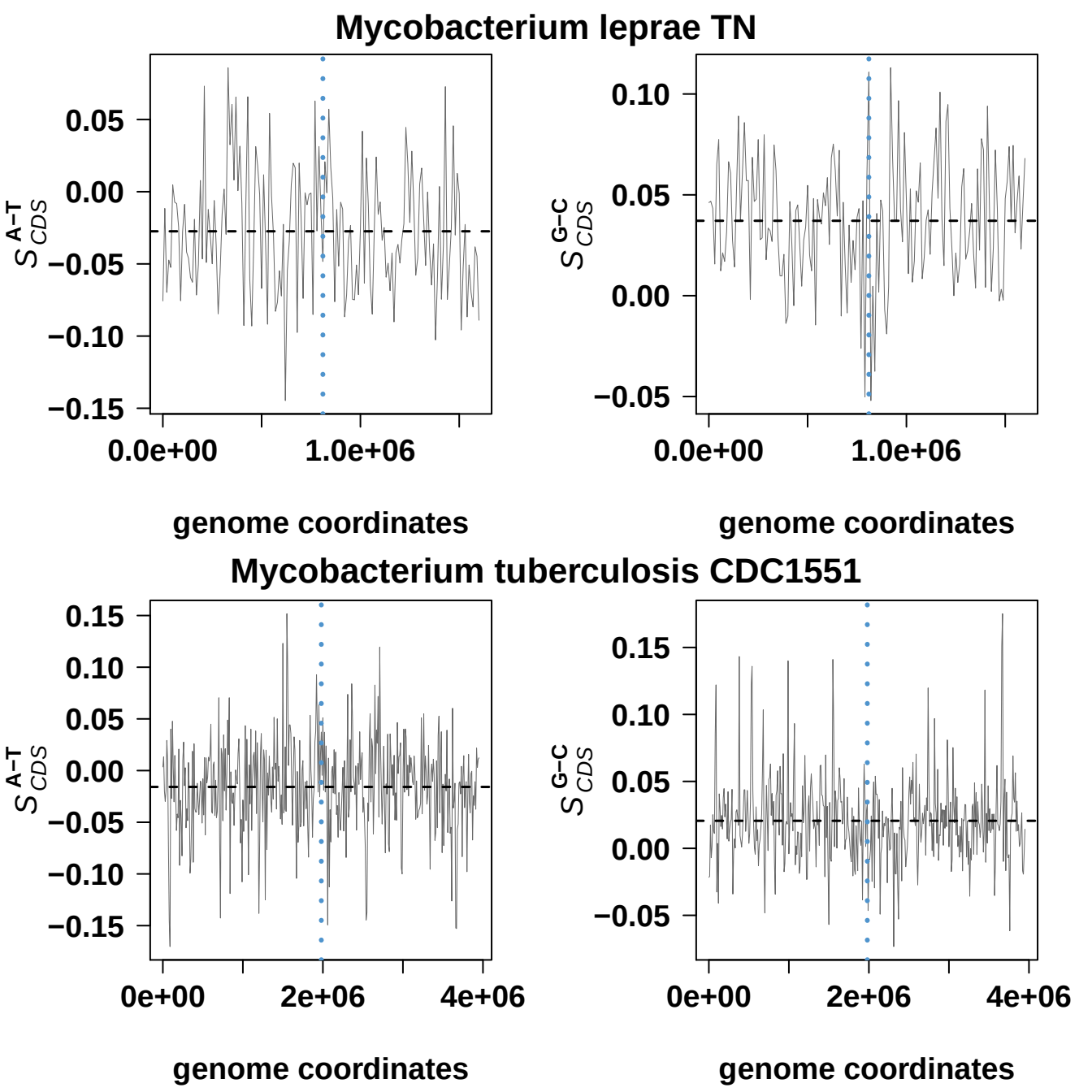
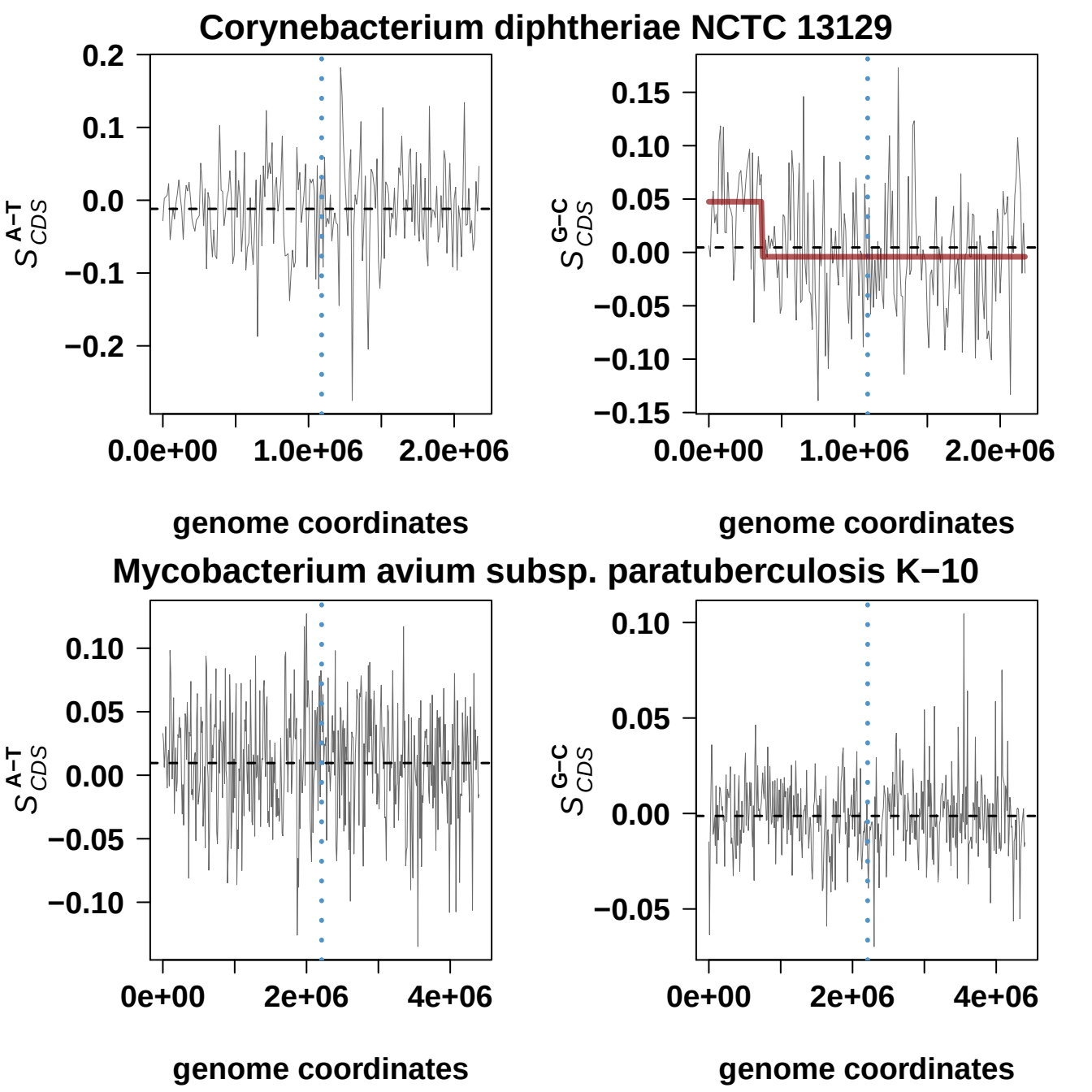
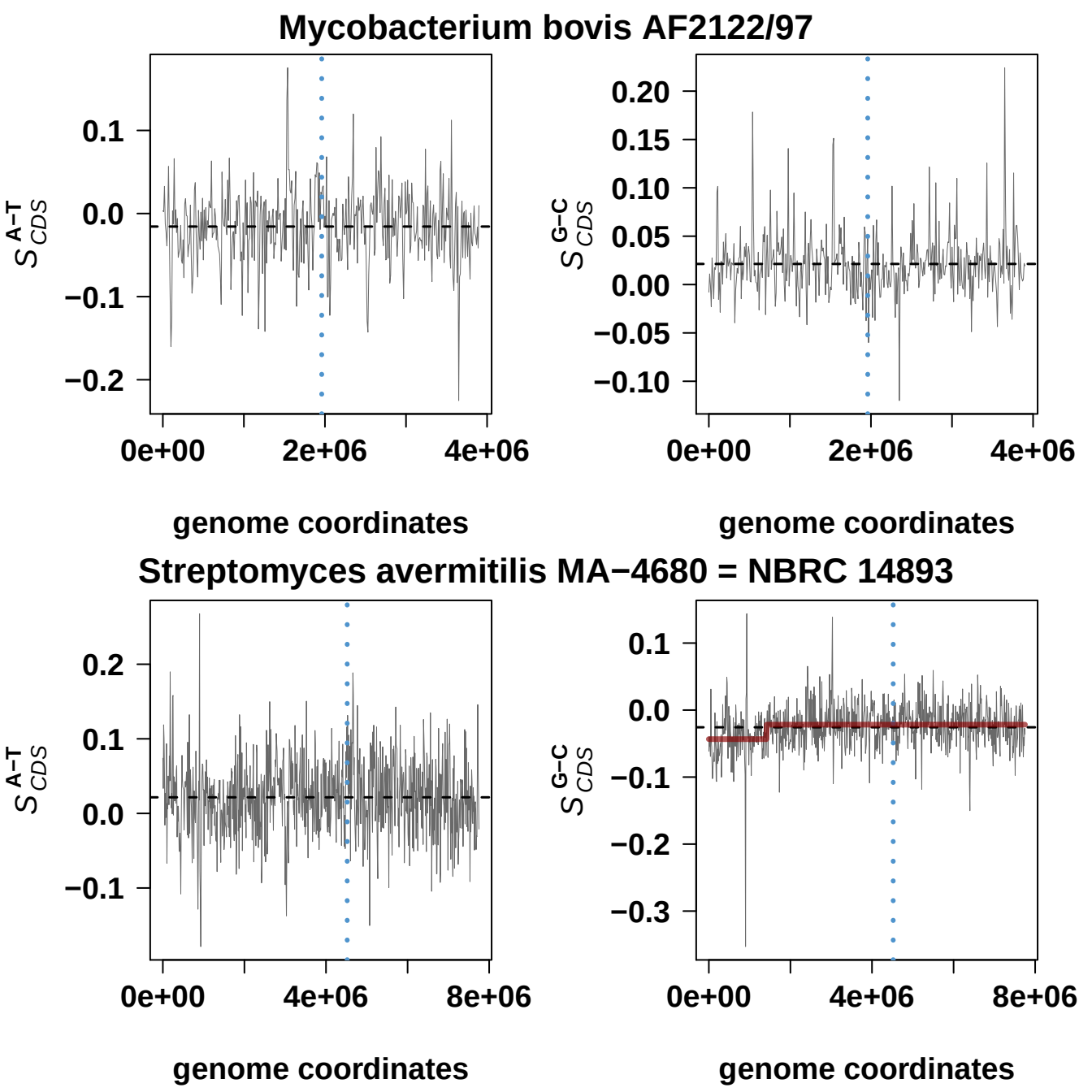
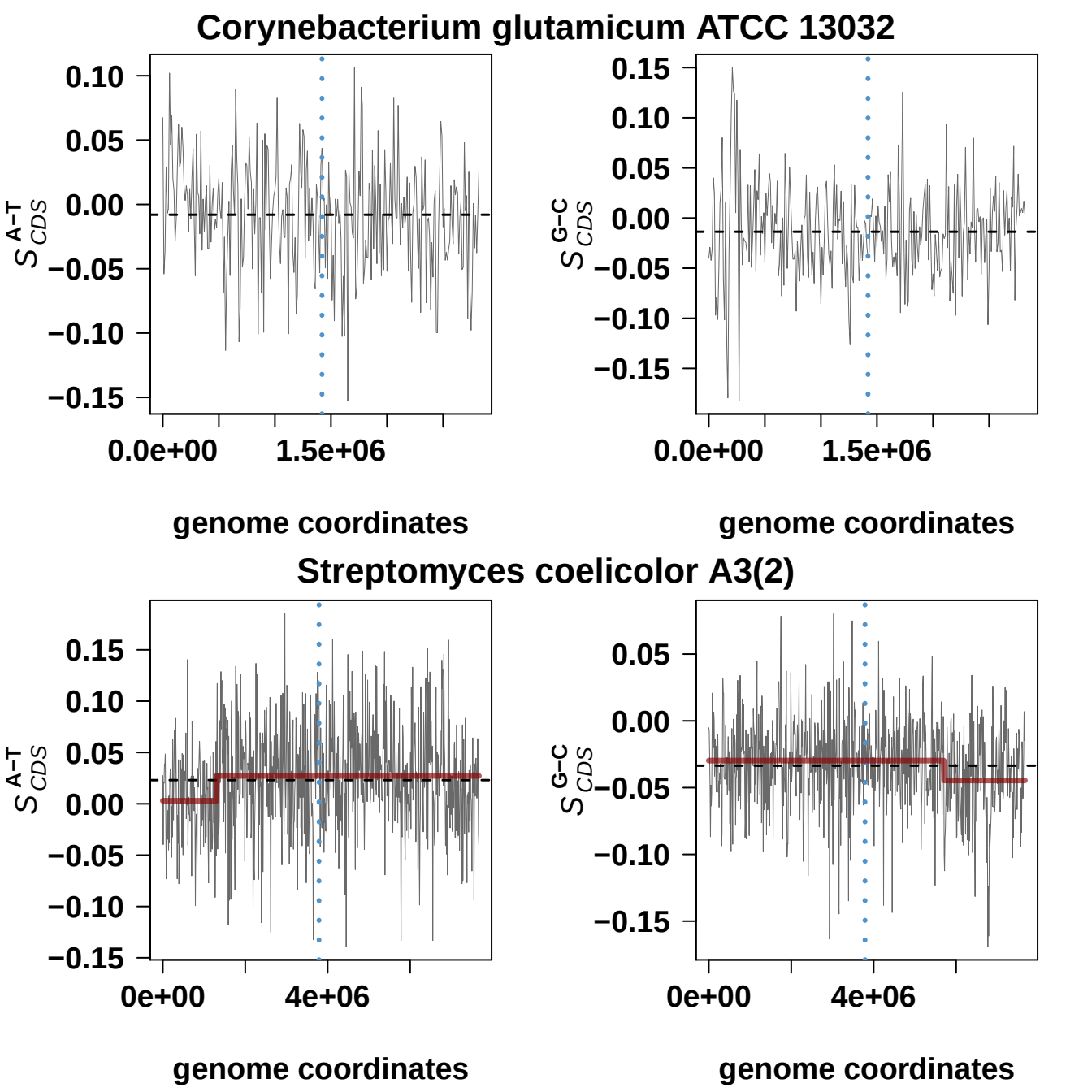
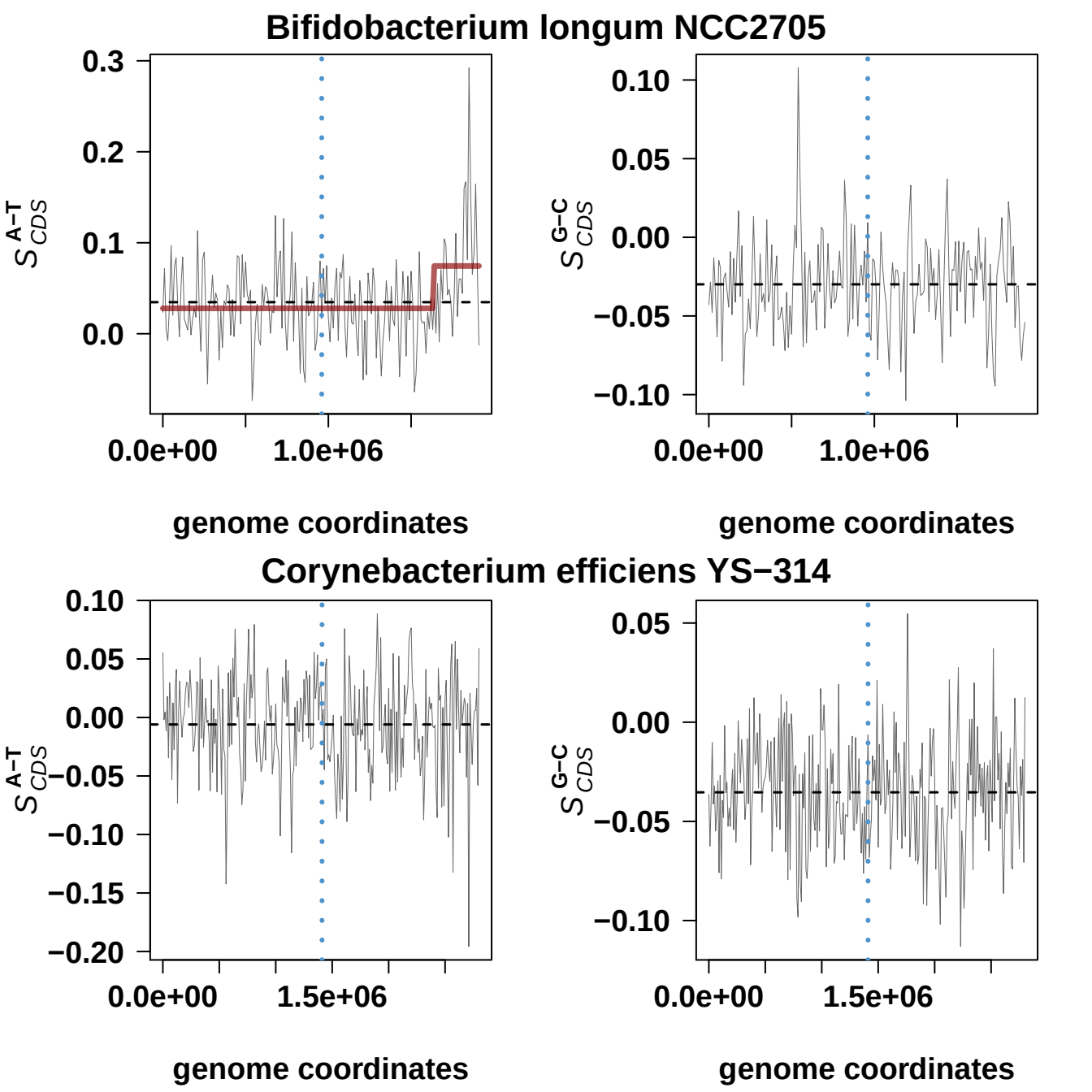
Diagrams (gray curve) and fitted linear models (red thick line) for mononucleotide skews (S_{CDS}^{A-T} and S_{CDS}^{G-C}) along the CDS concatenates of all bacteria chromosomes in our collection. Each step-like breakpoint of the red thick line corresponds to a statistically significant structural change of the skew pattern. In cases where no significant structural changes are detected, the red line is omitted. The vertical dotted blue line indicates the origin of replication (*ori*). There are three distinct types of skew patterns; "sharp": at least one step-like breakpoint is located close to the *ori,* "vague": at least one step-like breakpoint is detected, but all breakpoints are far from the *ori*, and "flat": no step-like breakpoints are detected. The horizontal dashed black line is drawn at the mean value of the skew.

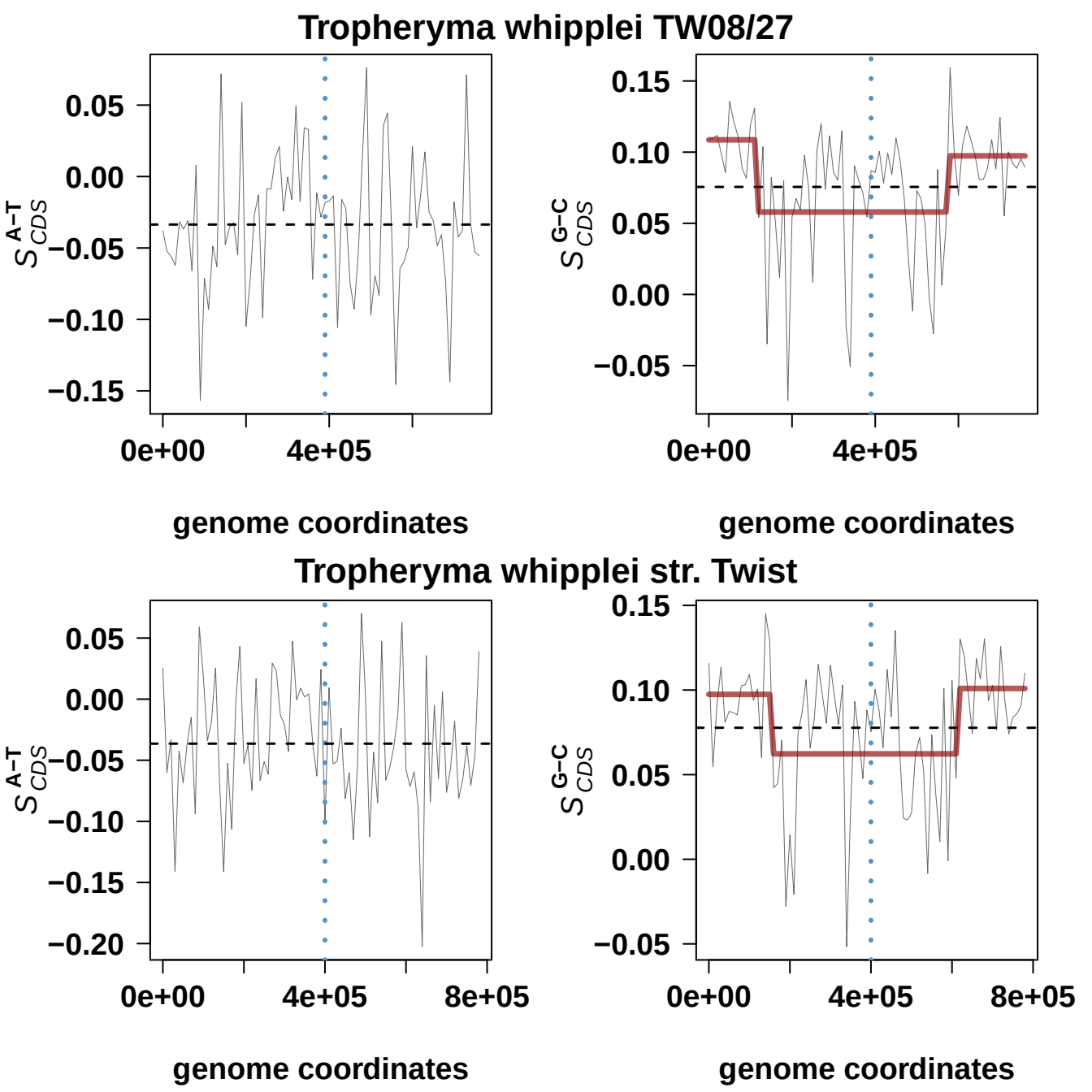

Mycobacterium leprae TN
S^{A-T}_{CDS}
0.05
0.00
−0.05
−0.10
−0.15
0.0e+00
1.0e+06
genome coordinates
S^{G-C}_{CDS}
0.10
0.05
0.00
−0.05
0.0e+00
1.0e+06
genome coordinates
Mycobacterium tuberculosis CDC1551
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
−0.05
−0.10
−0.15
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{CDS}
0.15
0.10
0.05
0.00
−0.05
0e+00
2e+06
4e+06
genome coordinates

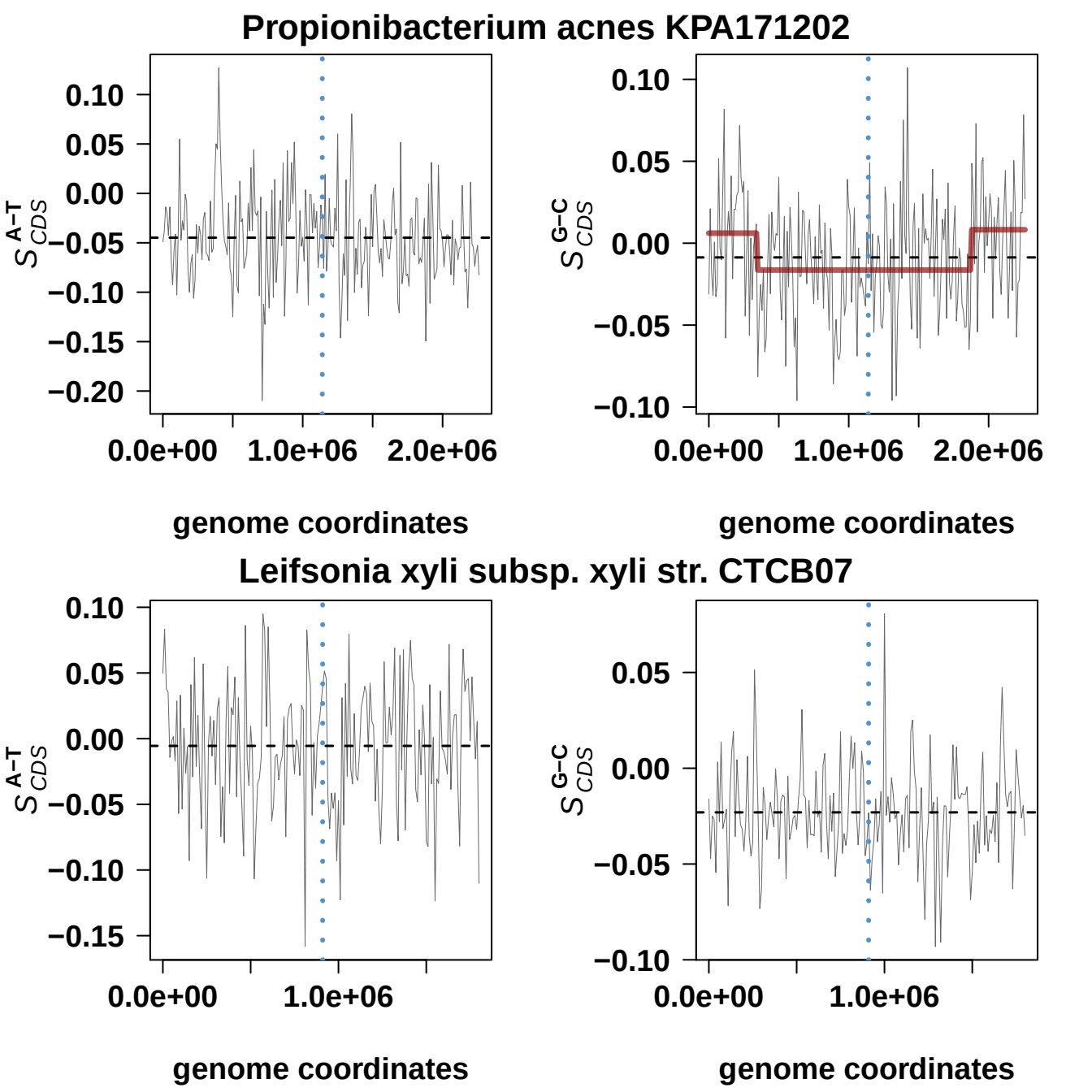

Corynebacterium diphtheriae NCTC 13129
S^{A-T}_{CDS}
0.2
0.1
0.0
−0.1
−0.2
0.0e+00
1.0e+06
2.0e+06
genome coordinates
S^{G-C}_{CDS}
0.15
0.10
0.05
0.00
−0.05
−0.10
−0.15
0.0e+00
1.0e+06
2.0e+06
genome coordinates
Mycobacterium avium subsp. paratuberculosis K−10
S^{A-T}_{CDS}
0.10
0.05
0.00
−0.05
−0.10
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{CDS}
0.10
0.05
0.00
−0.05
0e+00
2e+06
4e+06
genome coordinates

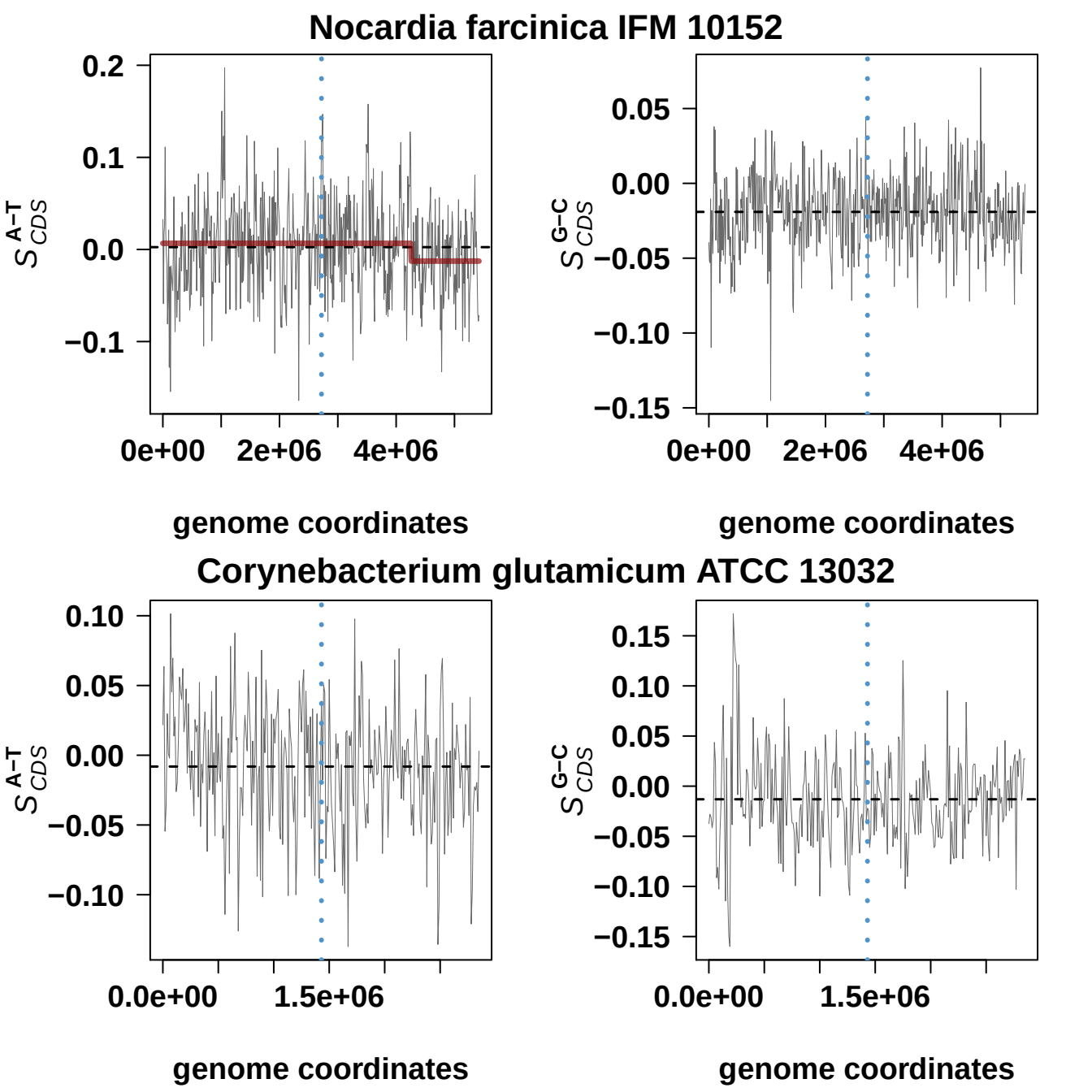

Mycobacterium bovis AF2122/97
S^{A-T}_{CDS}
0.1
0.0
−0.1
−0.2
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{CDS}
0.20
0.15
0.10
0.05
0.00
−0.05
−0.10
0e+00
2e+06
4e+06
genome coordinates
Streptomyces avermitilis MA−4680 = NBRC 14893
S^{A-T}_{CDS}
0.2
0.1
0.0
−0.1
0e+00
4e+06
8e+06
genome coordinates
S^{G-C}_{CDS}
0.1
0.0
−0.1
−0.2
−0.3
0e+00
4e+06
8e+06
genome coordinates

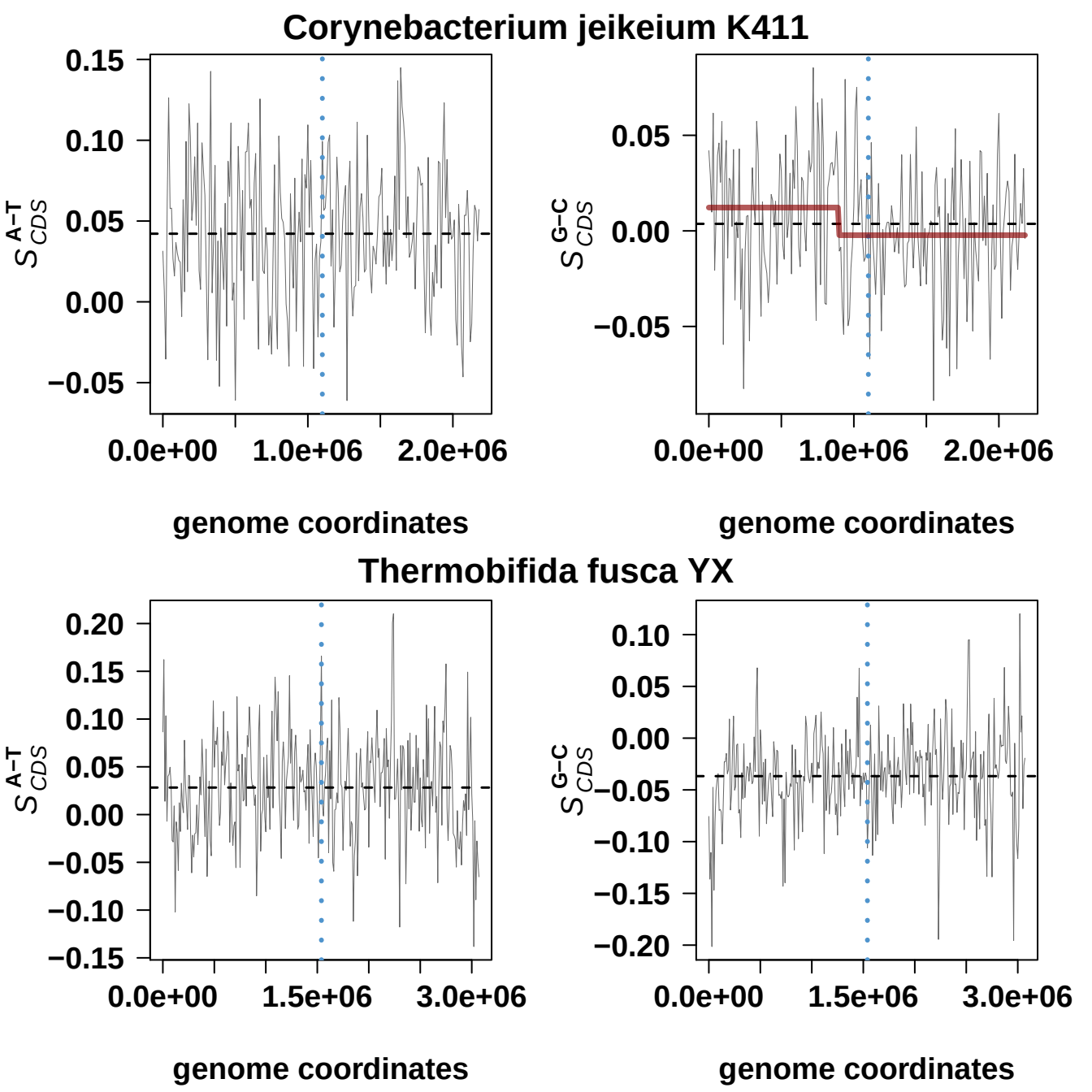

Corynebacterium glutamicum ATCC 13032
S^{A-T}_{CDS}
0.10
0.05
0.00
−0.05
−0.10
−0.15
0.0e+00
1.5e+06
genome coordinates
S^{G-C}_{CDS}
0.15
0.10
0.05
0.00
−0.05
−0.10
−0.15
0.0e+00
1.5e+06
genome coordinates
Streptomyces coelicolor A3(2)
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
−0.05
−0.10
−0.15
0e+00
4e+06
genome coordinates
S^{G-C}_{CDS}
0.05
0.00
−0.05
−0.10
−0.15
0e+00
4e+06
genome coordinates

