5
−10
−15
0.0e+00
1.0e+06
genome coordinates

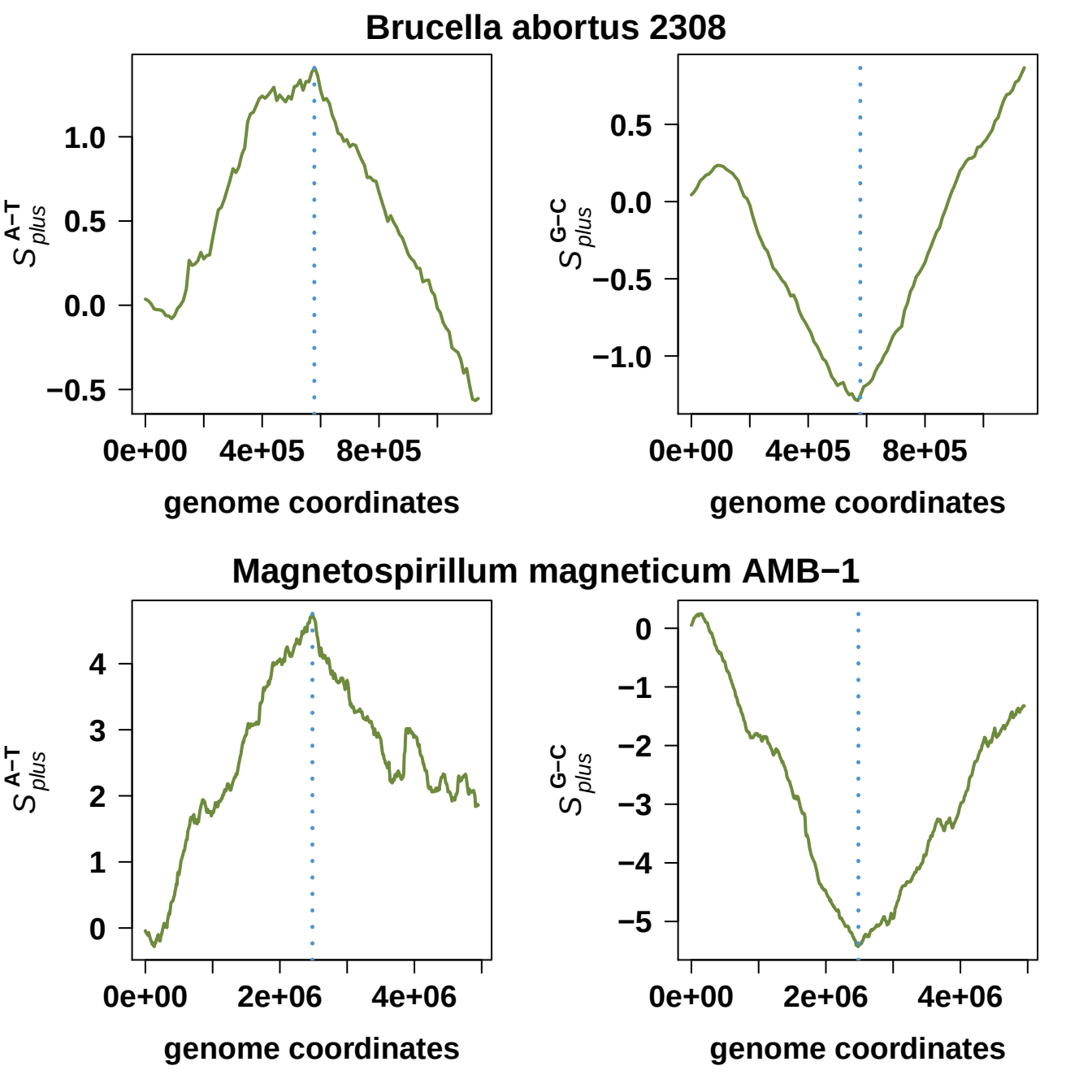

Wolbachia endosymbiont strain TRS of Brugia malayi
1.2
1.0
0.8
0.6
0.4
0.2
0.0
S^{A-T}_{plus}
0e+00
4e+05
8e+05
genome coordinates
0
−1
−2
−3
S^{G-C}_{plus}
0e+00
4e+05
8e+05
genome coordinates
Brucella abortus bv. 1 str. 9−941
2.5
2.0
1.5
1.0
0.5
0.0
S^{A-T}_{plus}
0.0e+00
1.0e+06
2.0e+06
genome coordinates
0
−1
−2
−3
−4
S^{G-C}_{plus}
0.0e+00
1.0e+06
2.0e+06
genome coordinates

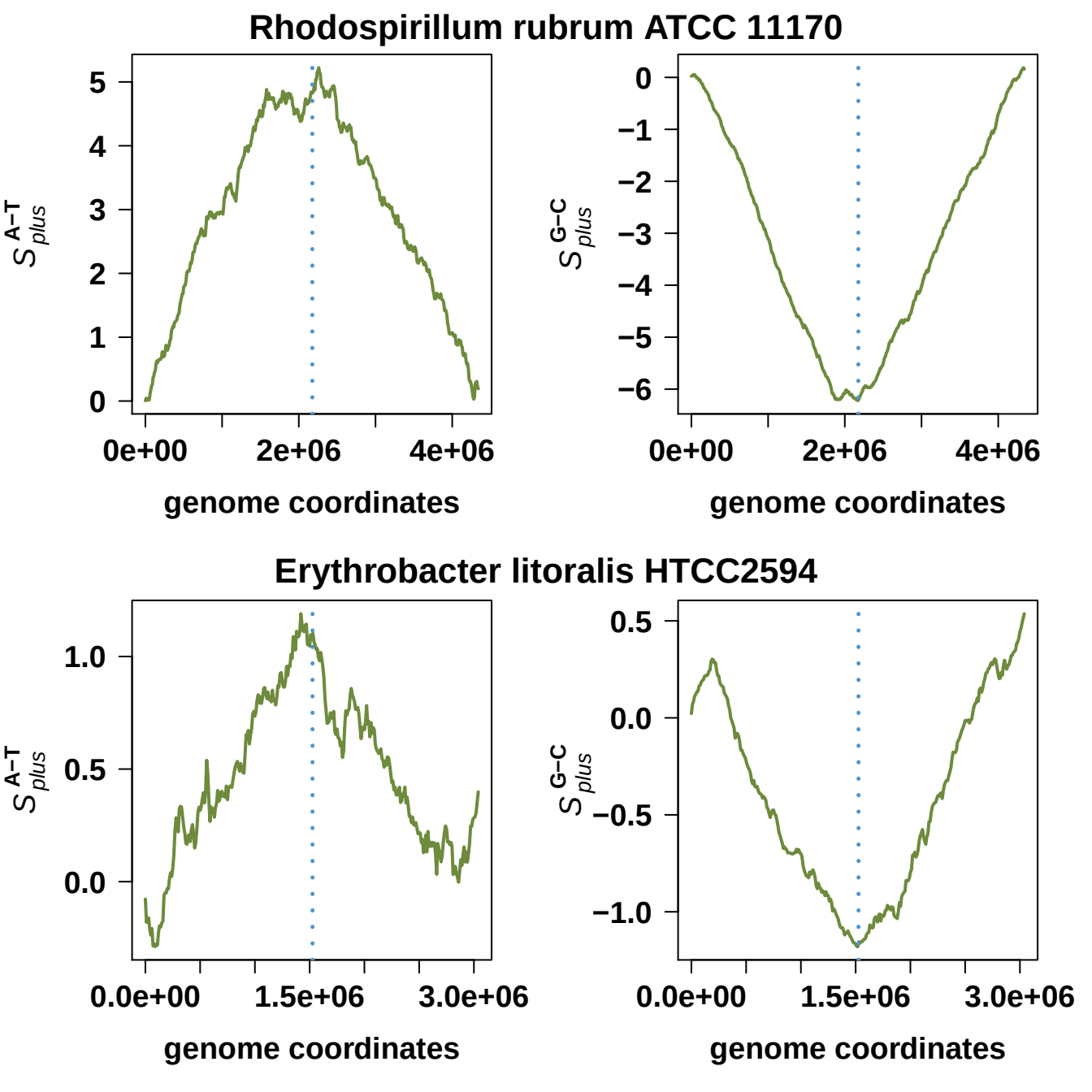

Brucella abortus bv. 1 str. 9−941
S^{A-T}_{plus}
1.0
0.5
0.0
−0.5
0e+00
4e+05
8e+05
genome coordinates
S^{G-C}_{plus}
0.5
0.0
−0.5
−1.0
0e+00
4e+05
8e+05
genome coordinates
Rickettsia felis URRWXCal2
S^{A-T}_{plus}
1.0
0.8
0.6
0.4
0.2
0.0e+00
1.0e+06
genome coordinates
S^{G-C}_{plus}
1
0
−1
−2
0.0e+00
1.0e+06
genome coordinates

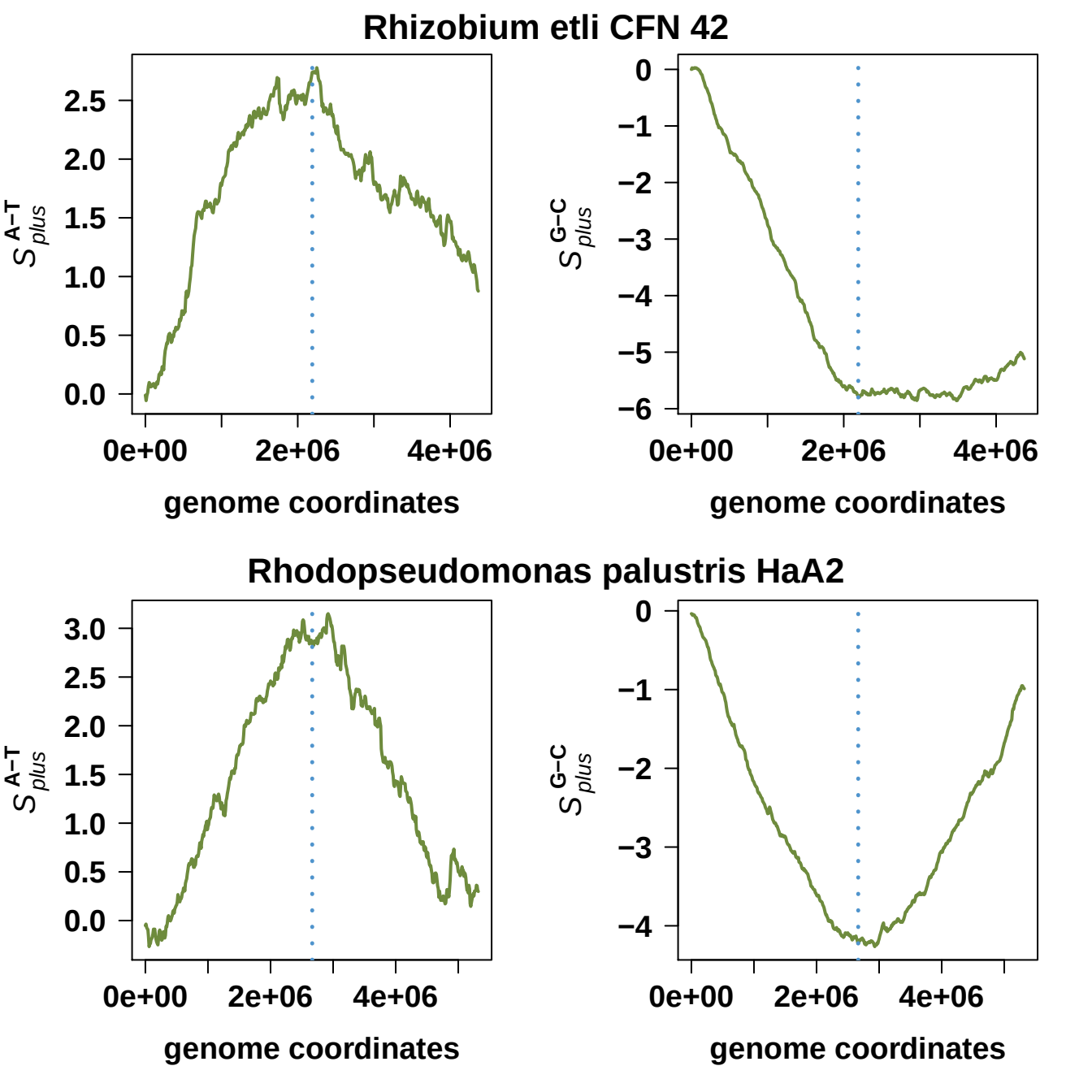

Candidatus Pelagibacter ubique HTCC1062
0.5
0.0
−0.5
−1.0
S^{A-T}_{plus}
0.0e+00
6.0e+05
1.2e+06
genome coordinates
0
−1
−2
−3
S^{G-C}_{plus}
0.0e+00
6.0e+05
1.2e+06
genome coordinates
Ehrlichia canis str. Jake
5
4
3
2
1
0
S^{A-T}_{plus}
0.0e+00
6.0e+05
1.2e+06
genome coordinates
0
−2
−4
−6
−8
−10
−12
−14
S^{G-C}_{plus}
0.0e+00
6.0e+05
1.2e+06
genome coordinates

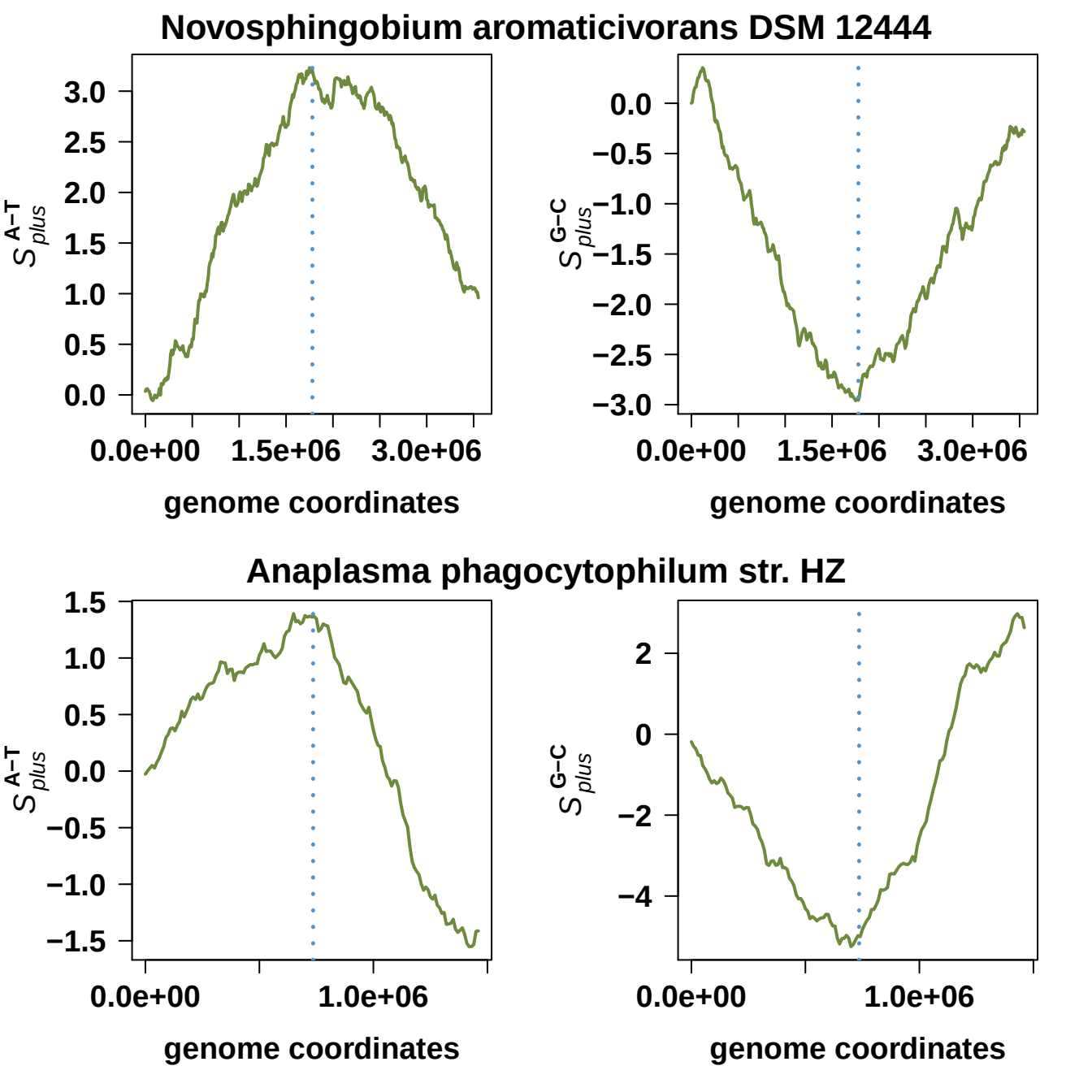

Nitrobacter winogradskyi Nb−255
S^{A-T}_{plus}
4
3
2
1
0
0.0e+00
1.5e+06
3.0e+06
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
−4
0.0e+00
1.5e+06
3.0e+06
genome coordinates
Rhodobacter sphaeroides 2.4.1
S^{A-T}_{plus}
1.0
0.5
0.0
0.0e+00
1.5e+06
3.0e+06
genome coordinates
S^{G-C}_{plus}
0.0
−0.5
−1.0
−1.5
−2.0
−2.5
−3.0
−3.5
0.0e+00
1.5e+06
3.0e+06
genome coordinates

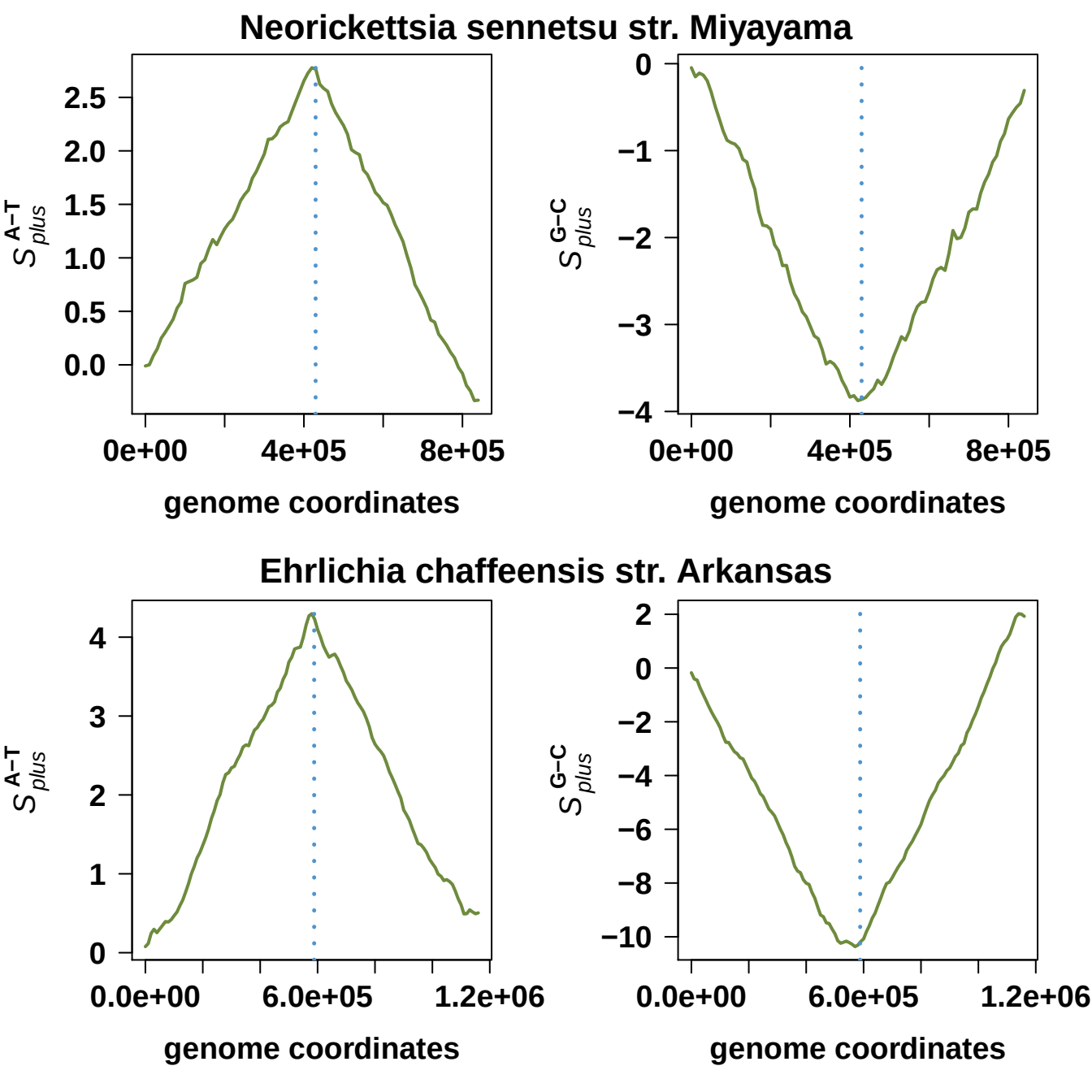

Rhodobacter sphaeroides 2.4.1
S^{A-T}_{plus}
0.8
0.6
0.4
0.2
0.0
0e+00
4e+05
8e+05
genome coordinates
S^{G-C}_{plus}
0.1
0.0
−0.1
−0.2
−0.3
−0.4
0e+00
4e+05
8e+05
genome coordinates
Brucella abortus 2308
S^{A-T}_{plus}
2.5
2.0
1.5
1.0
0.5
0.0
0.0e+00
1.0e+06
2.0e+06
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
−4
0.0e+00
1.0e+06
2.0e+06
genome coordinates

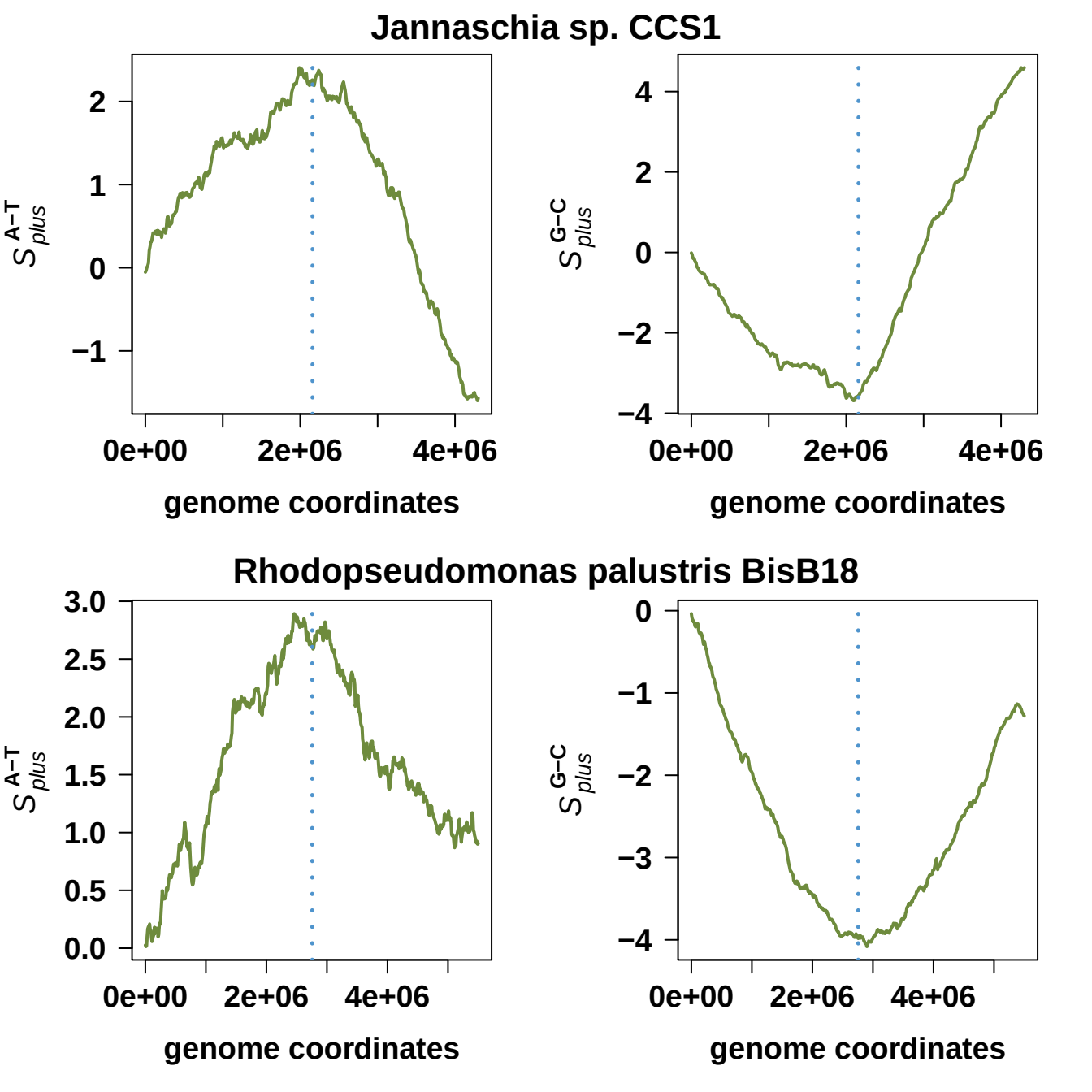

Brucella abortus 2308
S^{A-T}_{plus}
1.0
0.5
0.0
−0.5
0e+00
4e+05
8e+05
genome coordinates
S^{G-C}_{plus}
0.5
0.0
−0.5
−1.0
0e+00
4e+05
8e+05
genome coordinates
Magnetospirillum magneticum AMB−1
S^{A-T}_{plus}
4
3
2
1
0
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
−4
−5
0e+00
2e+06
4e+06
genome coordinates

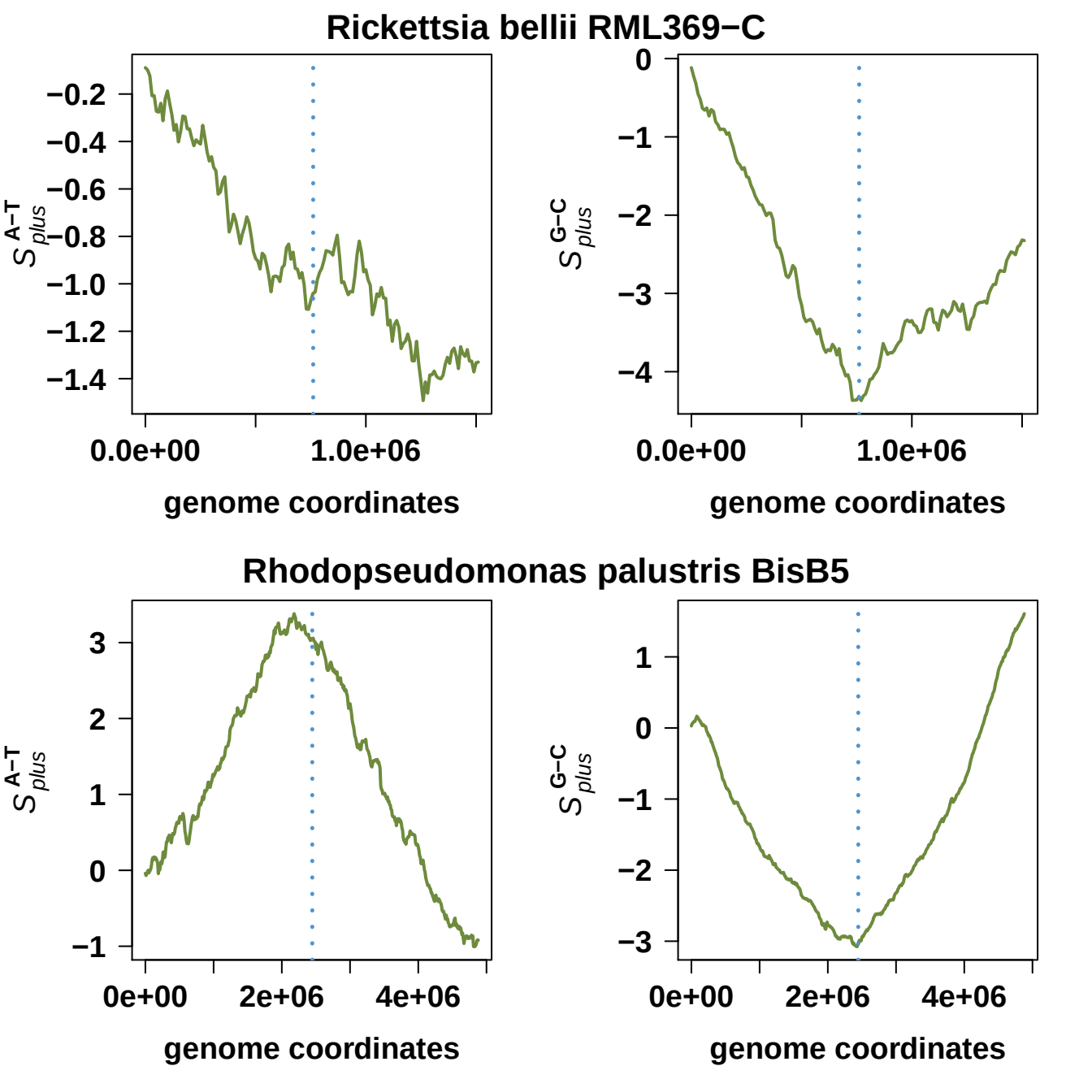

Rhodospirillum rubrum ATCC 11170
S^{A-T}_{plus}
5
4
3
2
1
0
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
−4
−5
−6
0e+00
2e+06
4e+06
genome coordinates
Erythrobacter litoralis HTCC2594
S^{A-T}_{plus}
1.0
0.5
0.0
0.0e+00
1.5e+06
3.0e+06
genome coordinates
S^{G-C}_{plus}
0.5
0.0
−0.5
−1.0
0.0e+00
1.5e+06
3.0e+06
genome coordinates

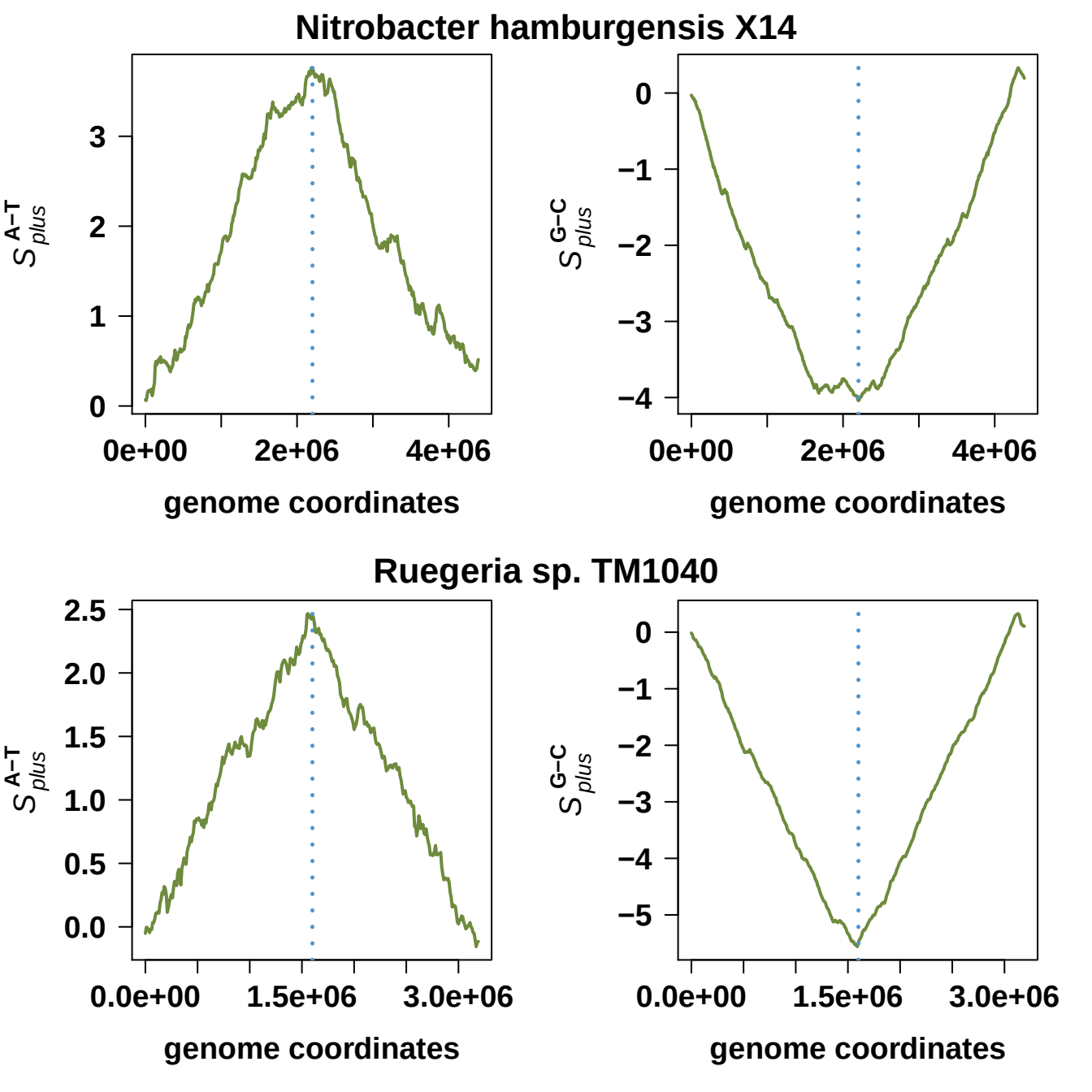

Rhizobium etli CFN 42
S^{A-T}_{plus}
2.5
2.0
1.5
1.0
0.5
0.0
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
−4
−5
−6
0e+00
2e+06
4e+06
genome coordinates
Rhodopseudomonas palustris HaA2
S^{A-T}_{plus}
3.0
2.5
2.0
1.5
1.0
0.5
0.0
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
−4
0e+00
2e+06
4e+06
genome coordinates

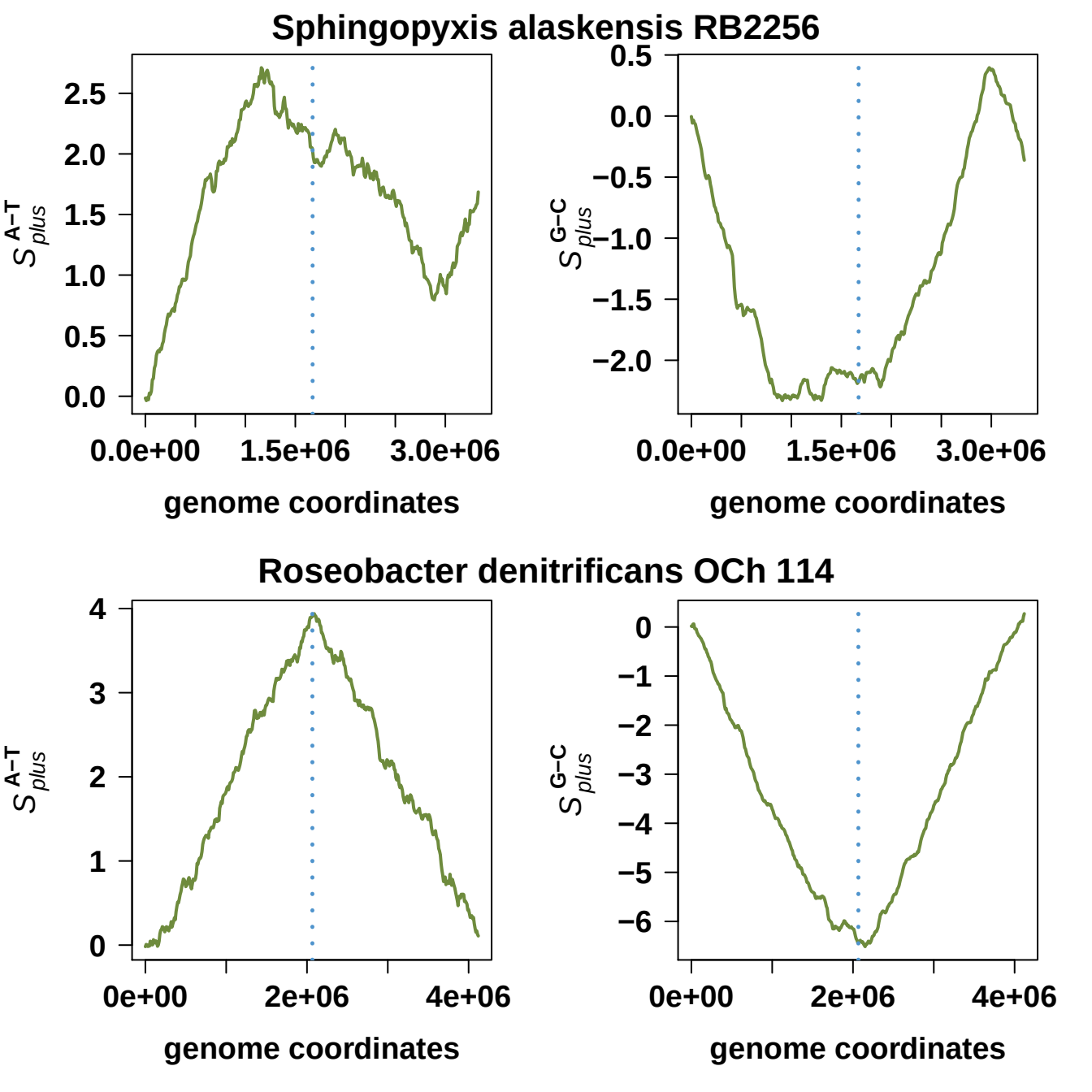

Novosphingobium aromaticivorans DSM 12444
3.0
2.5
2.0
1.5
1.0
0.5
0.0
S^{A-T}_{plus}
0.0e+00
1.5e+06
3.0e+06
genome coordinates
0.0
−0.5
−1.0
−1.5
−2.0
−2.5
−3.0
S^{G-C}_{plus}
0.0e+00
1.5e+06
3.0e+06
genome coordinates
Anaplasma phagocytophilum str. HZ
1.5
1.0
0.5
0.0
−0.5
−1.0
−1.5
S^{A-T}_{plus}
0.0e+00
1.0e+06
genome coordinates
2
0
−2
−4
S^{G-C}_{plus}
0.0e+00
1.0e+06
genome coordinates

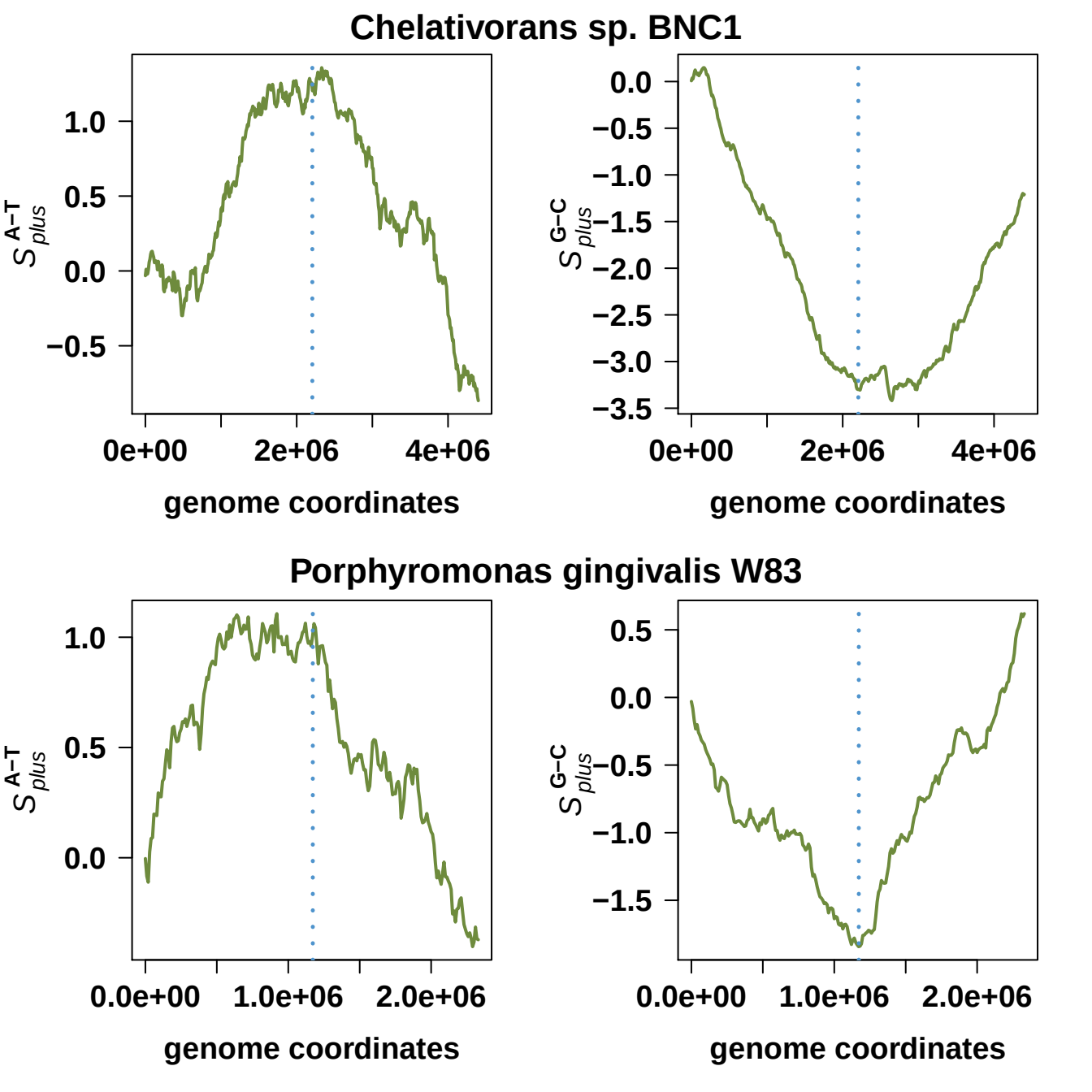

Neorickettsia sennetsu str. Miyayama
S^{A-T}_{plus}
2.5
2.0
1.5
1.0
0.5
0.0
0e+00
4e+05
8e+05
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
−4
0e+00
4e+05
8e+05
genome coordinates
Ehrlichia chaffeensis str. Arkansas
S^{A-T}_{plus}
4
3
2
1
0
0.0e+00
6.0e+05
1.2e+06
genome coordinates
S^{G-C}_{plus}
2
0
−2
−4
−6
−8
−10
0.0e+00
6.0e+05
1.2e+06
genome coordinates

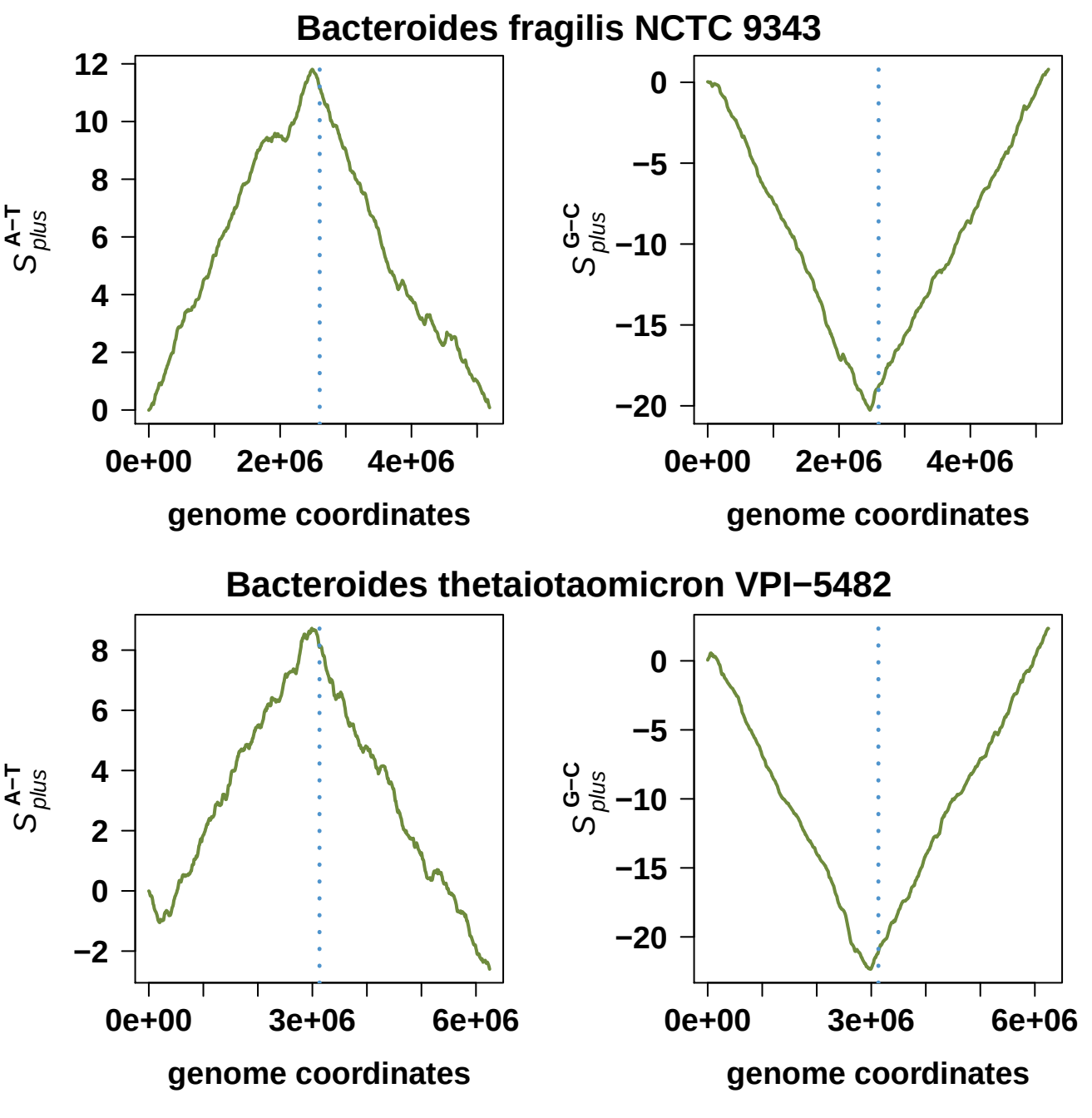

Jannaschia sp. CCS1
S^{A-T}_{plus}
2
1
0
−1
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
4
2
0
−2
−4
0e+00
2e+06
4e+06
genome coordinates
Rhodopseudomonas palustris BisB18
S^{A-T}_{plus}
3.0
2.5
2.0
1.5
1.0
0.5
0.0
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
−4
0e+00
2e+06
4e+06
genome coordinates

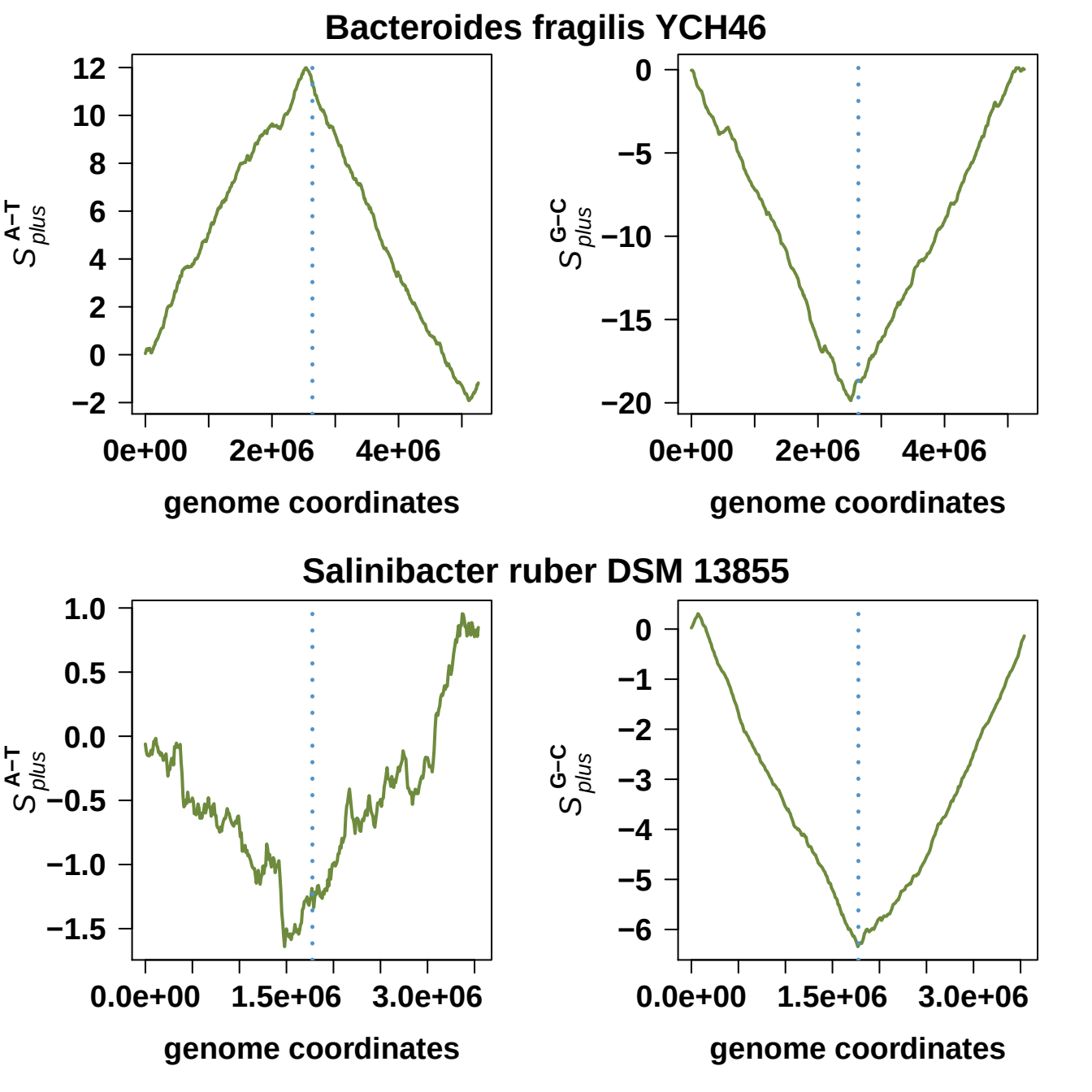

Rickettsia bellii RML369−C
S^{A-T}_{plus}
−0.2
−0.4
−0.6
−0.8
−1.0
−1.2
−1.4
0.0e+00
1.0e+06
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
−4
0.0e+00
1.0e+06
genome coordinates
Rhodopseudomonas palustris BisB5
S^{A-T}_{plus}
3
2
1
0
−1
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
1
0
−1
−2
−3
0e+00
2e+06
4e+06
genome coordinates

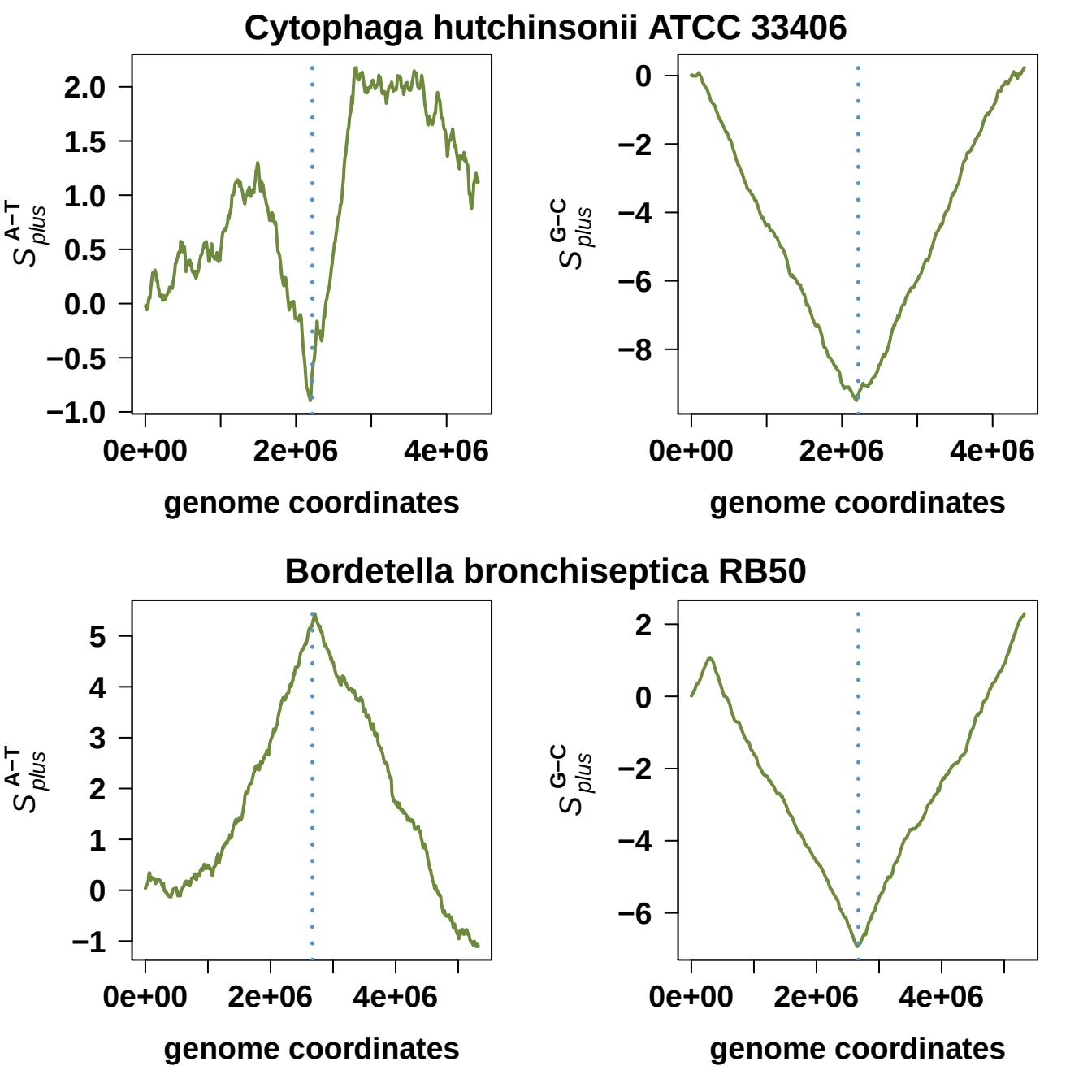

Nitrobacter hamburgensis X14
S^{A-T}_{plus}
3
2
1
0
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
−4
0e+00
2e+06
4e+06
genome coordinates
Ruegeria sp. TM1040
S^{A-T}_{plus}
2.5
2.0
1.5
1.0
0.5
0.0
0.0e+00
1.5e+06
3.0e+06
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
−4
−5
0.0e+00
1.5e+06
3.0e+06
genome coordinates

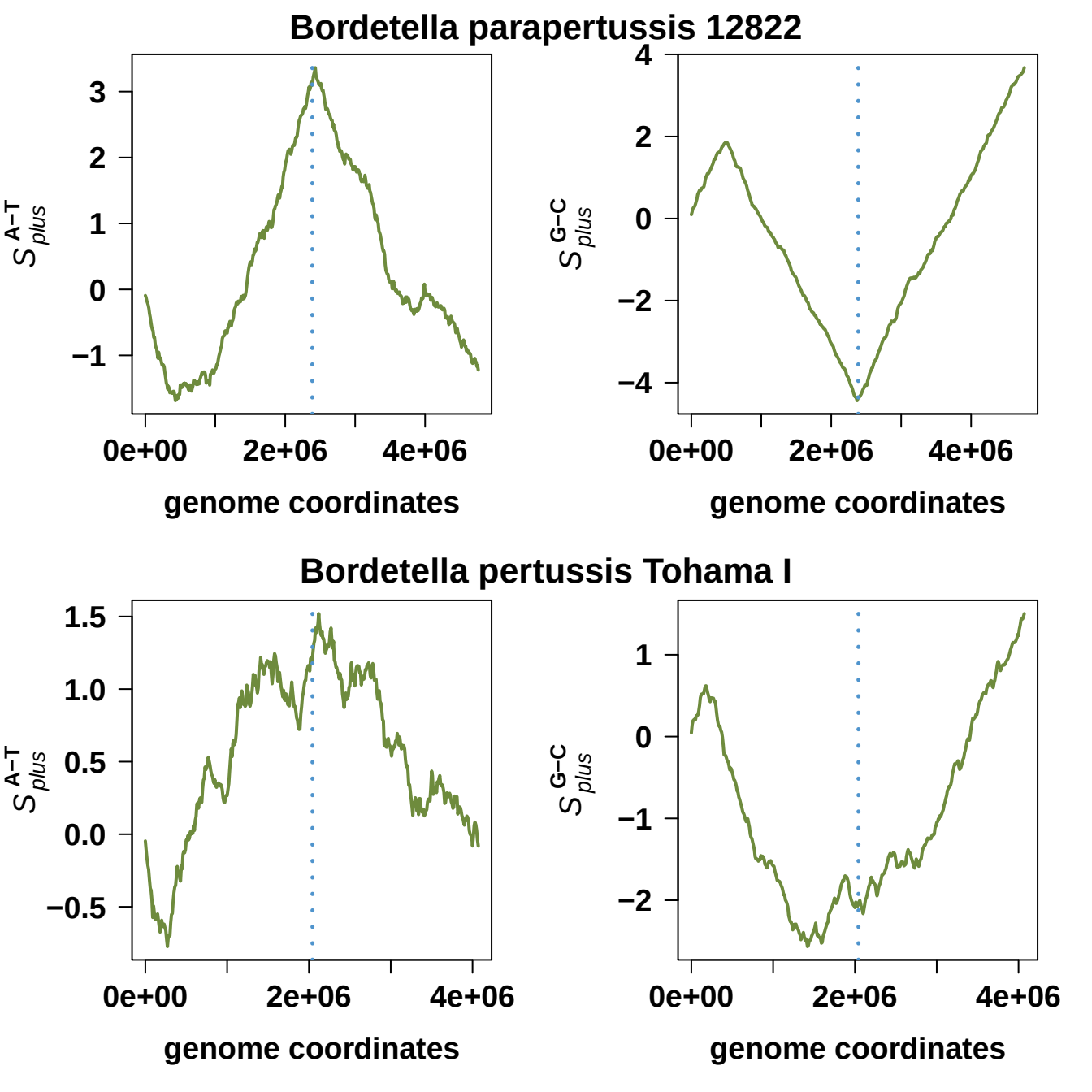

Sphingopyxis alaskensis RB2256
S^{A-T}_{plus}
2.5
2.0
1.5
1.0
0.5
0.0
0.0e+00
1.5e+06
3.0e+06
genome coordinates
S^{G-C}_{plus}
0.5
0.0
−0.5
−1.0
−1.5
−2.0
0.0e+00
1.5e+06
3.0e+06
genome coordinates
Roseobacter denitrificans OCh 114
S^{A-T}_{plus}
4
3
2
1
0
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
−4
−5
−6
0e+00
2e+06
4e+06
genome coordinates

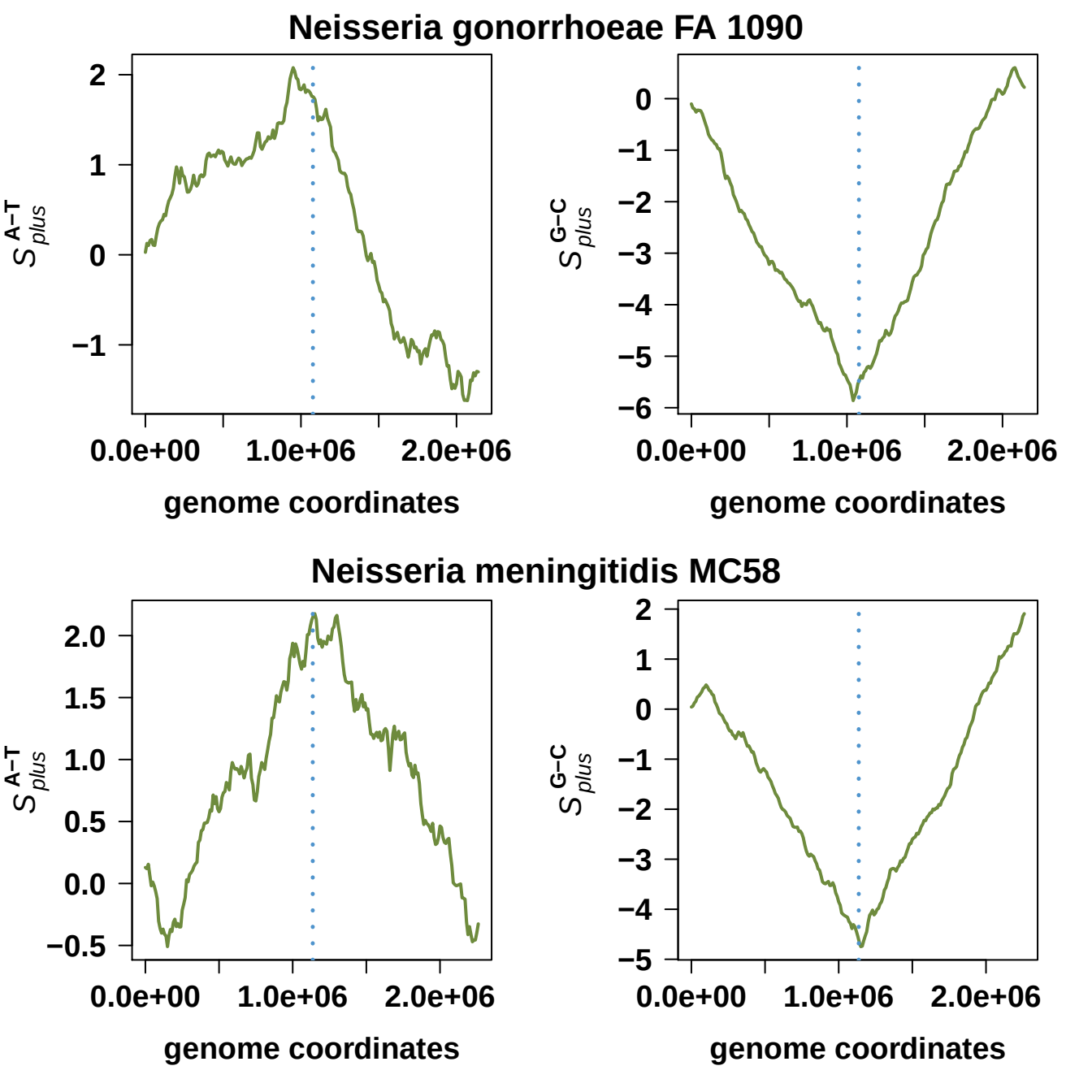

Chelativorans sp. BNC1
1.0
0.5
0.0
−0.5
S^{A-T}_{plus}
0e+00
2e+06
4e+06
genome coordinates
0.0
−0.5
−1.0
−1.5
−2.0
−2.5
−3.0
−3.5
S^{G-C}_{plus}
0e+00
2e+06
4e+06
genome coordinates
Porphyromonas gingivalis W83
1.0
0.5
0.0
S^{A-T}_{plus}
0.0e+00
1.0e+06
2.0e+06
genome coordinates
0.5
0.0
−0.5
−1.0
−1.5
S^{G-C}_{plus}
0.0e+00
1.0e+06
2.0e+06
genome coordinates

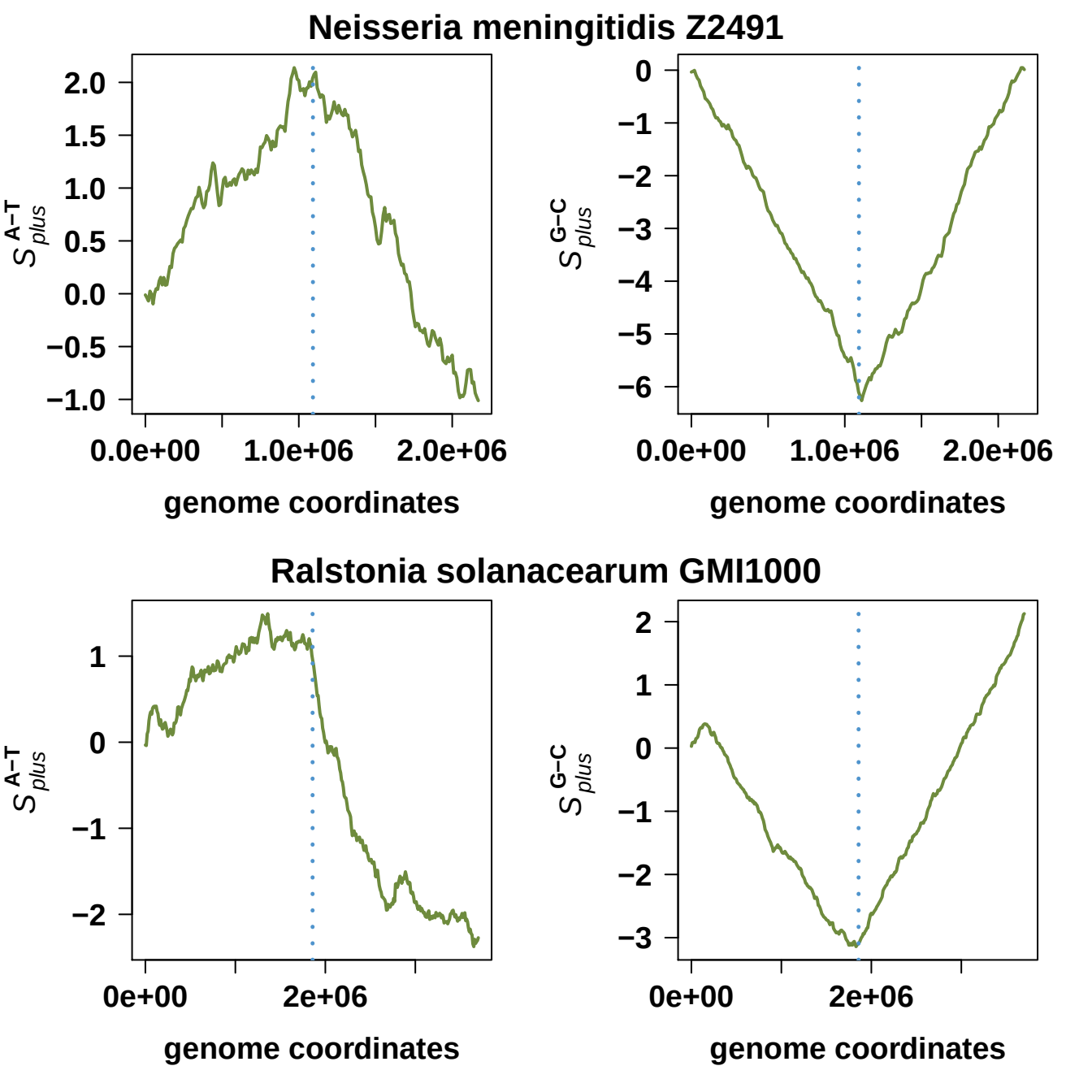

Bacteroides fragilis NCTC 9343
S^{A-T}_{plus}
12
10
8
6
4
2
0
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
0
−5
−10
−15
−20
0e+00
2e+06
4e+06
genome coordinates
Bacteroides thetaiotaomicron VPI−5482
S^{A-T}_{plus}
8
6
4
2
0
−2
0e+00
3e+06
6e+06
genome coordinates
S^{G-C}_{plus}
0
−5
−10
−15
−20
0e+00
3e+06
6e+06
genome coordinates

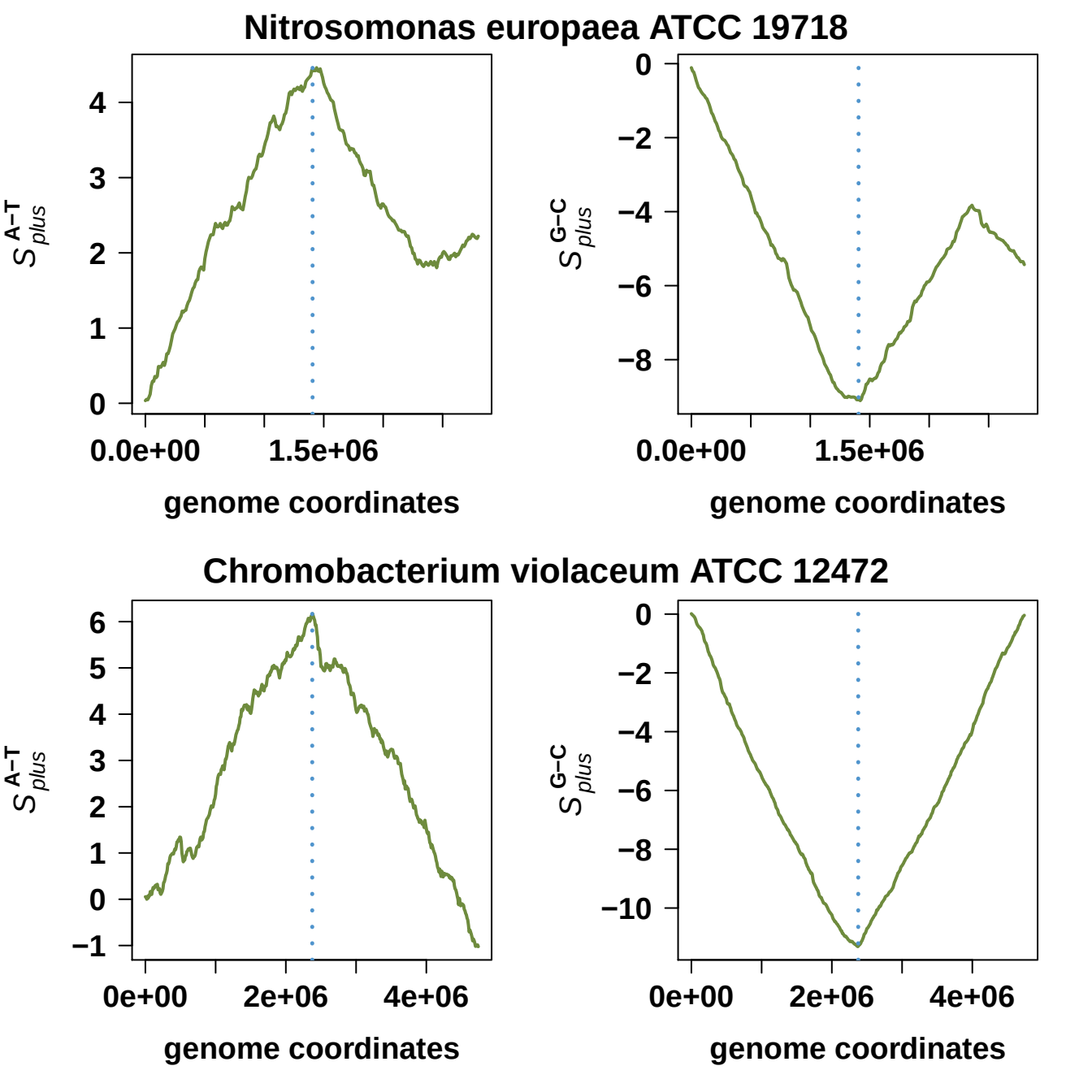

Bacteroides fragilis YCH46
S^{A-T}_{plus}
12
10
8
6
4
2
0
−2
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
0
−5
−10
−15
−20
0e+00
2e+06
4e+06
genome coordinates
Salinibacter ruber DSM 13855
S^{A-T}_{plus}
1.0
0.5
0.0
−0.5
−1.0
−1.5
0.0e+00
1.5e+06
3.0e+06
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
−4
−5
−6
0.0e+00
1.5e+06
3.0e+06
genome coordinates

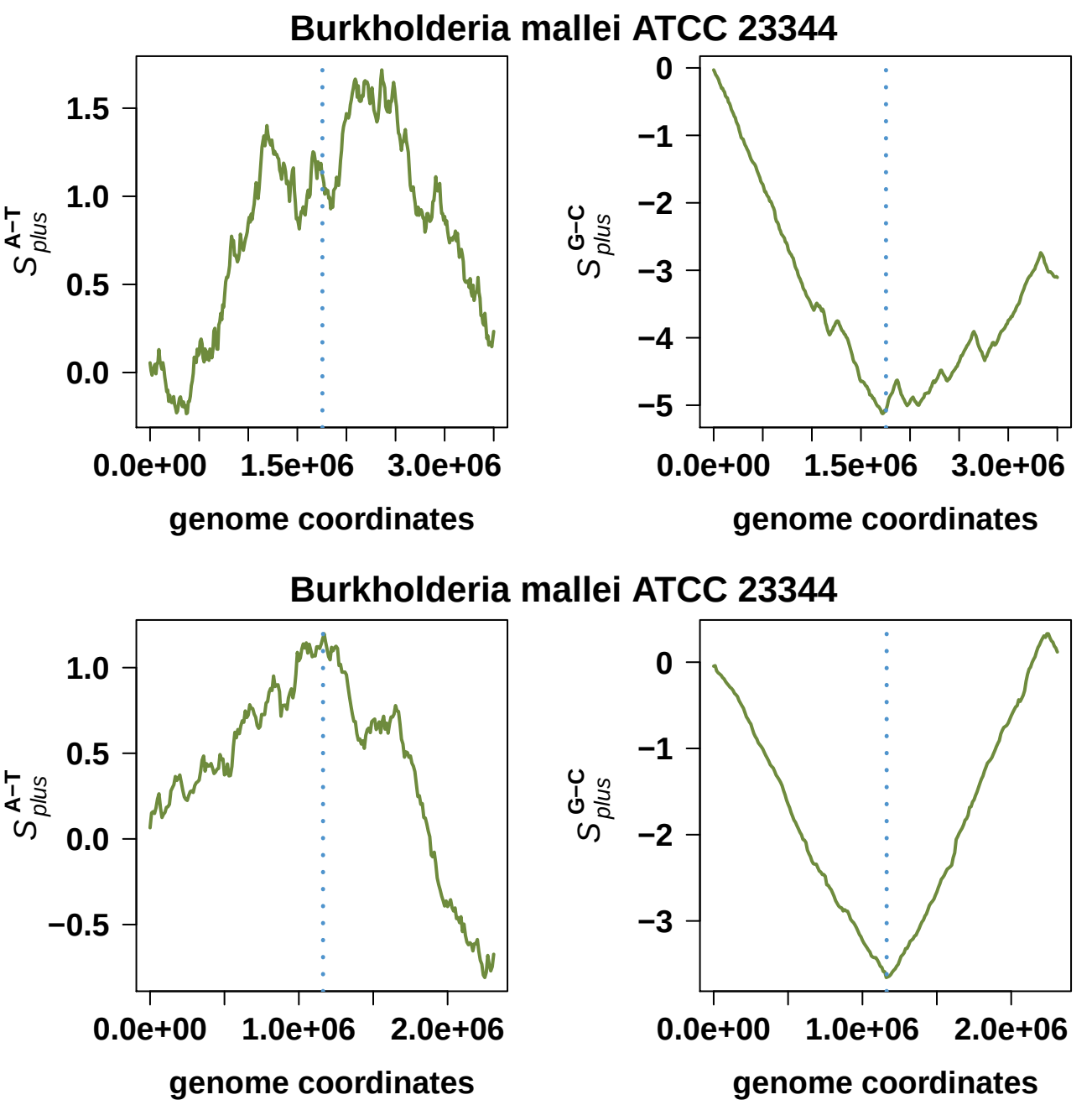

Cytophaga hutchinsonii ATCC 33406
S^{A-T}_{plus}
2.0
1.5
1.0
0.5
0.0
−0.5
−1.0
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
0
−2
−4
−6
−8
0e+00
2e+06
4e+06
genome coordinates
Bordetella bronchiseptica RB50
S^{A-T}_{plus}
5
4
3
2
1
0
−1
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
2
0
−2
−4
−6
0e+00
2e+06
4e+06
genome coordinates

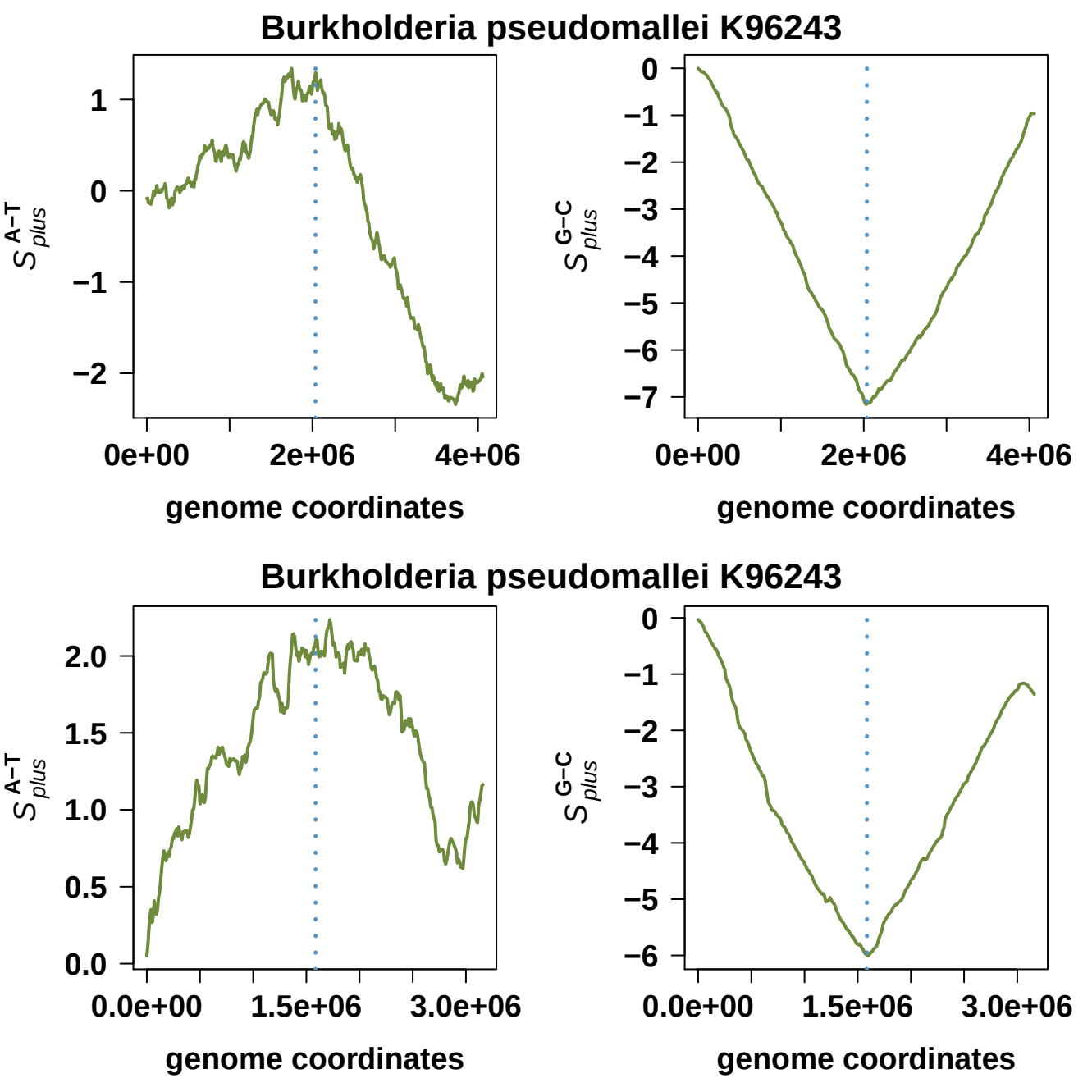

Bordetella parapertussis 12822
S^{A-T}_{plus}
3
2
1
0
−1
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
4
2
0
−2
−4
0e+00
2e+06
4e+06
genome coordinates
Bordetella pertussis Tohama I
S^{A-T}_{plus}
1.5
1.0
0.5
0.0
−0.5
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
1
0
−1
−2
0e+00
2e+06
4e+06
genome coordinates

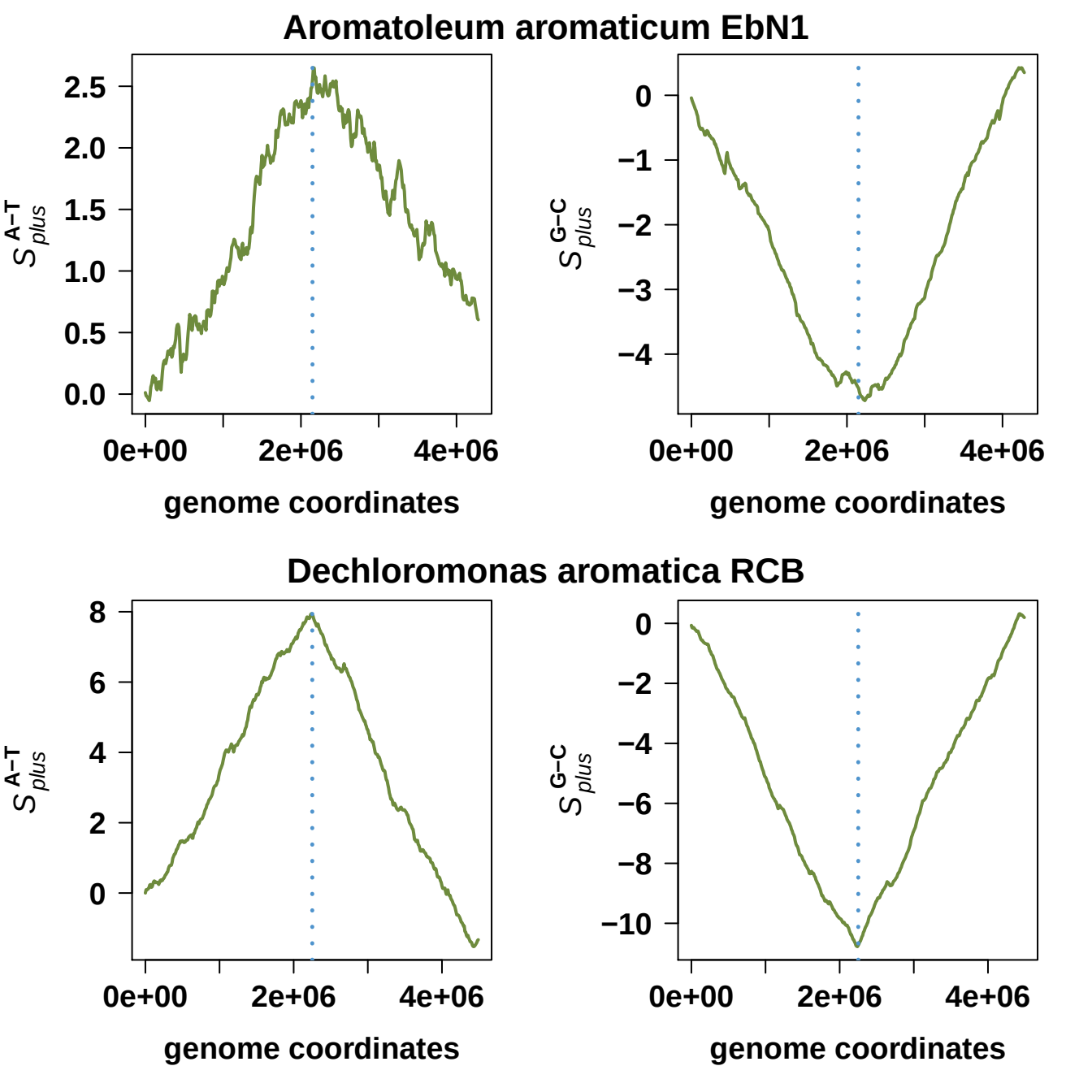

Neisseria gonorrhoeae FA 1090
S^{A-T}_{plus}
2
1
0
−1
0.0e+00
1.0e+06
2.0e+06
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
−4
−5
−6
0.0e+00
1.0e+06
2.0e+06
genome coordinates
Neisseria meningitidis MC58
S^{A-T}_{plus}
2.0
1.5
1.0
0.5
0.0
−0.5
0.0e+00
1.0e+06
2.0e+06
genome coordinates
S^{G-C}_{plus}
2
1
0
−1
−2
−3
−4
−5
0.0e+00
1.0e+06
2.0e+06
genome coordinates

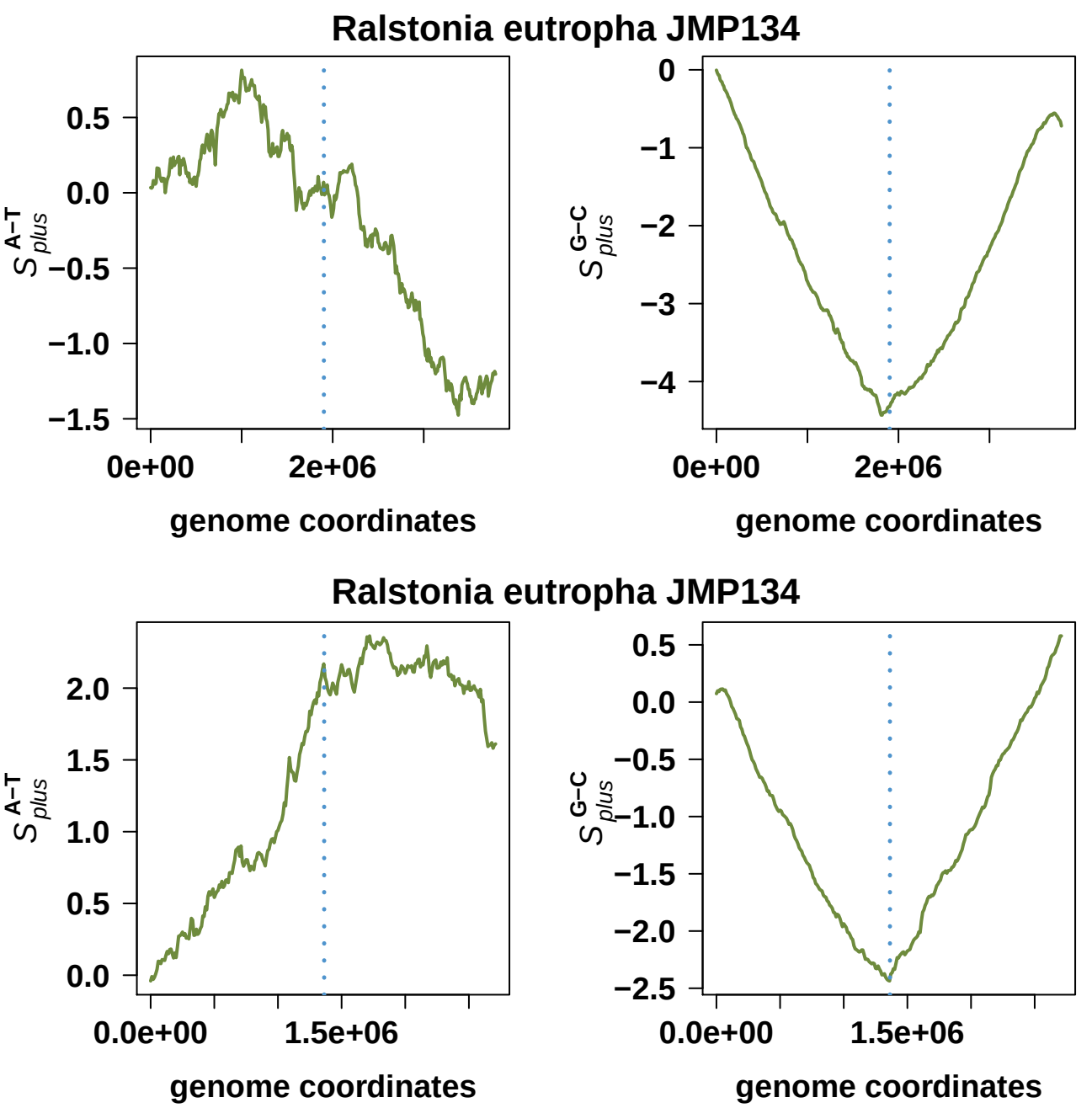

Neisseria meningitidis Z2491
S^{A-T}_{plus}
2.0
1.5
1.0
0.5
0.0
−0.5
−1.0
0.0e+00
1.0e+06
2.0e+06
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
−4
−5
−6
0.0e+00
1.0e+06
2.0e+06
genome coordinates
Ralstonia solanacearum GMI1000
S^{A-T}_{plus}
1
0
−1
−2
0e+00
2e+06
genome coordinates
S^{G-C}_{plus}
2
1
0
−1
−2
−3
0e+00
2e+06
genome coordinates

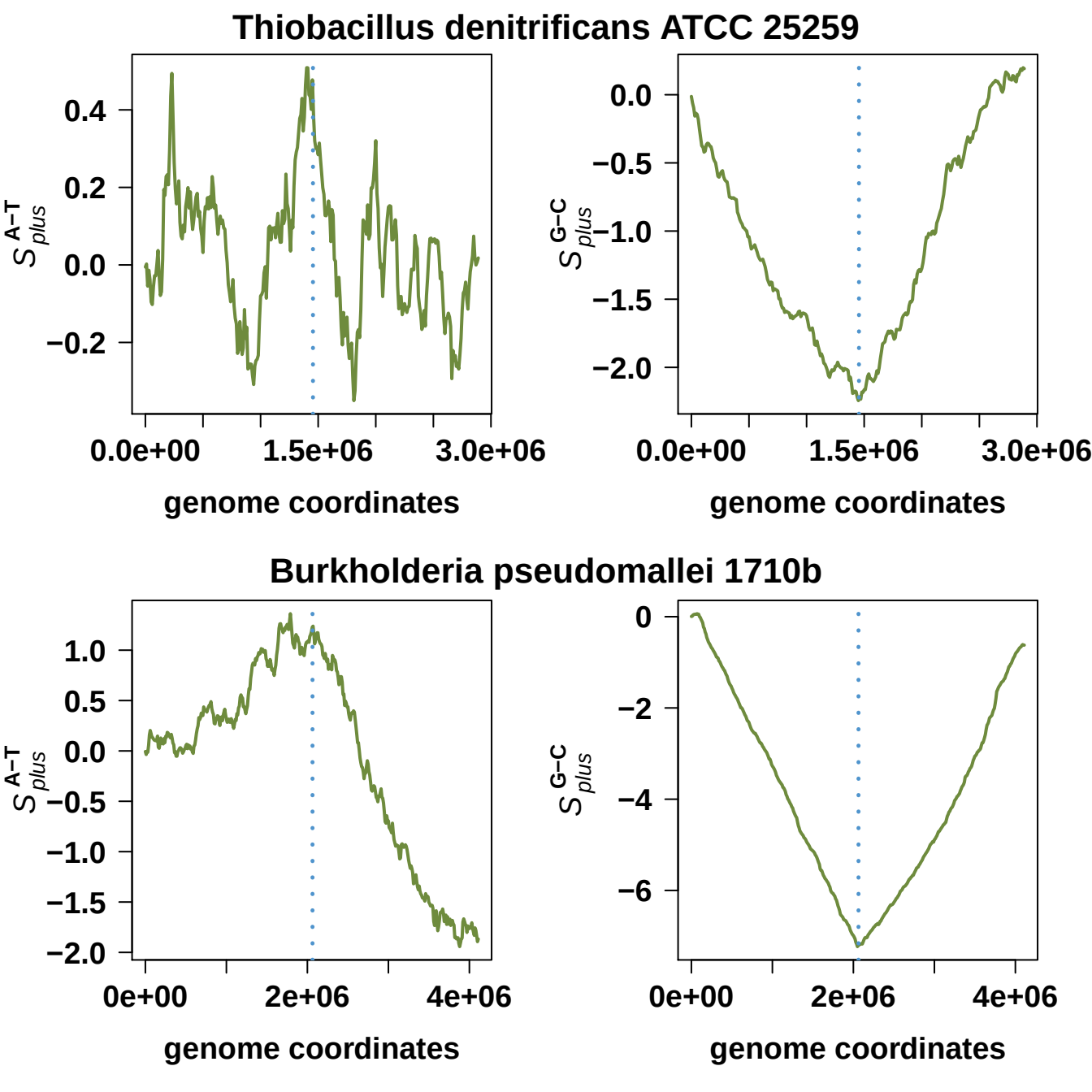

Nitrosomonas europaea ATCC 19718
S^{A-T}_{plus}
4
3
2
1
0
0.0e+00
1.5e+06
genome coordinates
S^{G-C}_{plus}
0
−2
−4
−6
−8
0.0e+00
1.5e+06
genome coordinates
Chromobacterium violaceum ATCC 12472
S^{A-T}_{plus}
6
5
4
3
2
1
0
−1
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
0
−2
−4
−6
−8
−10
0e+00
2e+06
4e+06
genome coordinates

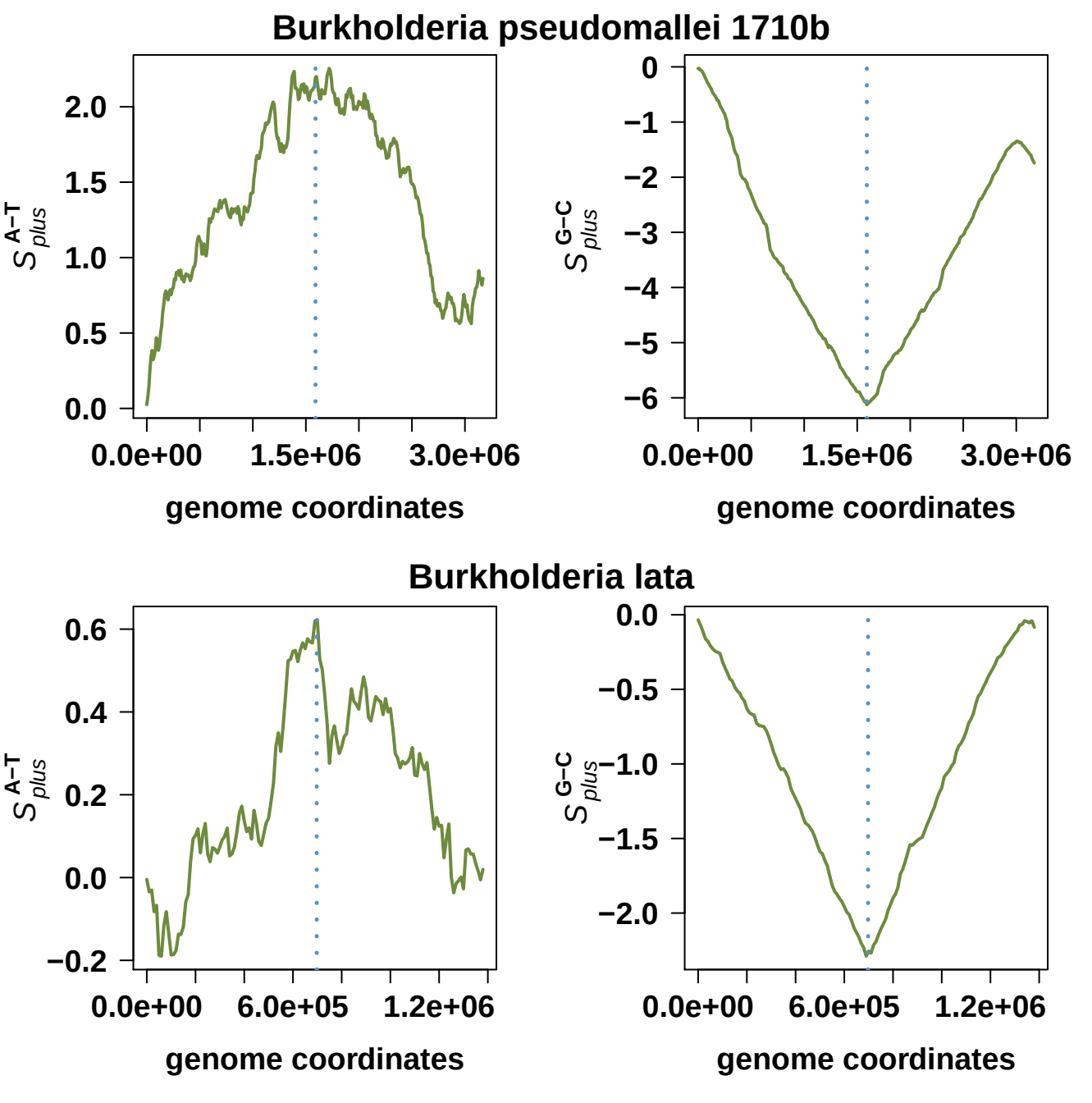

Burkholderia mallei ATCC 23344
S^{A-T}_{plus}
1.5
1.0
0.5
0.0
0.0e+00
1.5e+06
3.0e+06
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
−4
−5
0.0e+00
1.5e+06
3.0e+06
genome coordinates
Burkholderia mallei ATCC 23344
S^{A-T}_{plus}
1.0
0.5
0.0
−0.5
0.0e+00
1.0e+06
2.0e+06
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
0.0e+00
1.0e+06
2.0e+06
genome coordinates

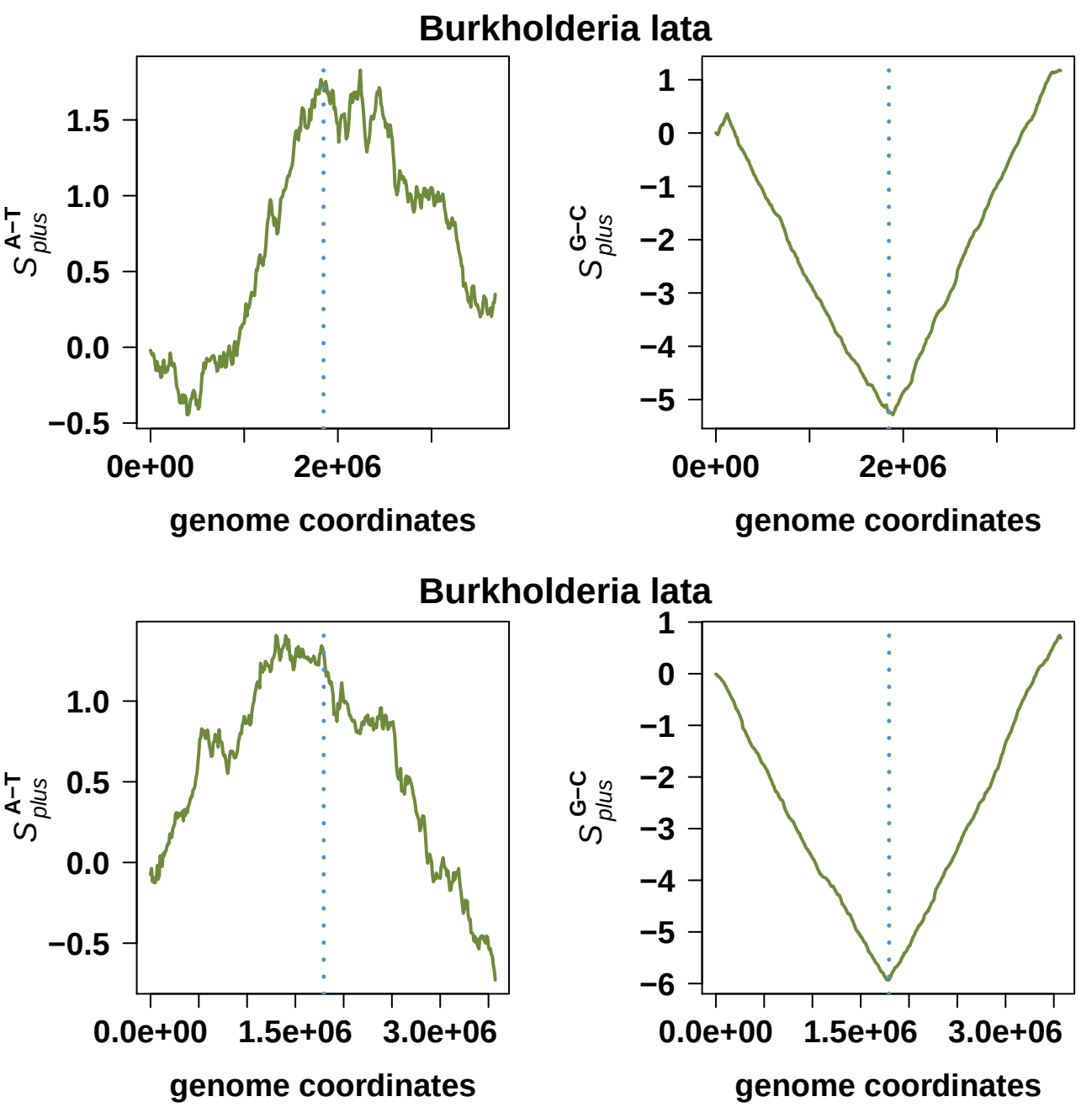

Burkholderia pseudomallei K96243
S^{A-T}_{plus}
1
0
−1
−2
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
−4
−5
−6
−7
0e+00
2e+06
4e+06
genome coordinates
Burkholderia pseudomallei K96243
S^{A-T}_{plus}
2.0
1.5
1.0
0.5
0.0
0.0e+00
1.5e+06
3.0e+06
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
−4
−5
−6
0.0e+00
1.5e+06
3.0e+06
genome coordinates

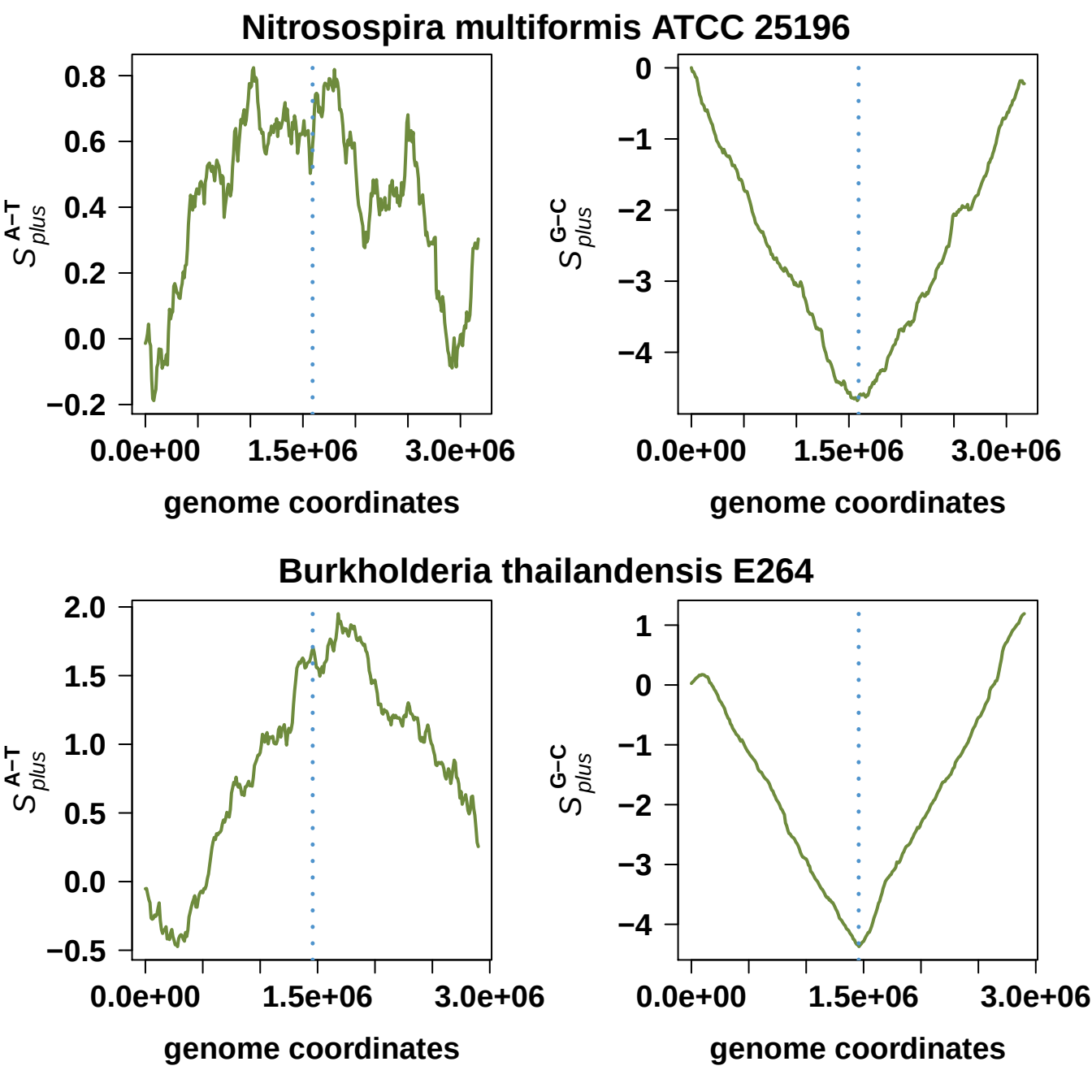

Aromatoleum aromaticum EbN1
S^{A-T}_{plus}
2.5
2.0
1.5
1.0
0.5
0.0
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
−4
0e+00
2e+06
4e+06
genome coordinates
Dechloromonas aromatica RCB
S^{A-T}_{plus}
8
6
4
2
0
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
0
−2
−4
−6
−8
−10
0e+00
2e+06
4e+06
genome coordinates

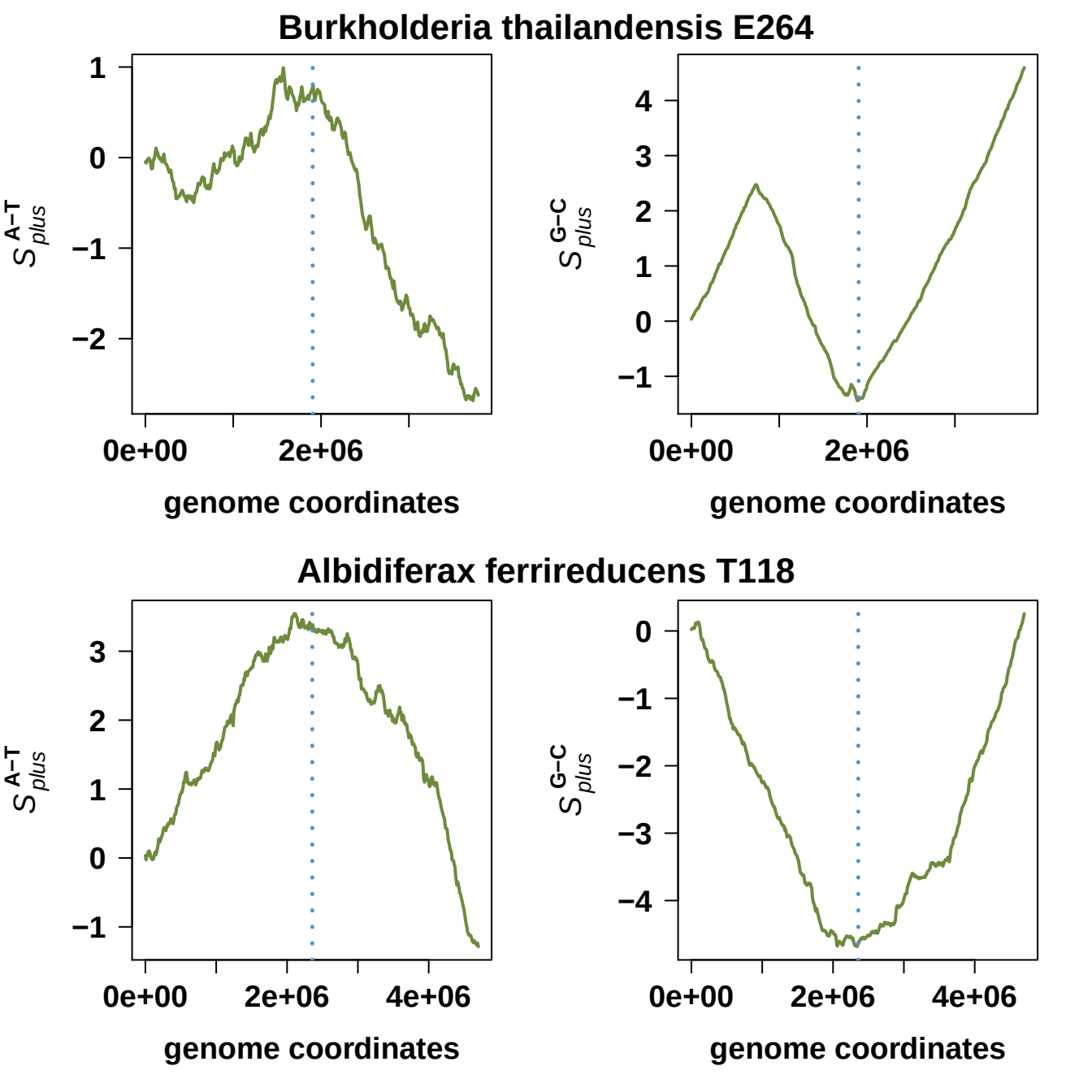

Ralstonia eutropha JMP134
S^{A-T}_{plus}
0.5
0.0
−0.5
−1.0
−1.5
0e+00
2e+06
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
−4
0e+00
2e+06
genome coordinates
Ralstonia eutropha JMP134
S^{A-T}_{plus}
2.0
1.5
1.0
0.5
0.0
0.0e+00
1.5e+06
genome coordinates
S^{G-C}_{plus}
0.5
0.0
−0.5
−1.0
−1.5
−2.0
−2.5
0.0e+00
1.5e+06
genome coordinates

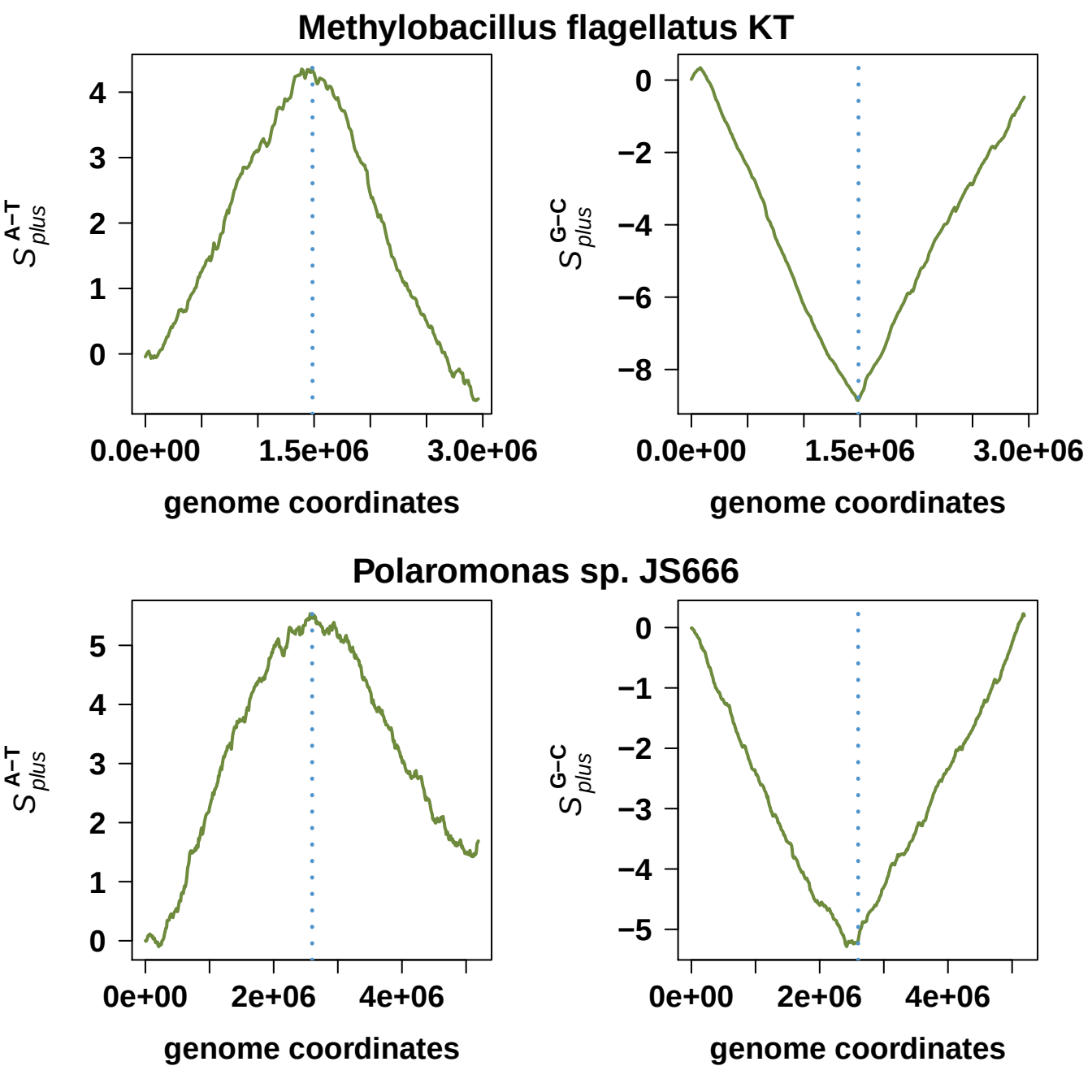

Thiobacillus denitrificans ATCC 25259
S^{A-T}_{plus}
0.4
0.2
0.0
−0.2
0.0e+00
1.5e+06
3.0e+06
genome coordinates
S^{G-C}_{plus}
0.0
−0.5
−1.0
−1.5
−2.0
0.0e+00
1.5e+06
3.0e+06
genome coordinates
Burkholderia pseudomallei 1710b
S^{A-T}_{plus}
1.0
0.5
0.0
−0.5
−1.0
−1.5
−2.0
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
0
−2
−4
−6
0e+00
2e+06
4e+06
genome coordinates

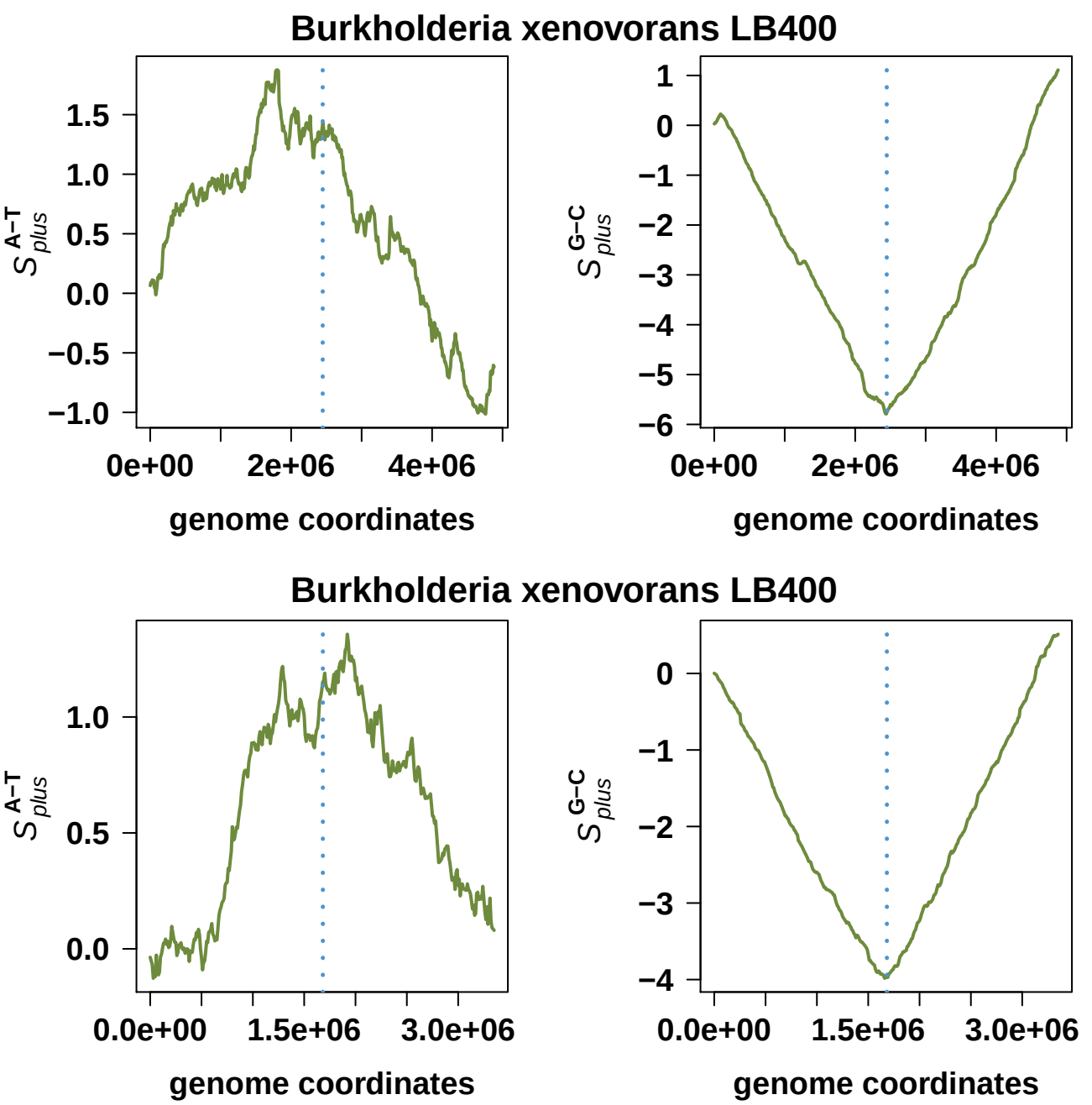

Burkholderia pseudomallei 1710b
S^{A-T}_{plus}
2.0
1.5
1.0
0.5
0.0
0.0e+00
1.5e+06
3.0e+06
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
−4
−5
−6
0.0e+00
1.5e+06
3.0e+06
genome coordinates
Burkholderia lata
S^{A-T}_{plus}
0.6
0.4
0.2
0.0
−0.2
0.0e+00
6.0e+05
1.2e+06
genome coordinates
S^{G-C}_{plus}
0.0
−0.5
−1.0
−1.5
−2.0
0.0e+00
6.0e+05
1.2e+06
genome coordinates

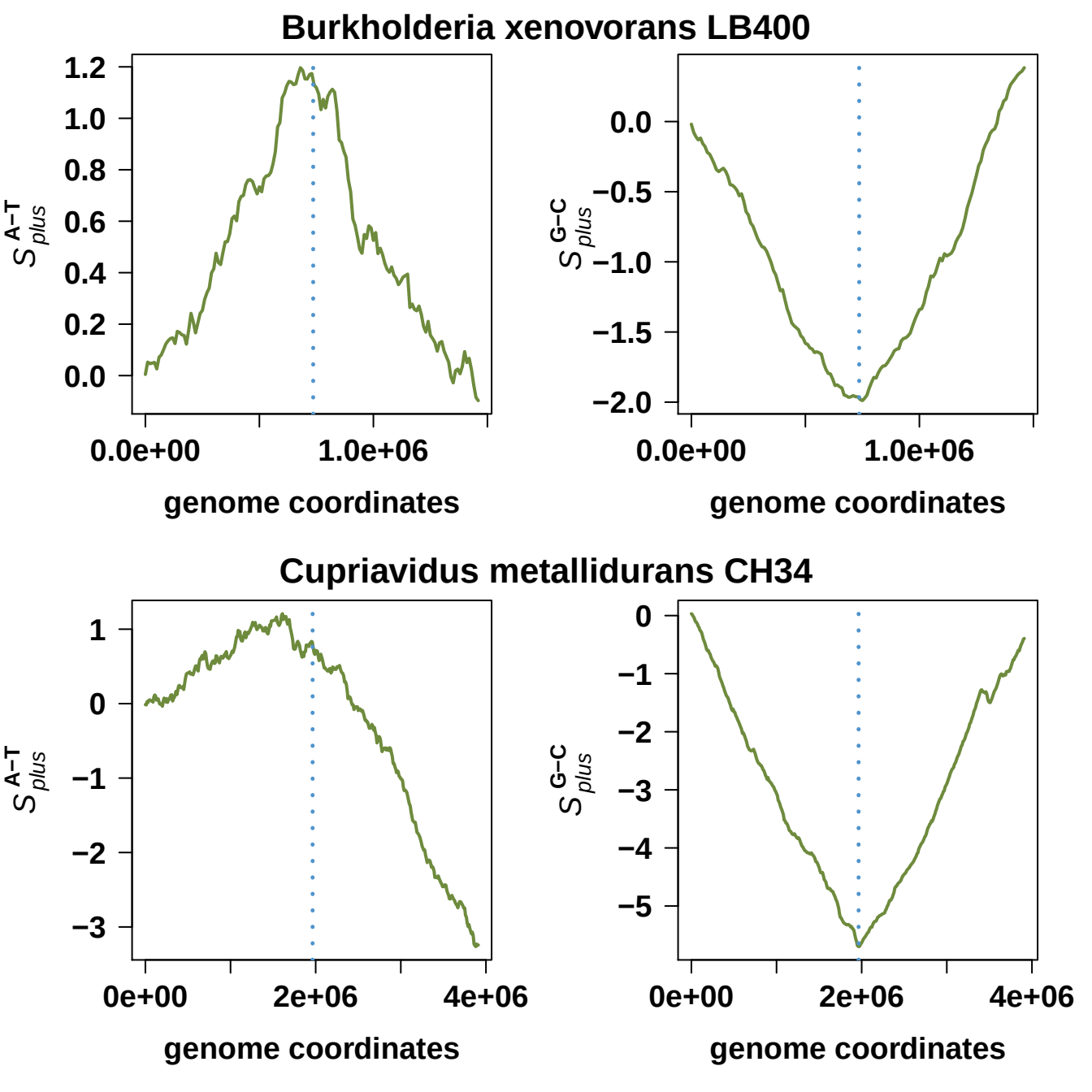

Burkholderia lata
1.5
1.0
0.5
0.0
−0.5
S^{A-T}_{plus}
0e+00
2e+06
genome coordinates
1
0
−1
−2
−3
−4
−5
S^{G-c}_{plus}
0e+00
2e+06
genome coordinates
Burkholderia lata
1.0
0.5
0.0
−0.5
S^{A-T}_{plus}
0.0e+00
1.5e+06
3.0e+06
genome coordinates
1
0
−1
−2
−3
−4
−5
−6
S^{G-c}_{plus}
0.0e+00
1.5e+06
3.0e+06
genome coordinates

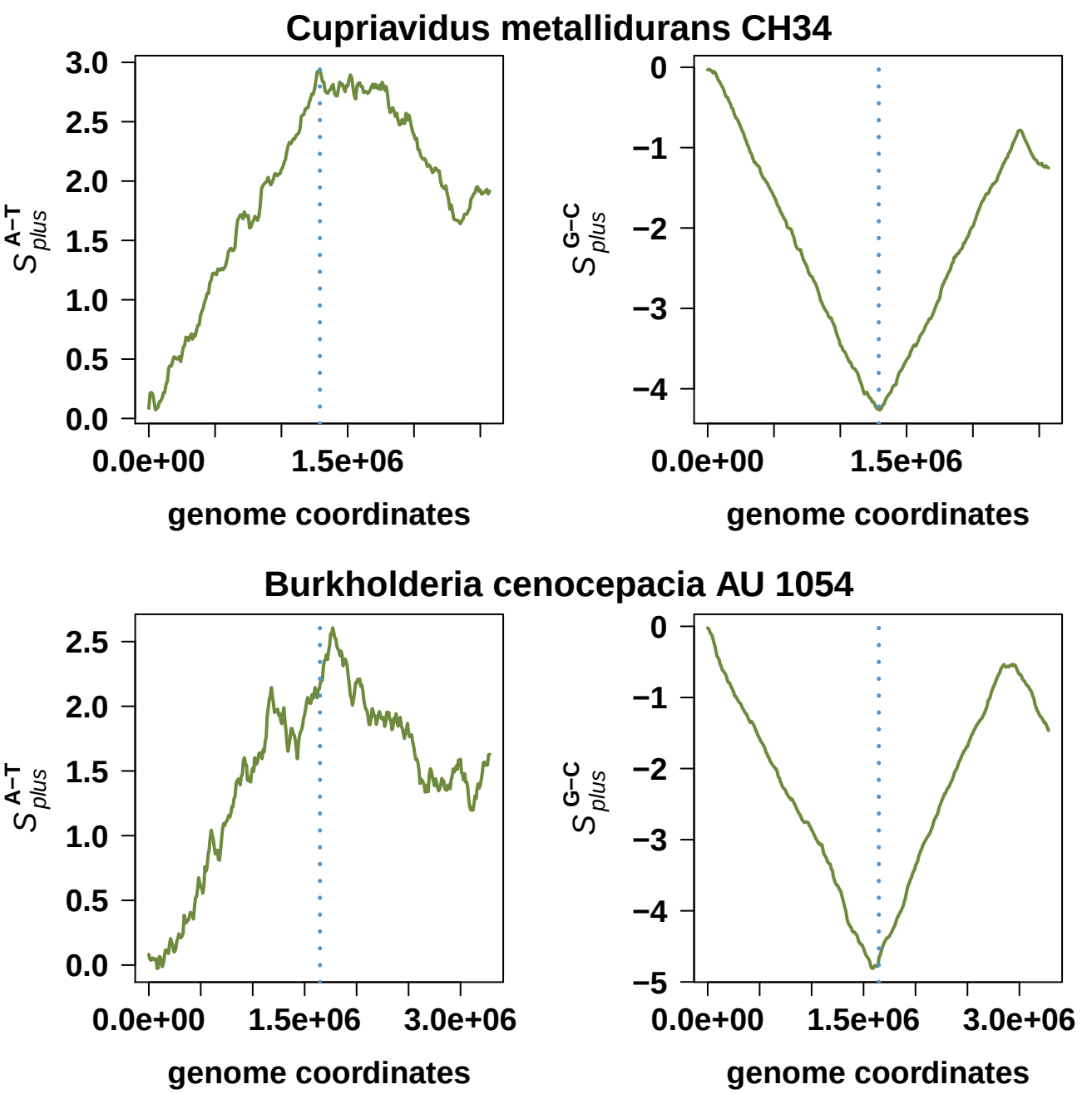

Nitrosospira multiformis ATCC 25196
S^{A-T}_{plus}
0.8
0.6
0.4
0.2
0.0
−0.2
0.0e+00
1.5e+06
3.0e+06
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
−4
0.0e+00
1.5e+06
3.0e+06
genome coordinates
Burkholderia thailandensis E264
S^{A-T}_{plus}
2.0
1.5
1.0
0.5
0.0
−0.5
0.0e+00
1.5e+06
3.0e+06
genome coordinates
S^{G-C}_{plus}
1
0
−1
−2
−3
−4
0.0e+00
1.5e+06
3.0e+06
genome coordinates

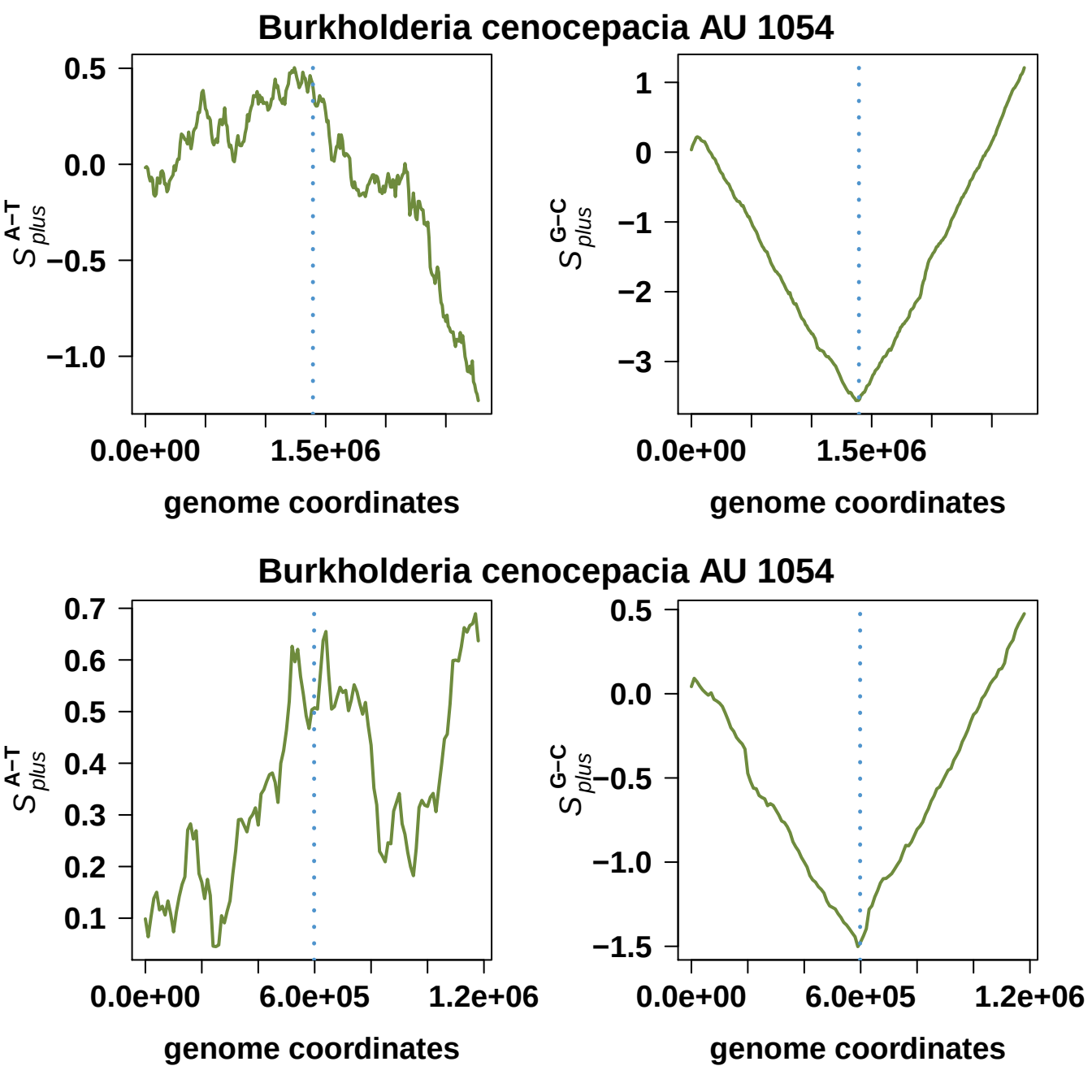

Burkholderia thailandensis E264
S^{A-T}_{plus}
1
0
−1
−2
0e+00
2e+06
genome coordinates
S^{G-C}_{plus}
4
3
2
1
0
−1
0e+00
2e+06
genome coordinates
Albidiferax ferrireducens T118
S^{A-T}_{plus}
3
2
1
0
−1
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
−4
0e+00
2e+06
4e+06
genome coordinates

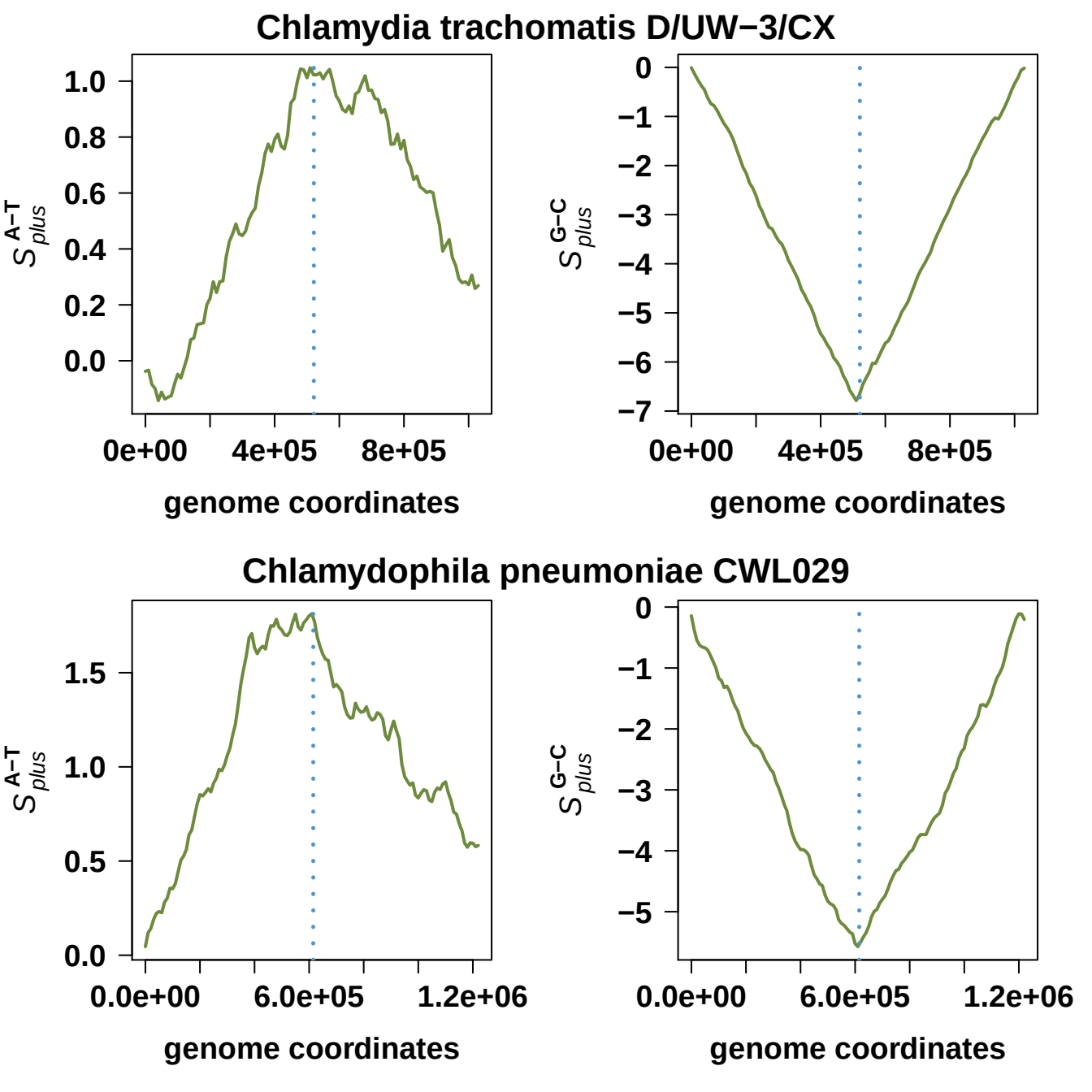

Methylobacillus flagellatus KT
S^{A-T}_{plus}
4
3
2
1
0
0.0e+00
1.5e+06
3.0e+06
genome coordinates
S^{G-C}_{plus}
0
−2
−4
−6
−8
0.0e+00
1.5e+06
3.0e+06
genome coordinates
Polaromonas sp. JS666
S^{A-T}_{plus}
5
4
3
2
1
0
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
−4
−5
0e+00
2e+06
4e+06
genome coordinates

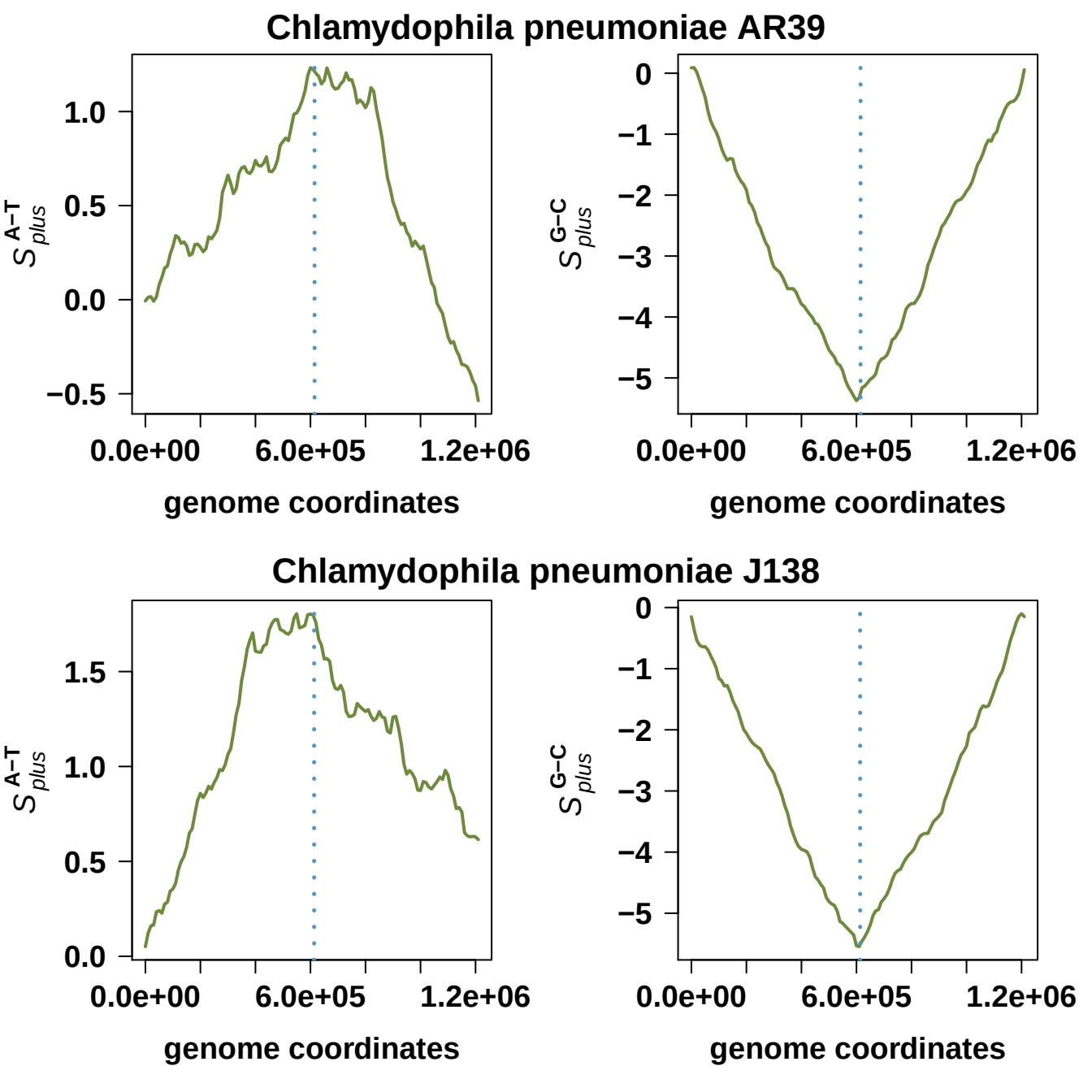

Burkholderia xenovorans LB400
S^{A-T}_{plus}
1.5
1.0
0.5
0.0
−0.5
−1.0
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
1
0
−1
−2
−3
−4
−5
−6
0e+00
2e+06
4e+06
genome coordinates
Burkholderia xenovorans LB400
S^{A-T}_{plus}
1.0
0.5
0.0
0.0e+00
1.5e+06
3.0e+06
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
−4
0.0e+00
1.5e+06
3.0e+06
genome coordinates

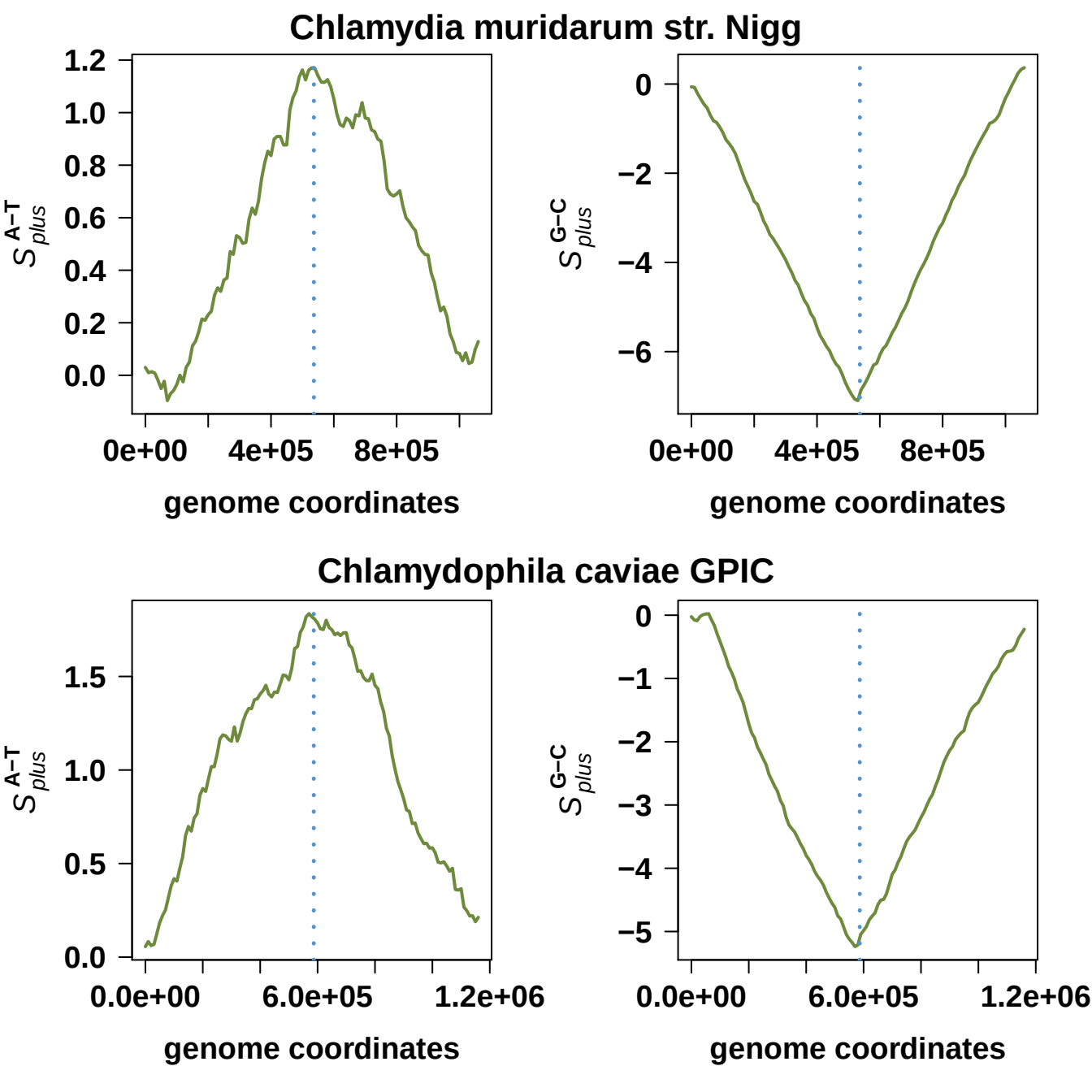

Burkholderia xenovorans LB400
1.2
1.0
0.8
0.6
0.4
0.2
0.0
S^{A-T}_{plus}
0.0e+00
1.0e+06
genome coordinates
0.0
−0.5
−1.0
−1.5
−2.0
S^{G-C}_{plus}
0.0e+00
1.0e+06
genome coordinates
Cupriavidus metallidurans CH34
1
0
−1
−2
−3
S^{A-T}_{plus}
0e+00
2e+06
4e+06
genome coordinates
0
−1
−2
−3
−4
−5
S^{G-C}_{plus}
0e+00
2e+06
4e+06
genome coordinates

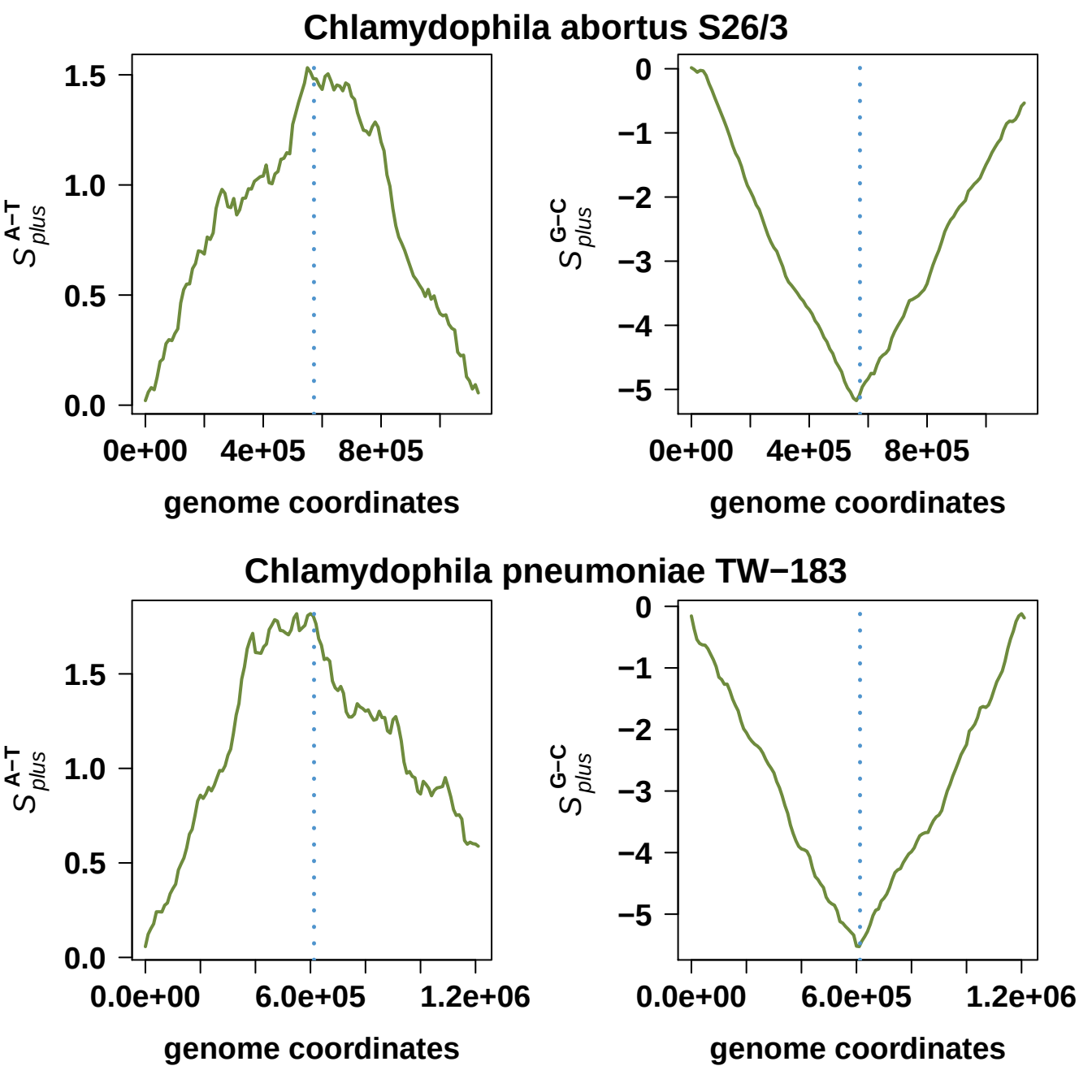

Cupriavidus metallidurans CH34
3.0
2.5
2.0
1.5
1.0
0.5
0.0
S^{A-T}_{plus}
0.0e+00
1.5e+06
genome coordinates
0
−1
−2
−3
−4
S^{G-C}_{plus}
0.0e+00
1.5e+06
genome coordinates
Burkholderia cenocepacia AU 1054
2.5
2.0
1.5
1.0
0.5
0.0
S^{A-T}_{plus}
0.0e+00
1.5e+06
3.0e+06
genome coordinates
0
−1
−2
−3
−4
−5
S^{G-C}_{plus}
0.0e+00
1.5e+06
3.0e+06
genome coordinates

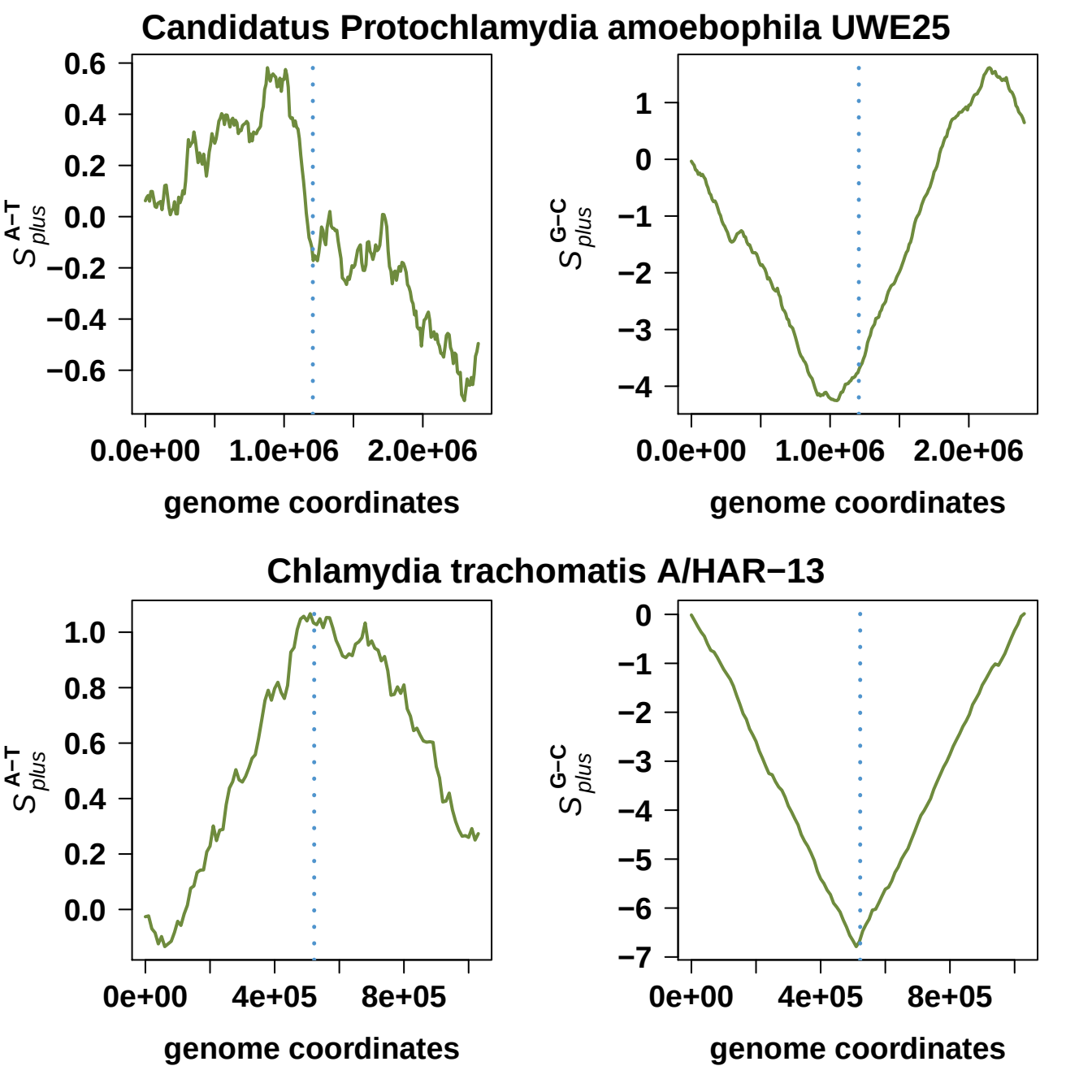

Burkholderia cenocepacia AU 1054
0.5
0.0
−0.5
−1.0
S^{A-T}_{plus}
0.0e+00
1.5e+06
genome coordinates
1
0
−1
−2
−3
S^{G-C}_{plus}
0.0e+00
1.5e+06
genome coordinates
Burkholderia cenocepacia AU 1054
0.7
0.6
0.5
0.4
0.3
0.2
0.1
S^{A-T}_{plus}
0.0e+00
6.0e+05
1.2e+06
genome coordinates
0.5
0.0
−0.5
−1.0
−1.5
S^{G-C}_{plus}
0.0e+00
6.0e+05
1.2e+06
genome coordinates