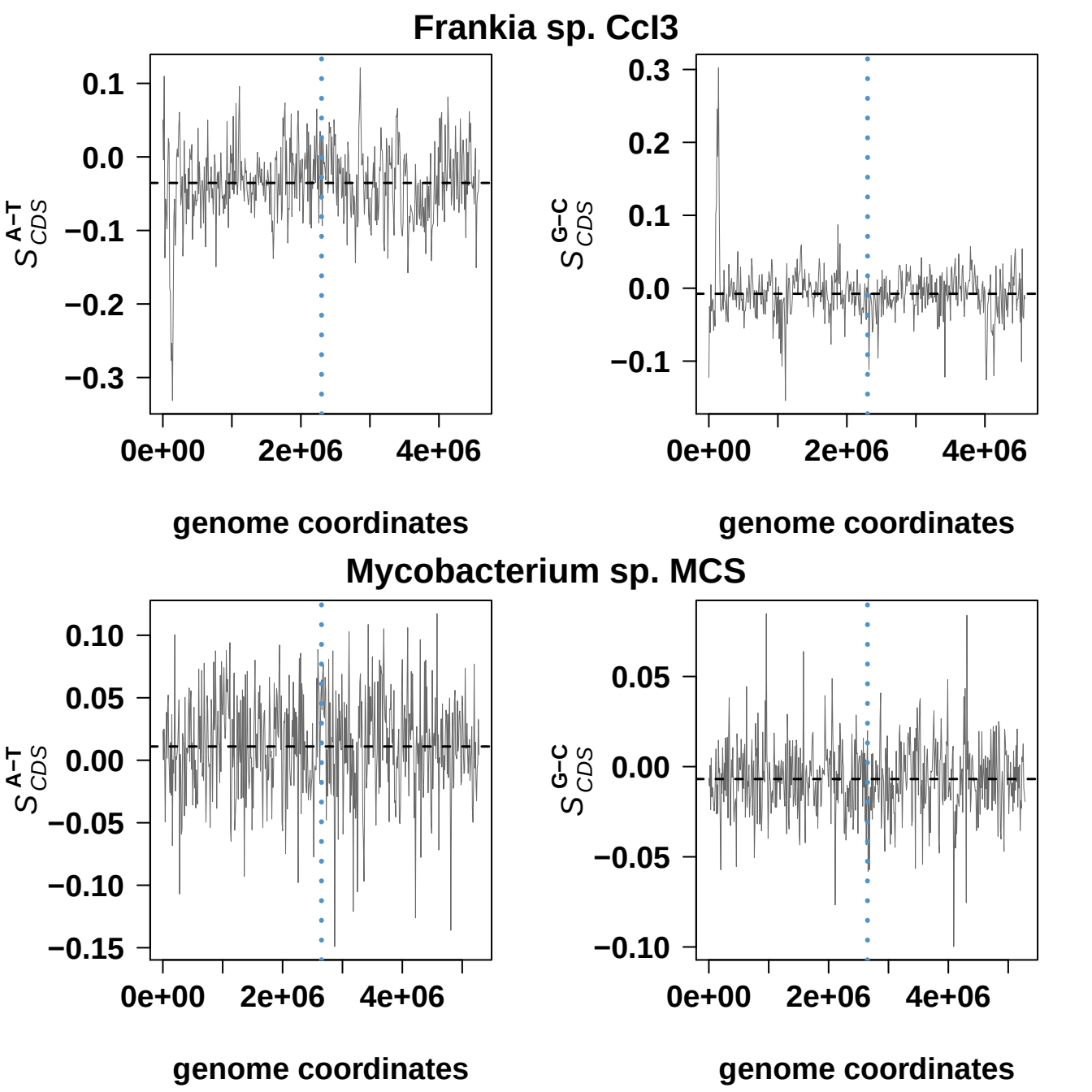

Bifidobacterium longum NCC2705
S^{A-T}_{CDS}
0.3
0.2
0.1
0.0
0.0e+00
1.0e+06
genome coordinates
S^{G-C}_{CDS}
0.10
0.05
0.00
−0.05
−0.10
0.0e+00
1.0e+06
genome coordinates
Corynebacterium efficiens YS−314
S^{A-T}_{CDS}
0.10
0.05
0.00
−0.05
−0.10
−0.15
−0.20
0.0e+00
1.5e+06
genome coordinates
S^{G-C}_{CDS}
0.05
0.00
−0.05
−0.10
0.0e+00
1.5e+06
genome coordinates

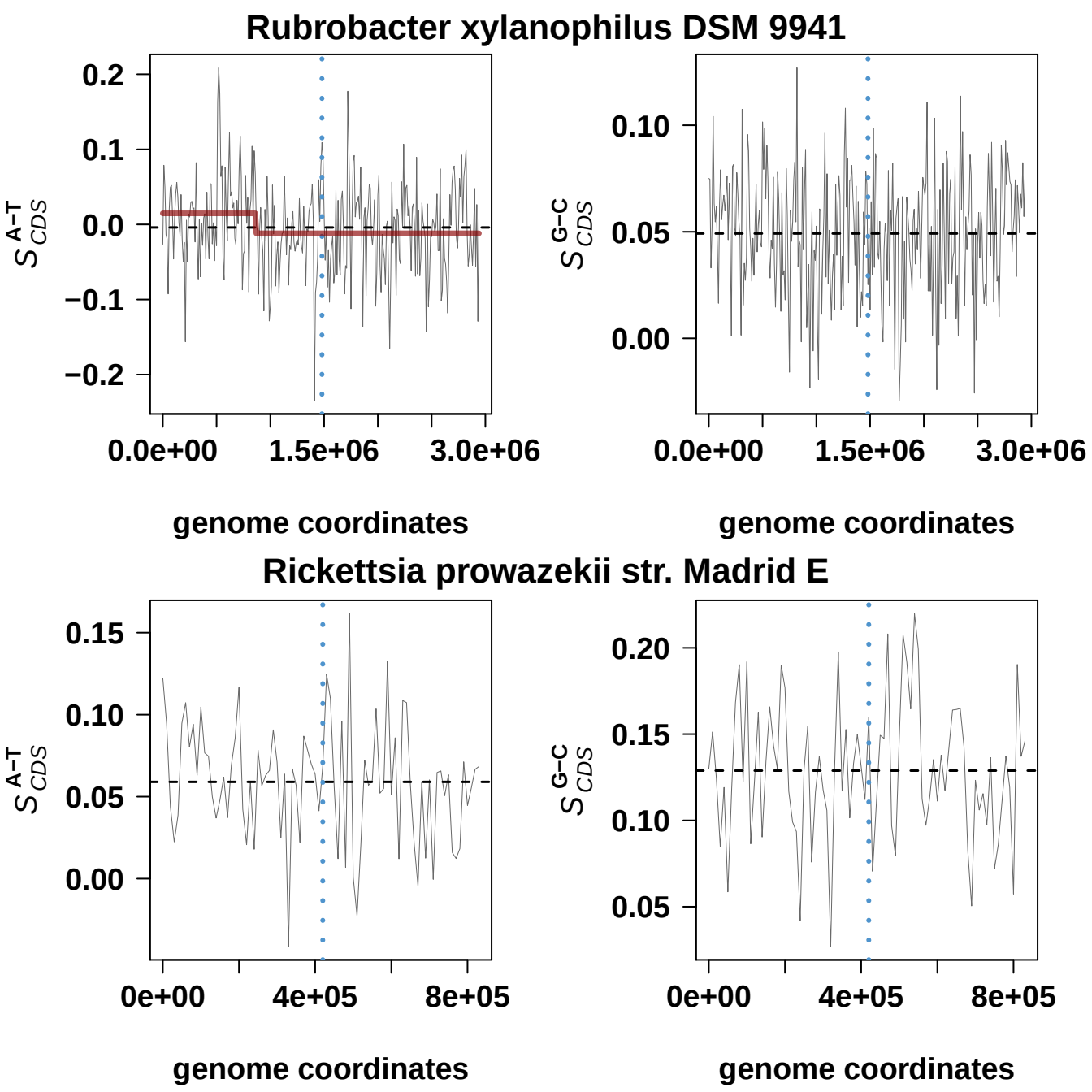

Tropheryma whipplei TW08/27
0.05
0.00
−0.05
−0.10
−0.15
S^{A-T}_{CDS}
0e+00
4e+05
genome coordinates
0.15
0.10
0.05
0.00
−0.05
S^{G-C}_{CDS}
0e+00
4e+05
genome coordinates
Tropheryma whipplei str. Twist
0.05
0.00
−0.05
−0.10
−0.15
−0.20
S^{A-T}_{CDS}
0e+00
4e+05
8e+05
genome coordinates
0.15
0.10
0.05
0.00
−0.05
S^{G-C}_{CDS}
0e+00
4e+05
8e+05
genome coordinates

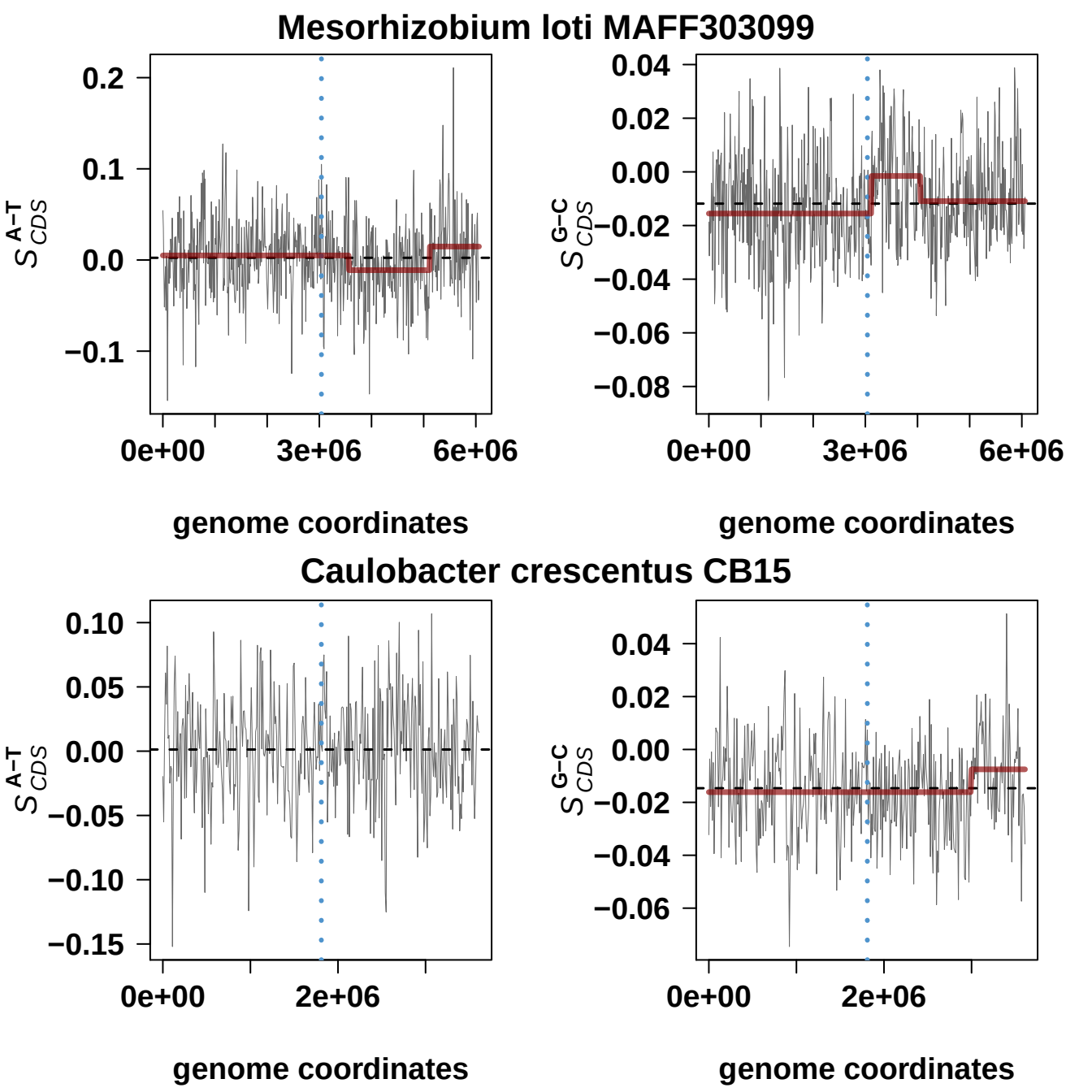

Propionibacterium acnes KPA171202
S^{A-T}_{CDS}
0.10
0.05
0.00
−0.05
−0.10
−0.15
−0.20
0.0e+00
1.0e+06
2.0e+06
genome coordinates
S^{G-C}_{CDS}
0.10
0.05
0.00
−0.05
−0.10
0.0e+00
1.0e+06
2.0e+06
genome coordinates
Leifsonia xyli subsp. xyli str. CTCB07
S^{A-T}_{CDS}
0.10
0.05
0.00
−0.05
−0.10
−0.15
0.0e+00
1.0e+06
genome coordinates
S^{G-C}_{CDS}
0.05
0.00
−0.05
−0.10
0.0e+00
1.0e+06
genome coordinates

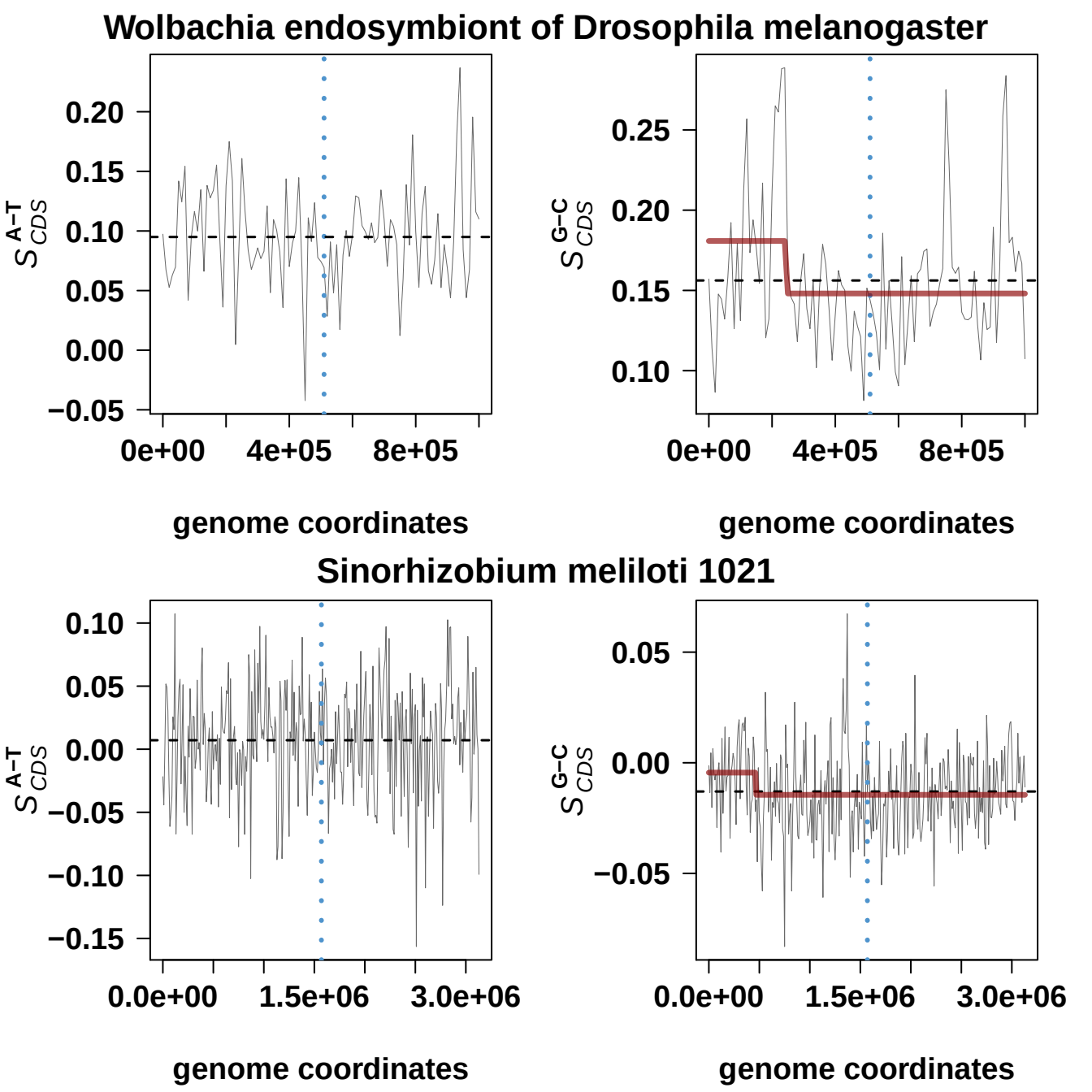

Nocardia farcinica IFM 10152
S^{A-T}_{CDS}
0.2
0.1
0.0
−0.1
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{CDS}
0.05
0.00
−0.05
−0.10
−0.15
0e+00
2e+06
4e+06
genome coordinates
Corynebacterium glutamicum ATCC 13032
S^{A-T}_{CDS}
0.10
0.05
0.00
−0.05
−0.10
0.0e+00
1.5e+06
genome coordinates
S^{G-C}_{CDS}
0.15
0.10
0.05
0.00
−0.05
−0.10
−0.15
0.0e+00
1.5e+06
genome coordinates

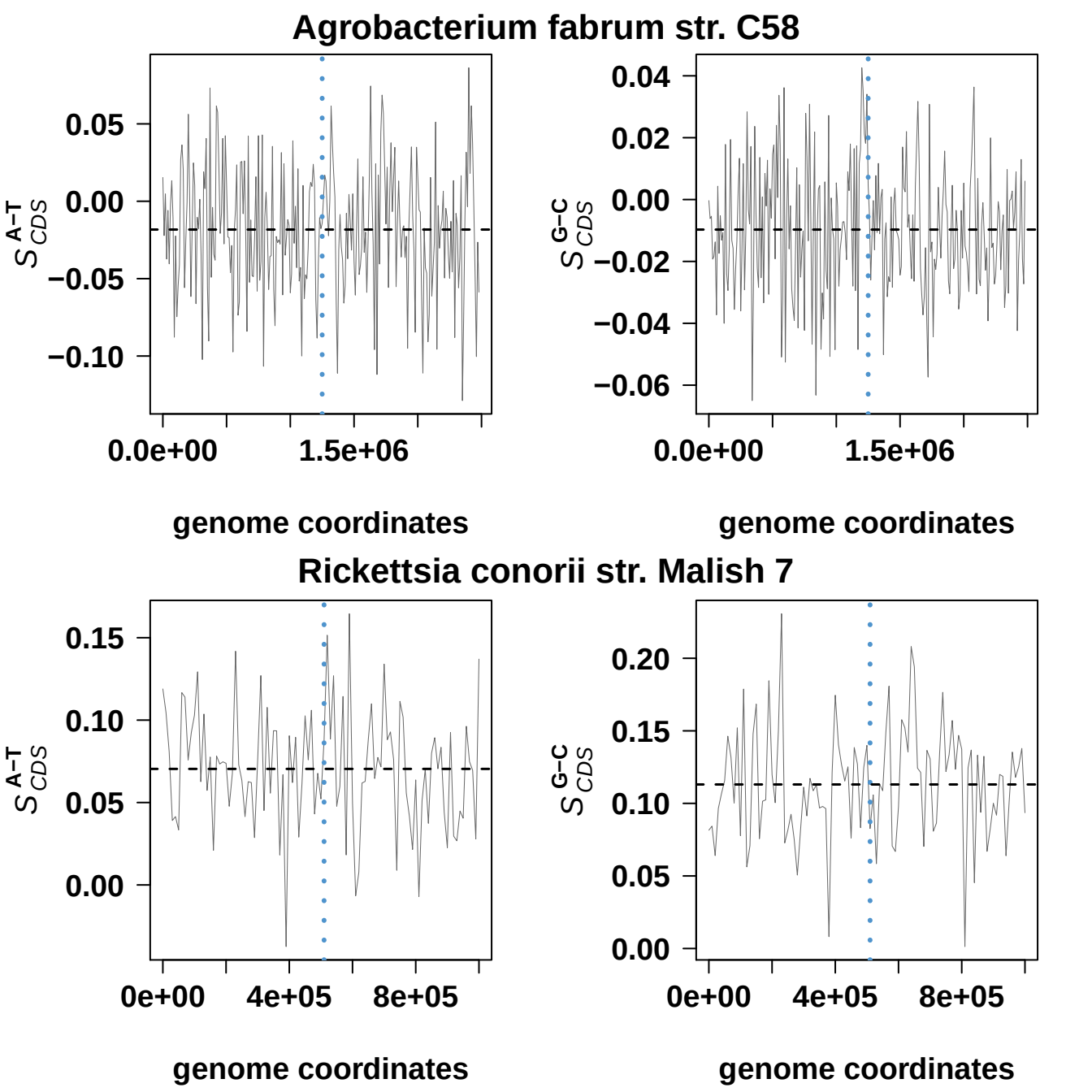

Corynebacterium jeikeium K411
0.15
0.10
0.05
0.00
−0.05
S^{A-T}_{CDS}
0.0e+00
1.0e+06
2.0e+06
genome coordinates
0.05
0.00
−0.05
S^{G-C}_{CDS}
0.0e+00
1.0e+06
2.0e+06
genome coordinates
Thermobifida fusca YX
0.20
0.15
0.10
0.05
0.00
−0.05
−0.10
−0.15
S^{A-T}_{CDS}
0.0e+00
1.5e+06
3.0e+06
genome coordinates
0.10
0.05
0.00
−0.05
−0.10
−0.15
−0.20
S^{G-C}_{CDS}
0.0e+00
1.5e+06
3.0e+06
genome coordinates

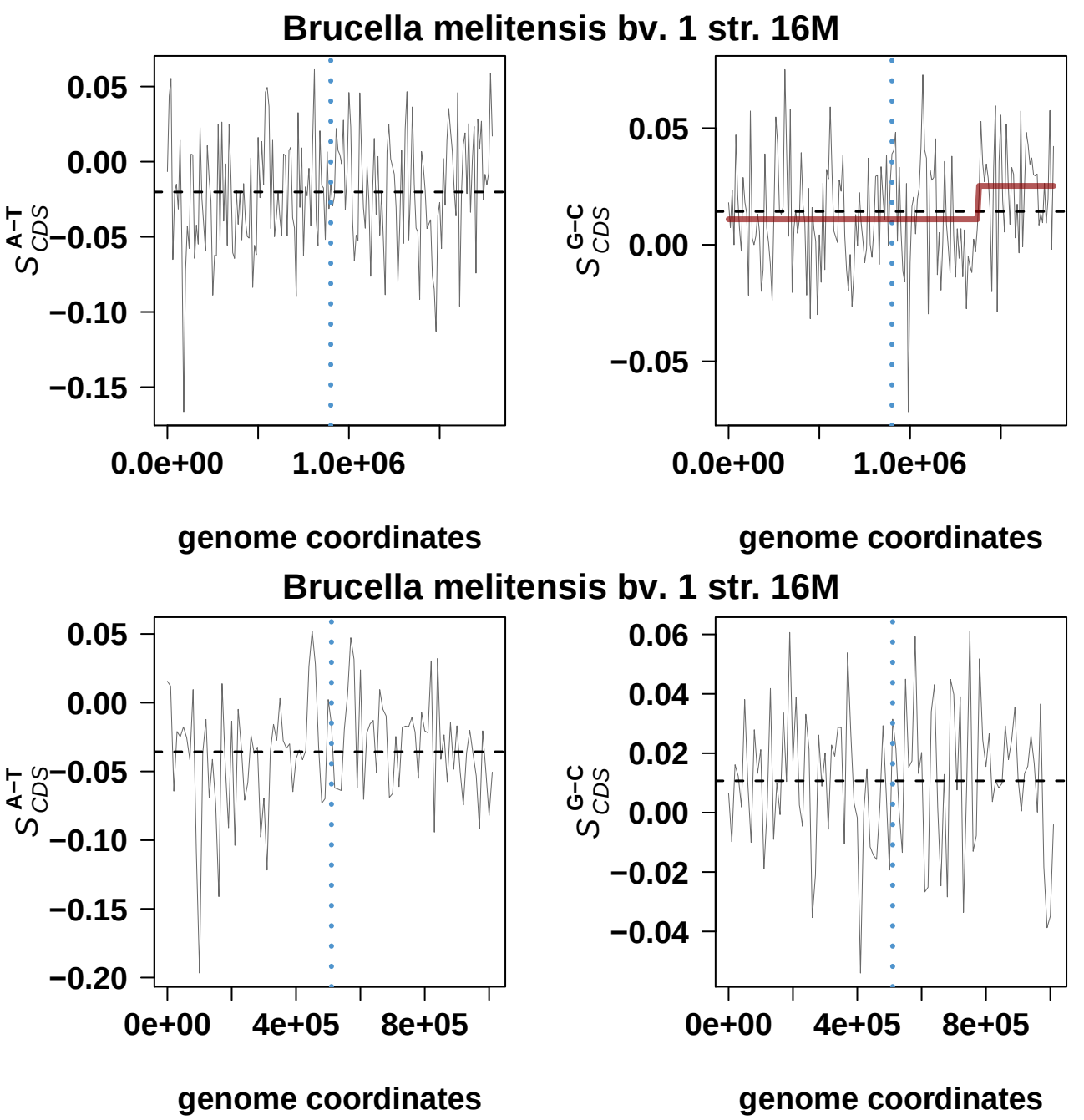

Frankia sp. CcI3
S^{A-T}_{CDS}
0.1
0.0
−0.1
−0.2
−0.3
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{CDS}
0.3
0.2
0.1
0.0
−0.1
0e+00
2e+06
4e+06
genome coordinates
Mycobacterium sp. MCS
S^{A-T}_{CDS}
0.10
0.05
0.00
−0.05
−0.10
−0.15
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{CDS}
0.05
0.00
−0.05
−0.10
0e+00
2e+06
4e+06
genome coordinates

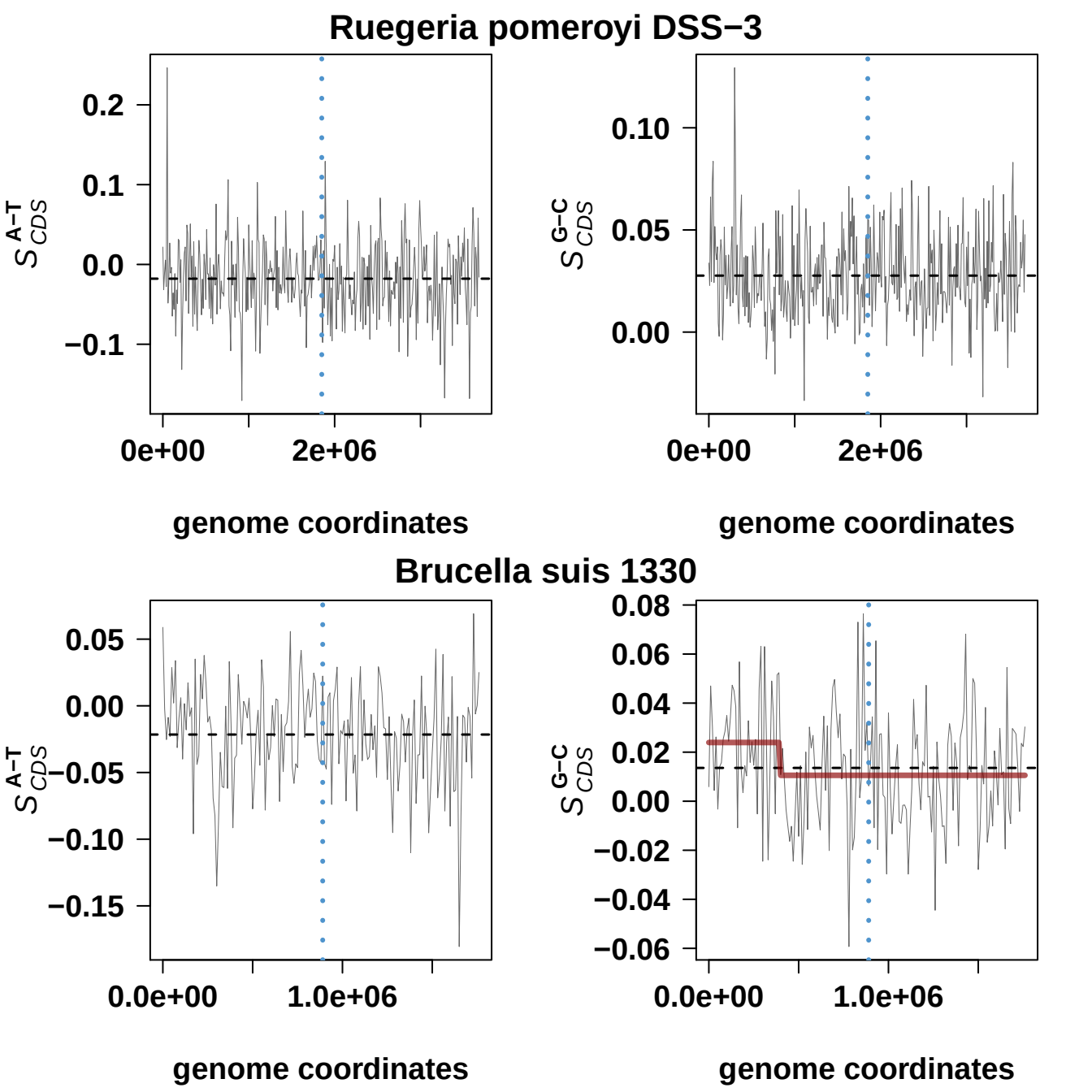

Rubrobacter xylanophilus DSM 9941
S^{A-T}_{CDS}
0.2
0.1
0.0
−0.1
−0.2
0.0e+00
1.5e+06
3.0e+06
genome coordinates
S^{G-C}_{CDS}
0.10
0.05
0.00
0.0e+00
1.5e+06
3.0e+06
genome coordinates
Rickettsia prowazekii str. Madrid E
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
0e+00
4e+05
8e+05
genome coordinates
S^{G-C}_{CDS}
0.20
0.15
0.10
0.05
0e+00
4e+05
8e+05
genome coordinates

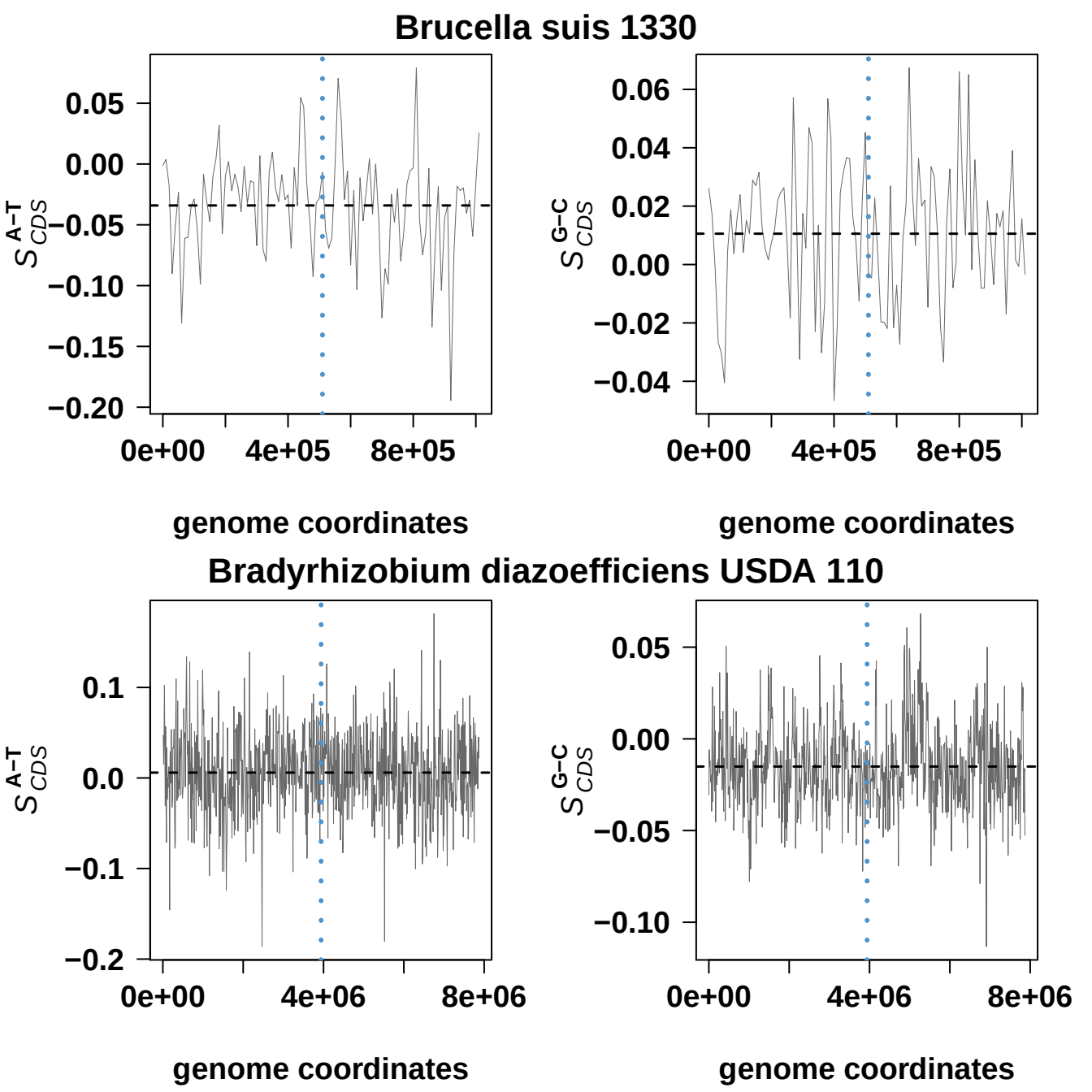

Mesorhizobium loti MAFF303099
S^{A-T}_{CDS}
0.2
0.1
0.0
−0.1
0e+00
3e+06
6e+06
genome coordinates
S^{G-C}_{CDS}
0.04
0.02
0.00
−0.02
−0.04
−0.06
−0.08
0e+00
3e+06
6e+06
genome coordinates
Caulobacter crescentus CB15
S^{A-T}_{CDS}
0.10
0.05
0.00
−0.05
−0.10
−0.15
0e+00
2e+06
genome coordinates
S^{G-C}_{CDS}
0.04
0.02
0.00
−0.02
−0.04
−0.06
0e+00
2e+06
genome coordinates