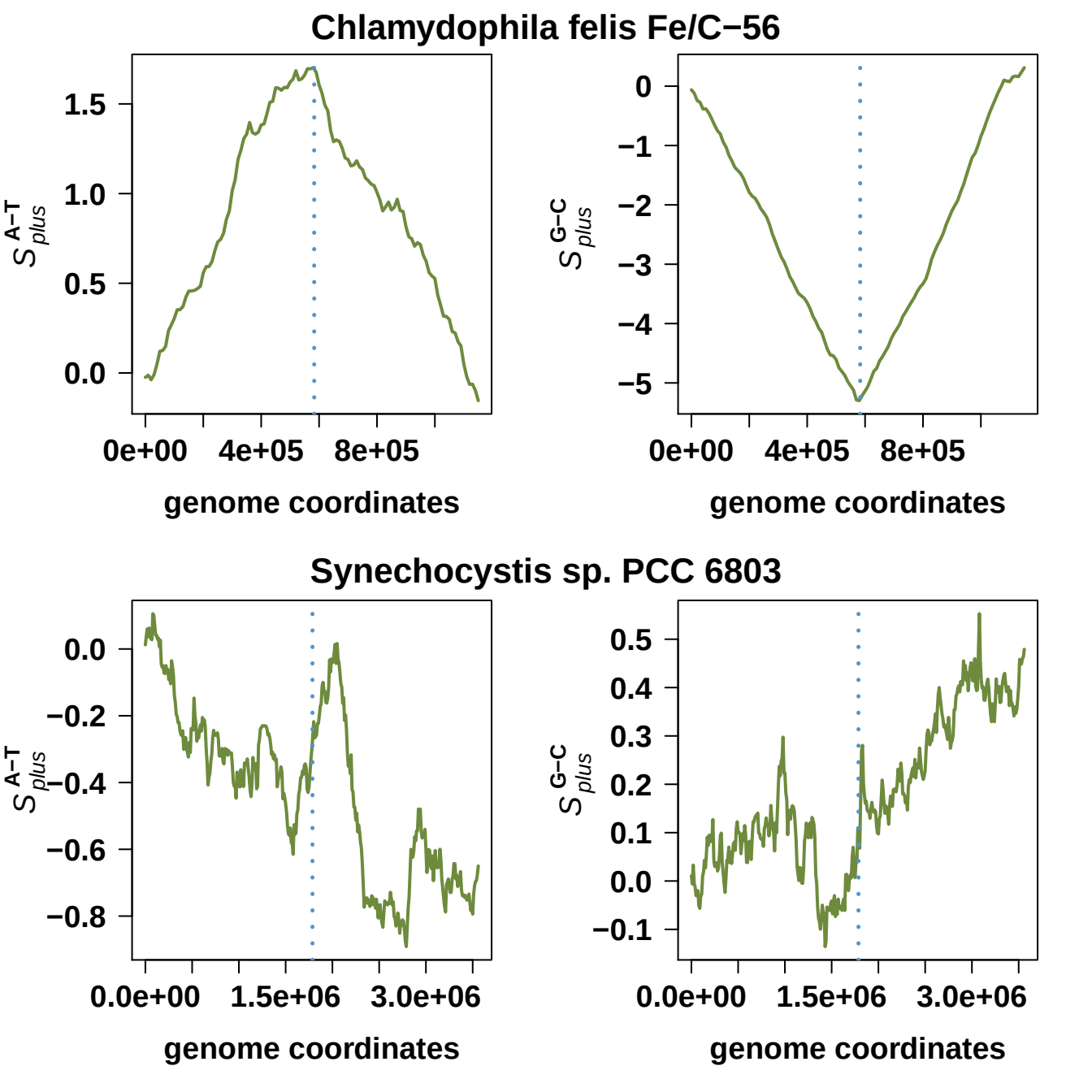

Chlamydia trachomatis D/UW−3/CX
1.0
0.8
0.6
0.4
0.2
0.0
S^{A-T}_{plus}
0e+00
4e+05
8e+05
genome coordinates
0
−1
−2
−3
−4
−5
−6
−7
S^{G-C}_{plus}
0e+00
4e+05
8e+05
genome coordinates
Chlamydophila pneumoniae CWL029
1.5
1.0
0.5
0.0
S^{A-T}_{plus}
0.0e+00
6.0e+05
1.2e+06
genome coordinates
0
−1
−2
−3
−4
−5
S^{G-C}_{plus}
0.0e+00
6.0e+05
1.2e+06
genome coordinates

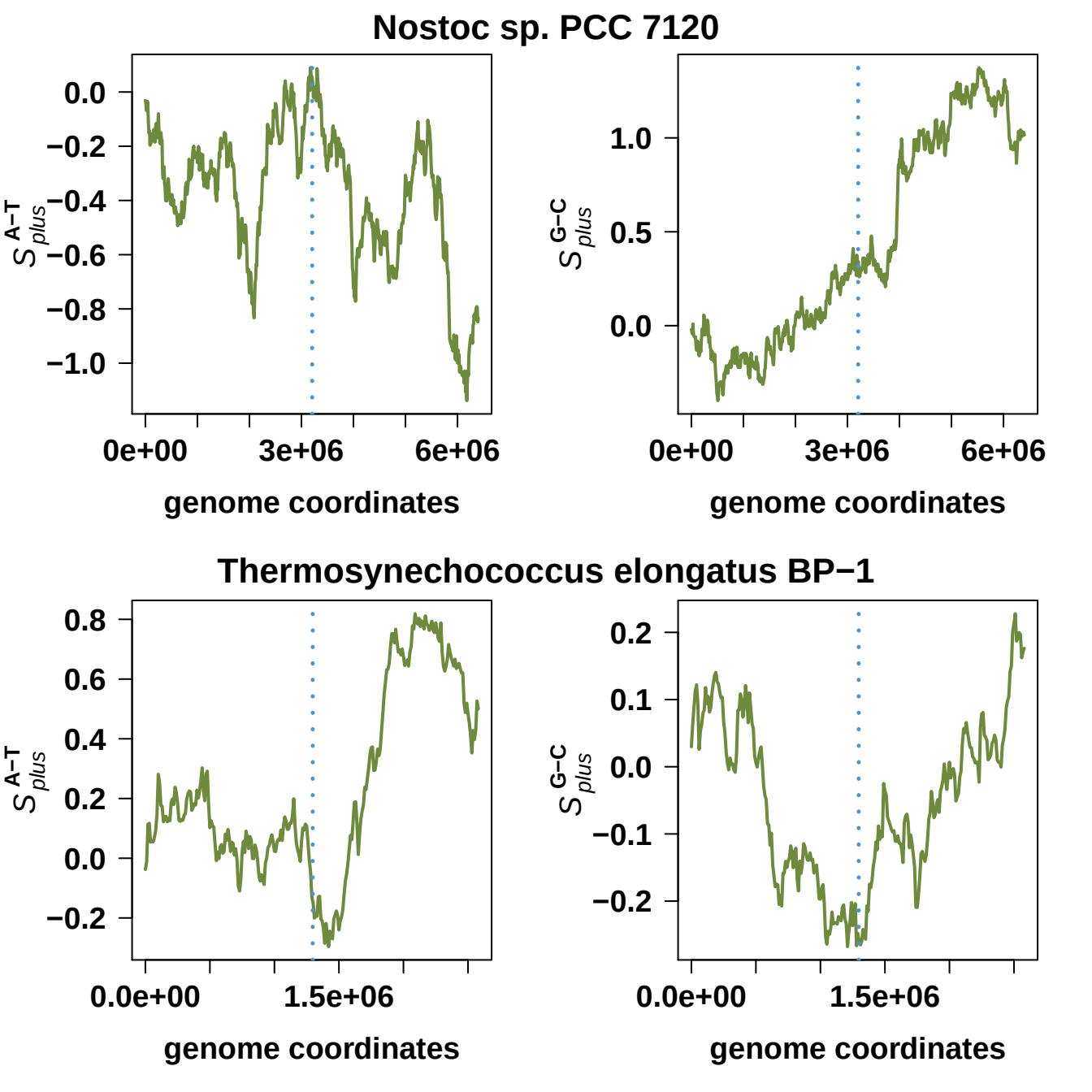

Chlamydophila pneumoniae AR39
S^{A-T}_{plus}
1.0
0.5
0.0
−0.5
0.0e+00
6.0e+05
1.2e+06
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
−4
−5
0.0e+00
6.0e+05
1.2e+06
genome coordinates
Chlamydophila pneumoniae J138
S^{A-T}_{plus}
1.5
1.0
0.5
0.0
0.0e+00
6.0e+05
1.2e+06
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
−4
−5
0.0e+00
6.0e+05
1.2e+06
genome coordinates

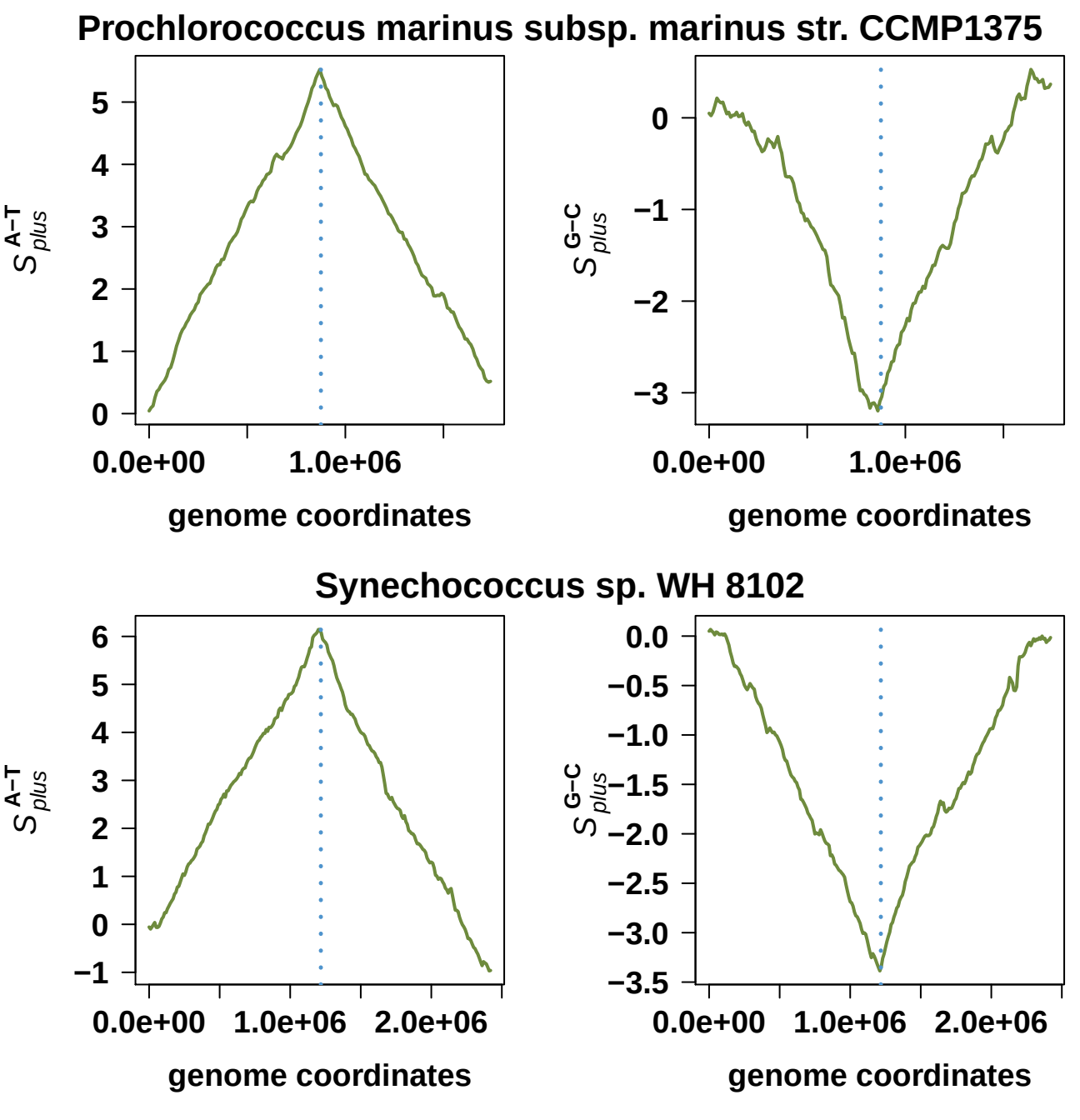

Chlamydia muridarum str. Nigg
1.2
1.0
0.8
0.6
0.4
0.2
0.0
S^{A-T}_{plus}
0e+00
4e+05
8e+05
genome coordinates
0
−2
−4
−6
S^{G-C}_{plus}
0e+00
4e+05
8e+05
genome coordinates
Chlamydophila caviae GPIC
1.5
1.0
0.5
0.0
S^{A-T}_{plus}
0.0e+00
6.0e+05
1.2e+06
genome coordinates
0
−1
−2
−3
−4
−5
S^{G-C}_{plus}
0.0e+00
6.0e+05
1.2e+06
genome coordinates

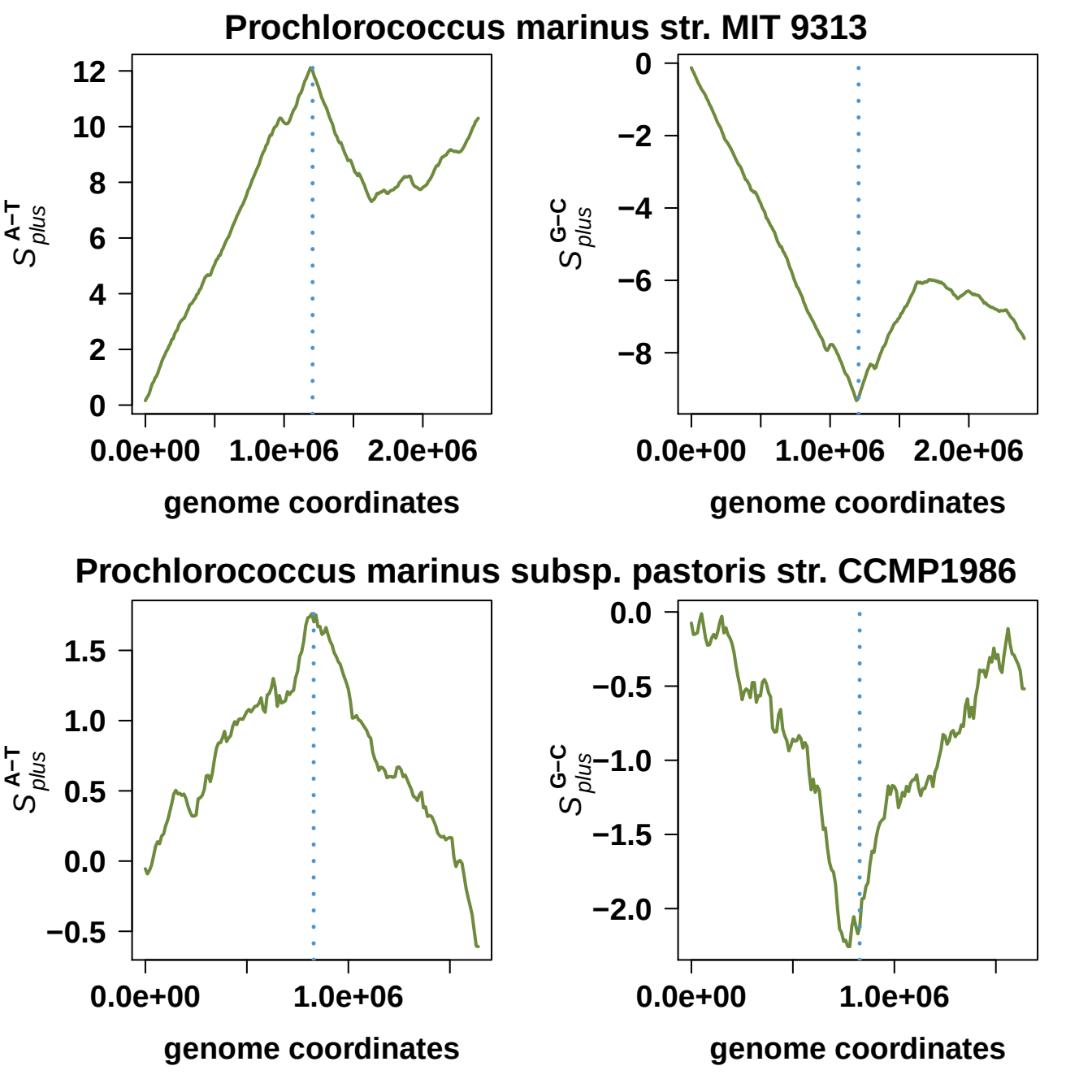

Chlamydophila abortus S26/3
1.5
1.0
0.5
0.0
S^{A-T}_{plus}
0e+00
4e+05
8e+05
genome coordinates
0
−1
−2
−3
−4
−5
S^{G-C}_{plus}
0e+00
4e+05
8e+05
genome coordinates
Chlamydophila pneumoniae TW−183
1.5
1.0
0.5
0.0
S^{A-T}_{plus}
0.0e+00
6.0e+05
1.2e+06
genome coordinates
0
−1
−2
−3
−4
−5
S^{G-C}_{plus}
0.0e+00
6.0e+05
1.2e+06
genome coordinates

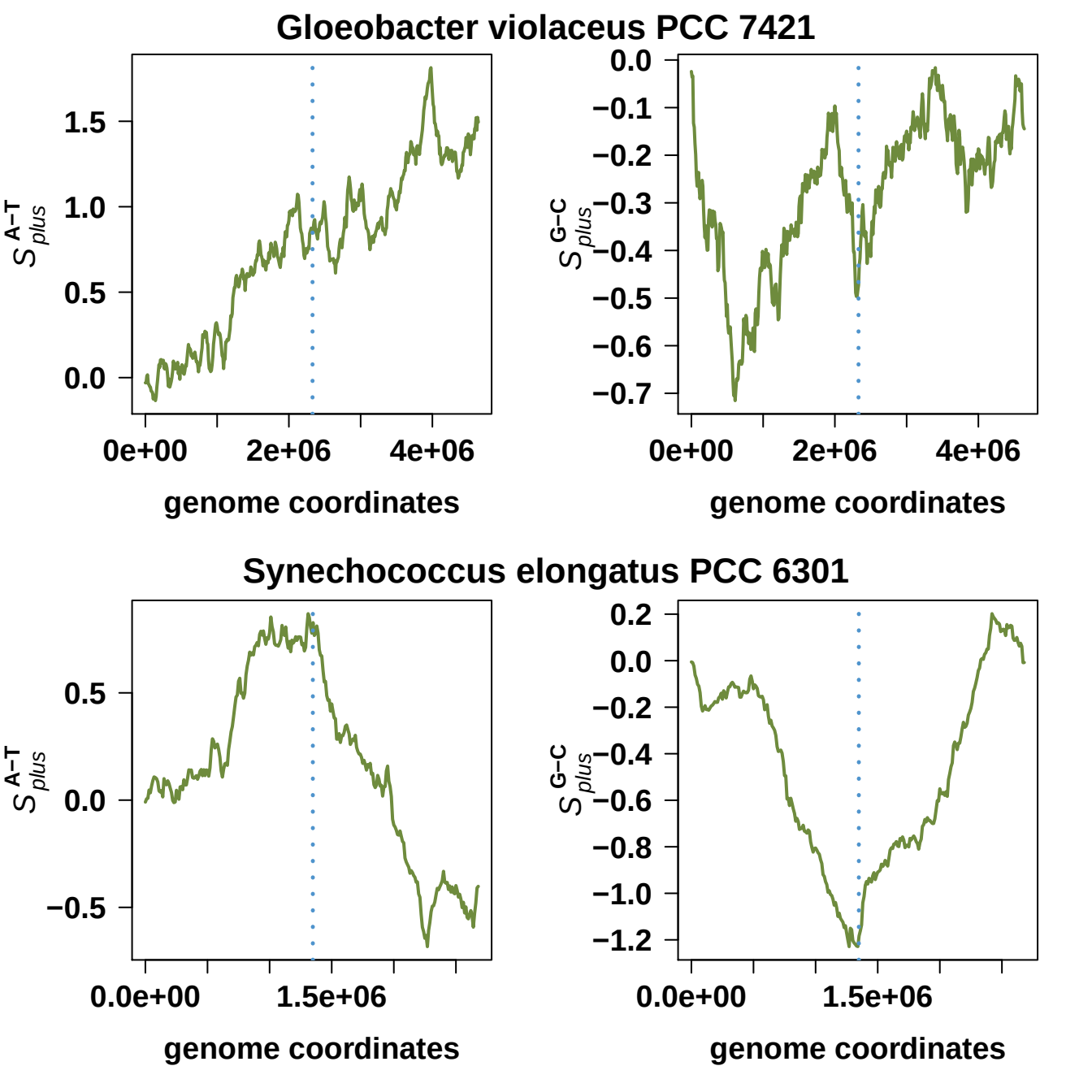

Candidatus Protochlamydia amoebophila UWE25
S^{A-T}_{plus}
0.6
0.4
0.2
0.0
−0.2
−0.4
−0.6
0.0e+00
1.0e+06
2.0e+06
genome coordinates
S^{G-C}_{plus}
1
0
−1
−2
−3
−4
0.0e+00
1.0e+06
2.0e+06
genome coordinates
Chlamydia trachomatis A/HAR−13
S^{A-T}_{plus}
1.0
0.8
0.6
0.4
0.2
0.0
0e+00
4e+05
8e+05
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
−4
−5
−6
−7
0e+00
4e+05
8e+05
genome coordinates

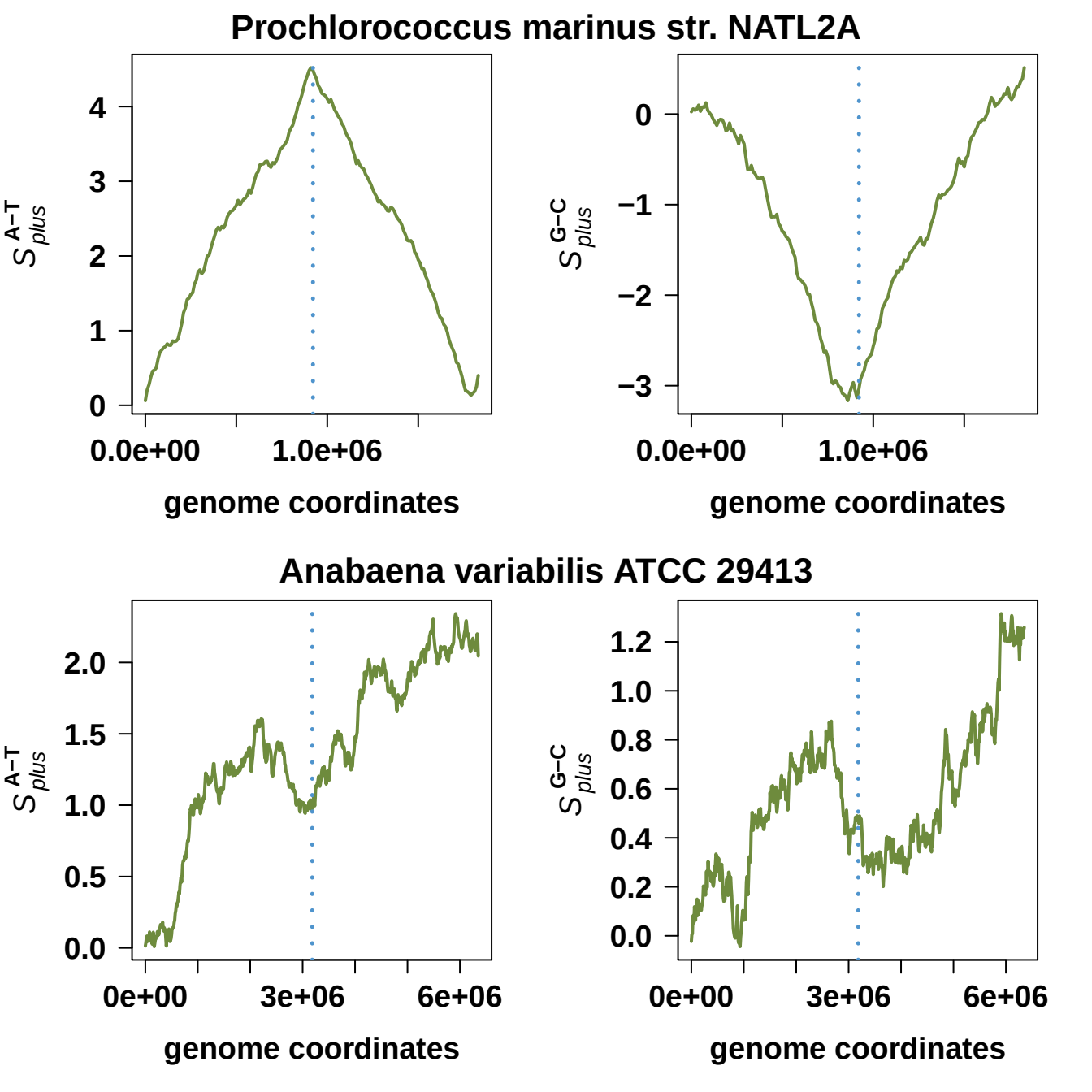

Chlamydophila felis Fe/C−56
S^{A-T}_{plus}
1.5
1.0
0.5
0.0
0e+00
4e+05
8e+05
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
−4
−5
0e+00
4e+05
8e+05
genome coordinates
Synechocystis sp. PCC 6803
S^{A-T}_{plus}
0.0
−0.2
−0.4
−0.6
−0.8
0.0e+00
1.5e+06
3.0e+06
genome coordinates
S^{G-C}_{plus}
0.5
0.4
0.3
0.2
0.1
0.0
−0.1
0.0e+00
1.5e+06
3.0e+06
genome coordinates

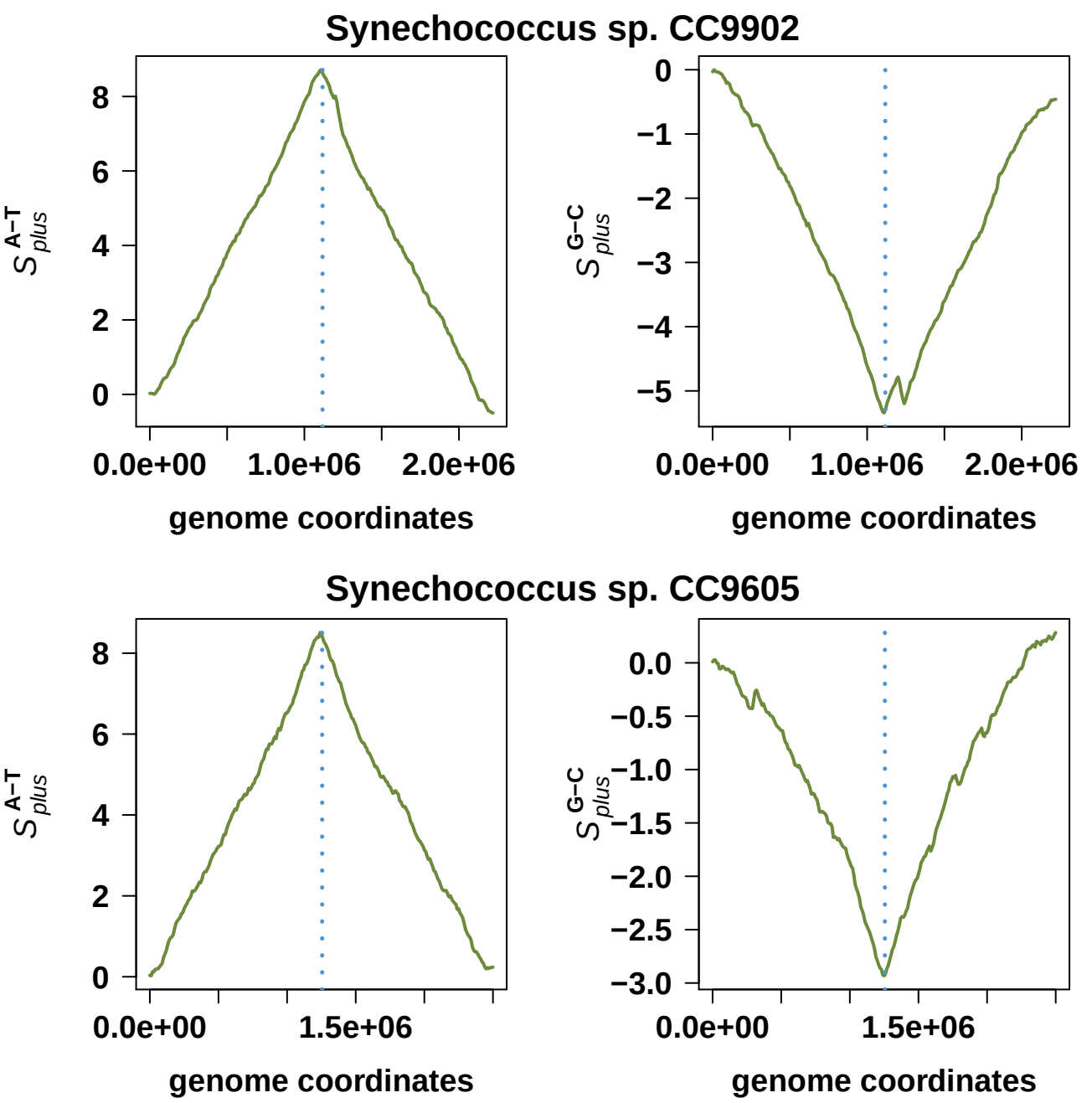

Nostoc sp. PCC 7120
0.0
−0.2
−0.4
−0.6
−0.8
−1.0
S^{A-T}_{plus}
0e+00
3e+06
6e+06
genome coordinates
1.0
0.5
0.0
S^{G-C}_{plus}
0e+00
3e+06
6e+06
genome coordinates
Thermosynechococcus elongatus BP−1
0.8
0.6
0.4
0.2
0.0
−0.2
S^{A-T}_{plus}
0.0e+00
1.5e+06
genome coordinates
0.2
0.1
0.0
−0.1
−0.2
S^{G-C}_{plus}
0.0e+00
1.5e+06
genome coordinates

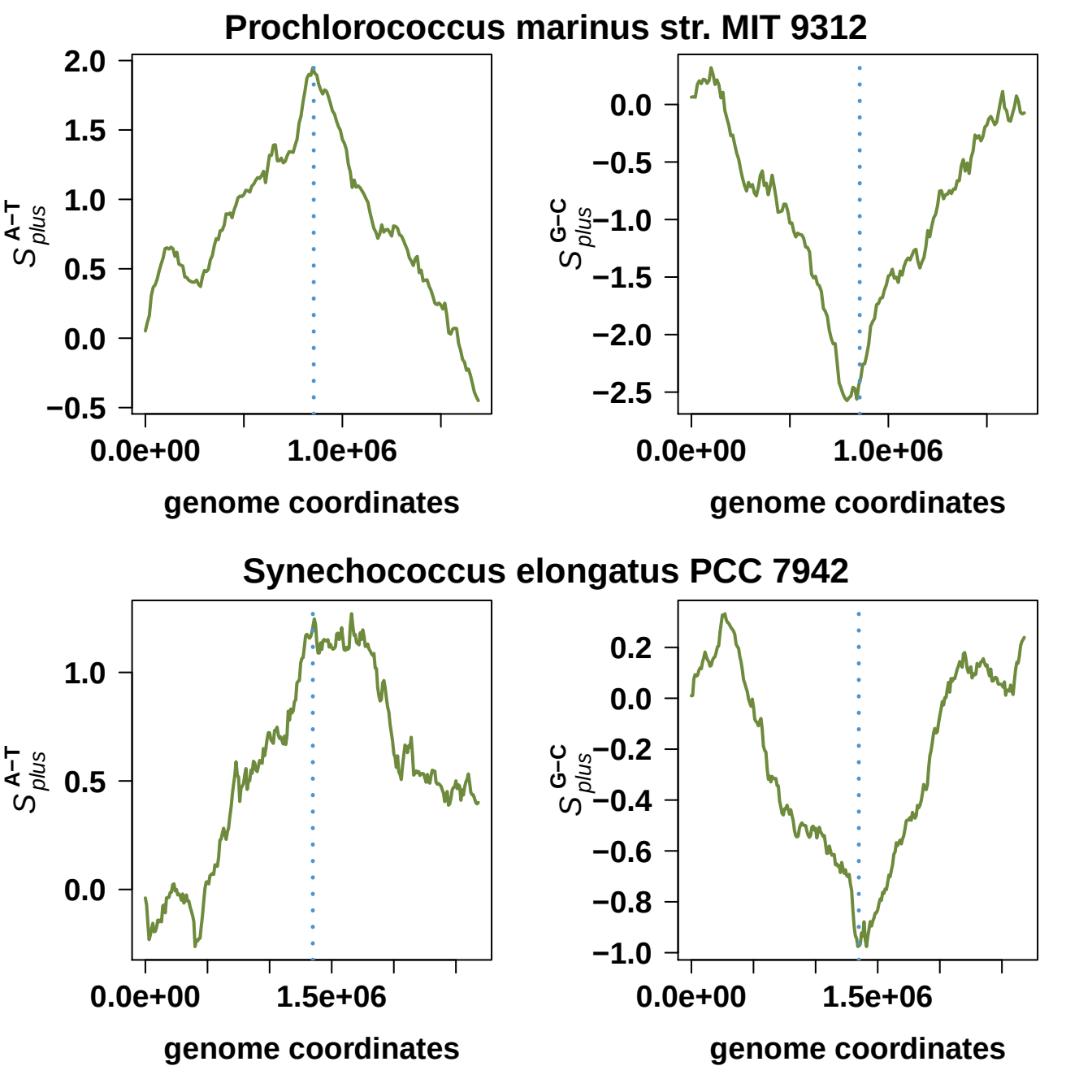

Prochlorococcus marinus subsp. marinus str. CCMP1375
S^{A-T}_{plus}
5
4
3
2
1
0
0.0e+00
1.0e+06
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
0.0e+00
1.0e+06
genome coordinates
Synechococcus sp. WH 8102
S^{A-T}_{plus}
6
5
4
3
2
1
0
−1
0.0e+00
1.0e+06
2.0e+06
genome coordinates
S^{G-C}_{plus}
0.0
−0.5
−1.0
−1.5
−2.0
−2.5
−3.0
−3.5
0.0e+00
1.0e+06
2.0e+06
genome coordinates

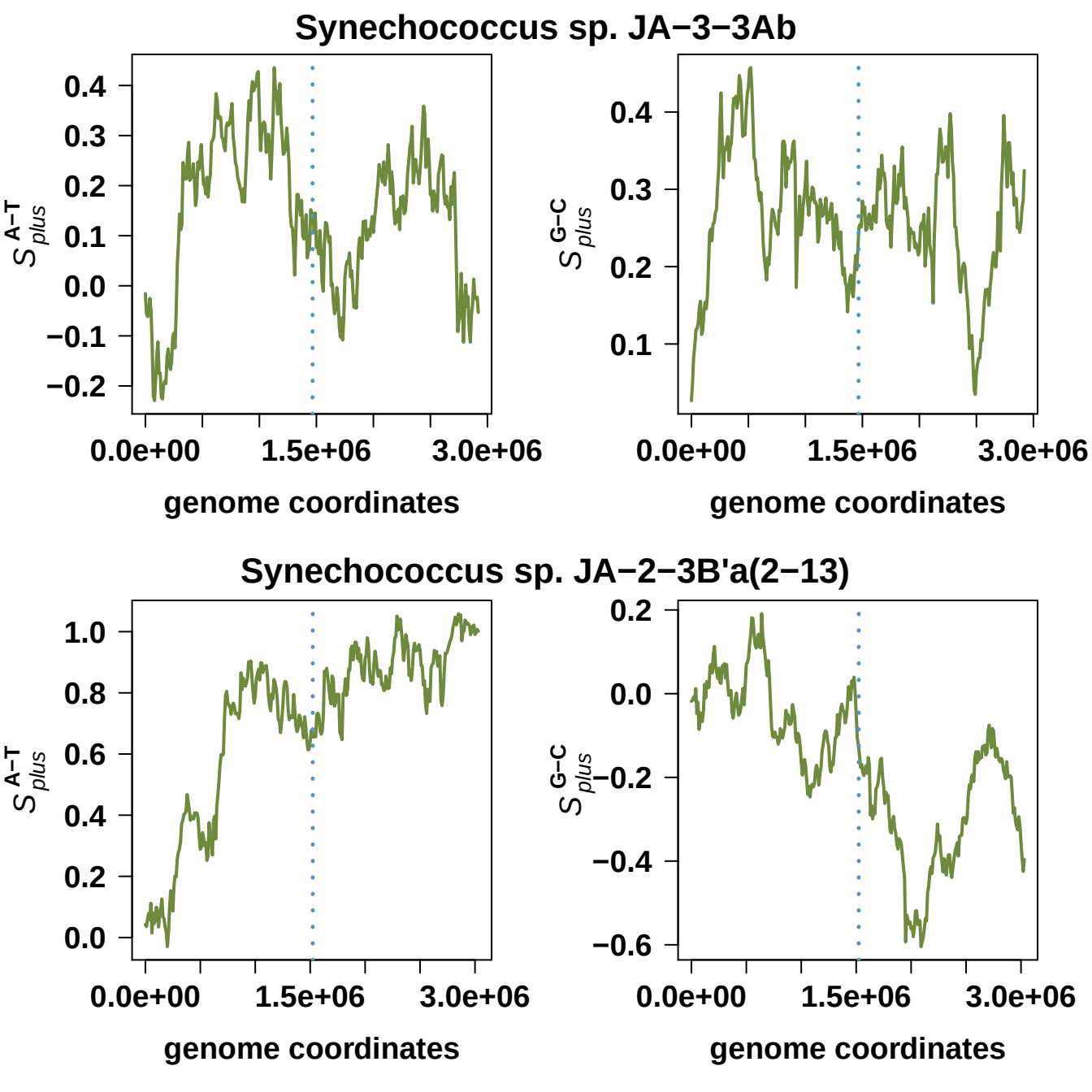

Prochlorococcus marinus str. MIT 9313
S^{A-T}_{plus}
12
10
8
6
4
2
0
0.0e+00
1.0e+06
2.0e+06
genome coordinates
S^{G-C}_{plus}
0
−2
−4
−6
−8
0.0e+00
1.0e+06
2.0e+06
genome coordinates
Prochlorococcus marinus subsp. pastoris str. CCMP1986
S^{A-T}_{plus}
1.5
1.0
0.5
0.0
−0.5
0.0e+00
1.0e+06
genome coordinates
S^{G-C}_{plus}
0.0
−0.5
−1.0
−1.5
−2.0
0.0e+00
1.0e+06
genome coordinates

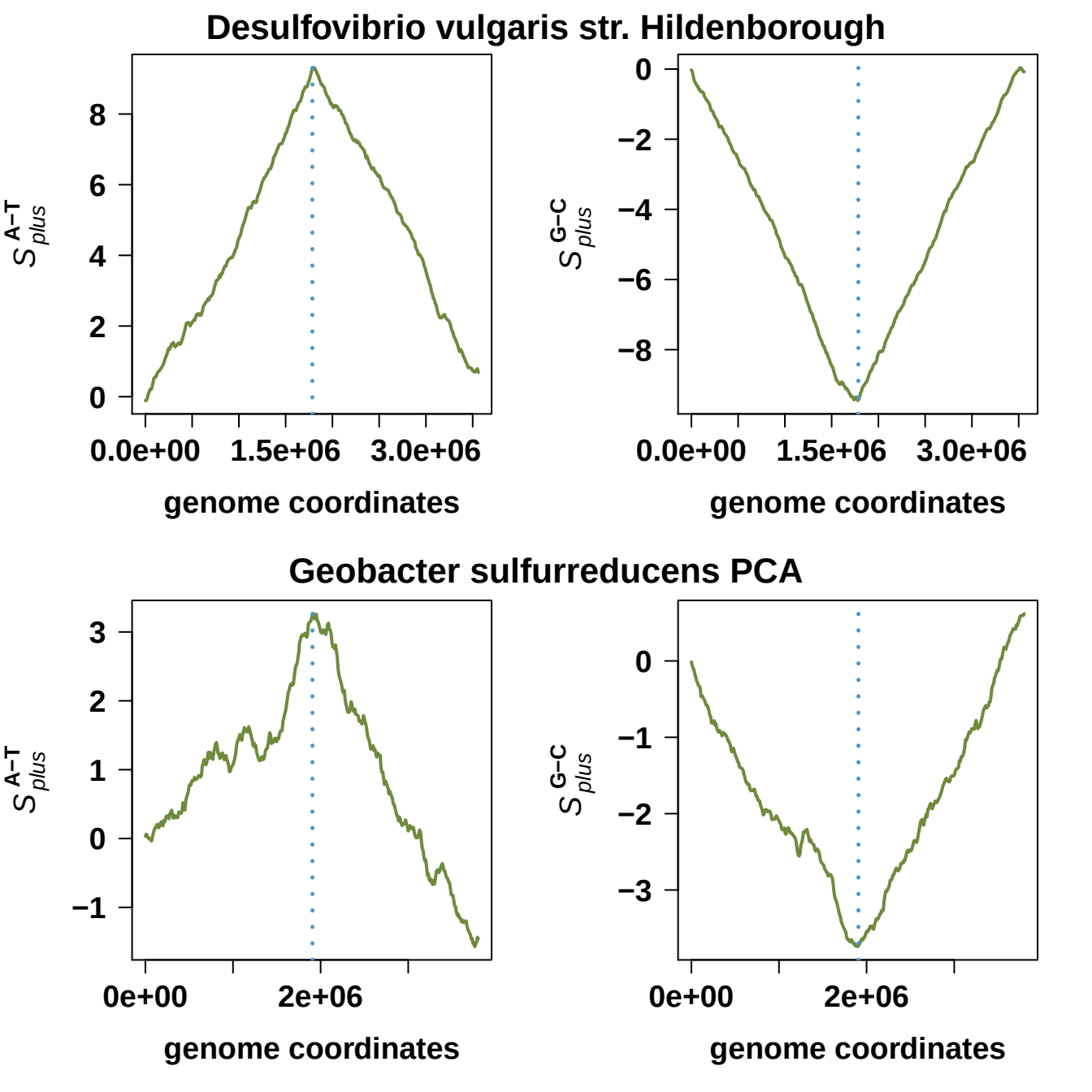

Gloeobacter violaceus PCC 7421
S^{A-T}_{plus}
1.5
1.0
0.5
0.0
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
0.0
−0.1
−0.2
−0.3
−0.4
−0.5
−0.6
−0.7
0e+00
2e+06
4e+06
genome coordinates
Synechococcus elongatus PCC 6301
S^{A-T}_{plus}
0.5
0.0
−0.5
0.0e+00
1.5e+06
genome coordinates
S^{G-C}_{plus}
0.2
0.0
−0.2
−0.4
−0.6
−0.8
−1.0
−1.2
0.0e+00
1.5e+06
genome coordinates

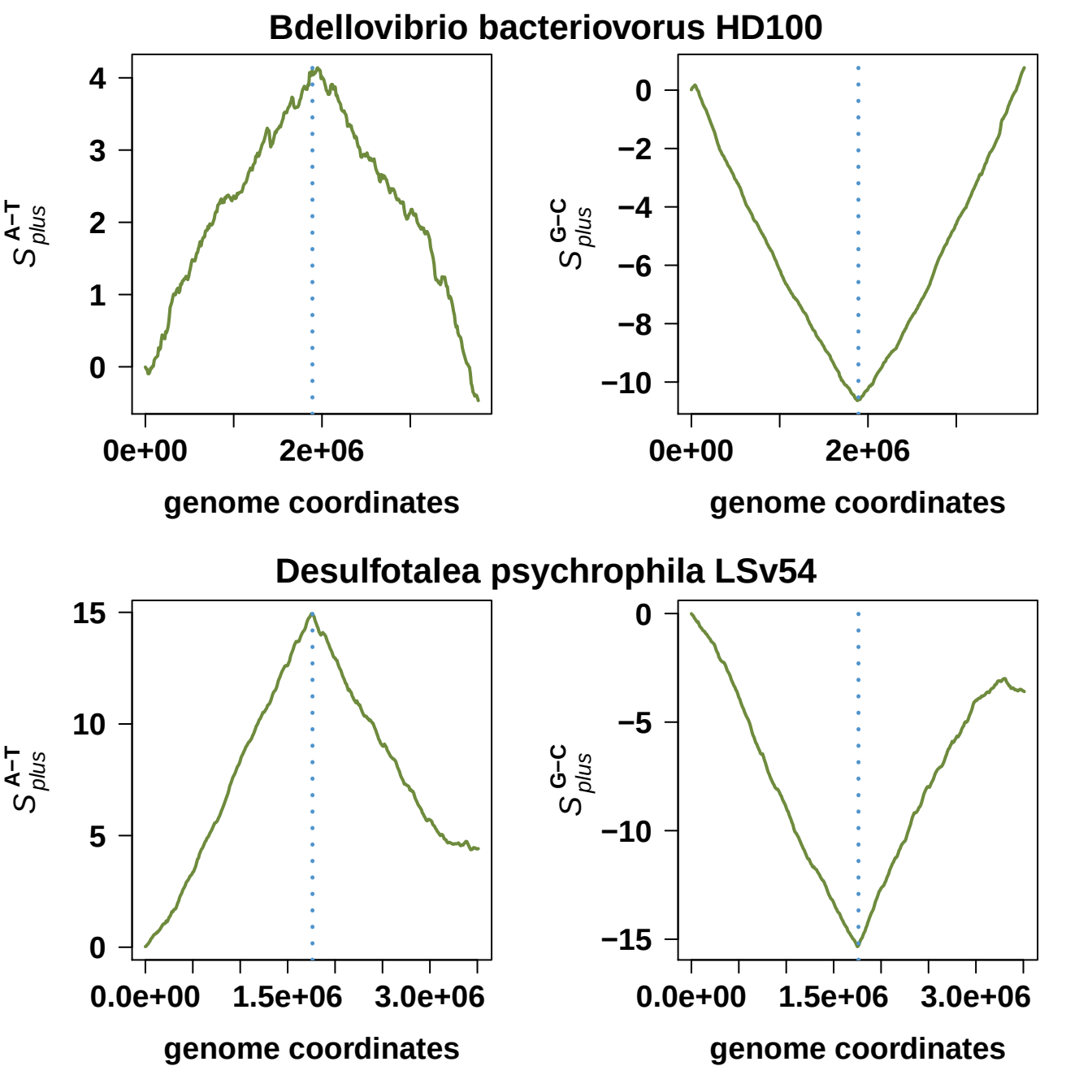

Prochlorococcus marinus str. NATL2A
S^{A-T}_{plus}
4
3
2
1
0
0.0e+00
1.0e+06
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
0.0e+00
1.0e+06
genome coordinates
Anabaena variabilis ATCC 29413
S^{A-T}_{plus}
2.0
1.5
1.0
0.5
0.0
0e+00
3e+06
6e+06
genome coordinates
S^{G-C}_{plus}
1.2
1.0
0.8
0.6
0.4
0.2
0.0
0e+00
3e+06
6e+06
genome coordinates

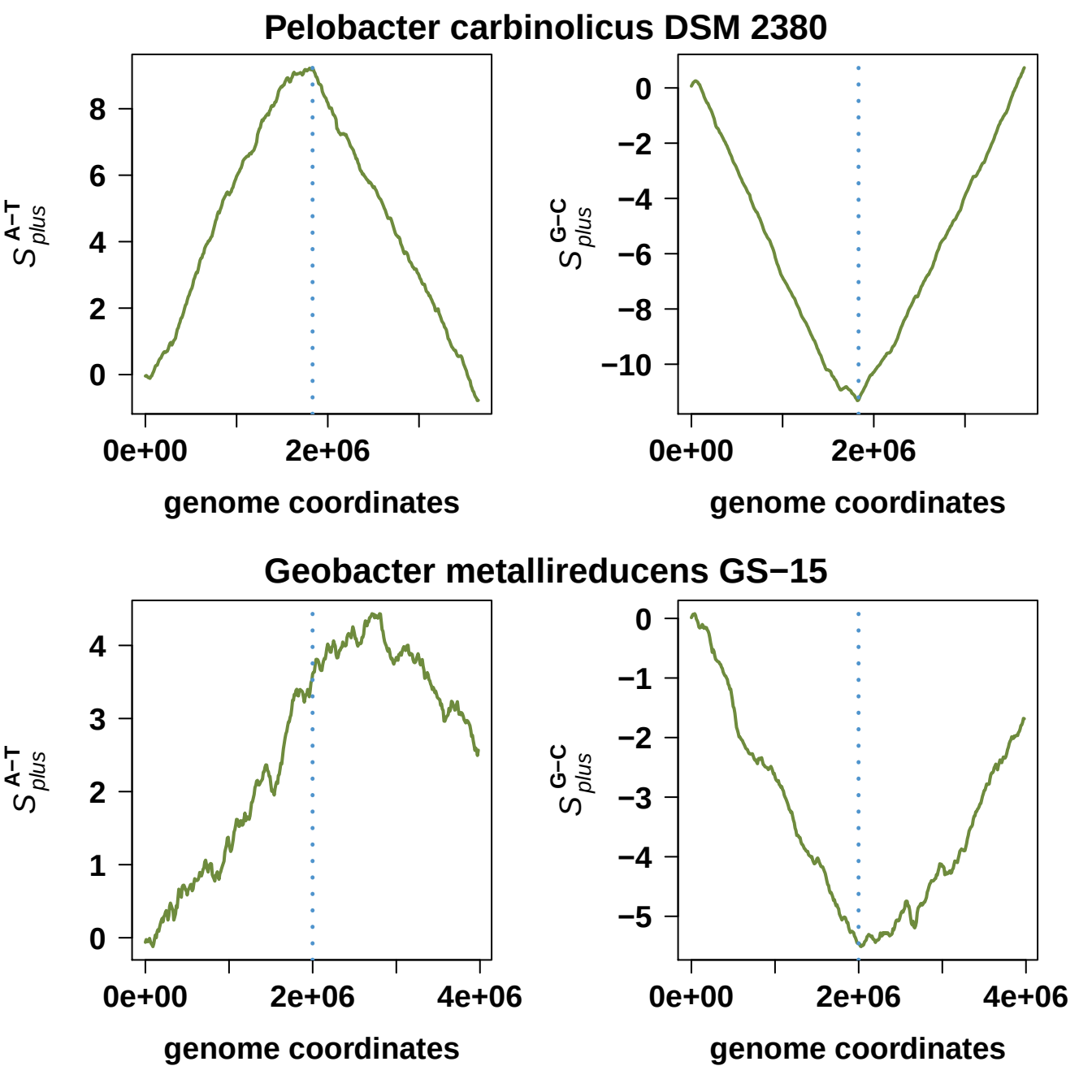

Synechococcus sp. CC9902
S^{A-T}_{plus}
8
6
4
2
0
0.0e+00
1.0e+06
2.0e+06
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
−4
−5
0.0e+00
1.0e+06
2.0e+06
genome coordinates
Synechococcus sp. CC9605
S^{A-T}_{plus}
8
6
4
2
0
0.0e+00
1.5e+06
genome coordinates
S^{G-C}_{plus}
0.0
−0.5
−1.0
−1.5
−2.0
−2.5
−3.0
0.0e+00
1.5e+06
genome coordinates

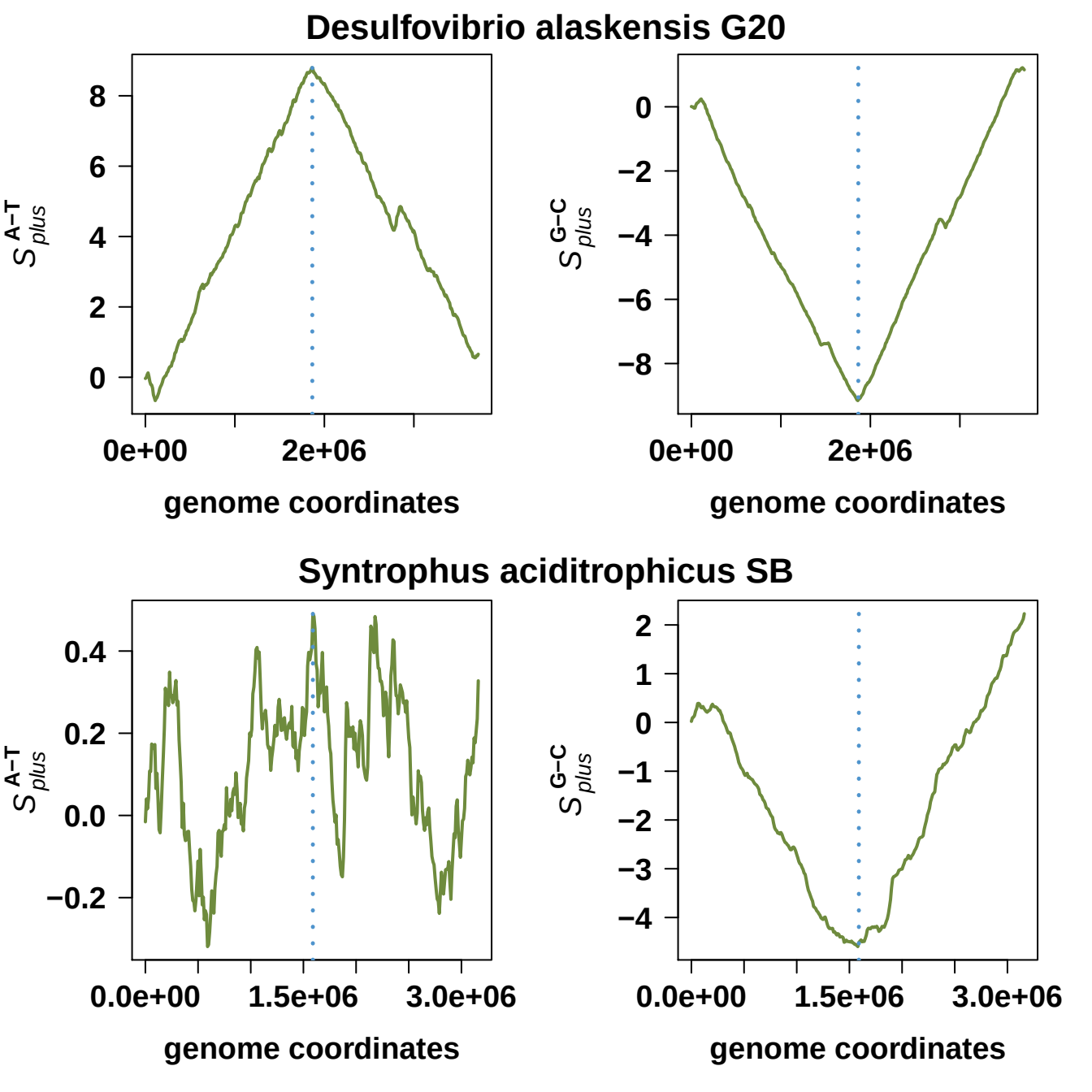

Prochlorococcus marinus str. MIT 9312
2.0
1.5
1.0
0.5
0.0
−0.5
S^{A-T}_{plus}
0.0e+00
1.0e+06
genome coordinates
0.0
−0.5
−1.0
−1.5
−2.0
−2.5
S^{G-C}_{plus}
0.0e+00
1.0e+06
genome coordinates
Synechococcus elongatus PCC 7942
1.0
0.5
0.0
S^{A-T}_{plus}
0.0e+00
1.5e+06
genome coordinates
0.2
0.0
−0.2
−0.4
−0.6
−0.8
−1.0
S^{G-C}_{plus}
0.0e+00
1.5e+06
genome coordinates

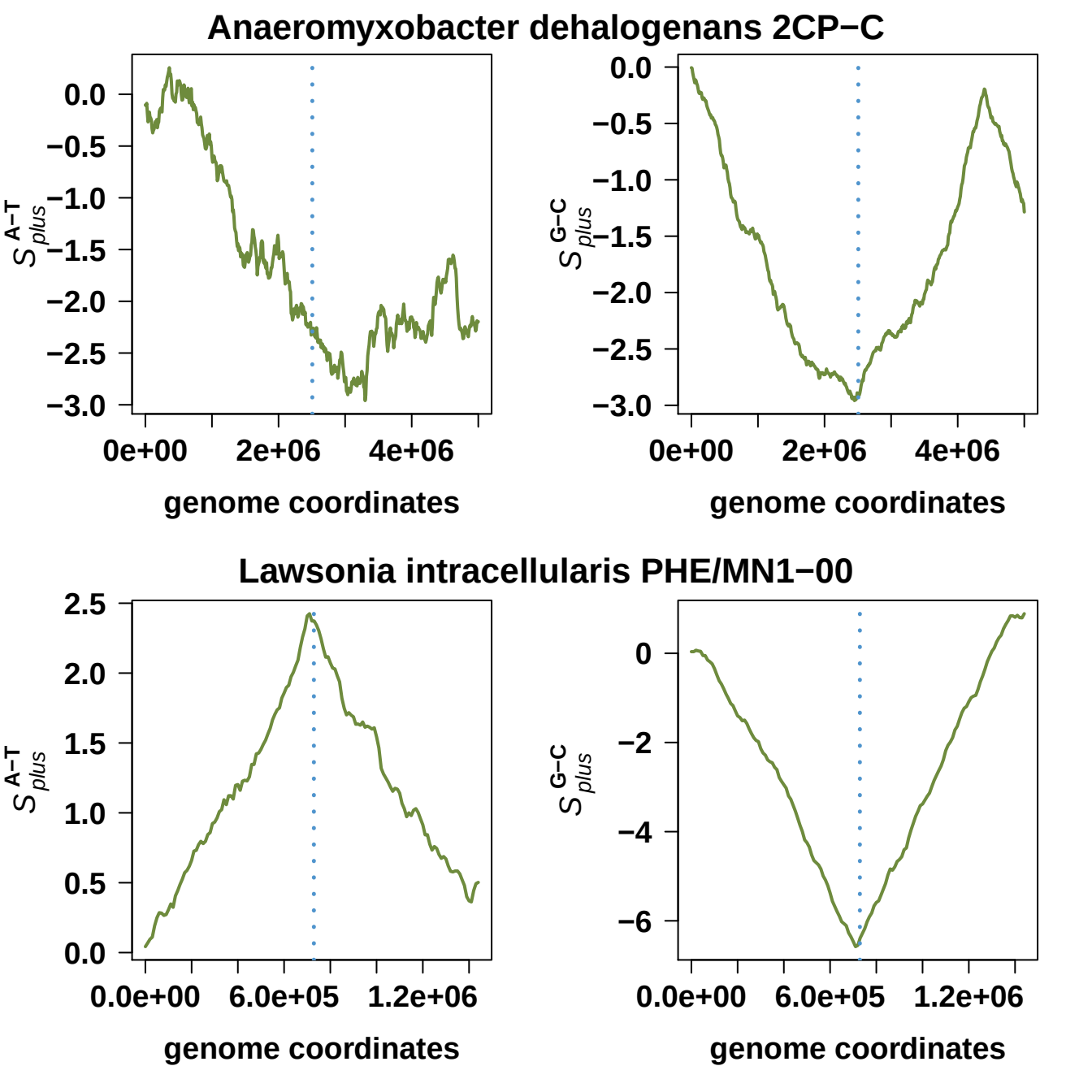

Synechococcus sp. JA−3−3Ab
S^{A-T}_{plus}
0.4
0.3
0.2
0.1
0.0
−0.1
−0.2
0.0e+00
1.5e+06
3.0e+06
genome coordinates
S^{G-C}_{plus}
0.4
0.3
0.2
0.1
0.0e+00
1.5e+06
3.0e+06
genome coordinates
Synechococcus sp. JA−2−3B'a(2−13)
S^{A-T}_{plus}
1.0
0.8
0.6
0.4
0.2
0.0
0.0e+00
1.5e+06
3.0e+06
genome coordinates
S^{G-C}_{plus}
0.2
0.0
−0.2
−0.4
−0.6
0.0e+00
1.5e+06
3.0e+06
genome coordinates

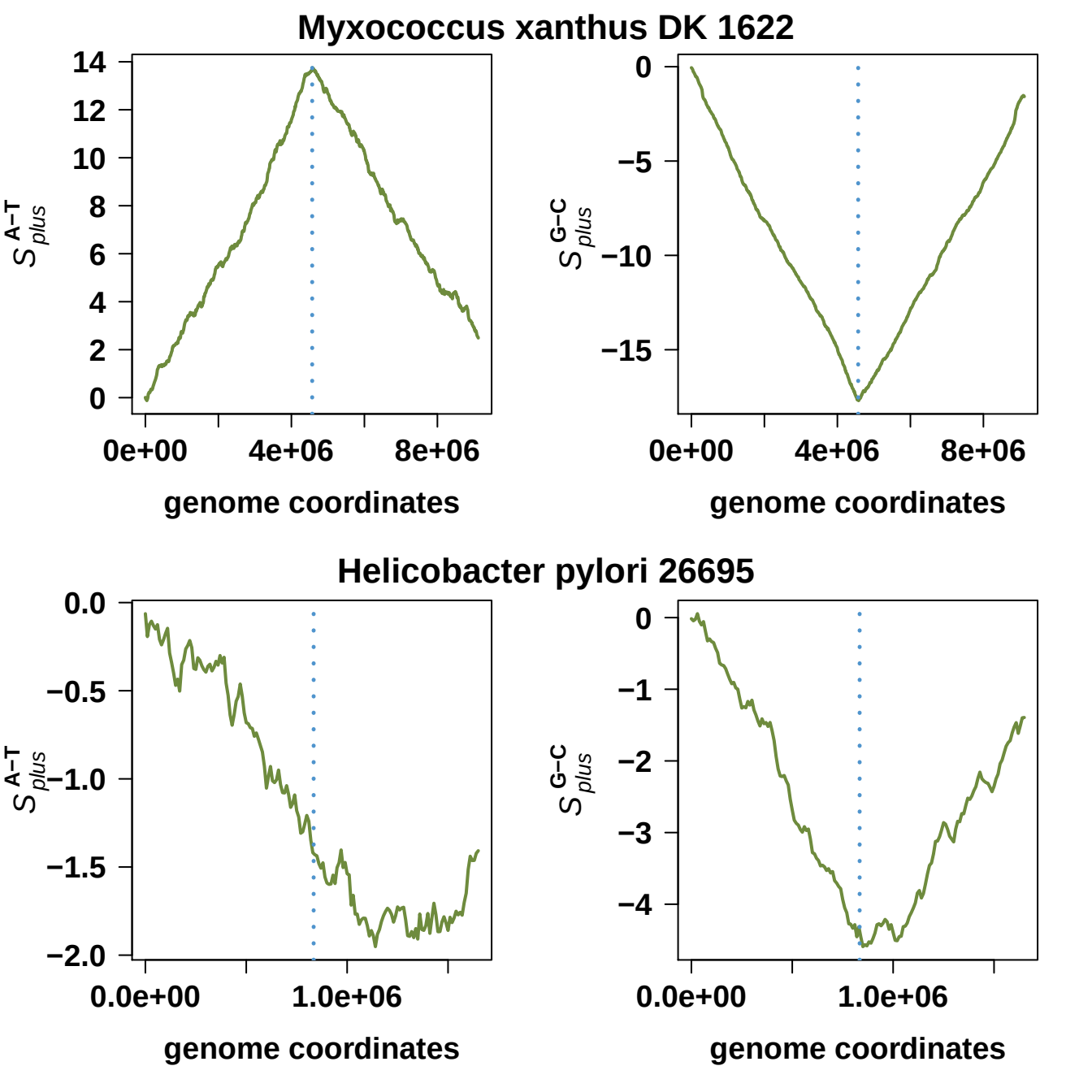

Desulfovibrio vulgaris str. Hildenborough
S^{A-T}_{plus}
8
6
4
2
0
0.0e+00
1.5e+06
3.0e+06
genome coordinates
S^{G-C}_{plus}
0
−2
−4
−6
−8
0.0e+00
1.5e+06
3.0e+06
genome coordinates
Geobacter sulfurreducens PCA
S^{A-T}_{plus}
3
2
1
0
−1
0e+00
2e+06
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
0e+00
2e+06
genome coordinates

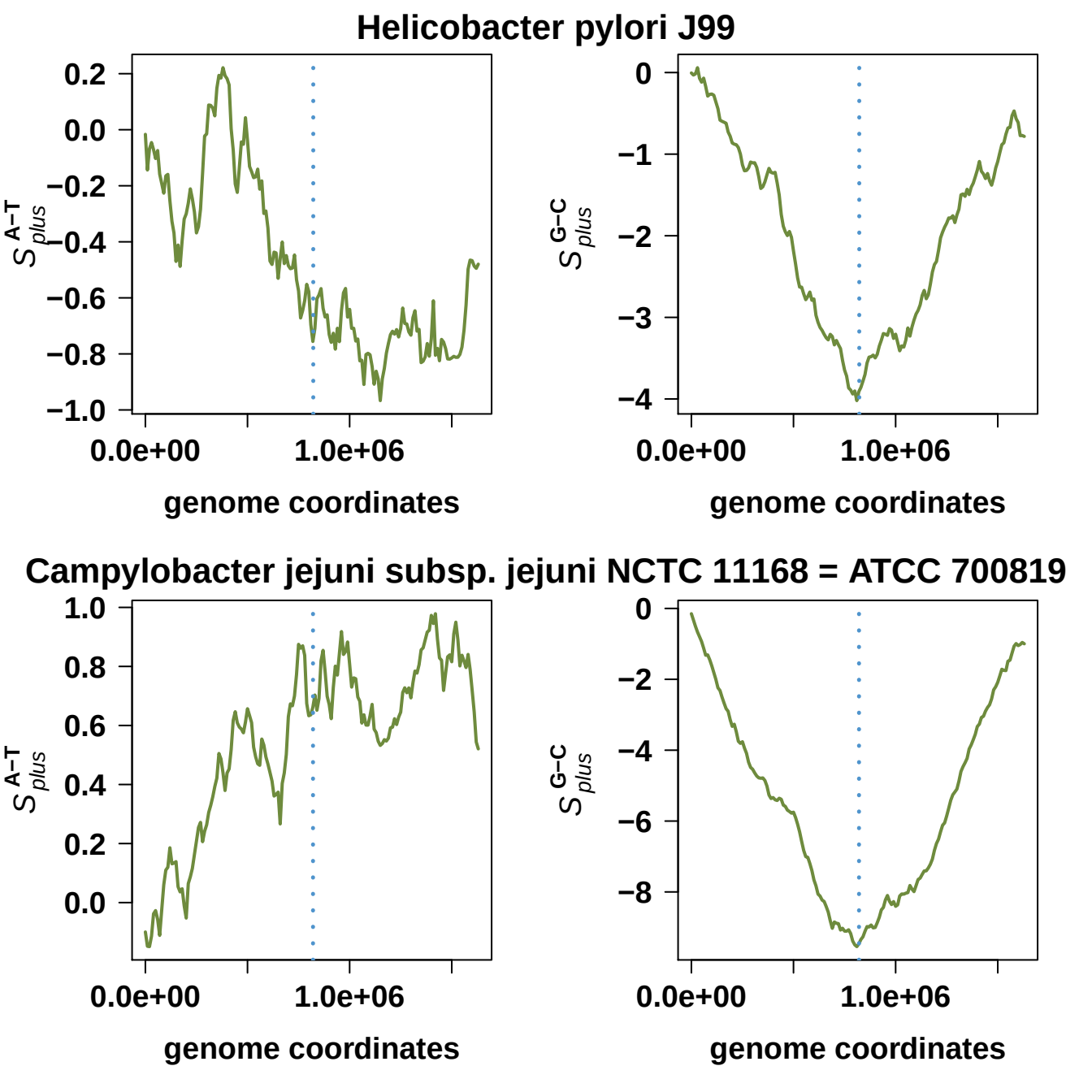

Bdellovibrio bacteriovorus HD100
S^{A-T}_{plus}
4
3
2
1
0
0e+00
2e+06
genome coordinates
S^{G-C}_{plus}
0
−2
−4
−6
−8
−10
0e+00
2e+06
genome coordinates
Desulfotalea psychrophila LSv54
S^{A-T}_{plus}
15
10
5
0
0.0e+00
1.5e+06
3.0e+06
genome coordinates
S^{G-C}_{plus}
0
−5
−10
−15
0.0e+00
1.5e+06
3.0e+06
genome coordinates

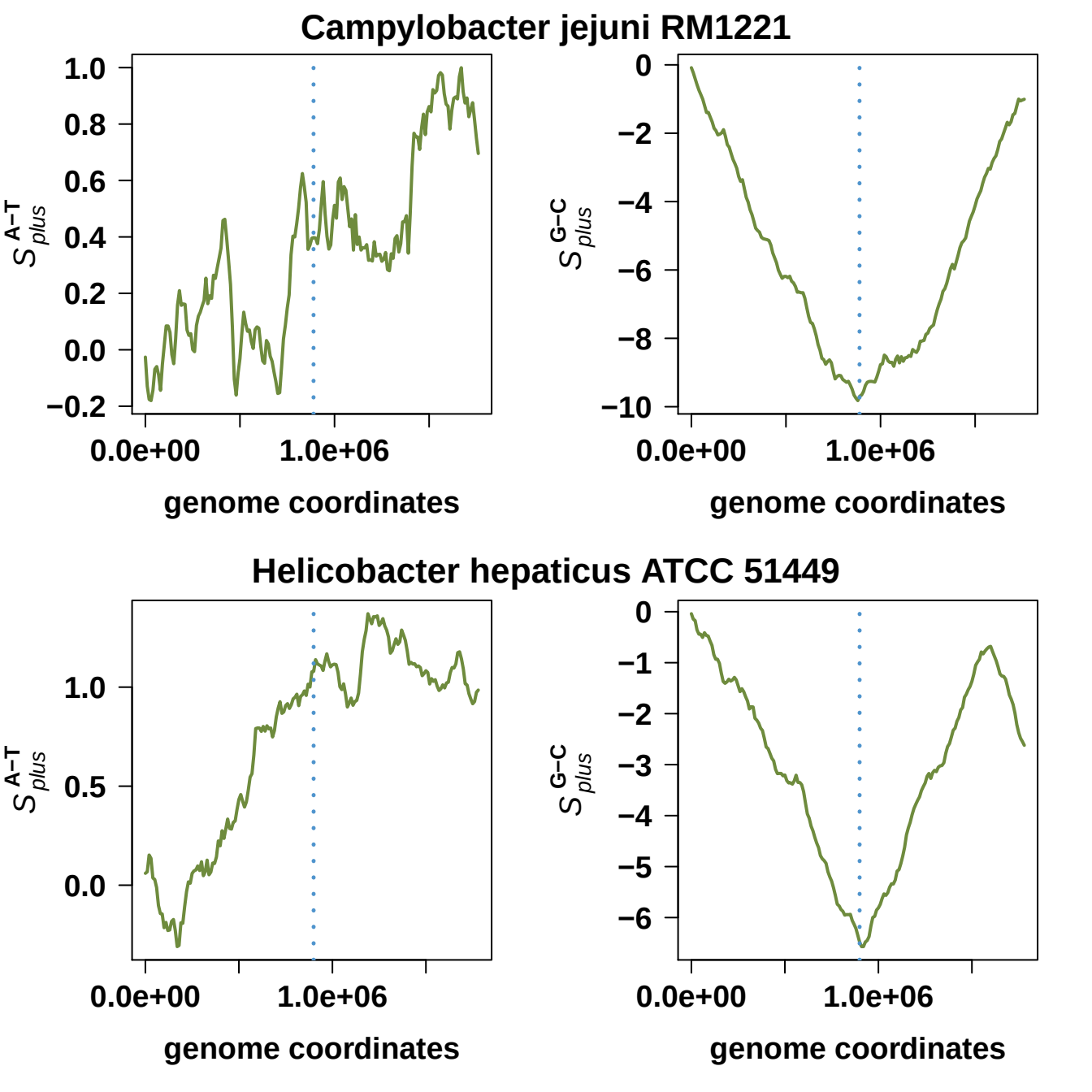

Pelobacter carbinolicus DSM 2380
S^{A-T}_{plus}
8
6
4
2
0
0e+00
2e+06
genome coordinates
S^{G-C}_{plus}
0
−2
−4
−6
−8
−10
0e+00
2e+06
genome coordinates
Geobacter metallireducens GS−15
S^{A-T}_{plus}
4
3
2
1
0
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
−4
−5
0e+00
2e+06
4e+06
genome coordinates

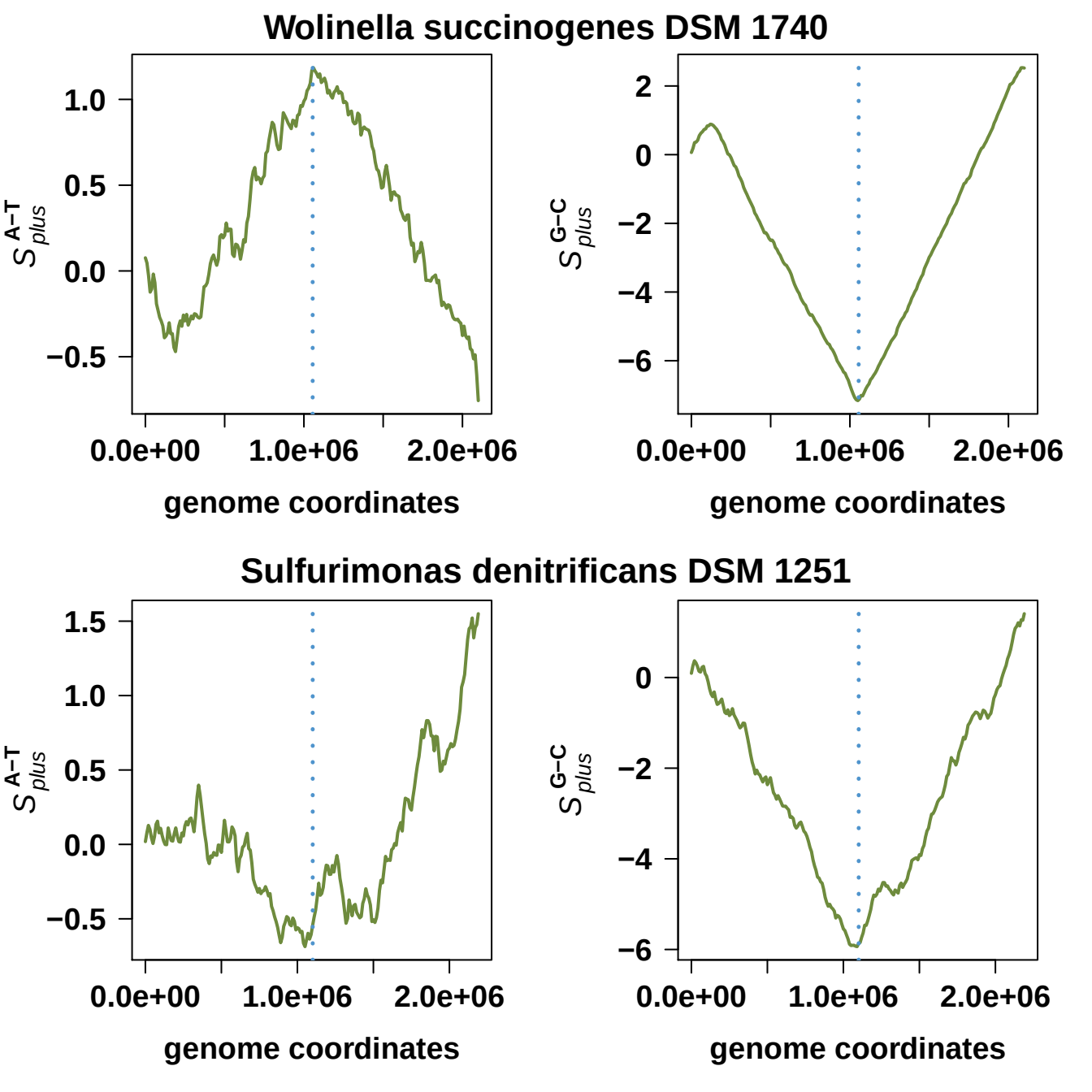

Desulfovibrio alaskensis G20
S^{A-T}_{plus}
8
6
4
2
0
0e+00
2e+06
genome coordinates
S^{G-C}_{plus}
0
−2
−4
−6
−8
0e+00
2e+06
genome coordinates
Syntrophus aciditrophicus SB
S^{A-T}_{plus}
0.4
0.2
0.0
−0.2
0.0e+00
1.5e+06
3.0e+06
genome coordinates
S^{G-C}_{plus}
2
1
0
−1
−2
−3
−4
0.0e+00
1.5e+06
3.0e+06
genome coordinates

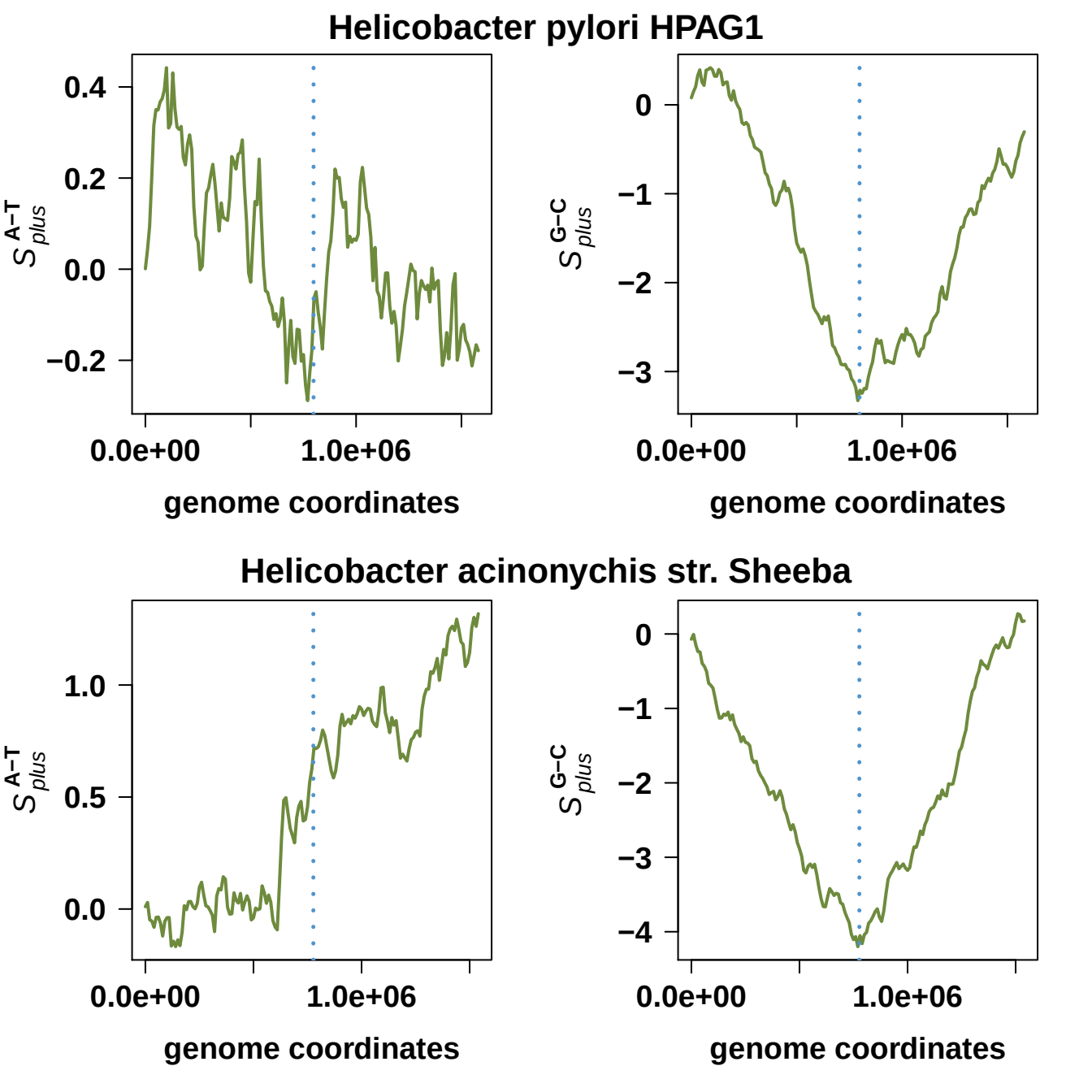

Anaeromyxobacter dehalogenans 2CP−C
S^{A-T}_{plus}
0.0
−0.5
−1.0
−1.5
−2.0
−2.5
−3.0
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
0.0
−0.5
−1.0
−1.5
−2.0
−2.5
−3.0
0e+00
2e+06
4e+06
genome coordinates
Lawsonia intracellularis PHE/MN1−00
S^{A-T}_{plus}
2.5
2.0
1.5
1.0
0.5
0.0
0.0e+00
6.0e+05
1.2e+06
genome coordinates
S^{G-C}_{plus}
0
−2
−4
−6
0.0e+00
6.0e+05
1.2e+06
genome coordinates

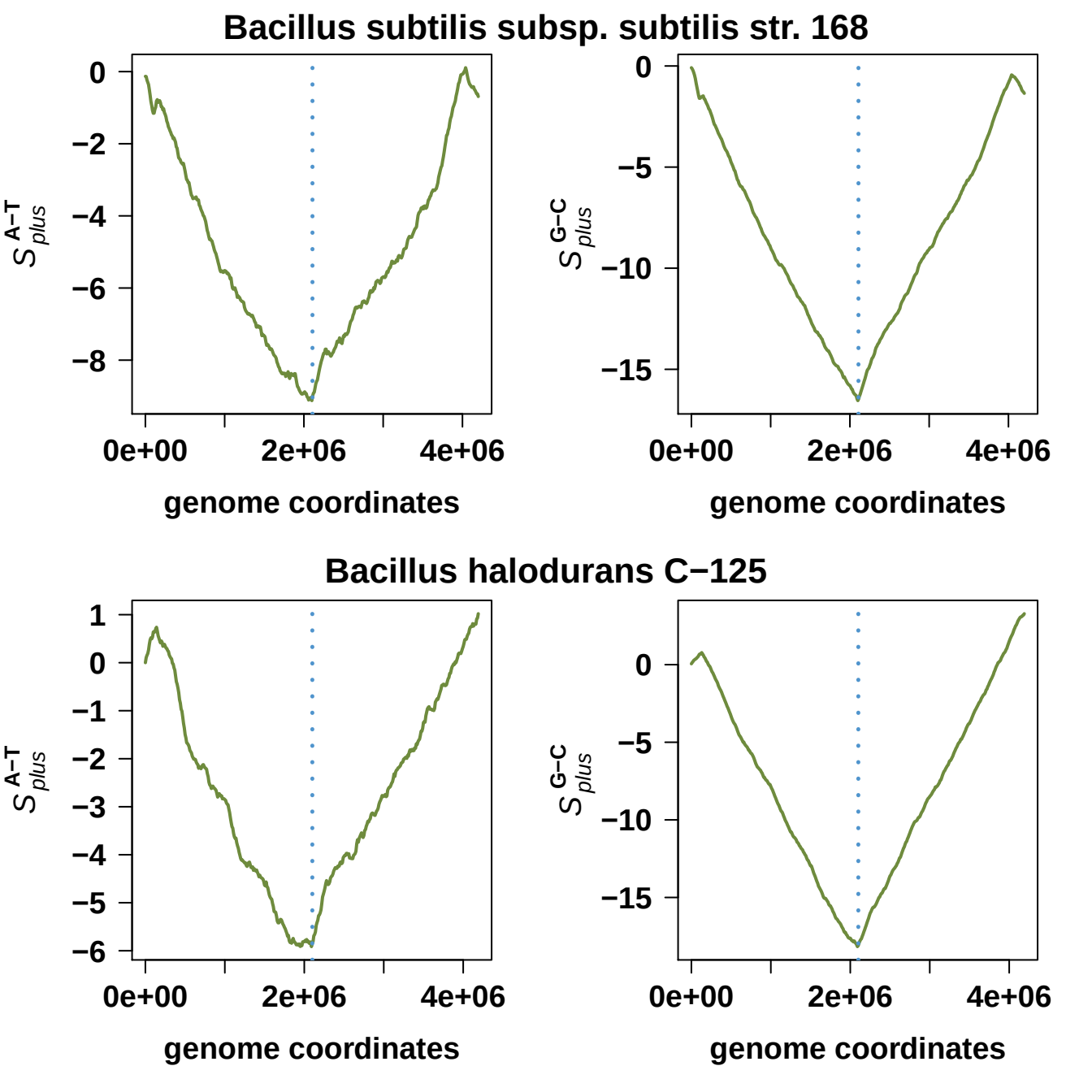

Myxococcus xanthus DK 1622
S^{A-T}_{plus}
14
12
10
8
6
4
2
0
0e+00
4e+06
8e+06
genome coordinates
S^{G-C}_{plus}
0
−5
−10
−15
0e+00
4e+06
8e+06
genome coordinates
Helicobacter pylori 26695
S^{A-T}_{plus}
0.0
−0.5
−1.0
−1.5
−2.0
0.0e+00
1.0e+06
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
−4
0.0e+00
1.0e+06
genome coordinates

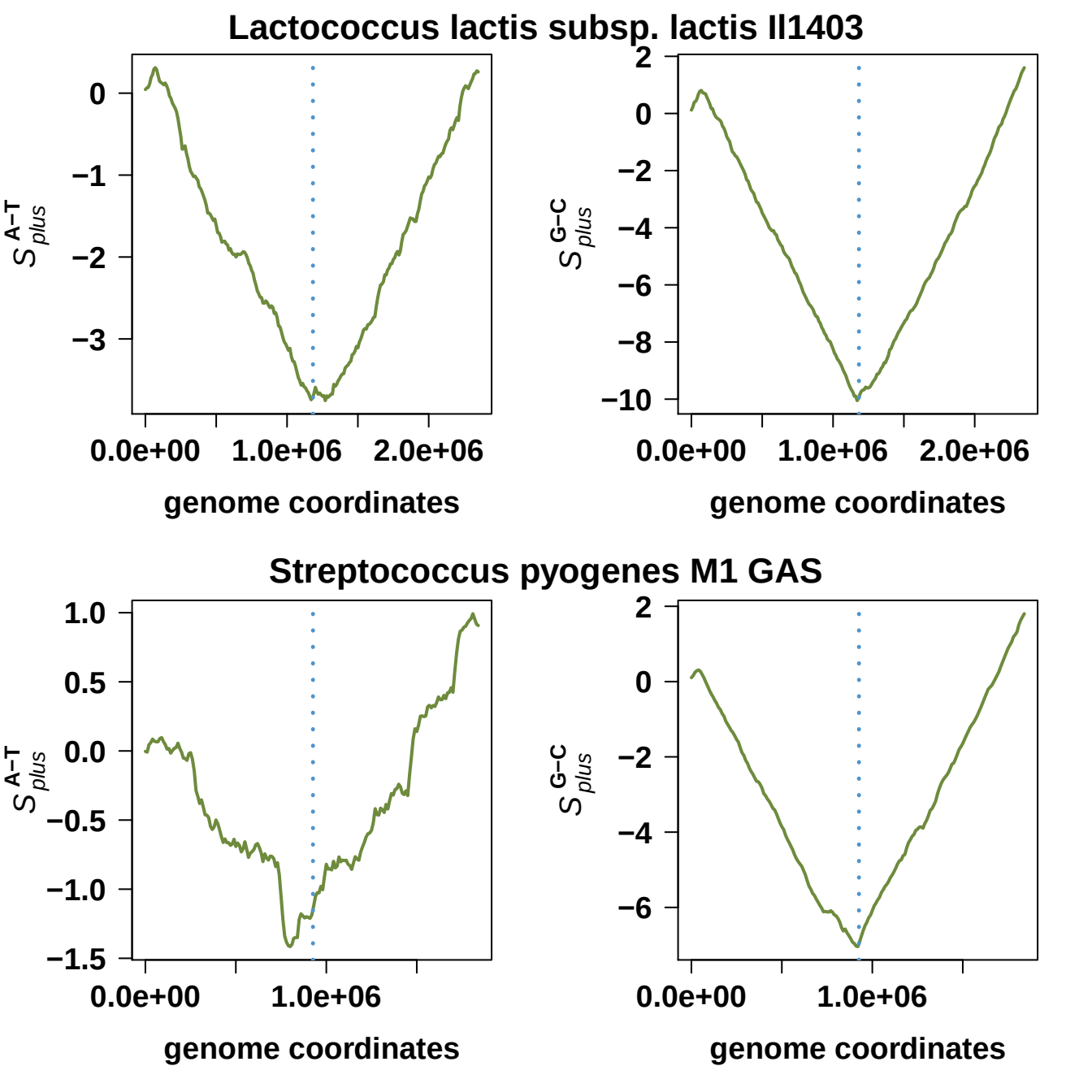

Helicobacter pylori J99
0.2
0.0
−0.2
−0.4
−0.6
−0.8
−1.0
S^{A-T}_{plus}
0.0e+00
1.0e+06
genome coordinates
0
−1
−2
−3
−4
S^{G-C}_{plus}
0.0e+00
1.0e+06
genome coordinates
Campylobacter jejuni subsp. jejuni NCTC 11168 = ATCC 700819
1.0
0.8
0.6
0.4
0.2
0.0
S^{A-T}_{plus}
0.0e+00
1.0e+06
genome coordinates
0
−2
−4
−6
−8
S^{G-C}_{plus}
0.0e+00
1.0e+06
genome coordinates

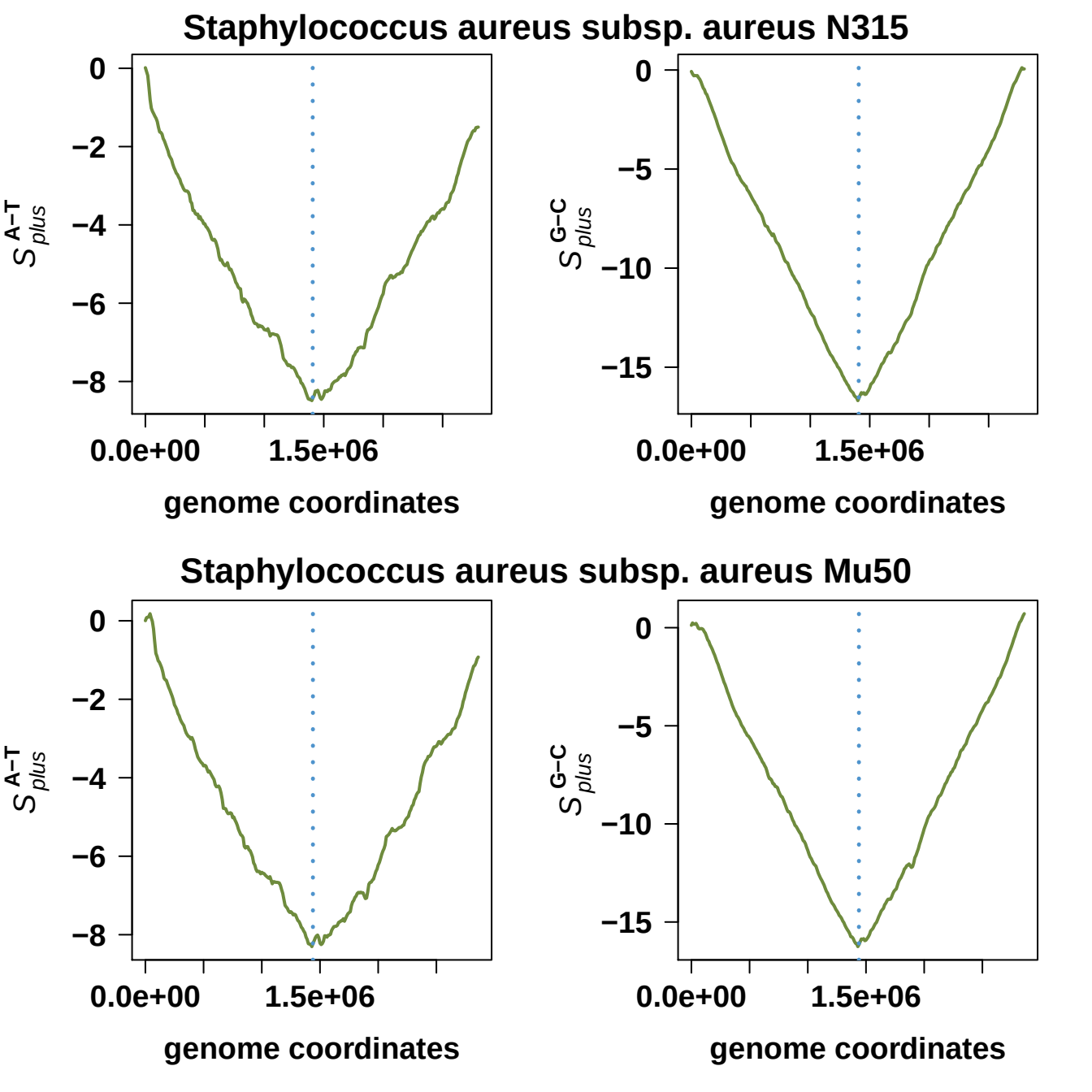

Campylobacter jejuni RM1221
1.0
0.8
0.6
0.4
0.2
0.0
−0.2
S^{A-T}_{plus}
0.0e+00
1.0e+06
genome coordinates
0
−2
−4
−6
−8
−10
S^{G-C}_{plus}
0.0e+00
1.0e+06
genome coordinates
Helicobacter hepaticus ATCC 51449
1.0
0.5
0.0
S^{A-T}_{plus}
0.0e+00
1.0e+06
genome coordinates
0
−1
−2
−3
−4
−5
−6
S^{G-C}_{plus}
0.0e+00
1.0e+06
genome coordinates

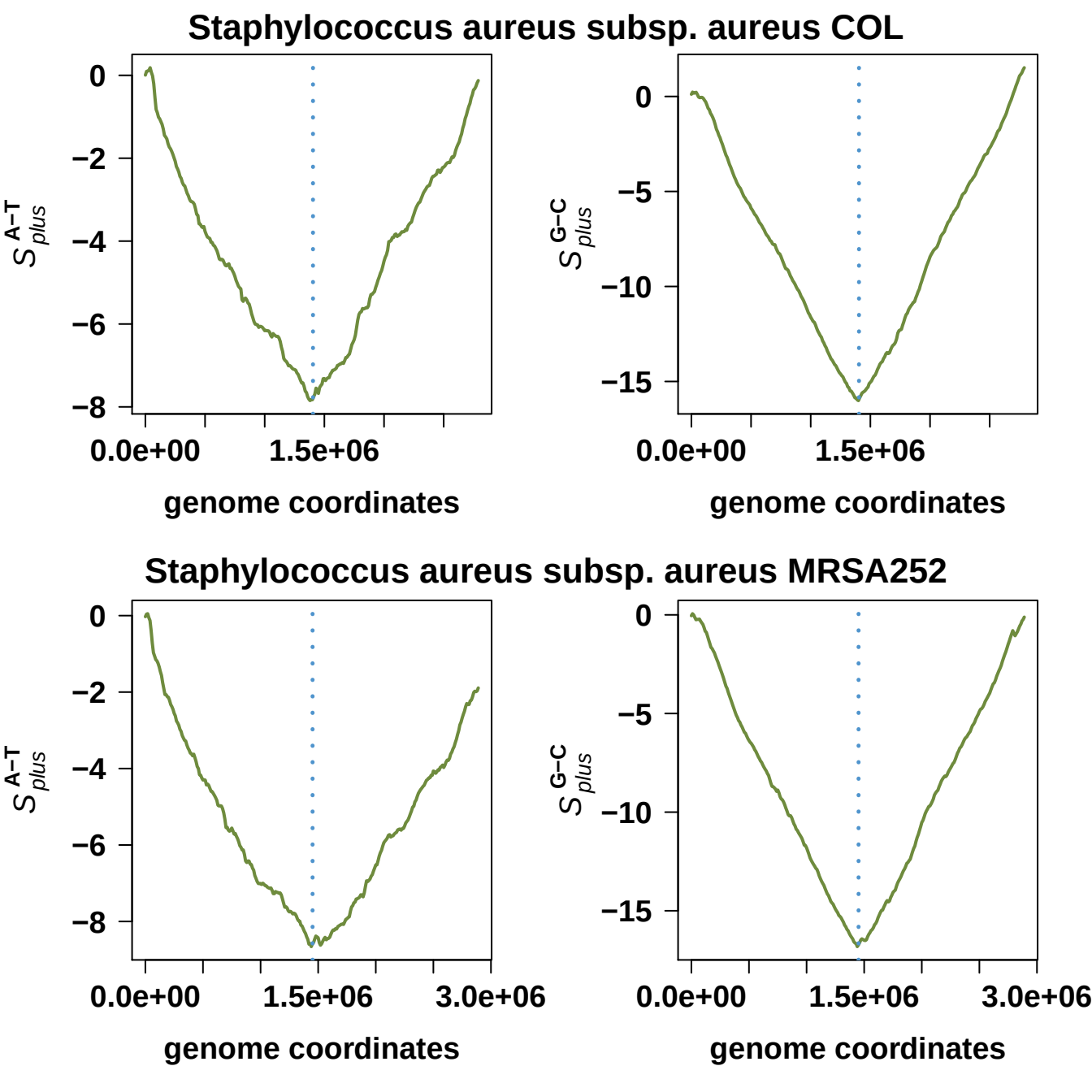

Wolinella succinogenes DSM 1740
S^{A-T}_{plus}
1.0
0.5
0.0
−0.5
0.0e+00
1.0e+06
2.0e+06
genome coordinates
S^{G-C}_{plus}
2
0
−2
−4
−6
0.0e+00
1.0e+06
2.0e+06
genome coordinates
Sulfurimonas denitrificans DSM 1251
S^{A-T}_{plus}
1.5
1.0
0.5
0.0
−0.5
0.0e+00
1.0e+06
2.0e+06
genome coordinates
S^{G-C}_{plus}
0
−2
−4
−6
0.0e+00
1.0e+06
2.0e+06
genome coordinates

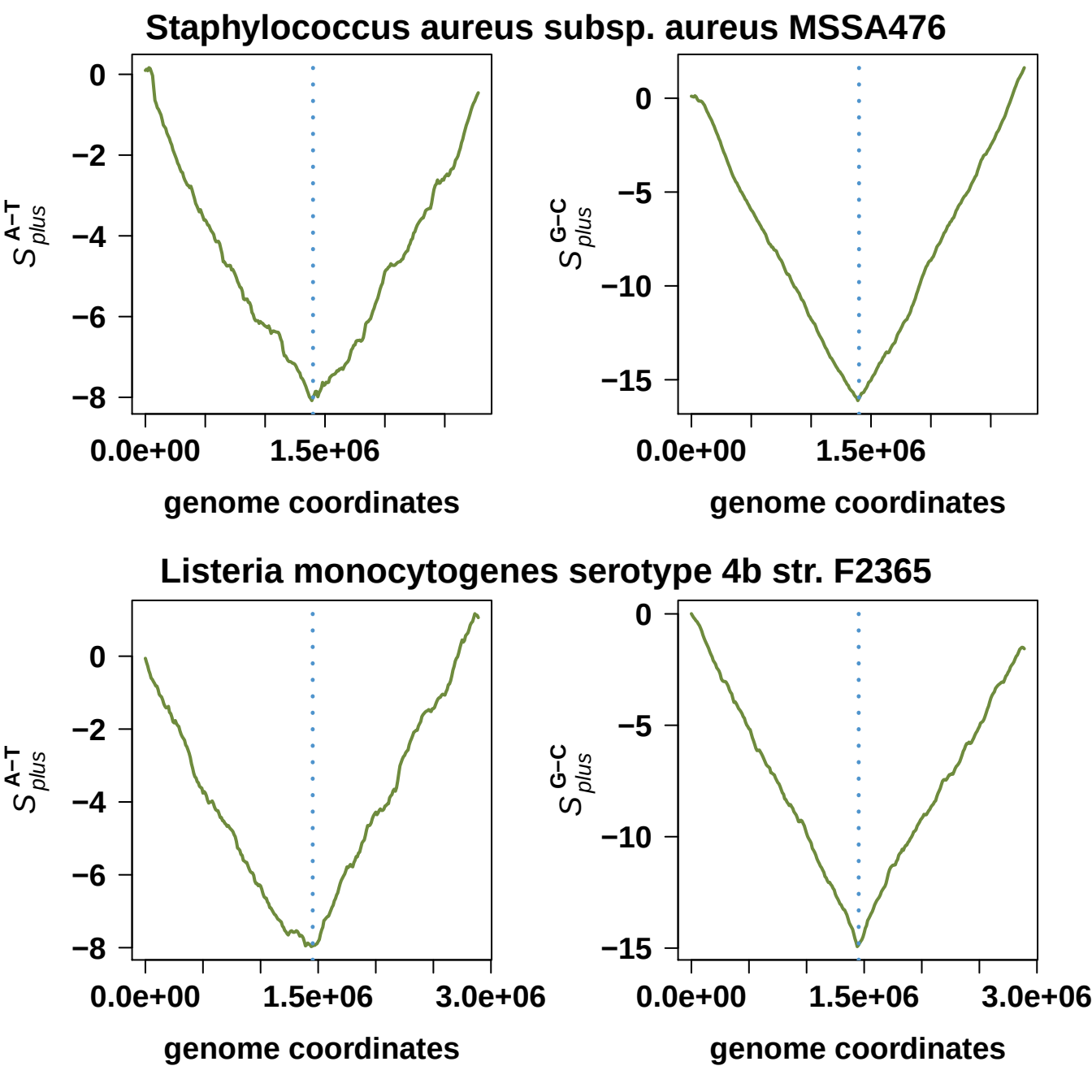

Helicobacter pylori HPAG1
S^{A-T}_{plus}
0.4
0.2
0.0
−0.2
0.0e+00
1.0e+06
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
0.0e+00
1.0e+06
genome coordinates
Helicobacter acinonychis str. Sheeba
S^{A-T}_{plus}
1.0
0.5
0.0
0.0e+00
1.0e+06
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
−4
0.0e+00
1.0e+06
genome coordinates

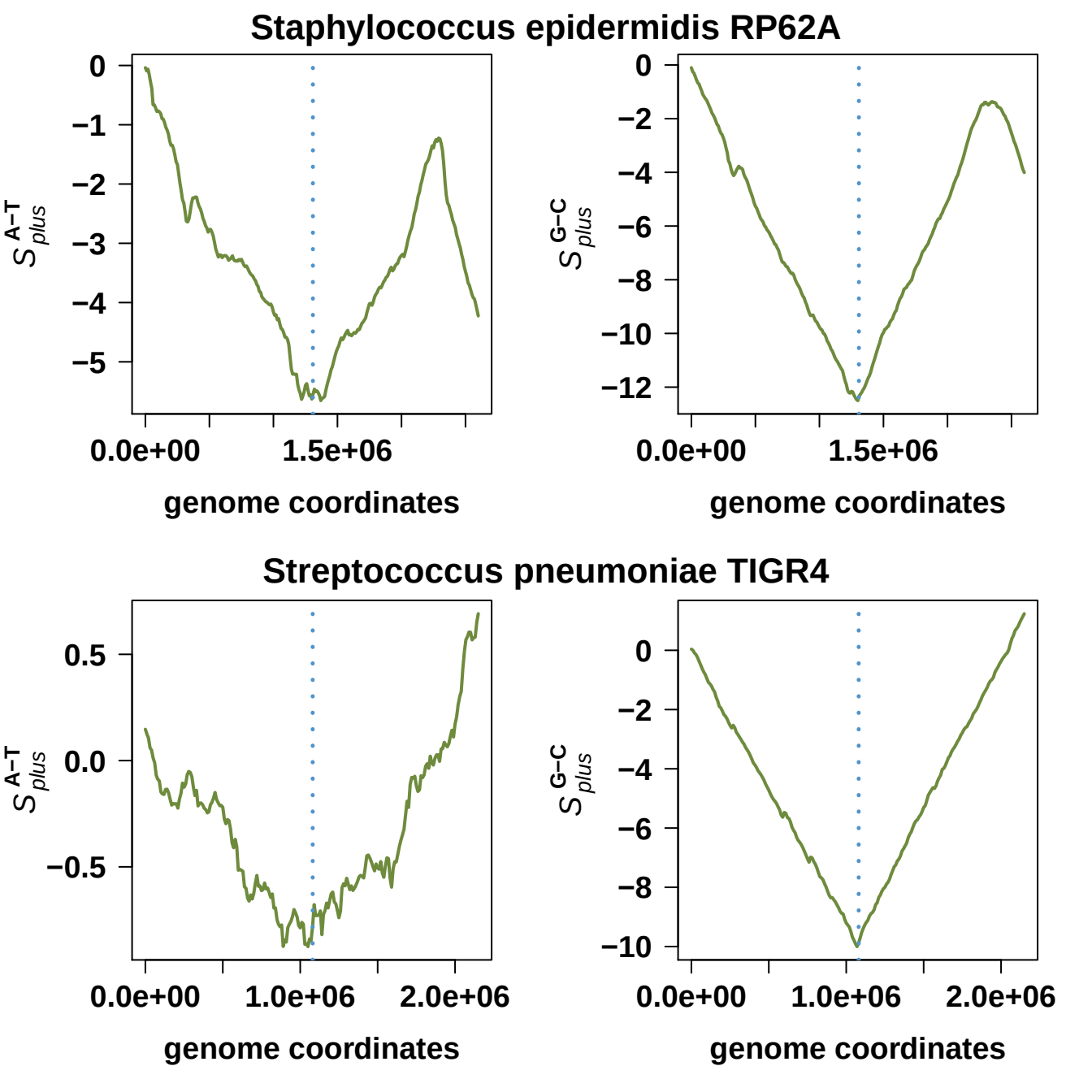

Bacillus subtilis subsp. subtilis str. 168
S^{A-T}_{plus}
0
−2
−4
−6
−8
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
0
−5
−10
−15
0e+00
2e+06
4e+06
genome coordinates
Bacillus halodurans C−125
S^{A-T}_{plus}
1
0
−1
−2
−3
−4
−5
−6
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
0
−5
−10
−15
0e+00
2e+06
4e+06
genome coordinates

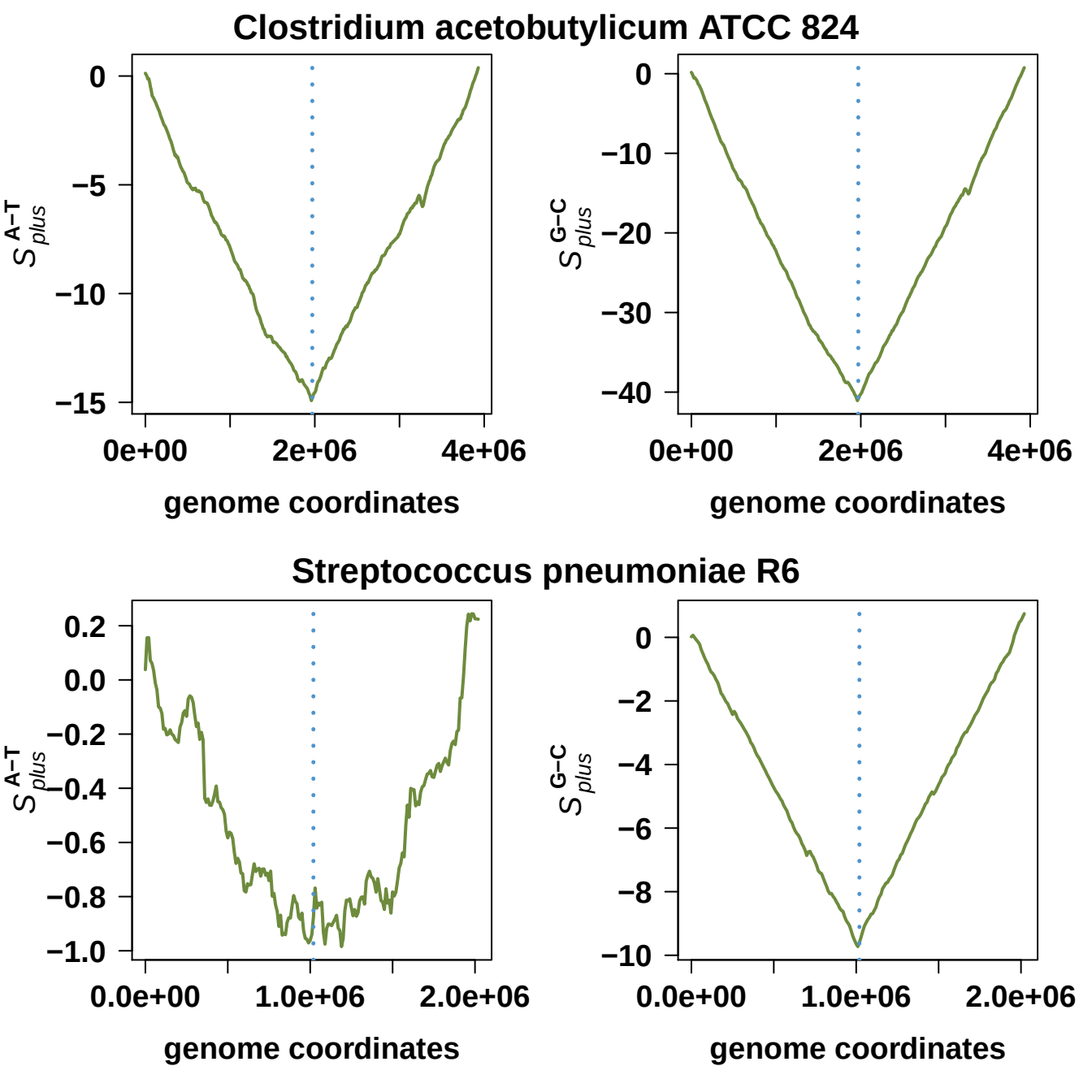

Lactococcus lactis subsp. lactis Il1403
S^{A-T}_{plus}
0
−1
−2
−3
0.0e+00
1.0e+06
2.0e+06
genome coordinates
S^{G-C}_{plus}
2
0
−2
−4
−6
−8
−10
0.0e+00
1.0e+06
2.0e+06
genome coordinates
Streptococcus pyogenes M1 GAS
S^{A-T}_{plus}
1.0
0.5
0.0
−0.5
−1.0
−1.5
0.0e+00
1.0e+06
genome coordinates
S^{G-C}_{plus}
2
0
−2
−4
−6
0.0e+00
1.0e+06
genome coordinates

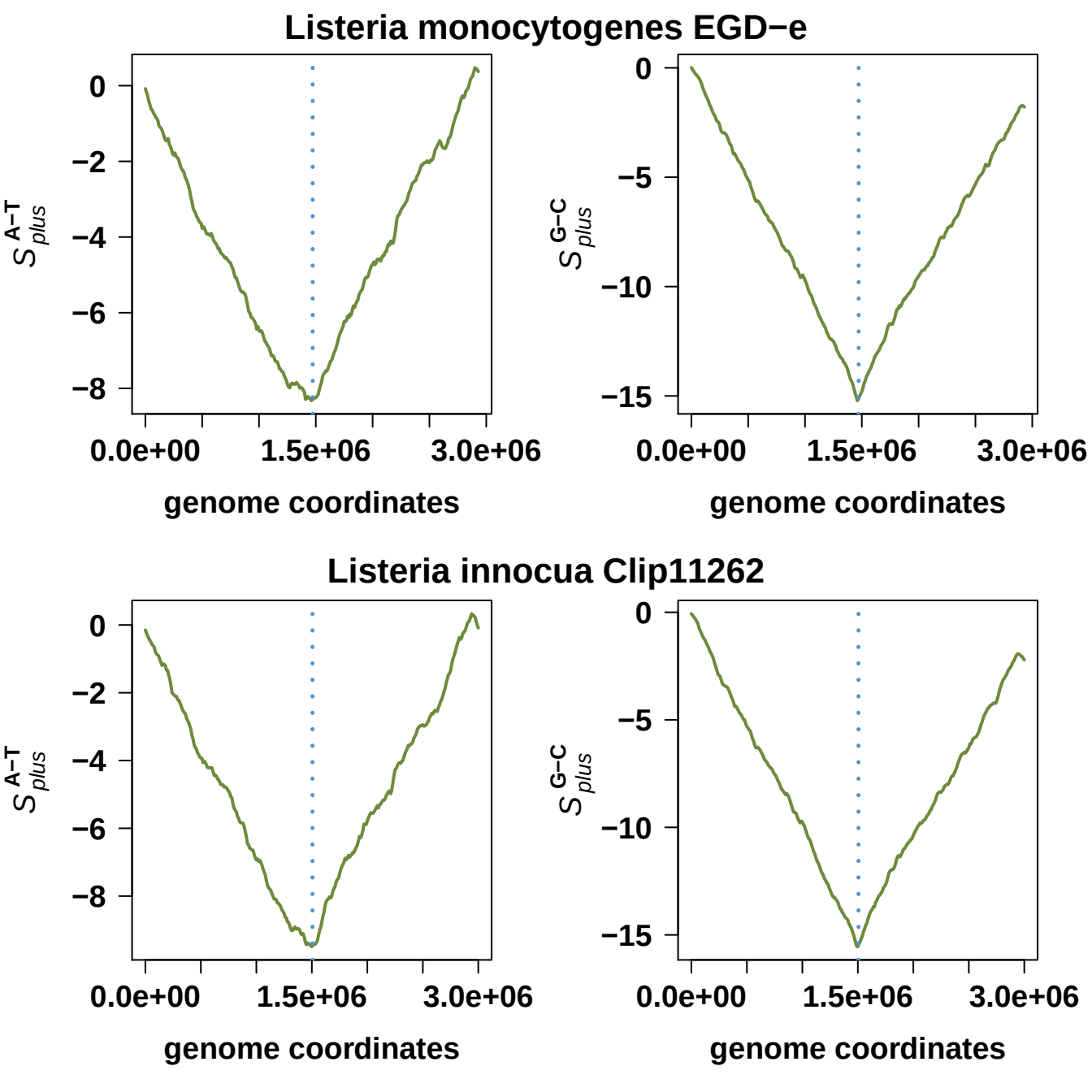

Staphylococcus aureus subsp. aureus N315
0
−2
−4
−6
−8
S^{A-T}_{plus}
0.0e+00
1.5e+06
genome coordinates
0
−5
−10
−15
S^{G-C}_{plus}
0.0e+00
1.5e+06
genome coordinates
Staphylococcus aureus subsp. aureus Mu50
0
−2
−4
−6
−8
S^{A-T}_{plus}
0.0e+00
1.5e+06
genome coordinates
0
−5
−10
−15
S^{G-C}_{plus}
0.0e+00
1.5e+06
genome coordinates

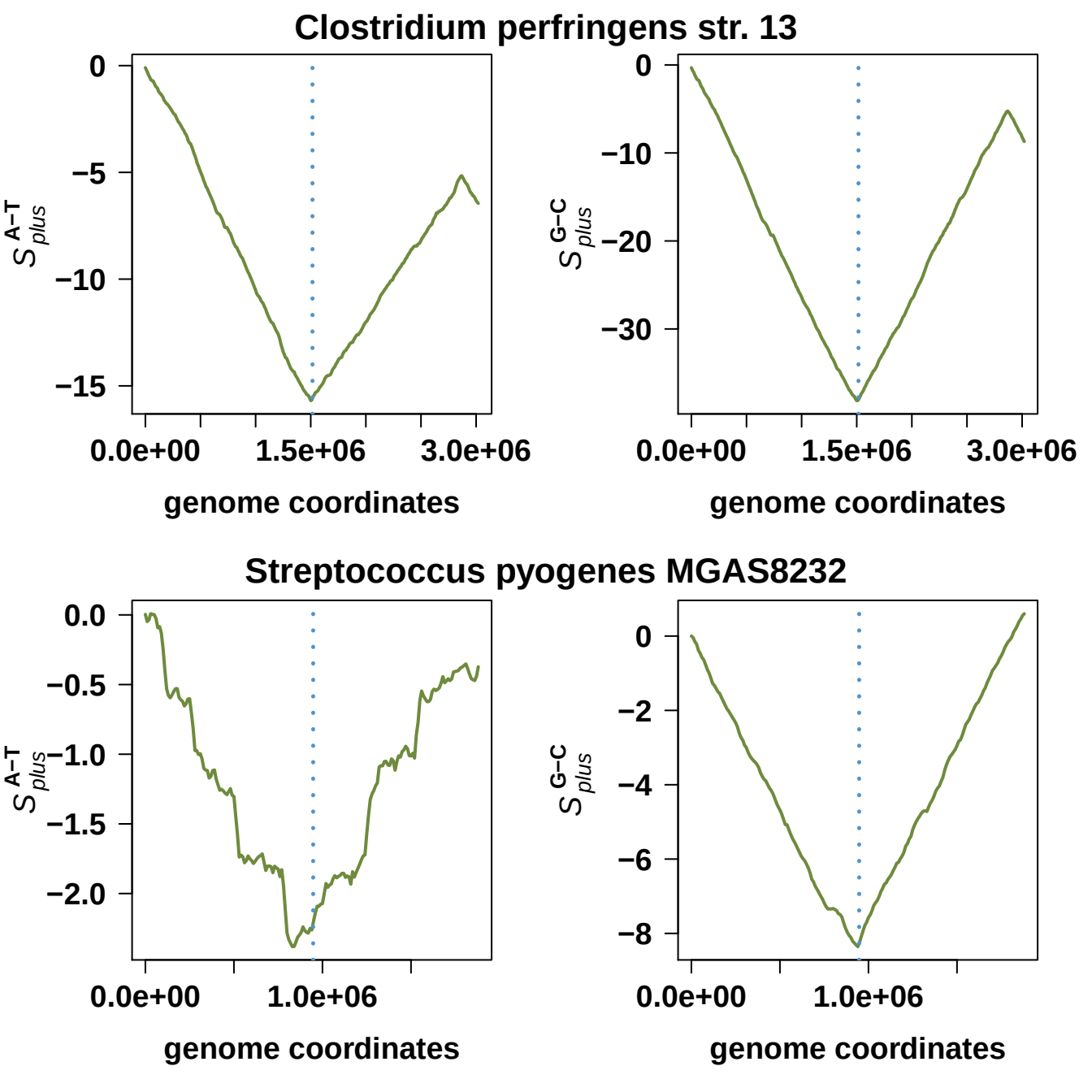

Staphylococcus aureus subsp. aureus COL
0
−2
−4
−6
−8
S^{A-T}_{plus}
0.0e+00
1.5e+06
genome coordinates
0
−5
−10
−15
S^{G-C}_{plus}
0.0e+00
1.5e+06
genome coordinates
Staphylococcus aureus subsp. aureus MRSA252
0
−2
−4
−6
−8
S^{A-T}_{plus}
0.0e+00
1.5e+06
3.0e+06
genome coordinates
0
−5
−10
−15
S^{G-C}_{plus}
0.0e+00
1.5e+06
3.0e+06
genome coordinates

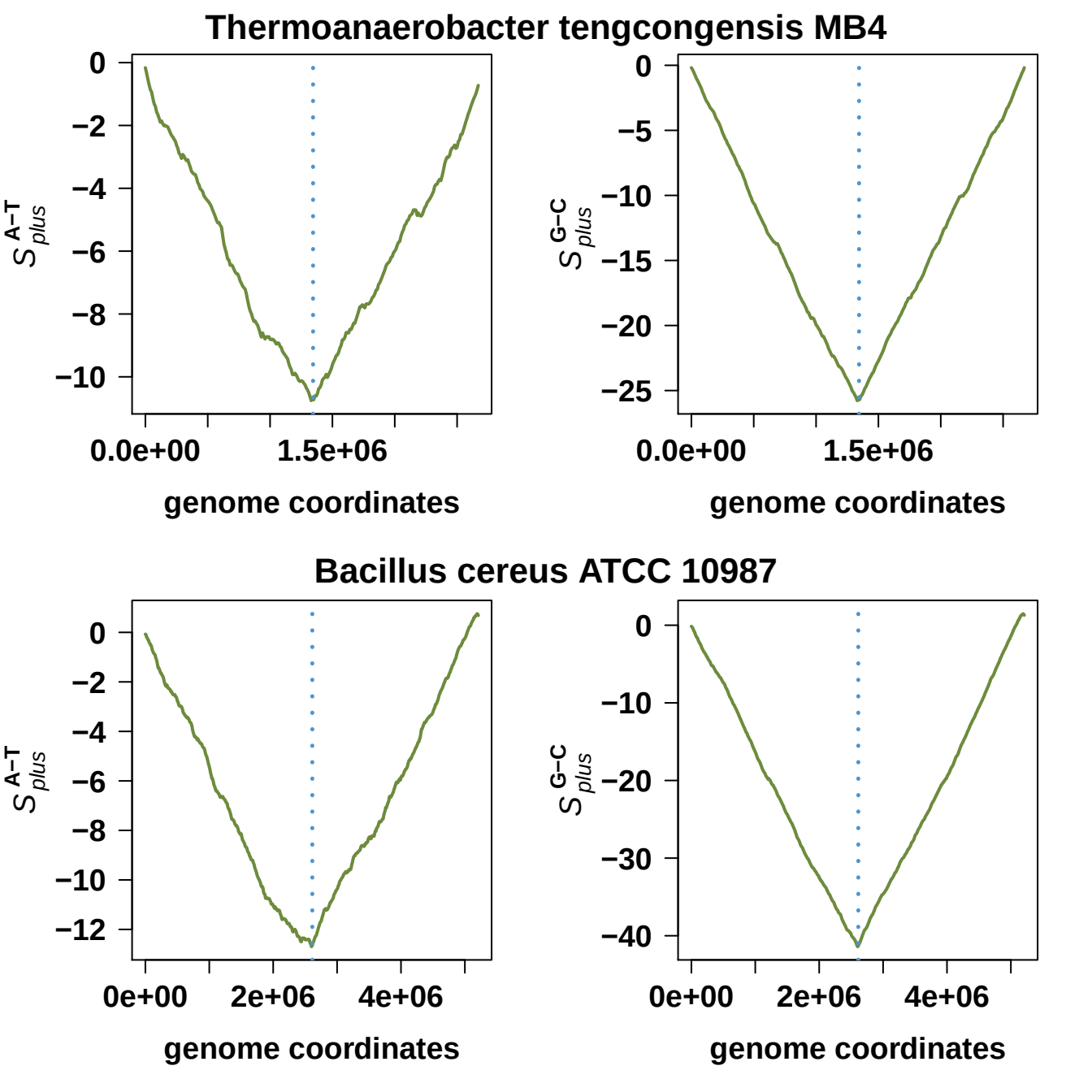

Staphylococcus aureus subsp. aureus MSSA476
S^{A-T}_{plus}
0
−2
−4
−6
−8
0.0e+00
1.5e+06
genome coordinates
S^{G-C}_{plus}
0
−5
−10
−15
0.0e+00
1.5e+06
genome coordinates
Listeria monocytogenes serotype 4b str. F2365
S^{A-T}_{plus}
0
−2
−4
−6
−8
0.0e+00
1.5e+06
3.0e+06
genome coordinates
S^{G-C}_{plus}
0
−5
−10
−15
0.0e+00
1.5e+06
3.0e+06
genome coordinates

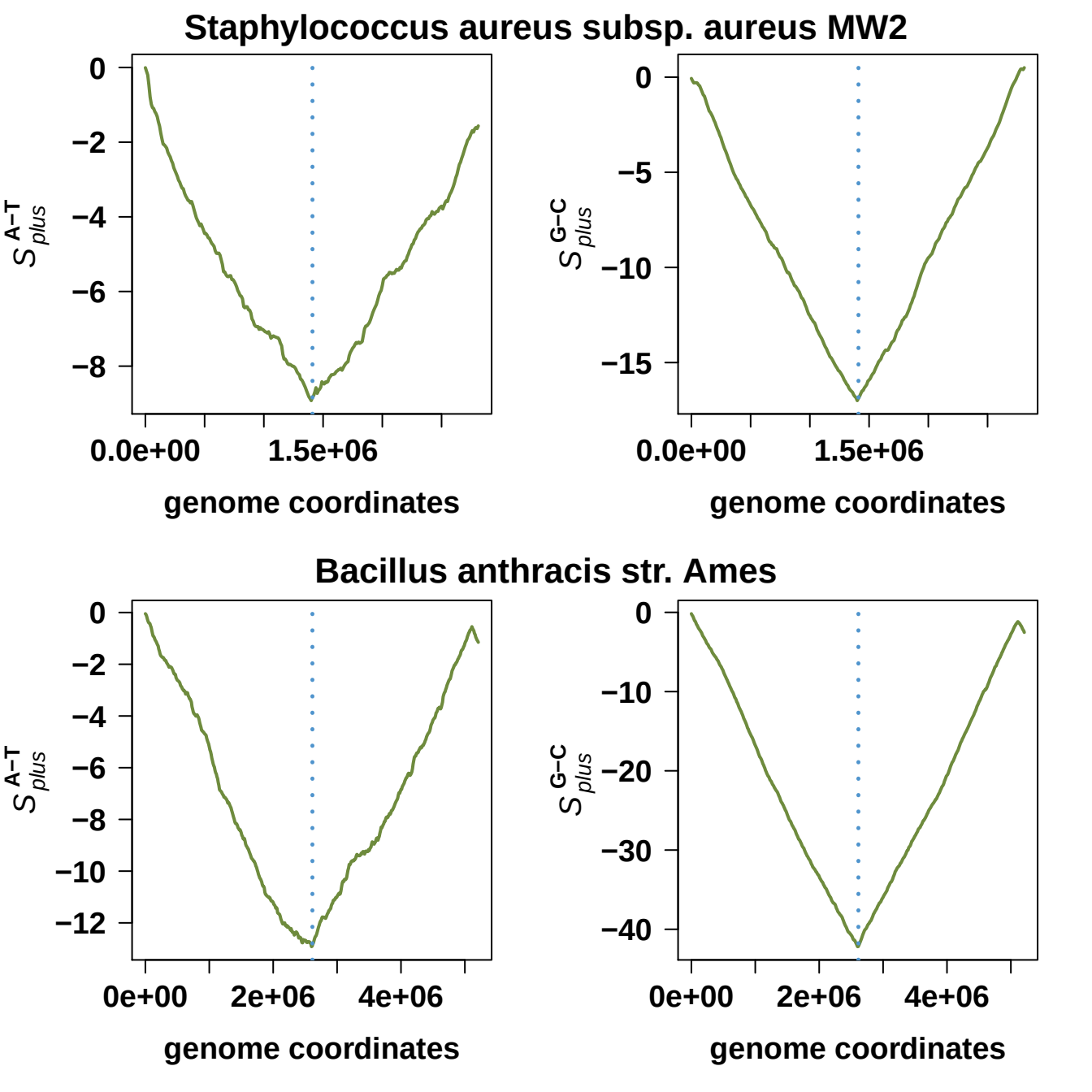

Staphylococcus epidermidis RP62A
0
−1
−2
−3
−4
−5
S^{A-T}_{plus}
0.0e+00
1.5e+06
genome coordinates
0
−2
−4
−6
−8
−10
−12
S^{G-C}_{plus}
0.0e+00
1.5e+06
genome coordinates
Streptococcus pneumoniae TIGR4
0.5
0.0
−0.5
S^{A-T}_{plus}
0.0e+00
1.0e+06
2.0e+06
genome coordinates
0
−2
−4
−6
−8
−10
S^{G-C}_{plus}
0.0e+00
1.0e+06
2.0e+06
genome coordinates

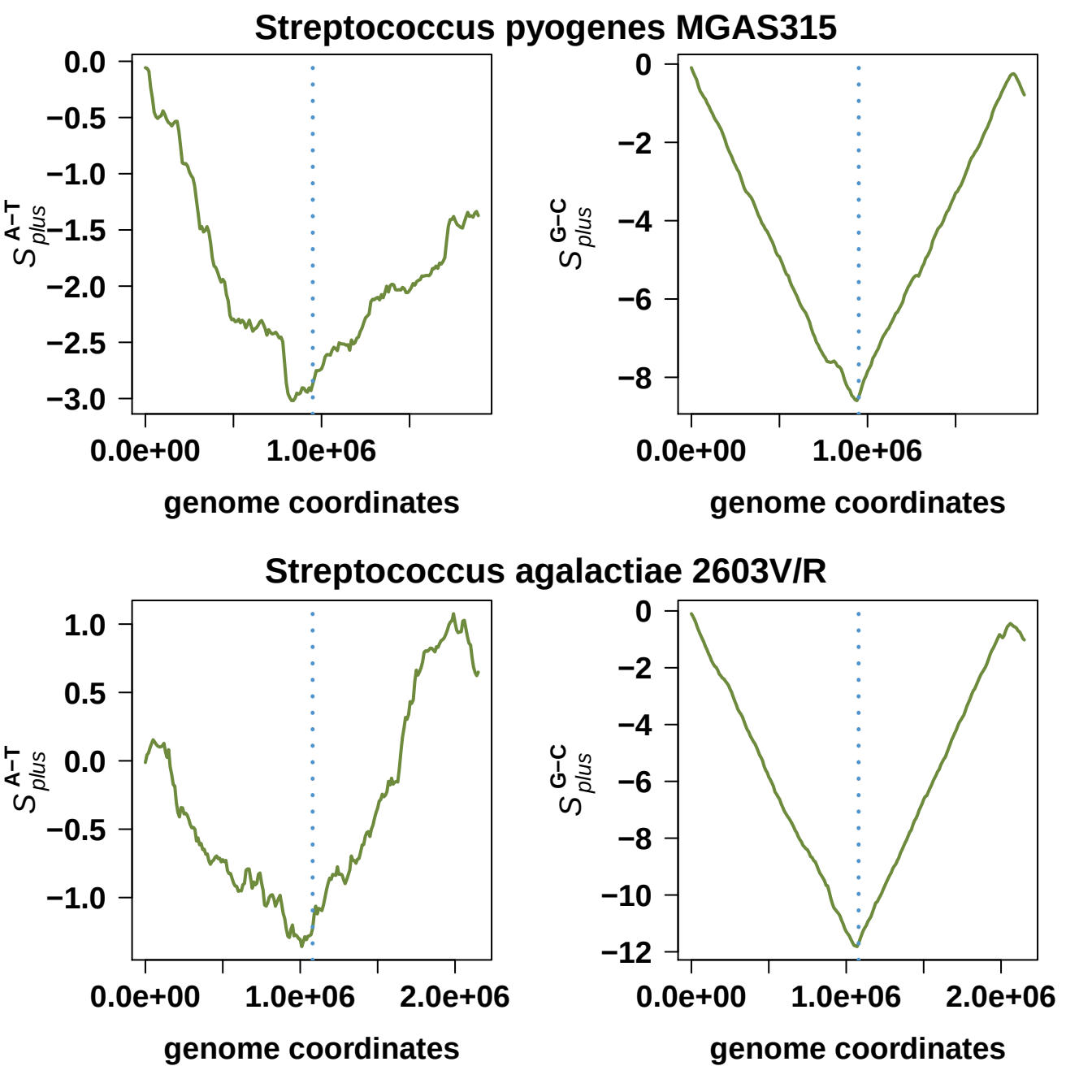

Clostridium acetobutylicum ATCC 824
S^{A-T}_{plus}
0
−5
−10
−15
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
0
−10
−20
−30
−40
0e+00
2e+06
4e+06
genome coordinates
Streptococcus pneumoniae R6
S^{A-T}_{plus}
0.2
0.0
−0.2
−0.4
−0.6
−0.8
−1.0
0.0e+00
1.0e+06
2.0e+06
genome coordinates
S^{G-C}_{plus}
0
−2
−4
−6
−8
−10
0.0e+00
1.0e+06
2.0e+06
genome coordinates

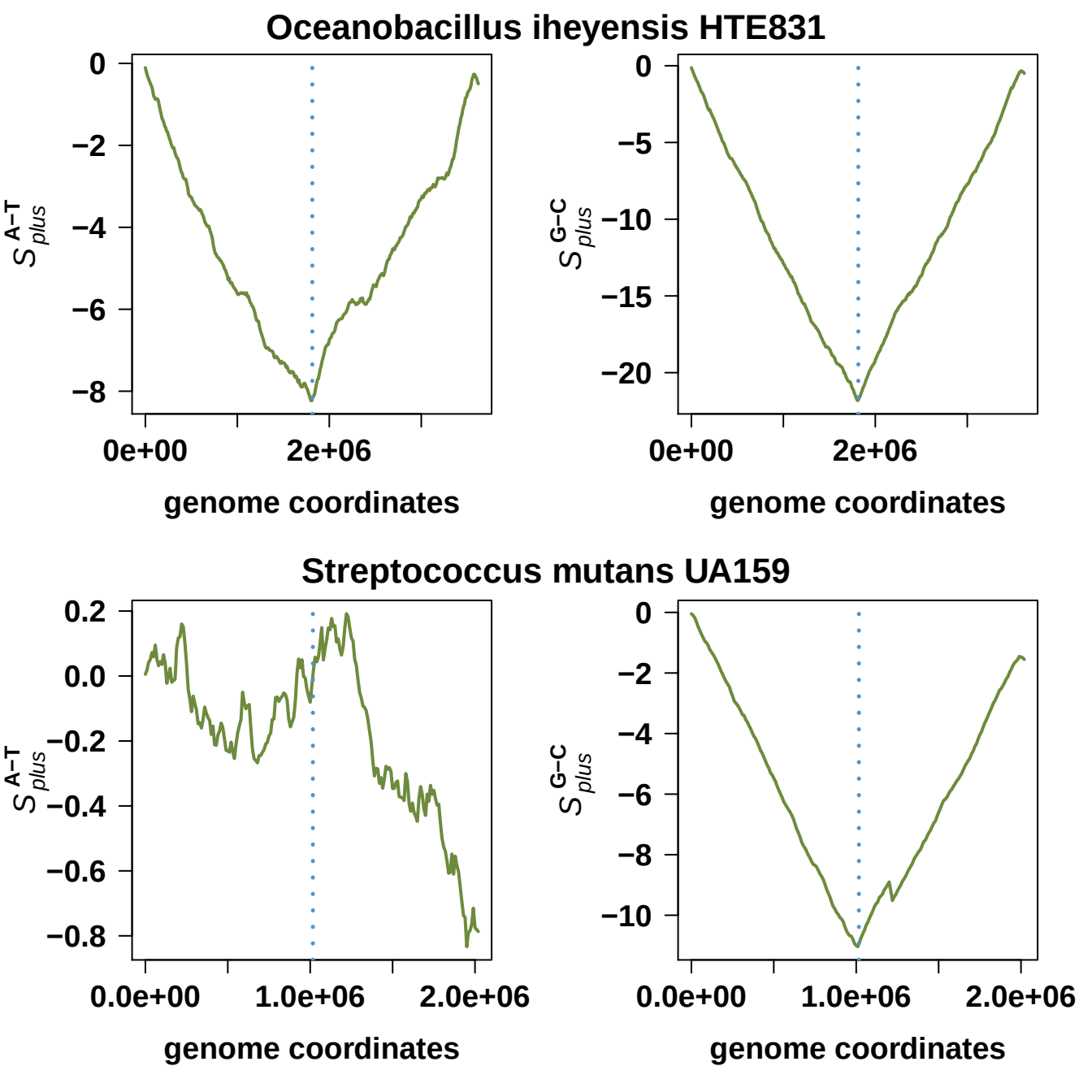

Listeria monocytogenes EGD−e
S^{A-T}_{plus}
0
−2
−4
−6
−8
0.0e+00
1.5e+06
3.0e+06
genome coordinates
S^{G-C}_{plus}
0
−5
−10
−15
0.0e+00
1.5e+06
3.0e+06
genome coordinates
Listeria innocua Clip11262
S^{A-T}_{plus}
0
−2
−4
−6
−8
0.0e+00
1.5e+06
3.0e+06
genome coordinates
S^{G-C}_{plus}
0
−5
−10
−15
0.0e+00
1.5e+06
3.0e+06
genome coordinates

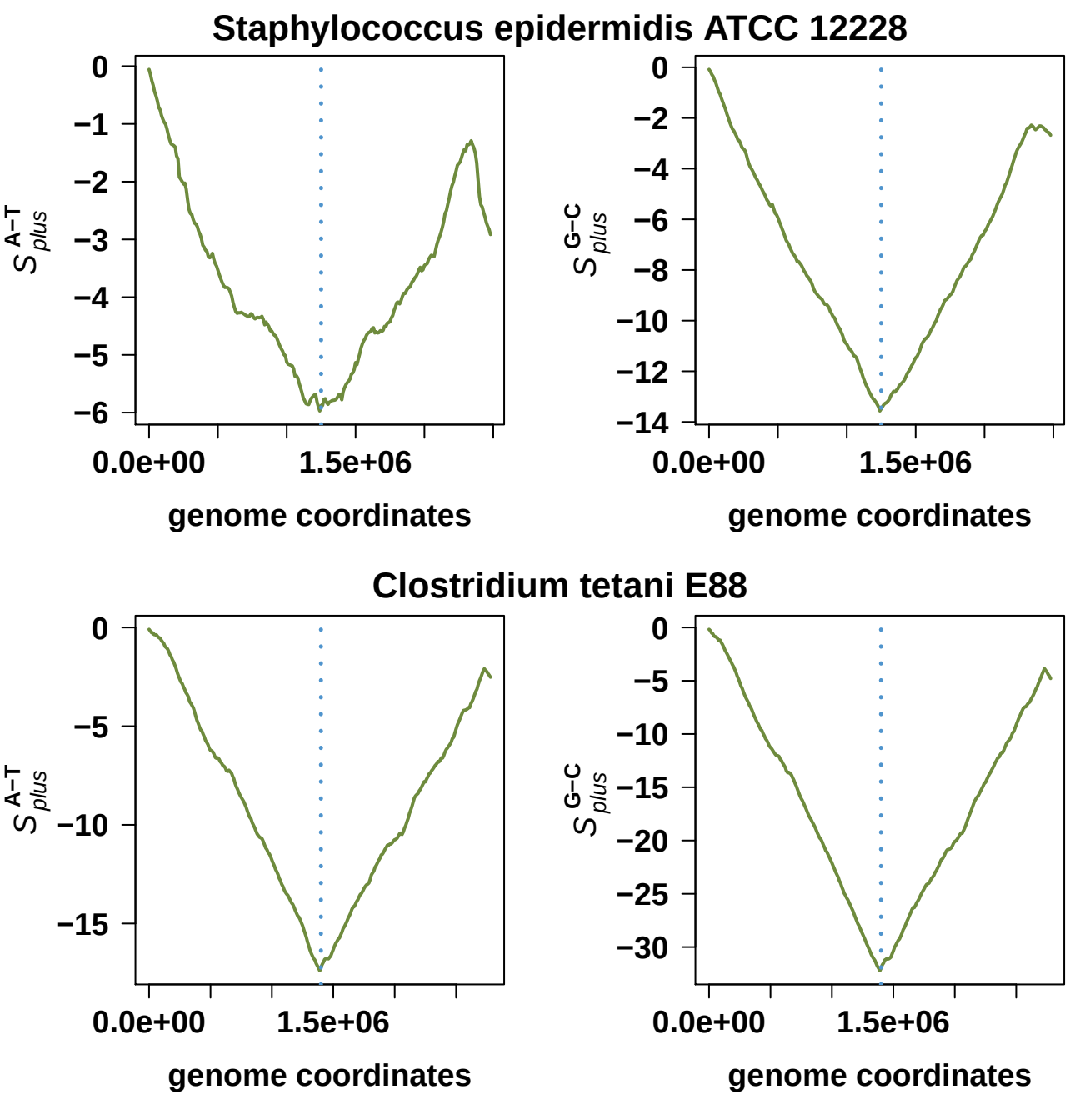

Clostridium perfringens str. 13
S^{A-T}_{plus}
0
−5
−10
−15
0.0e+00
1.5e+06
3.0e+06
genome coordinates
S^{G-C}_{plus}
0
−10
−20
−30
0.0e+00
1.5e+06
3.0e+06
genome coordinates
Streptococcus pyogenes MGAS8232
S^{A-T}_{plus}
0.0
−0.5
−1.0
−1.5
−2.0
0.0e+00
1.0e+06
genome coordinates
S^{G-C}_{plus}
0
−2
−4
−6
−8
0.0e+00
1.0e+06
genome coordinates

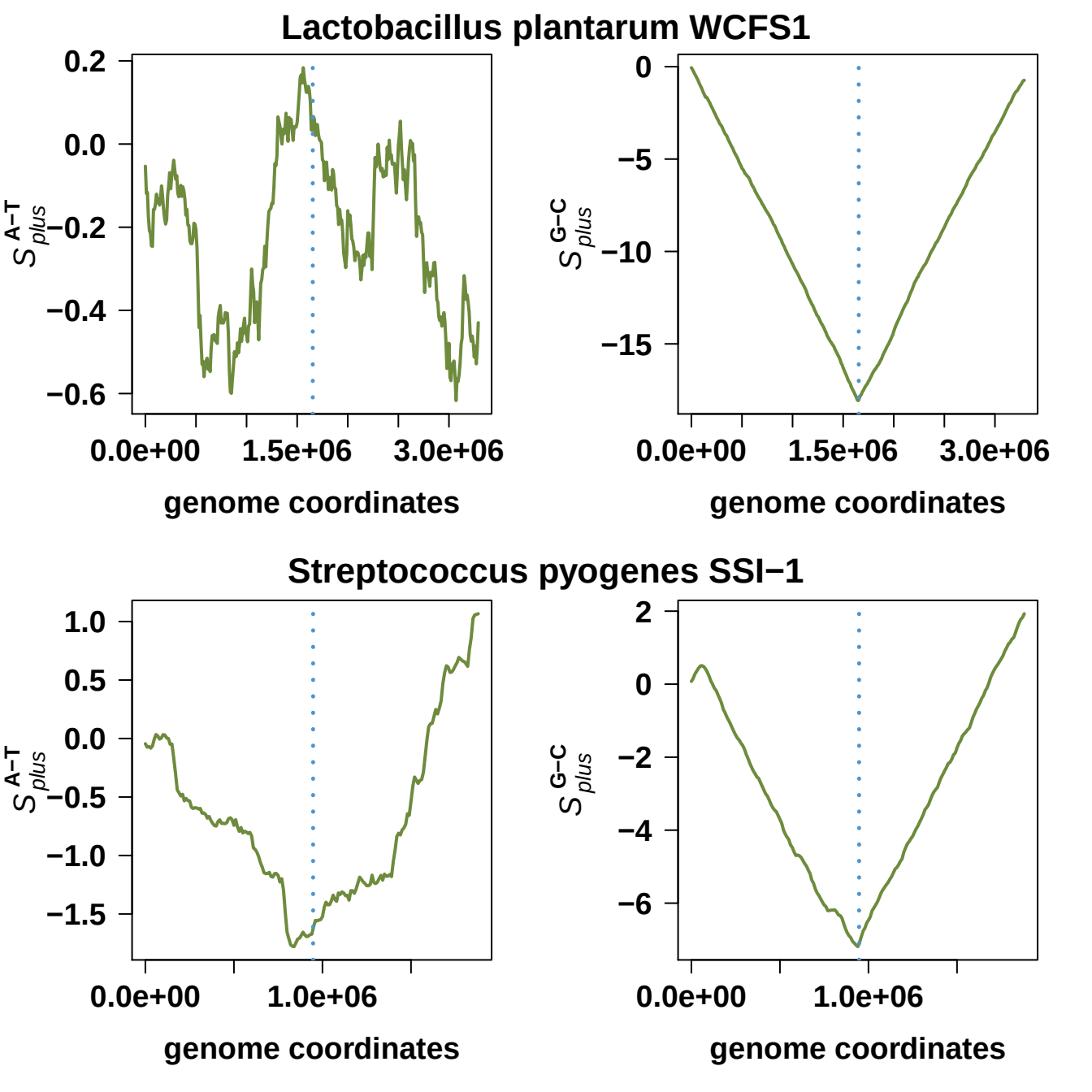

Thermoanaerobacter tengcongensis MB4
S^{A-T}_{plus}
0
−2
−4
−6
−8
−10
0.0e+00
1.5e+06
genome coordinates
S^{G-C}_{plus}
0
−5
−10
−15
−20
−25
0.0e+00
1.5e+06
genome coordinates
Bacillus cereus ATCC 10987
S^{A-T}_{plus}
0
−2
−4
−6
−8
−10
−12
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
0
−10
−20
−30
−40
0e+00
2e+06
4e+06
genome coordinates

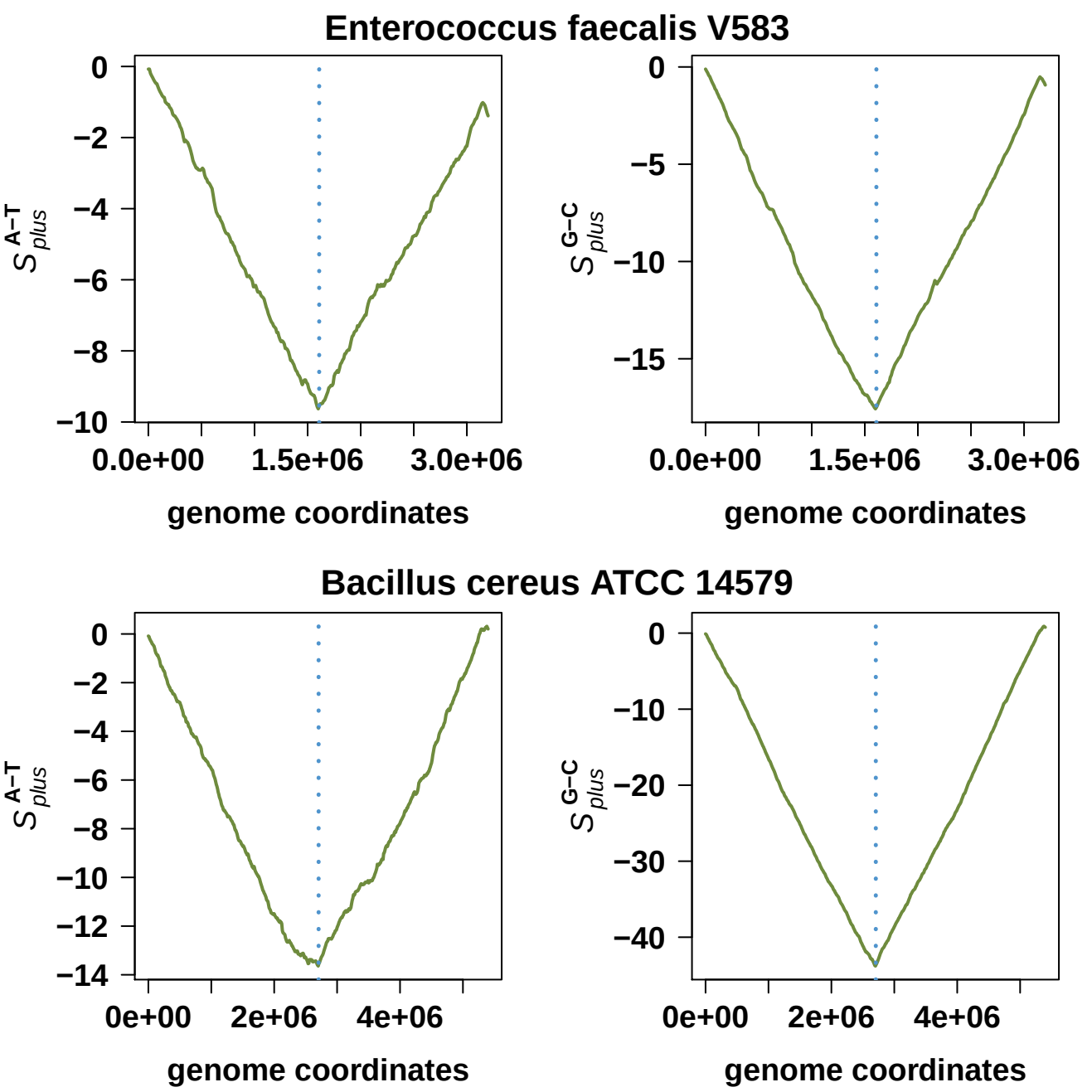

Staphylococcus aureus subsp. aureus MW2
0
−2
−4
−6
−8
S^{A-T}_{plus}
0.0e+00
1.5e+06
genome coordinates
0
−5
−10
−15
S^{G-C}_{plus}
0.0e+00
1.5e+06
genome coordinates
Bacillus anthracis str. Ames
0
−2
−4
−6
−8
−10
−12
S^{A-T}_{plus}
0e+00
2e+06
4e+06
genome coordinates
0
−10
−20
−30
−40
S^{G-C}_{plus}
0e+00
2e+06
4e+06
genome coordinates

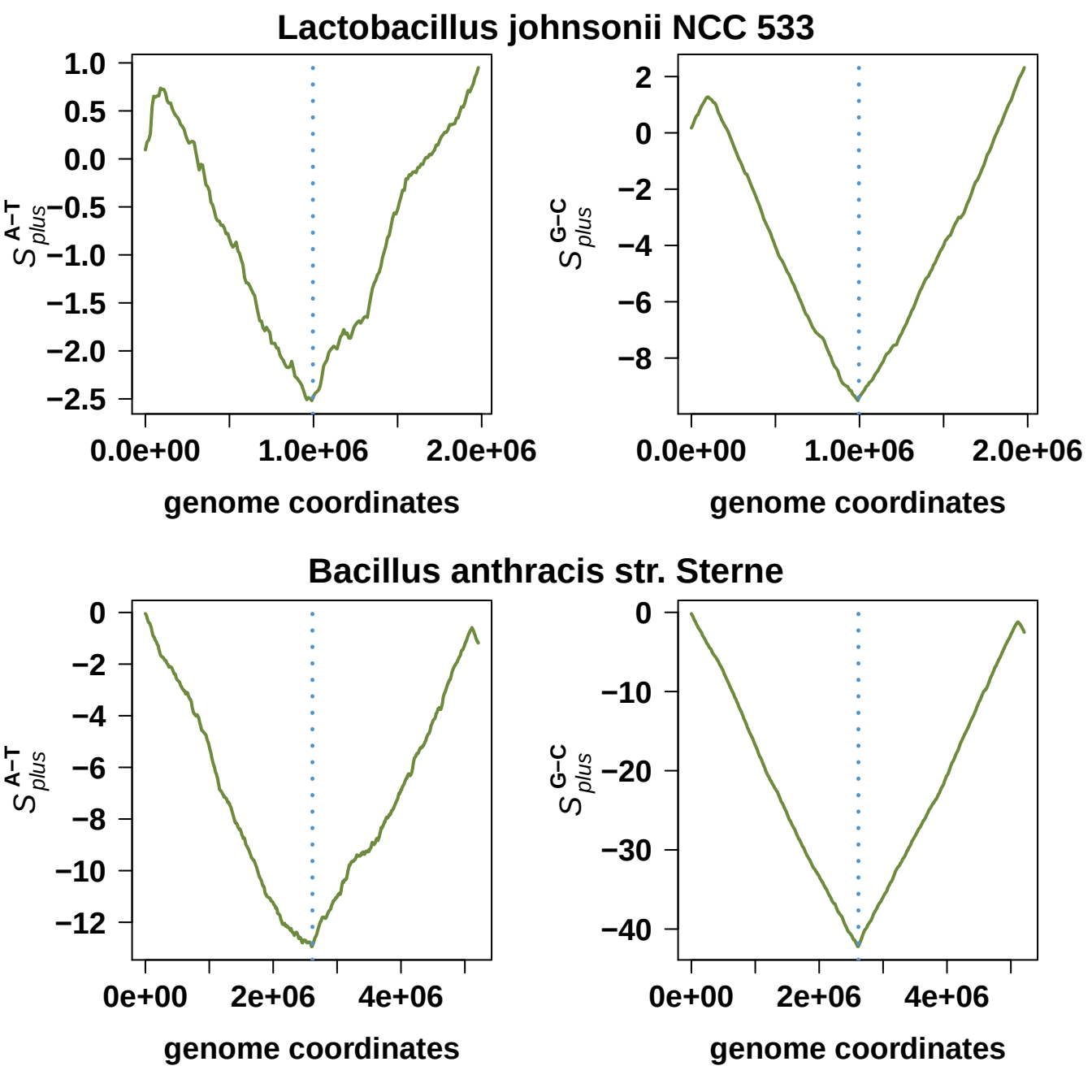

Streptococcus pyogenes MGAS315
0.0
−0.5
−1.0
−1.5
−2.0
−2.5
−3.0
S^{A-T}_{plus}
0.0e+00
1.0e+06
genome coordinates
0
−2
−4
−6
−8
S^{G-C}_{plus}
0.0e+00
1.0e+06
genome coordinates
Streptococcus agalactiae 2603V/R
1.0
0.5
0.0
−0.5
−1.0
S^{A-T}_{plus}
0.0e+00
1.0e+06
2.0e+06
genome coordinates
0
−2
−4
−6
−8
−10
−12
S^{G-C}_{plus}
0.0e+00
1.0e+06
2.0e+06
genome coordinates