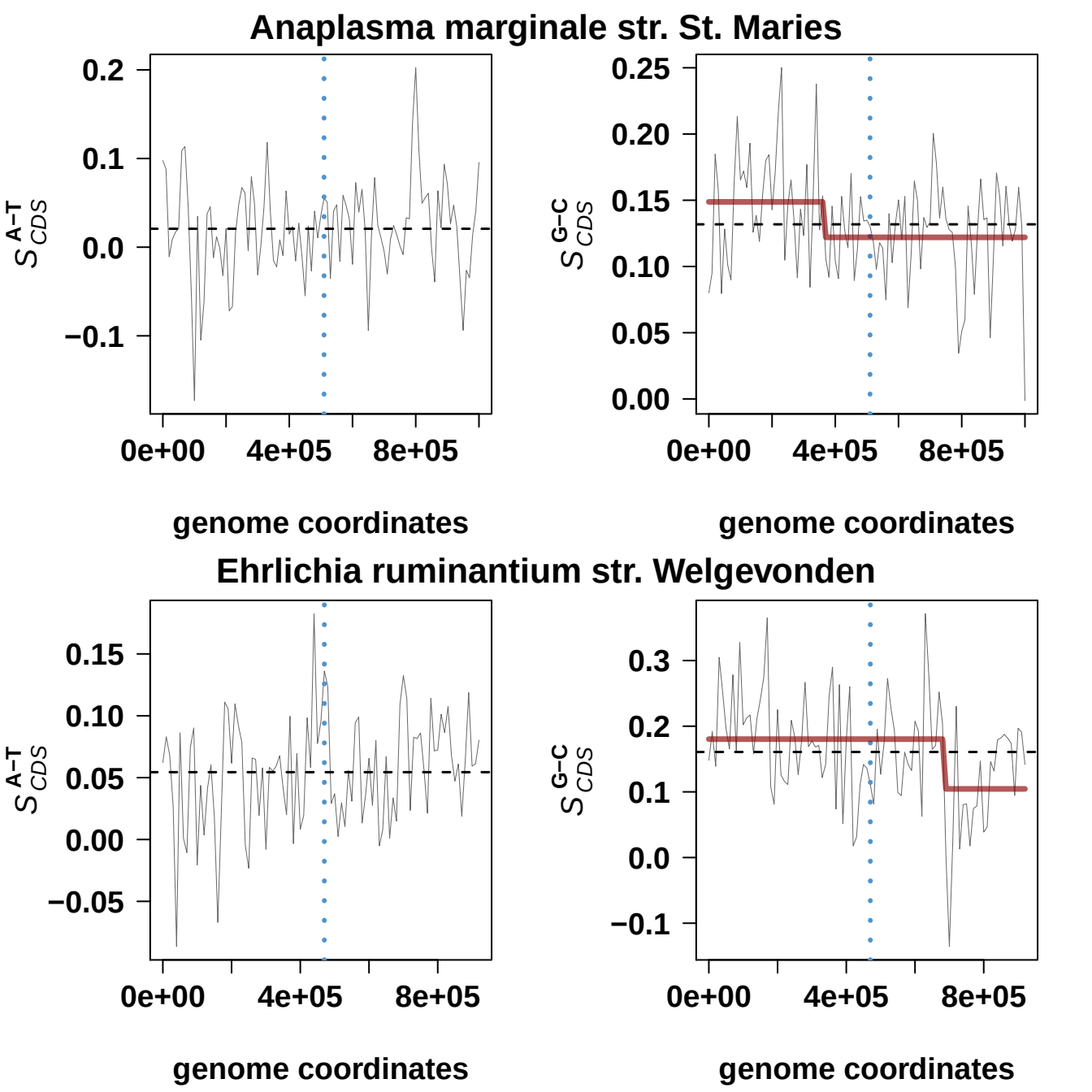

Wolbachia endosymbiont of Drosophila melanogaster
S^{A-T}_{CDS}
0.20
0.15
0.10
0.05
0.00
−0.05
0e+00
4e+05
8e+05
genome coordinates
S^{G-C}_{CDS}
0.25
0.20
0.15
0.10
0e+00
4e+05
8e+05
genome coordinates
Sinorhizobium meliloti 1021
S^{A-T}_{CDS}
0.10
0.05
0.00
−0.05
−0.10
−0.15
0.0e+00
1.5e+06
3.0e+06
genome coordinates
S^{G-C}_{CDS}
0.05
0.00
−0.05
0.0e+00
1.5e+06
3.0e+06
genome coordinates

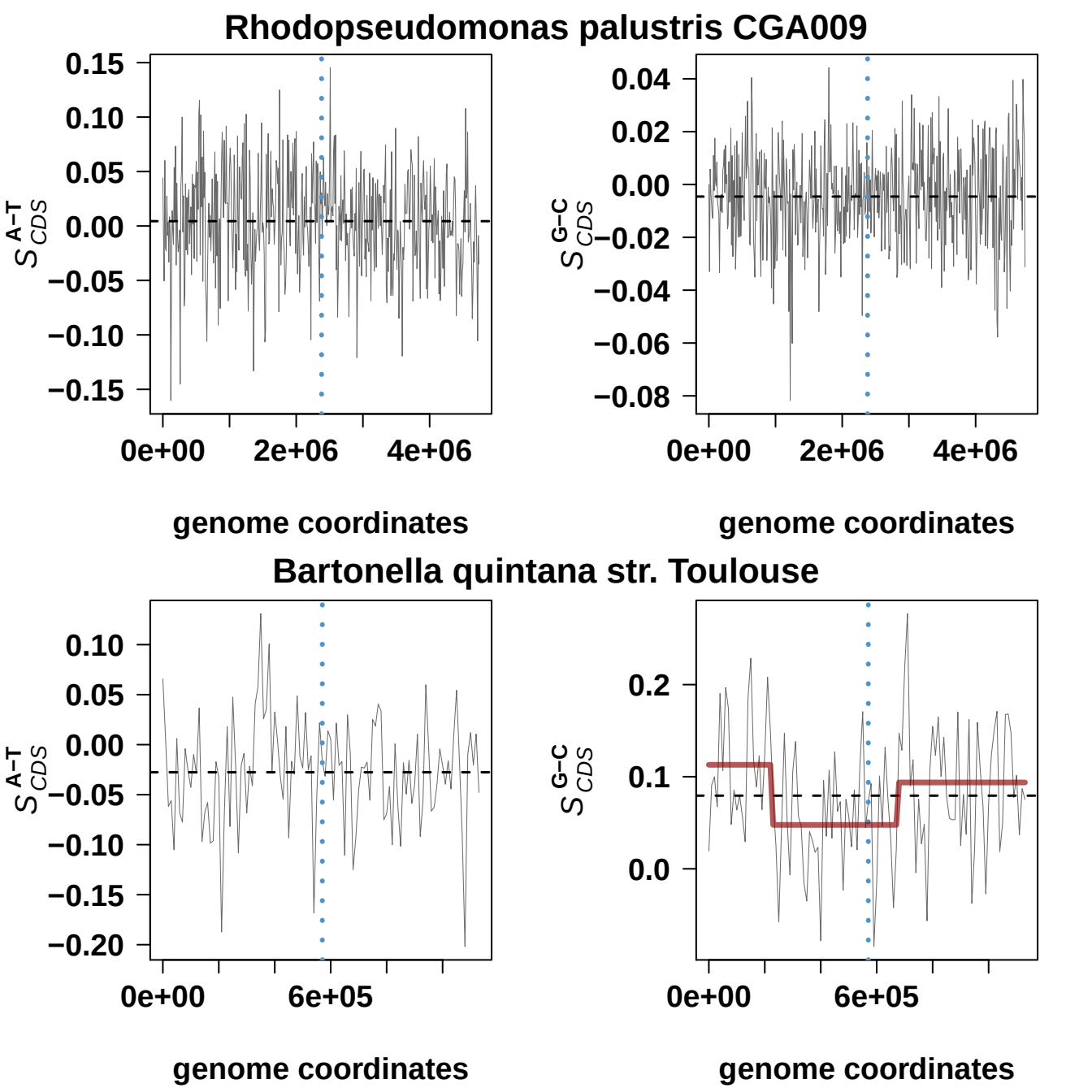

Agrobacterium fabrum str. C58
S^{A-T}_{CDS}
0.05
0.00
−0.05
−0.10
0.0e+00
1.5e+06
genome coordinates
S^{G-C}_{CDS}
0.04
0.02
0.00
−0.02
−0.04
−0.06
0.0e+00
1.5e+06
genome coordinates
Rickettsia conorii str. Malish 7
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
0e+00
4e+05
8e+05
genome coordinates
S^{G-C}_{CDS}
0.20
0.15
0.10
0.05
0.00
0e+00
4e+05
8e+05
genome coordinates

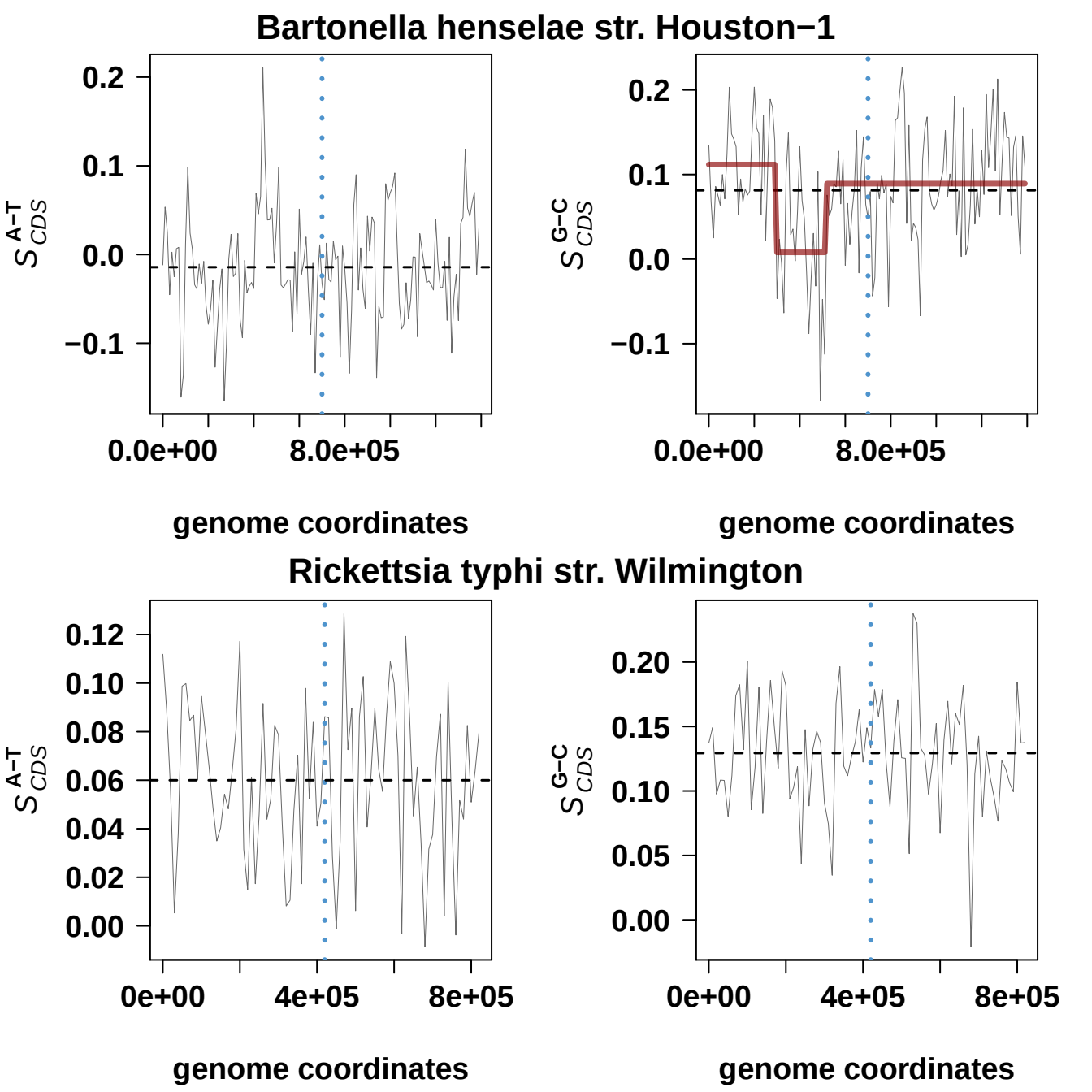

Brucella melitensis bv. 1 str. 16M
0.05
0.00
−0.05
−0.10
−0.15
S^{A-T}_{CDS}
0.0e+00
1.0e+06
genome coordinates
Brucella melitensis bv. 1 str. 16M
0.05
0.00
−0.05
−0.10
−0.15
−0.20
S^{A-T}_{CDS}
0e+00
4e+05
8e+05
genome coordinates
0.05
0.00
−0.05
S^{G-C}_{CDS}
0.0e+00
1.0e+06
genome coordinates
0.06
0.04
0.02
0.00
−0.02
−0.04
S^{G-C}_{CDS}
0e+00
4e+05
8e+05
genome coordinates

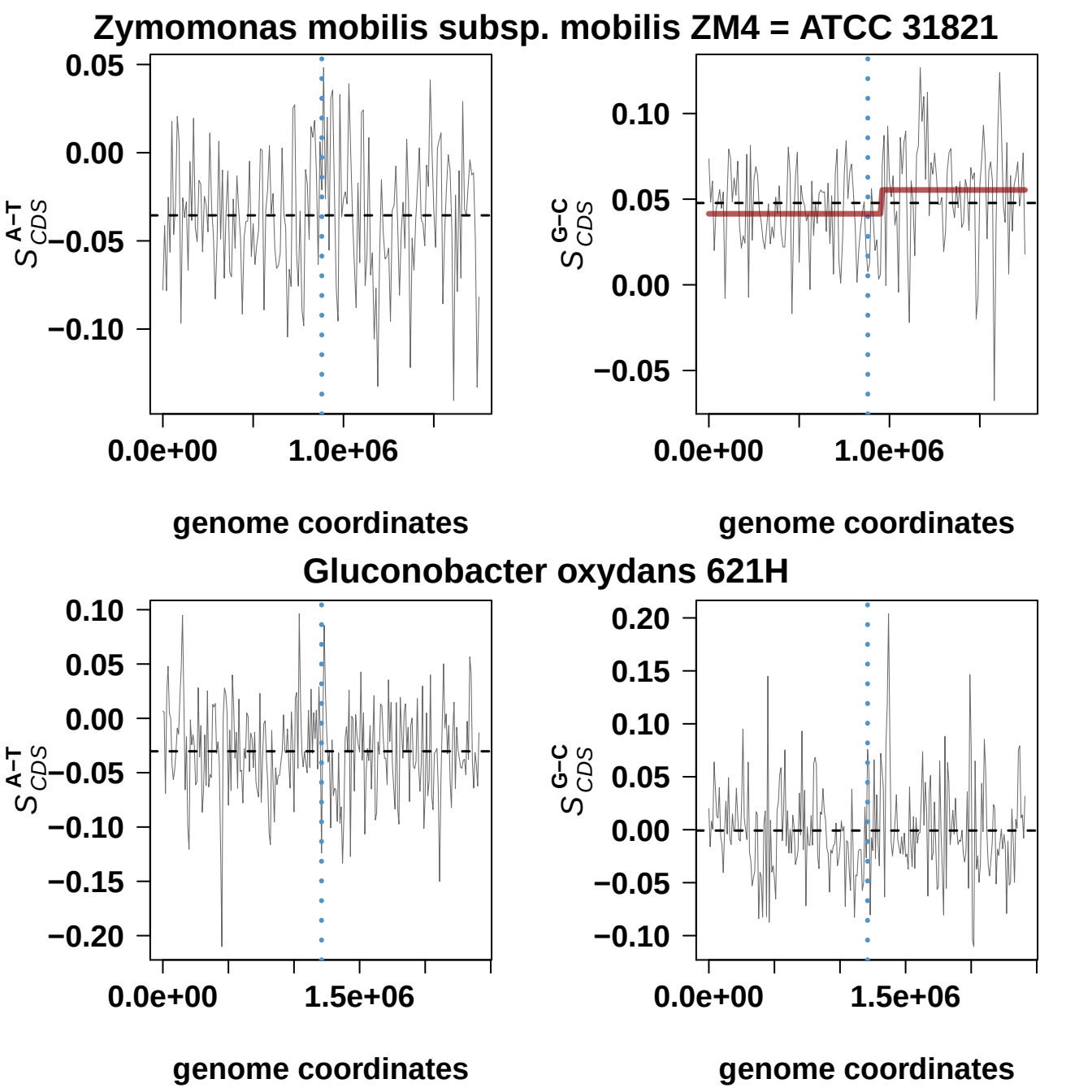

Ruegeria pomeroyi DSS−3
S^{A-T}_{CDS}
0.2
0.1
0.0
−0.1
0e+00
2e+06
genome coordinates
S^{G-C}_{CDS}
0.10
0.05
0.00
0e+00
2e+06
genome coordinates
Brucella suis 1330
S^{A-T}_{CDS}
0.05
0.00
−0.05
−0.10
−0.15
0.0e+00
1.0e+06
genome coordinates
S^{G-C}_{CDS}
0.08
0.06
0.04
0.02
0.00
−0.02
−0.04
−0.06
0.0e+00
1.0e+06
genome coordinates

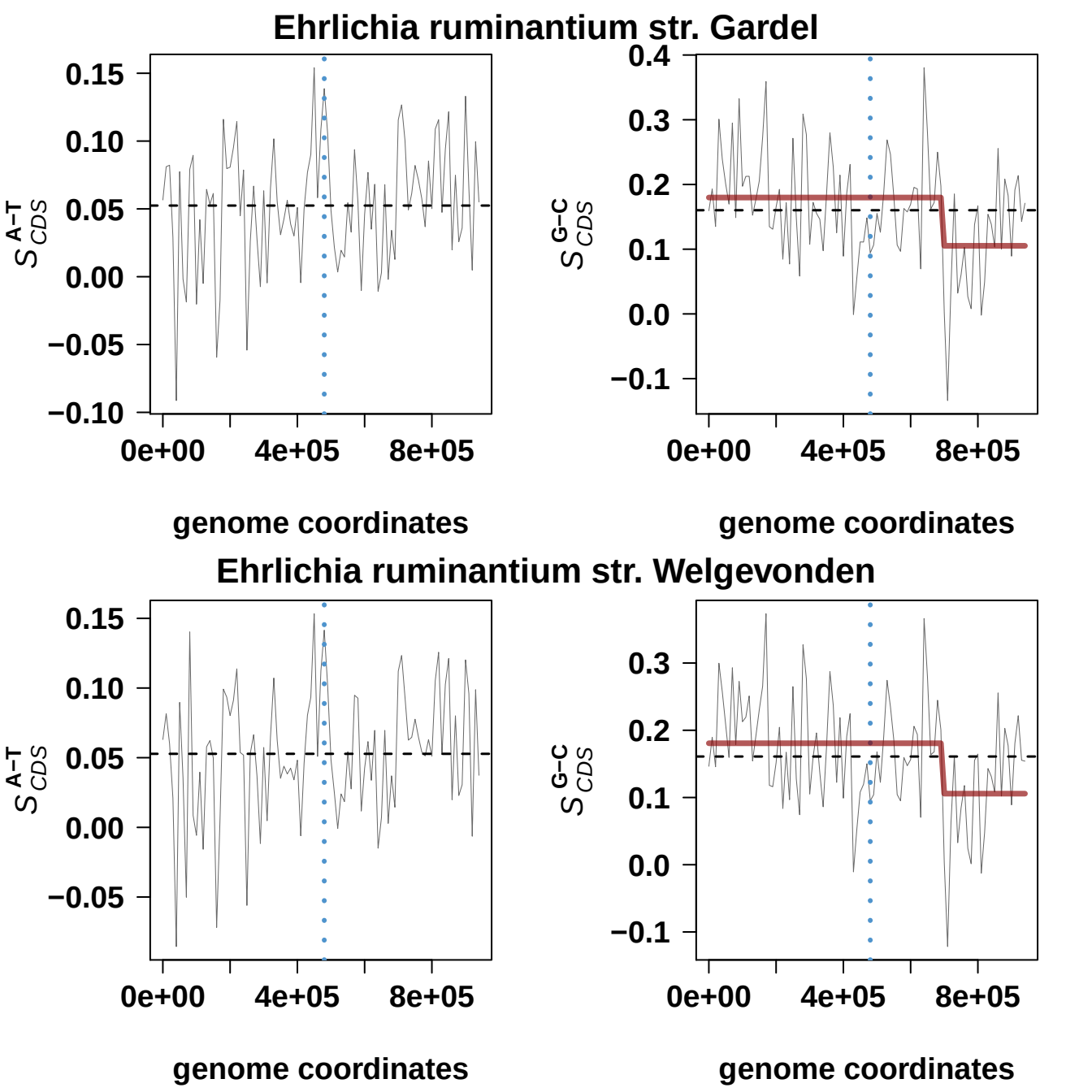

Brucella suis 1330
0.05
0.00
−0.05
−0.10
−0.15
−0.20
S^{A-T}_{CDS}
0e+00
4e+05
8e+05
genome coordinates
0.06
0.04
0.02
0.00
−0.02
−0.04
S^{G-C}_{CDS}
0e+00
4e+05
8e+05
genome coordinates
Bradyrhizobium diazoefficiens USDA 110
0.1
0.0
−0.1
−0.2
S^{A-T}_{CDS}
0e+00
4e+06
8e+06
genome coordinates
0.05
0.00
−0.05
−0.10
S^{G-C}_{CDS}
0e+00
4e+06
8e+06
genome coordinates

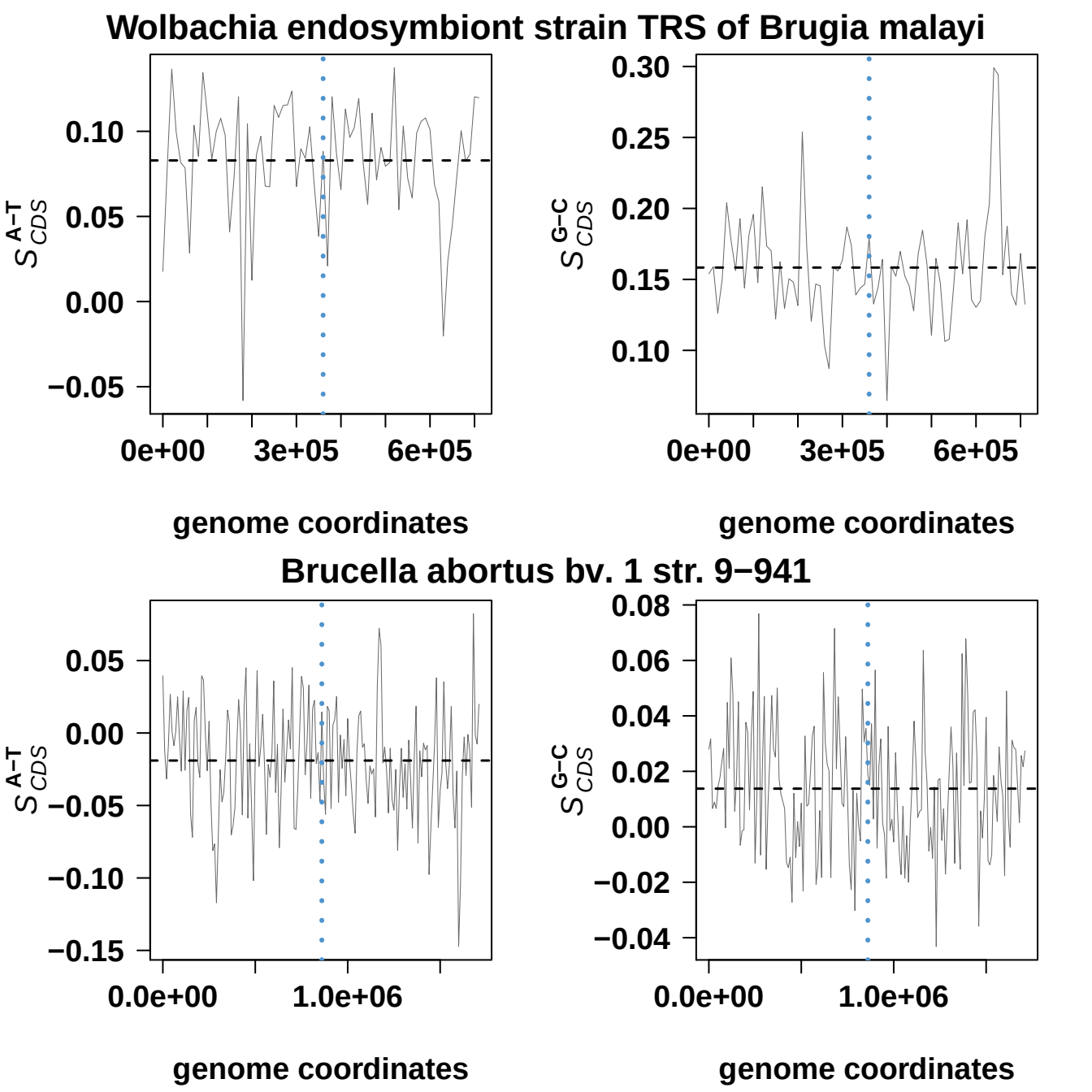

Anaplasma marginale str. St. Maries
S^{A-T}_{CDS}
0.2
0.1
0.0
−0.1
0e+00
4e+05
8e+05
genome coordinates
S^{G-C}_{CDS}
0.25
0.20
0.15
0.10
0.05
0.00
0e+00
4e+05
8e+05
genome coordinates
Ehrlichia ruminantium str. Welgevonden
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
−0.05
0e+00
4e+05
8e+05
genome coordinates
S^{G-C}_{CDS}
0.3
0.2
0.1
0.0
−0.1
0e+00
4e+05
8e+05
genome coordinates

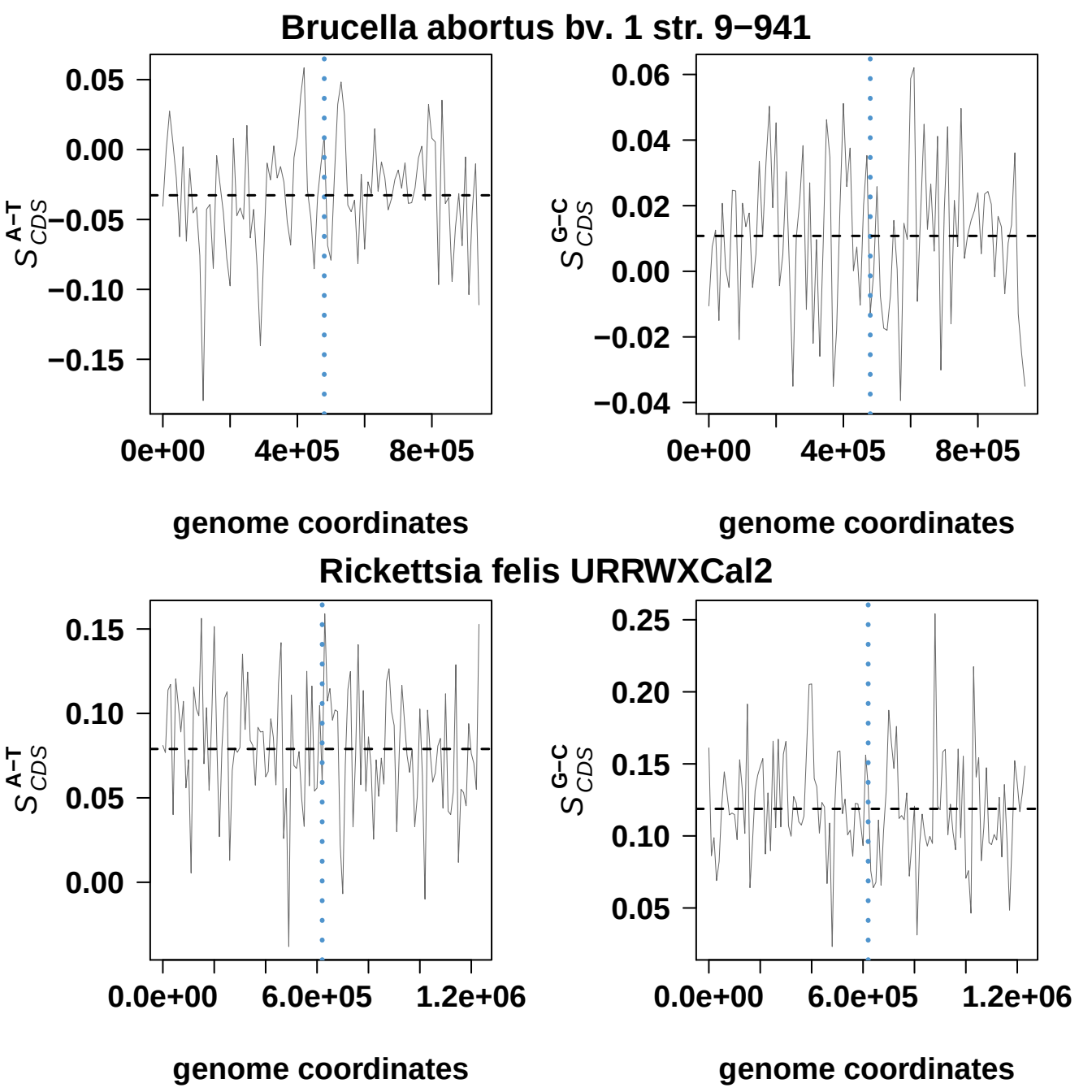

Rhodopseudomonas palustris CGA009
0.15
0.10
0.05
0.00
−0.05
−0.10
−0.15
S^{A-T}_{CDS}
0e+00
2e+06
4e+06
genome coordinates
0.04
0.02
0.00
−0.02
−0.04
−0.06
−0.08
S^{G-C}_{CDS}
0e+00
2e+06
4e+06
genome coordinates
Bartonella quintana str. Toulouse
0.10
0.05
0.00
−0.05
−0.10
−0.15
−0.20
S^{A-T}_{CDS}
0e+00
6e+05
genome coordinates
0.2
0.1
0.0
S^{G-C}_{CDS}
0e+00
6e+05
genome coordinates

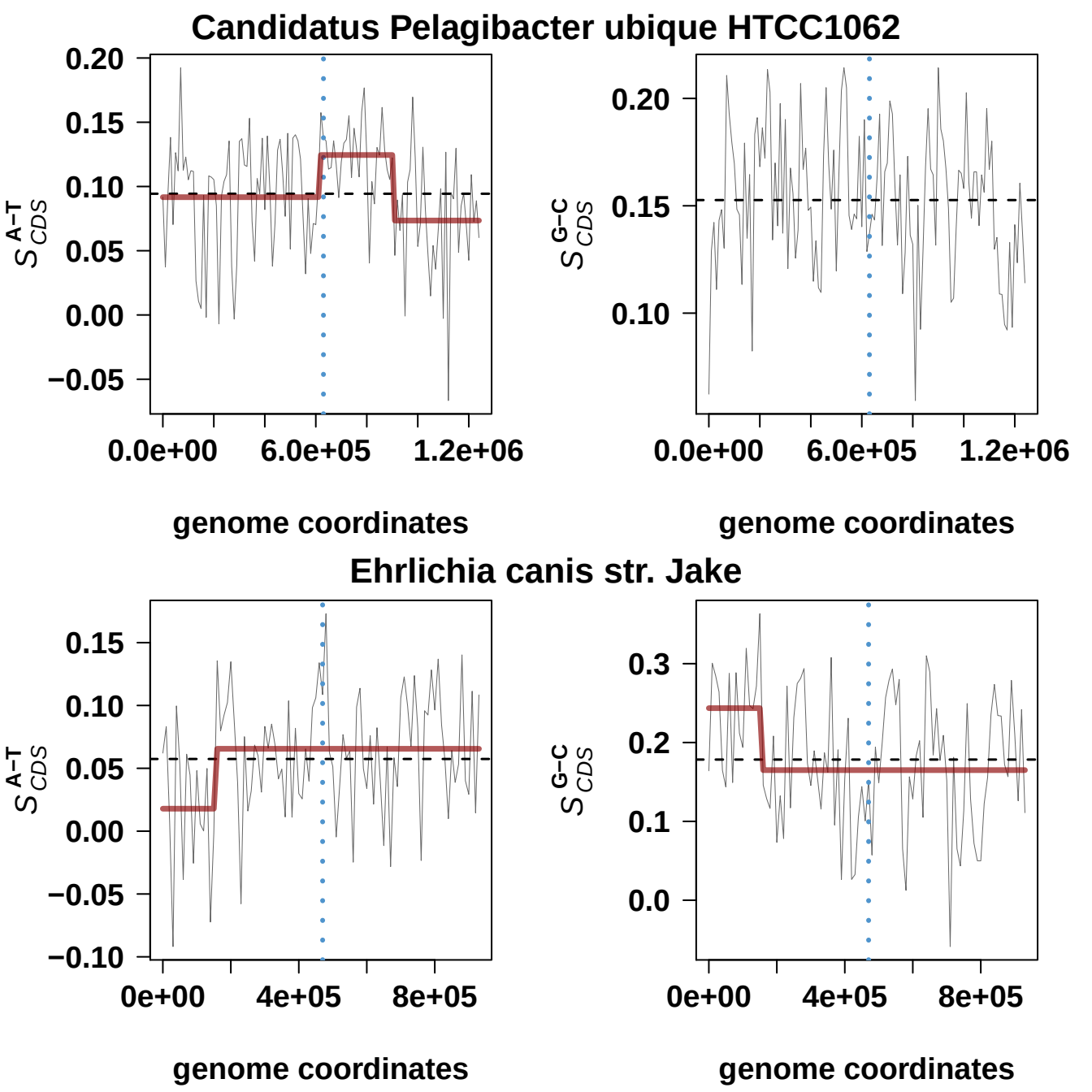

Bartonella henselae str. Houston−1
S^{A-T}_{CDS}
0.2
0.1
0.0
−0.1
0.0e+00
8.0e+05
genome coordinates
S^{G-C}_{CDS}
0.2
0.1
0.0
−0.1
0.0e+00
8.0e+05
genome coordinates
Rickettsia typhi str. Wilmington
S^{A-T}_{CDS}
0.12
0.10
0.08
0.06
0.04
0.02
0.00
0e+00
4e+05
8e+05
genome coordinates
S^{G-C}_{CDS}
0.20
0.15
0.10
0.05
0.00
0e+00
4e+05
8e+05
genome coordinates

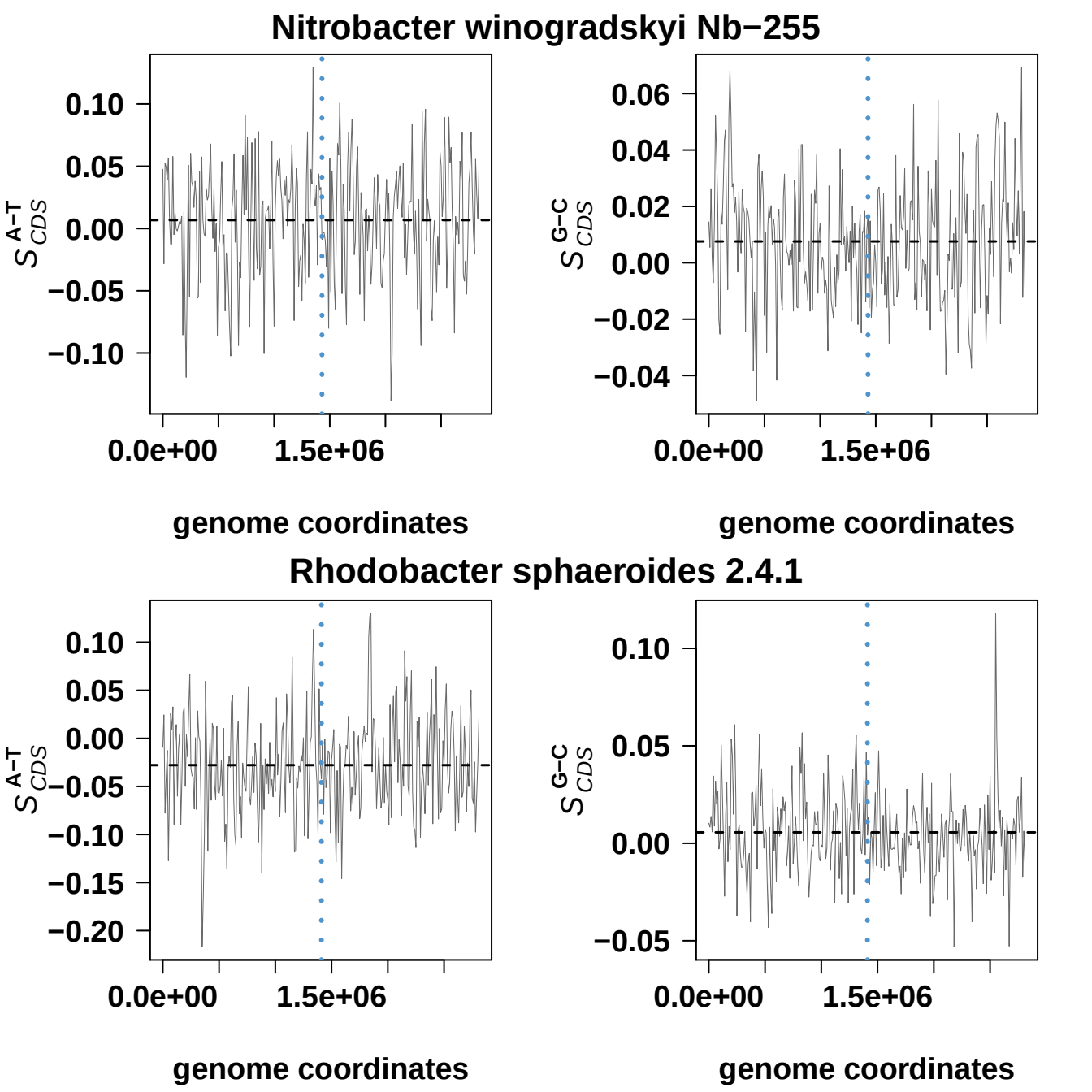

Zymomonas mobilis subsp. mobilis ZM4 = ATCC 31821
0.05
0.00
−0.05
−0.10
S^{A-T}_{CDS}
0.0e+00
1.0e+06
genome coordinates
0.10
0.05
0.00
−0.05
S^{G-C}_{CDS}
0.0e+00
1.0e+06
genome coordinates
Gluconobacter oxydans 621H
0.10
0.05
0.00
−0.05
−0.10
−0.15
−0.20
S^{A-T}_{CDS}
0.0e+00
1.5e+06
genome coordinates
0.20
0.15
0.10
0.05
0.00
−0.05
−0.10
S^{G-C}_{CDS}
0.0e+00
1.5e+06
genome coordinates

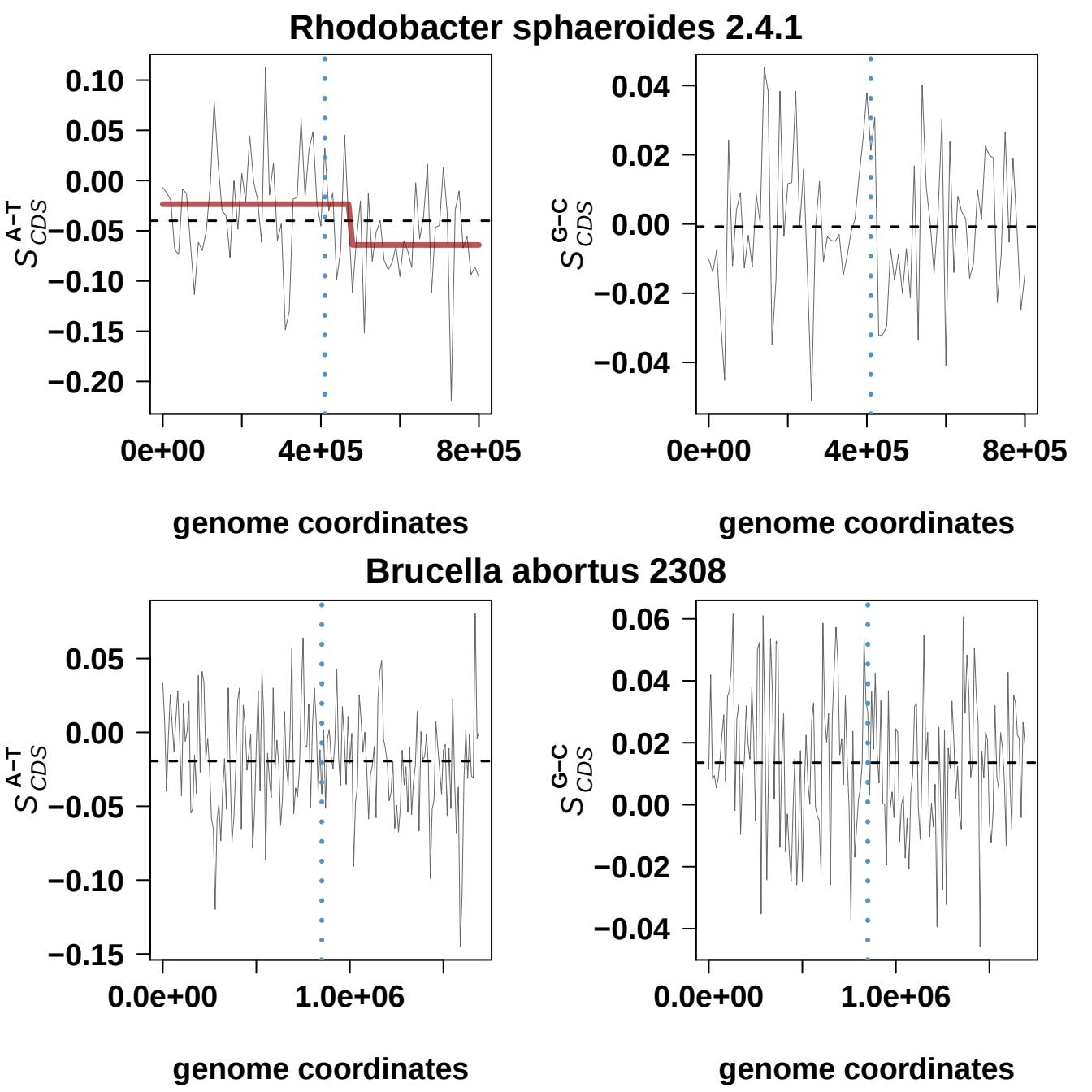

Ehrlichia ruminantium str. Gardel
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
−0.05
−0.10
0e+00
4e+05
8e+05
genome coordinates
S^{G-C}_{CDS}
0.4
0.3
0.2
0.1
0.0
−0.1
0e+00
4e+05
8e+05
genome coordinates
Ehrlichia ruminantium str. Welgevonden
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
−0.05
0e+00
4e+05
8e+05
genome coordinates
S^{G-C}_{CDS}
0.3
0.2
0.1
0.0
−0.1
0e+00
4e+05
8e+05
genome coordinates

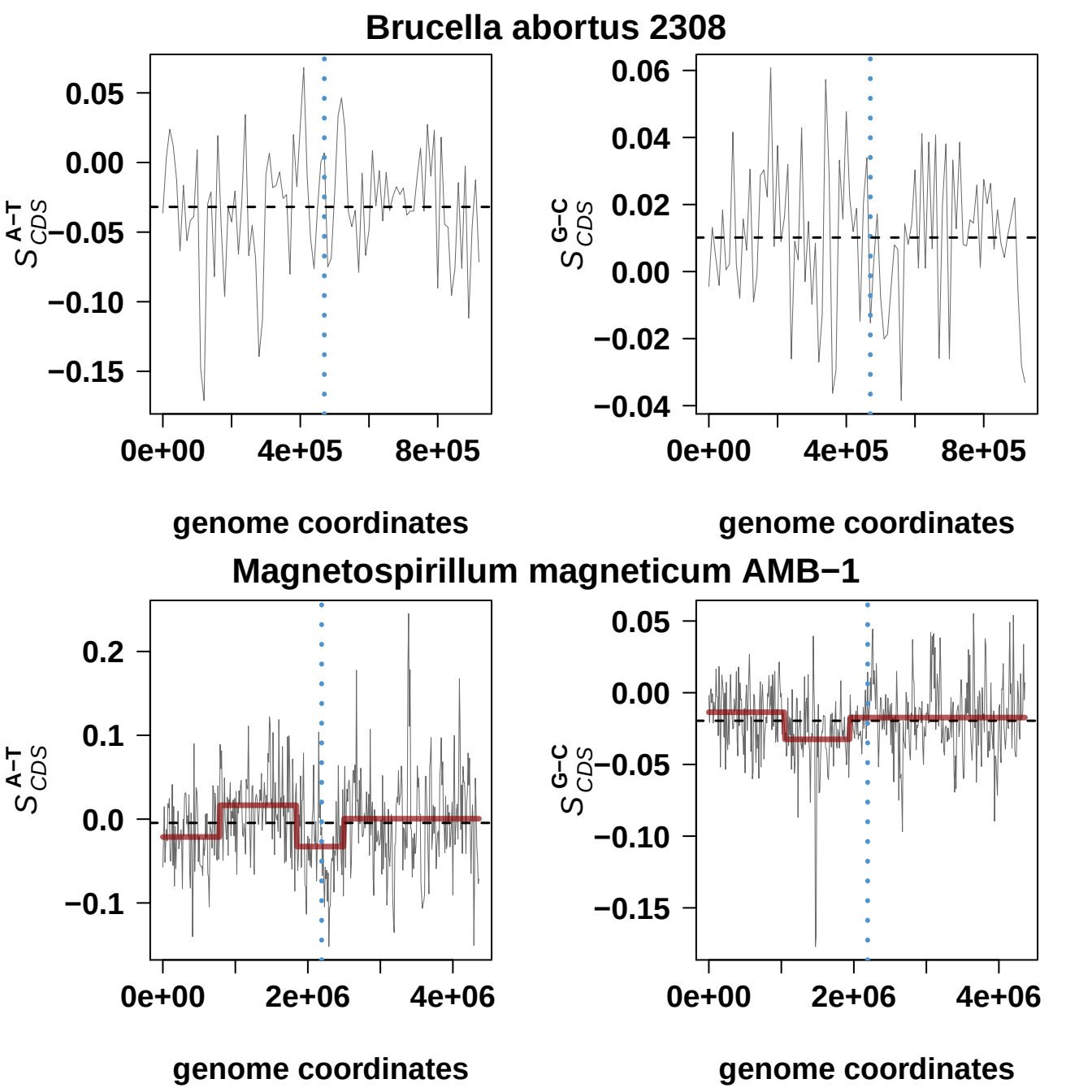

Wolbachia endosymbiont strain TRS of Brugia malayi
S^{A-T}_{CDS}
0.10
0.05
0.00
−0.05
0e+00
3e+05
6e+05
genome coordinates
S^{G-C}_{CDS}
0.30
0.25
0.20
0.15
0.10
0e+00
3e+05
6e+05
genome coordinates
Brucella abortus bv. 1 str. 9−941
S^{A-T}_{CDS}
0.05
0.00
−0.05
−0.10
−0.15
0.0e+00
1.0e+06
genome coordinates
S^{G-C}_{CDS}
0.08
0.06
0.04
0.02
0.00
−0.02
−0.04
0.0e+00
1.0e+06
genome coordinates

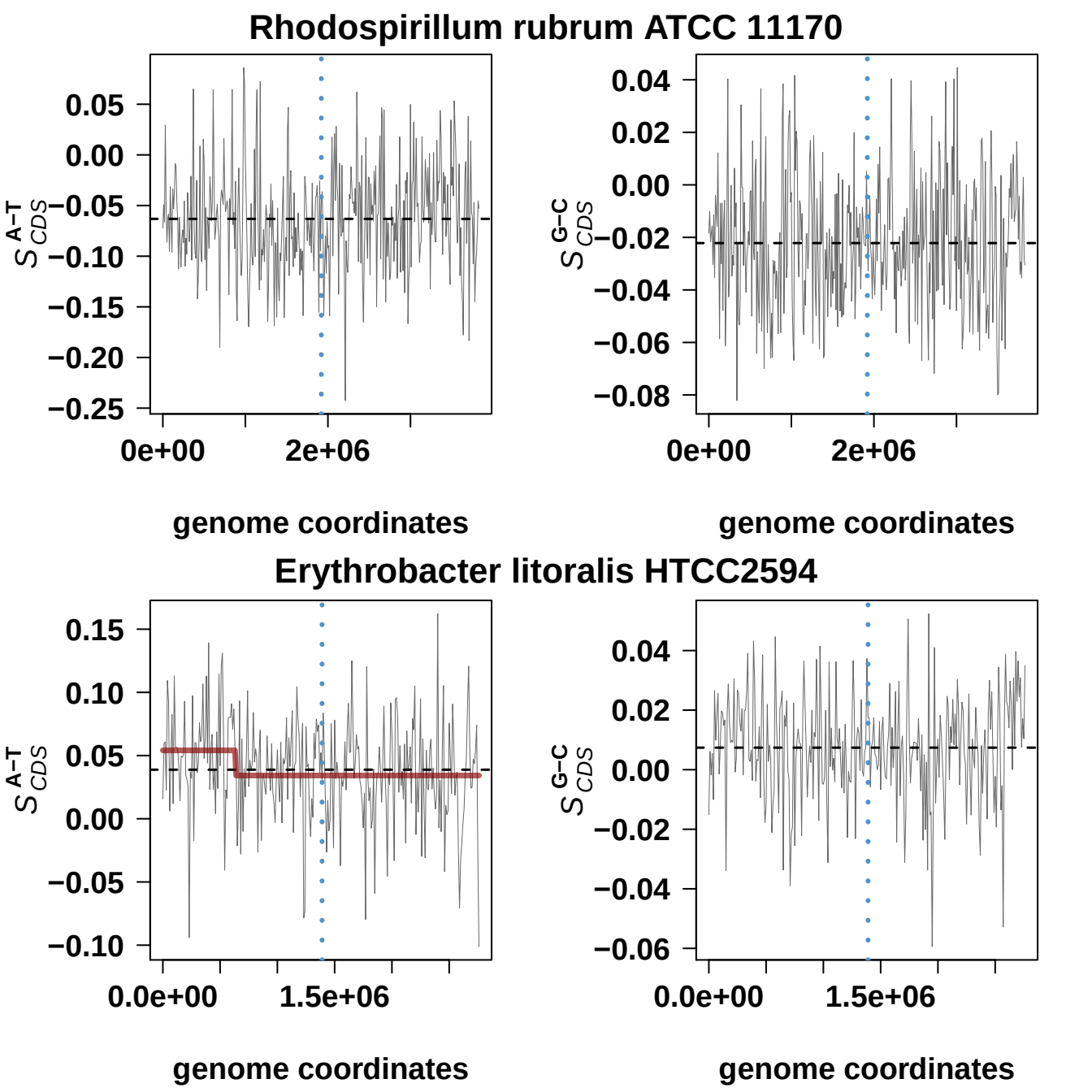

Brucella abortus bv. 1 str. 9−941
0.05
0.00
−0.05
−0.10
−0.15
S^{A-T}_{CDS}
0e+00
4e+05
8e+05
genome coordinates
0.06
0.04
0.02
0.00
−0.02
−0.04
S^{G-C}_{CDS}
0e+00
4e+05
8e+05
genome coordinates
Rickettsia felis URRWXCal2
0.15
0.10
0.05
0.00
S^{A-T}_{CDS}
0.0e+00
6.0e+05
1.2e+06
genome coordinates
0.25
0.20
0.15
0.10
0.05
S^{G-C}_{CDS}
0.0e+00
6.0e+05
1.2e+06
genome coordinates

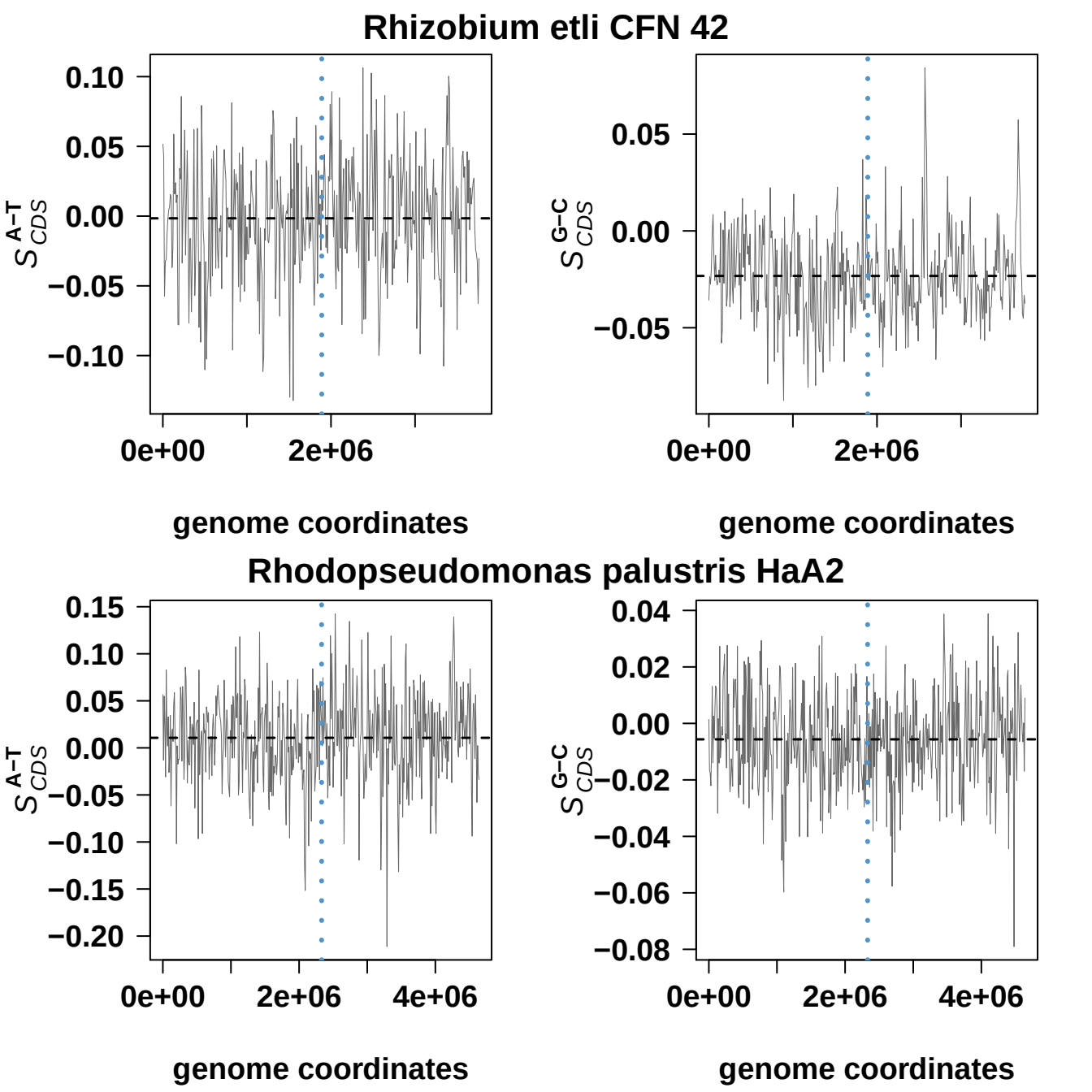

Candidatus Pelagibacter ubique HTCC1062
S^{A-T}_{CDS}
0.20
0.15
0.10
0.05
0.00
−0.05
0.0e+00
6.0e+05
1.2e+06
genome coordinates
S^{G-C}_{CDS}
0.20
0.15
0.10
0.0e+00
6.0e+05
1.2e+06
genome coordinates
Ehrlichia canis str. Jake
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
−0.05
−0.10
0e+00
4e+05
8e+05
genome coordinates
S^{G-C}_{CDS}
0.3
0.2
0.1
0.0
0e+00
4e+05
8e+05
genome coordinates

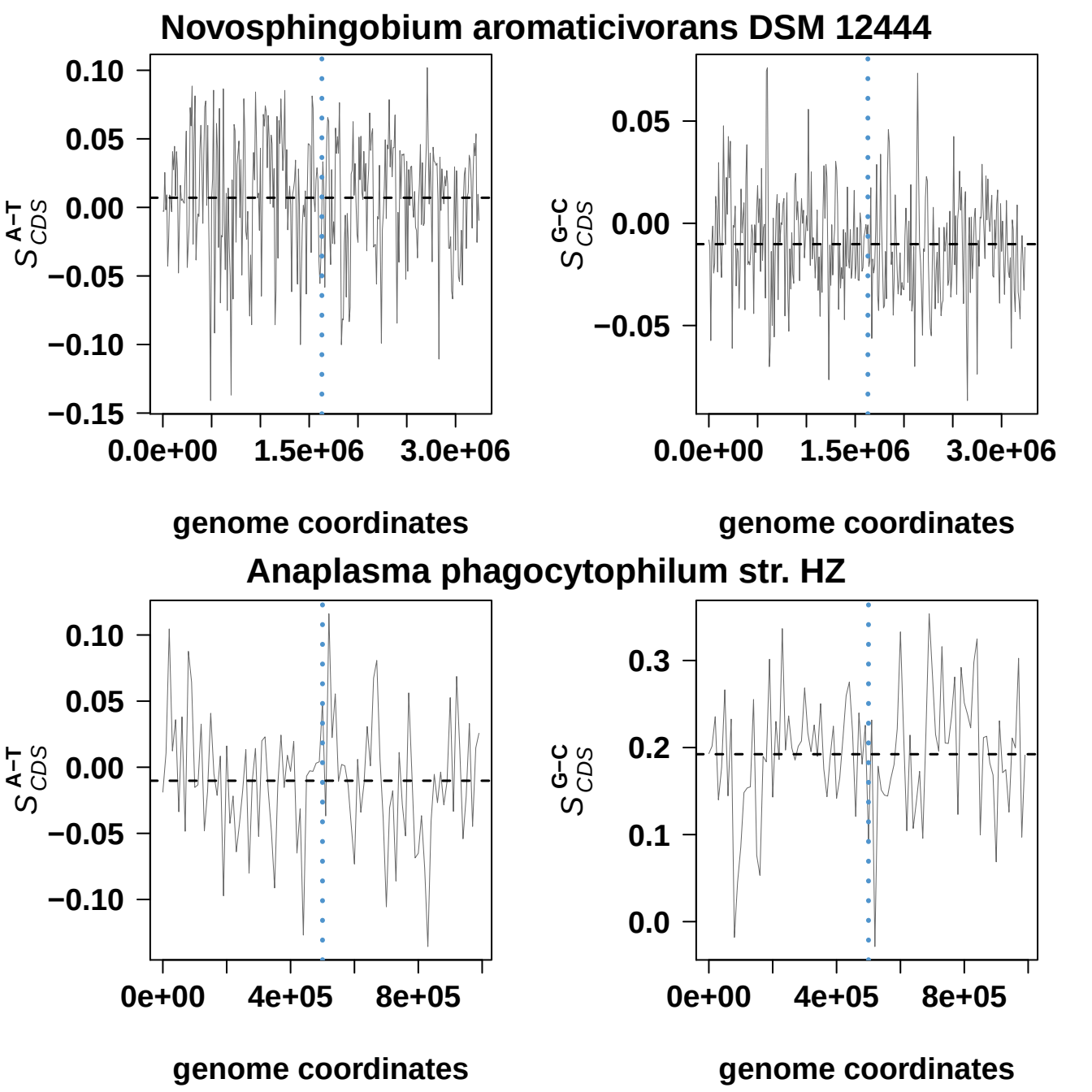

Nitrobacter winogradskyi Nb−255
S^{A-T}_{CDS}
0.10
0.05
0.00
−0.05
−0.10
0.0e+00
1.5e+06
genome coordinates
S^{G-C}_{CDS}
0.06
0.04
0.02
0.00
−0.02
−0.04
0.0e+00
1.5e+06
genome coordinates
Rhodobacter sphaeroides 2.4.1
S^{A-T}_{CDS}
0.10
0.05
0.00
−0.05
−0.10
−0.15
−0.20
0.0e+00
1.5e+06
genome coordinates
S^{G-C}_{CDS}
0.10
0.05
0.00
−0.05
0.0e+00
1.5e+06
genome coordinates

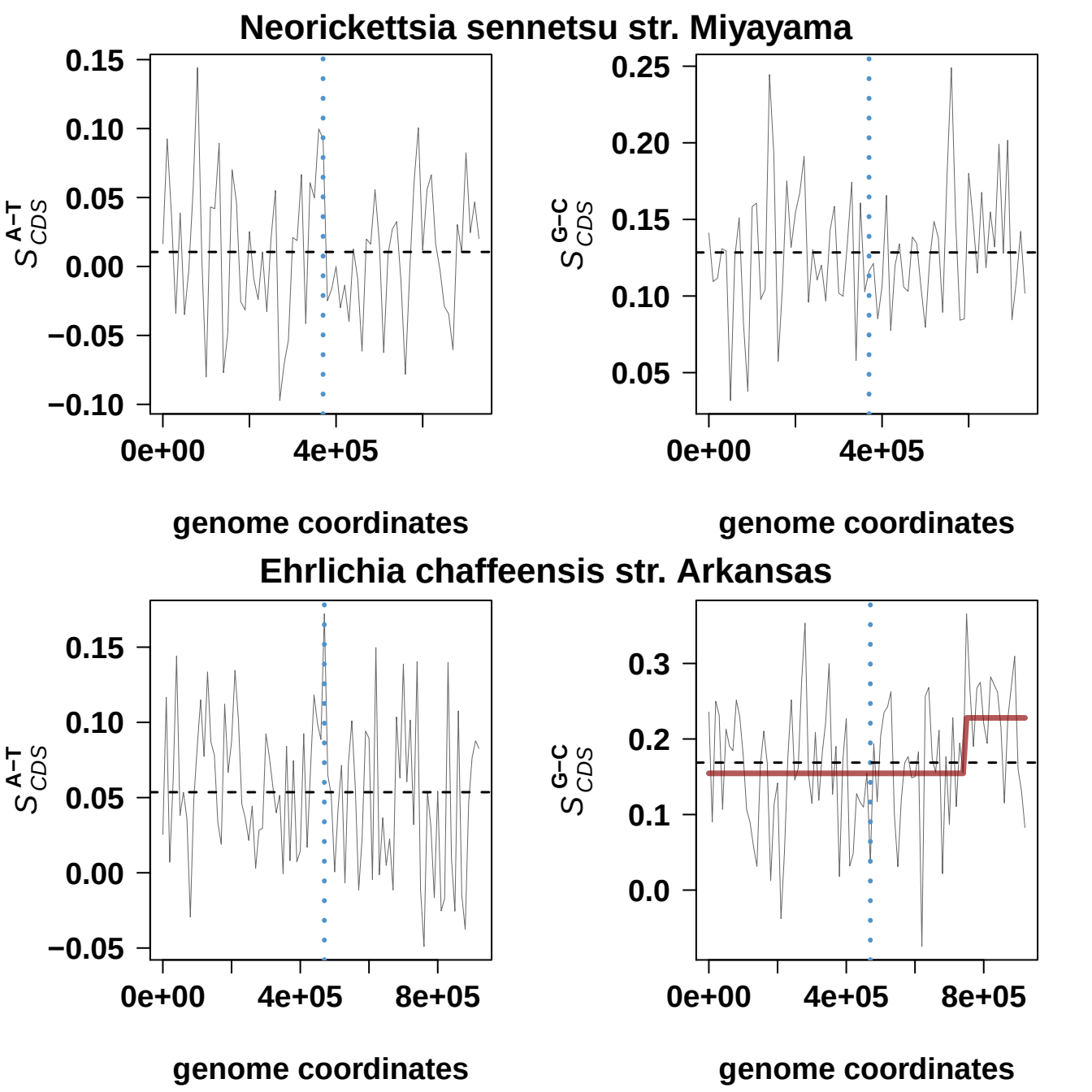

Rhodobacter sphaeroides 2.4.1
S^{A-T}_{CDS}
0.10
0.05
0.00
−0.05
−0.10
−0.15
−0.20
0e+00
4e+05
8e+05
genome coordinates
S^{G-C}_{CDS}
0.04
0.02
0.00
−0.02
−0.04
0e+00
4e+05
8e+05
genome coordinates
Brucella abortus 2308
S^{A-T}_{CDS}
0.05
0.00
−0.05
−0.10
−0.15
0.0e+00
1.0e+06
genome coordinates
S^{G-C}_{CDS}
0.06
0.04
0.02
0.00
−0.02
−0.04
0.0e+00
1.0e+06
genome coordinates

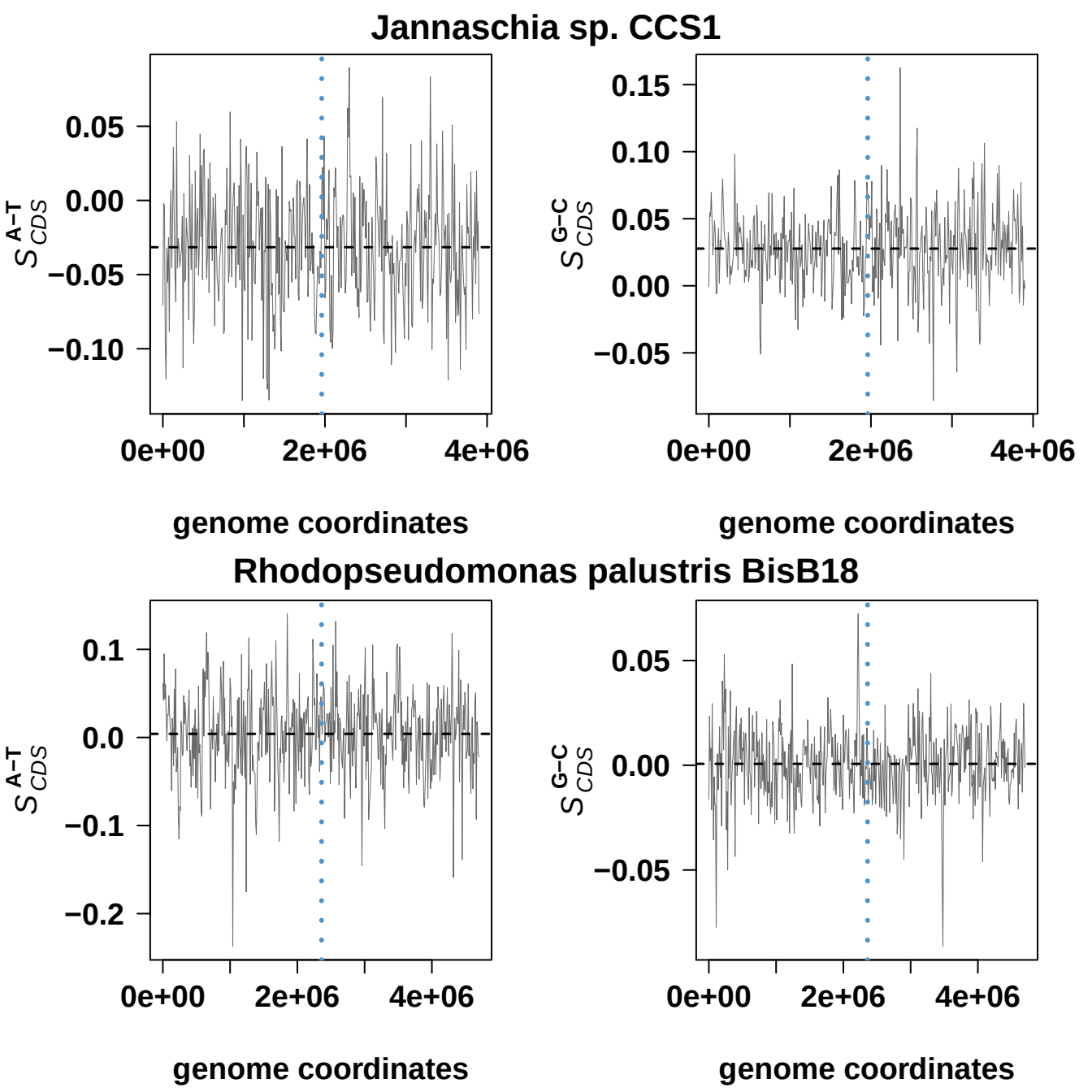

Brucella abortus 2308
S^{A-T}_{CDS}
0.05
0.00
−0.05
−0.10
−0.15
0e+00
4e+05
8e+05
genome coordinates
S^{G-C}_{CDS}
0.06
0.04
0.02
0.00
−0.02
−0.04
0e+00
4e+05
8e+05
genome coordinates
Magnetospirillum magneticum AMB−1
S^{A-T}_{CDS}
0.2
0.1
0.0
−0.1
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{CDS}
0.05
0.00
−0.05
−0.10
−0.15
0e+00
2e+06
4e+06
genome coordinates

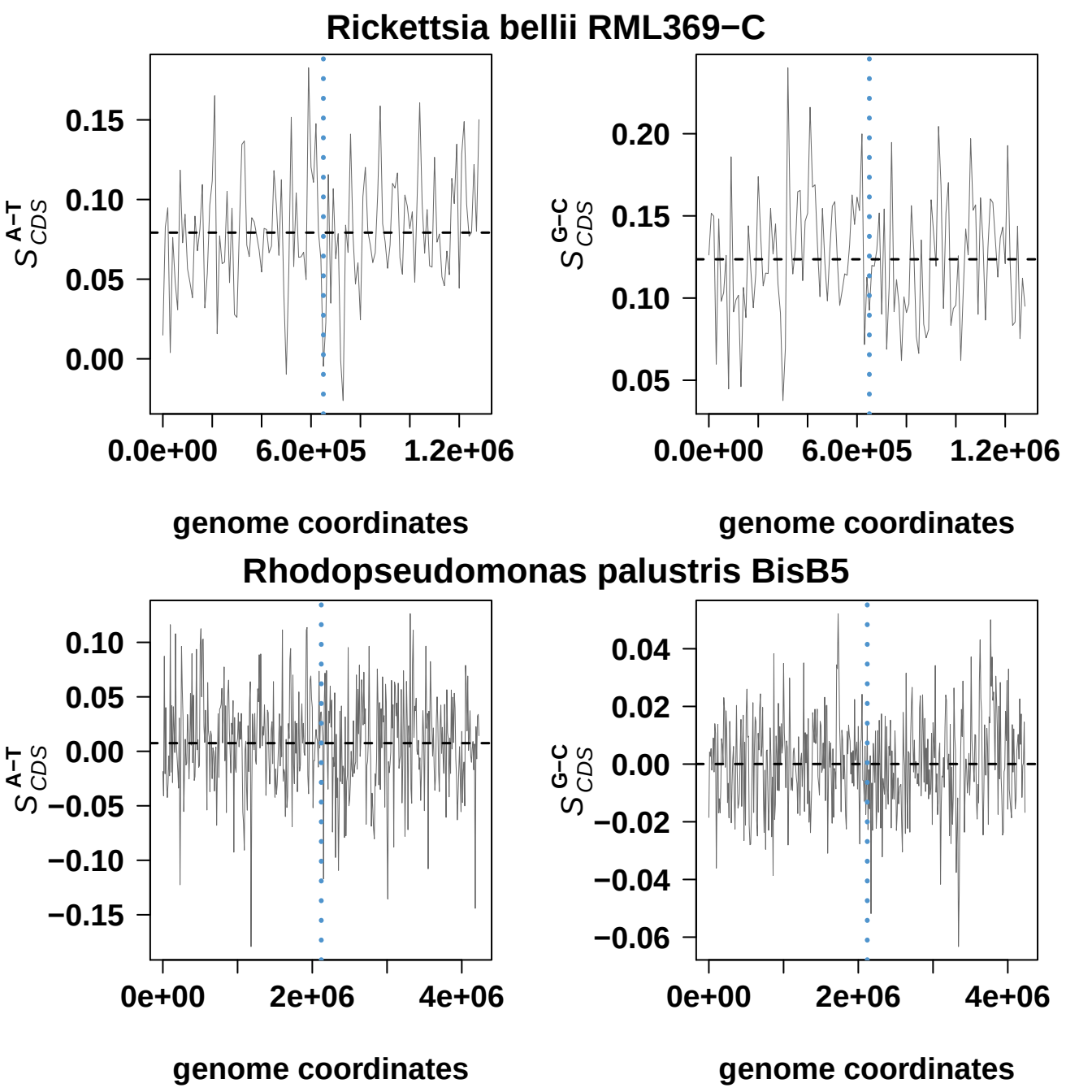

Rhodospirillum rubrum ATCC 11170
0.05
0.00
−0.05
−0.10
−0.15
−0.20
−0.25
S^{A-T}_{CDS}
0e+00
2e+06
genome coordinates
0.04
0.02
0.00
−0.02
−0.04
−0.06
−0.08
S^{G-C}_{CDS}
0e+00
2e+06
genome coordinates
Erythrobacter litoralis HTCC2594
0.15
0.10
0.05
0.00
−0.05
−0.10
S^{A-T}_{CDS}
0.0e+00
1.5e+06
genome coordinates
0.04
0.02
0.00
−0.02
−0.04
−0.06
S^{G-C}_{CDS}
0.0e+00
1.5e+06
genome coordinates