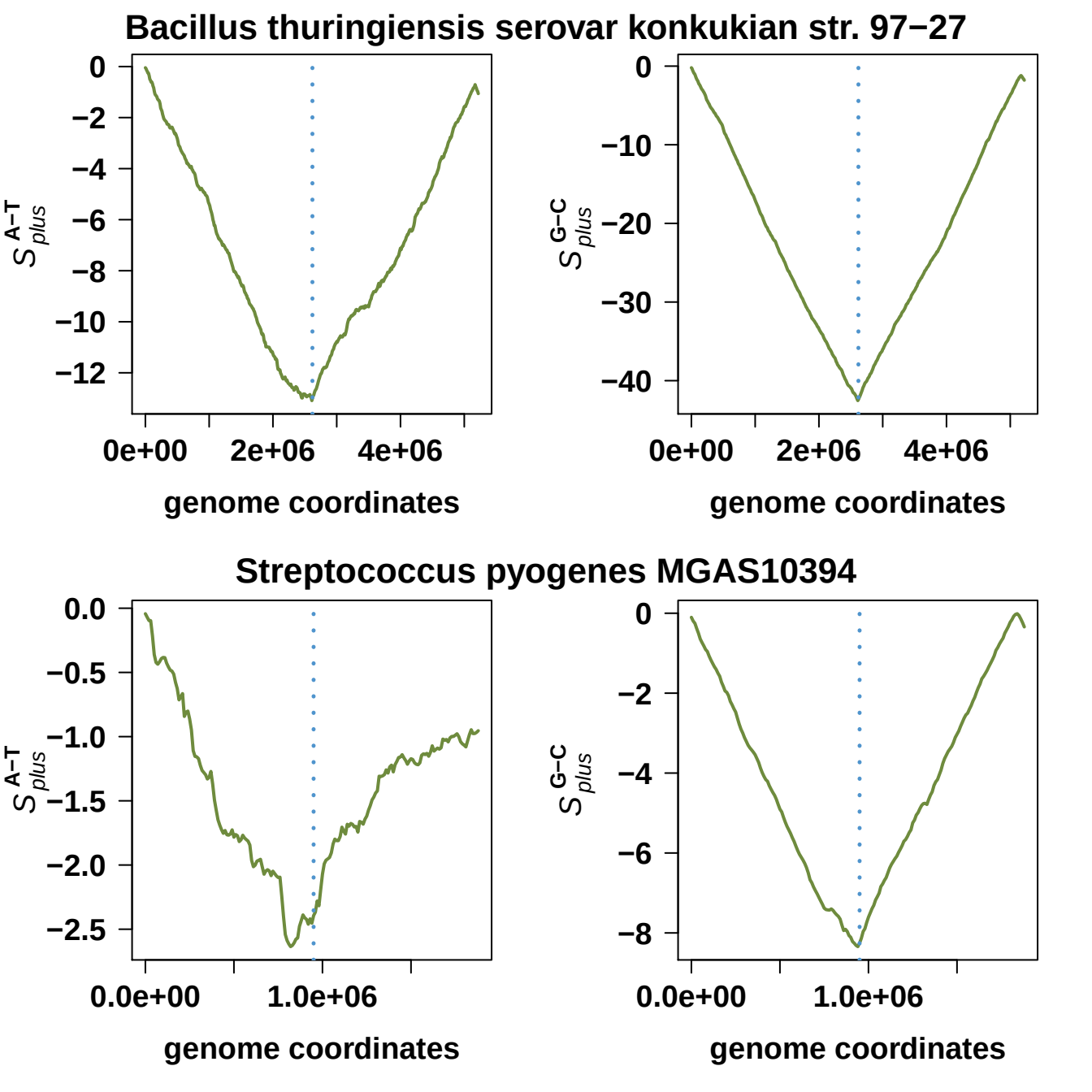

Oceanobacillus iheyensis HTE831
0
−2
−4
−6
−8
S^{A-T}_{plus}
0e+00
2e+06
genome coordinates
0
−5
−10
−15
−20
S^{G-C}_{plus}
0e+00
2e+06
genome coordinates
Streptococcus mutans UA159
0.2
0.0
−0.2
−0.4
−0.6
−0.8
S^{A-T}_{plus}
0.0e+00
1.0e+06
2.0e+06
genome coordinates
0
−2
−4
−6
−8
−10
S^{G-C}_{plus}
0.0e+00
1.0e+06
2.0e+06
genome coordinates

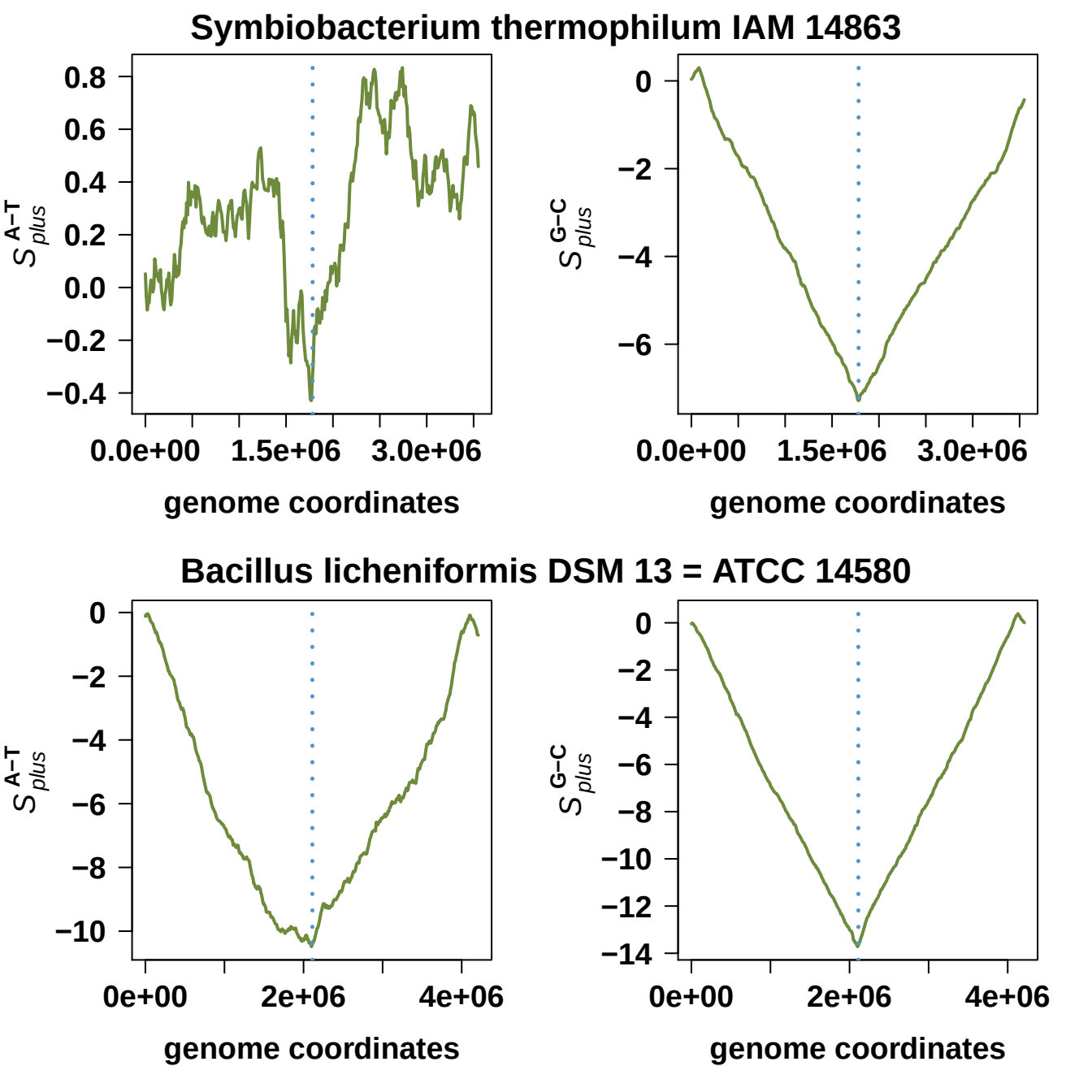

Staphylococcus epidermidis ATCC 12228
S^{A-T}_{plus}
0
−1
−2
−3
−4
−5
−6
0.0e+00
1.5e+06
genome coordinates
S^{G-C}_{plus}
0
−2
−4
−6
−8
−10
−12
−14
0.0e+00
1.5e+06
genome coordinates
Clostridium tetani E88
S^{A-T}_{plus}
0
−5
−10
−15
0.0e+00
1.5e+06
genome coordinates
S^{G-C}_{plus}
0
−5
−10
−15
−20
−25
−30
0.0e+00
1.5e+06
genome coordinates

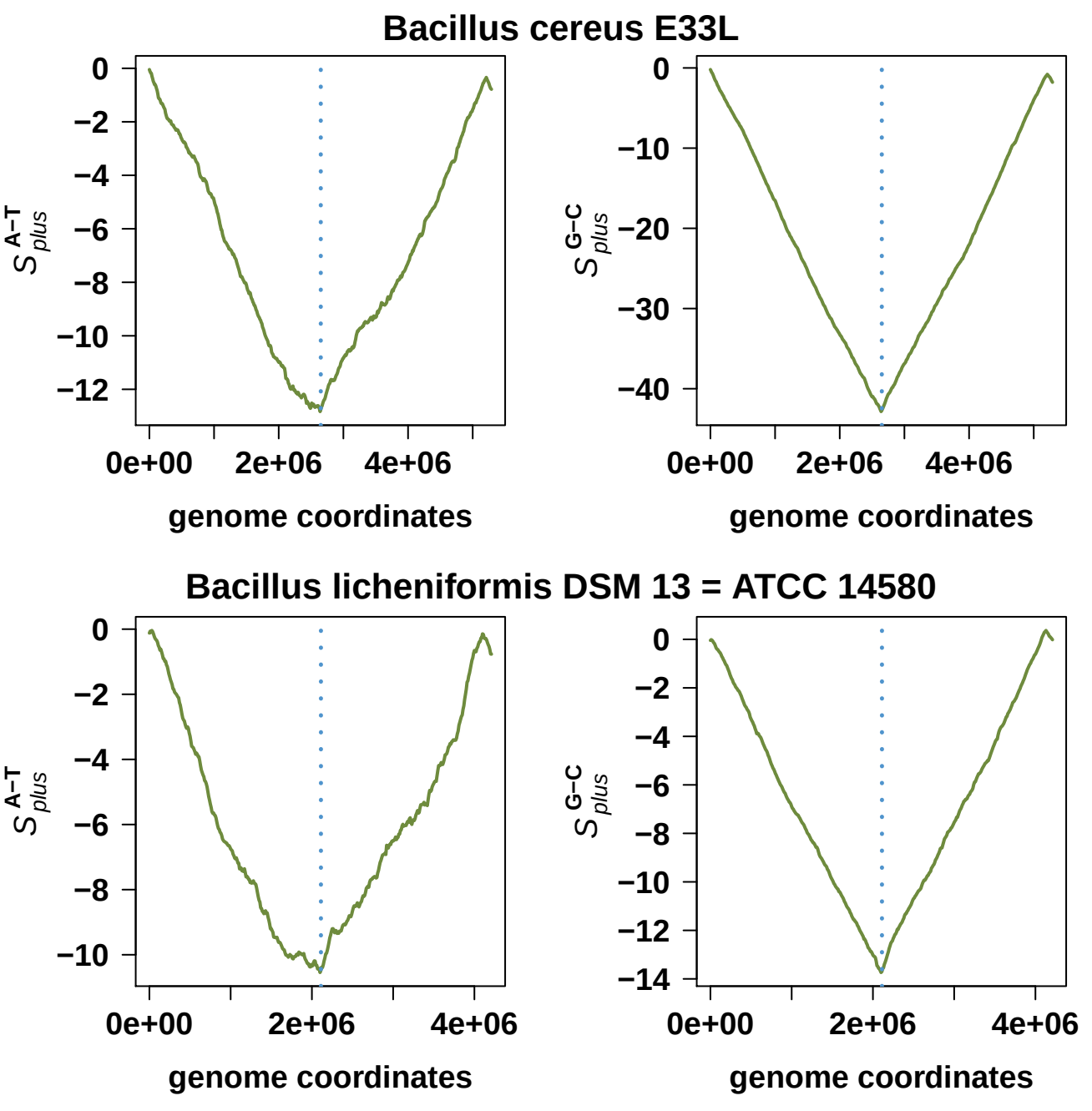

Lactobacillus plantarum WCFS1
0.2
0.0
−0.2
−0.4
−0.6
S^{A-T}_{plus}
0.0e+00
1.5e+06
3.0e+06
genome coordinates
0
−5
−10
−15
S^{G-C}_{plus}
0.0e+00
1.5e+06
3.0e+06
genome coordinates
Streptococcus pyogenes SSI−1
1.0
0.5
0.0
−0.5
−1.0
−1.5
S^{A-T}_{plus}
0.0e+00
1.0e+06
genome coordinates
2
0
−2
−4
−6
S^{G-C}_{plus}
0.0e+00
1.0e+06
genome coordinates

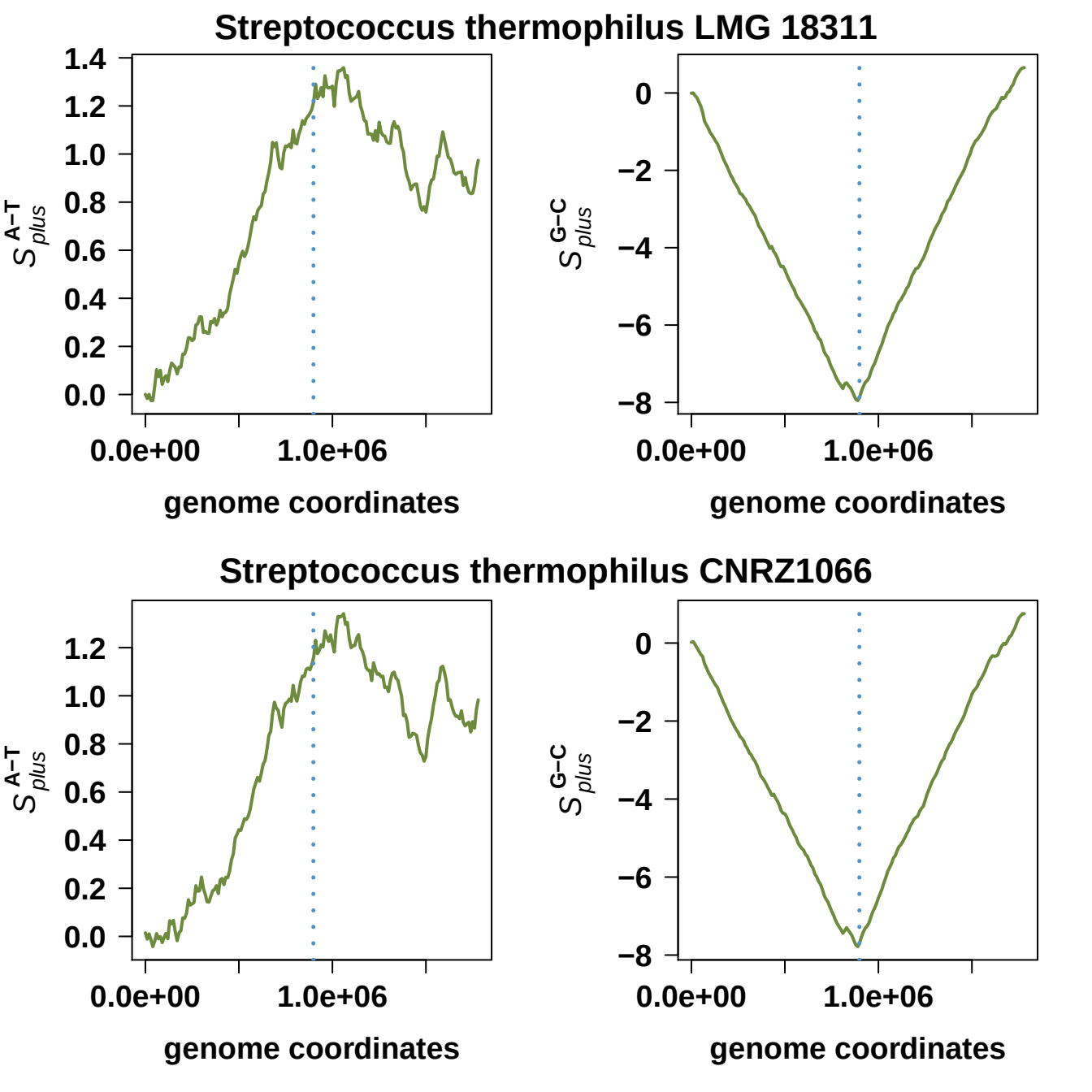

Enterococcus faecalis V583
S^{A-T}_{plus}
0
−2
−4
−6
−8
−10
0.0e+00
1.5e+06
3.0e+06
genome coordinates
S^{G-C}_{plus}
0
−5
−10
−15
0.0e+00
1.5e+06
3.0e+06
genome coordinates
Bacillus cereus ATCC 14579
S^{A-T}_{plus}
0
−2
−4
−6
−8
−10
−12
−14
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
0
−10
−20
−30
−40
0e+00
2e+06
4e+06
genome coordinates

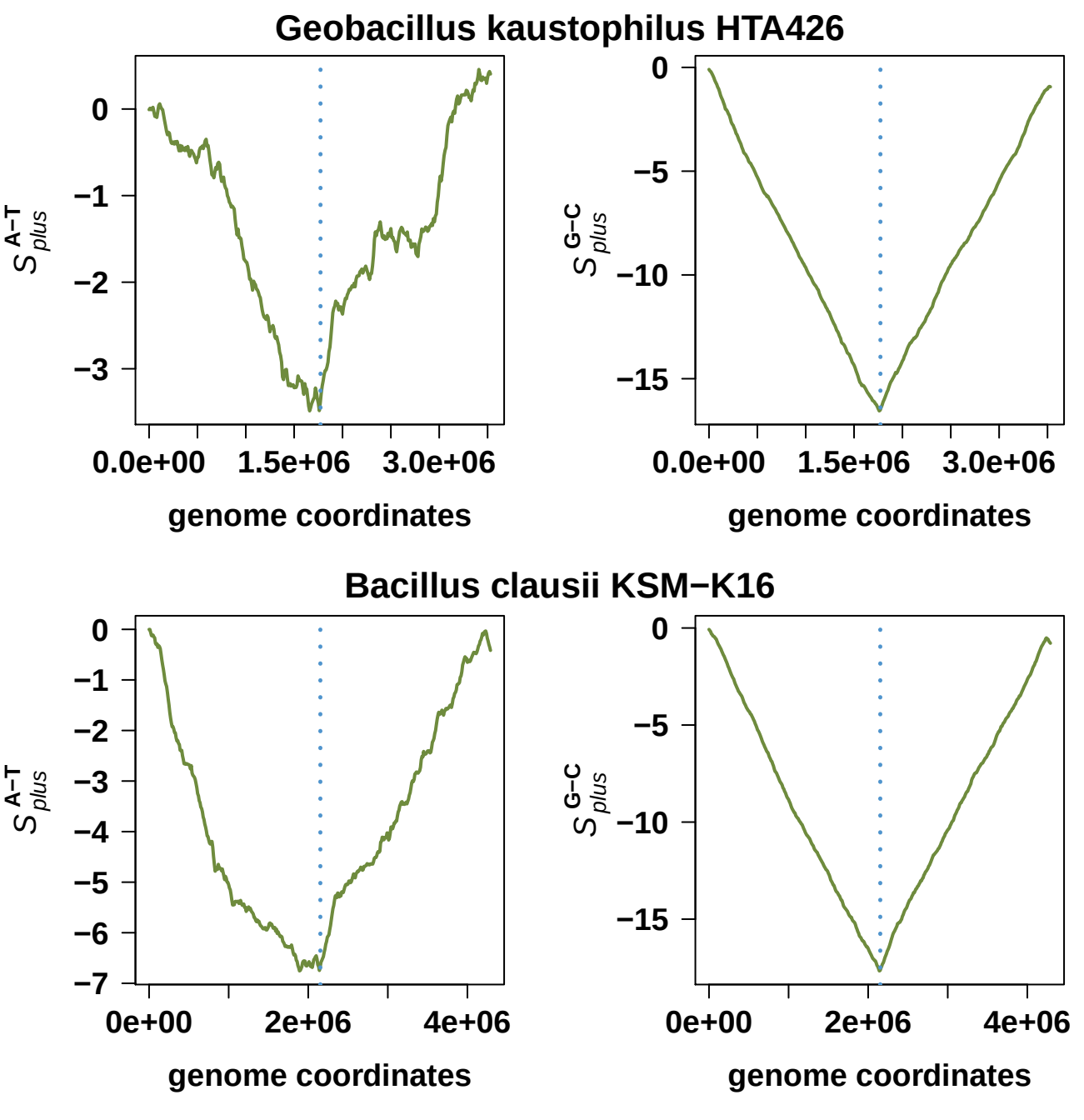

Lactobacillus johnsonii NCC 533
1.0
0.5
0.0
−0.5
−1.0
−1.5
−2.0
−2.5
S^{A-T}_{plus}
0.0e+00
1.0e+06
2.0e+06
genome coordinates
2
0
−2
−4
−6
−8
S^{G-C}_{plus}
0.0e+00
1.0e+06
2.0e+06
genome coordinates
Bacillus anthracis str. Sterne
0
−2
−4
−6
−8
−10
−12
S^{A-T}_{plus}
0e+00
2e+06
4e+06
genome coordinates
0
−10
−20
−30
−40
S^{G-C}_{plus}
0e+00
2e+06
4e+06
genome coordinates

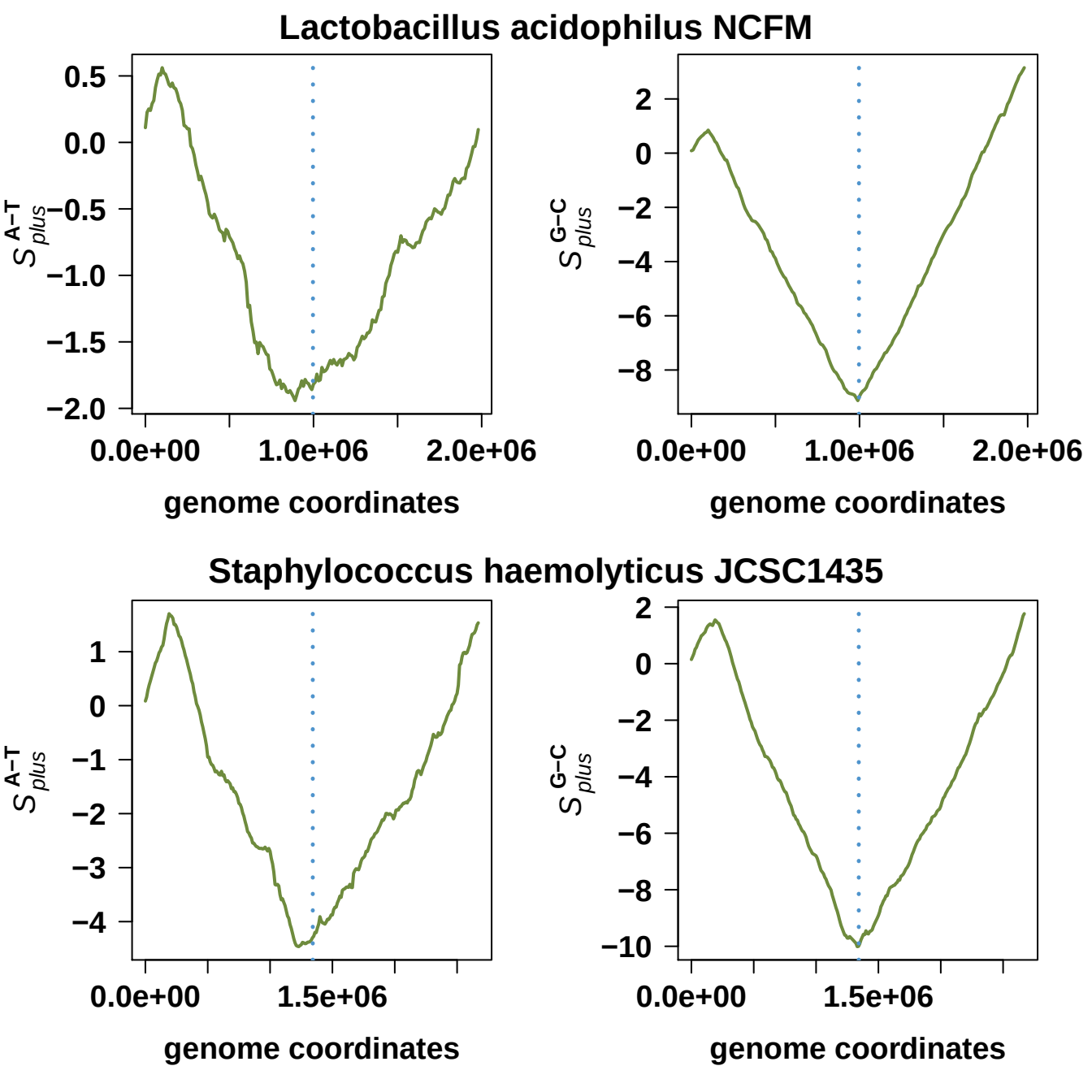

Bacillus thuringiensis serovar konkukian str. 97−27
0
−2
−4
−6
−8
−10
−12
S^{A-T}_{plus}
0e+00
2e+06
4e+06
genome coordinates
0
−10
−20
−30
−40
S^{G-C}_{plus}
0e+00
2e+06
4e+06
genome coordinates
Streptococcus pyogenes MGAS10394
0.0
−0.5
−1.0
−1.5
−2.0
−2.5
S^{A-T}_{plus}
0.0e+00
1.0e+06
genome coordinates
0
−2
−4
−6
−8
S^{G-C}_{plus}
0.0e+00
1.0e+06
genome coordinates

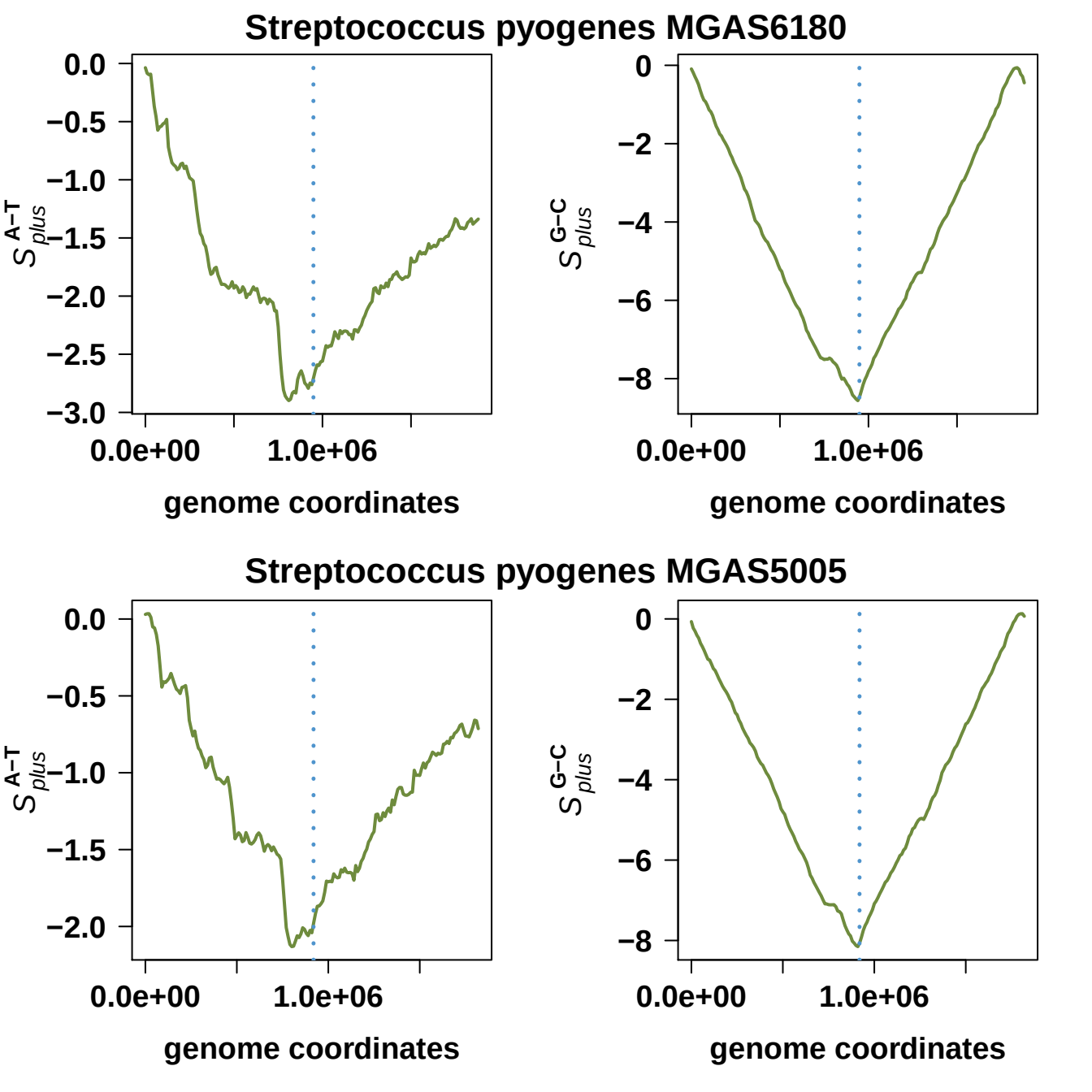

Symbiobacterium thermophilum IAM 14863
0.8
0.6
0.4
0.2
0.0
−0.2
−0.4
S^{A-T}_{plus}
0.0e+00
1.5e+06
3.0e+06
genome coordinates
0
−2
−4
−6
S^{G-C}_{plus}
0.0e+00
1.5e+06
3.0e+06
genome coordinates
Bacillus licheniformis DSM 13 = ATCC 14580
0
−2
−4
−6
−8
−10
S^{A-T}_{plus}
0e+00
2e+06
4e+06
genome coordinates
0
−2
−4
−6
−8
−10
−12
−14
S^{G-C}_{plus}
0e+00
2e+06
4e+06
genome coordinates

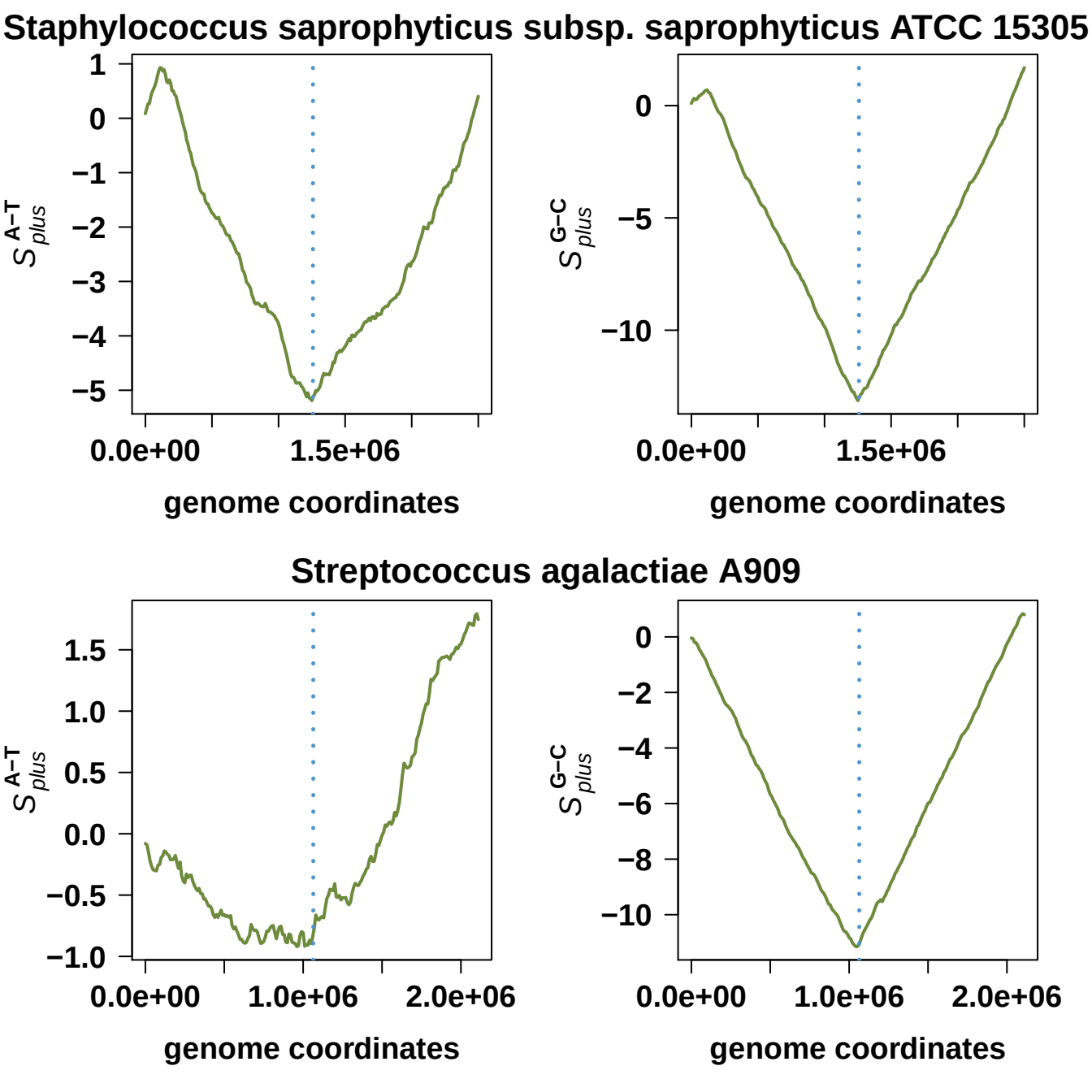

Bacillus cereus E33L
0
−2
−4
−6
−8
−10
−12
S^{A-T}_{plus}
0e+00
2e+06
4e+06
genome coordinates
0
−10
−20
−30
−40
S^{G-C}_{plus}
0e+00
2e+06
4e+06
genome coordinates
Bacillus licheniformis DSM 13 = ATCC 14580
0
−2
−4
−6
−8
−10
S^{A-T}_{plus}
0e+00
2e+06
4e+06
genome coordinates
0
−2
−4
−6
−8
−10
−12
−14
S^{G-C}_{plus}
0e+00
2e+06
4e+06
genome coordinates

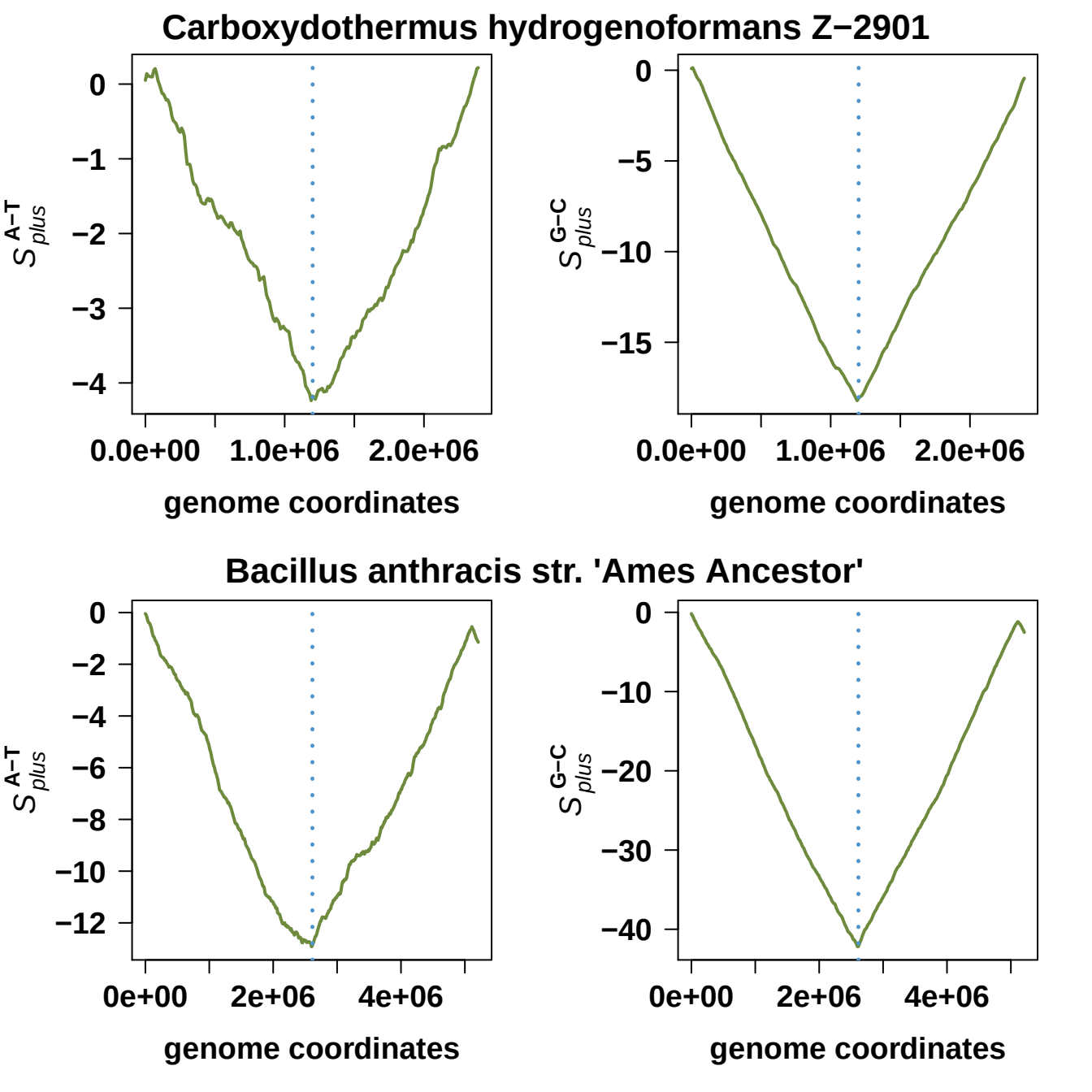

Streptococcus thermophilus LMG 18311
1.4
1.2
1.0
0.8
0.6
0.4
0.2
0.0
S^{A-T}_{plus}
0.0e+00
1.0e+06
genome coordinates
0
−2
−4
−6
−8
S^{G-C}_{plus}
0.0e+00
1.0e+06
genome coordinates
Streptococcus thermophilus CNRZ1066
1.2
1.0
0.8
0.6
0.4
0.2
0.0
S^{A-T}_{plus}
0.0e+00
1.0e+06
genome coordinates
0
−2
−4
−6
−8
S^{G-C}_{plus}
0.0e+00
1.0e+06
genome coordinates

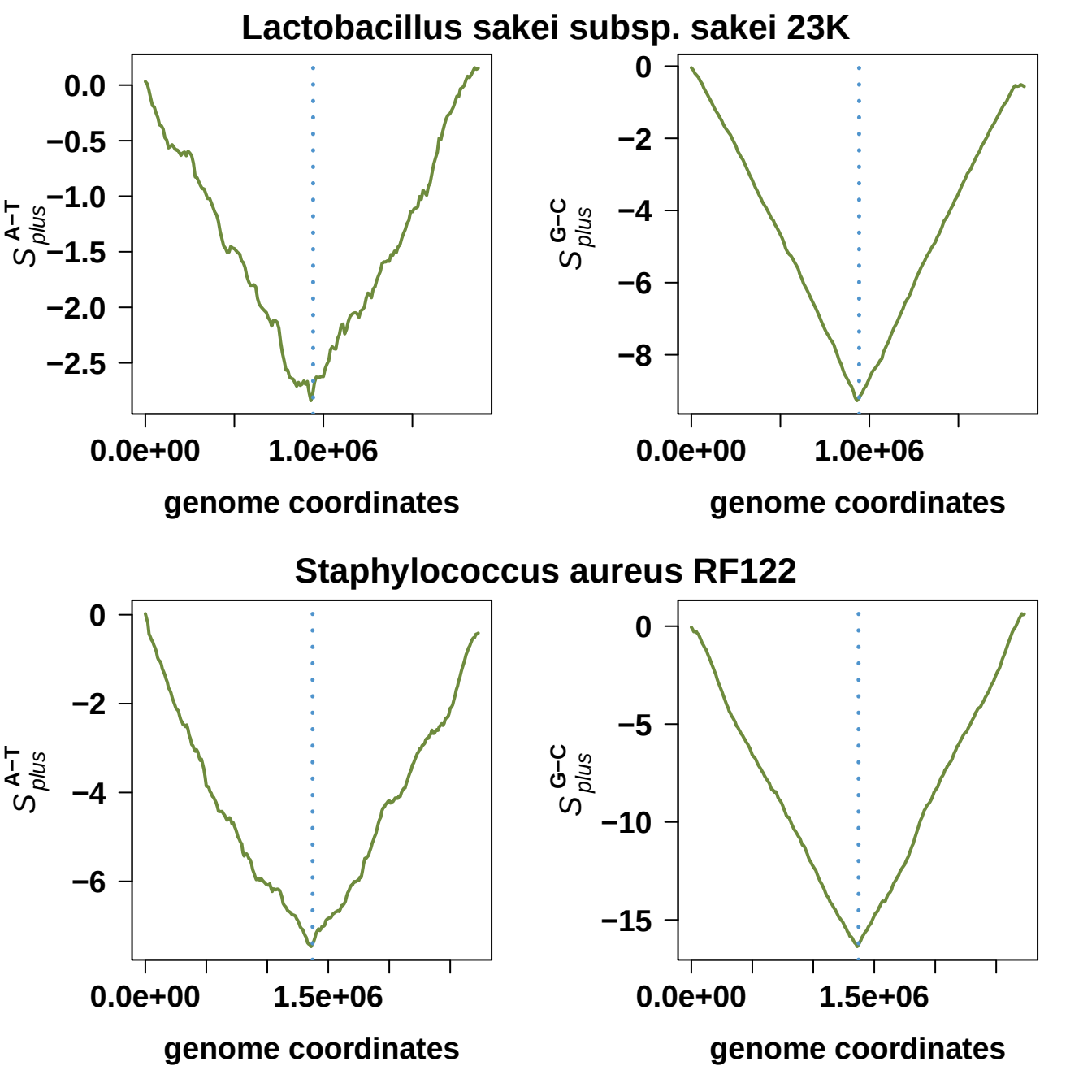

Geobacillus kaustophilus HTA426
S^{A-T}_{plus}
0
−1
−2
−3
0.0e+00
1.5e+06
3.0e+06
genome coordinates
S^{G-C}_{plus}
0
−5
−10
−15
0.0e+00
1.5e+06
3.0e+06
genome coordinates
Bacillus clausii KSM−K16
S^{A-T}_{plus}
0
−1
−2
−3
−4
−5
−6
−7
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
0
−5
−10
−15
0e+00
2e+06
4e+06
genome coordinates

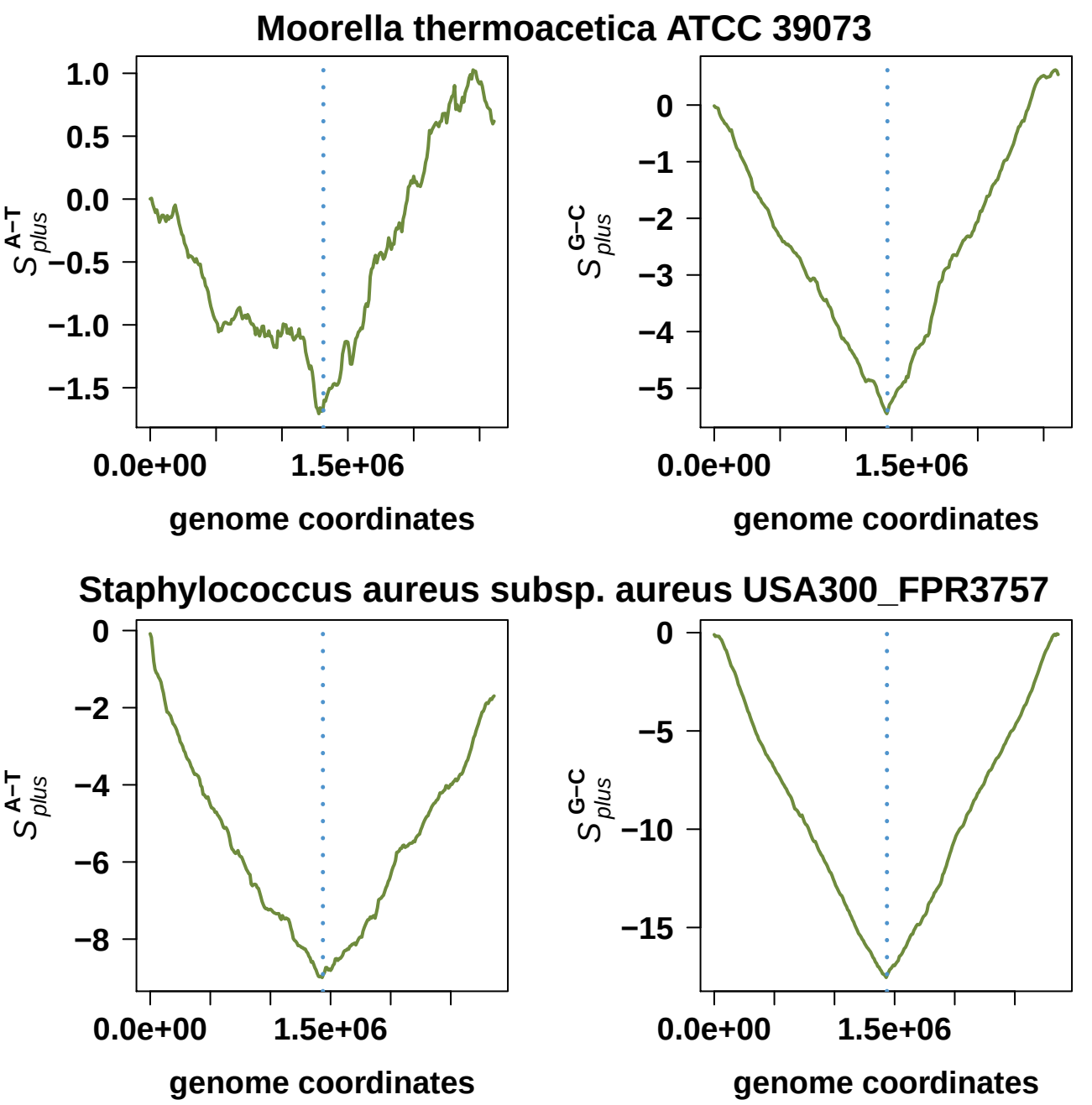

Lactobacillus acidophilus NCFM
S^{A-T}_{plus}
0.5
0.0
−0.5
−1.0
−1.5
−2.0
0.0e+00
1.0e+06
2.0e+06
genome coordinates
S^{G-C}_{plus}
2
0
−2
−4
−6
−8
0.0e+00
1.0e+06
2.0e+06
genome coordinates
Staphylococcus haemolyticus JCSC1435
S^{A-T}_{plus}
1
0
−1
−2
−3
−4
0.0e+00
1.5e+06
genome coordinates
S^{G-C}_{plus}
2
0
−2
−4
−6
−8
−10
0.0e+00
1.5e+06
genome coordinates

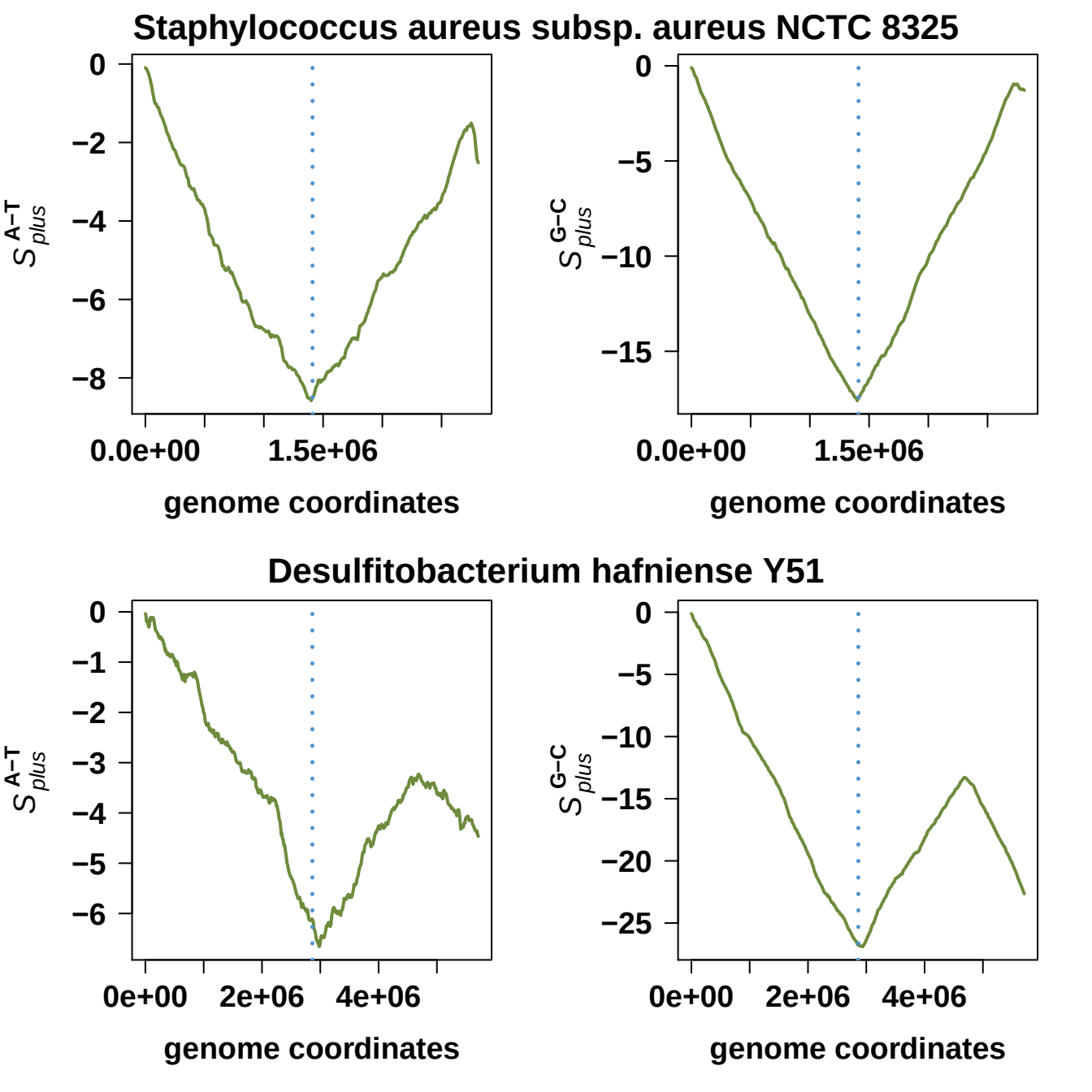

Streptococcus pyogenes MGAS6180
0.0
−0.5
−1.0
−1.5
−2.0
−2.5
−3.0
S^{A-T}_{plus}
0.0e+00
1.0e+06
genome coordinates
0
−2
−4
−6
−8
S^{G-C}_{plus}
0.0e+00
1.0e+06
genome coordinates
Streptococcus pyogenes MGAS5005
0.0
−0.5
−1.0
−1.5
−2.0
S^{A-T}_{plus}
0.0e+00
1.0e+06
genome coordinates
0
−2
−4
−6
−8
S^{G-C}_{plus}
0.0e+00
1.0e+06
genome coordinates

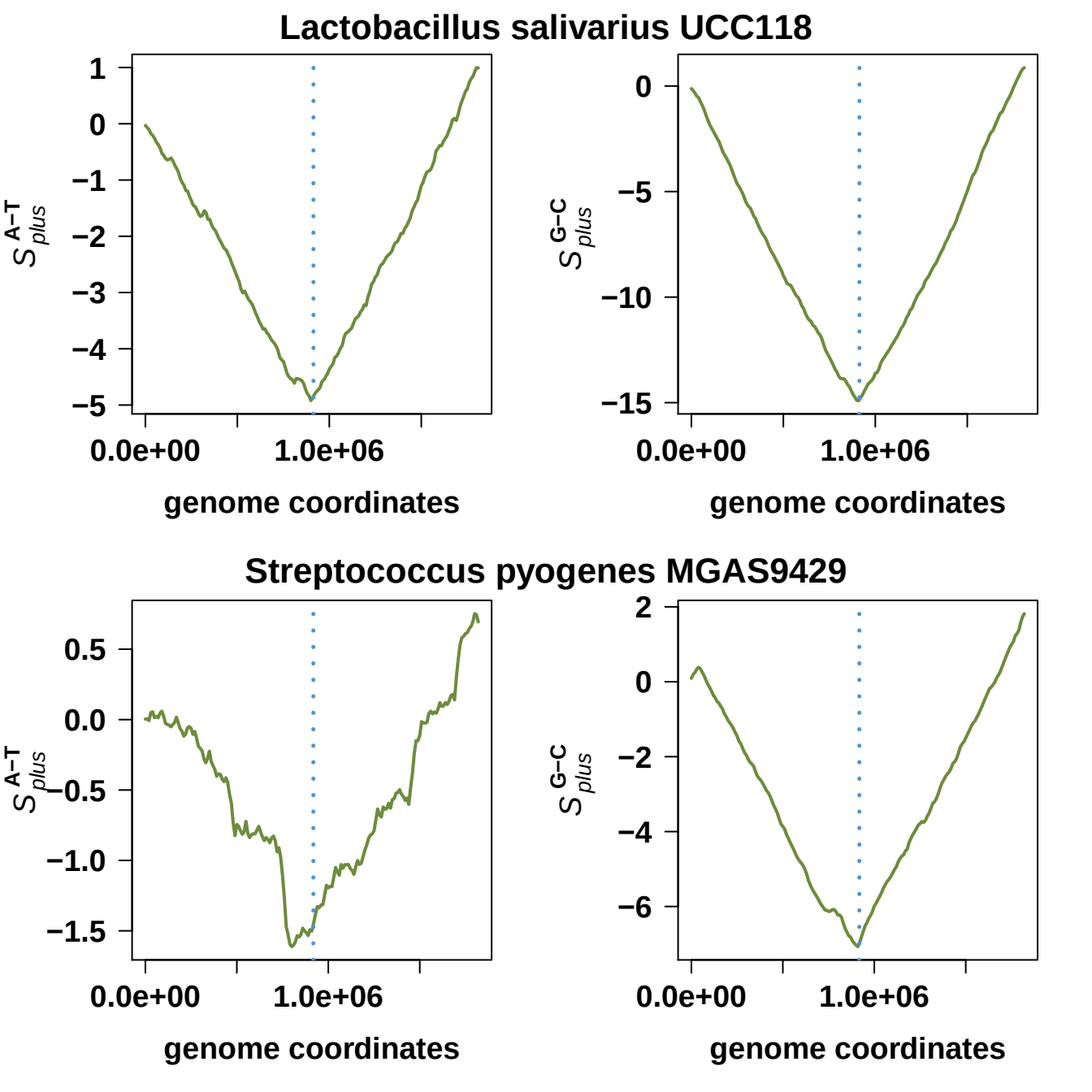

Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305
S^{A-T}_{plus}
1
0
−1
−2
−3
−4
−5
0.0e+00
1.5e+06
genome coordinates
S^{G-C}_{plus}
0
−5
−10
0.0e+00
1.5e+06
genome coordinates
Streptococcus agalactiae A909
S^{A-T}_{plus}
1.5
1.0
0.5
0.0
−0.5
−1.0
0.0e+00
1.0e+06
2.0e+06
genome coordinates
S^{G-C}_{plus}
0
−2
−4
−6
−8
−10
0.0e+00
1.0e+06
2.0e+06
genome coordinates

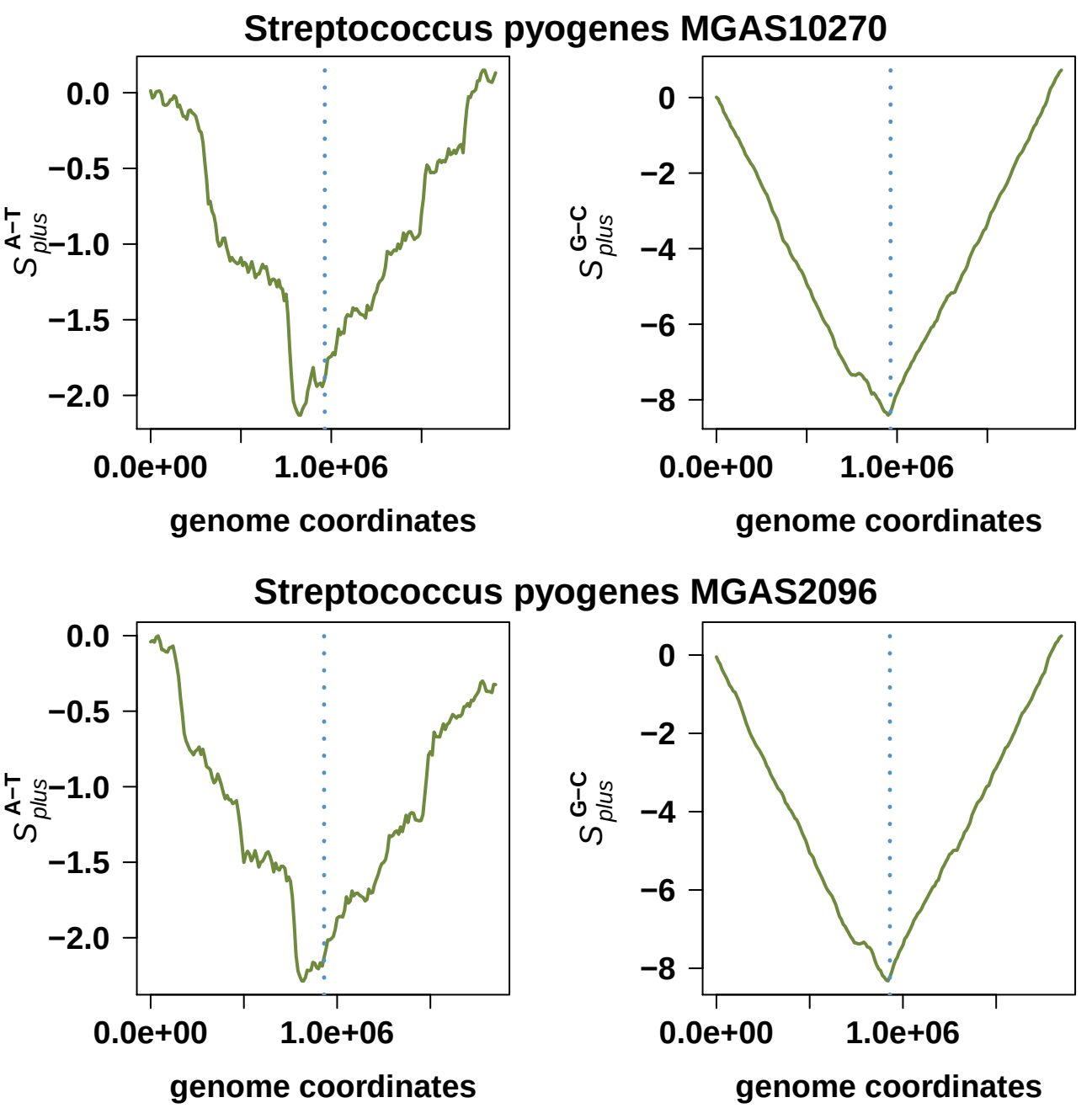

Carboxydothermus hydrogenoformans Z−2901
S^{A-T}_{plus}
0
−1
−2
−3
−4
0.0e+00
1.0e+06
2.0e+06
genome coordinates
S^{G-C}_{plus}
0
−5
−10
−15
0.0e+00
1.0e+06
2.0e+06
genome coordinates
Bacillus anthracis str. 'Ames Ancestor'
S^{A-T}_{plus}
0
−2
−4
−6
−8
−10
−12
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
0
−10
−20
−30
−40
0e+00
2e+06
4e+06
genome coordinates

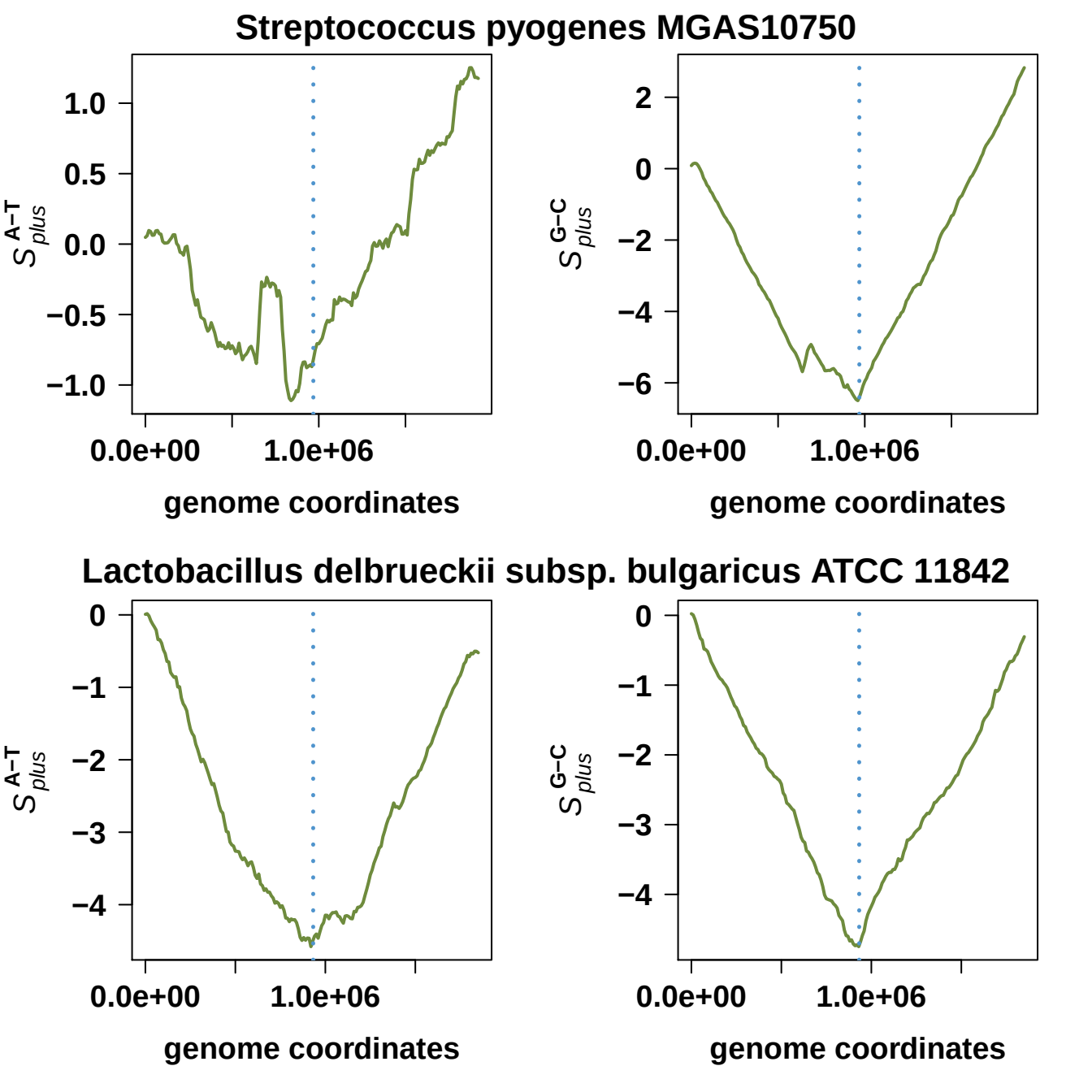

Lactobacillus sakei subsp. sakei 23K
0.0
−0.5
−1.0
−1.5
−2.0
−2.5
S^{A-T}_{plus}
0.0e+00
1.0e+06
genome coordinates
0
−2
−4
−6
−8
S^{G-C}_{plus}
0.0e+00
1.0e+06
genome coordinates
Staphylococcus aureus RF122
0
−2
−4
−6
S^{A-T}_{plus}
0.0e+00
1.5e+06
genome coordinates
0
−5
−10
−15
S^{G-C}_{plus}
0.0e+00
1.5e+06
genome coordinates

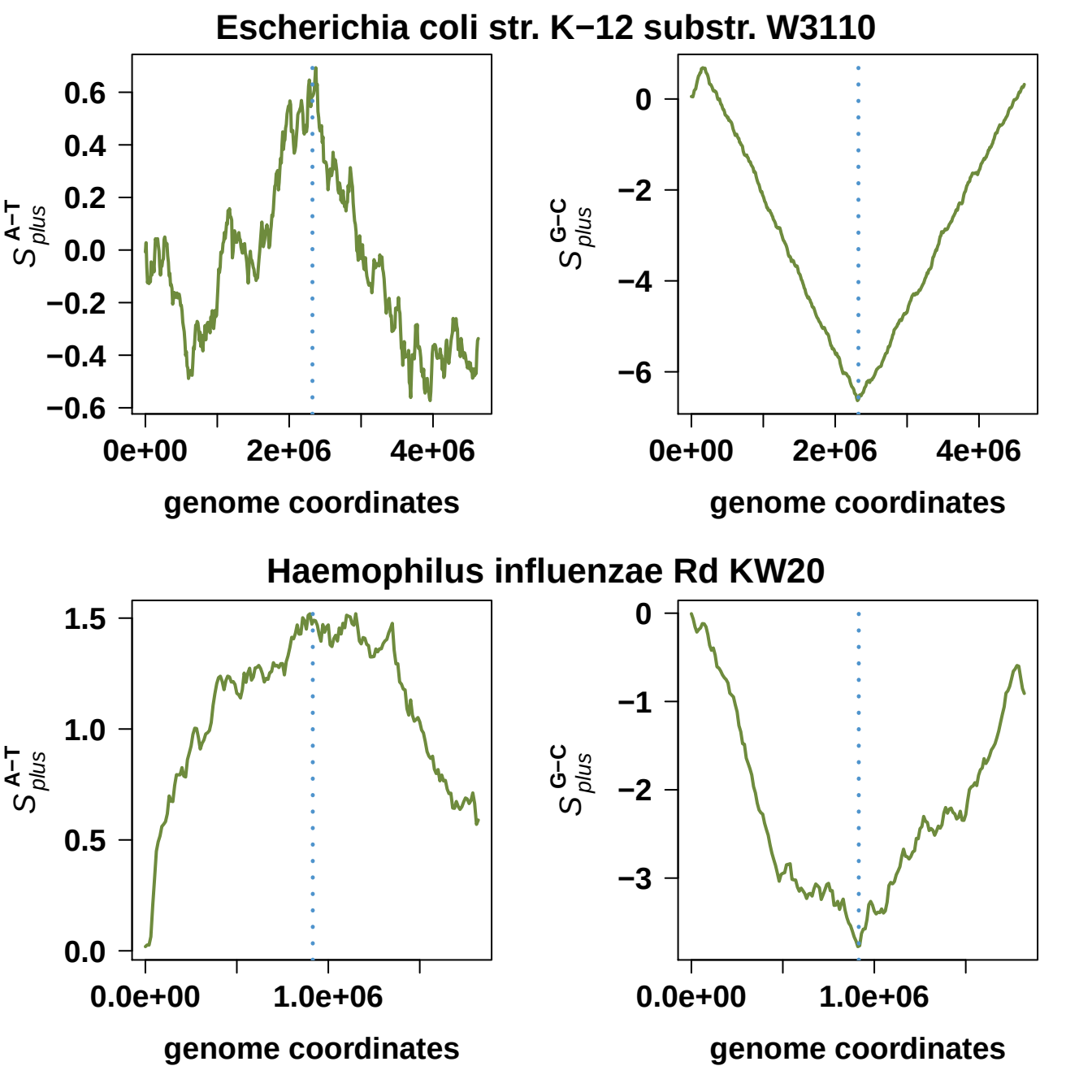

Moorella thermoacetica ATCC 39073
1.0
0.5
0.0
−0.5
−1.0
−1.5
S^{A-T}_{plus}
0.0e+00
1.5e+06
genome coordinates
0
−1
−2
−3
−4
−5
S^{G-C}_{plus}
0.0e+00
1.5e+06
genome coordinates
Staphylococcus aureus subsp. aureus USA300_FPR3757
0
−2
−4
−6
−8
S^{A-T}_{plus}
0.0e+00
1.5e+06
genome coordinates
0
−5
−10
−15
S^{G-C}_{plus}
0.0e+00
1.5e+06
genome coordinates

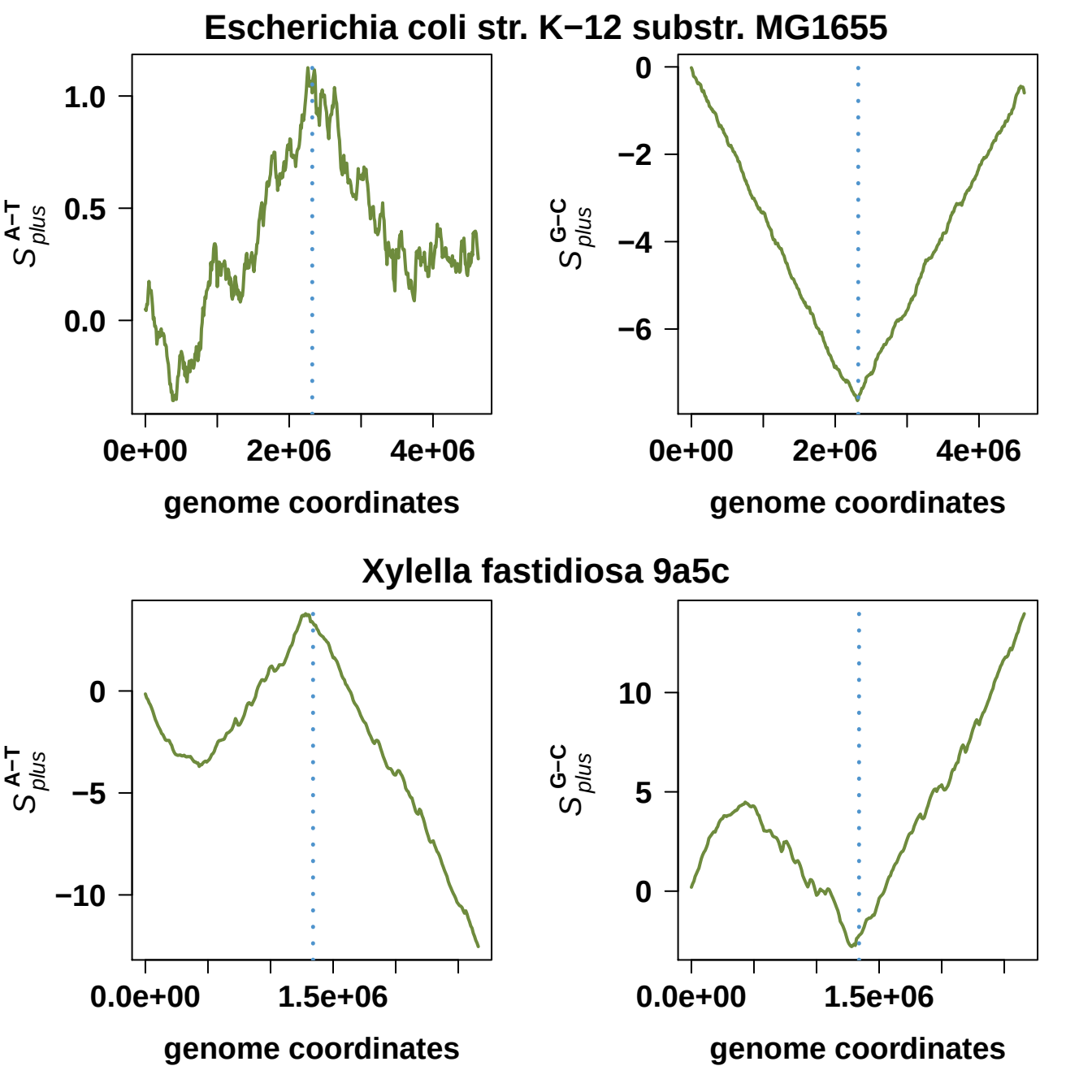

Staphylococcus aureus subsp. aureus NCTC 8325
S^{A-T}_{plus}
0
−2
−4
−6
−8
0.0e+00
1.5e+06
genome coordinates
S^{G-C}_{plus}
0
−5
−10
−15
0.0e+00
1.5e+06
genome coordinates
Desulfitobacterium hafniense Y51
S^{A-T}_{plus}
0
−1
−2
−3
−4
−5
−6
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
0
−5
−10
−15
−20
−25
0e+00
2e+06
4e+06
genome coordinates

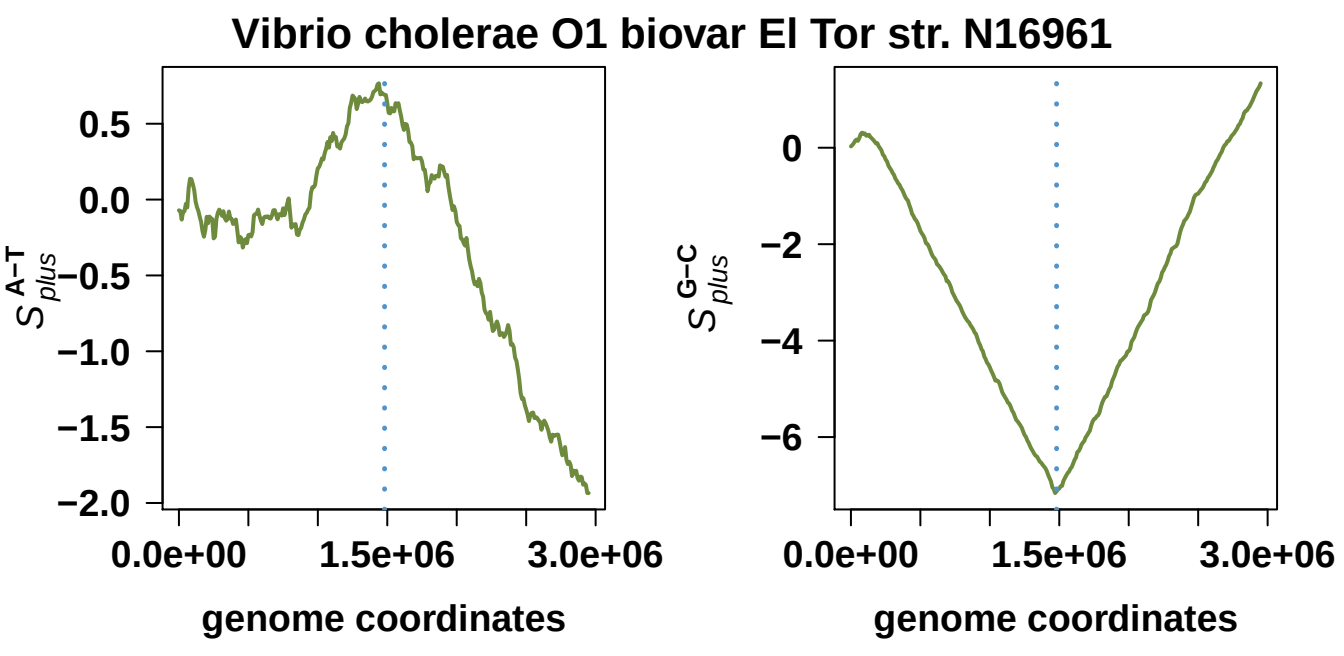

Lactobacillus salivarius UCC118
S^{A-T}_{plus}
1
0
−1
−2
−3
−4
−5
0.0e+00
1.0e+06
genome coordinates
S^{G-C}_{plus}
0
−5
−10
−15
0.0e+00
1.0e+06
genome coordinates
Streptococcus pyogenes MGAS9429
S^{A-T}_{plus}
0.5
0.0
−0.5
−1.0
−1.5
0.0e+00
1.0e+06
genome coordinates
S^{G-C}_{plus}
2
0
−2
−4
−6
0.0e+00
1.0e+06
genome coordinates