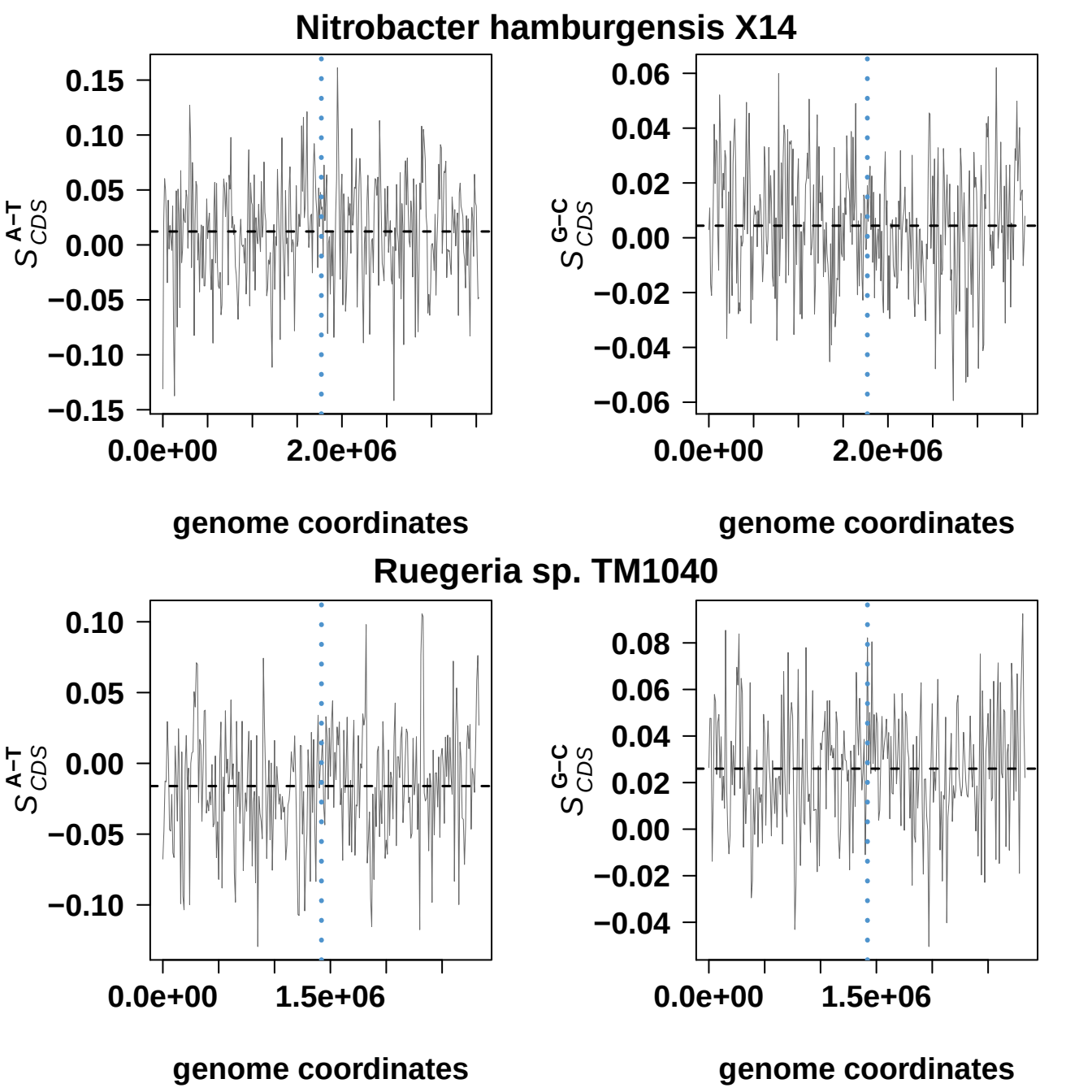

Rhizobium etli CFN 42
S^{A-T}_{CDS}
0.10
0.05
0.00
−0.05
−0.10
0e+00
2e+06
genome coordinates
S^{G-C}_{CDS}
0.05
0.00
−0.05
0e+00
2e+06
genome coordinates
Rhodopseudomonas palustris HaA2
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
−0.05
−0.10
−0.15
−0.20
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{CDS}
0.04
0.02
0.00
−0.02
−0.04
−0.06
−0.08
0e+00
2e+06
4e+06
genome coordinates


Novosphingobium aromaticivorans DSM 12444
0.10
0.05
0.00
−0.05
−0.10
−0.15
S^{A-T}_{CDS}
0.0e+00
1.5e+06
3.0e+06
genome coordinates
0.05
0.00
−0.05
S^{G-C}_{CDS}
0.0e+00
1.5e+06
3.0e+06
genome coordinates
Anaplasma phagocytophilum str. HZ
0.10
0.05
0.00
−0.05
−0.10
S^{A-T}_{CDS}
0e+00
4e+05
8e+05
genome coordinates
0.3
0.2
0.1
0.0
S^{G-C}_{CDS}
0e+00
4e+05
8e+05
genome coordinates


Neorickettsia sennetsu str. Miyayama
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
−0.05
−0.10
0e+00
4e+05
genome coordinates
S^{G-C}_{CDS}
0.25
0.20
0.15
0.10
0.05
0e+00
4e+05
genome coordinates
Ehrlichia chaffeensis str. Arkansas
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
−0.05
0e+00
4e+05
8e+05
genome coordinates
S^{G-C}_{CDS}
0.3
0.2
0.1
0.0
0e+00
4e+05
8e+05
genome coordinates


Jannaschia sp. CCS1
S^{A-T}_{CDS}
0.05
0.00
−0.05
−0.10
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{CDS}
0.15
0.10
0.05
0.00
−0.05
0e+00
2e+06
4e+06
genome coordinates
Rhodopseudomonas palustris BisB18
S^{A-T}_{CDS}
0.1
0.0
−0.1
−0.2
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{CDS}
0.05
0.00
−0.05
0e+00
2e+06
4e+06
genome coordinates


Rickettsia bellii RML369−C
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
0.0e+00
6.0e+05
1.2e+06
genome coordinates
S^{G-C}_{CDS}
0.20
0.15
0.10
0.05
0.0e+00
6.0e+05
1.2e+06
genome coordinates
Rhodopseudomonas palustris BisB5
S^{A-T}_{CDS}
0.10
0.05
0.00
−0.05
−0.10
−0.15
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{CDS}
0.04
0.02
0.00
−0.02
−0.04
−0.06
0e+00
2e+06
4e+06
genome coordinates


Nitrobacter hamburgensis X14
S^{A-T}_{CDS}
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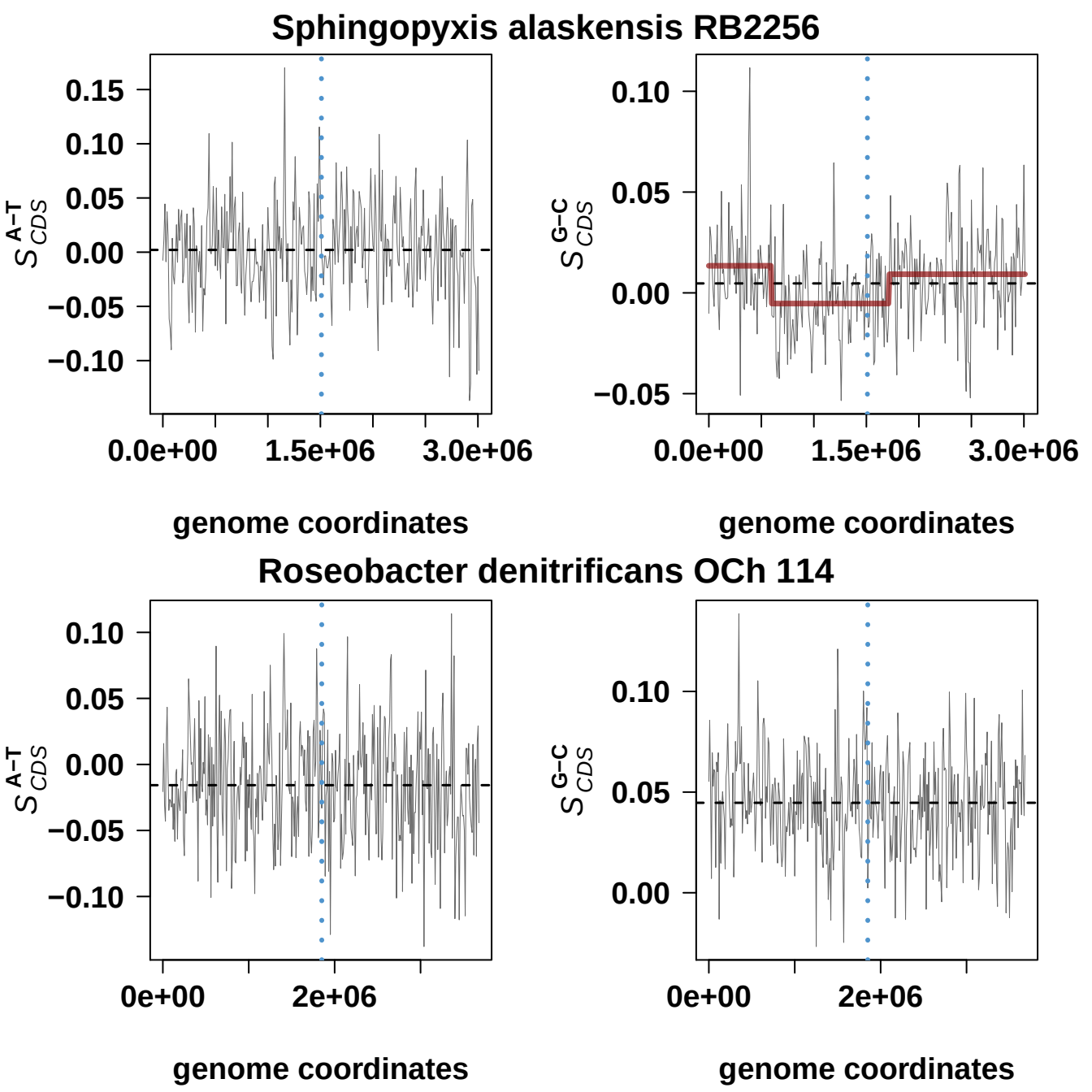
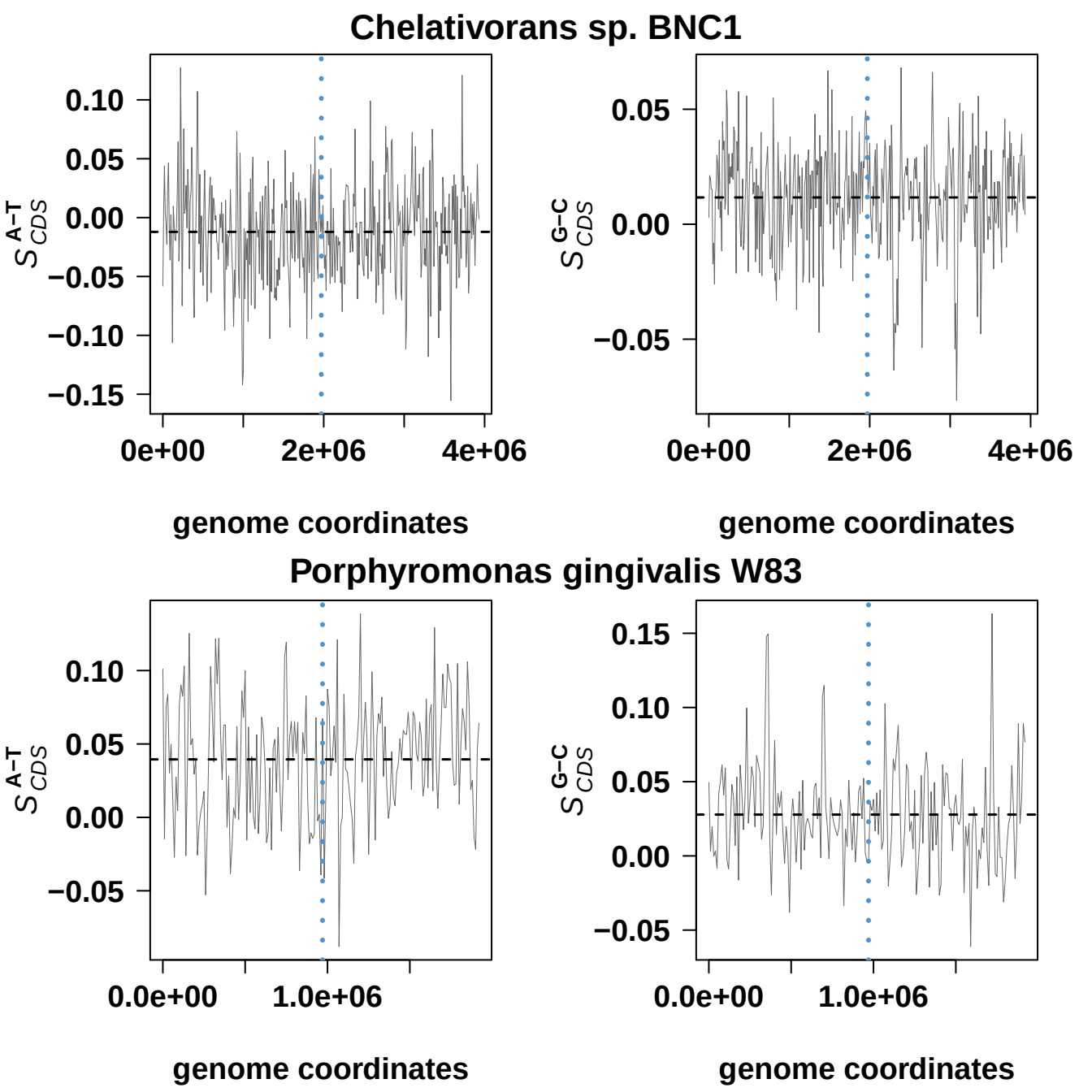
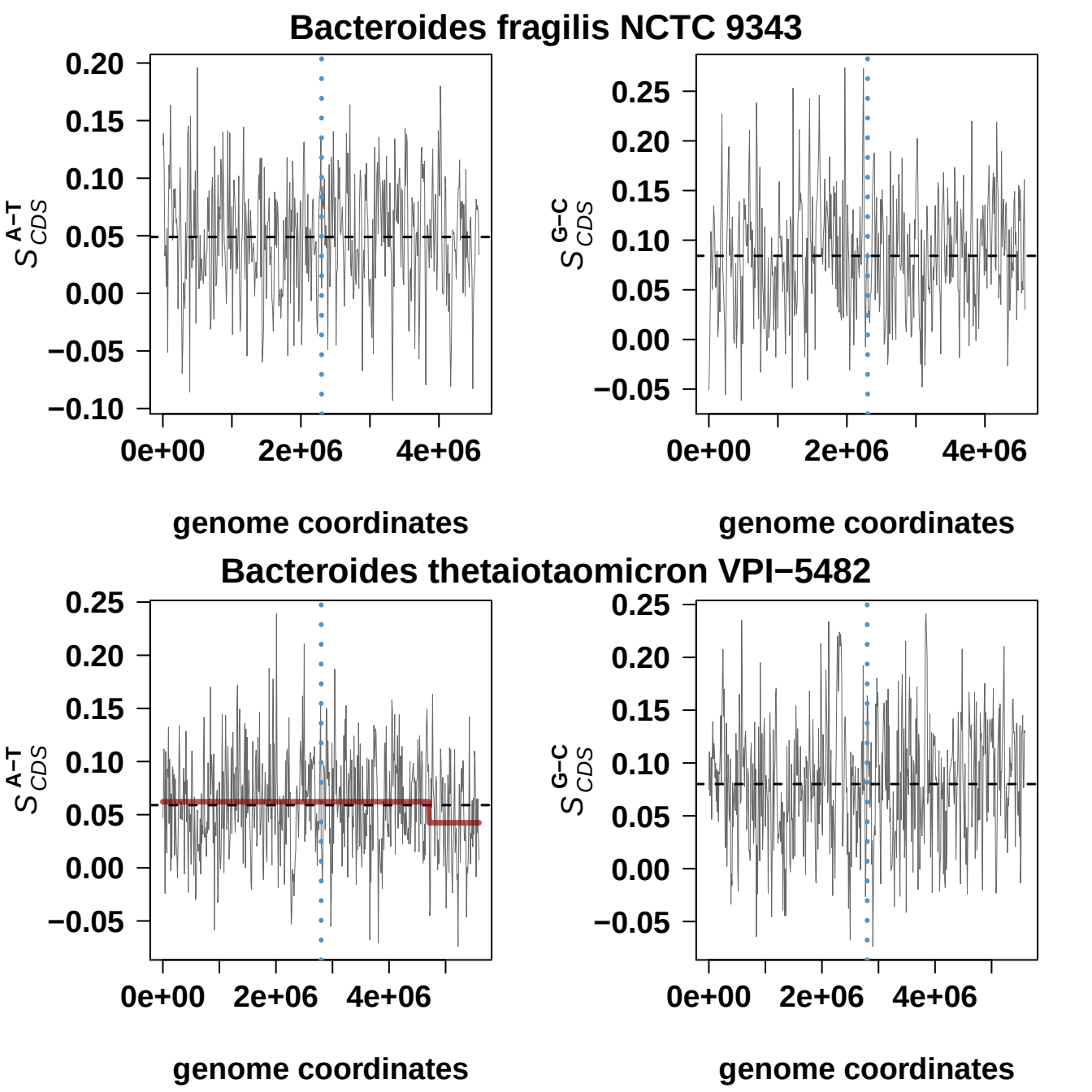
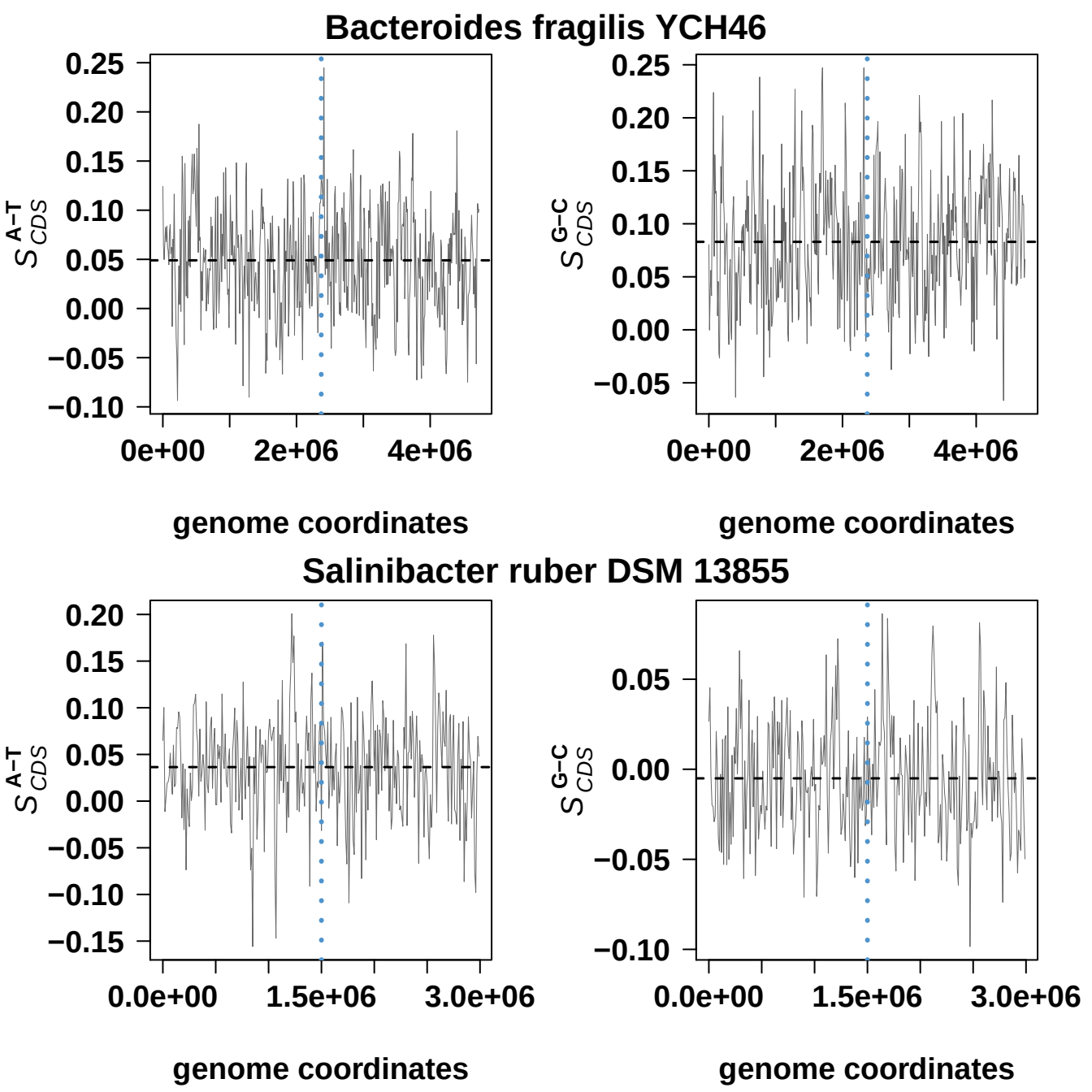
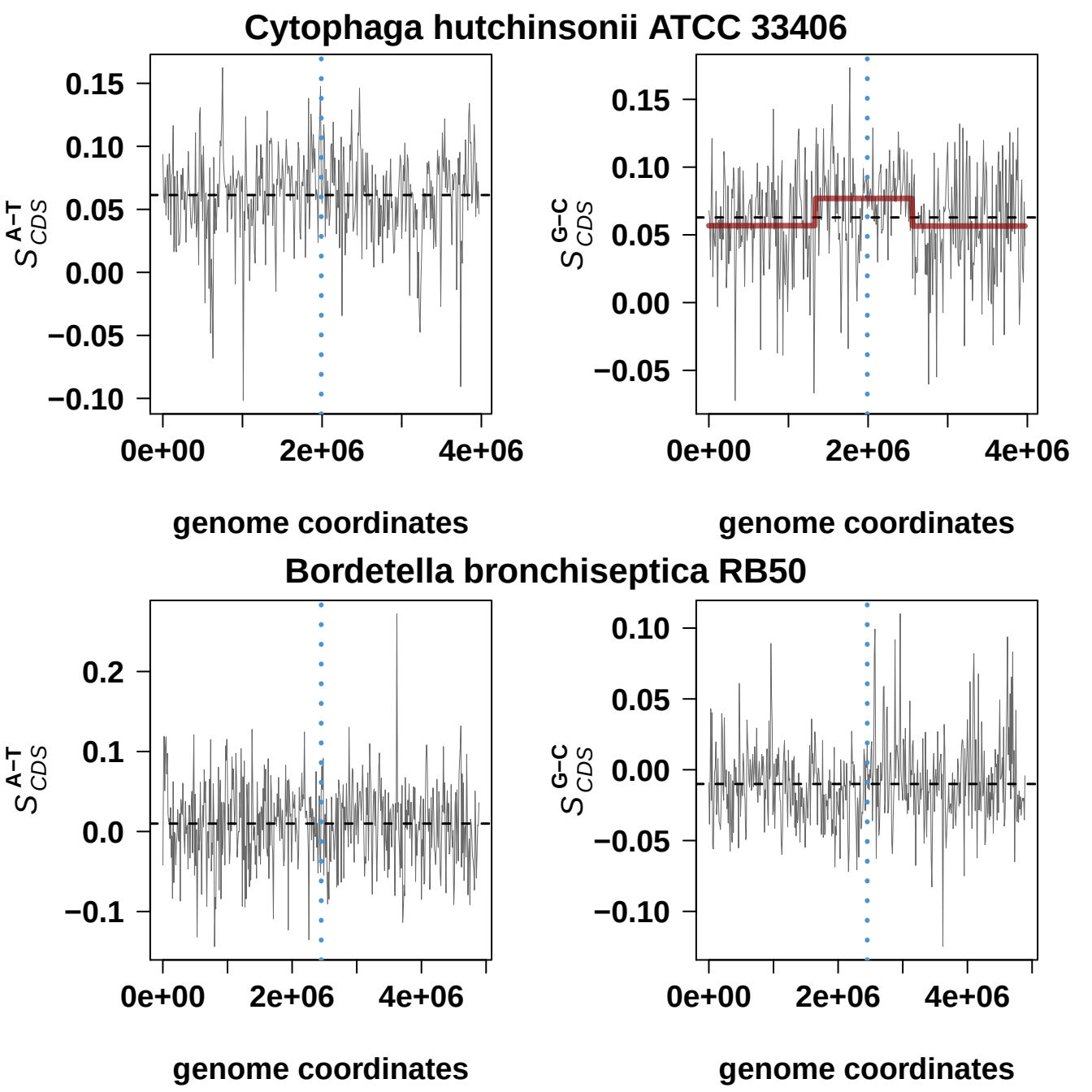
0.10
0.05
0.00
−0.05
−0.10
−0.15
0.0e+00
2.0e+06
genome coordinates
S^{G-C}_{CDS}
0.06
0.04
0.02
0.00
−0.02
−0.04
−0.06
0.0e+00
2.0e+06
genome coordinates
Ruegeria sp. TM1040
S^{A-T}_{CDS}
0.10
0.05
0.00
−0.05
−0.10
0.0e+00
1.5e+06
genome coordinates
S^{G-C}_{CDS}
0.08
0.06
0.04
0.02
0.00
−0.02
−0.04
0.0e+00
1.5e+06
genome coordinates

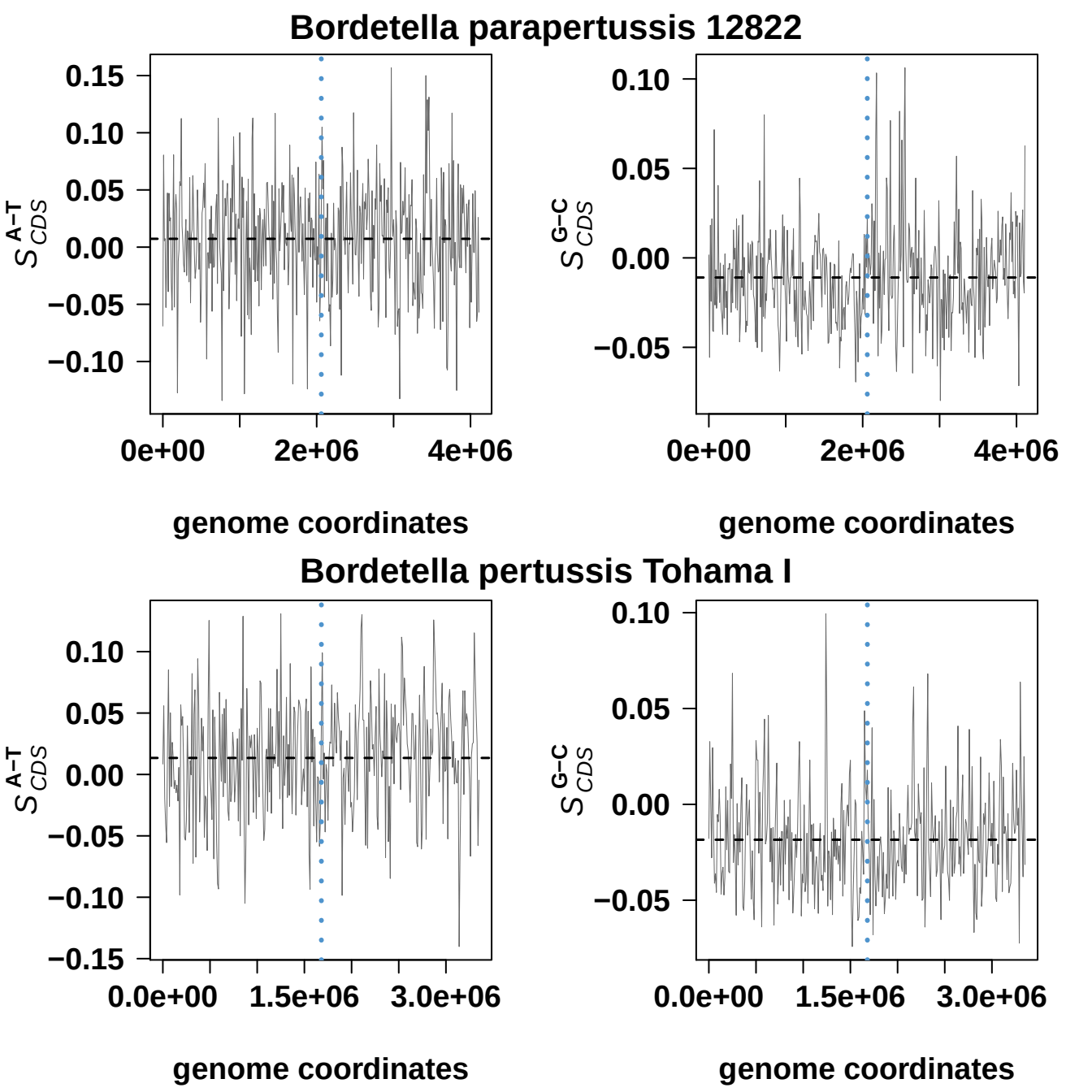

Sphingopyxis alaskensis RB2256
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
−0.05
−0.10
0.0e+00
1.5e+06
3.0e+06
genome coordinates
S^{G-C}_{CDS}
0.10
0.05
0.00
−0.05
0.0e+00
1.5e+06
3.0e+06
genome coordinates
Roseobacter denitrificans OCh 114
S^{A-T}_{CDS}
0.10
0.05
0.00
−0.05
−0.10
0e+00
2e+06
genome coordinates
S^{G-C}_{CDS}
0.10
0.05
0.00
0e+00
2e+06
genome coordinates

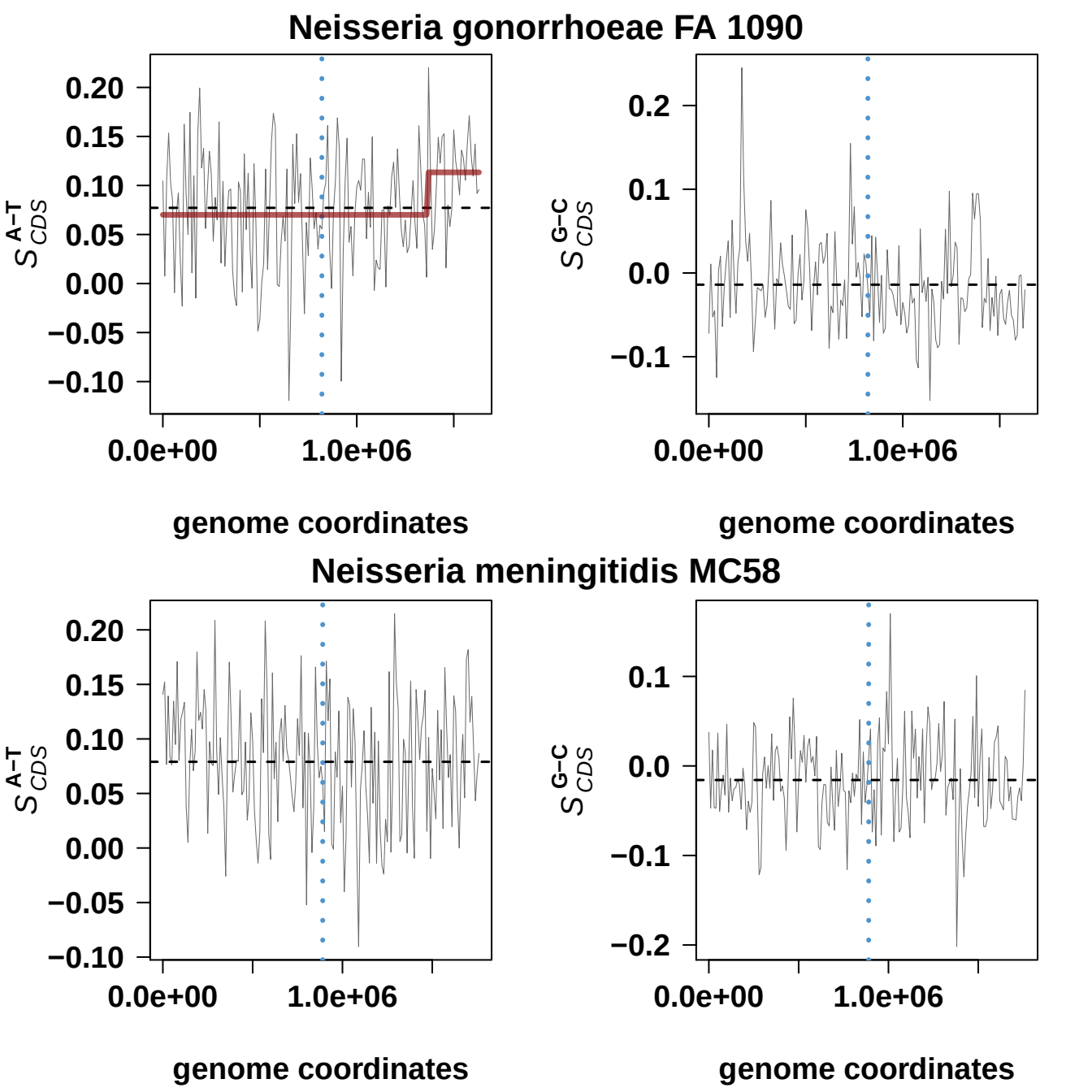

Chelativorans sp. BNC1
0.10
0.05
0.00
−0.05
−0.10
−0.15
S^{A-T}_{CDS}
0e+00
2e+06
4e+06
genome coordinates
0.05
0.00
−0.05
S^{G-C}_{CDS}
0e+00
2e+06
4e+06
genome coordinates
Porphyromonas gingivalis W83
0.10
0.05
0.00
−0.05
S^{A-T}_{CDS}
0.0e+00
1.0e+06
genome coordinates
0.15
0.10
0.05
0.00
−0.05
S^{G-C}_{CDS}
0.0e+00
1.0e+06
genome coordinates

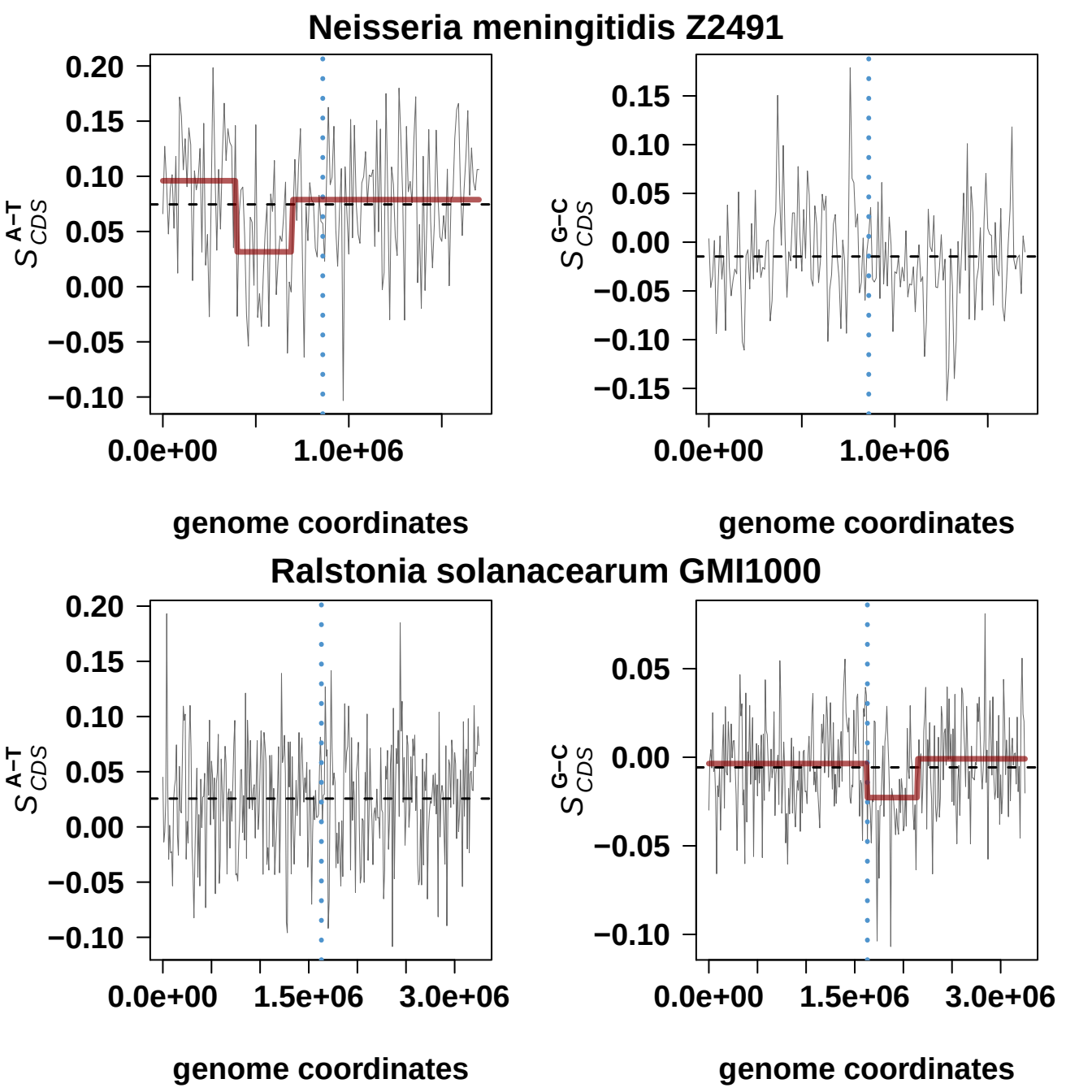

Bacteroides fragilis NCTC 9343
Bacteroides thetaiotaomicron VPI−5482
S^{A-T}_{CDS}
S^{G-C}_{CDS}
0.20
0.15
0.10
0.05
0.00
−0.05
−0.10
0.25
0e+00
2e+06
4e+06
genome coordinates

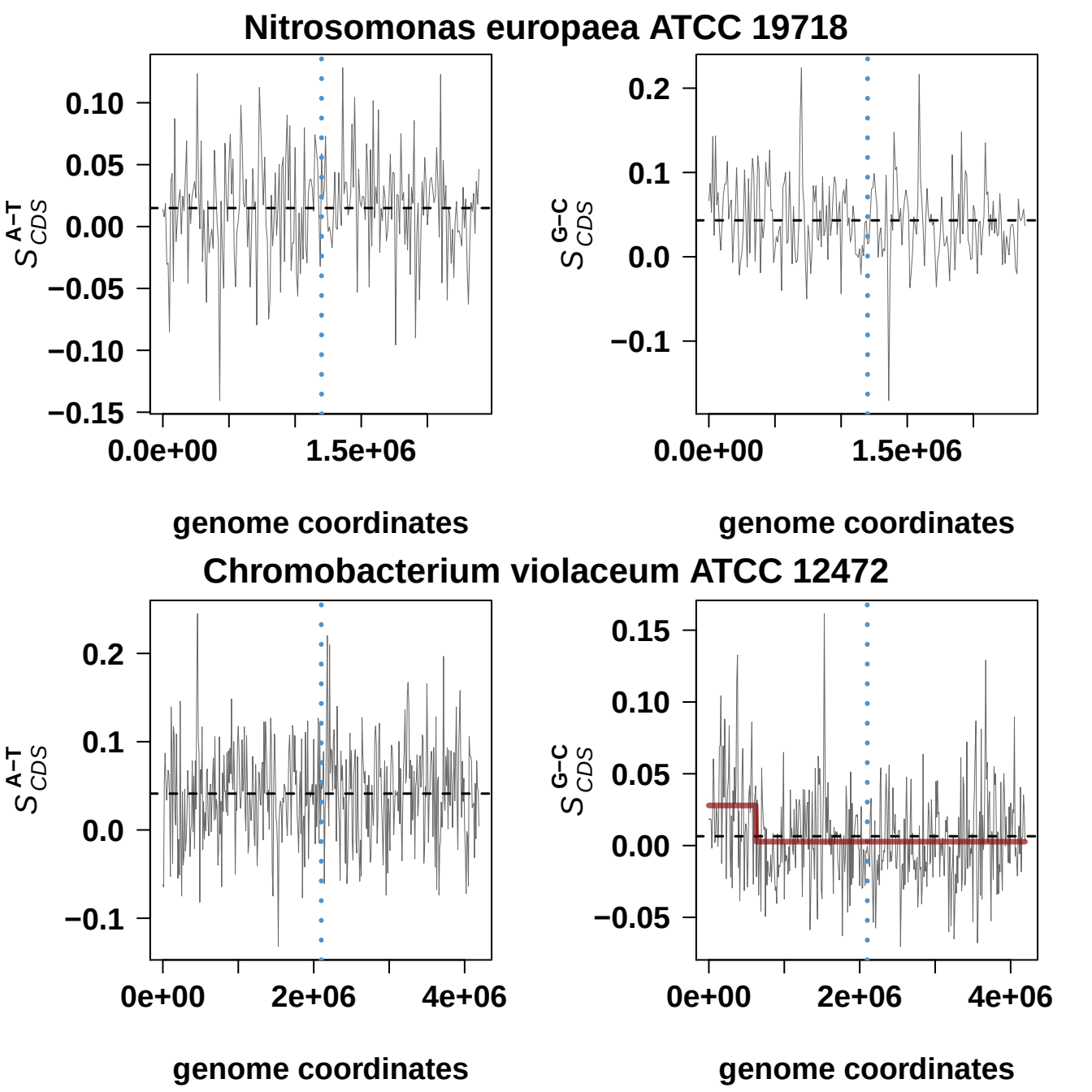

Bacteroides fragilis YCH46
S^{A-T}_{CDS}
0.25
0.20
0.15
0.10
0.05
0.00
−0.05
−0.10
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{CDS}
0.25
0.20
0.15
0.10
0.05
0.00
−0.05
0e+00
2e+06
4e+06
genome coordinates
Salinibacter ruber DSM 13855
S^{A-T}_{CDS}
0.20
0.15
0.10
0.05
0.00
−0.05
−0.10
−0.15
0.0e+00
1.5e+06
3.0e+06
genome coordinates
S^{G-C}_{CDS}
0.05
0.00
−0.05
−0.10
0.0e+00
1.5e+06
3.0e+06
genome coordinates

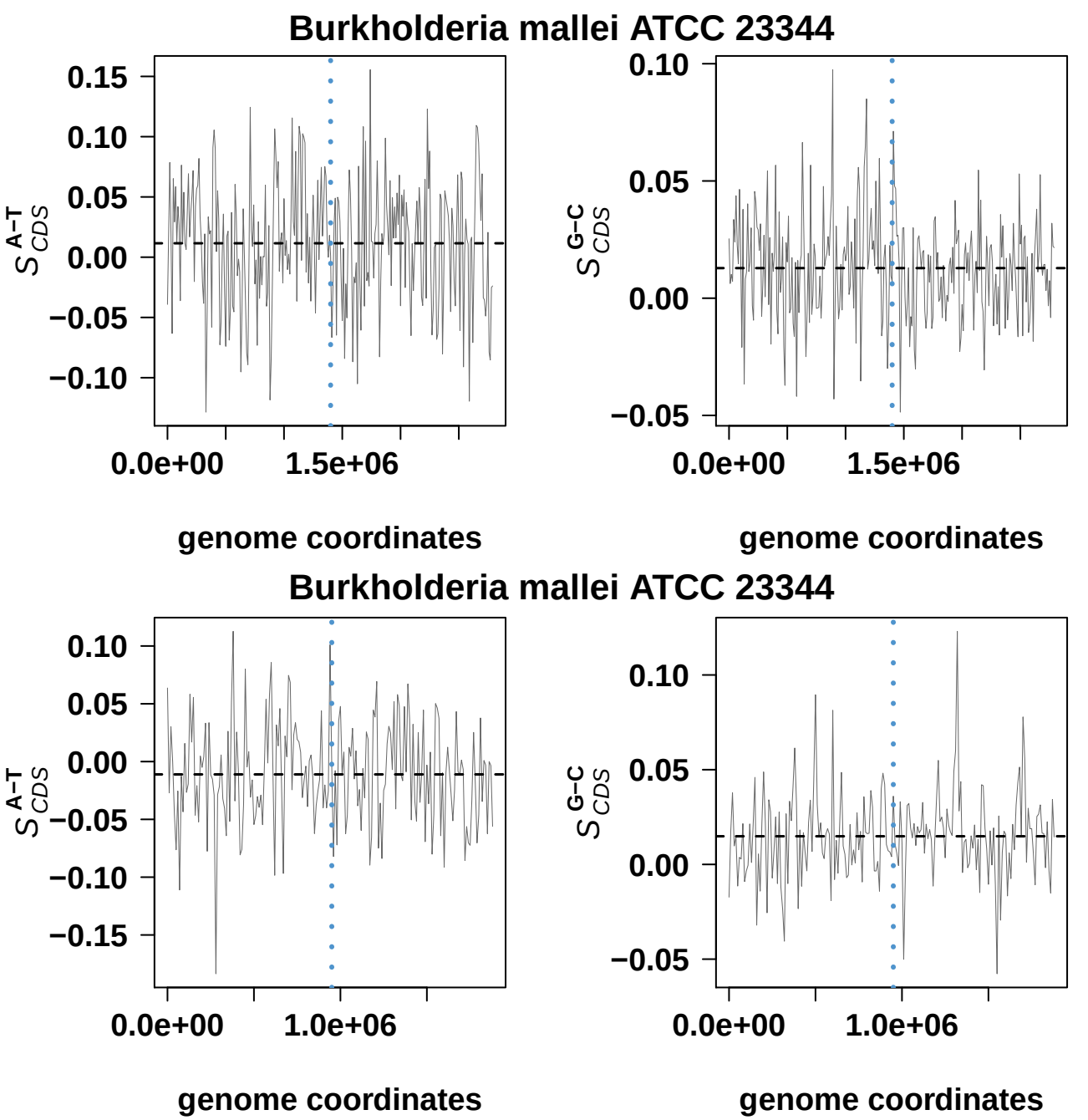

Cytophaga hutchinsonii ATCC 33406
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
−0.05
−0.10
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{CDS}
0.15
0.10
0.05
0.00
−0.05
0e+00
2e+06
4e+06
genome coordinates
Bordetella bronchiseptica RB50
S^{A-T}_{CDS}
0.2
0.1
0.0
−0.1
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{CDS}
0.10
0.05
0.00
−0.05
−0.10
0e+00
2e+06
4e+06
genome coordinates

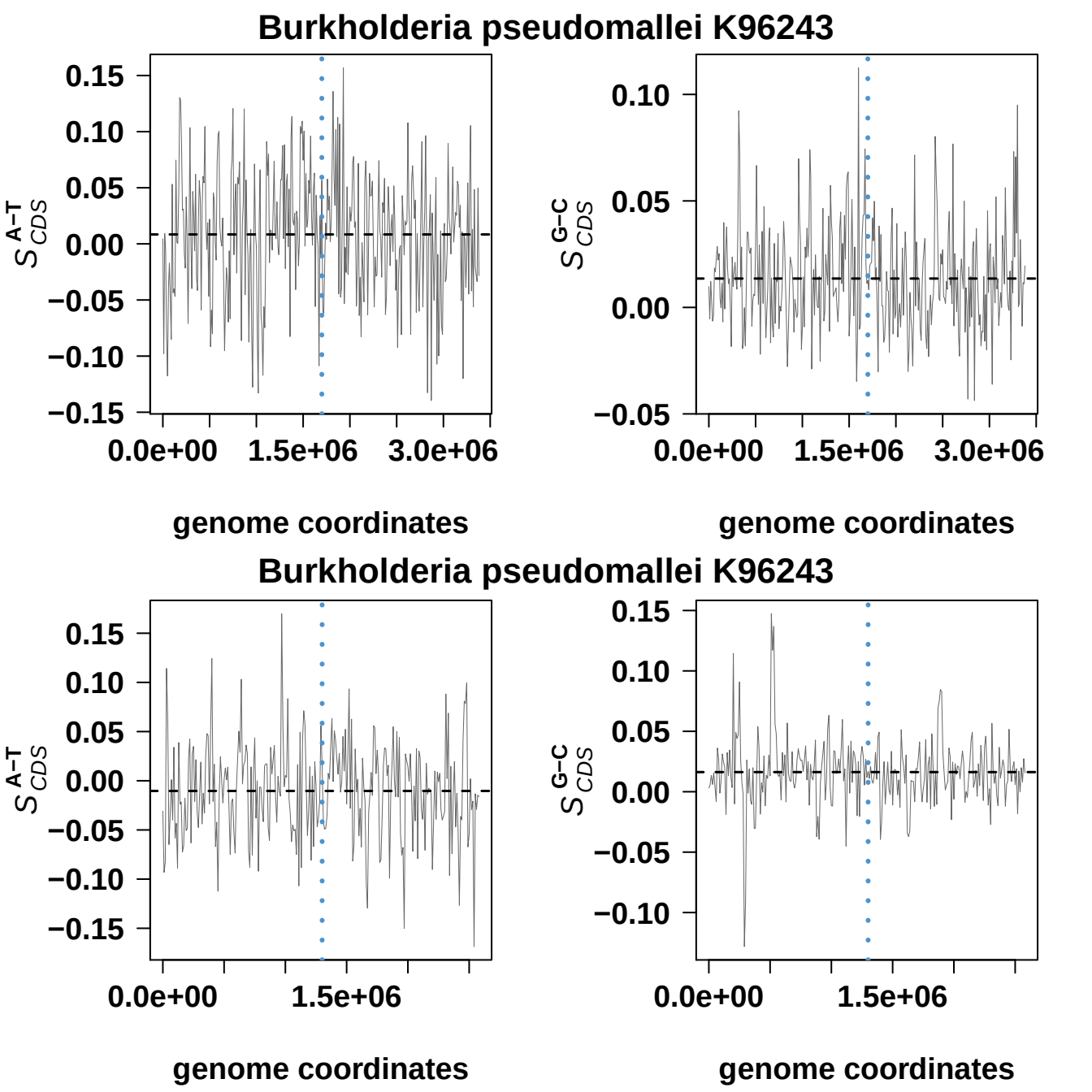

Bordetella parapertussis 12822
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
−0.05
−0.10
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{CDS}
0.10
0.05
0.00
−0.05
0e+00
2e+06
4e+06
genome coordinates
Bordetella pertussis Tohama I
S^{A-T}_{CDS}
0.10
0.05
0.00
−0.05
−0.10
−0.15
0.0e+00
1.5e+06
3.0e+06
genome coordinates
S^{G-C}_{CDS}
0.10
0.05
0.00
−0.05
0.0e+00
1.5e+06
3.0e+06
genome coordinates

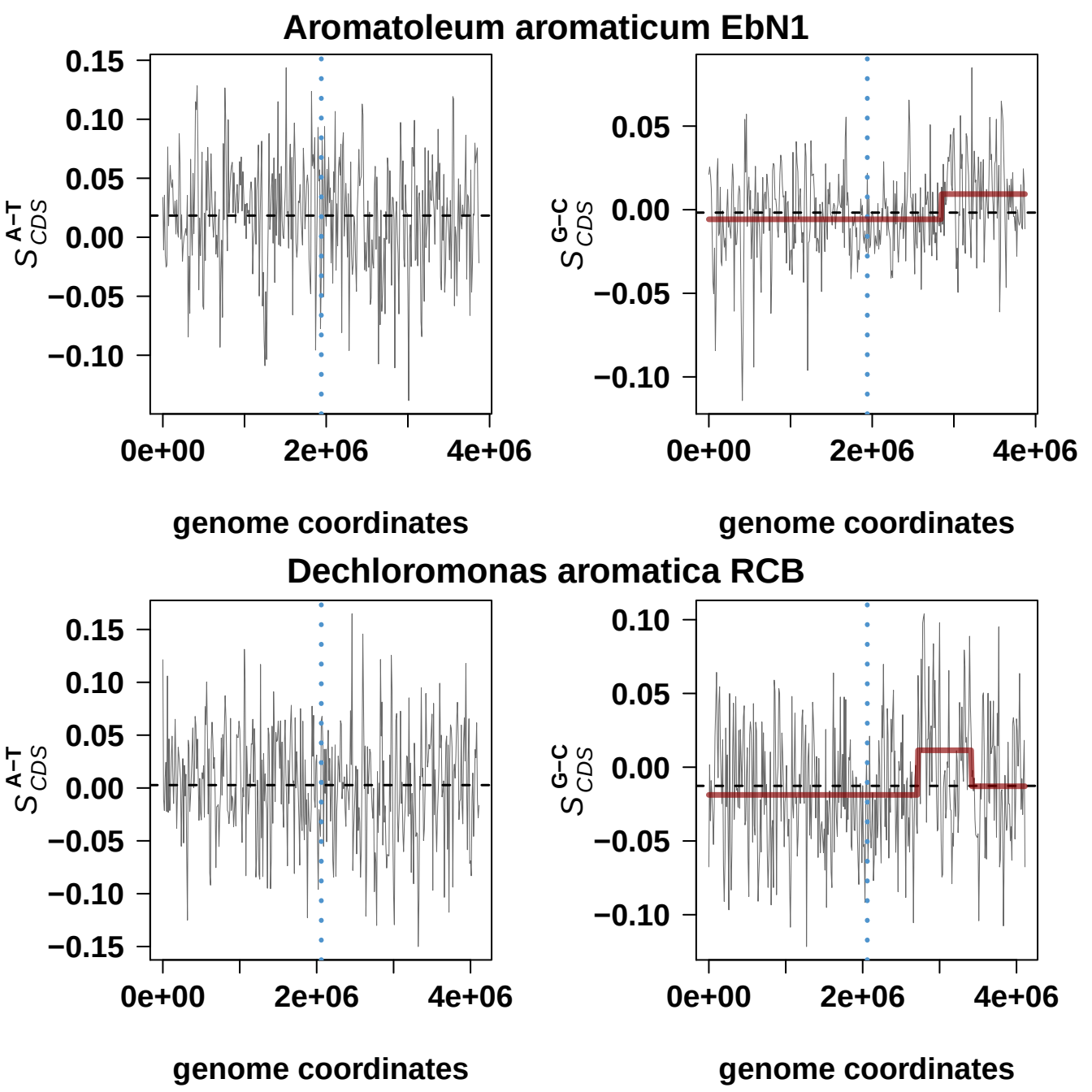

Neisseria gonorrhoeae FA 1090
S^{A-T}_{CDS}
0.20
0.15
0.10
0.05
0.00
−0.05
−0.10
0.0e+00
1.0e+06
genome coordinates
S^{G-C}_{CDS}
0.2
0.1
0.0
−0.1
0.0e+00
1.0e+06
genome coordinates
Neisseria meningitidis MC58
S^{A-T}_{CDS}
0.20
0.15
0.10
0.05
0.00
−0.05
−0.10
0.0e+00
1.0e+06
genome coordinates
S^{G-C}_{CDS}
0.1
0.0
−0.1
−0.2
0.0e+00
1.0e+06
genome coordinates

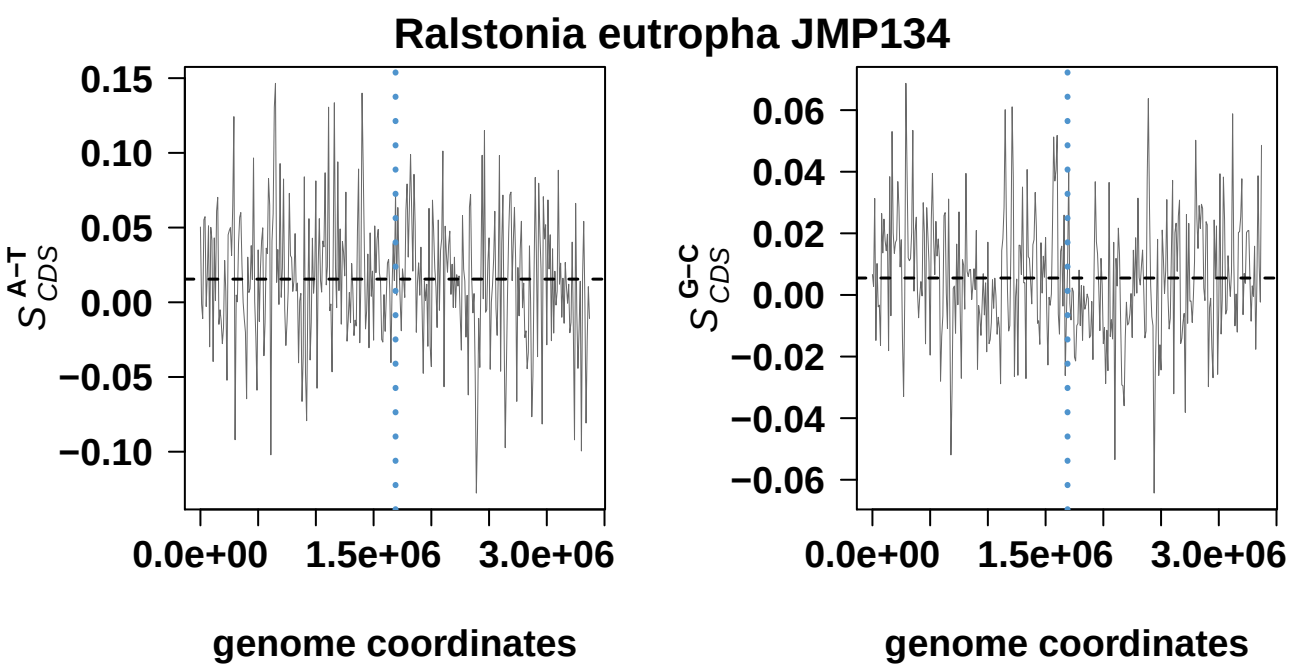

Neisseria meningitidis Z2491
S^{A-T}_{CDS}
0.20
0.15
0.10
0.05
0.00
−0.05
−0.10
0.0e+00
1.0e+06
genome coordinates
S^{G-C}_{CDS}
0.15
0.10
0.05
0.00
−0.05
−0.10
−0.15
0.0e+00
1.0e+06
genome coordinates
Ralstonia solanacearum GMI1000
S^{A-T}_{CDS}
0.20
0.15
0.10
0.05
0.00
−0.05
−0.10
0.0e+00
1.5e+06
3.0e+06
genome coordinates
S^{G-C}_{CDS}
0.05
0.00
−0.05
−0.10
0.0e+00
1.5e+06
3.0e+06
genome coordinates

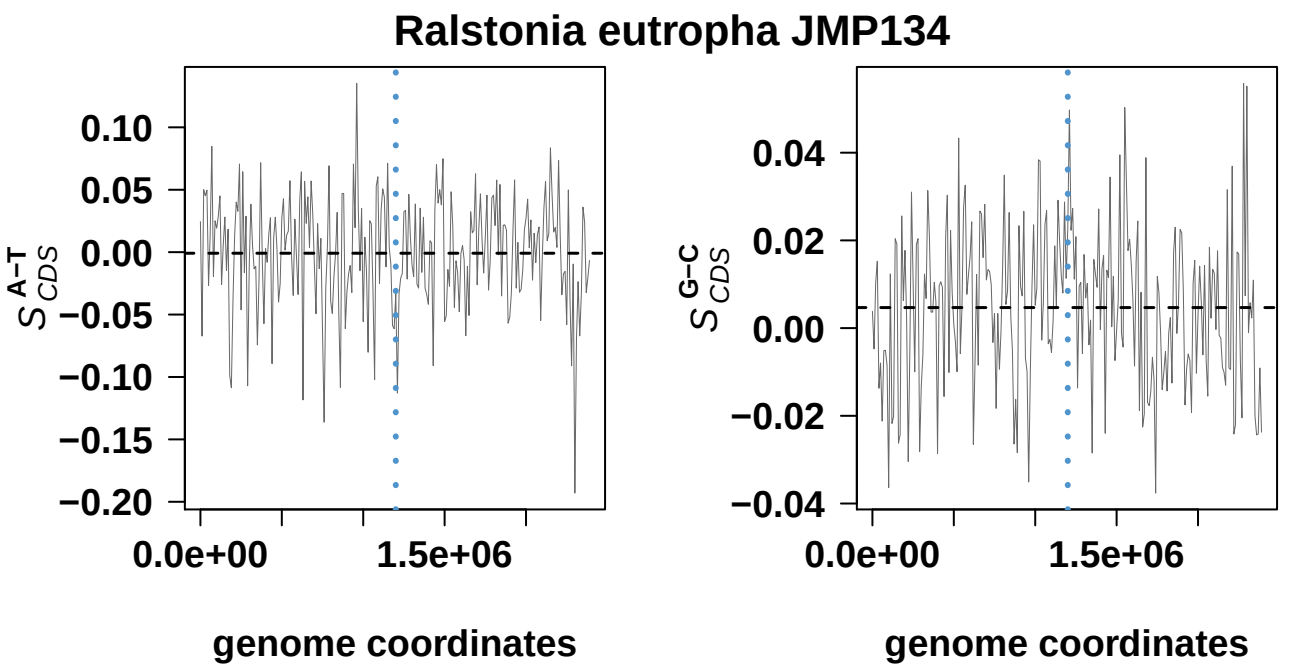

Nitrosomonas europaea ATCC 19718
S^{A-T}_{CDS}
0.10
0.05
0.00
−0.05
−0.10
−0.15
0.0e+00
1.5e+06
genome coordinates
S^{G-C}_{CDS}
0.2
0.1
0.0
−0.1
0.0e+00
1.5e+06
genome coordinates
Chromobacterium violaceum ATCC 12472
S^{A-T}_{CDS}
0.2
0.1
0.0
−0.1
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{CDS}
0.15
0.10
0.05
0.00
−0.05
0e+00
2e+06
4e+06
genome coordinates

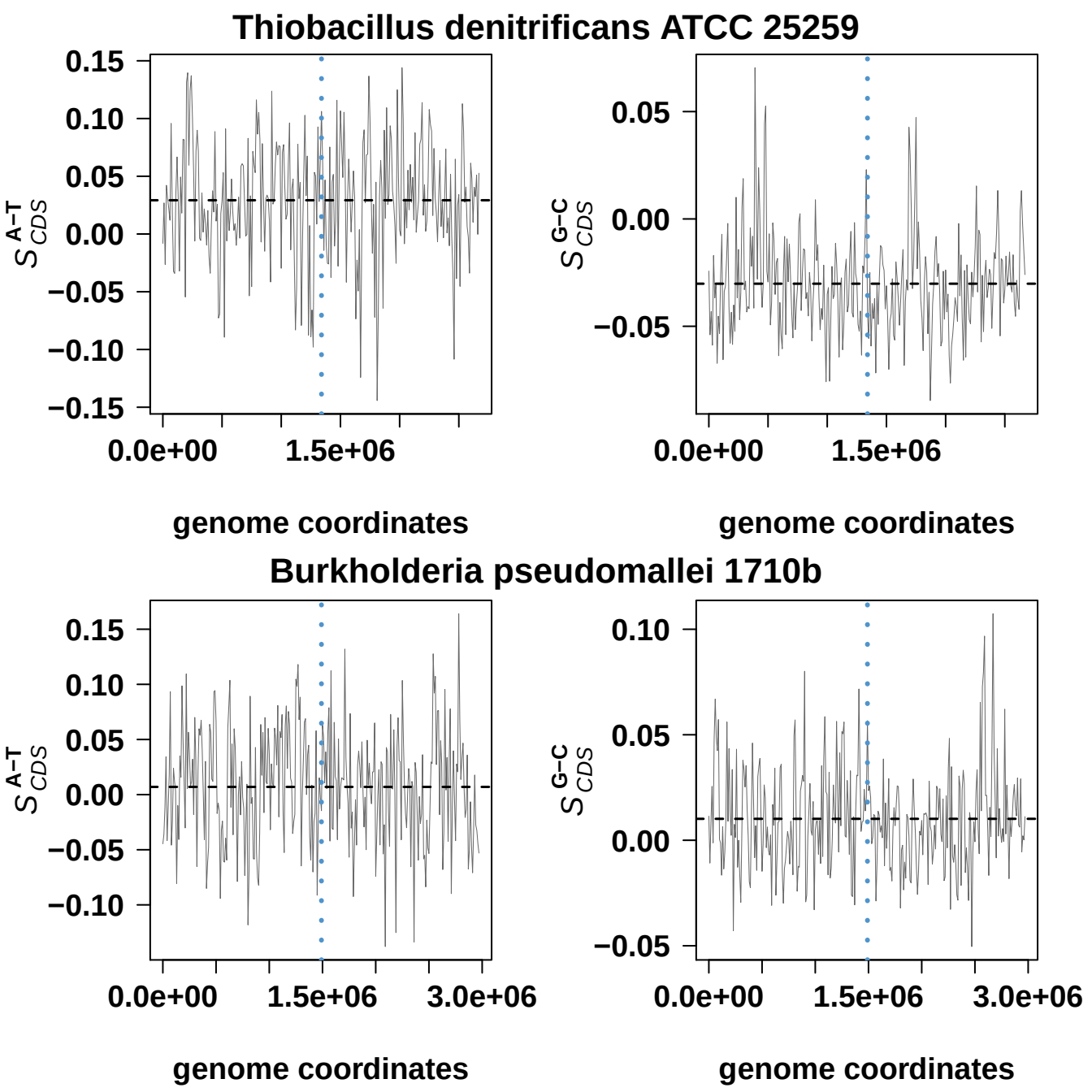

Burkholderia mallei ATCC 23344
0.15
0.10
0.05
0.00
−0.05
−0.10
S^{A-T}_{CDS}
0.0e+00
1.5e+06
genome coordinates
0.10
0.05
0.00
−0.05
S^{G-C}_{CDS}
0.0e+00
1.5e+06
genome coordinates
Burkholderia mallei ATCC 23344
0.10
0.05
0.00
−0.05
−0.10
−0.15
S^{A-T}_{CDS}
0.0e+00
1.0e+06
genome coordinates
0.10
0.05
0.00
−0.05
S^{G-C}_{CDS}
0.0e+00
1.0e+06
genome coordinates

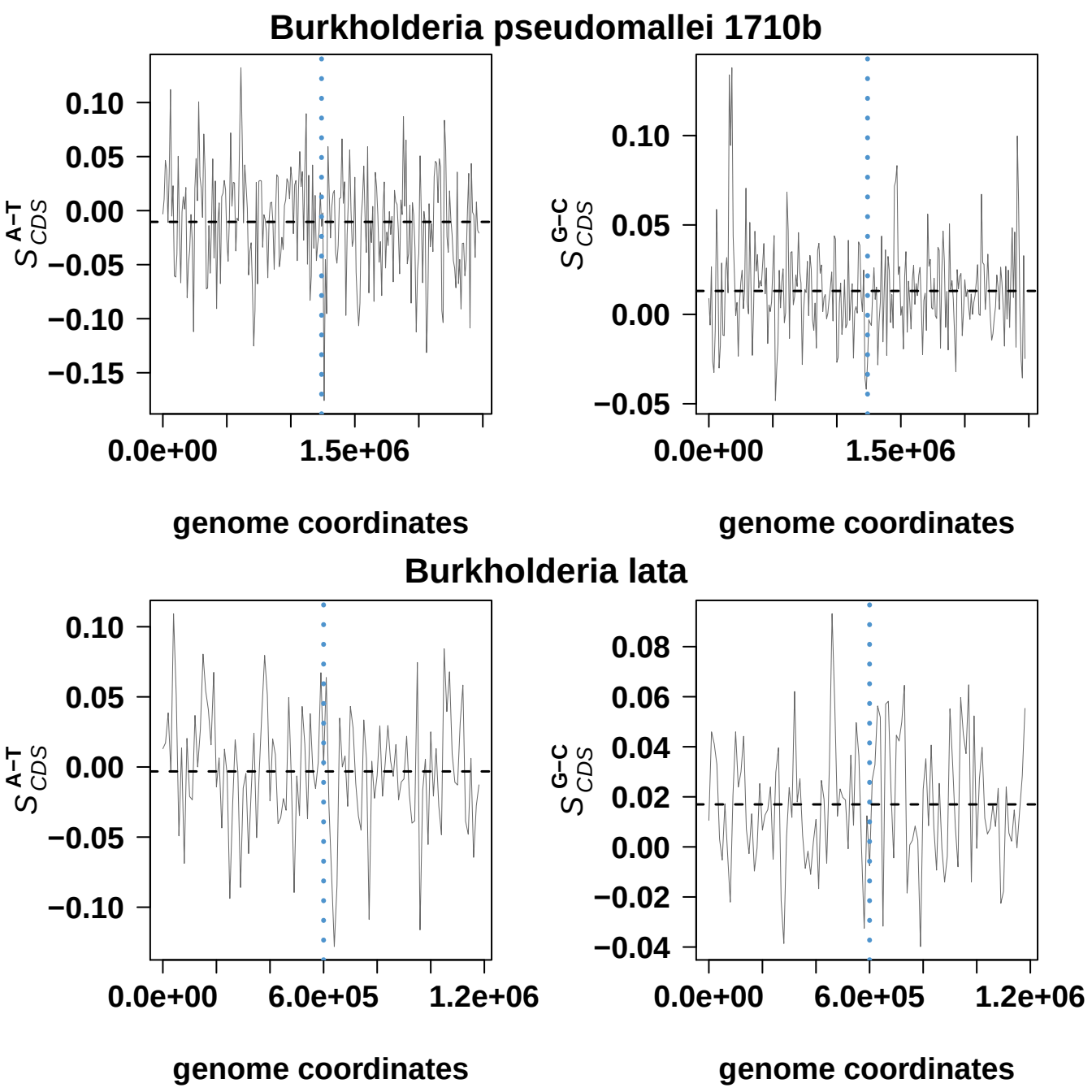

Burkholderia pseudomallei K96243
0.15
0.10
0.05
0.00
−0.05
−0.10
−0.15
S^{A-T}_{CDS}
0.0e+00
1.5e+06
3.0e+06
genome coordinates
0.10
0.05
0.00
−0.05
S^{G-C}_{CDS}
0.0e+00
1.5e+06
3.0e+06
genome coordinates
Burkholderia pseudomallei K96243
0.15
0.10
0.05
0.00
−0.05
−0.10
−0.15
S^{A-T}_{CDS}
0.0e+00
1.5e+06
genome coordinates
0.15
0.10
0.05
0.00
−0.05
−0.10
S^{G-C}_{CDS}
0.0e+00
1.5e+06
genome coordinates