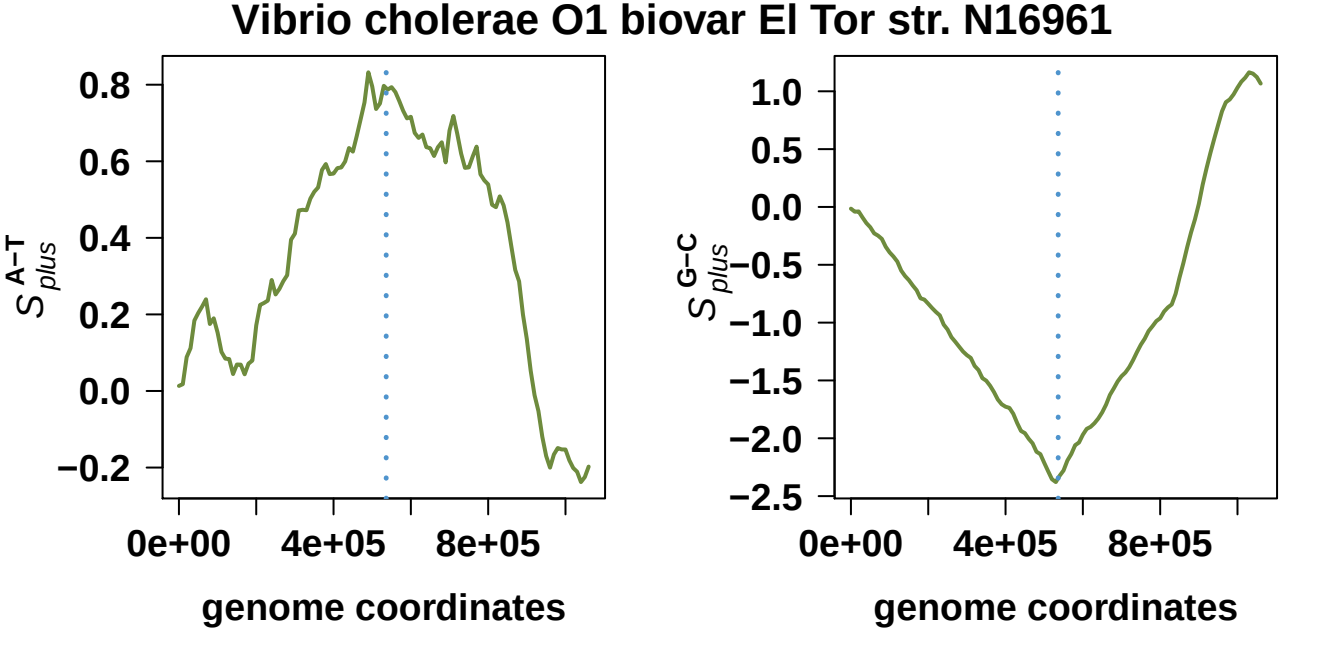

Streptococcus pyogenes MGAS10270
0.0
−0.5
−1.0
−1.5
−2.0
S^{A-T}_{plus}
0.0e+00
1.0e+06
genome coordinates
0
−2
−4
−6
−8
S^{G-C}_{plus}
0.0e+00
1.0e+06
genome coordinates
Streptococcus pyogenes MGAS2096
0.0
−0.5
−1.0
−1.5
−2.0
S^{A-T}_{plus}
0.0e+00
1.0e+06
genome coordinates
0
−2
−4
−6
−8
S^{G-C}_{plus}
0.0e+00
1.0e+06
genome coordinates

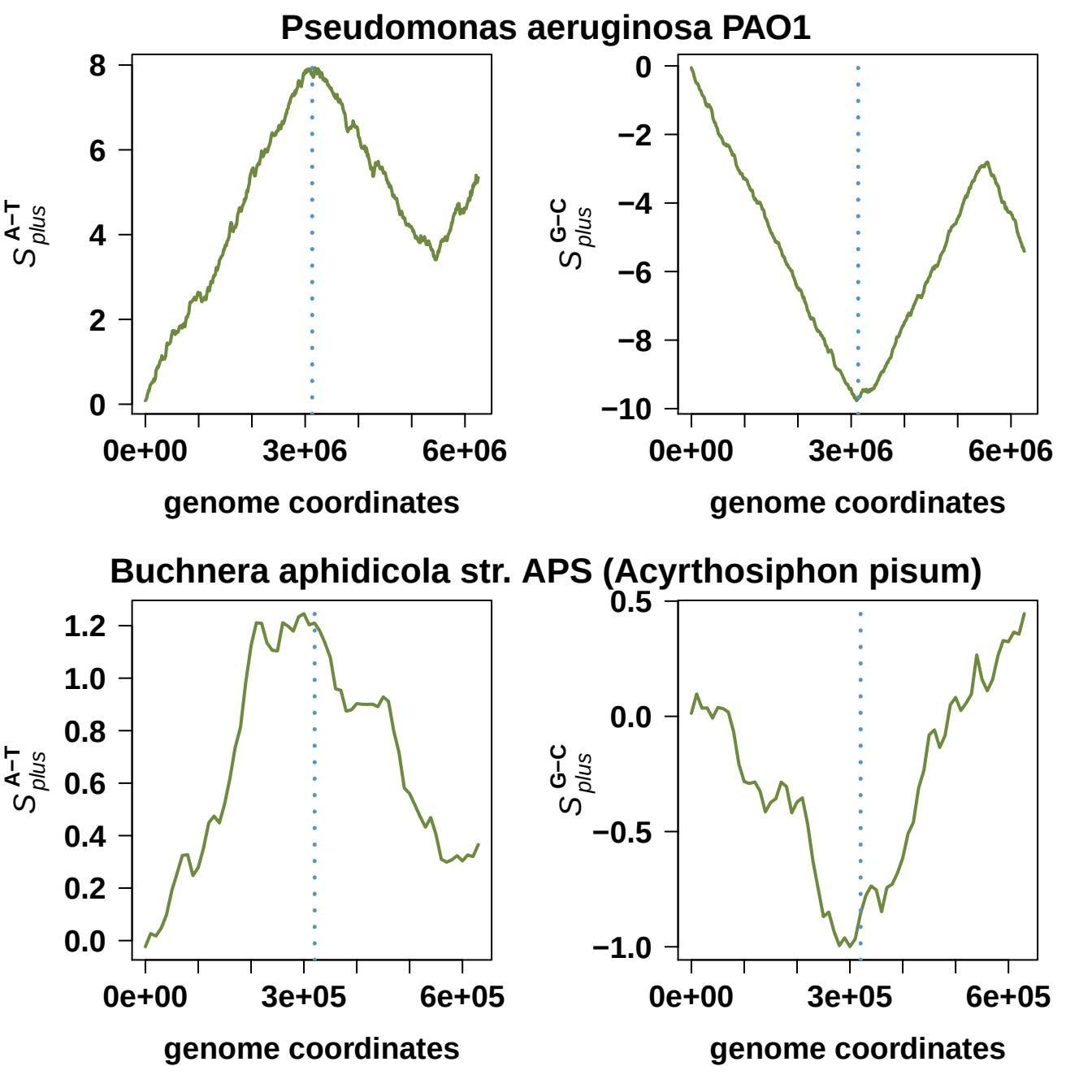

Streptococcus pyogenes MGAS10750
S^{A-T}_{plus}
1.0
0.5
0.0
−0.5
−1.0
0.0e+00
1.0e+06
genome coordinates
S^{G-C}_{plus}
2
0
−2
−4
−6
0.0e+00
1.0e+06
genome coordinates
Lactobacillus delbrueckii subsp. bulgaricus ATCC 11842
S^{A-T}_{plus}
0
−1
−2
−3
−4
0.0e+00
1.0e+06
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
−4
0.0e+00
1.0e+06
genome coordinates

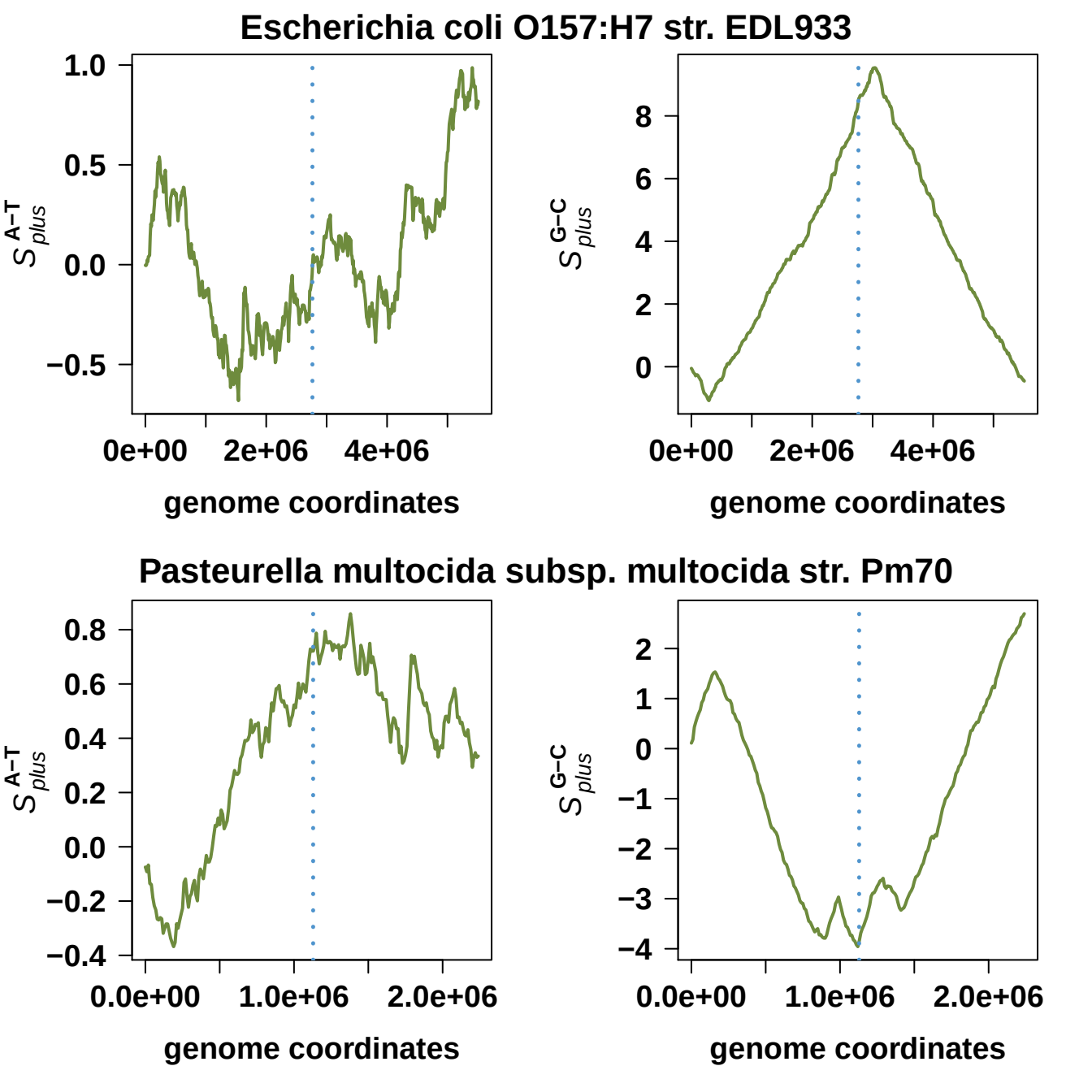

Escherichia coli str. K−12 substr. W3110
S^{A-T}_{plus}
0.6
0.4
0.2
0.0
−0.2
−0.4
−0.6
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
0
−2
−4
−6
0e+00
2e+06
4e+06
genome coordinates
Haemophilus influenzae Rd KW20
S^{A-T}_{plus}
1.5
1.0
0.5
0.0
0.0e+00
1.0e+06
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
0.0e+00
1.0e+06
genome coordinates

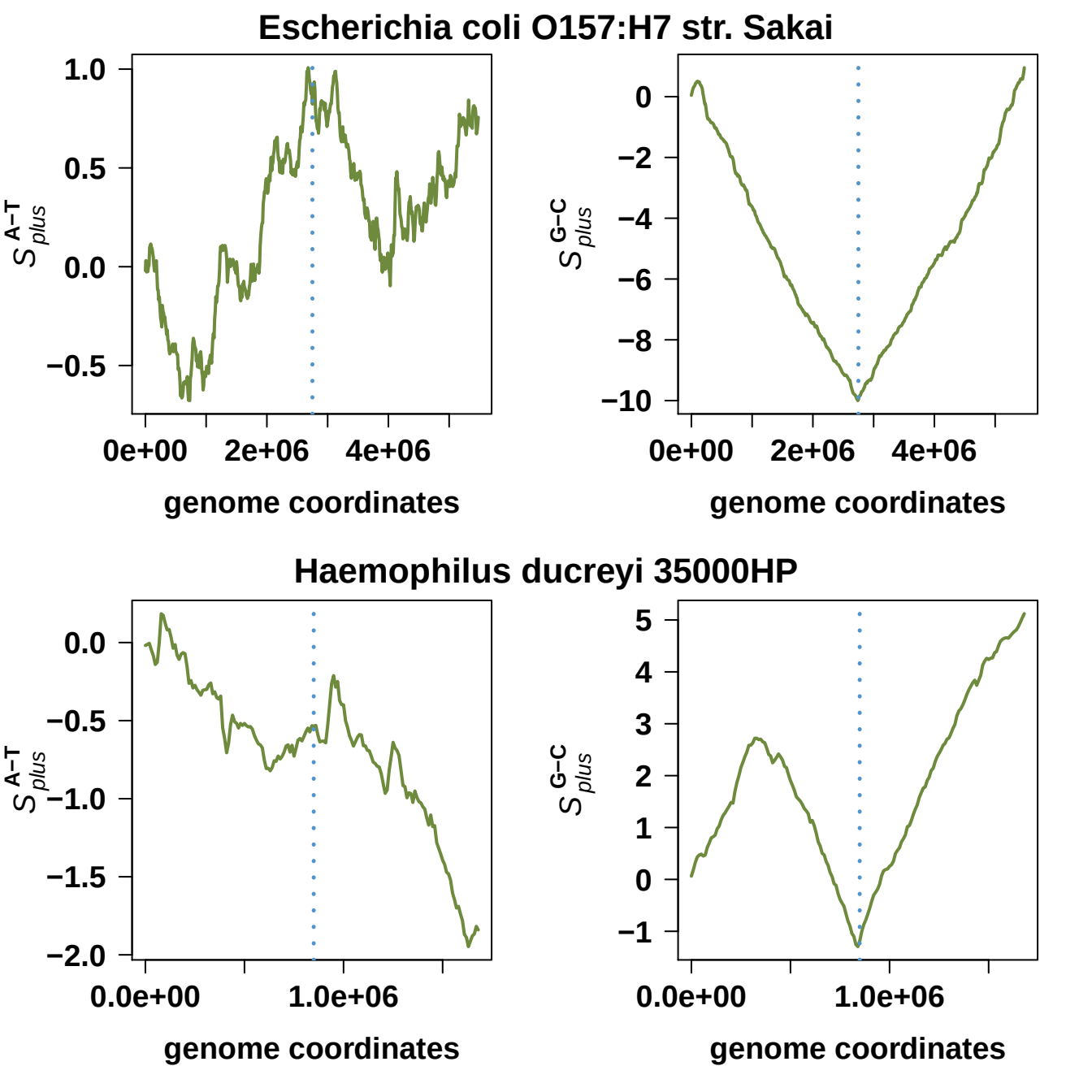

Escherichia coli str. K−12 substr. MG1655
1.0
0.5
0.0
S^{A-T}_{plus}
0e+00
2e+06
4e+06
genome coordinates
0
−2
−4
−6
S^{G-C}_{plus}
0e+00
2e+06
4e+06
genome coordinates
Xylella fastidiosa 9a5c
0
−5
−10
S^{A-T}_{plus}
0.0e+00
1.5e+06
genome coordinates
10
5
0
S^{G-C}_{plus}
0.0e+00
1.5e+06
genome coordinates

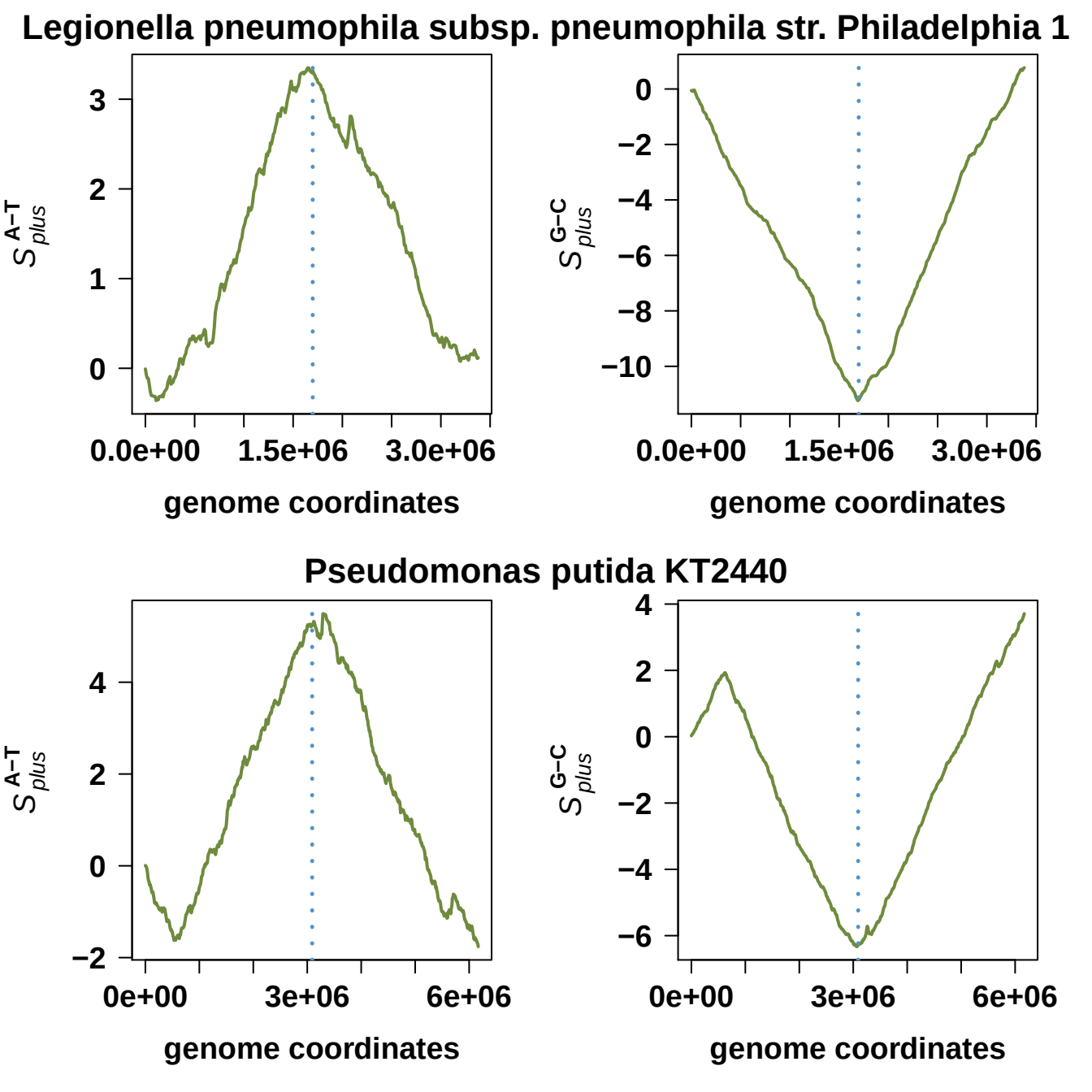

Vibrio cholerae O1 biovar El Tor str. N16961
S^{A-T}_{plus}
0.5
0.0
−0.5
−1.0
−1.5
−2.0
0.0e+00
1.5e+06
3.0e+06
genome coordinates
S^{G-C}_{plus}
0
−2
−4
−6
0.0e+00
1.5e+06
3.0e+06
genome coordinates

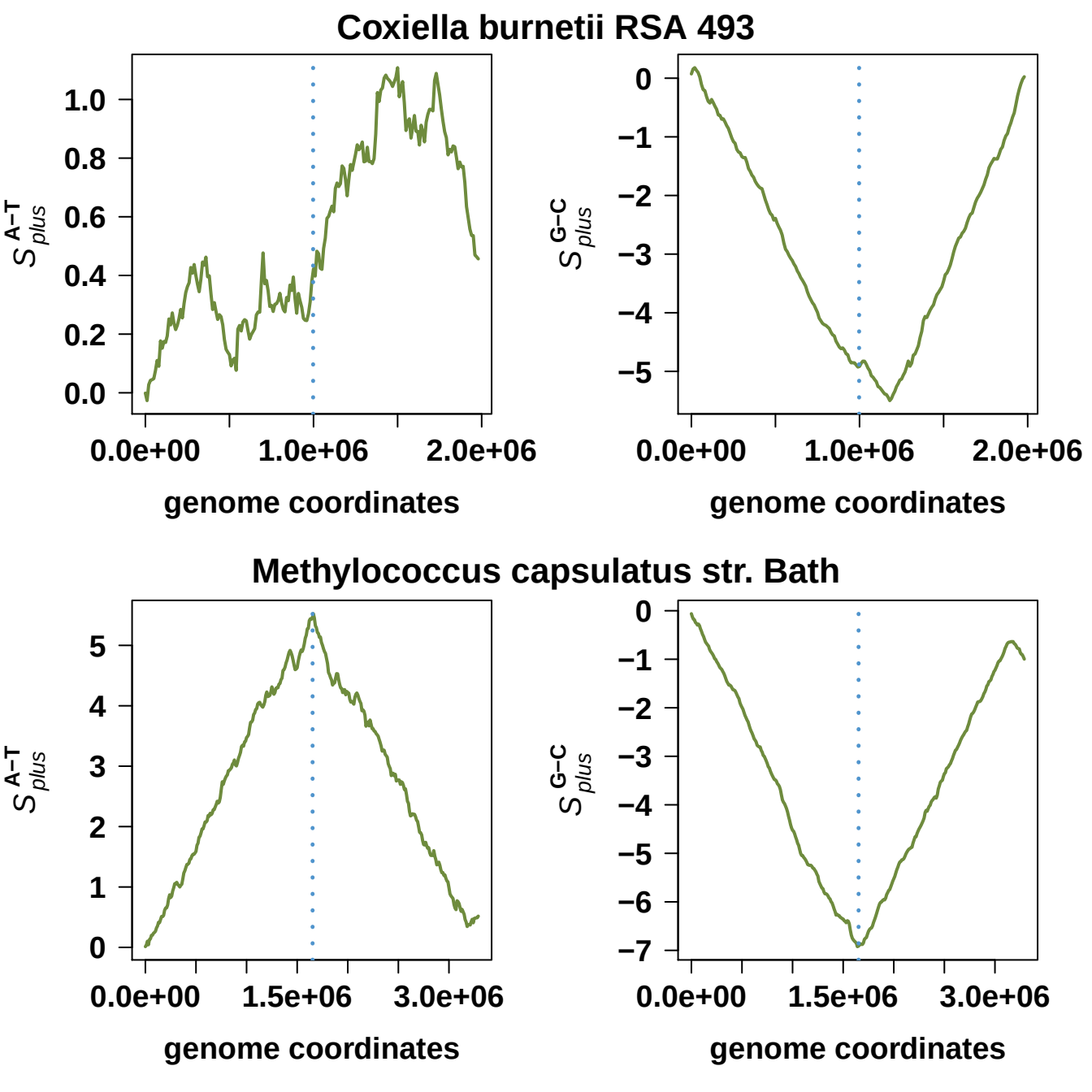

Vibrio cholerae O1 biovar El Tor str. N16961
S^{A-T}_{plus}
0.8
0.6
0.4
0.2
0.0
−0.2
0e+00
4e+05
8e+05
genome coordinates
S^{G-C}_{plus}
1.0
0.5
0.0
−0.5
−1.0
−1.5
−2.0
−2.5
0e+00
4e+05
8e+05
genome coordinates

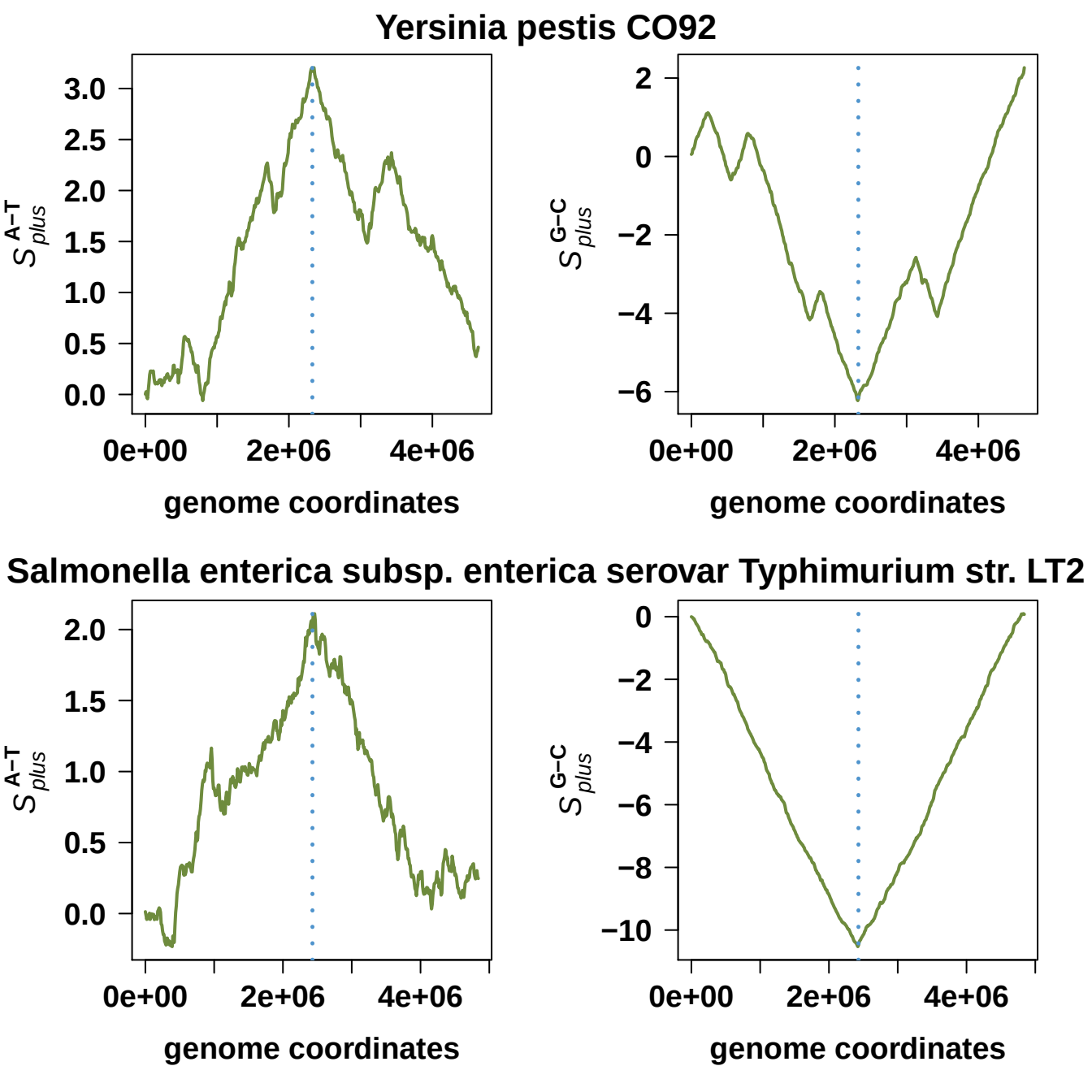

Pseudomonas aeruginosa PAO1
S^{A-T}_{plus}
8
6
4
2
0
0e+00
3e+06
6e+06
genome coordinates
S^{G-C}_{plus}
0
−2
−4
−6
−8
−10
0e+00
3e+06
6e+06
genome coordinates
Buchnera aphidicola str. APS (Acyrthosiphon pisum)
S^{A-T}_{plus}
1.2
1.0
0.8
0.6
0.4
0.2
0.0
0e+00
3e+05
6e+05
genome coordinates
S^{G-C}_{plus}
0.5
0.0
−0.5
−1.0
0e+00
3e+05
6e+05
genome coordinates

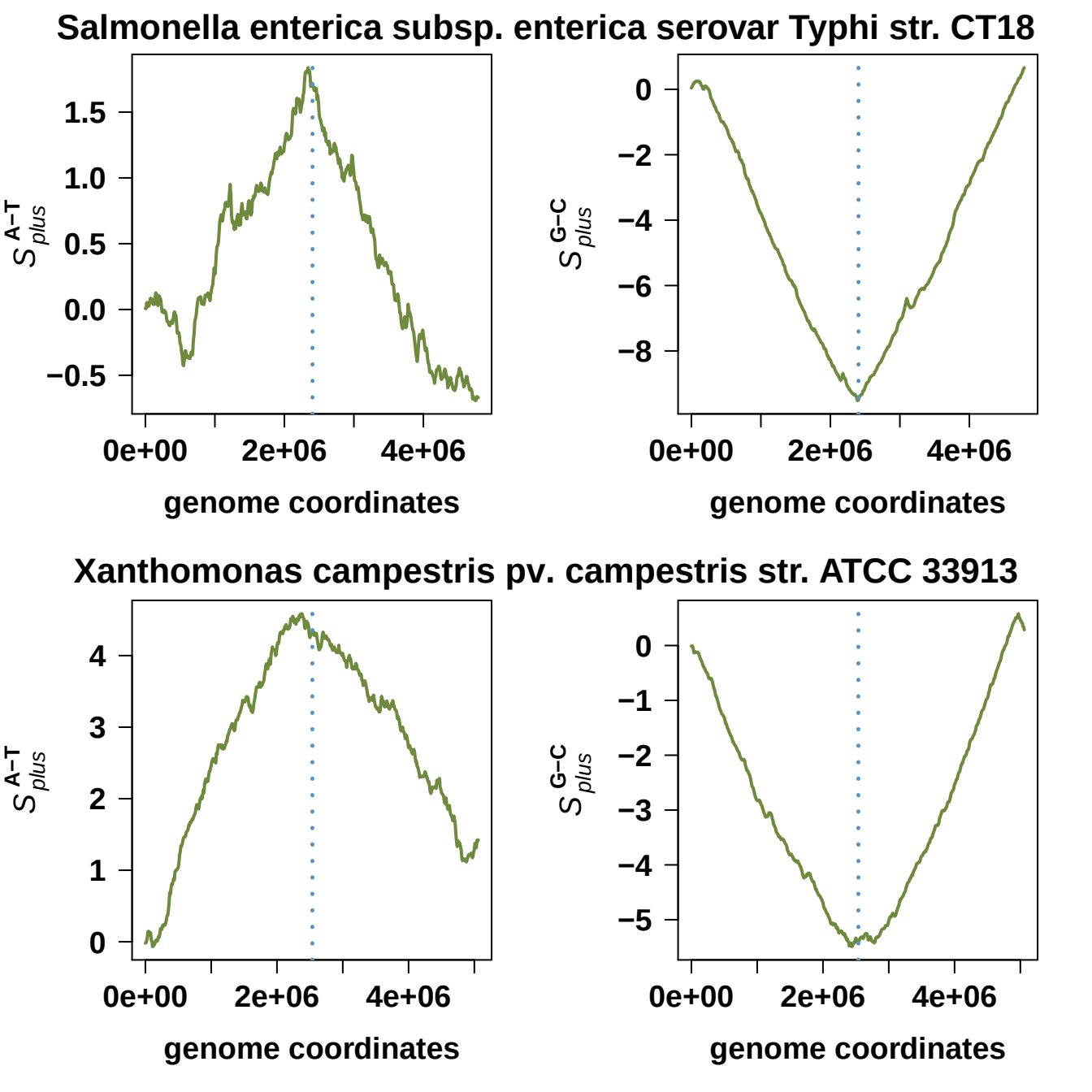

Escherichia coli O157:H7 str. EDL933
1.0
0.5
0.0
−0.5
S^{A-T}_{plus}
0e+00
2e+06
4e+06
genome coordinates
8
6
4
2
0
S^{G-C}_{plus}
0e+00
2e+06
4e+06
genome coordinates
Pasteurella multocida subsp. multocida str. Pm70
0.8
0.6
0.4
0.2
0.0
−0.2
−0.4
S^{A-T}_{plus}
0.0e+00
1.0e+06
2.0e+06
genome coordinates
2
1
0
−1
−2
−3
−4
S^{G-C}_{plus}
0.0e+00
1.0e+06
2.0e+06
genome coordinates

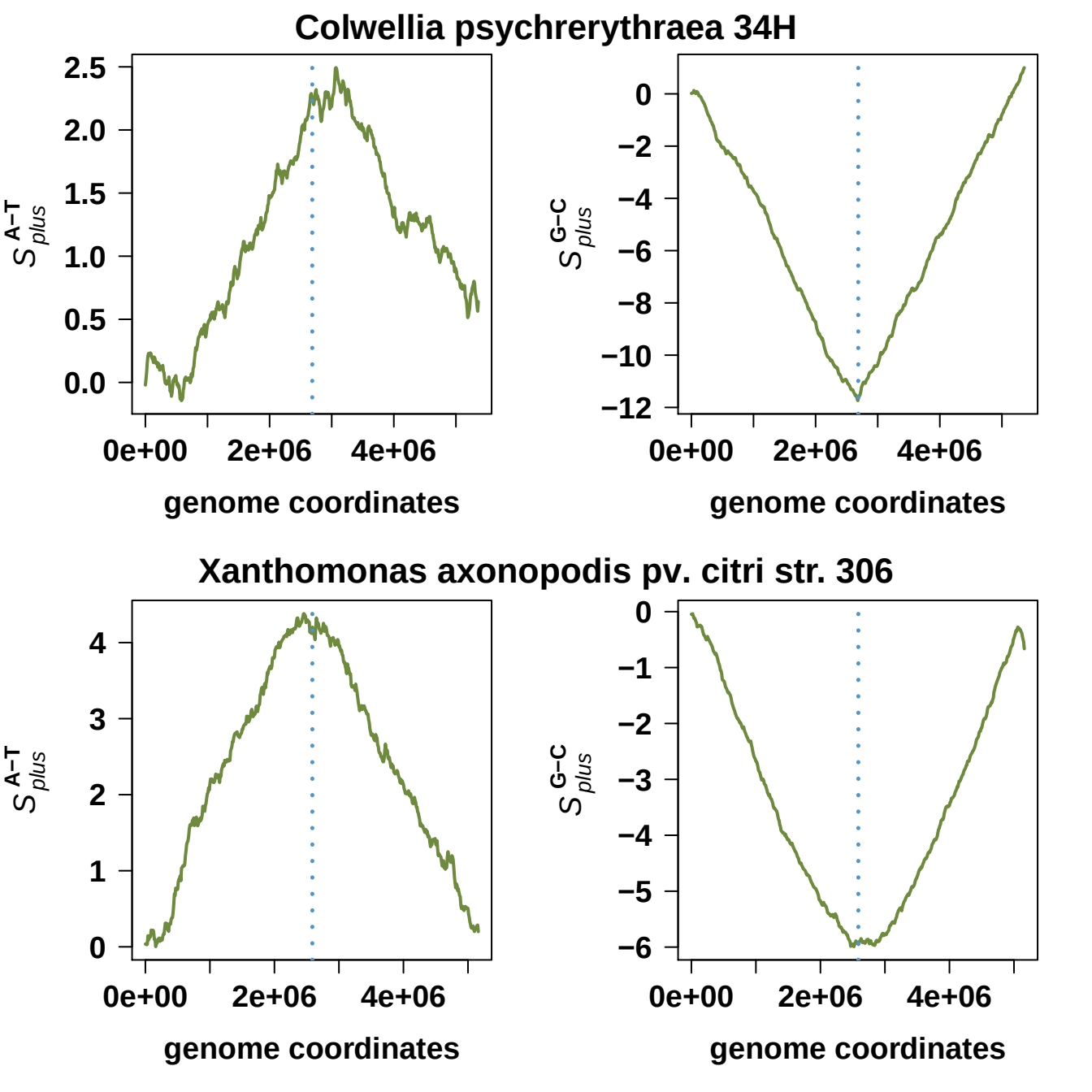

Escherichia coli O157:H7 str. Sakai
1.0
0.5
0.0
−0.5
S^{A-T}_{plus}
0e+00
2e+06
4e+06
genome coordinates
0
−2
−4
−6
−8
−10
S^{G-C}_{plus}
0e+00
2e+06
4e+06
genome coordinates
Haemophilus ducreyi 35000HP
0.0
−0.5
−1.0
−1.5
−2.0
S^{A-T}_{plus}
0.0e+00
1.0e+06
genome coordinates
5
4
3
2
1
0
−1
S^{G-C}_{plus}
0.0e+00
1.0e+06
genome coordinates

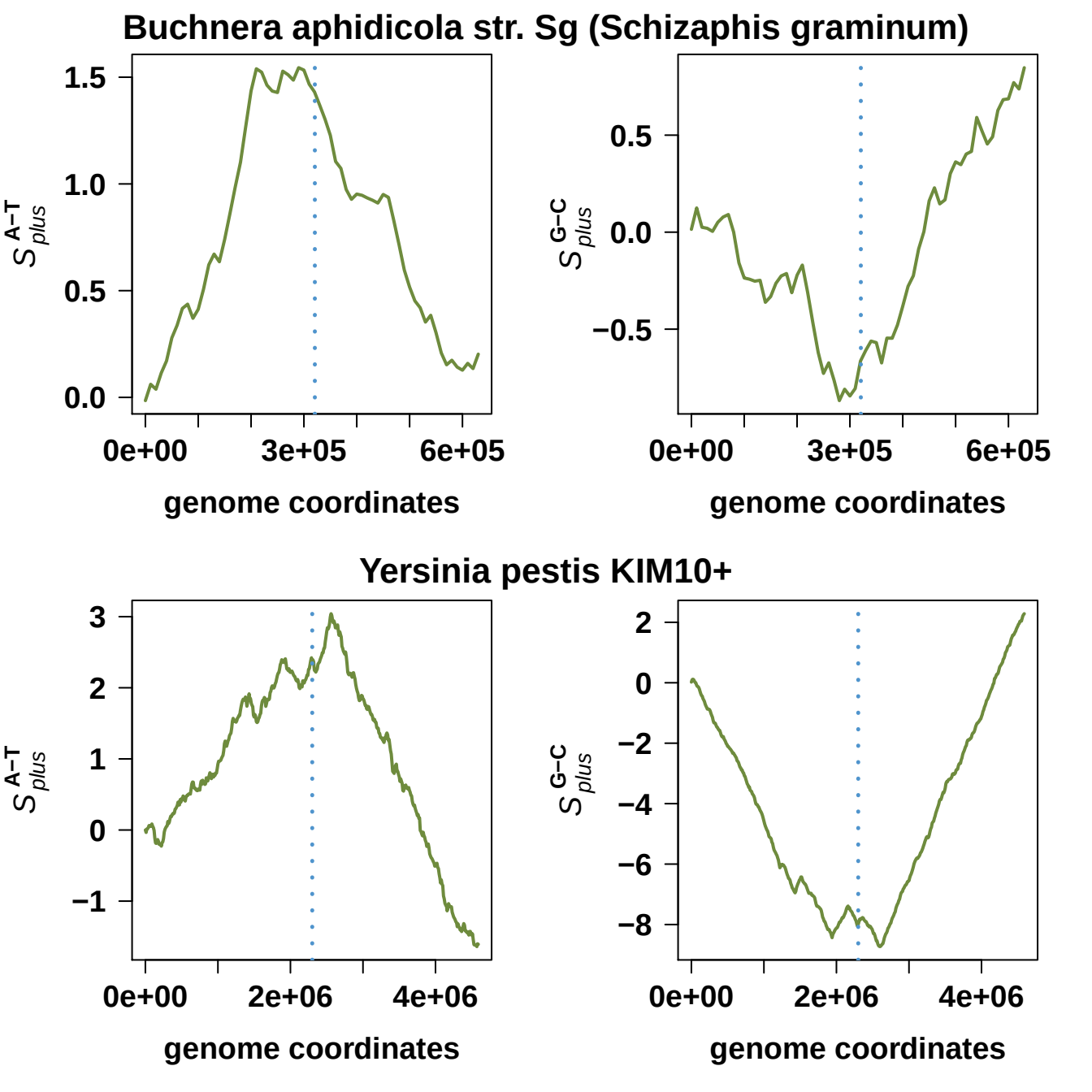

Legionella pneumophila subsp. pneumophila str. Philadelphia 1
S^{A-T}_{plus}
3
2
1
0
0.0e+00
1.5e+06
3.0e+06
genome coordinates
S^{G-C}_{plus}
0
−2
−4
−6
−8
−10
0.0e+00
1.5e+06
3.0e+06
genome coordinates
Pseudomonas putida KT2440
S^{A-T}_{plus}
4
2
0
−2
0e+00
3e+06
6e+06
genome coordinates
S^{G-C}_{plus}
4
2
0
−2
−4
−6
0e+00
3e+06
6e+06
genome coordinates

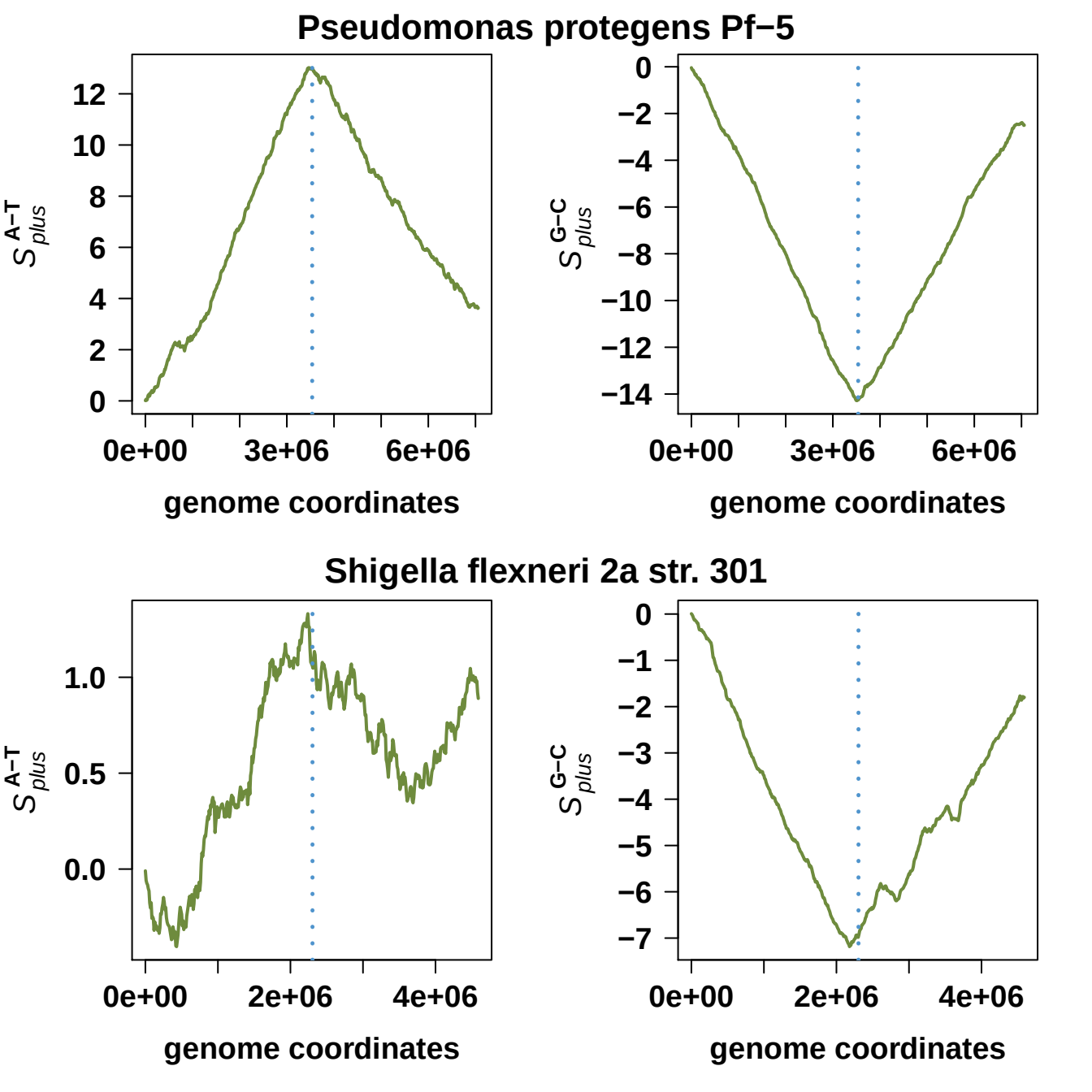

Coxiella burnetii RSA 493
S^{A-T}_{plus}
1.0
0.8
0.6
0.4
0.2
0.0
0.0e+00
1.0e+06
2.0e+06
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
−4
−5
0.0e+00
1.0e+06
2.0e+06
genome coordinates
Methylococcus capsulatus str. Bath
S^{A-T}_{plus}
5
4
3
2
1
0
0.0e+00
1.5e+06
3.0e+06
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
−4
−5
−6
−7
0.0e+00
1.5e+06
3.0e+06
genome coordinates

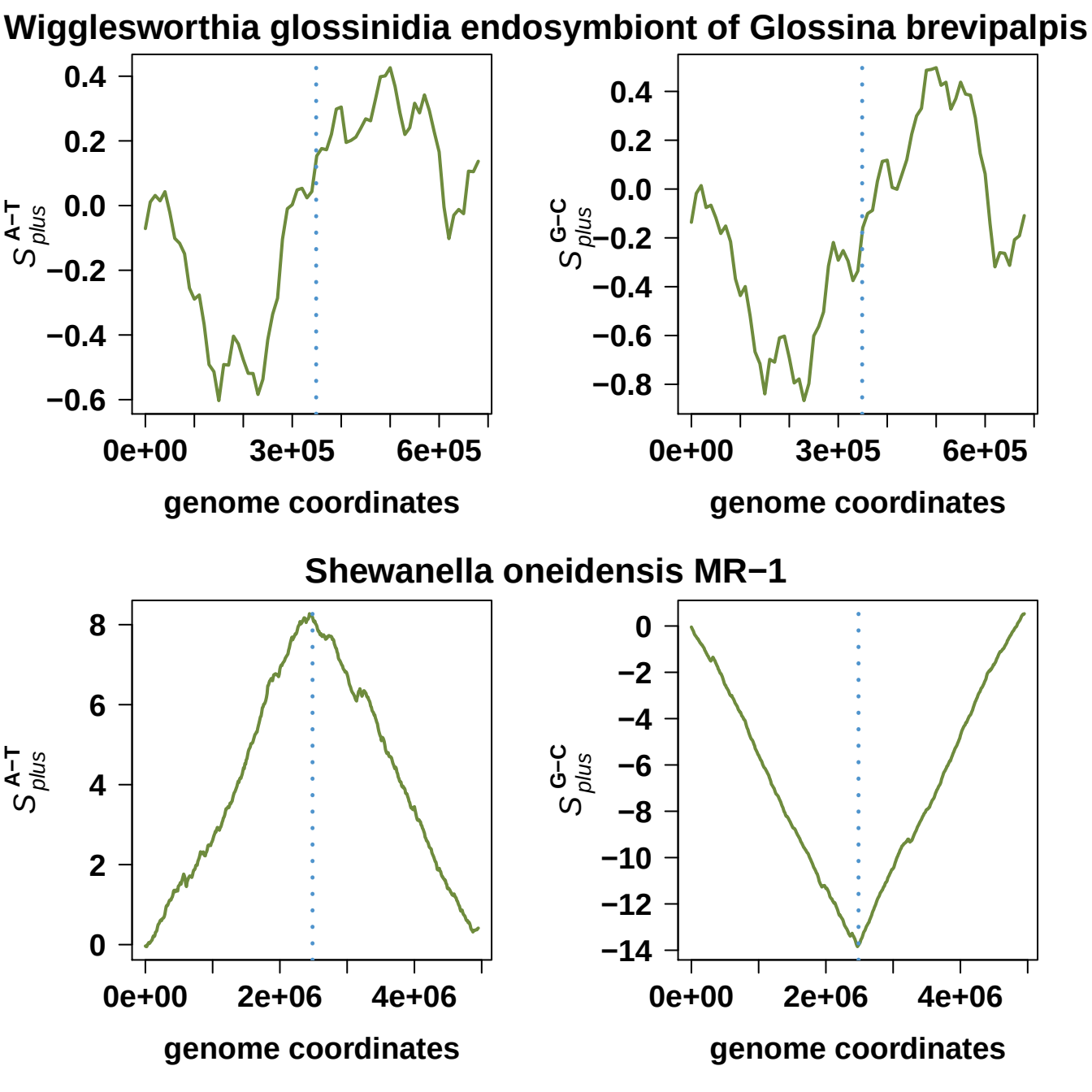

Yersinia pestis CO92
S^{A-T}_{plus}
3.0
2.5
2.0
1.5
1.0
0.5
0.0
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
2
0
−2
−4
−6
0e+00
2e+06
4e+06
genome coordinates
Salmonella enterica subsp. enterica serovar Typhimurium str. LT2
S^{A-T}_{plus}
2.0
1.5
1.0
0.5
0.0
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
0
−2
−4
−6
−8
−10
0e+00
2e+06
4e+06
genome coordinates

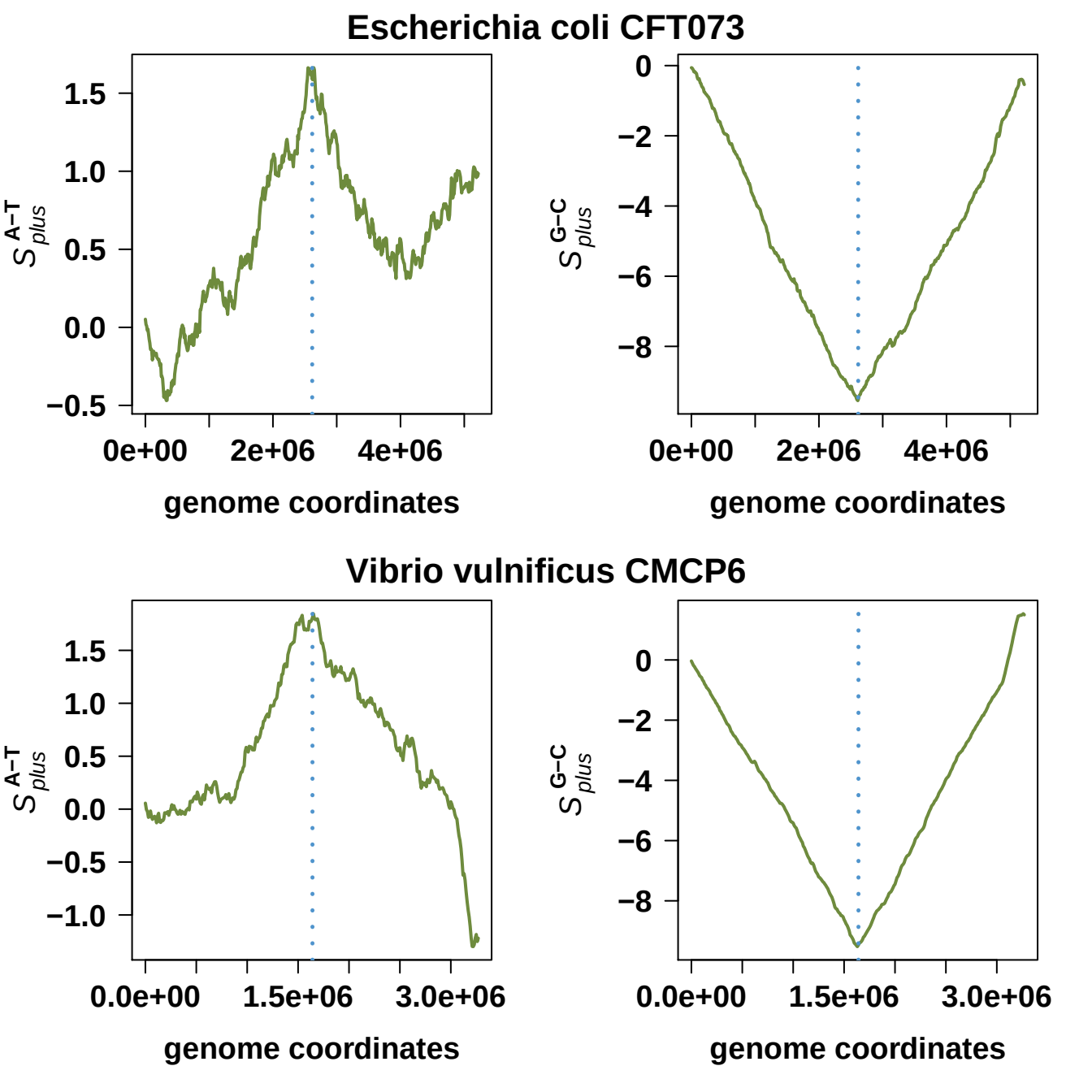

Salmonella enterica subsp. enterica serovar Typhi str. CT18
S^{A-T}_{plus}
1.5
1.0
0.5
0.0
−0.5
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
0
−2
−4
−6
−8
0e+00
2e+06
4e+06
genome coordinates
Xanthomonas campestris pv. campestris str. ATCC 33913
S^{A-T}_{plus}
4
3
2
1
0
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
−4
−5
0e+00
2e+06
4e+06
genome coordinates

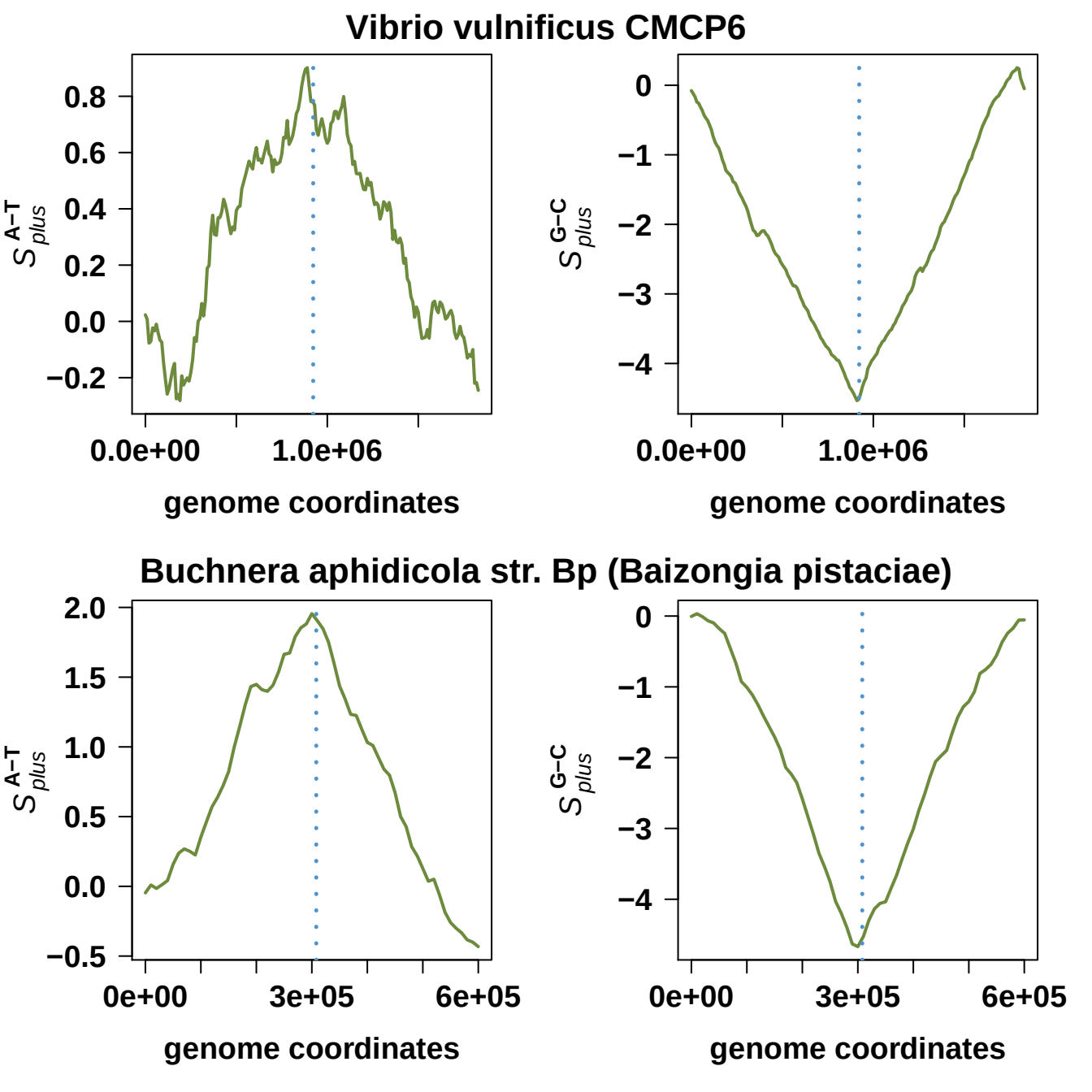

Colwellia psychrerythraea 34H
S^{A-T}_{plus}
2.5
2.0
1.5
1.0
0.5
0.0
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
0
−2
−4
−6
−8
−10
−12
0e+00
2e+06
4e+06
genome coordinates
Xanthomonas axonopodis pv. citri str. 306
S^{A-T}_{plus}
4
3
2
1
0
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
−4
−5
−6
0e+00
2e+06
4e+06
genome coordinates

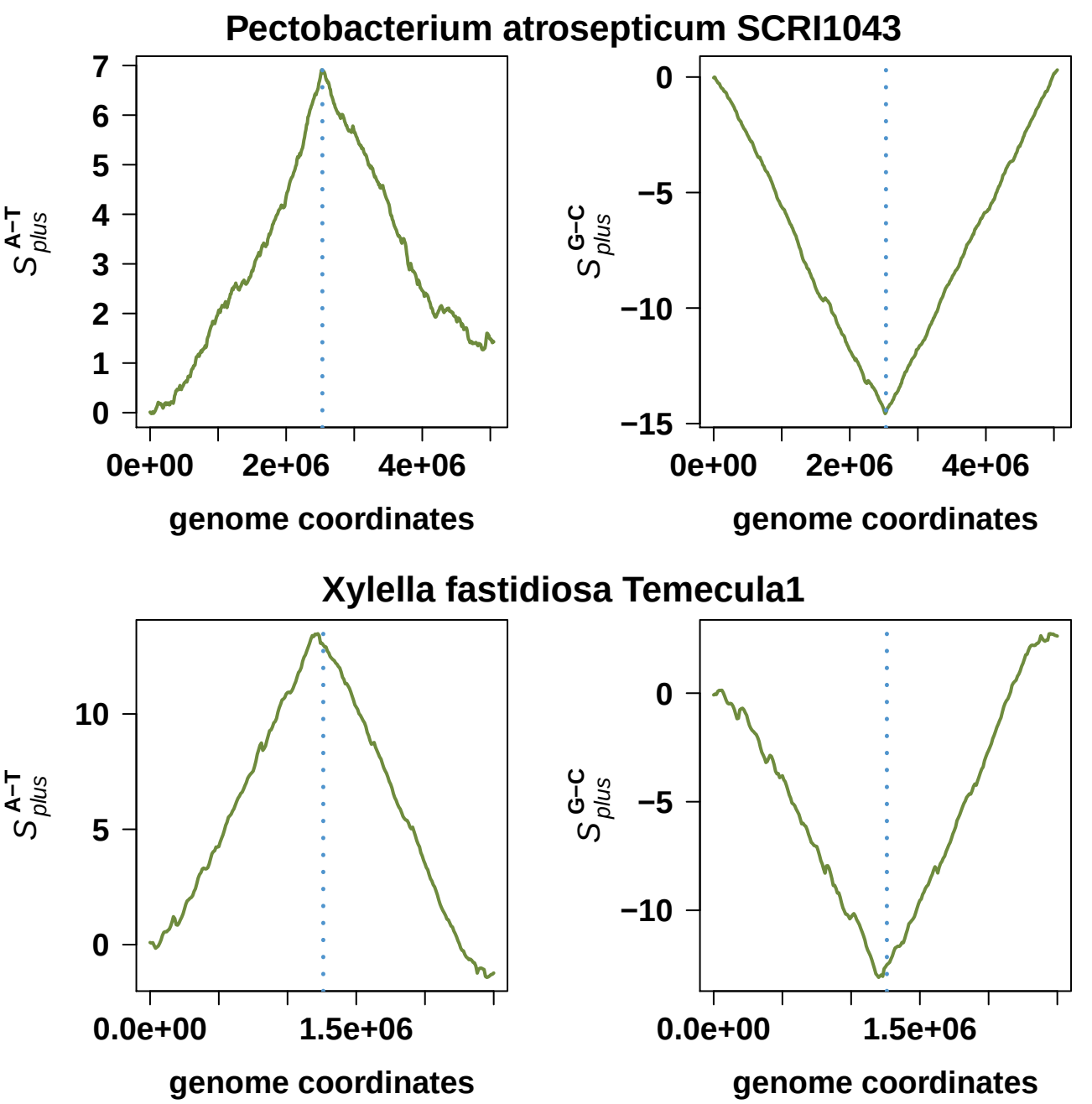

Buchnera aphidicola str. Sg (Schizaphis graminum)
1.5
1.0
0.5
0.0
S^{A-T}_{plus}
0e+00
3e+05
6e+05
genome coordinates
0.5
0.0
−0.5
S^{G-C}_{plus}
0e+00
3e+05
6e+05
genome coordinates
Yersinia pestis KIM10+
3
2
1
0
−1
S^{A-T}_{plus}
0e+00
2e+06
4e+06
genome coordinates
2
0
−2
−4
−6
−8
S^{G-C}_{plus}
0e+00
2e+06
4e+06
genome coordinates

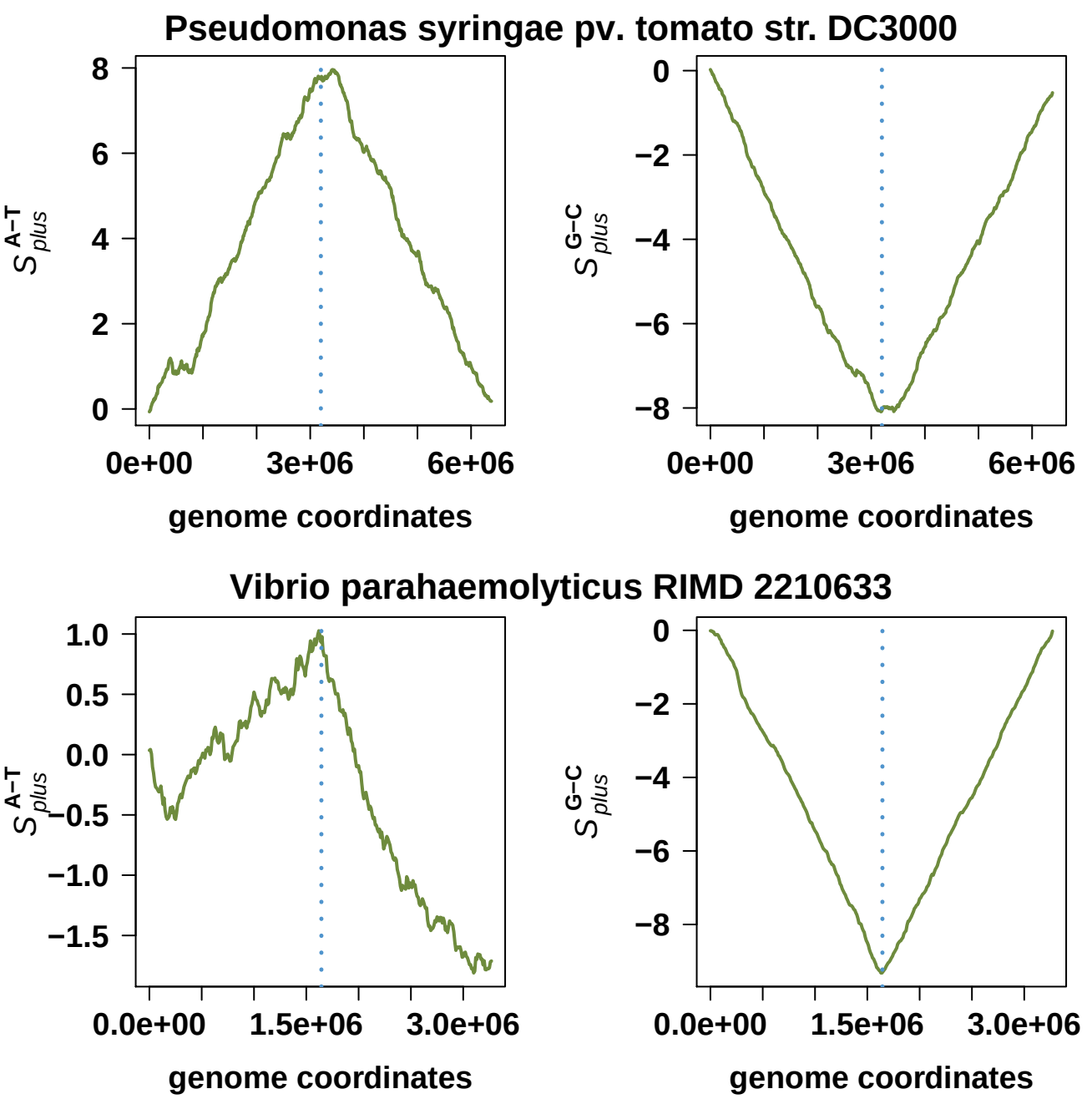

Pseudomonas protegens Pf−5
S^{A-T}_{plus}
12
10
8
6
4
2
0
0e+00
3e+06
6e+06
genome coordinates
S^{G-C}_{plus}
0
−2
−4
−6
−8
−10
−12
−14
0e+00
3e+06
6e+06
genome coordinates
Shigella flexneri 2a str. 301
S^{A-T}_{plus}
1.0
0.5
0.0
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
−4
−5
−6
−7
0e+00
2e+06
4e+06
genome coordinates

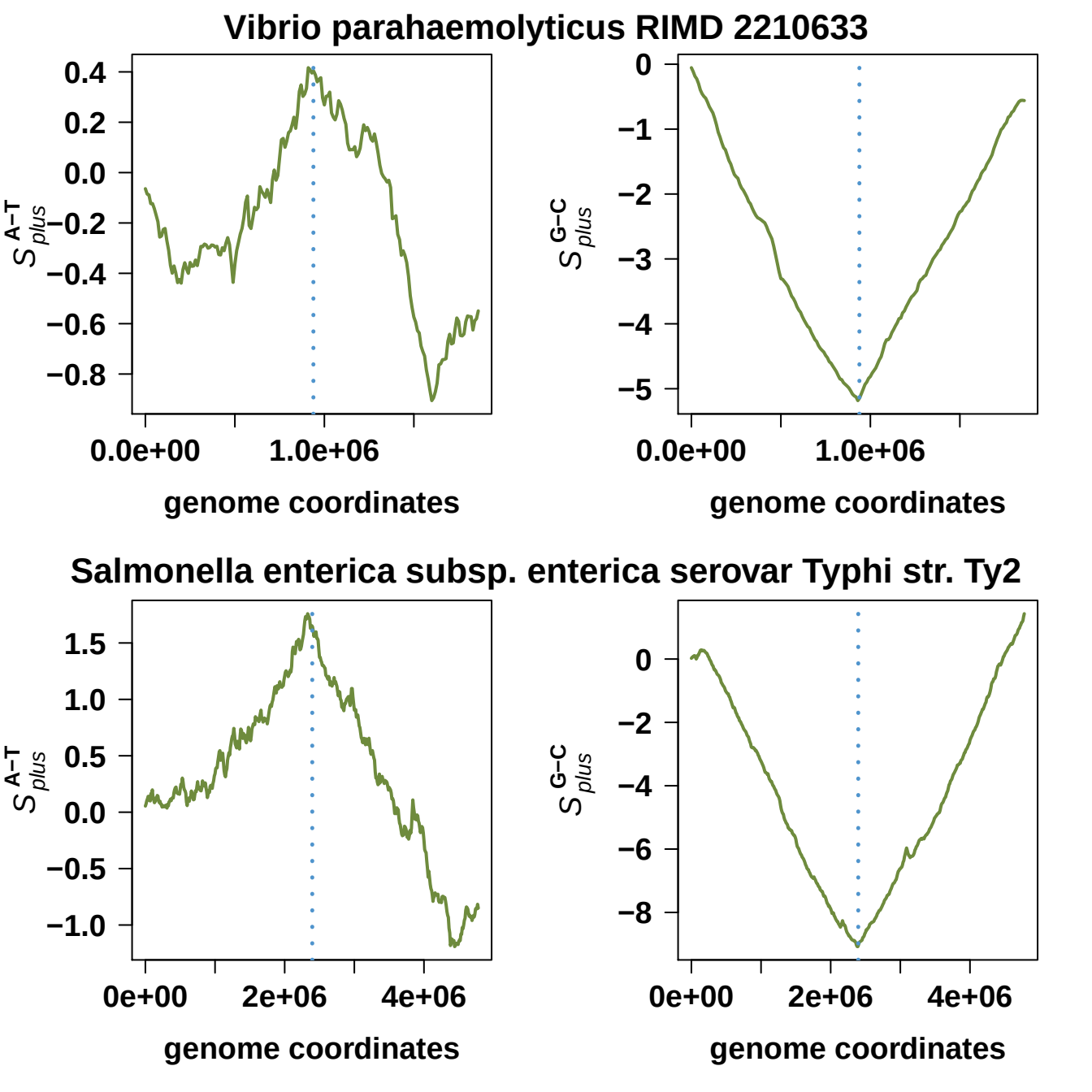

Wigglesworthia glossinidia endosymbiont of Glossina brevipalpis
0.4
0.2
0.0
−0.2
−0.4
−0.6
S^{A-T}_{plus}
0e+00
3e+05
6e+05
genome coordinates
0.4
0.2
0.0
−0.2
−0.4
−0.6
−0.8
S^{G-C}_{plus}
0e+00
3e+05
6e+05
genome coordinates
Shewanella oneidensis MR−1
8
6
4
2
0
S^{A-T}_{plus}
0e+00
2e+06
4e+06
genome coordinates
0
−2
−4
−6
−8
−10
−12
−14
S^{G-C}_{plus}
0e+00
2e+06
4e+06
genome coordinates

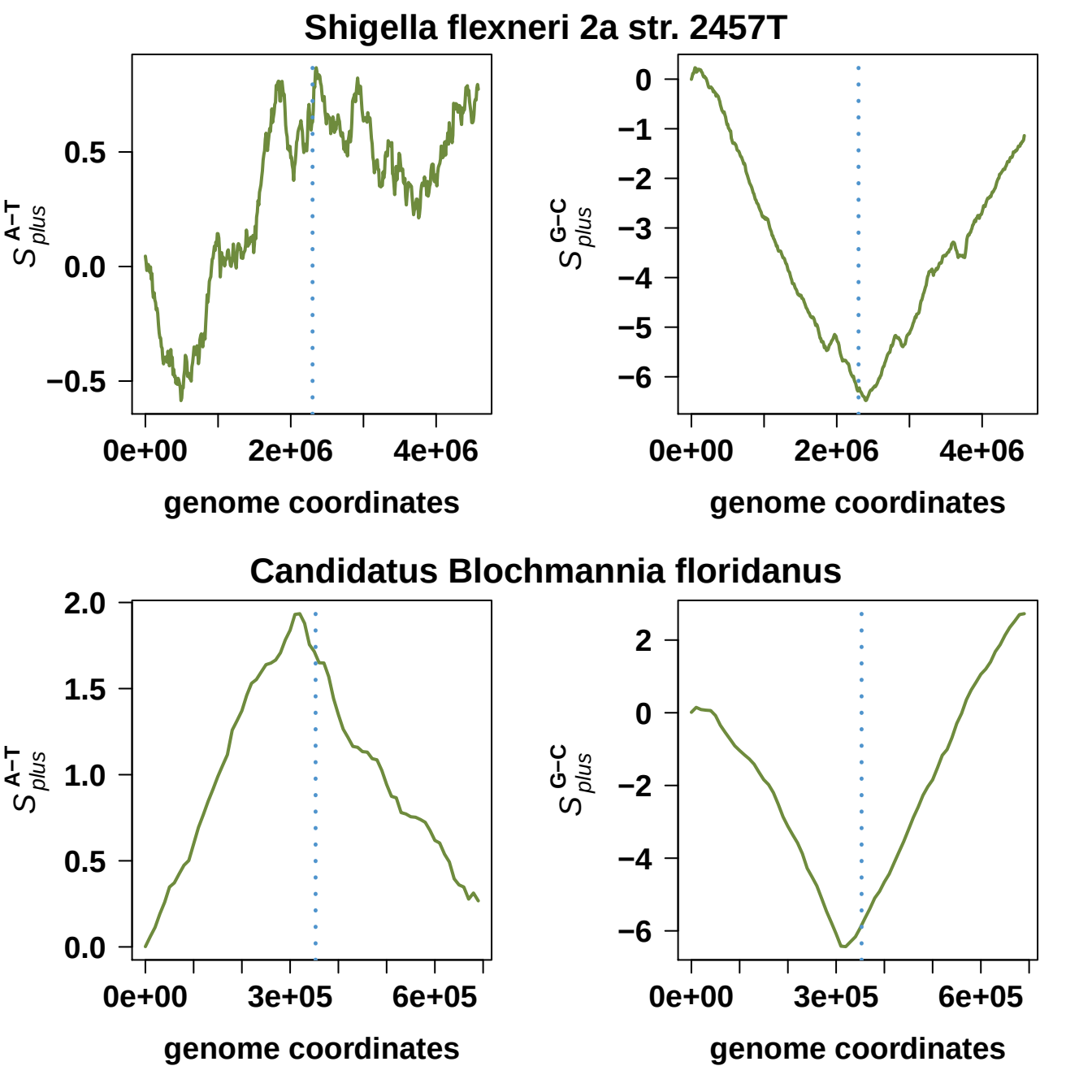

Escherichia coli CFT073
1.5
1.0
0.5
0.0
−0.5
S^{A-T}_{plus}
0e+00
2e+06
4e+06
genome coordinates
0
−2
−4
−6
−8
S^{G-C}_{plus}
0e+00
2e+06
4e+06
genome coordinates
Vibrio vulnificus CMCP6
1.5
1.0
0.5
0.0
−0.5
−1.0
S^{A-T}_{plus}
0.0e+00
1.5e+06
3.0e+06
genome coordinates
0
−2
−4
−6
−8
S^{G-C}_{plus}
0.0e+00
1.5e+06
3.0e+06
genome coordinates

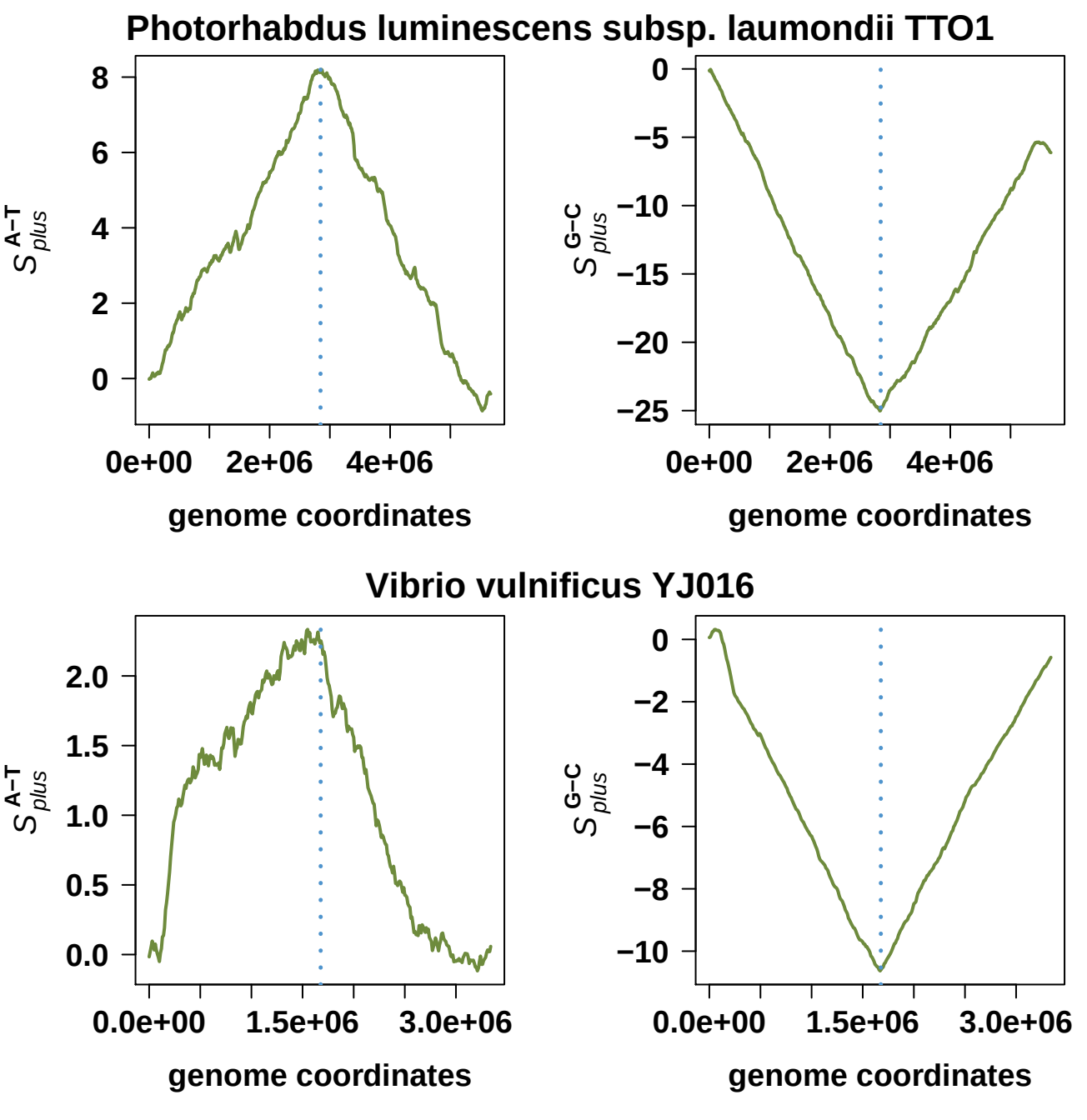

Vibrio vulnificus CMCP6
0.8
0.6
0.4
0.2
0.0
−0.2
S^{A-T}_{plus}
0.0e+00
1.0e+06
genome coordinates
0
−1
−2
−3
−4
S^{G-C}_{plus}
0.0e+00
1.0e+06
genome coordinates
Buchnera aphidicola str. Bp (Baizongia pistaciae)
2.0
1.5
1.0
0.5
0.0
−0.5
S^{A-T}_{plus}
0e+00
3e+05
6e+05
genome coordinates
0
−1
−2
−3
−4
S^{G-C}_{plus}
0e+00
3e+05
6e+05
genome coordinates

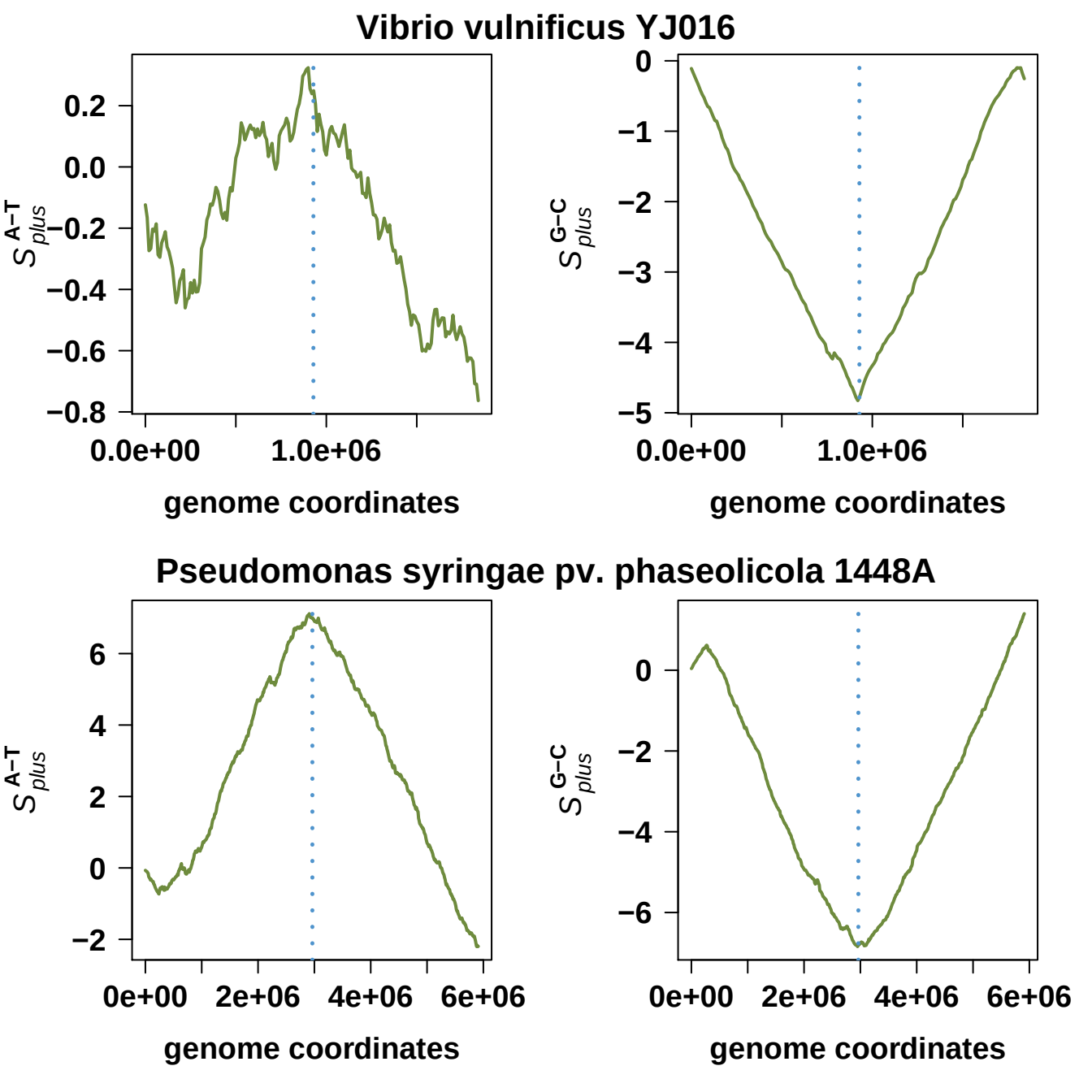

Pectobacterium atrosepticum SCRI1043
S^{A-T}_{plus}
7
6
5
4
3
2
1
0
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
0
−5
−10
−15
0e+00
2e+06
4e+06
genome coordinates
Xylella fastidiosa Temecula1
S^{A-T}_{plus}
10
5
0
0.0e+00
1.5e+06
genome coordinates
S^{G-C}_{plus}
0
−5
−10
0.0e+00
1.5e+06
genome coordinates

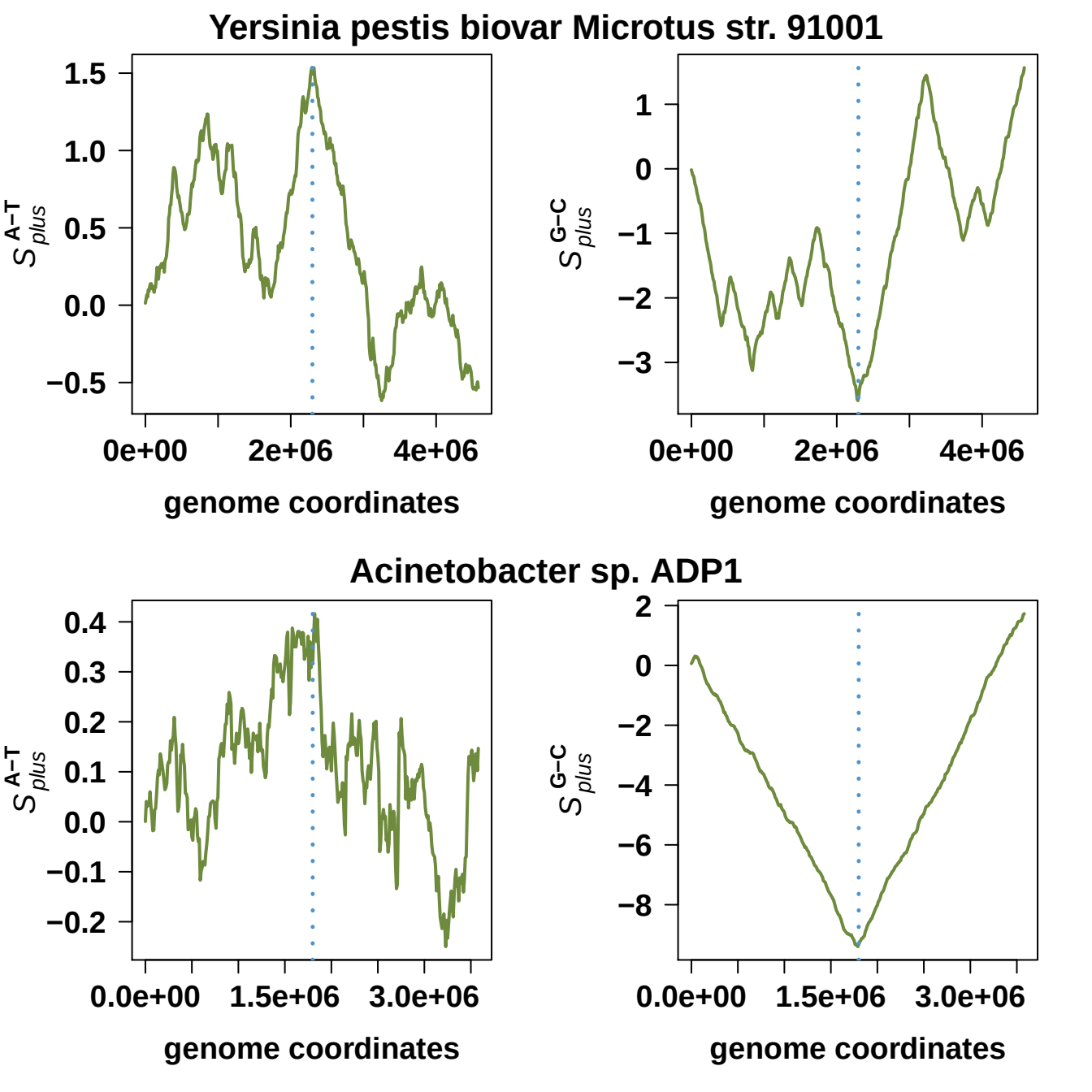

Pseudomonas syringae pv. tomato str. DC3000
S^{A-T}_{plus}
8
6
4
2
0
0e+00
3e+06
6e+06
genome coordinates
S^{G-C}_{plus}
0
−2
−4
−6
−8
0e+00
3e+06
6e+06
genome coordinates
Vibrio parahaemolyticus RIMD 2210633
S^{A-T}_{plus}
1.0
0.5
0.0
−0.5
−1.0
−1.5
0.0e+00
1.5e+06
3.0e+06
genome coordinates
S^{G-C}_{plus}
0
−2
−4
−6
−8
0.0e+00
1.5e+06
3.0e+06
genome coordinates

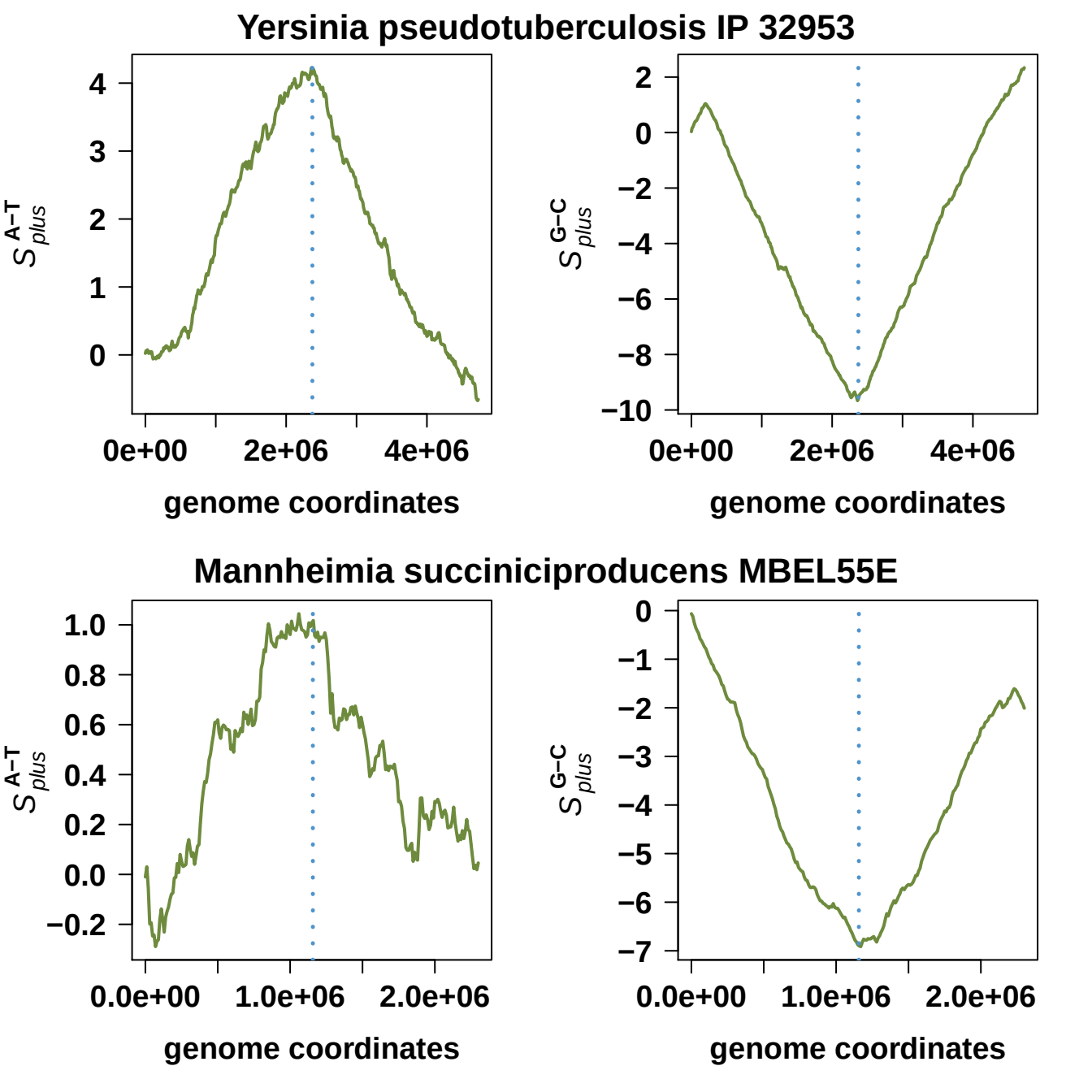

Vibrio parahaemolyticus RIMD 2210633
0.4
0.2
0.0
−0.2
−0.4
−0.6
−0.8
S^{A-T}_{plus}
0.0e+00
1.0e+06
genome coordinates
0
−1
−2
−3
−4
−5
S^{G-C}_{plus}
0.0e+00
1.0e+06
genome coordinates
Salmonella enterica subsp. enterica serovar Typhi str. Ty2
1.5
1.0
0.5
0.0
−0.5
−1.0
S^{A-T}_{plus}
0e+00
2e+06
4e+06
genome coordinates
0
−2
−4
−6
−8
S^{G-C}_{plus}
0e+00
2e+06
4e+06
genome coordinates

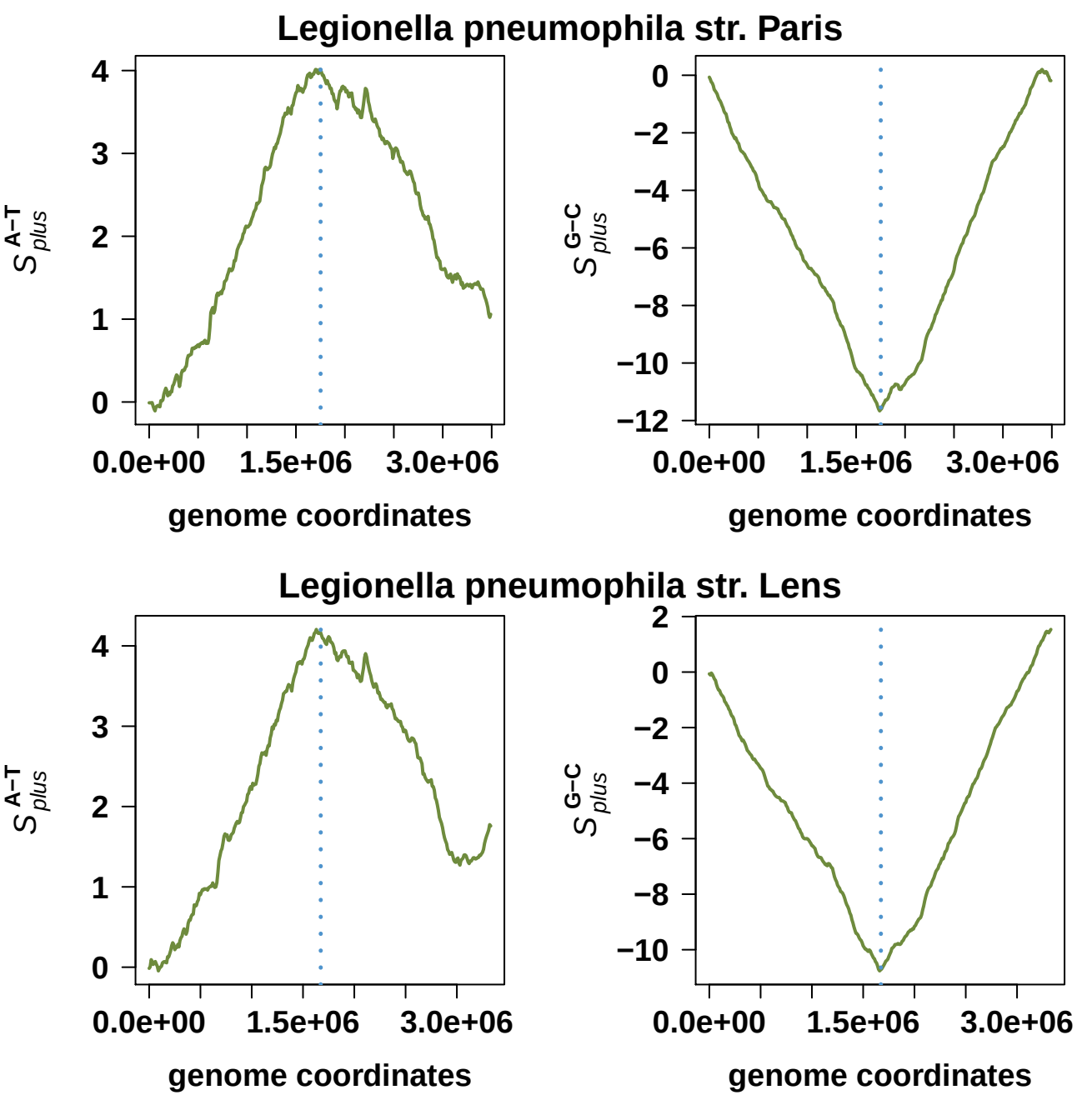

Shigella flexneri 2a str. 2457T
S^{A-T}_{plus}
0.5
0.0
−0.5
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
−4
−5
−6
0e+00
2e+06
4e+06
genome coordinates
Candidatus Blochmannia floridanus
S^{A-T}_{plus}
2.0
1.5
1.0
0.5
0.0
0e+00
3e+05
6e+05
genome coordinates
S^{G-C}_{plus}
2
0
−2
−4
−6
0e+00
3e+05
6e+05
genome coordinates

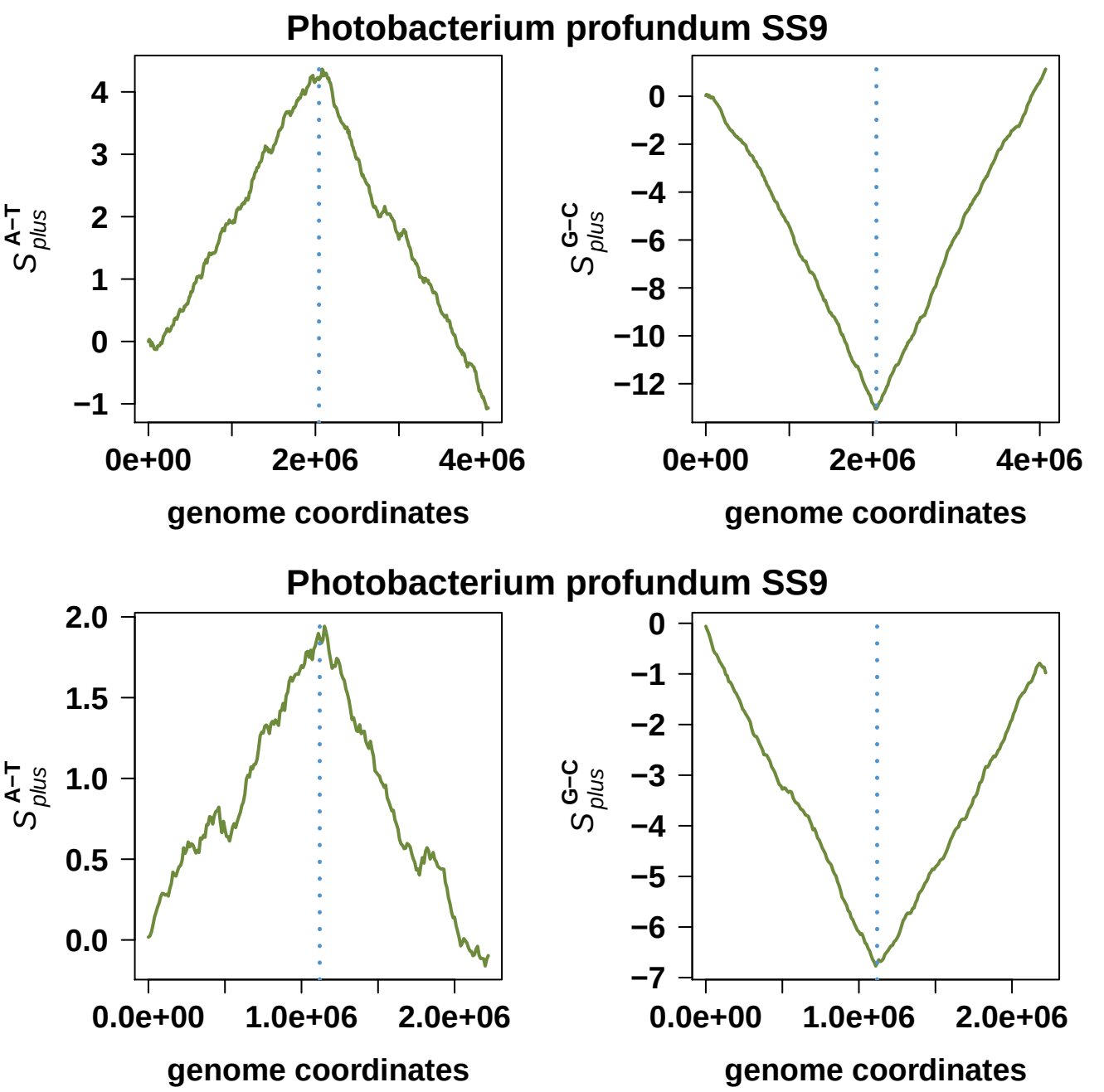

Photorhabdus luminescens subsp. laumondii TTO1
S^{A-T}_{plus}
8
6
4
2
0
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
0
−5
−10
−15
−20
−25
0e+00
2e+06
4e+06
genome coordinates
Vibrio vulnificus YJ016
S^{A-T}_{plus}
2.0
1.5
1.0
0.5
0.0
0.0e+00
1.5e+06
3.0e+06
genome coordinates
S^{G-C}_{plus}
0
−2
−4
−6
−8
−10
0.0e+00
1.5e+06
3.0e+06
genome coordinates

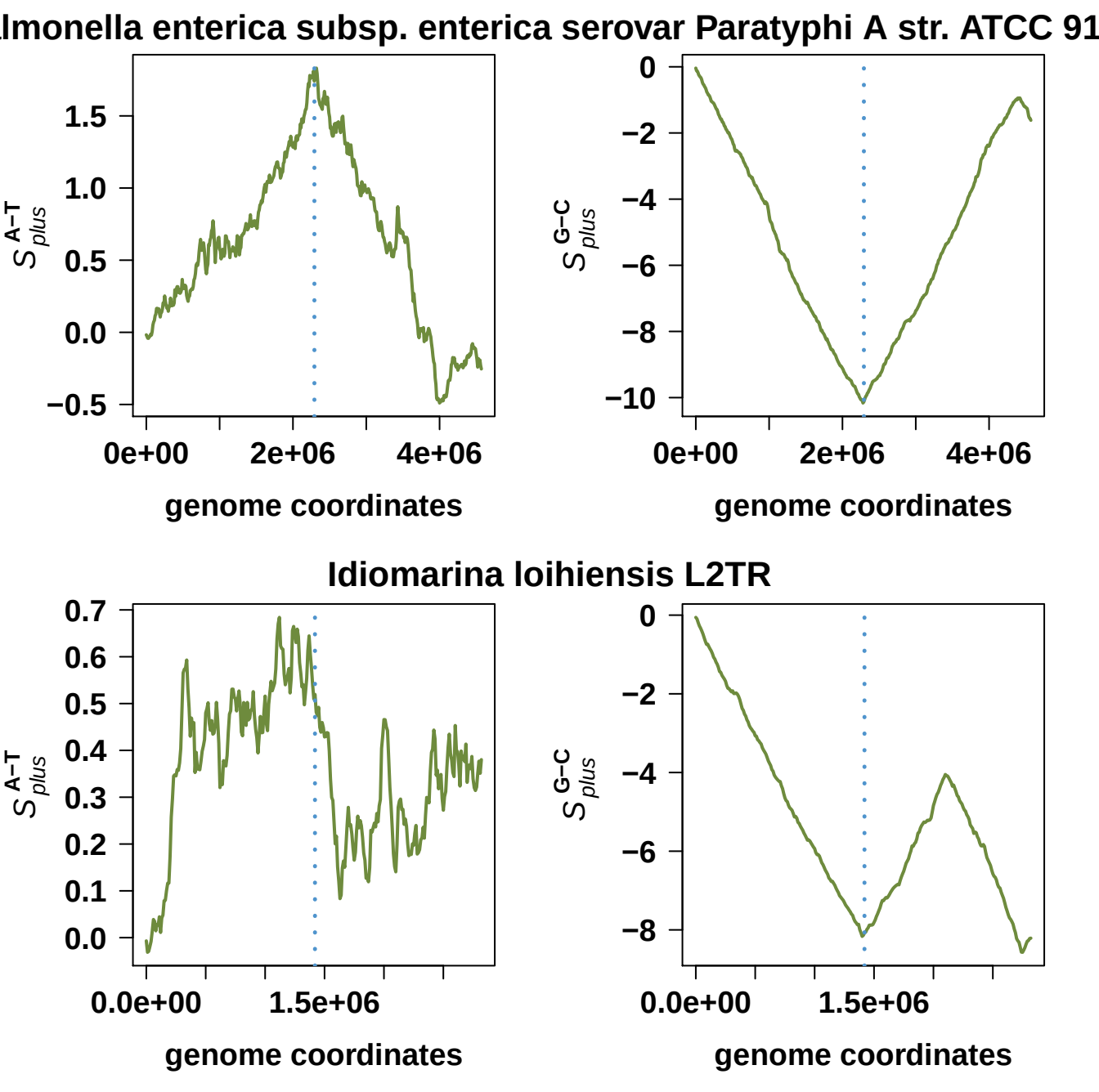

Vibrio vulnificus YJ016
S^{A-T}_{plus}
0.2
0.0
−0.2
−0.4
−0.6
−0.8
0.0e+00
1.0e+06
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
−4
−5
0.0e+00
1.0e+06
genome coordinates
Pseudomonas syringae pv. phaseolicola 1448A
S^{A-T}_{plus}
6
4
2
0
−2
0e+00
2e+06
4e+06
6e+06
genome coordinates
S^{G-C}_{plus}
0
−2
−4
−6
0e+00
2e+06
4e+06
6e+06
genome coordinates

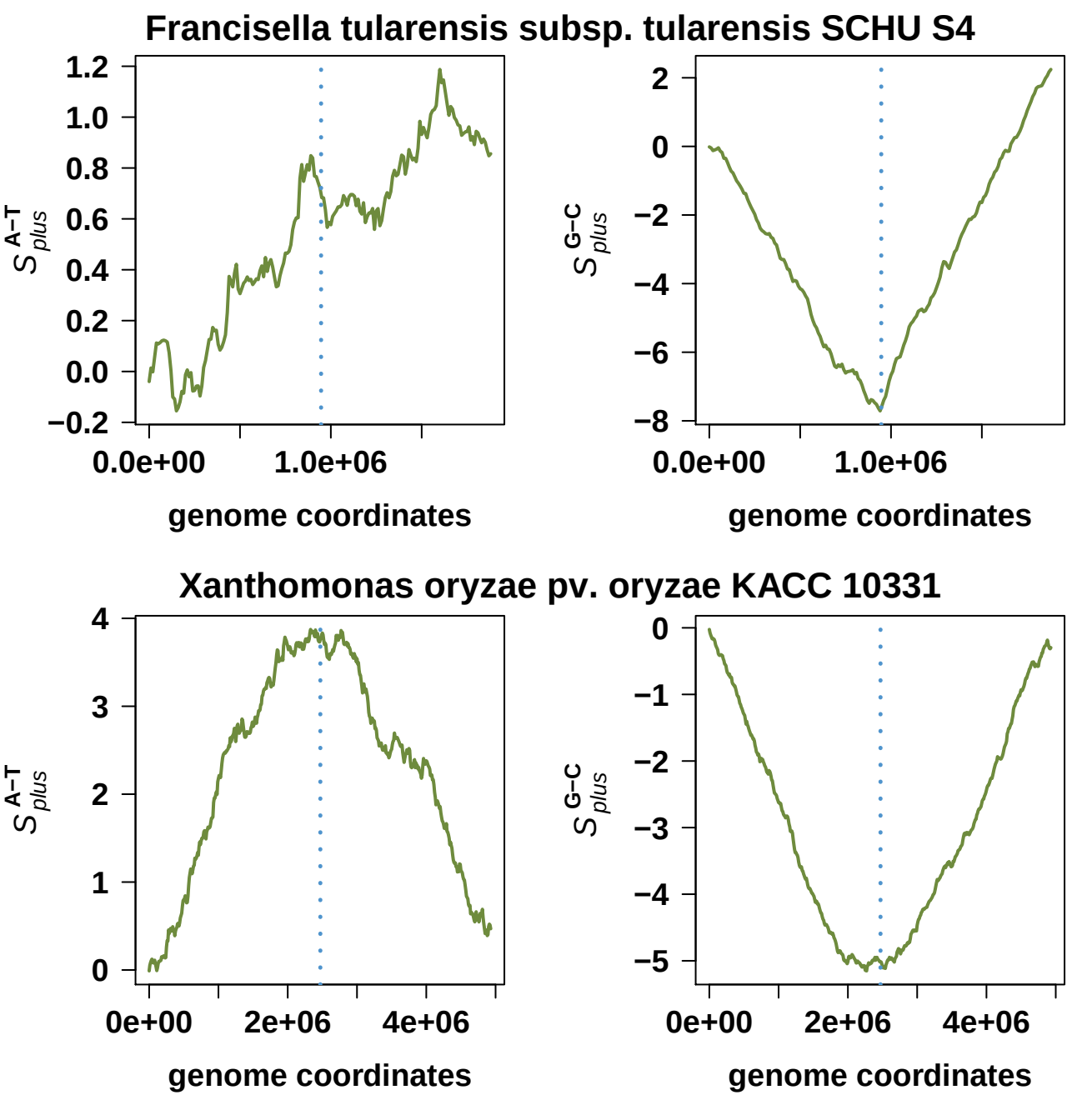

Yersinia pestis biovar Microtus str. 91001
1.5
1.0
0.5
0.0
−0.5
S^{A-T}_{plus}
0e+00
2e+06
4e+06
genome coordinates
1
0
−1
−2
−3
S^{G-C}_{plus}
0e+00
2e+06
4e+06
genome coordinates
Acinetobacter sp. ADP1
0.4
0.3
0.2
0.1
0.0
−0.1
−0.2
S^{A-T}_{plus}
0.0e+00
1.5e+06
3.0e+06
genome coordinates
2
0
−2
−4
−6
−8
S^{G-C}_{plus}
0.0e+00
1.5e+06
3.0e+06
genome coordinates

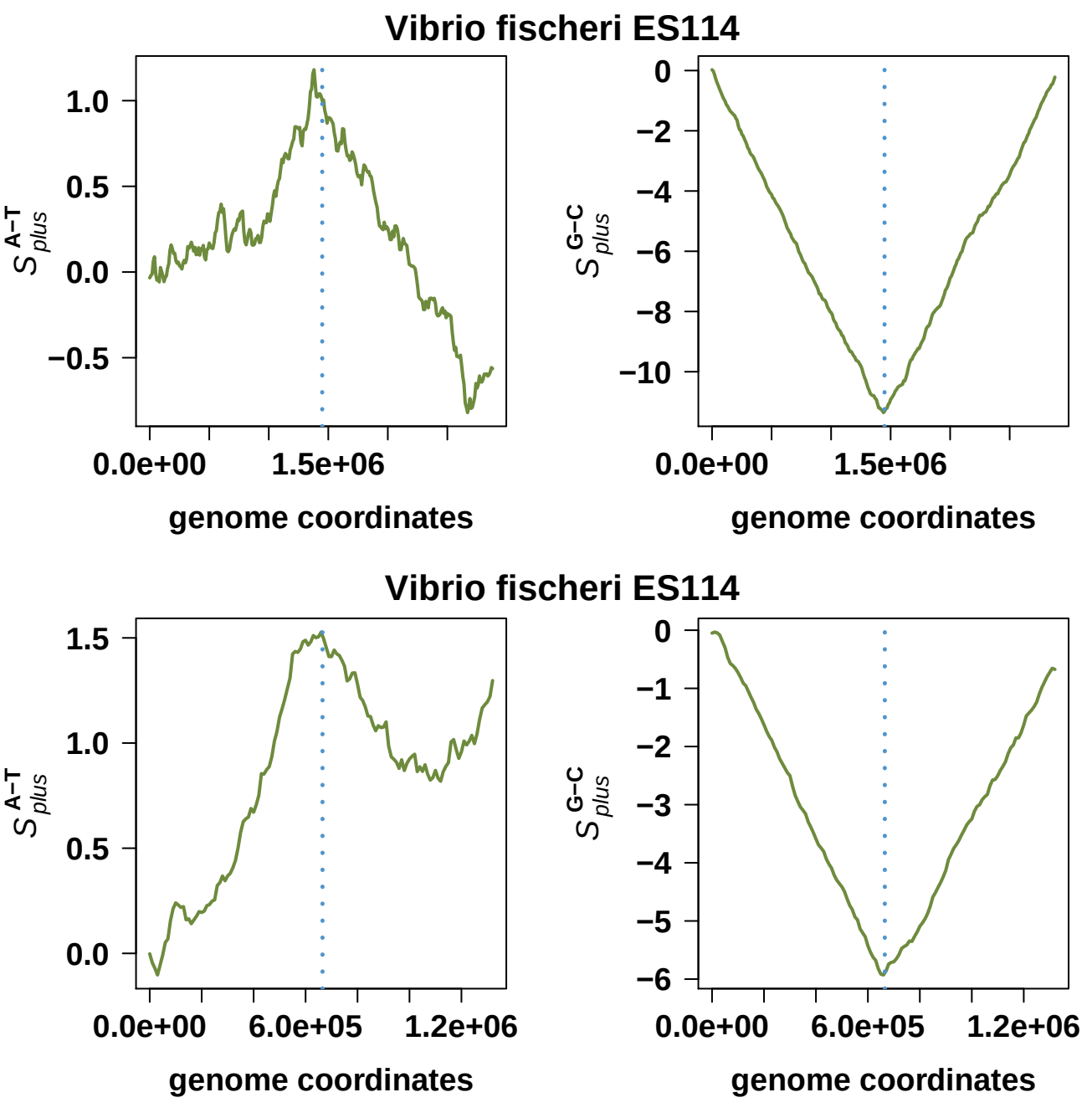

Yersinia pseudotuberculosis IP 32953
S^{A-T}_{plus}
4
3
2
1
0
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
2
0
−2
−4
−6
−8
−10
0e+00
2e+06
4e+06
genome coordinates
Mannheimia succiniciproducens MBEL55E
S^{A-T}_{plus}
1.0
0.8
0.6
0.4
0.2
0.0
−0.2
0.0e+00
1.0e+06
2.0e+06
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
−4
−5
−6
−7
0.0e+00
1.0e+06
2.0e+06
genome coordinates

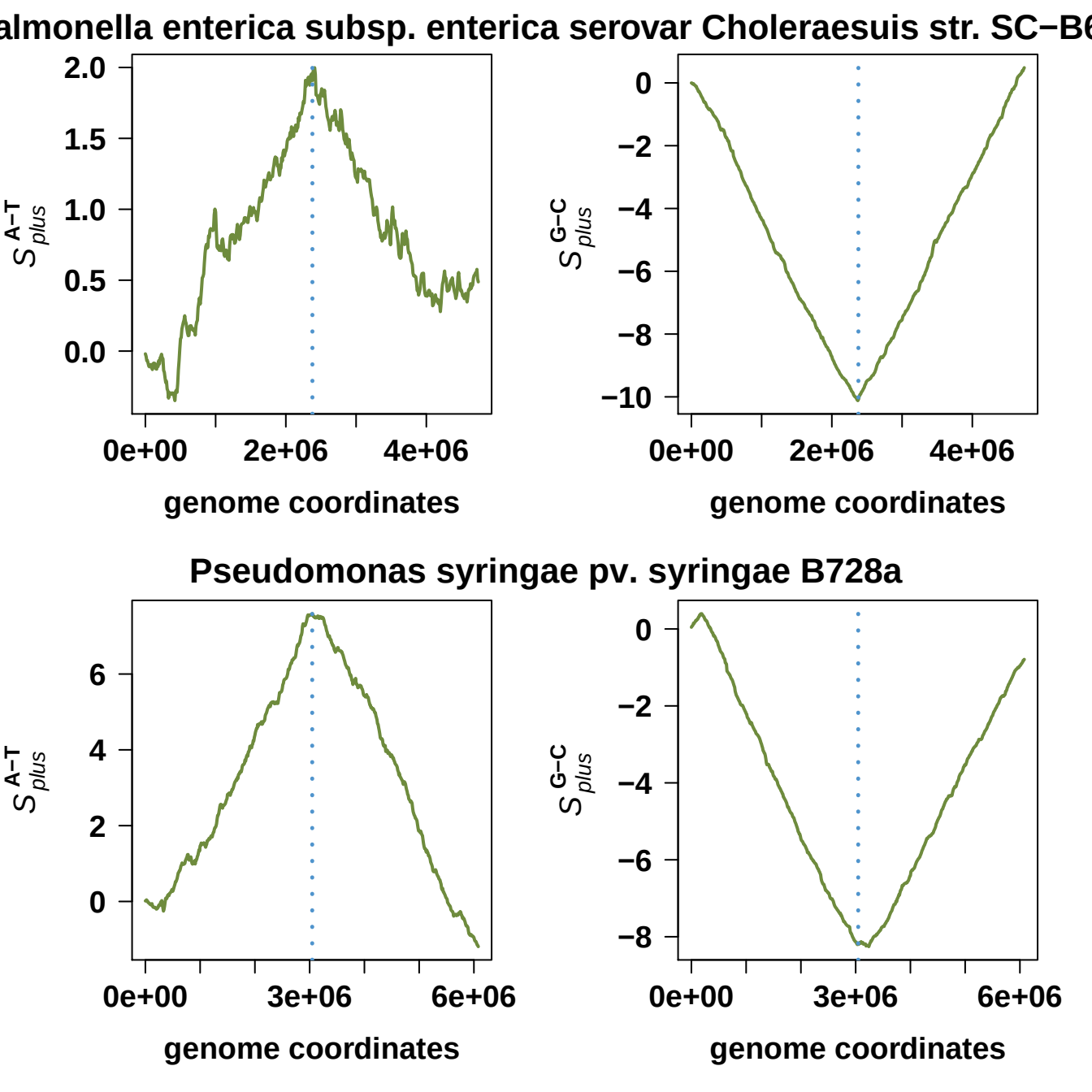

Legionella pneumophila str. Paris
S^{A-T}_{plus}
4
3
2
1
0
0.0e+00
1.5e+06
3.0e+06
genome coordinates
S^{G-C}_{plus}
0
−2
−4
−6
−8
−10
−12
0.0e+00
1.5e+06
3.0e+06
genome coordinates
Legionella pneumophila str. Lens
S^{A-T}_{plus}
4
3
2
1
0
0.0e+00
1.5e+06
3.0e+06
genome coordinates
S^{G-C}_{plus}
2
0
−2
−4
−6
−8
−10
0.0e+00
1.5e+06
3.0e+06
genome coordinates

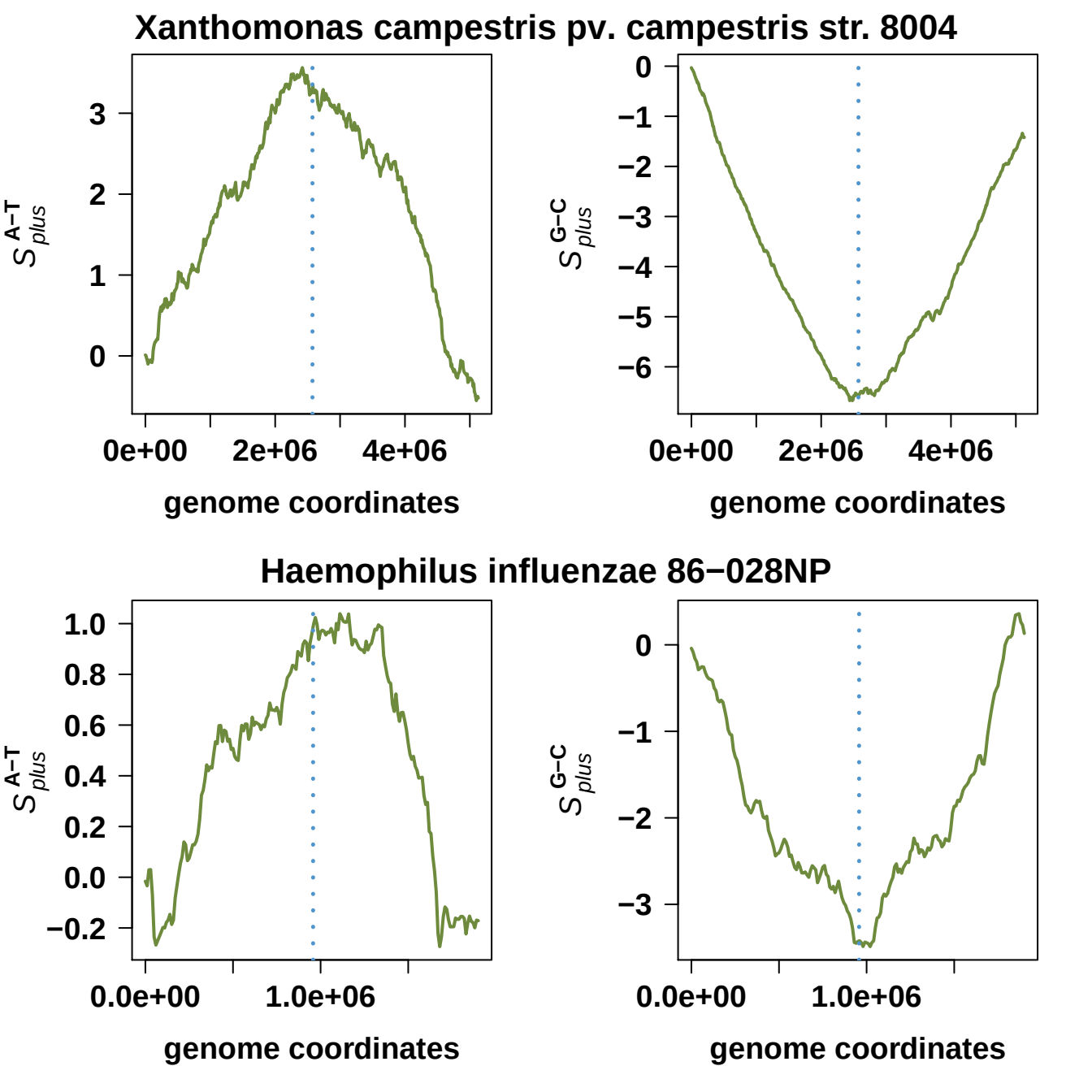

Photobacterium profundum SS9
S^{A-T}_{plus}
4
3
2
1
0
−1
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
0
−2
−4
−6
−8
−10
−12
0e+00
2e+06
4e+06
genome coordinates
Photobacterium profundum SS9
S^{A-T}_{plus}
2.0
1.5
1.0
0.5
0.0
0.0e+00
1.0e+06
2.0e+06
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
−4
−5
−6
−7
0.0e+00
1.0e+06
2.0e+06
genome coordinates

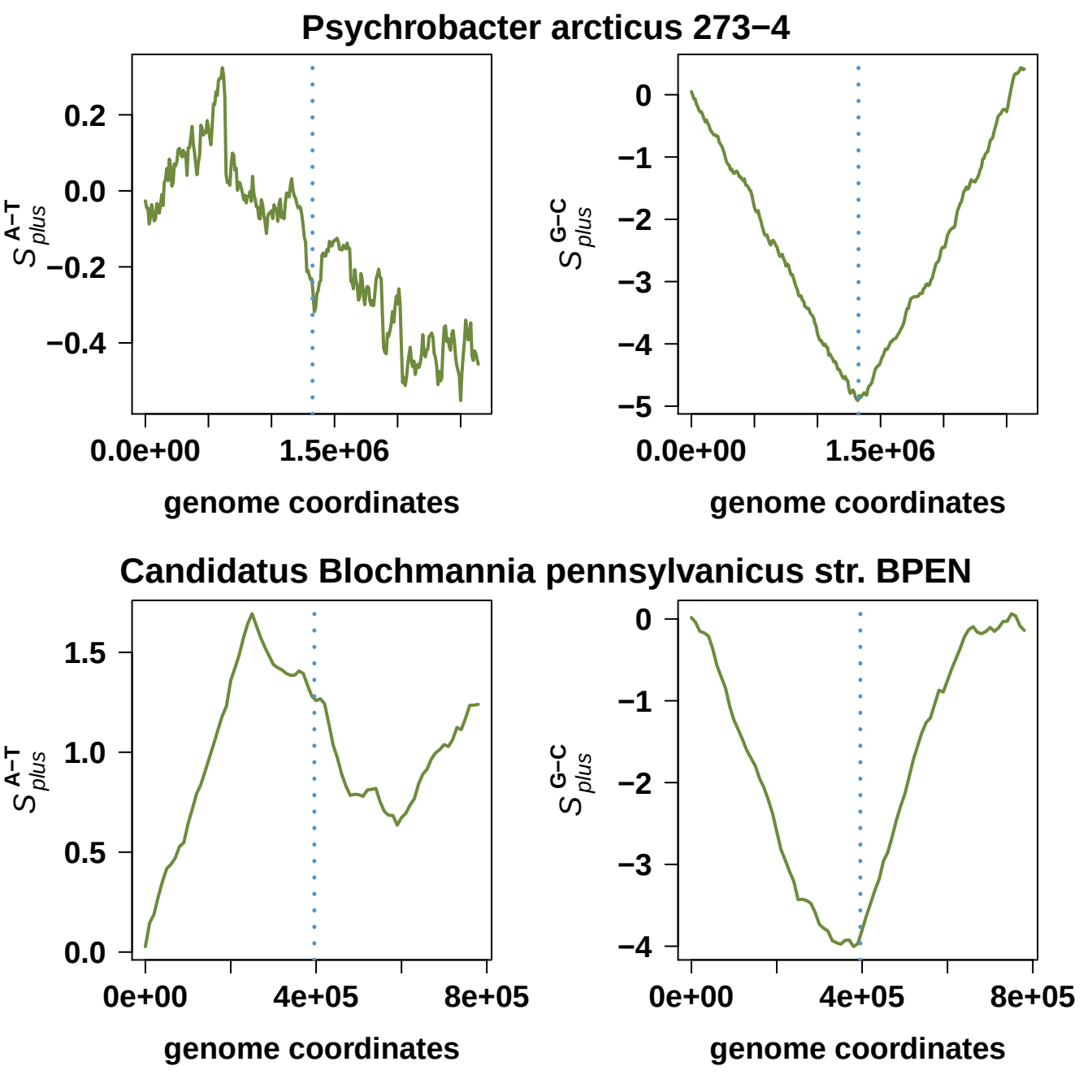

lmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 91
1.5
1.0
0.5
0.0
−0.5
S^{A-T}_{plus}
0e+00
2e+06
4e+06
genome coordinates
0
−2
−4
−6
−8
−10
S^{G-C}_{plus}
0e+00
2e+06
4e+06
genome coordinates
Idiomarina loihiensis L2TR
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
S^{A-T}_{plus}
0.0e+00
1.5e+06
genome coordinates
0
−2
−4
−6
−8
S^{G-C}_{plus}
0.0e+00
1.5e+06
genome coordinates

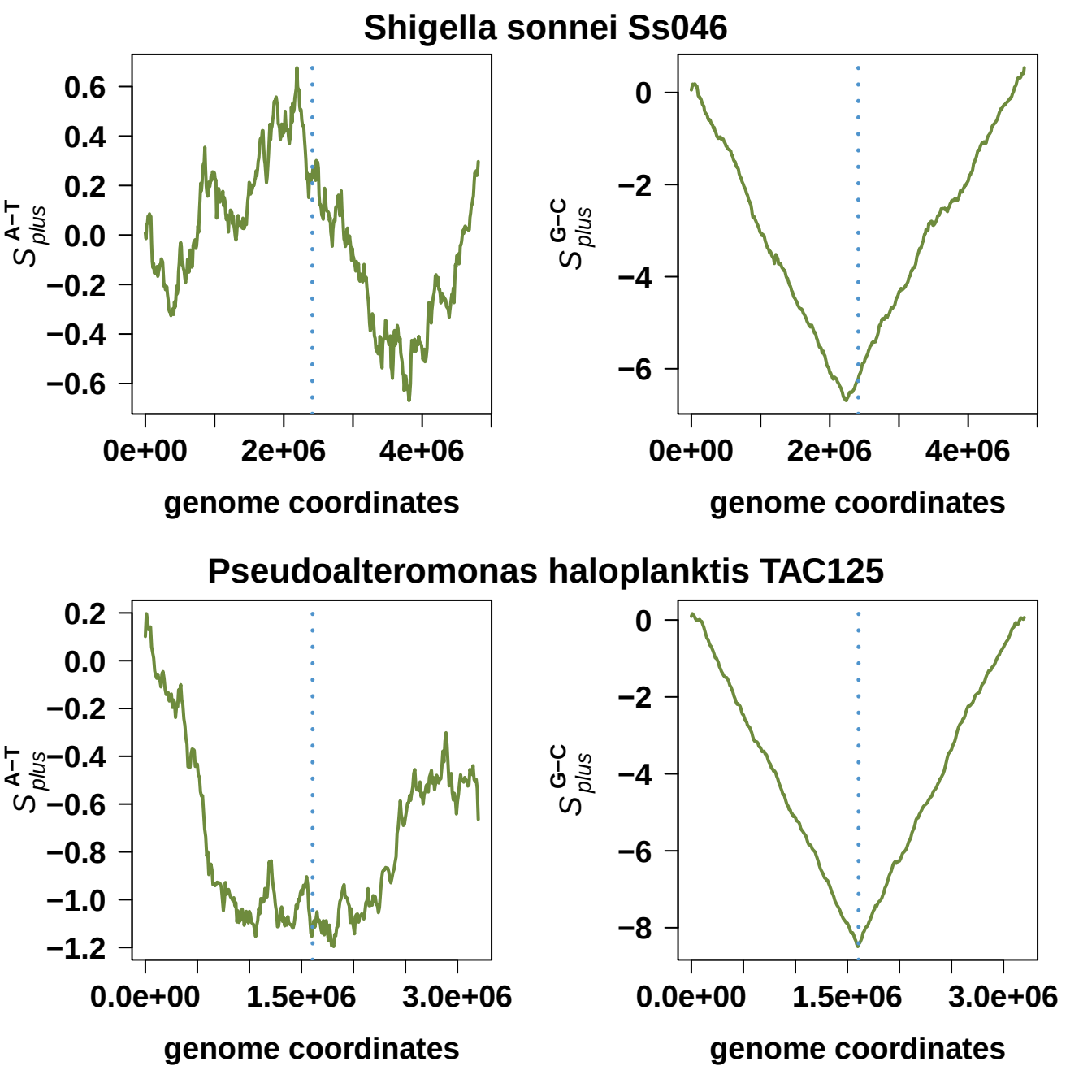

Francisella tularensis subsp. tularensis SCHU S4
1.2
1.0
0.8
0.6
0.4
0.2
0.0
−0.2
S^{A-T}_{plus}
0.0e+00
1.0e+06
genome coordinates
2
0
−2
−4
−6
−8
S^{G-C}_{plus}
0.0e+00
1.0e+06
genome coordinates
Xanthomonas oryzae pv. oryzae KACC 10331
4
3
2
1
0
S^{A-T}_{plus}
0e+00
2e+06
4e+06
genome coordinates
0
−1
−2
−3
−4
−5
S^{G-C}_{plus}
0e+00
2e+06
4e+06
genome coordinates

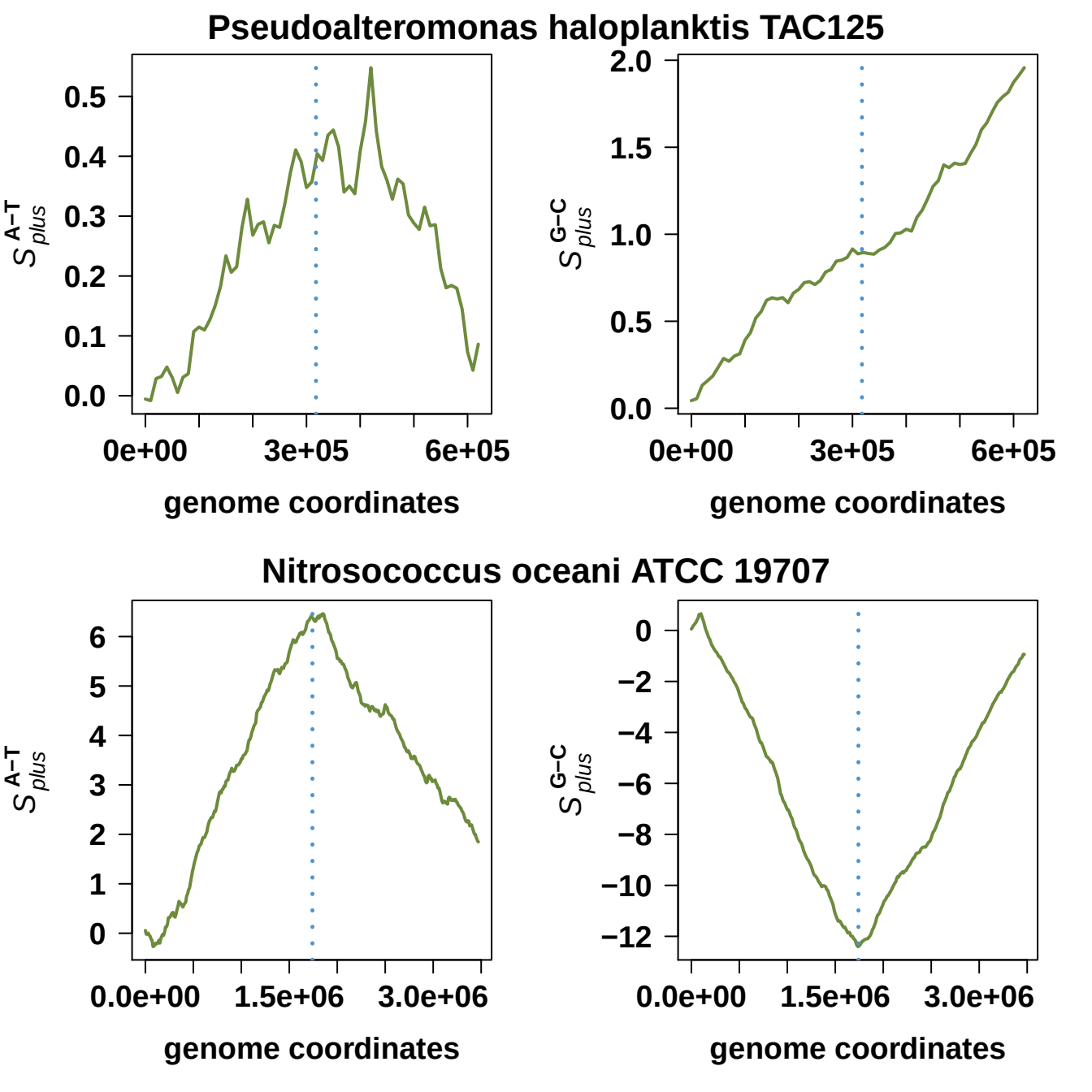

Vibrio fischeri ES114
1.0
0.5
0.0
−0.5
S^{A-T}_{plus}
0.0e+00
1.5e+06
genome coordinates
0
−2
−4
−6
−8
−10
S^{G-C}_{plus}
0.0e+00
1.5e+06
genome coordinates
Vibrio fischeri ES114
1.5
1.0
0.5
0.0
S^{A-T}_{plus}
0.0e+00
6.0e+05
1.2e+06
genome coordinates
0
−1
−2
−3
−4
−5
−6
S^{G-C}_{plus}
0.0e+00
6.0e+05
1.2e+06
genome coordinates

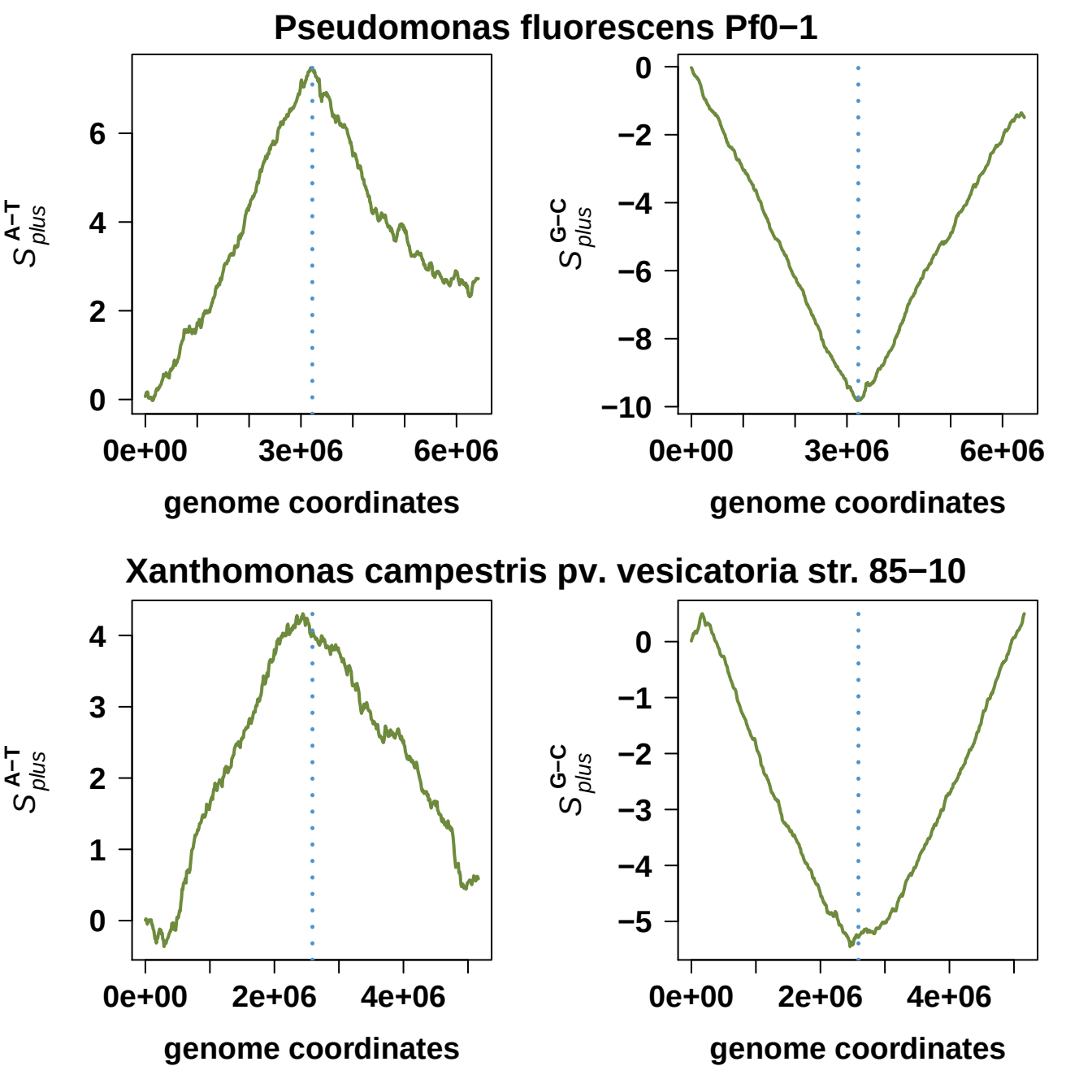

almonella enterica subsp. enterica serovar Choleraesuis str. SC−B6
2.0
1.5
1.0
0.5
0.0
S^{A-T}_{plus}
0e+00
2e+06
4e+06
genome coordinates
0
−2
−4
−6
−8
−10
S^{G-C}_{plus}
0e+00
2e+06
4e+06
genome coordinates
Pseudomonas syringae pv. syringae B728a
6
4
2
0
S^{A-T}_{plus}
0e+00
3e+06
6e+06
genome coordinates
0
−2
−4
−6
−8
S^{G-C}_{plus}
0e+00
3e+06
6e+06
genome coordinates

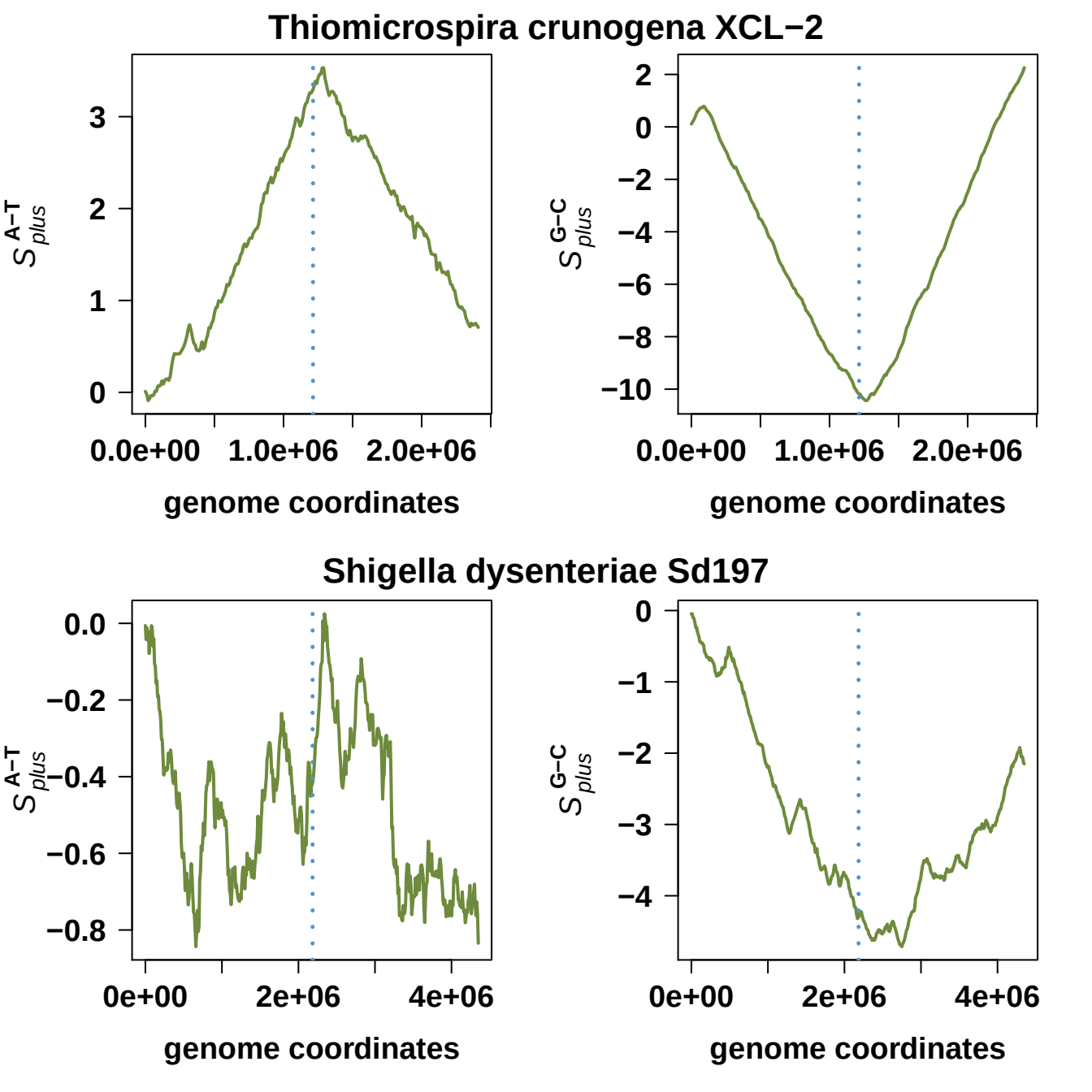

Xanthomonas campestris pv. campestris str. 8004
S^{A-T}_{plus}
3
2
1
0
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
−4
−5
−6
0e+00
2e+06
4e+06
genome coordinates
Haemophilus influenzae 86−028NP
S^{A-T}_{plus}
1.0
0.8
0.6
0.4
0.2
0.0
−0.2
0.0e+00
1.0e+06
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
0.0e+00
1.0e+06
genome coordinates

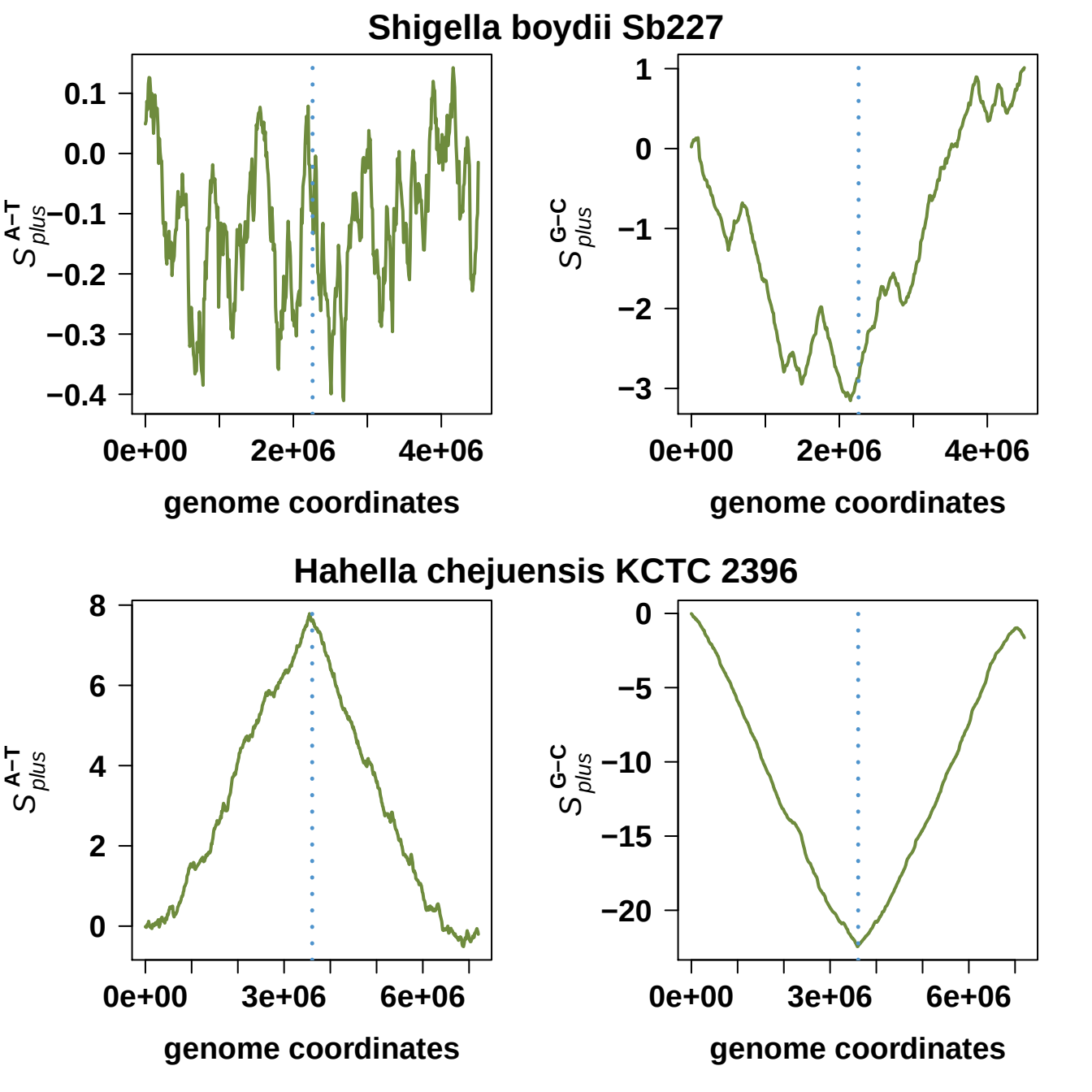

Psychrobacter arcticus 273−4
S^{A-T}_{plus}
0.2
0.0
−0.2
−0.4
0.0e+00
1.5e+06
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
−4
−5
0.0e+00
1.5e+06
genome coordinates
Candidatus Blochmannia pennsylvanicus str. BPEN
S^{A-T}_{plus}
1.5
1.0
0.5
0.0
0e+00
4e+05
8e+05
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
−4
0e+00
4e+05
8e+05
genome coordinates

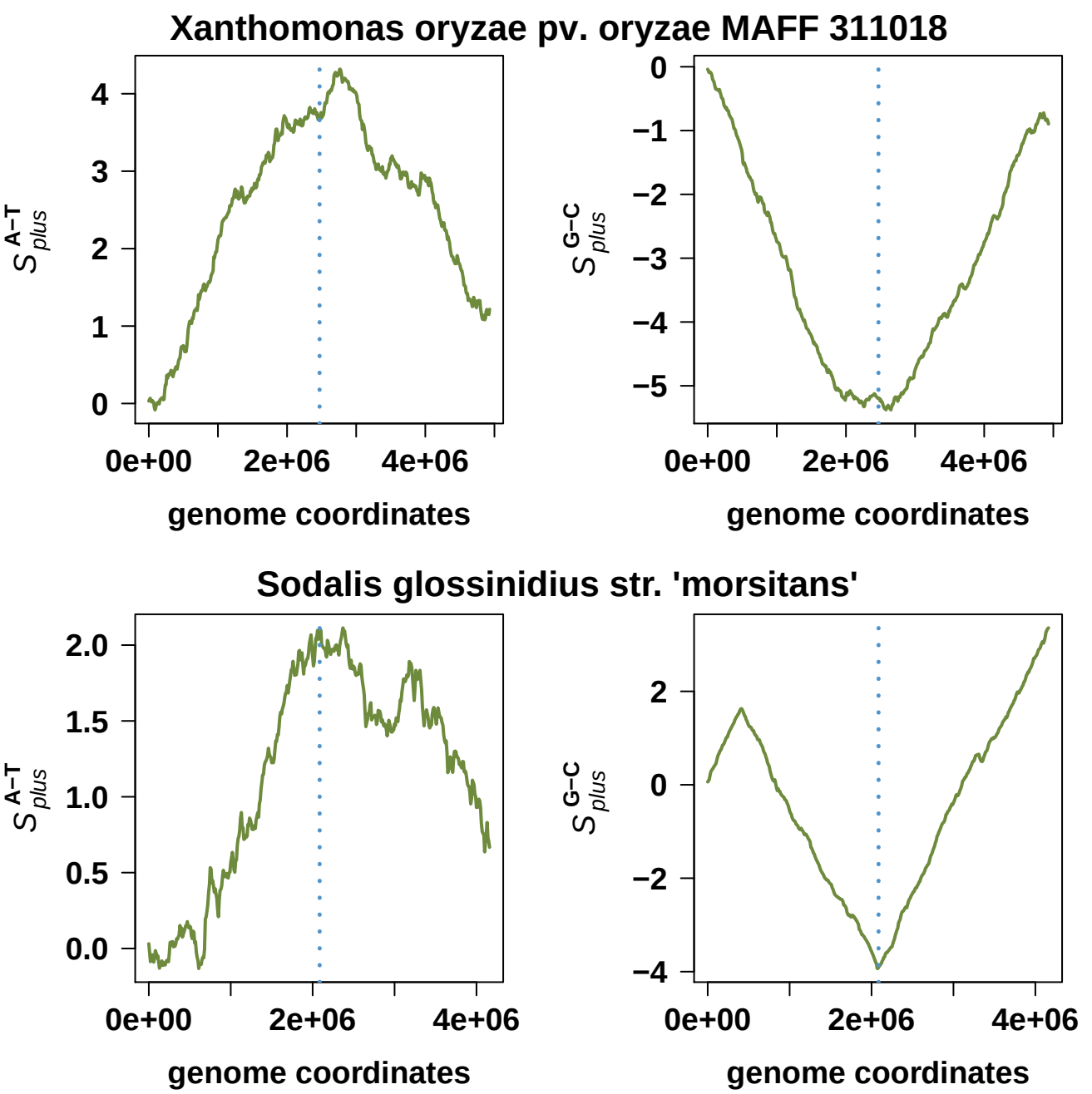

Shigella sonnei Ss046
0.6
0.4
0.2
0.0
−0.2
−0.4
−0.6
S^{A-T}_{plus}
0e+00
2e+06
4e+06
genome coordinates
0
−2
−4
−6
S^{G-C}_{plus}
0e+00
2e+06
4e+06
genome coordinates
Pseudoalteromonas haloplanktis TAC125
0.2
0.0
−0.2
−0.4
−0.6
−0.8
−1.0
−1.2
S^{A-T}_{plus}
0.0e+00
1.5e+06
3.0e+06
genome coordinates
0
−2
−4
−6
−8
S^{G-C}_{plus}
0.0e+00
1.5e+06
3.0e+06
genome coordinates

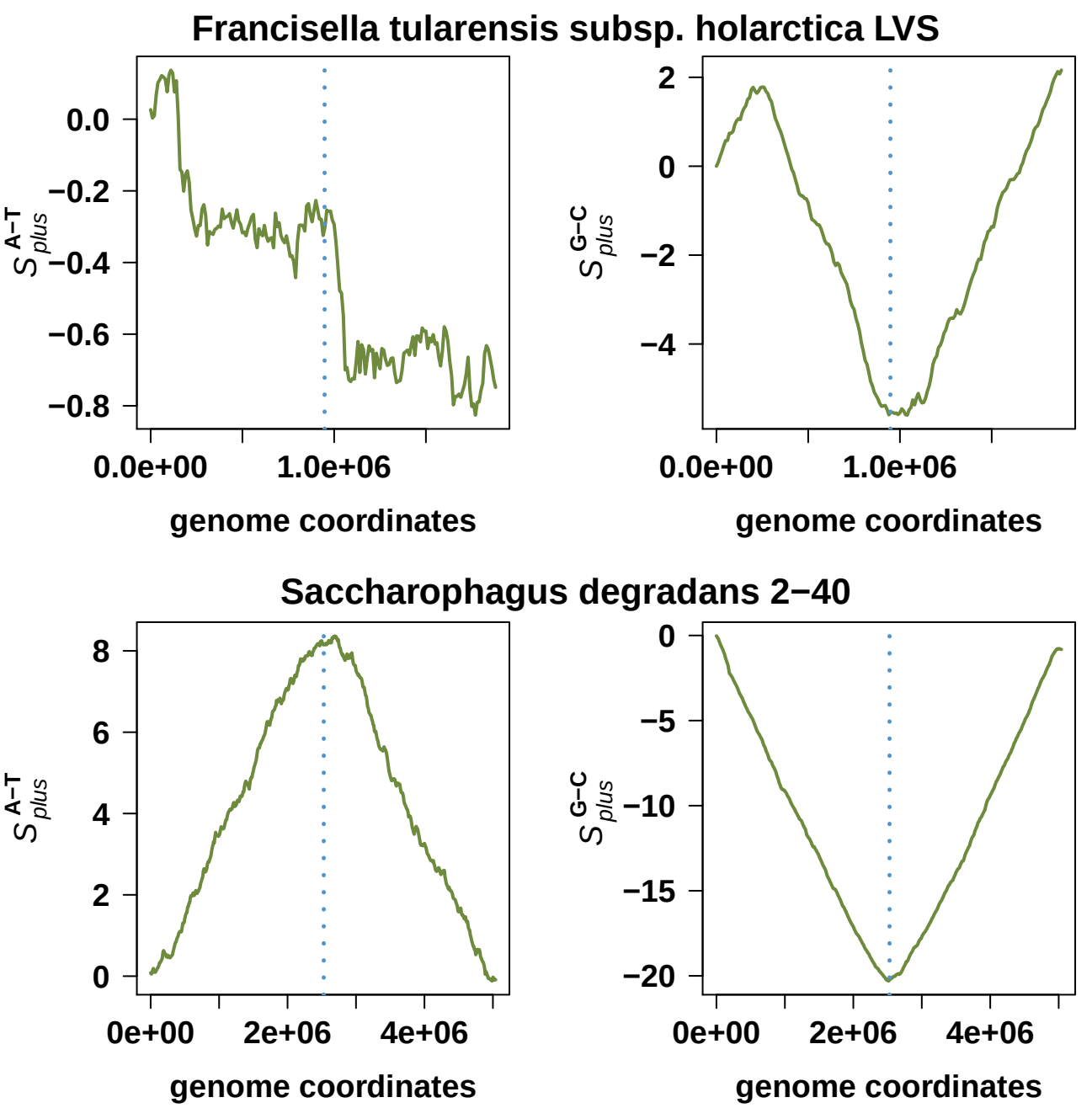

Pseudoalteromonas haloplanktis TAC125
S^{A-T}_{plus}
0.0
0.1
0.2
0.3
0.4
0.5
0e+00
3e+05
6e+05
genome coordinates
S^{G-C}_{plus}
0.0
0.5
1.0
1.5
2.0
0e+00
3e+05
6e+05
genome coordinates
Nitrosococcus oceani ATCC 19707
S^{A-T}_{plus}
0
1
2
3
4
5
6
0.0e+00
1.5e+06
3.0e+06
genome coordinates
S^{G-C}_{plus}
0
−2
−4
−6
−8
−10
−12
0.0e+00
1.5e+06
3.0e+06
genome coordinates