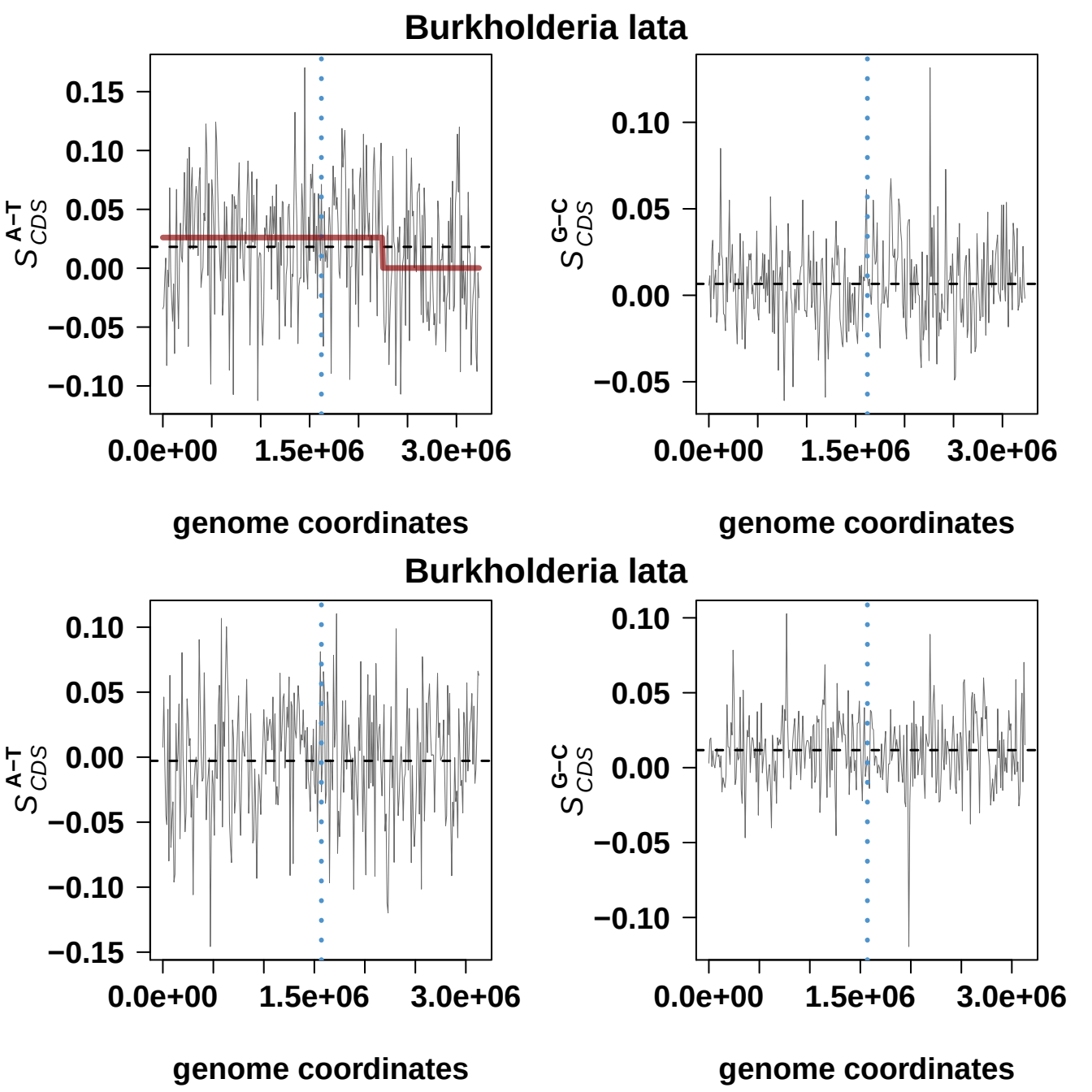

Aromatoleum aromaticum EbN1
0.15
0.10
0.05
0.00
−0.05
−0.10
S^{A-T}_{CDS}
0e+00
2e+06
4e+06
genome coordinates
0.05
0.00
−0.05
−0.10
S^{G-C}_{CDS}
0e+00
2e+06
4e+06
genome coordinates
Dechloromonas aromatica RCB
0.15
0.10
0.05
0.00
−0.05
−0.10
−0.15
S^{A-T}_{CDS}
0e+00
2e+06
4e+06
genome coordinates
0.10
0.05
0.00
−0.05
−0.10
S^{G-C}_{CDS}
0e+00
2e+06
4e+06
genome coordinates

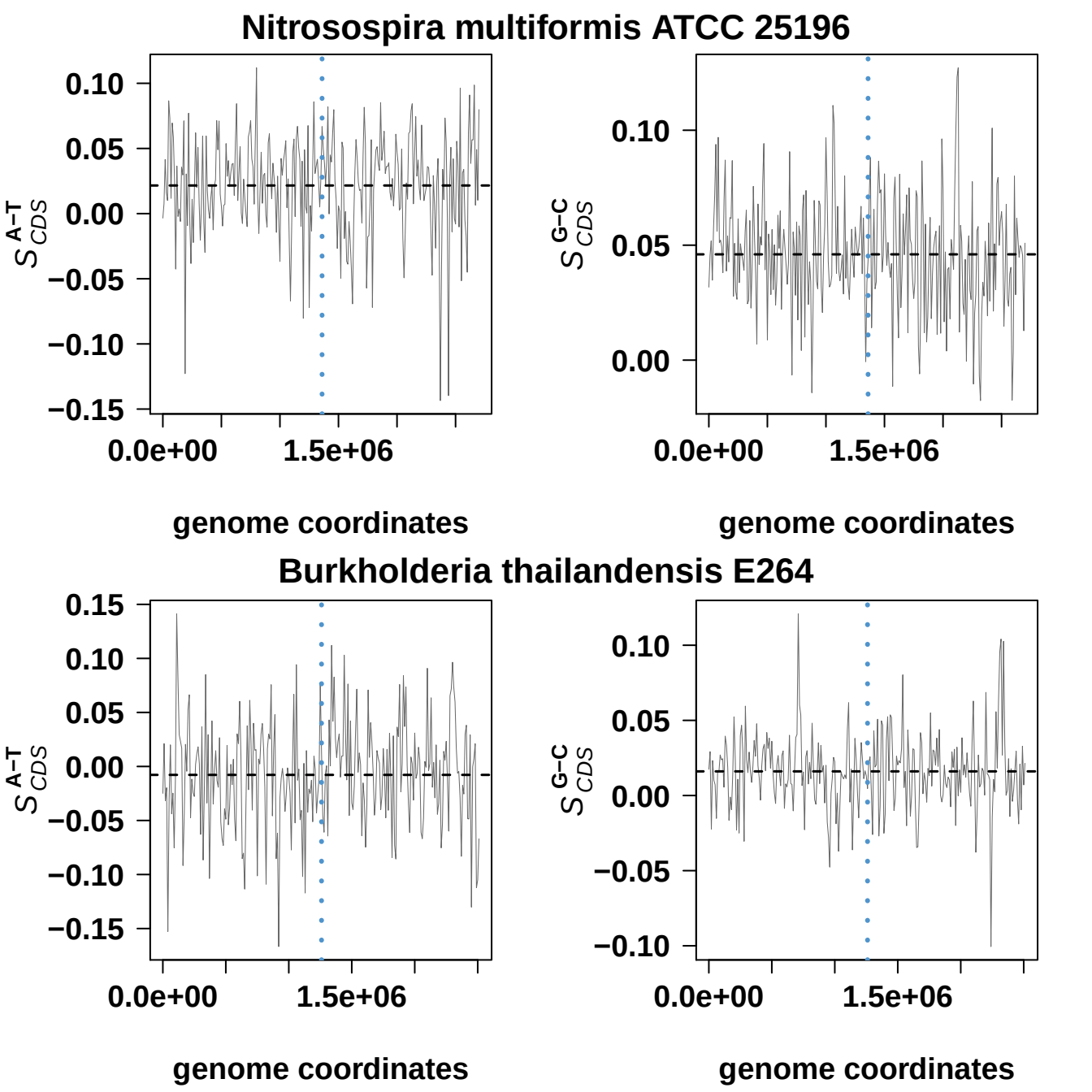

Ralstonia eutropha JMP134
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
−0.05
−0.10
0.0e+00
1.5e+06
3.0e+06
genome coordinates
S^{G-C}_{CDS}
0.06
0.04
0.02
0.00
−0.02
−0.04
−0.06
0.0e+00
1.5e+06
3.0e+06
genome coordinates

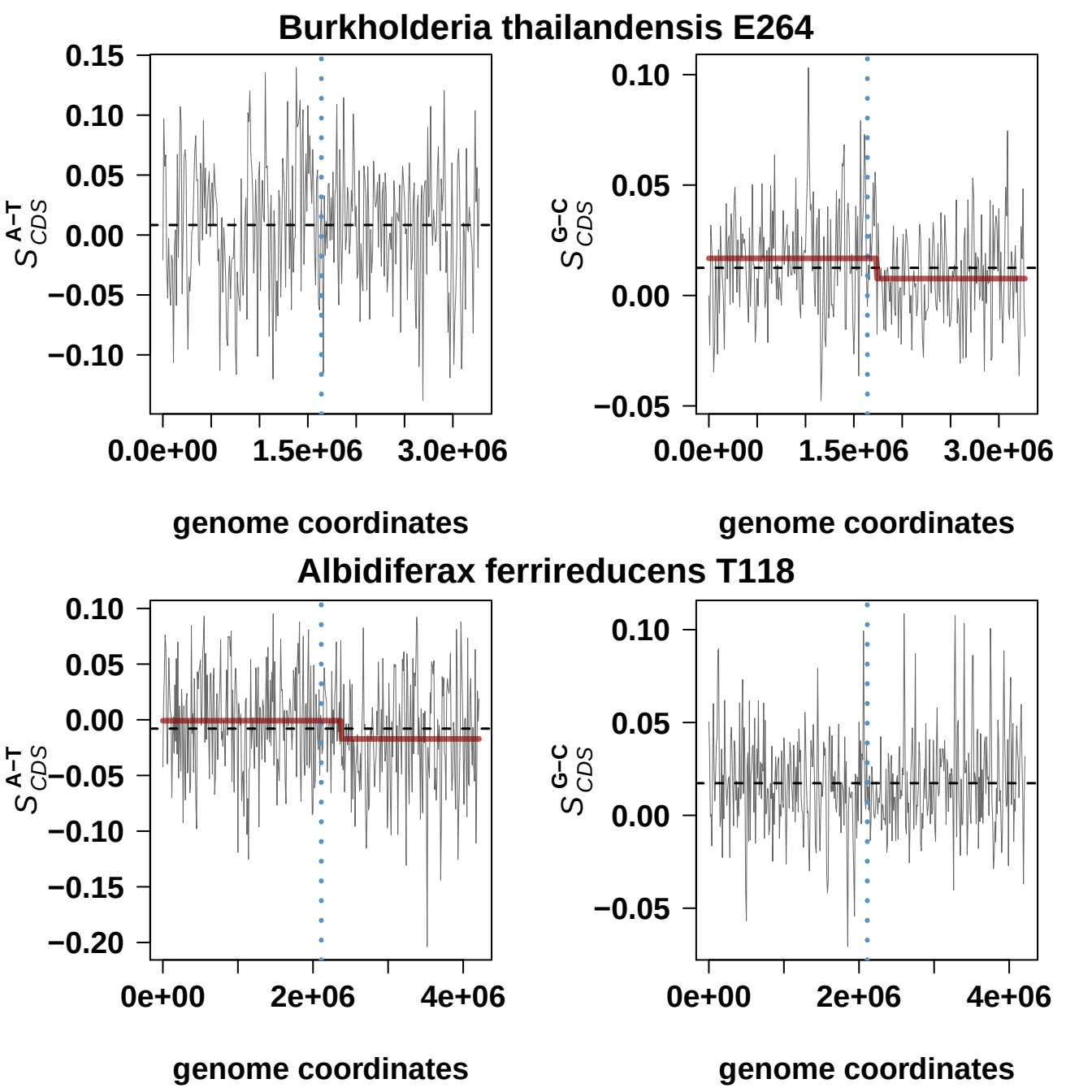

Ralstonia eutropha JMP134
S^{A-T}_{CDS}
0.10
0.05
0.00
−0.05
−0.10
−0.15
−0.20
0.0e+00
1.5e+06
genome coordinates
S^{G-C}_{CDS}
0.04
0.02
0.00
−0.02
−0.04
0.0e+00
1.5e+06
genome coordinates

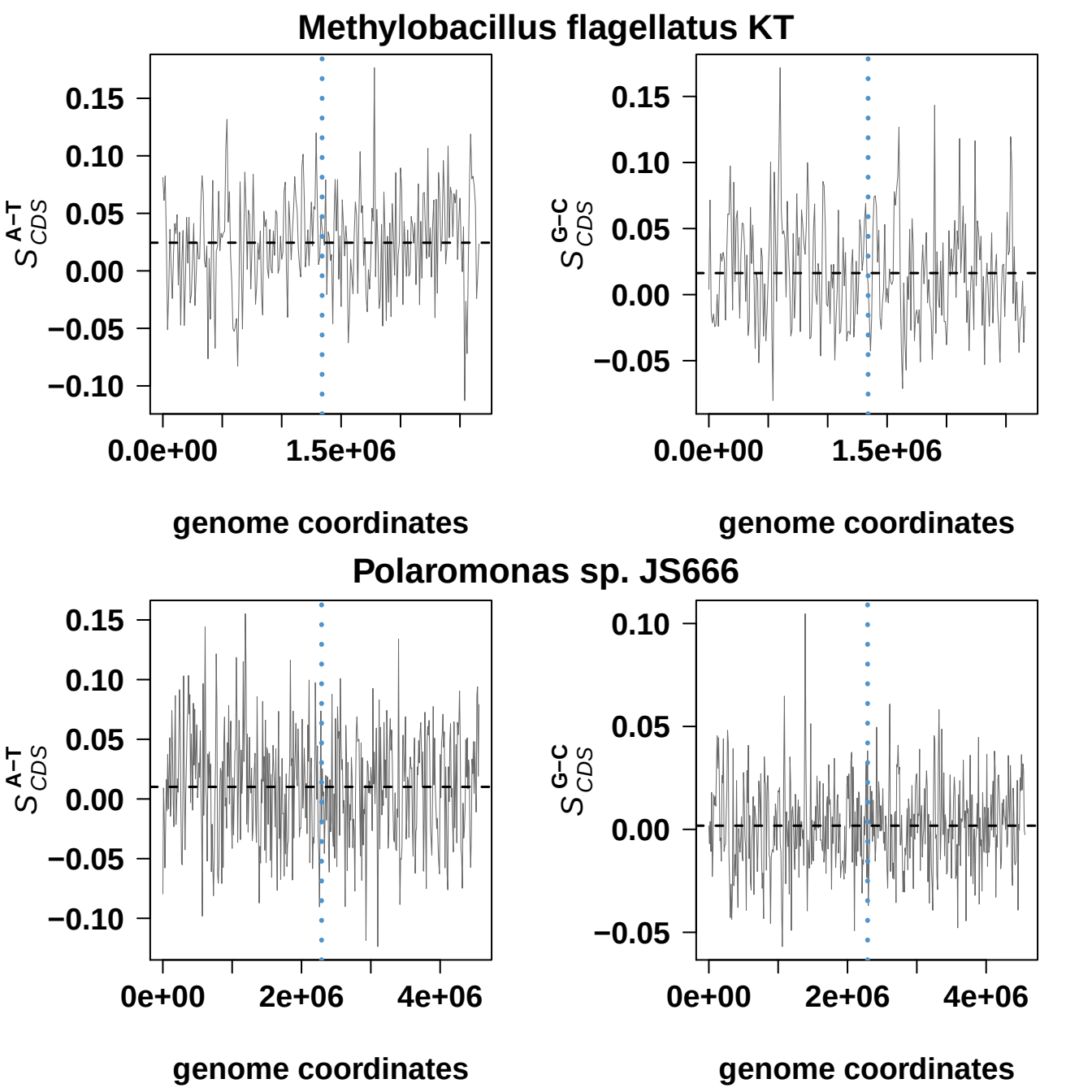

Thiobacillus denitrificans ATCC 25259
0.15
0.10
0.05
0.00
−0.05
−0.10
−0.15
S^{A-T}_{CDS}
0.0e+00
1.5e+06
genome coordinates
0.05
0.00
−0.05
S^{G-C}_{CDS}
0.0e+00
1.5e+06
genome coordinates
Burkholderia pseudomallei 1710b
0.15
0.10
0.05
0.00
−0.05
−0.10
S^{A-T}_{CDS}
0.0e+00
1.5e+06
3.0e+06
genome coordinates
0.10
0.05
0.00
−0.05
S^{G-C}_{CDS}
0.0e+00
1.5e+06
3.0e+06
genome coordinates

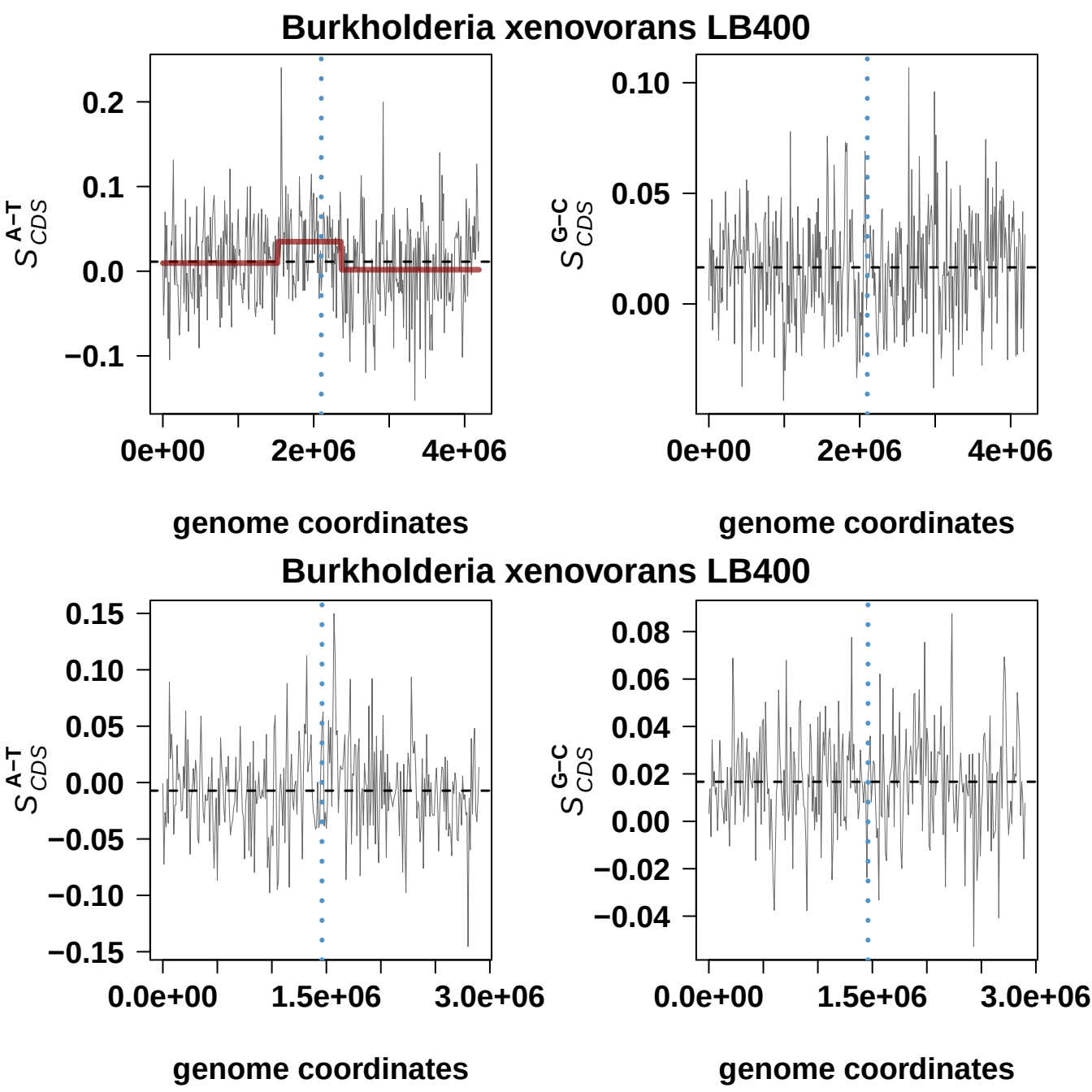

Burkholderia pseudomallei 1710b
S^{A-T}_{CDS}
0.10
0.05
0.00
−0.05
−0.10
−0.15
0.0e+00
1.5e+06
genome coordinates
S^{G-C}_{CDS}
0.10
0.05
0.00
−0.05
0.0e+00
1.5e+06
genome coordinates
Burkholderia lata
S^{A-T}_{CDS}
0.10
0.05
0.00
−0.05
−0.10
0.0e+00
6.0e+05
1.2e+06
genome coordinates
S^{G-C}_{CDS}
0.08
0.06
0.04
0.02
0.00
−0.02
−0.04
0.0e+00
6.0e+05
1.2e+06
genome coordinates

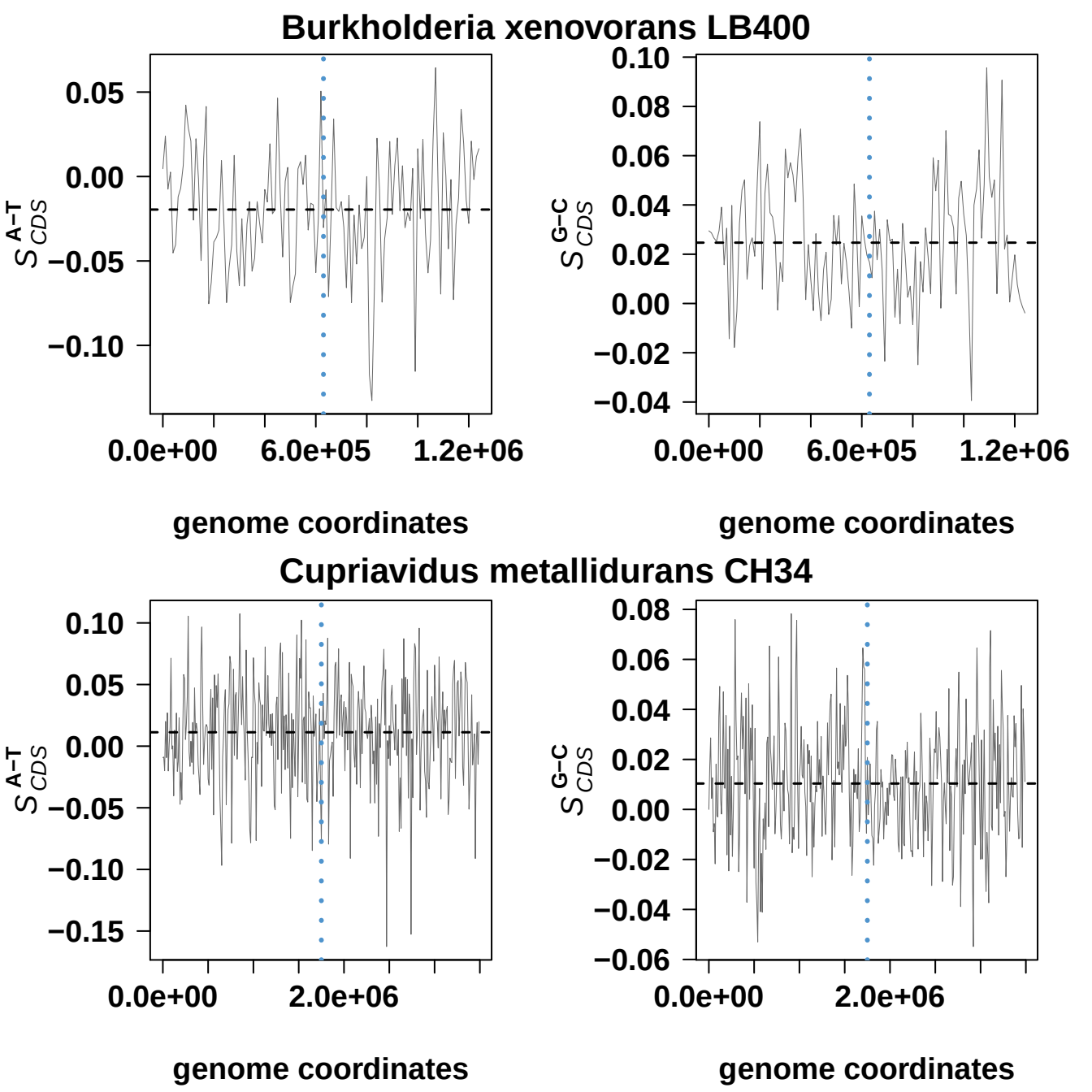

Burkholderia lata
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
−0.05
−0.10
0.0e+00
1.5e+06
3.0e+06
genome coordinates
S^{G-C}_{CDS}
0.10
0.05
0.00
−0.05
0.0e+00
1.5e+06
3.0e+06
genome coordinates
Burkholderia lata
S^{A-T}_{CDS}
0.10
0.05
0.00
−0.05
−0.10
−0.15
0.0e+00
1.5e+06
3.0e+06
genome coordinates
S^{G-C}_{CDS}
0.10
0.05
0.00
−0.05
−0.10
0.0e+00
1.5e+06
3.0e+06
genome coordinates

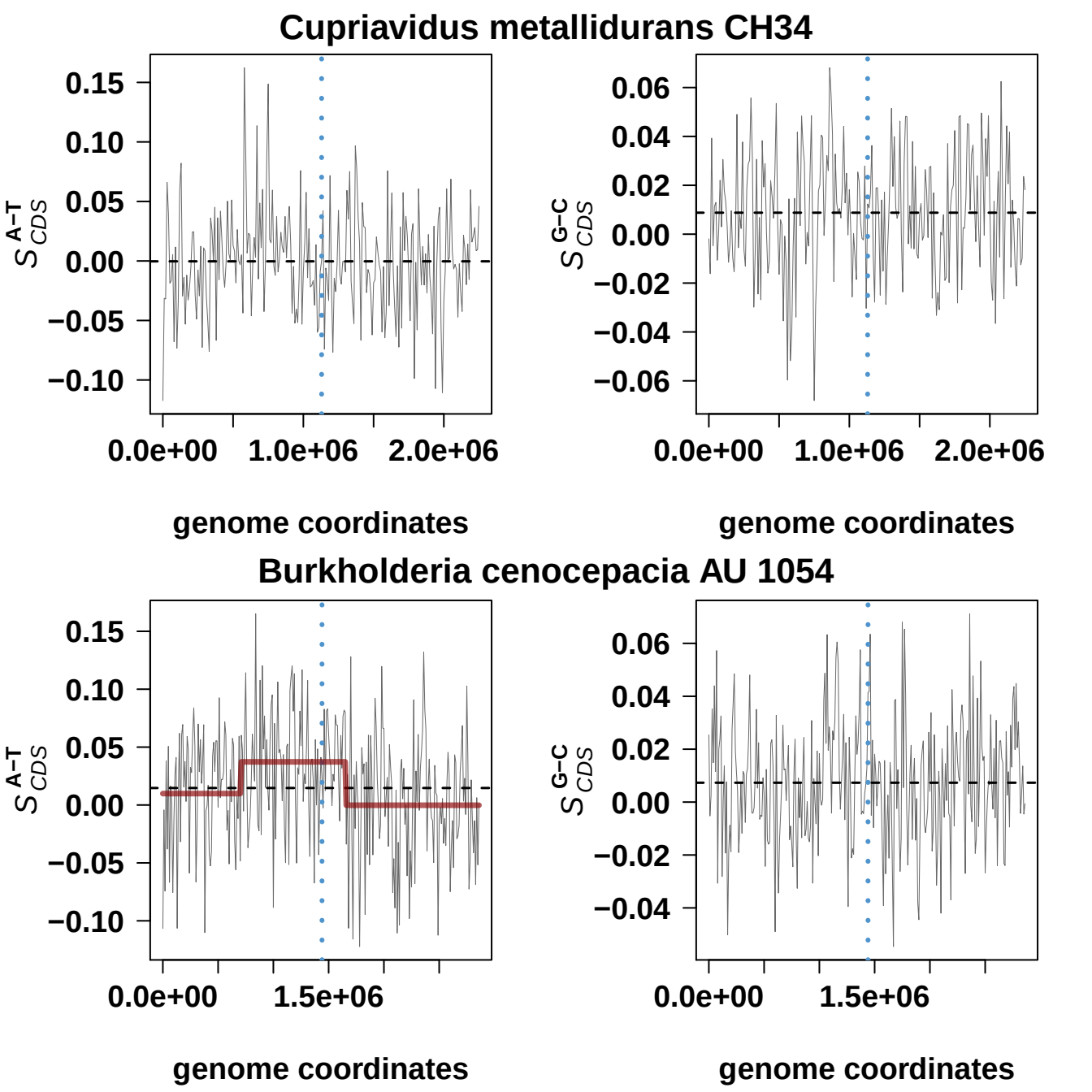

Nitrosospira multiformis ATCC 25196
S^{A-T}_{CDS}
0.10
0.05
0.00
−0.05
−0.10
−0.15
0.0e+00
1.5e+06
genome coordinates
S^{G-C}_{CDS}
0.10
0.05
0.00
0.0e+00
1.5e+06
genome coordinates
Burkholderia thailandensis E264
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
−0.05
−0.10
−0.15
0.0e+00
1.5e+06
genome coordinates
S^{G-C}_{CDS}
0.10
0.05
0.00
−0.05
−0.10
0.0e+00
1.5e+06
genome coordinates

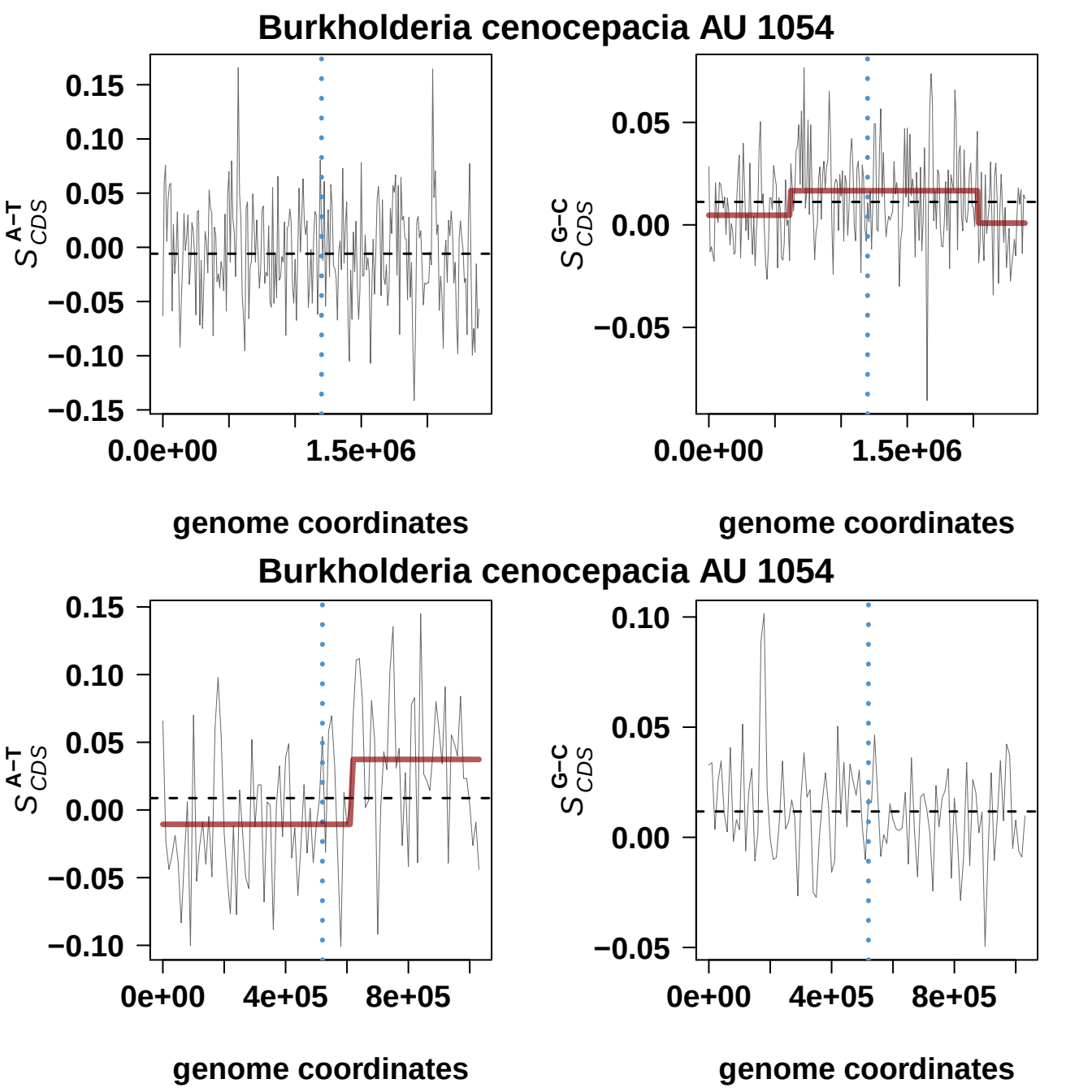

Burkholderia thailandensis E264
0.15
0.10
0.05
0.00
−0.05
−0.10
S^{A-T}_{CDS}
0.0e+00
1.5e+06
3.0e+06
genome coordinates
0.10
0.05
0.00
−0.05
S^{G-C}_{CDS}
0.0e+00
1.5e+06
3.0e+06
genome coordinates
Albidiferax ferrireducens T118
0.10
0.05
0.00
−0.05
−0.10
−0.15
−0.20
S^{A-T}_{CDS}
0e+00
2e+06
4e+06
genome coordinates
0.10
0.05
0.00
−0.05
S^{G-C}_{CDS}
0e+00
2e+06
4e+06
genome coordinates

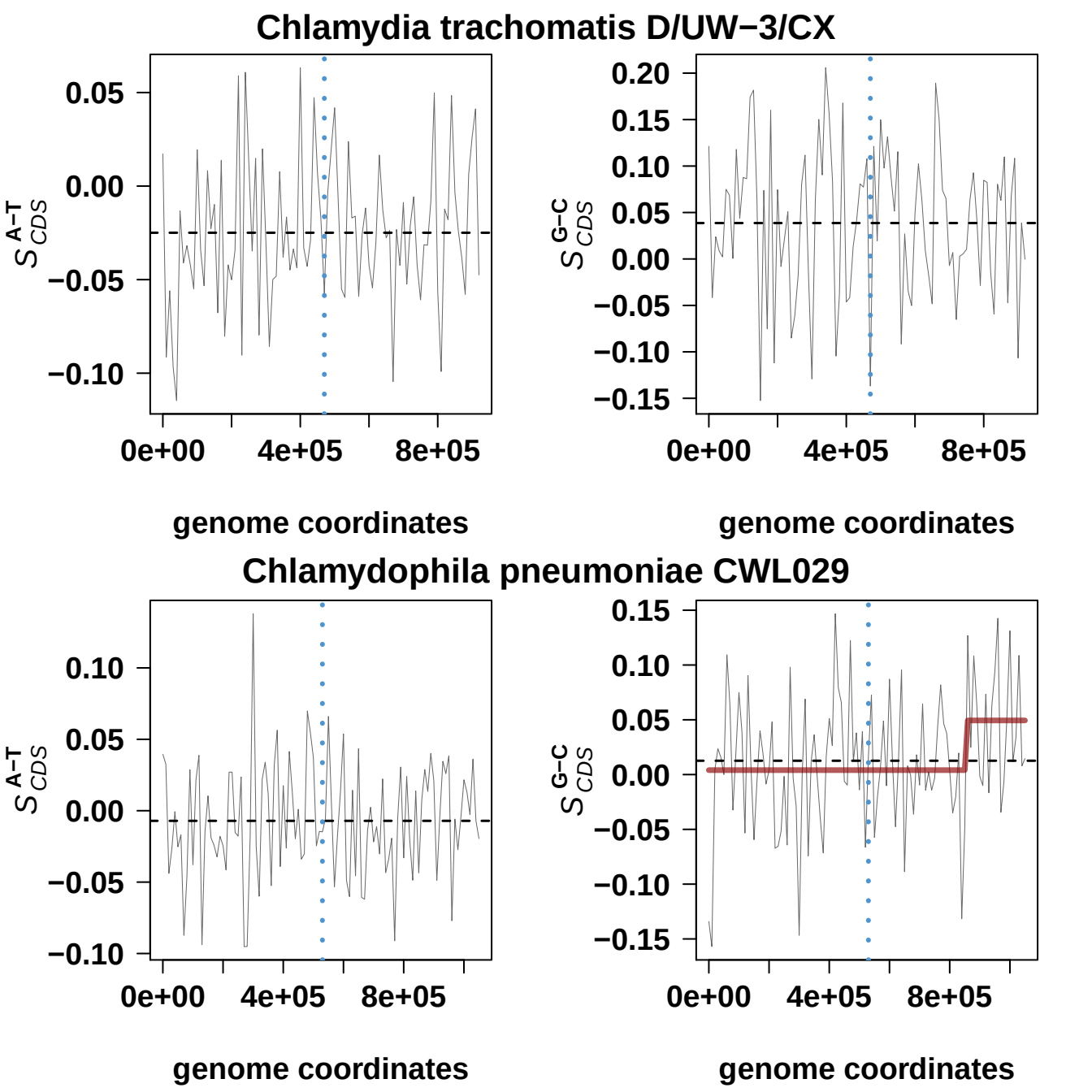

Methylobacillus flagellatus KT
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
−0.05
−0.10
0.0e+00
1.5e+06
genome coordinates
S^{G-C}_{CDS}
0.15
0.10
0.05
0.00
−0.05
0.0e+00
1.5e+06
genome coordinates
Polaromonas sp. JS666
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
−0.05
−0.10
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{CDS}
0.10
0.05
0.00
−0.05
0e+00
2e+06
4e+06
genome coordinates