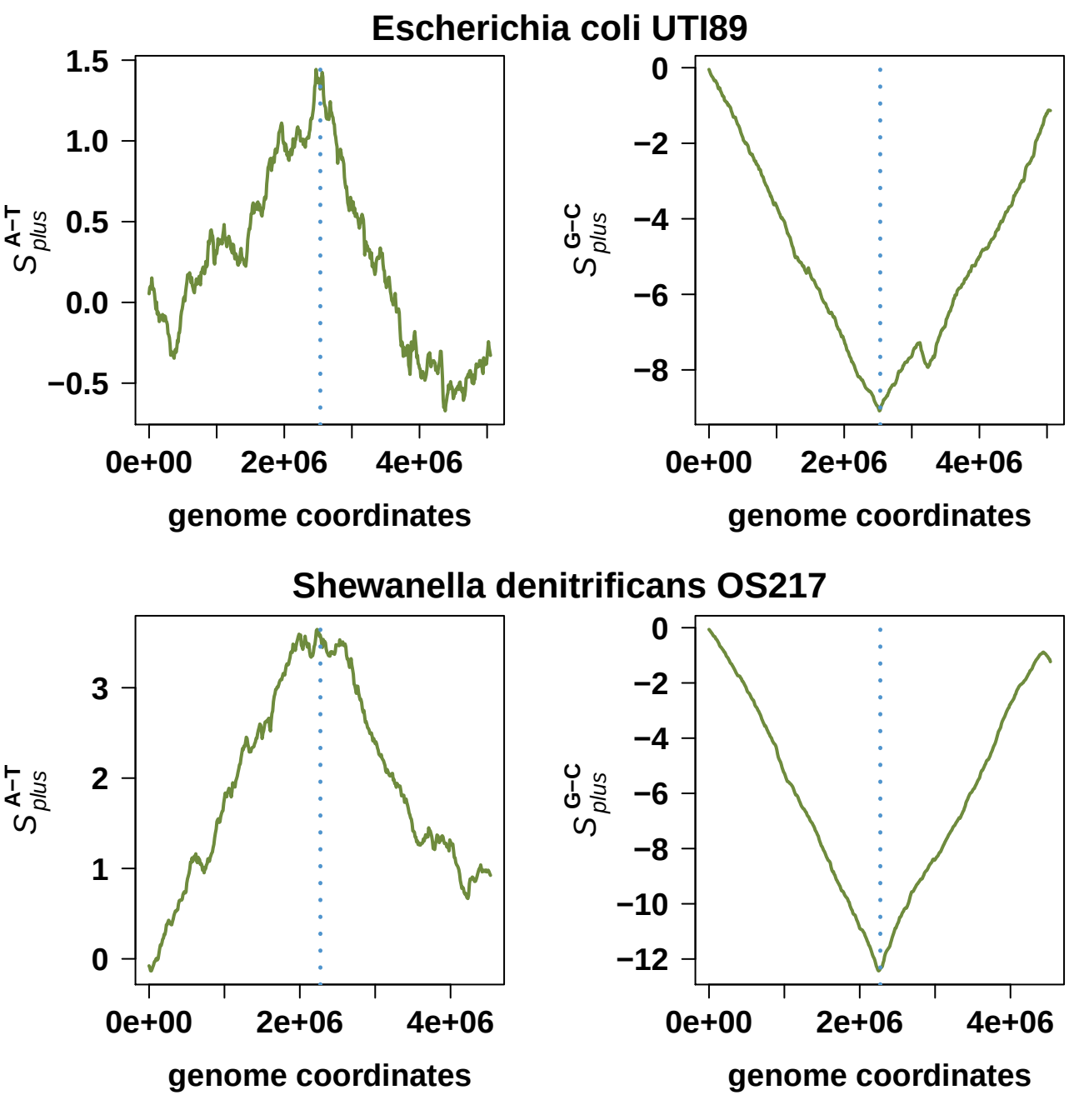

Pseudomonas fluorescens Pf0−1
S^{A-T}_{plus}
6
4
2
0
0e+00
3e+06
6e+06
genome coordinates
S^{G-C}_{plus}
0
−2
−4
−6
−8
−10
0e+00
3e+06
6e+06
genome coordinates
Xanthomonas campestris pv. vesicatoria str. 85−10
S^{A-T}_{plus}
4
3
2
1
0
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
−4
−5
0e+00
2e+06
4e+06
genome coordinates

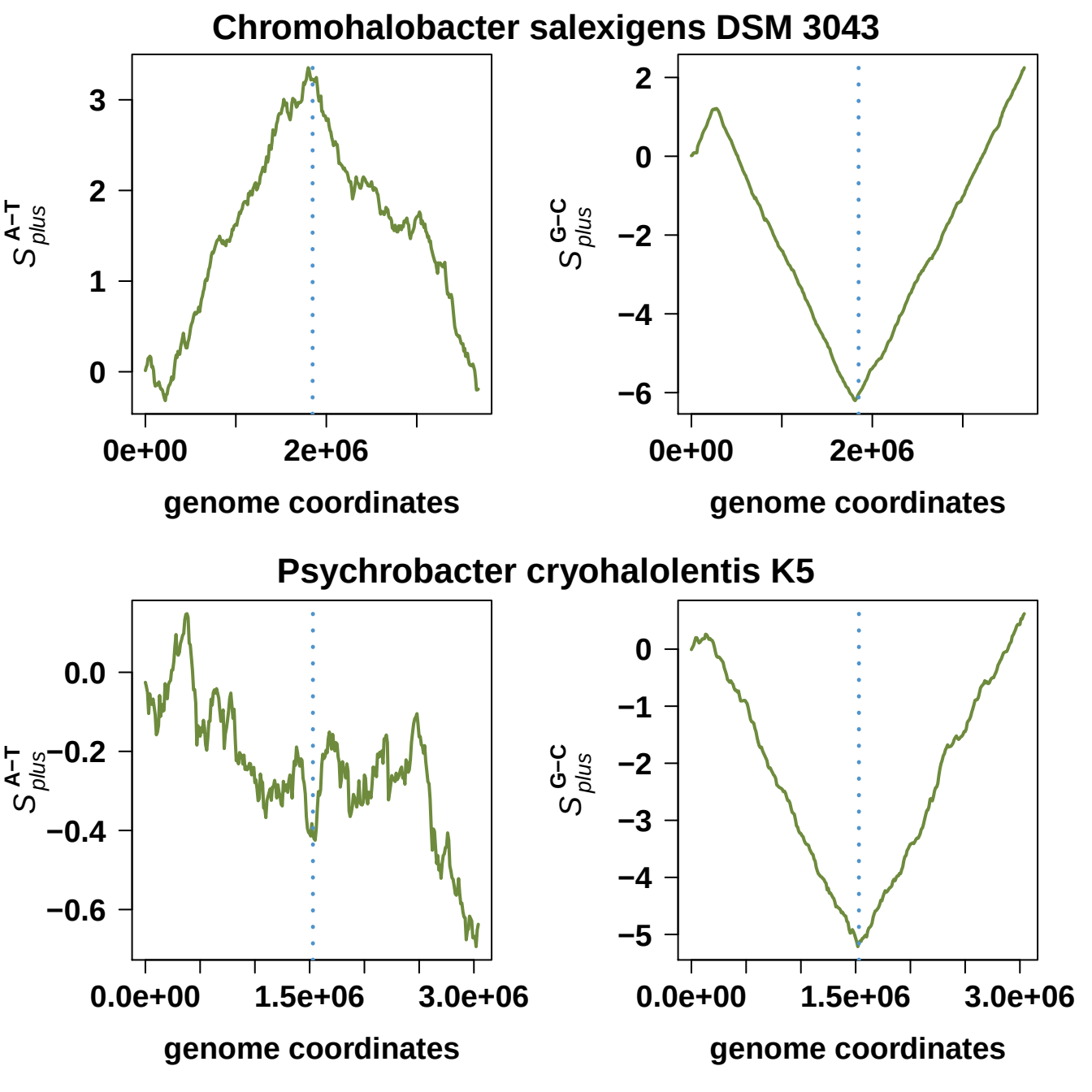

Thiomicrospira crunogena XCL−2
S^{A-T}_{plus}
3
2
1
0
0.0e+00
1.0e+06
2.0e+06
genome coordinates
S^{G-C}_{plus}
2
0
−2
−4
−6
−8
−10
0.0e+00
1.0e+06
2.0e+06
genome coordinates
Shigella dysenteriae Sd197
S^{A-T}_{plus}
0.0
−0.2
−0.4
−0.6
−0.8
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
−4
0e+00
2e+06
4e+06
genome coordinates

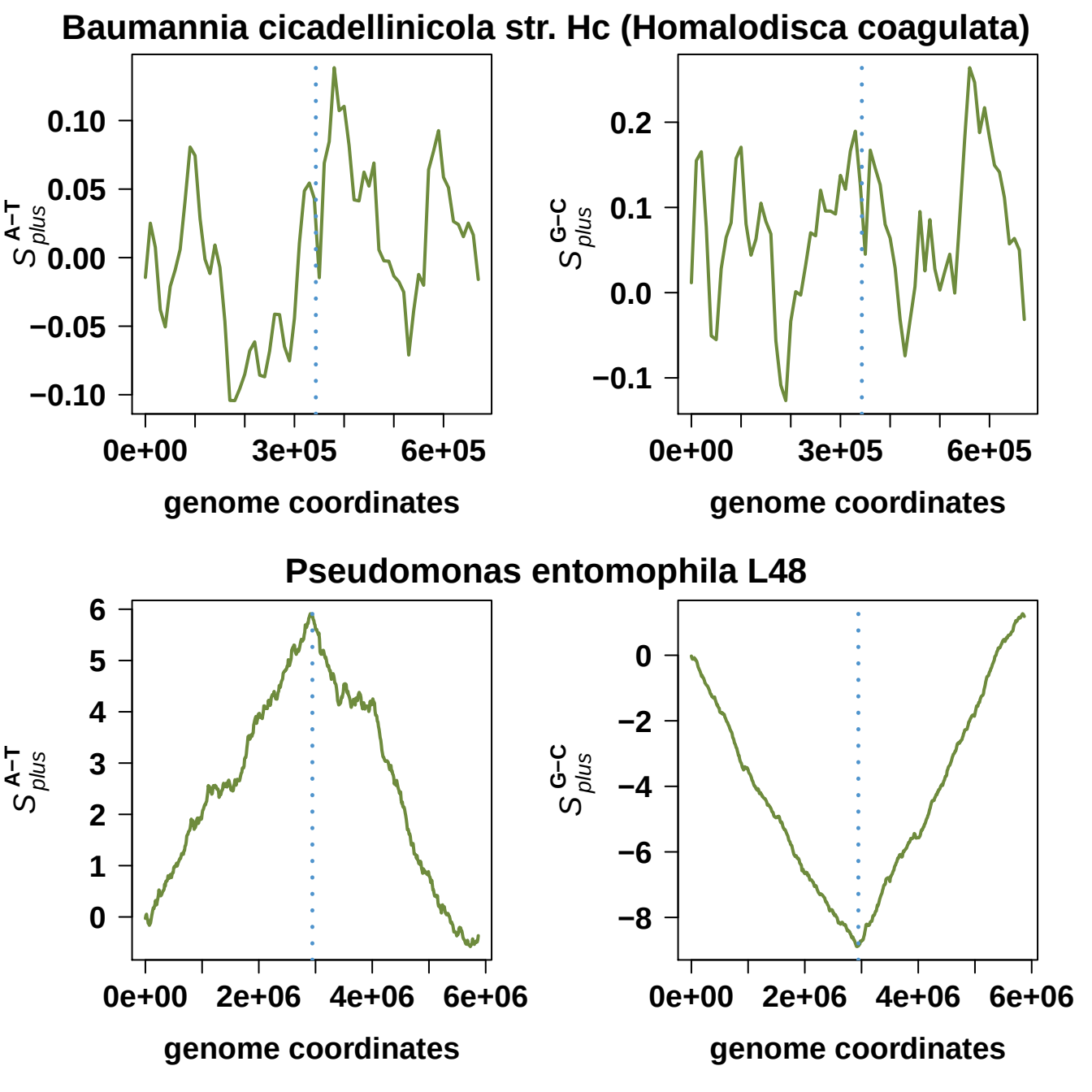

Shigella boydii Sb227
0.1
0.0
−0.1
−0.2
−0.3
−0.4
S^{A-T}_{plus}
0e+00
2e+06
4e+06
genome coordinates
1
0
−1
−2
−3
S^{G-C}_{plus}
0e+00
2e+06
4e+06
genome coordinates
Hahella chejuensis KCTC 2396
8
6
4
2
0
S^{A-T}_{plus}
0e+00
3e+06
6e+06
genome coordinates
0
−5
−10
−15
−20
S^{G-C}_{plus}
0e+00
3e+06
6e+06
genome coordinates

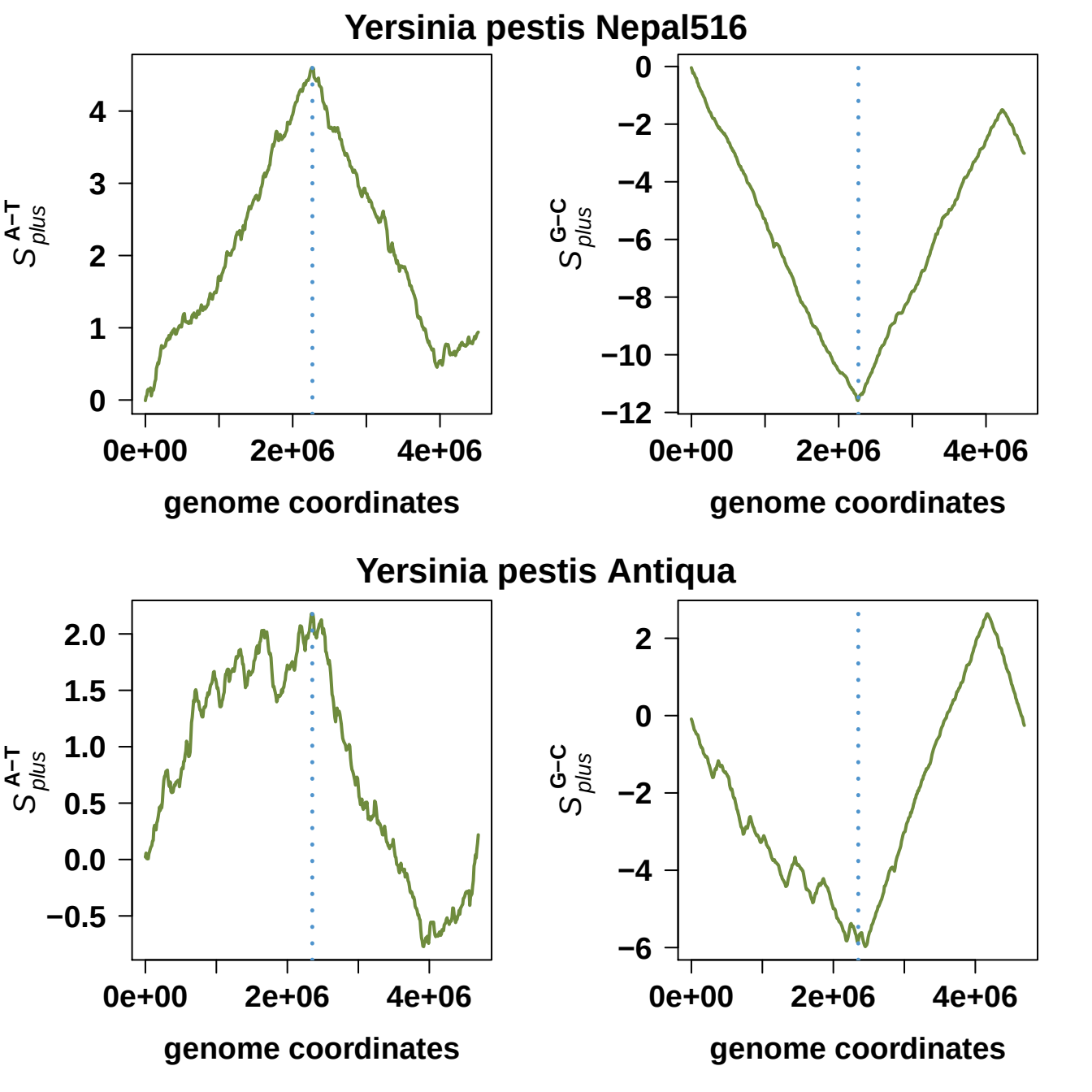

Xanthomonas oryzae pv. oryzae MAFF 311018
S^{A-T}_{plus}
4
3
2
1
0
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
−4
−5
0e+00
2e+06
4e+06
genome coordinates
Sodalis glossinidius str. 'morsitans'
S^{A-T}_{plus}
2.0
1.5
1.0
0.5
0.0
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
2
0
−2
−4
0e+00
2e+06
4e+06
genome coordinates

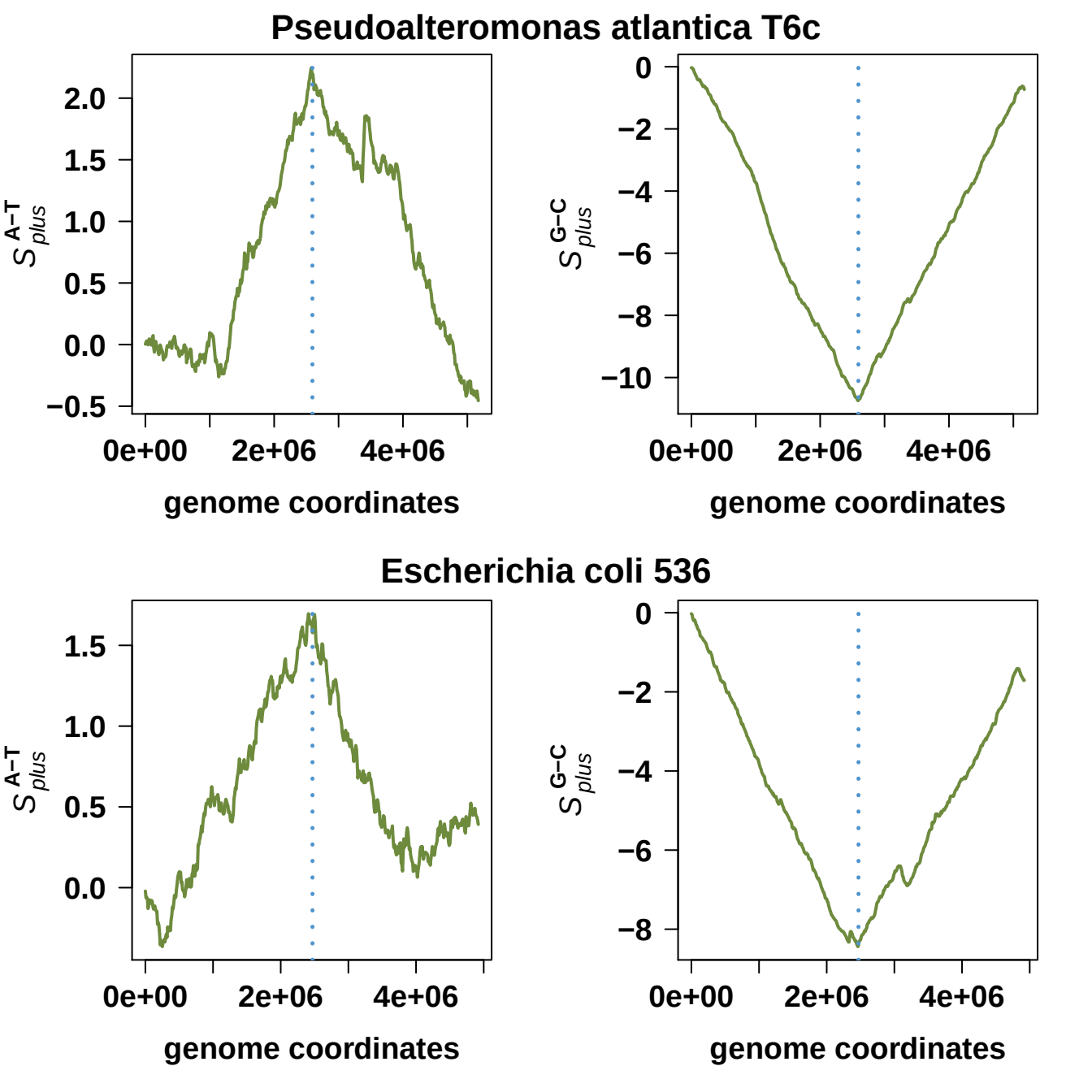

Francisella tularensis subsp. holarctica LVS
S^{A-T}_{plus}
0.0
−0.2
−0.4
−0.6
−0.8
0.0e+00
1.0e+06
genome coordinates
S^{G-C}_{plus}
2
0
−2
−4
0.0e+00
1.0e+06
genome coordinates
Saccharophagus degradans 2−40
S^{A-T}_{plus}
8
6
4
2
0
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
0
−5
−10
−15
−20
0e+00
2e+06
4e+06
genome coordinates

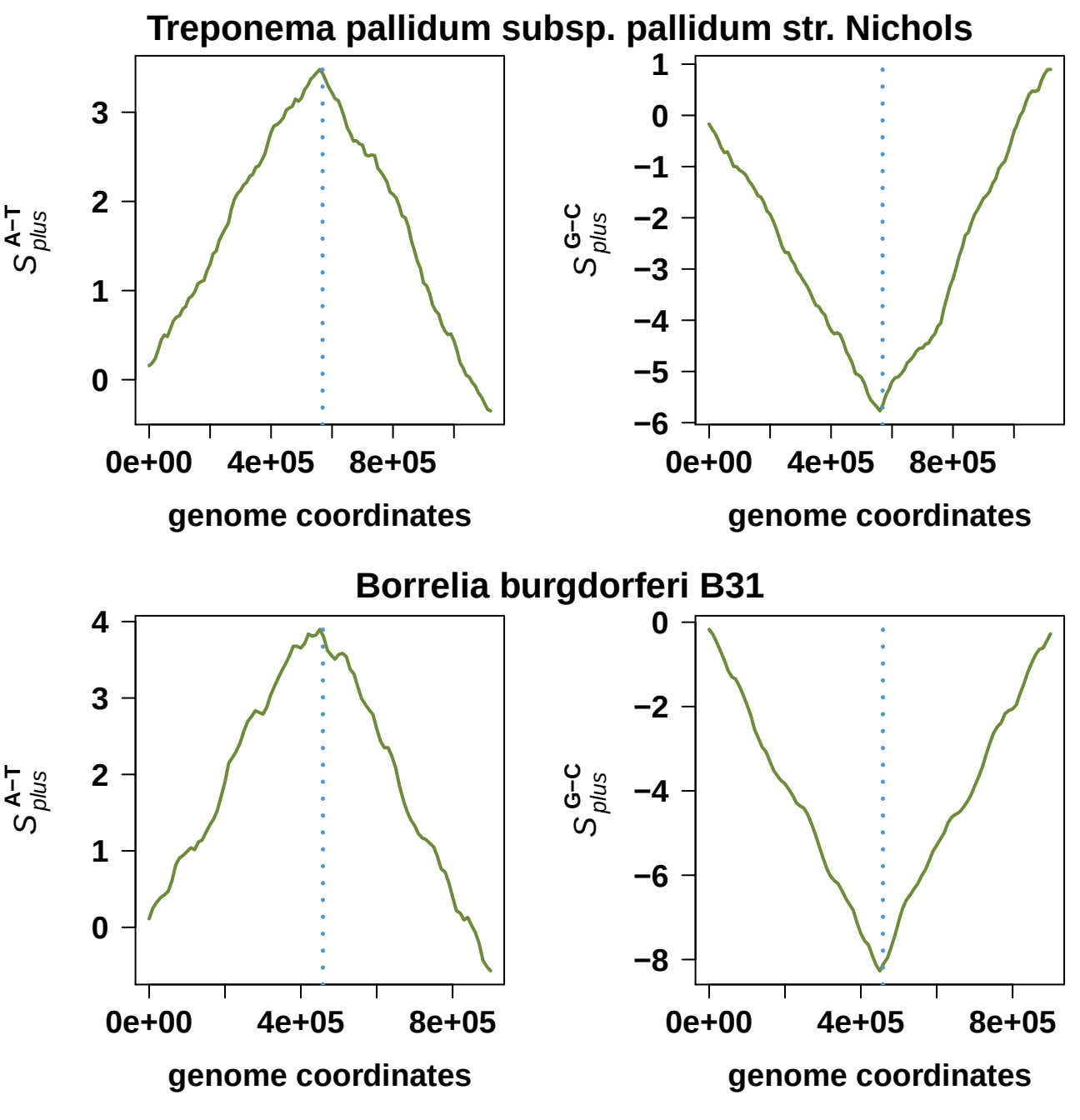

Escherichia coli UTI89
1.5
1.0
0.5
0.0
−0.5
S^{A-T}_{plus}
0e+00
2e+06
4e+06
genome coordinates
0
−2
−4
−6
−8
S^{G-C}_{plus}
0e+00
2e+06
4e+06
genome coordinates
Shewanella denitrificans OS217
3
2
1
0
S^{A-T}_{plus}
0e+00
2e+06
4e+06
genome coordinates
0
−2
−4
−6
−8
−10
−12
S^{G-C}_{plus}
0e+00
2e+06
4e+06
genome coordinates

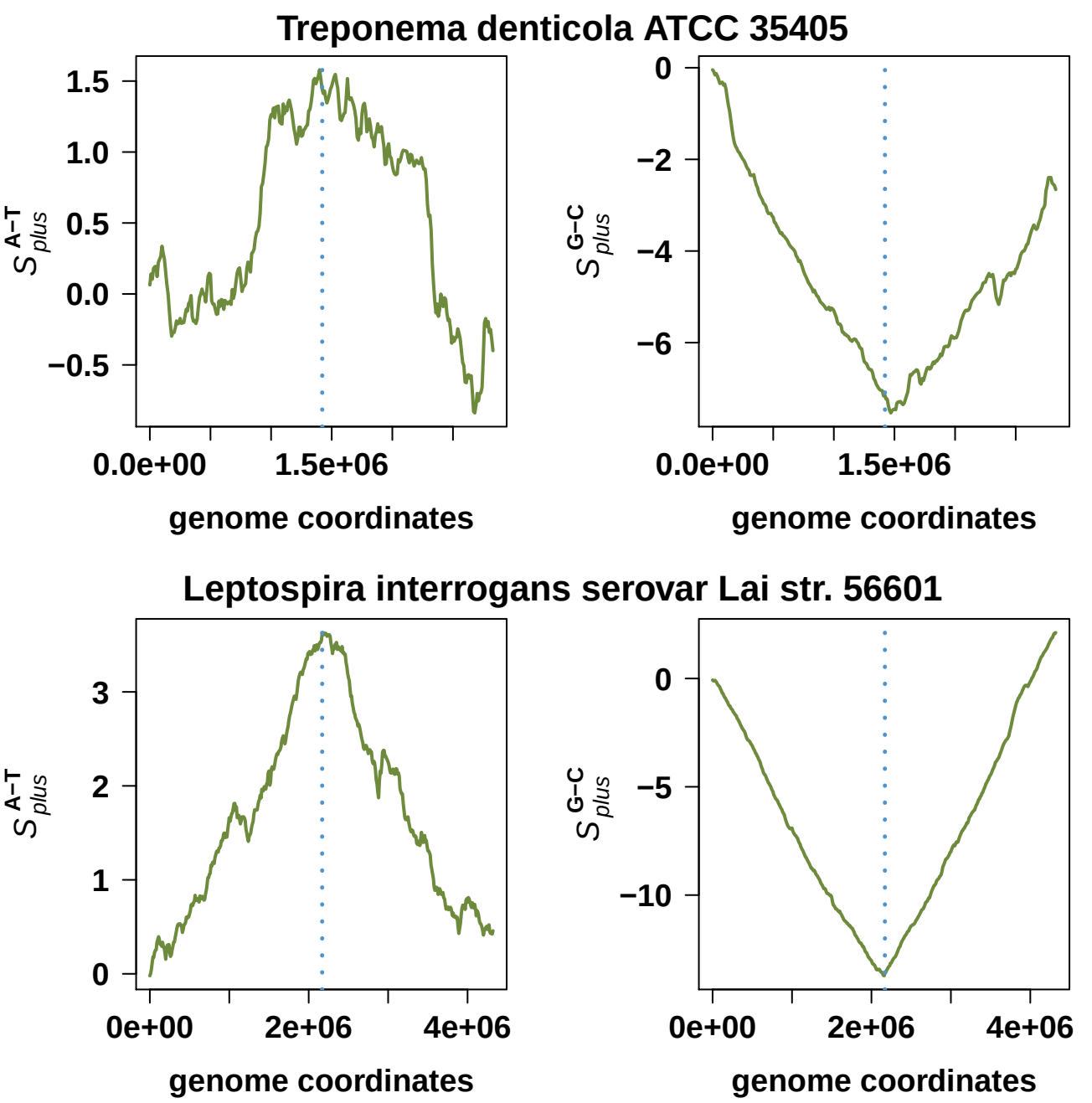

Chromohalobacter salexigens DSM 3043
S^{A-T}_{plus}
3
2
1
0
0e+00
2e+06
genome coordinates
S^{G-C}_{plus}
2
0
−2
−4
−6
0e+00
2e+06
genome coordinates
Psychrobacter cryohalolentis K5
S^{A-T}_{plus}
0.0
−0.2
−0.4
−0.6
0.0e+00
1.5e+06
3.0e+06
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
−4
−5
0.0e+00
1.5e+06
3.0e+06
genome coordinates

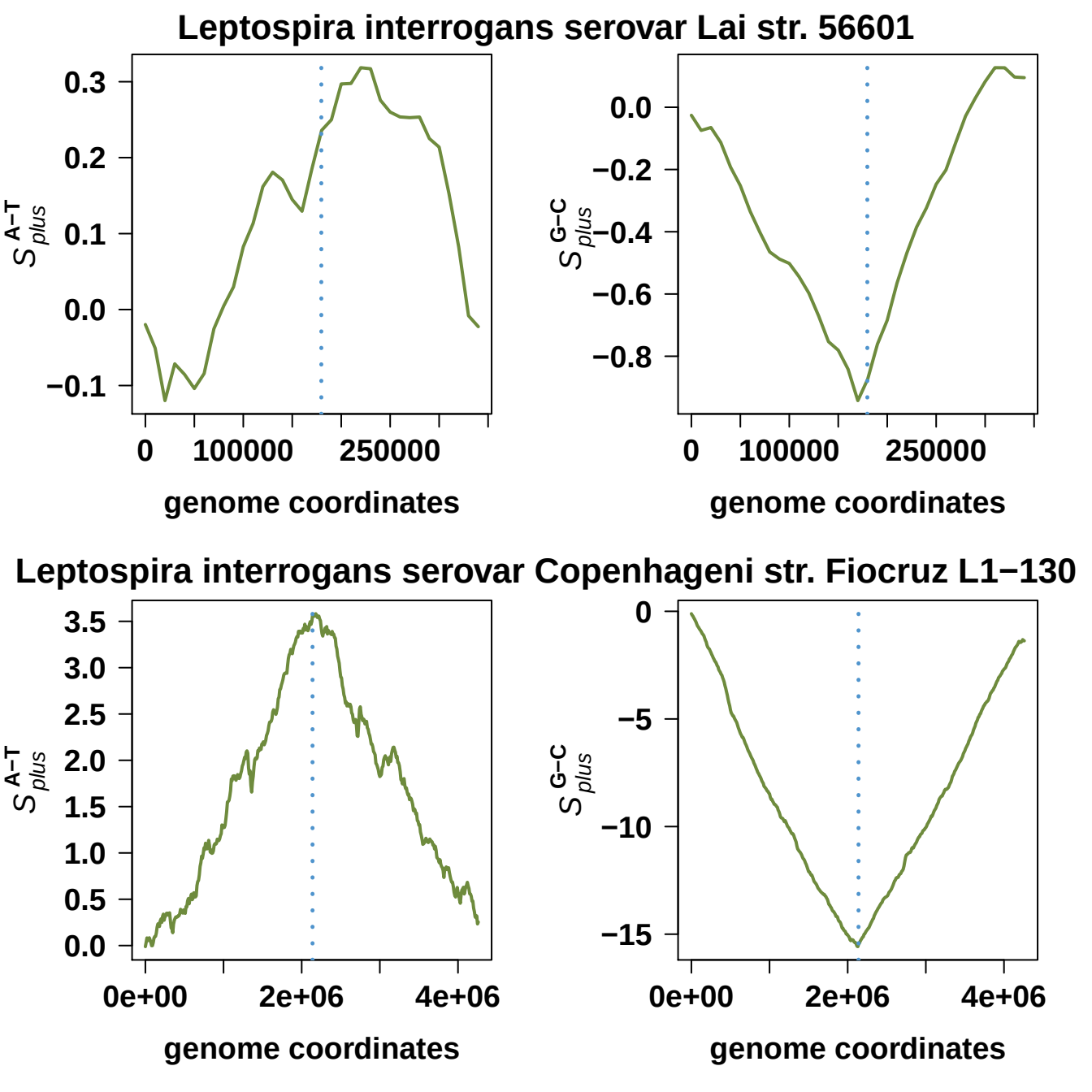

Baumannia cicadellinicola str. Hc (Homalodisca coagulata)
S^{A-T}_{plus}
0.10
0.05
0.00
−0.05
−0.10
0e+00
3e+05
6e+05
genome coordinates
S^{G-C}_{plus}
0.2
0.1
0.0
−0.1
0e+00
3e+05
6e+05
genome coordinates
Pseudomonas entomophila L48
S^{A-T}_{plus}
6
5
4
3
2
1
0
0e+00
2e+06
4e+06
6e+06
genome coordinates
S^{G-C}_{plus}
0
−2
−4
−6
−8
0e+00
2e+06
4e+06
6e+06
genome coordinates

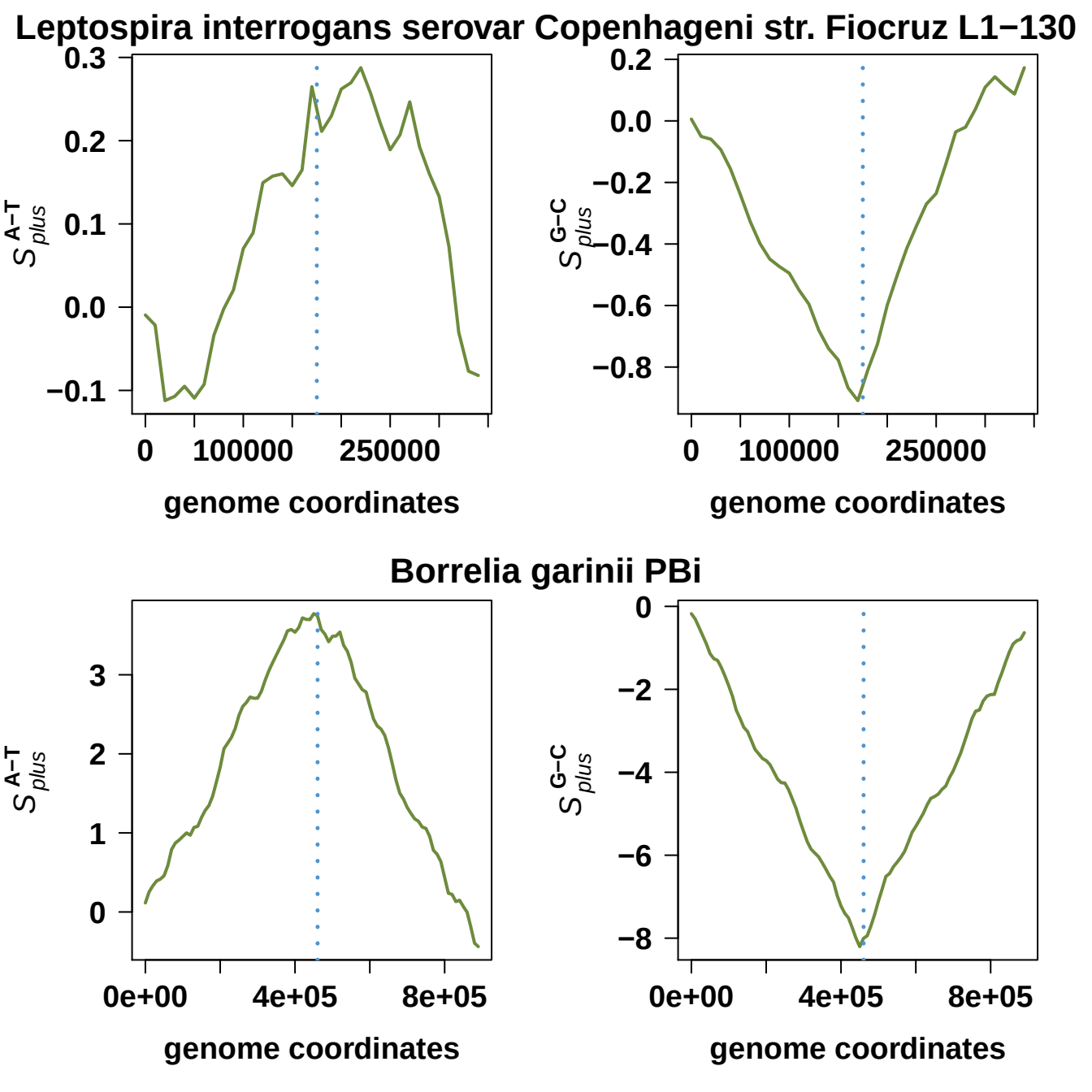

Yersinia pestis Nepal516
S^{A-T}_{plus}
4
3
2
1
0
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
0
−2
−4
−6
−8
−10
−12
0e+00
2e+06
4e+06
genome coordinates
Yersinia pestis Antiqua
S^{A-T}_{plus}
2.0
1.5
1.0
0.5
0.0
−0.5
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
2
0
−2
−4
−6
0e+00
2e+06
4e+06
genome coordinates

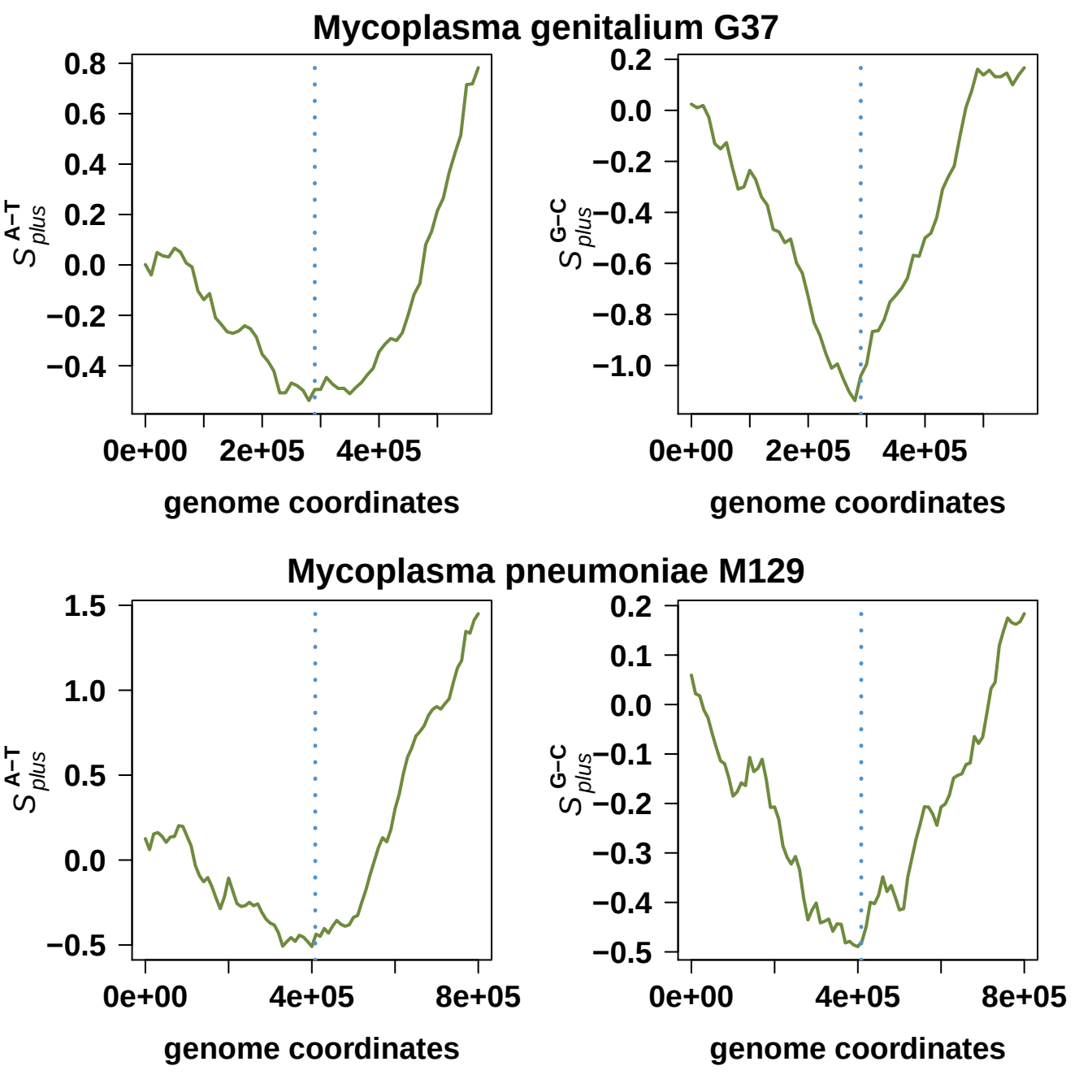

Pseudoalteromonas atlantica T6c
S^{A-T}_{plus}
2.0
1.5
1.0
0.5
0.0
−0.5
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
0
−2
−4
−6
−8
−10
0e+00
2e+06
4e+06
genome coordinates
Escherichia coli 536
S^{A-T}_{plus}
1.5
1.0
0.5
0.0
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
0
−2
−4
−6
−8
0e+00
2e+06
4e+06
genome coordinates

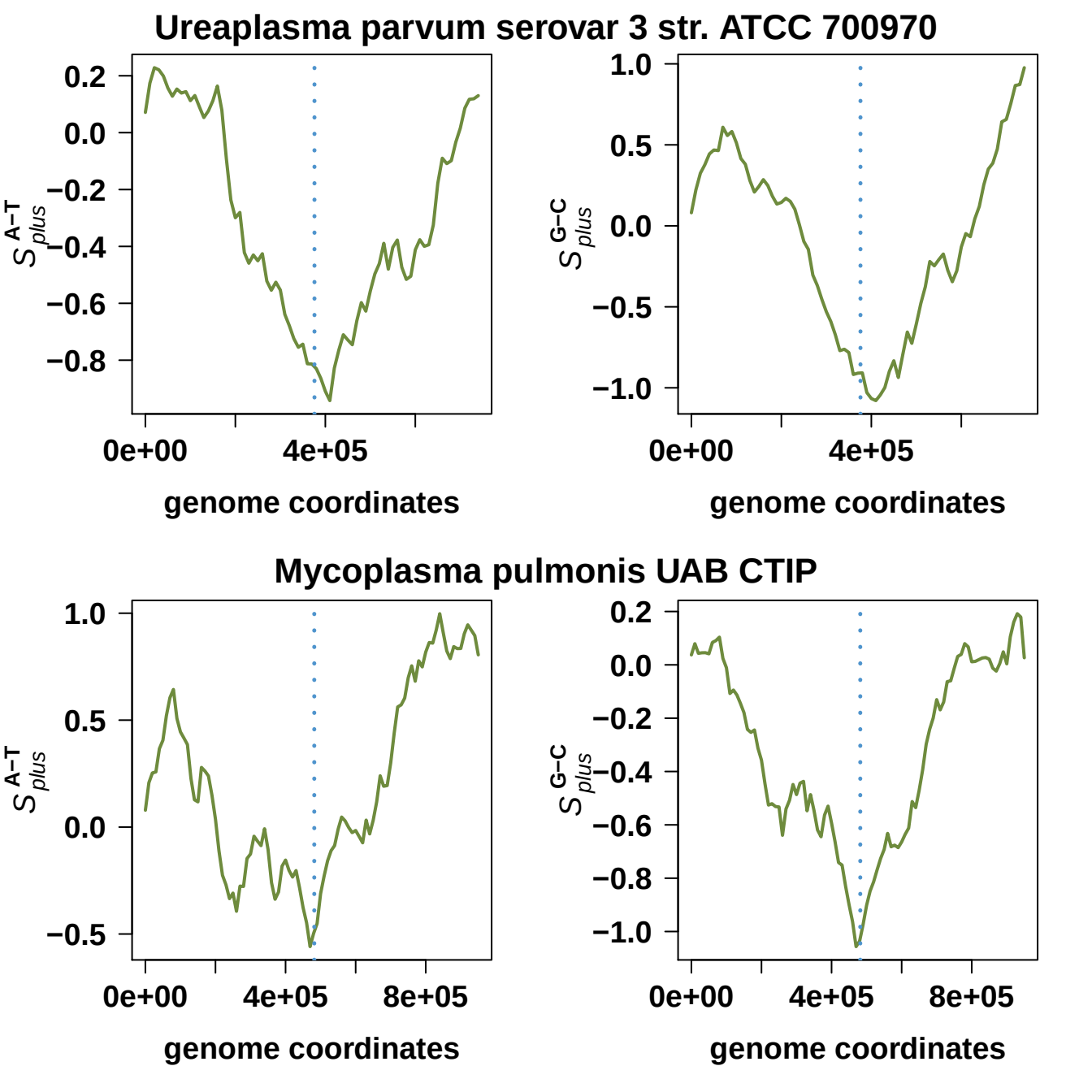

Treponema pallidum subsp. pallidum str. Nichols
S^{A-T}_{plus}
3
2
1
0
0e+00
4e+05
8e+05
genome coordinates
S^{G-C}_{plus}
1
0
−1
−2
−3
−4
−5
−6
0e+00
4e+05
8e+05
genome coordinates
Borrelia burgdorferi B31
S^{A-T}_{plus}
4
3
2
1
0
0e+00
4e+05
8e+05
genome coordinates
S^{G-C}_{plus}
0
−2
−4
−6
−8
0e+00
4e+05
8e+05
genome coordinates

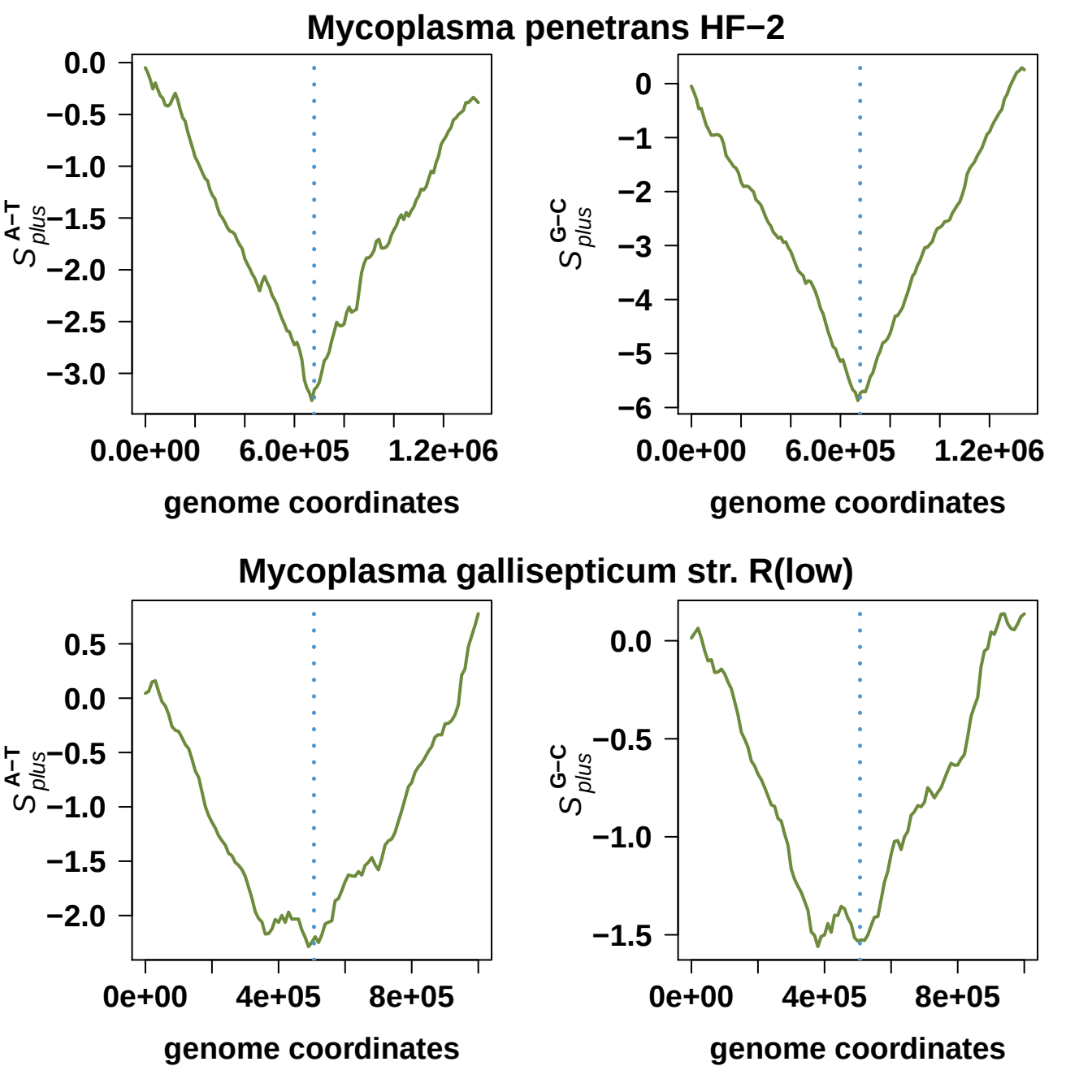

Treponema denticola ATCC 35405
1.5
1.0
0.5
0.0
−0.5
S^{A-T}_{plus}
0.0e+00
1.5e+06
genome coordinates
0
−2
−4
−6
S^{G-C}_{plus}
0.0e+00
1.5e+06
genome coordinates
Leptospira interrogans serovar Lai str. 56601
3
2
1
0
S^{A-T}_{plus}
0e+00
2e+06
4e+06
genome coordinates
0
−5
−10
S^{G-C}_{plus}
0e+00
2e+06
4e+06
genome coordinates

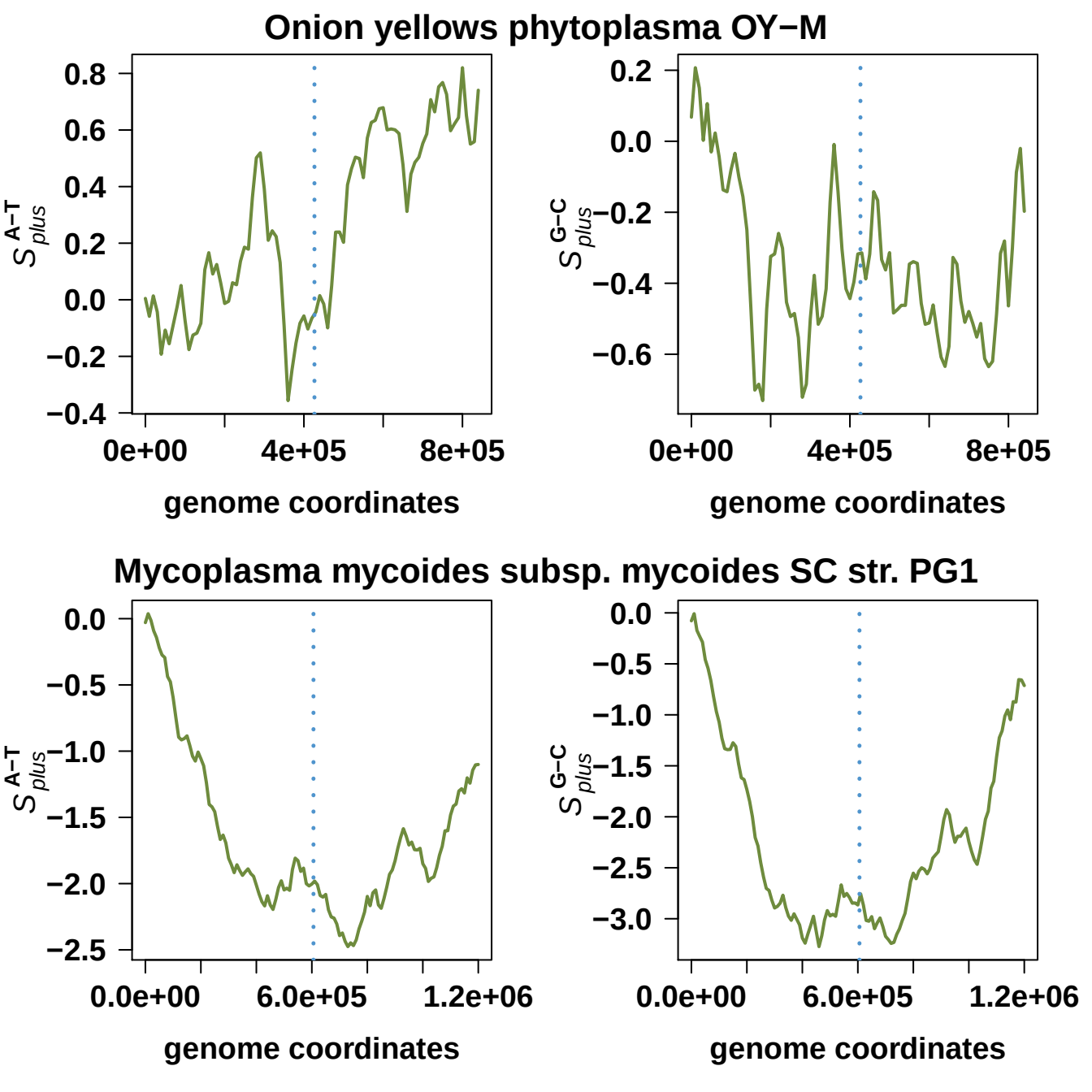

Leptospira interrogans serovar Lai str. 56601
S^{A-T}_{plus}
0.3
0.2
0.1
0.0
−0.1
0
100000
250000
genome coordinates
S^{G-C}_{plus}
0.0
−0.2
−0.4
−0.6
−0.8
0
100000
250000
genome coordinates
Leptospira interrogans serovar Copenhageni str. Fiocruz L1−130
S^{A-T}_{plus}
3.5
3.0
2.5
2.0
1.5
1.0
0.5
0.0
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{plus}
0
−5
−10
−15
0e+00
2e+06
4e+06
genome coordinates

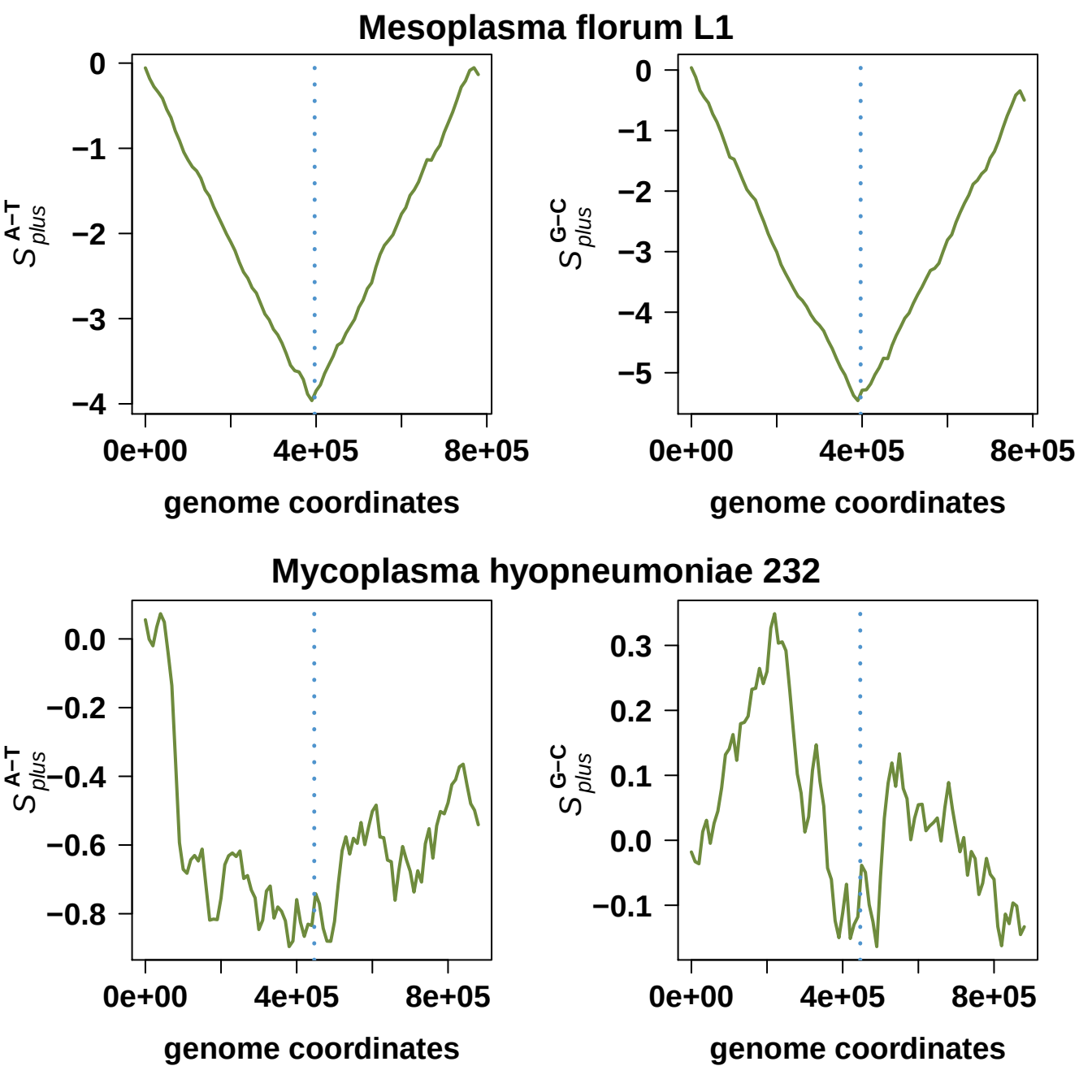

Leptospira interrogans serovar Copenhageni str. Fiocruz L1−130
0.3
0.2
0.1
0.0
−0.1
S^{A-T}_{plus}
0
100000
250000
genome coordinates
0.2
0.0
−0.2
−0.4
−0.6
−0.8
S^{G-C}_{plus}
0
100000
250000
genome coordinates
Borrelia garinii PBi
3
2
1
0
S^{A-T}_{plus}
0e+00
4e+05
8e+05
genome coordinates
0
−2
−4
−6
−8
S^{G-C}_{plus}
0e+00
4e+05
8e+05
genome coordinates

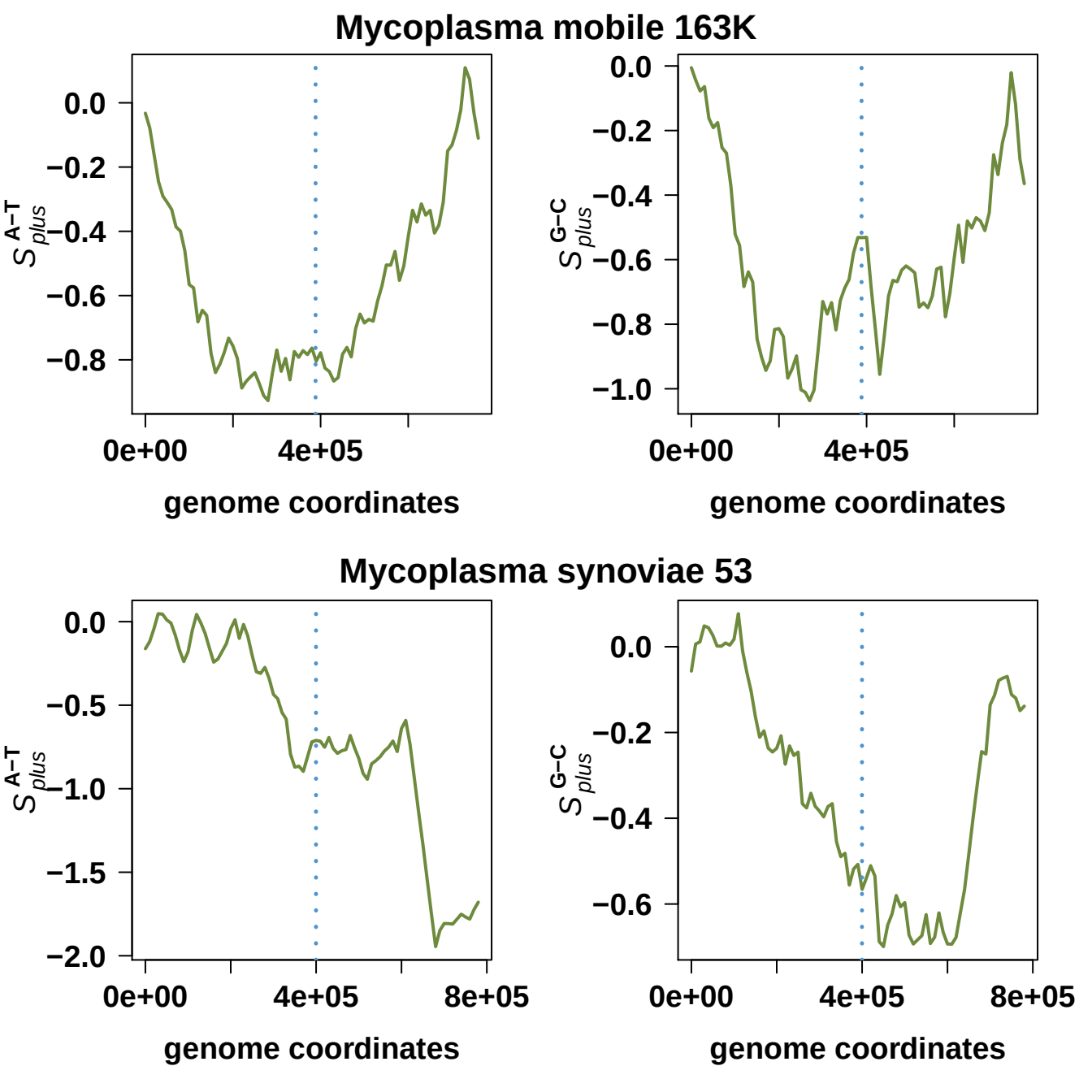

Mycoplasma genitalium G37
0.8
0.6
0.4
0.2
0.0
−0.2
−0.4
S^{A-T}_{plus}
0e+00
2e+05
4e+05
genome coordinates
0.2
0.0
−0.2
−0.4
−0.6
−0.8
−1.0
S^{G-C}_{plus}
0e+00
2e+05
4e+05
genome coordinates
Mycoplasma pneumoniae M129
1.5
1.0
0.5
0.0
−0.5
S^{A-T}_{plus}
0e+00
4e+05
8e+05
genome coordinates
0.2
0.1
0.0
−0.1
−0.2
−0.3
−0.4
−0.5
S^{G-C}_{plus}
0e+00
4e+05
8e+05
genome coordinates

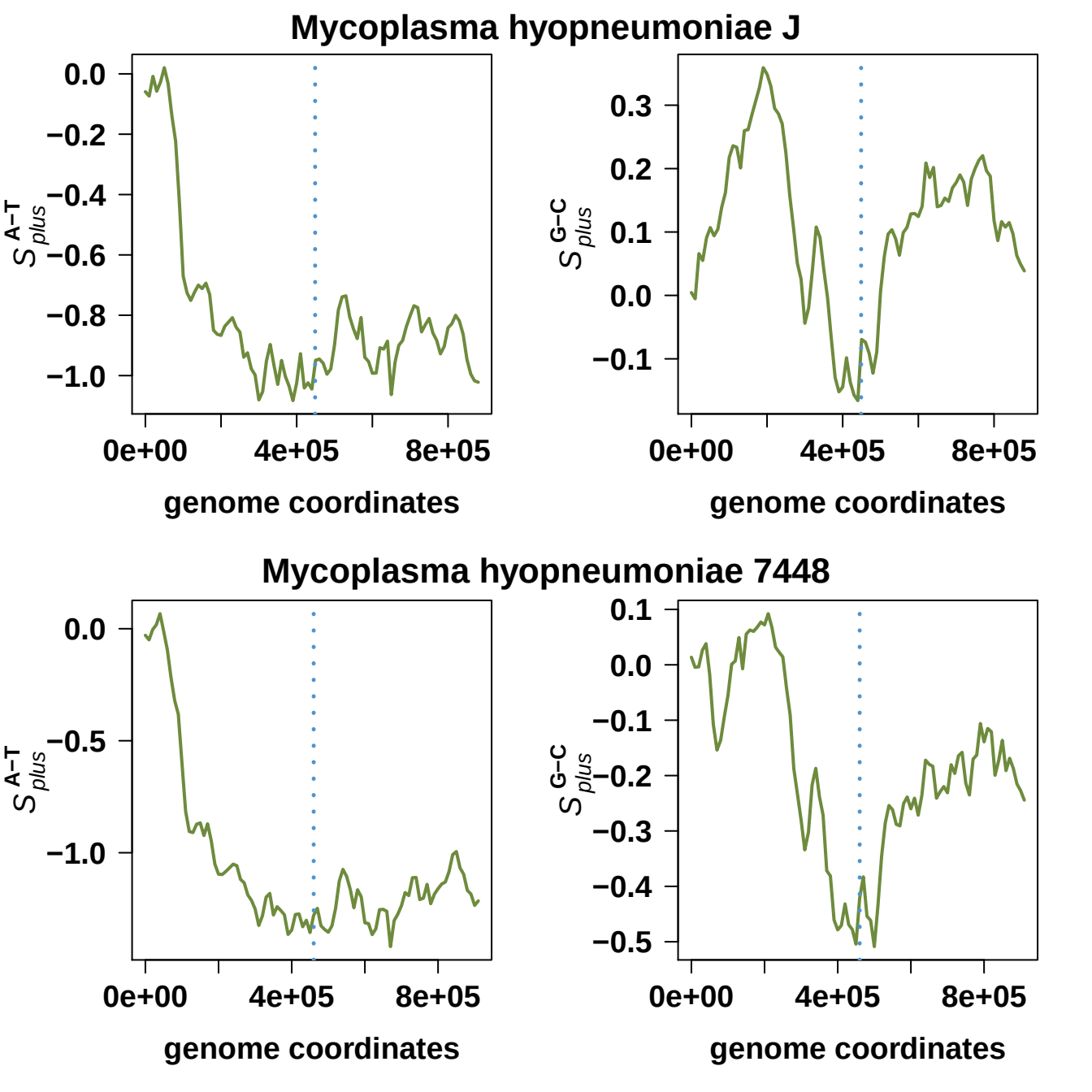

Ureaplasma parvum serovar 3 str. ATCC 700970
0.2
0.0
−0.2
−0.4
−0.6
−0.8
S A−T plus
0e+00
4e+05
genome coordinates
1.0
0.5
0.0
−0.5
−1.0
S G−C plus
0e+00
4e+05
genome coordinates
Mycoplasma pulmonis UAB CTIP
1.0
0.5
0.0
−0.5
S A−T plus
0e+00
4e+05
8e+05
genome coordinates
0.2
0.0
−0.2
−0.4
−0.6
−0.8
−1.0
S G−C plus
0e+00
4e+05
8e+05
genome coordinates

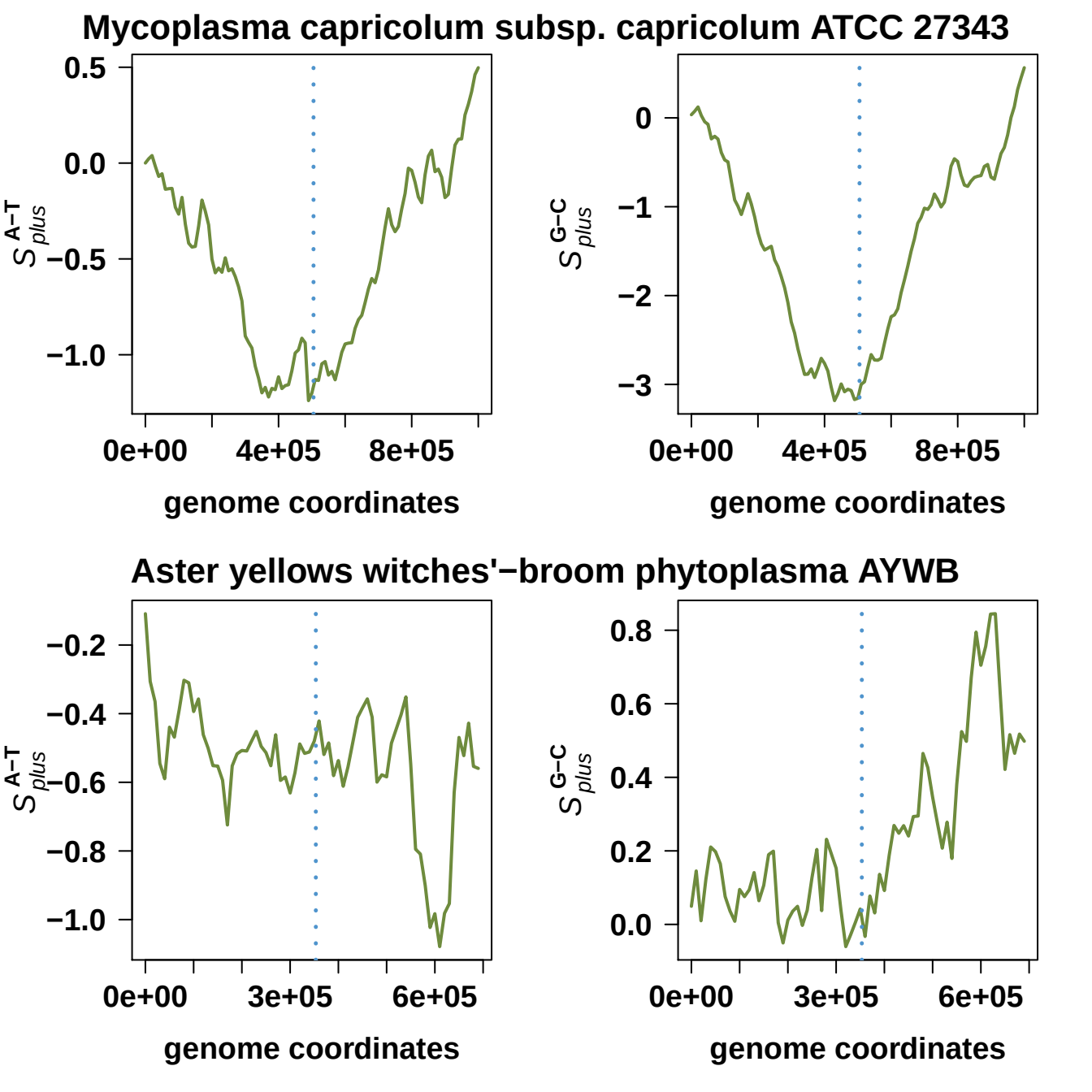

Mycoplasma penetrans HF−2
0.0
−0.5
−1.0
−1.5
−2.0
−2.5
−3.0
S^{A-T}_{plus}
0.0e+00
6.0e+05
1.2e+06
genome coordinates
0
−1
−2
−3
−4
−5
−6
S^{G-C}_{plus}
0.0e+00
6.0e+05
1.2e+06
genome coordinates
Mycoplasma gallisepticum str. R(low)
0.5
0.0
−0.5
−1.0
−1.5
−2.0
S^{A-T}_{plus}
0e+00
4e+05
8e+05
genome coordinates
0.0
−0.5
−1.0
−1.5
S^{G-C}_{plus}
0e+00
4e+05
8e+05
genome coordinates


Onion yellows phytoplasma OY−M
S^{A-T}_{plus}
0.8
0.6
0.4
0.2
0.0
−0.2
−0.4
0e+00
4e+05
8e+05
genome coordinates
S^{G-C}_{plus}
0.2
0.0
−0.2
−0.4
−0.6
0e+00
4e+05
8e+05
genome coordinates
Mycoplasma mycoides subsp. mycoides SC str. PG1
S^{A-T}_{plus}
0.0
−0.5
−1.0
−1.5
−2.0
−2.5
0.0e+00
6.0e+05
1.2e+06
genome coordinates
S^{G-C}_{plus}
0.0
−0.5
−1.0
−1.5
−2.0
−2.5
−3.0
0.0e+00
6.0e+05
1.2e+06
genome coordinates


Mesoplasma florum L1
S^{A-T}_{plus}
0
−1
−2
−3
−4
0e+00
4e+05
8e+05
genome coordinates
S^{G-C}_{plus}
0
−1
−2
−3
−4
−5
0e+00
4e+05
8e+05
genome coordinates
Mycoplasma hyopneumoniae 232
S^{A-T}_{plus}
0.0
−0.2
−0.4
−0.6
−0.8
0e+00
4e+05
8e+05
genome coordinates
S^{G-C}_{plus}
0.3
0.2
0.1
0.0
−0.1
0e+00
4e+05
8e+05
genome coordinates


Mycoplasma mobile 163K
S^{A-T}_{plus}
0.0
−0.2
−0.4
−0.6
−0.8
0e+00
4e+05
genome coordinates
S^{G-C}_{plus}
0.0
−0.2
−0.4
−0.6
−0.8
−1.0
0e+00
4e+05
genome coordinates
Mycoplasma synoviae 53
S^{A-T}_{plus}
0.0
−0.5
−1.0
−1.5
−2.0
0e+00
4e+05
8e+05
genome coordinates
S^{G-C}_{plus}
0.0
−0.2
−0.4
−0.6
0e+00
4e+05
8e+05
genome coordinates


Mycoplasma hyopneumoniae J
0.0
−0.2
−0.4
−0.6
−0.8
−1.0
S^{A-T}_{plus}
0e+00
4e+05
8e+05
genome coordinates
0.3
0.2
0.1
0.0
−0.1
S^{G-C}_{plus}
0e+00
4e+05
8e+05
genome coordinates
Mycoplasma hyopneumoniae 7448
0.0
−0.5
−1.0
S^{A-T}_{plus}
0e+00
4e+05
8e+05
genome coordinates
0.1
0.0
−0.1
−0.2
−0.3
−0.4
−0.5
S^{G-C}_{plus}
0e+00
4e+05
8e+05
genome coordinates


Mycoplasma capricolum subsp. capricolum ATCC 27343
0.5
0.0
−0.5
−1.0
S^{A-T}_{plus}
0e+00
4e+05
8e+05
genome coordinates
0
−1
−2
−3
S^{G-C}_{plus}
0e+00
4e+05
8e+05
genome coordinates
Aster yellows witches'−broom phytoplasma AYWB
−0.2
−0.4
−0.6
−0.8
−1.0
S^{A-T}_{plus}
0e+00
3e+05
6e+05
genome coordinates
0.8
0.6
0.4
0.2
0.0
S^{G-C}_{plus}
0e+00
3e+05
6e+05
genome coordinates