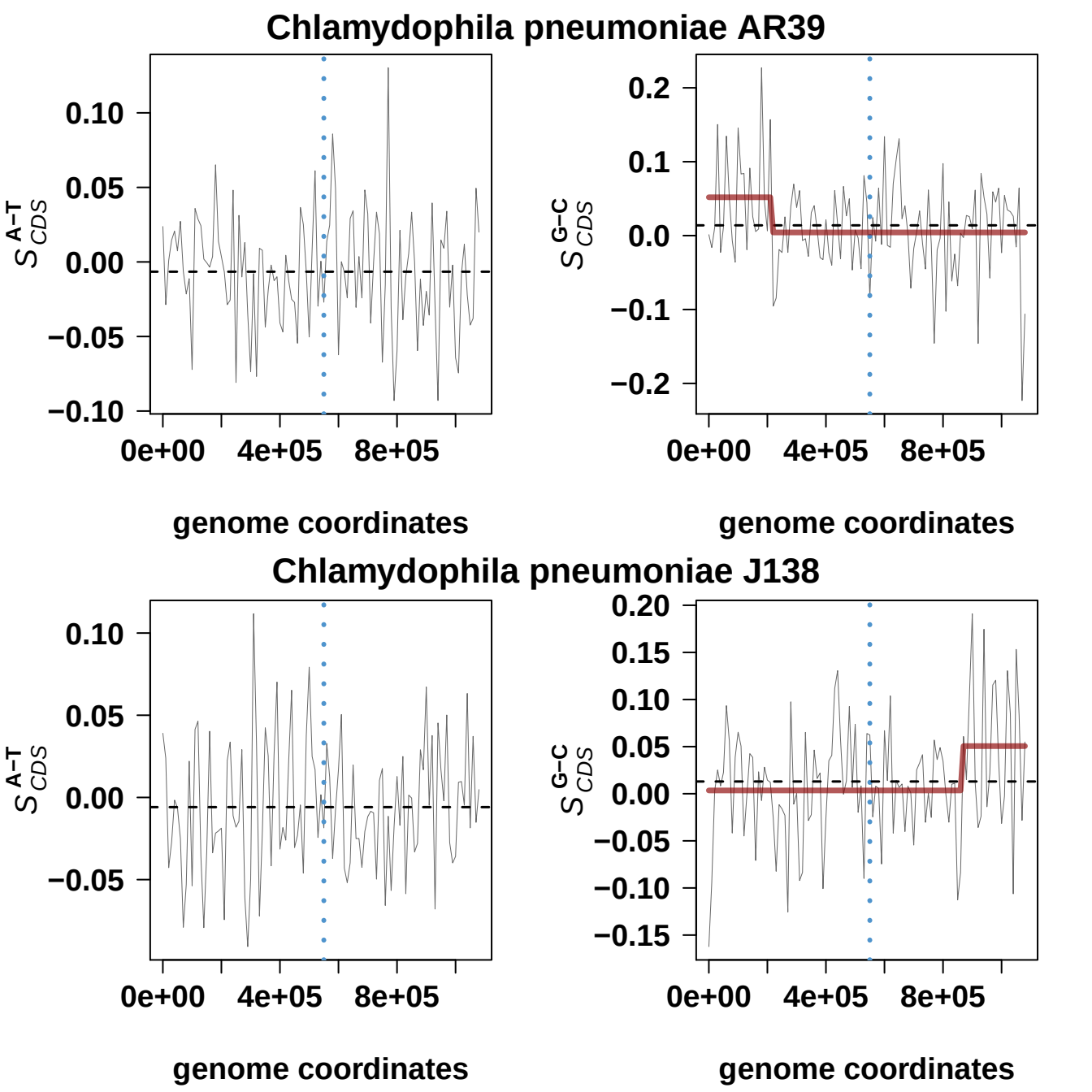

Burkholderia xenovorans LB400
S^{A-T}_{CDS}
0.2
0.1
0.0
−0.1
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{CDS}
0.10
0.05
0.00
0e+00
2e+06
4e+06
genome coordinates
Burkholderia xenovorans LB400
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
−0.05
−0.10
−0.15
0.0e+00
1.5e+06
3.0e+06
genome coordinates
S^{G-C}_{CDS}
0.08
0.06
0.04
0.02
0.00
−0.02
−0.04
0.0e+00
1.5e+06
3.0e+06
genome coordinates

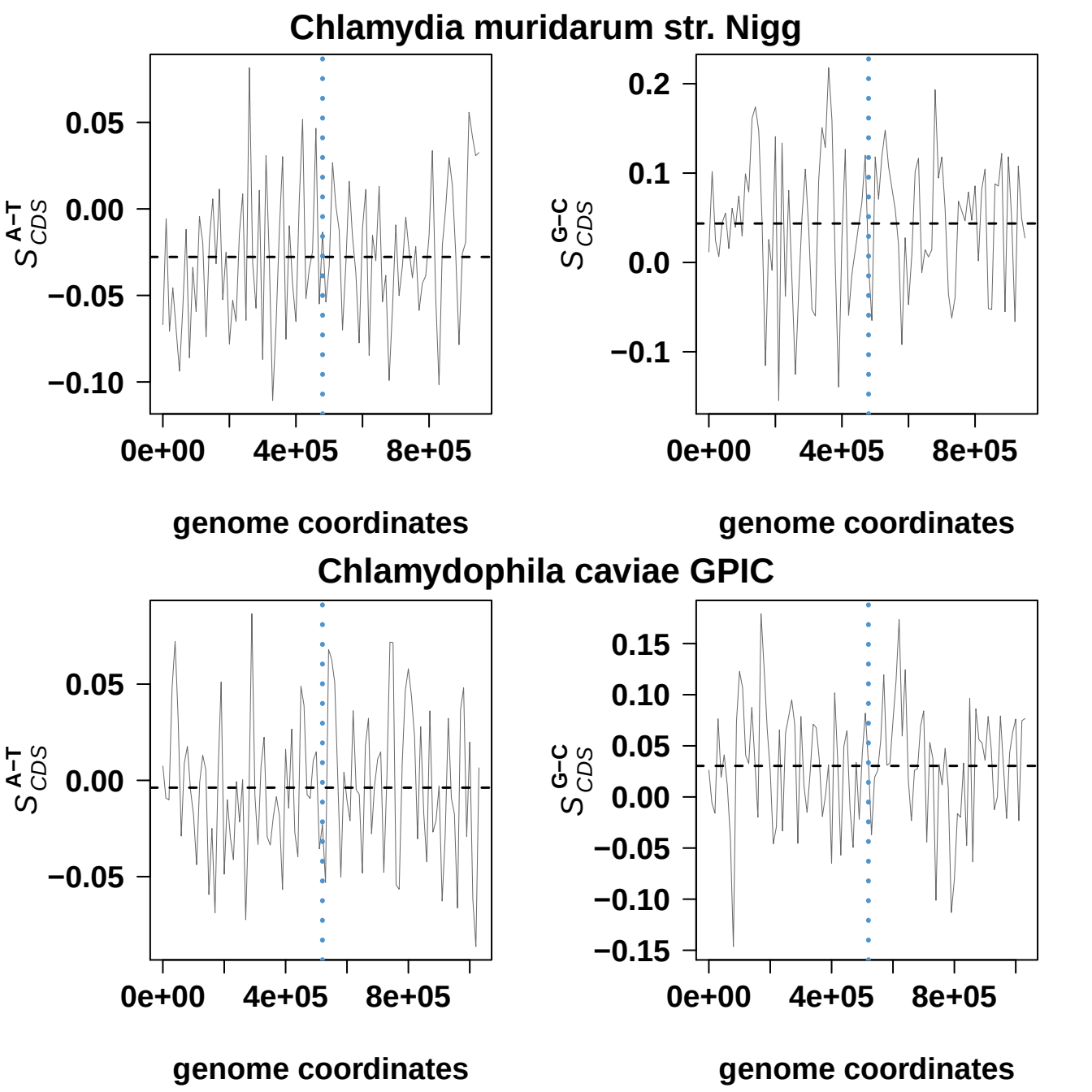

Burkholderia xenovorans LB400
S^{A-T}_{CDS}
0.05
0.00
−0.05
−0.10
0.0e+00
6.0e+05
1.2e+06
genome coordinates
S^{G-C}_{CDS}
0.10
0.08
0.06
0.04
0.02
0.00
−0.02
−0.04
0.0e+00
6.0e+05
1.2e+06
genome coordinates
Cupriavidus metallidurans CH34
S^{A-T}_{CDS}
0.10
0.05
0.00
−0.05
−0.10
−0.15
0.0e+00
2.0e+06
genome coordinates
S^{G-C}_{CDS}
0.08
0.06
0.04
0.02
0.00
−0.02
−0.04
−0.06
0.0e+00
2.0e+06
genome coordinates

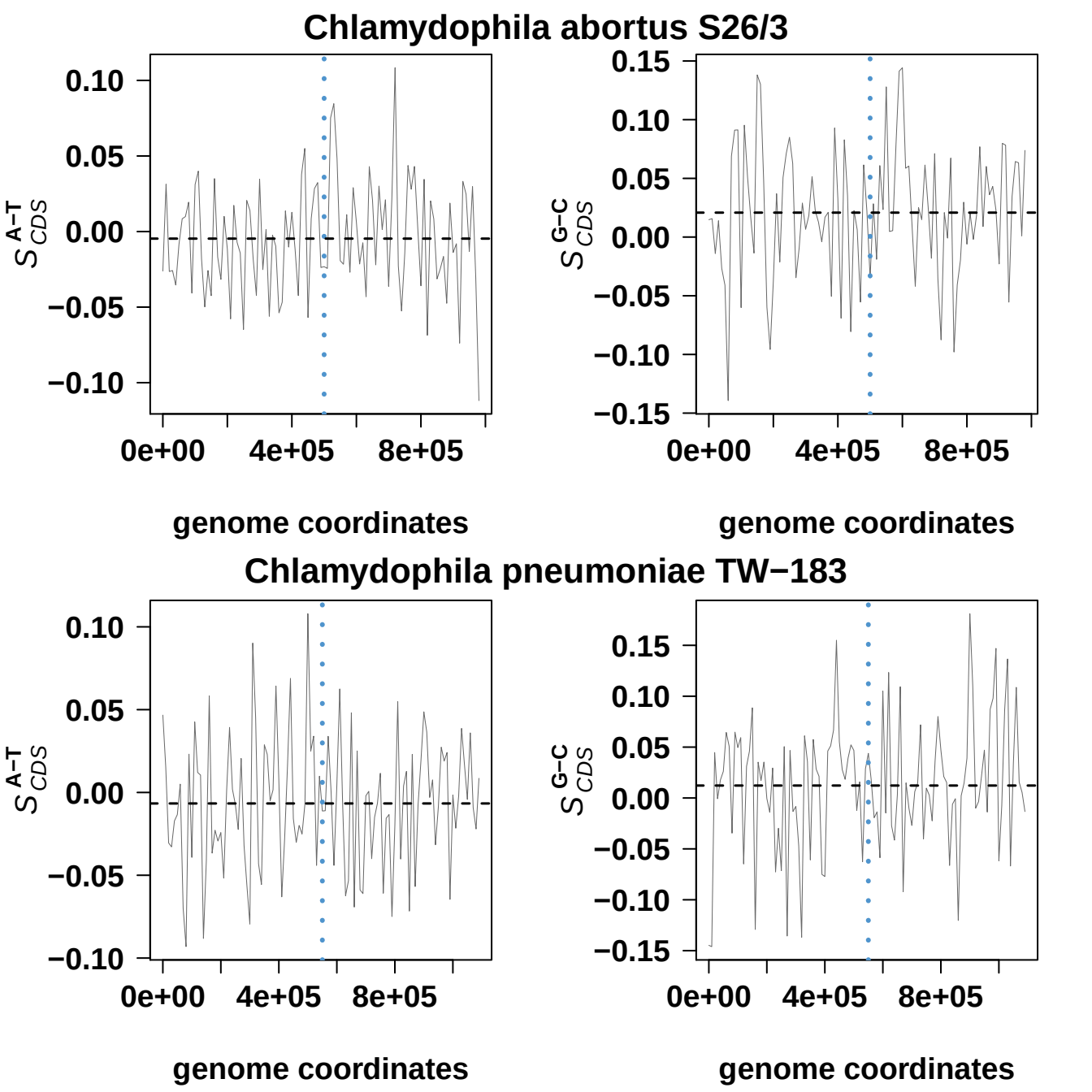

Cupriavidus metallidurans CH34
0.15
0.10
0.05
0.00
−0.05
−0.10
S^{A-T}_{CDS}
0.0e+00
1.0e+06
2.0e+06
genome coordinates
0.06
0.04
0.02
0.00
−0.02
−0.04
−0.06
S^{G-C}_{CDS}
0.0e+00
1.0e+06
2.0e+06
genome coordinates
Burkholderia cenocepacia AU 1054
0.15
0.10
0.05
0.00
−0.05
−0.10
S^{A-T}_{CDS}
0.0e+00
1.5e+06
genome coordinates
0.06
0.04
0.02
0.00
−0.02
−0.04
S^{G-C}_{CDS}
0.0e+00
1.5e+06
genome coordinates

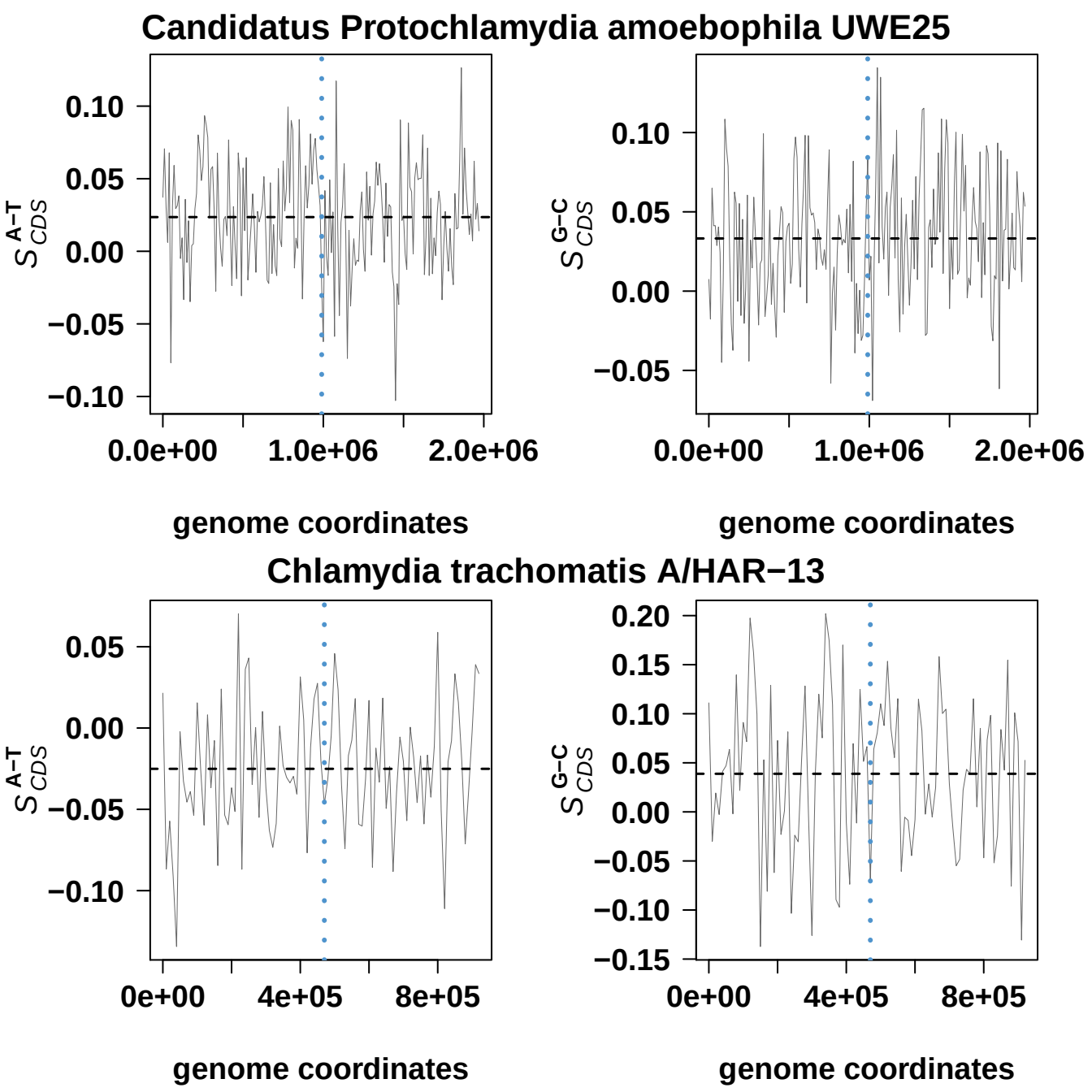

Burkholderia cenocepacia AU 1054
0.15
0.10
0.05
0.00
−0.05
−0.10
−0.15
S^{A-T}_{CDS}
0.0e+00
1.5e+06
genome coordinates
0.05
0.00
−0.05
S^{G-C}_{CDS}
0.0e+00
1.5e+06
genome coordinates
Burkholderia cenocepacia AU 1054
0.15
0.10
0.05
0.00
−0.05
−0.10
S^{A-T}_{CDS}
0e+00
4e+05
8e+05
genome coordinates
0.10
0.05
0.00
−0.05
S^{G-C}_{CDS}
0e+00
4e+05
8e+05
genome coordinates

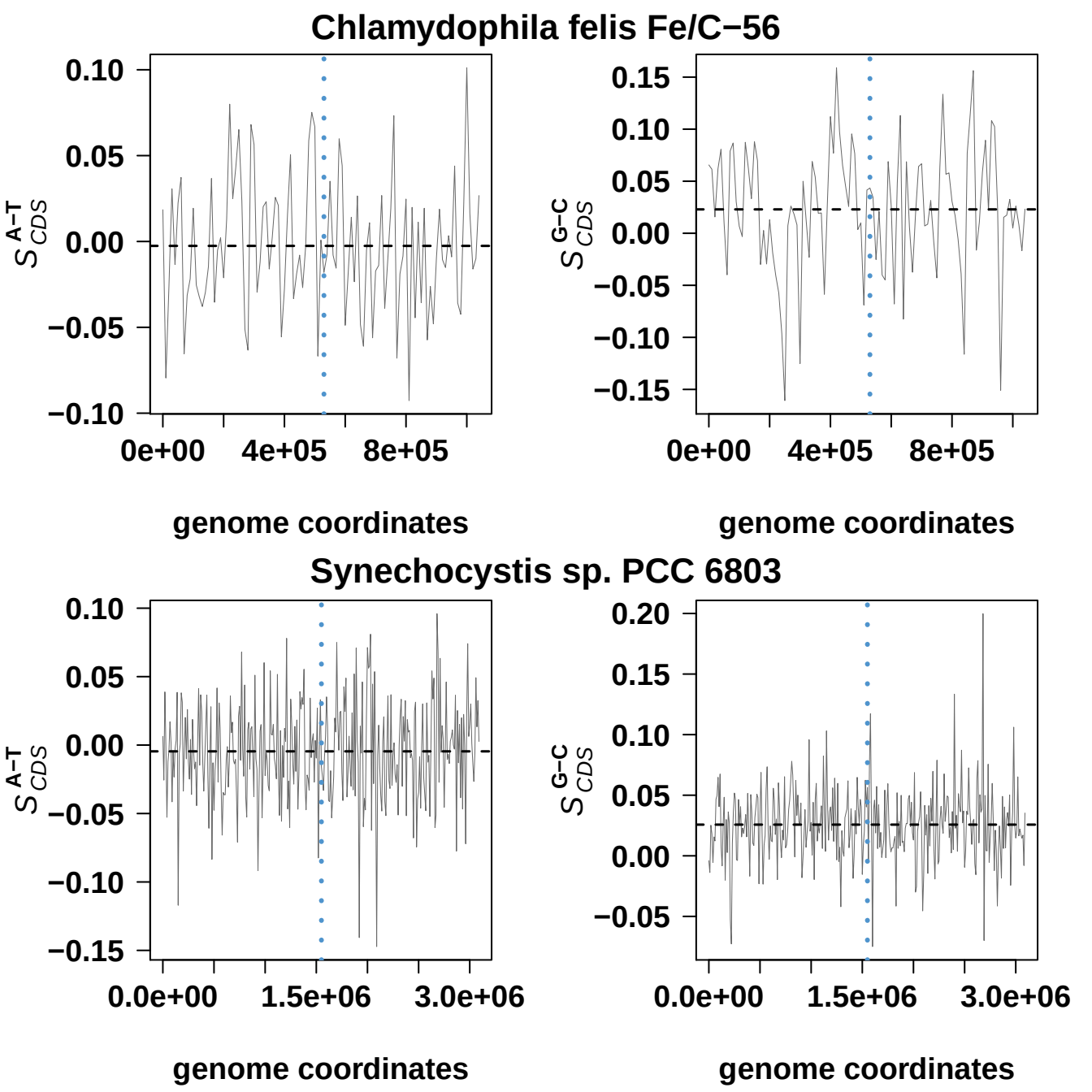

Chlamydia trachomatis D/UW−3/CX
S^{A-T}_{CDS}
0.05
0.00
−0.05
−0.10
0e+00
4e+05
8e+05
genome coordinates
S^{G-C}_{CDS}
0.20
0.15
0.10
0.05
0.00
−0.05
−0.10
−0.15
0e+00
4e+05
8e+05
genome coordinates
Chlamydophila pneumoniae CWL029
S^{A-T}_{CDS}
0.10
0.05
0.00
−0.05
−0.10
0e+00
4e+05
8e+05
genome coordinates
S^{G-C}_{CDS}
0.15
0.10
0.05
0.00
−0.05
−0.10
−0.15
0e+00
4e+05
8e+05
genome coordinates

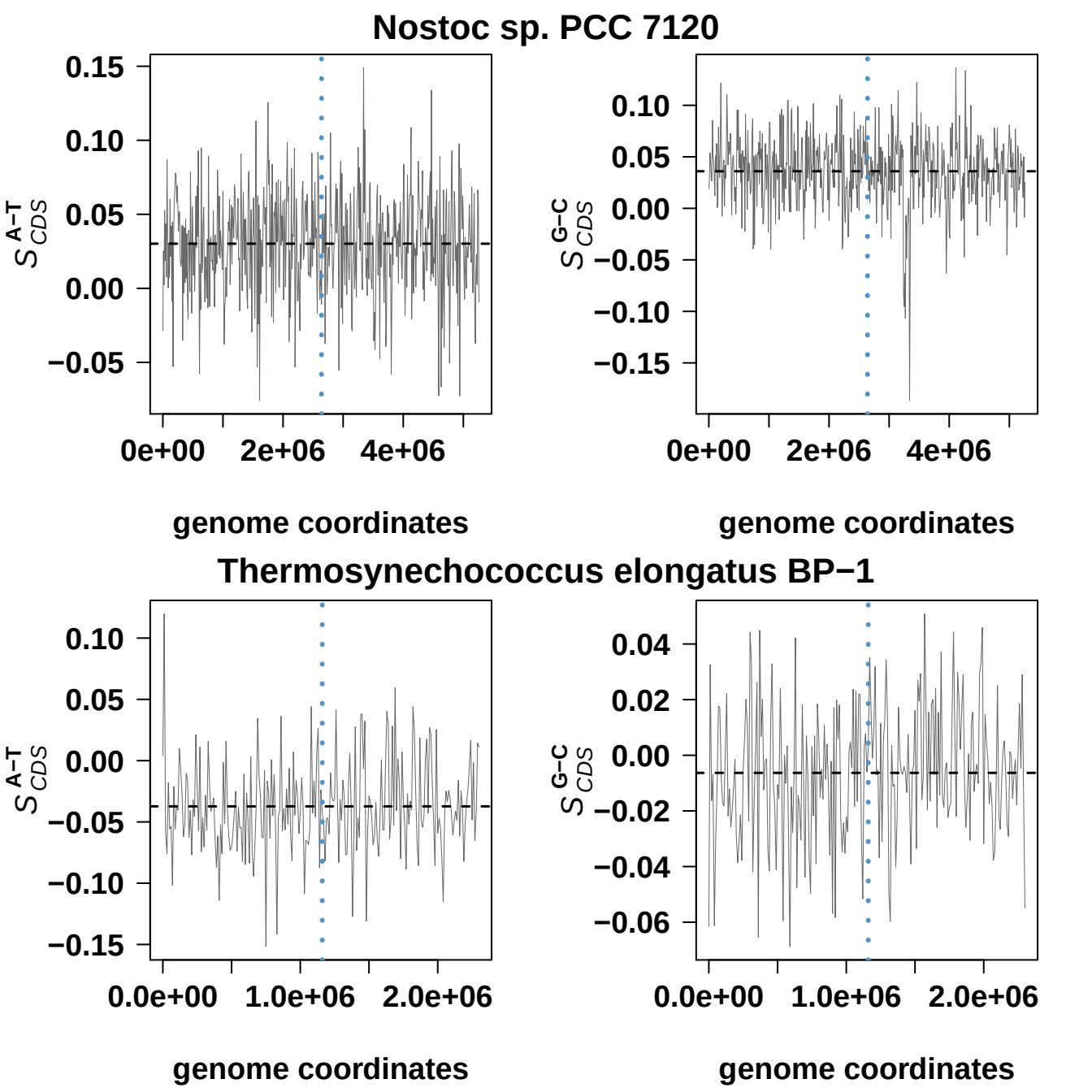

Chlamydophila pneumoniae AR39
S^{A-T}_{CDS}
0.10
0.05
0.00
−0.05
−0.10
0e+00
4e+05
8e+05
genome coordinates
S^{G-C}_{CDS}
0.2
0.1
0.0
−0.1
−0.2
0e+00
4e+05
8e+05
genome coordinates
Chlamydophila pneumoniae J138
S^{A-T}_{CDS}
0.10
0.05
0.00
−0.05
0e+00
4e+05
8e+05
genome coordinates
S^{G-C}_{CDS}
0.20
0.15
0.10
0.05
0.00
−0.05
−0.10
−0.15
0e+00
4e+05
8e+05
genome coordinates

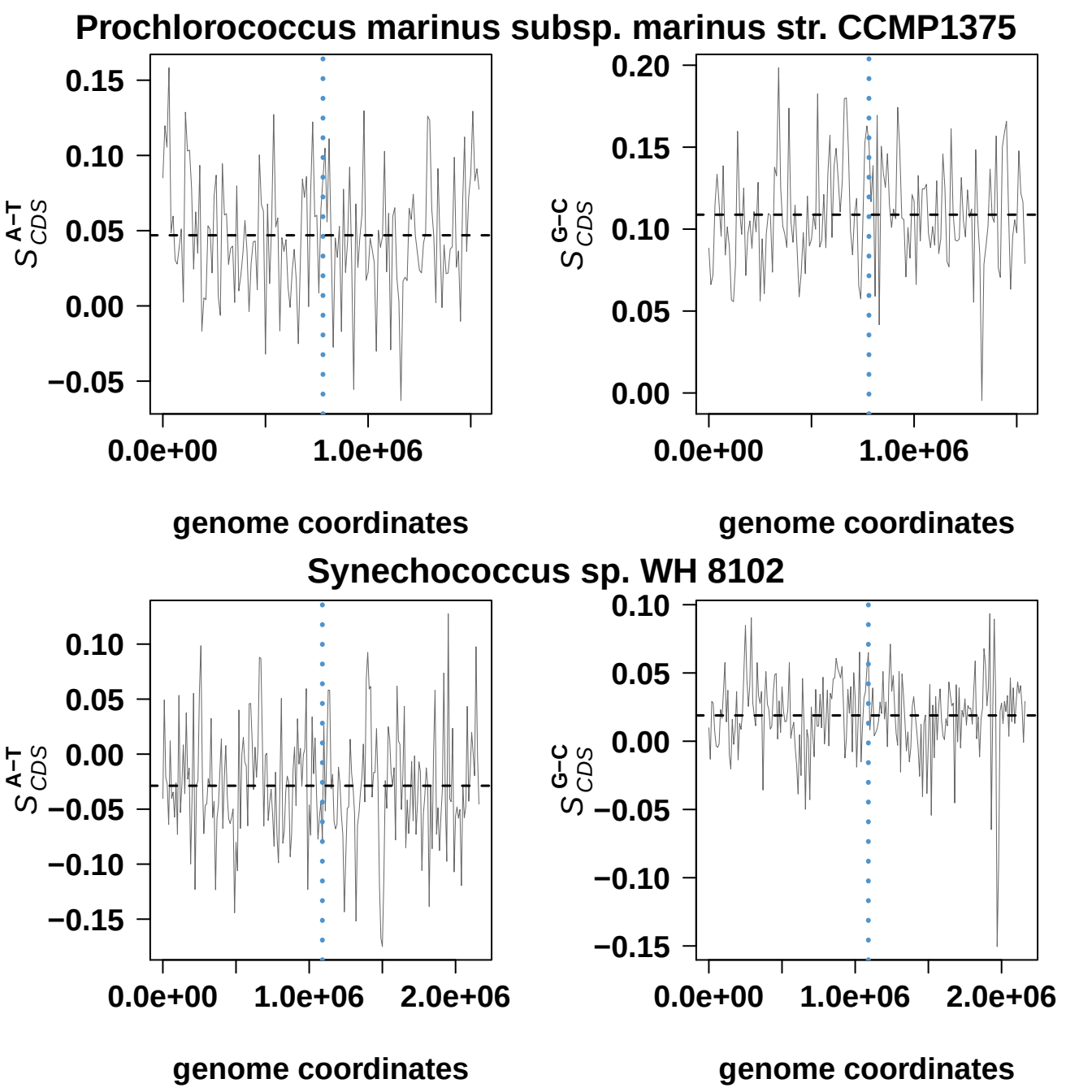

Chlamydia muridarum str. Nigg
S^{A-T}_{CDS}
0.05
0.00
−0.05
−0.10
0e+00
4e+05
8e+05
genome coordinates
S^{G-C}_{CDS}
0.2
0.1
0.0
−0.1
0e+00
4e+05
8e+05
genome coordinates
Chlamydophila caviae GPIC
S^{A-T}_{CDS}
0.05
0.00
−0.05
0e+00
4e+05
8e+05
genome coordinates
S^{G-C}_{CDS}
0.15
0.10
0.05
0.00
−0.05
−0.10
−0.15
0e+00
4e+05
8e+05
genome coordinates

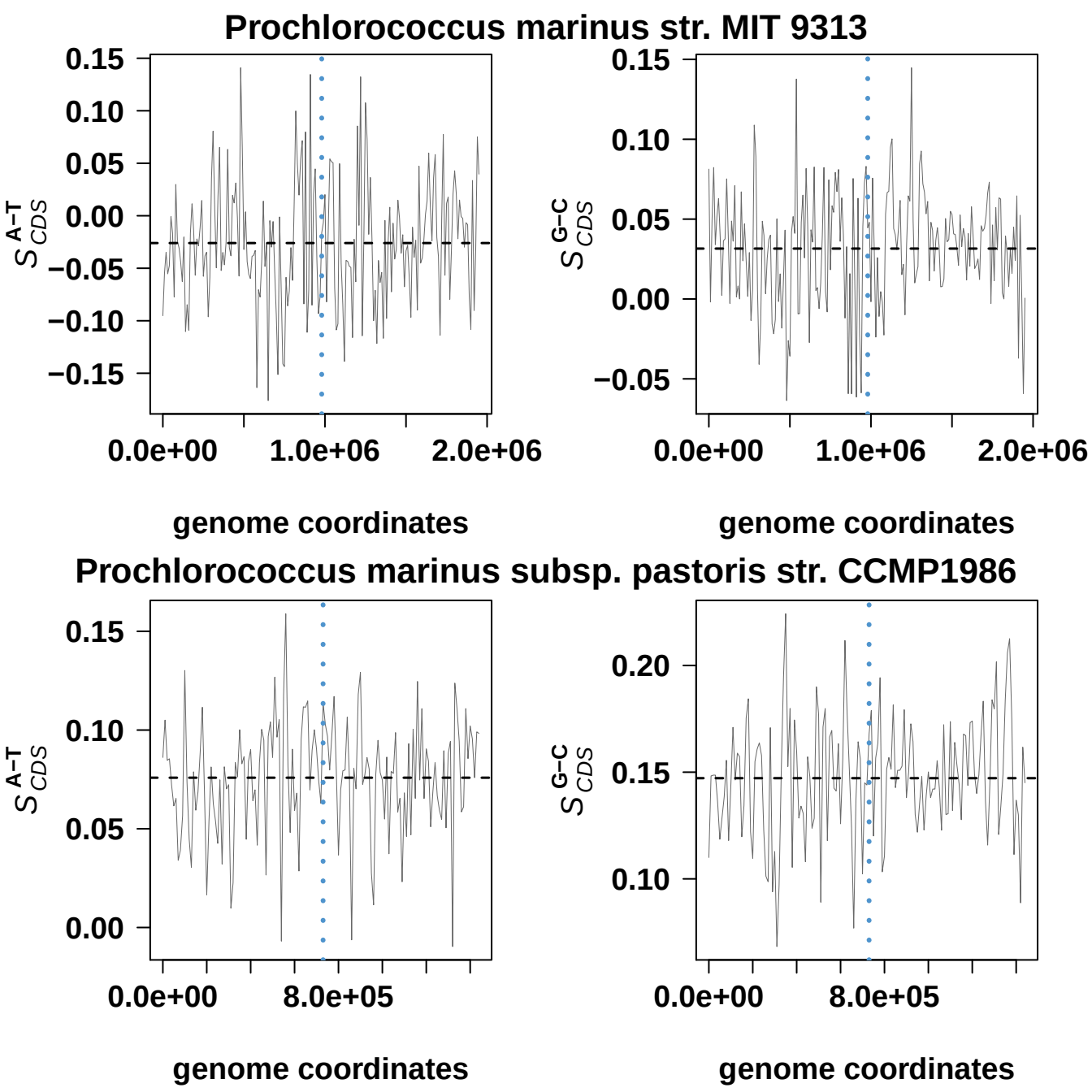

Chlamydophila abortus S26/3
S^{A-T}_{CDS}
0.10
0.05
0.00
−0.05
−0.10
0e+00
4e+05
8e+05
genome coordinates
S^{G-C}_{CDS}
0.15
0.10
0.05
0.00
−0.05
−0.10
−0.15
0e+00
4e+05
8e+05
genome coordinates
Chlamydophila pneumoniae TW−183
S^{A-T}_{CDS}
0.10
0.05
0.00
−0.05
−0.10
0e+00
4e+05
8e+05
genome coordinates
S^{G-C}_{CDS}
0.15
0.10
0.05
0.00
−0.05
−0.10
−0.15
0e+00
4e+05
8e+05
genome coordinates

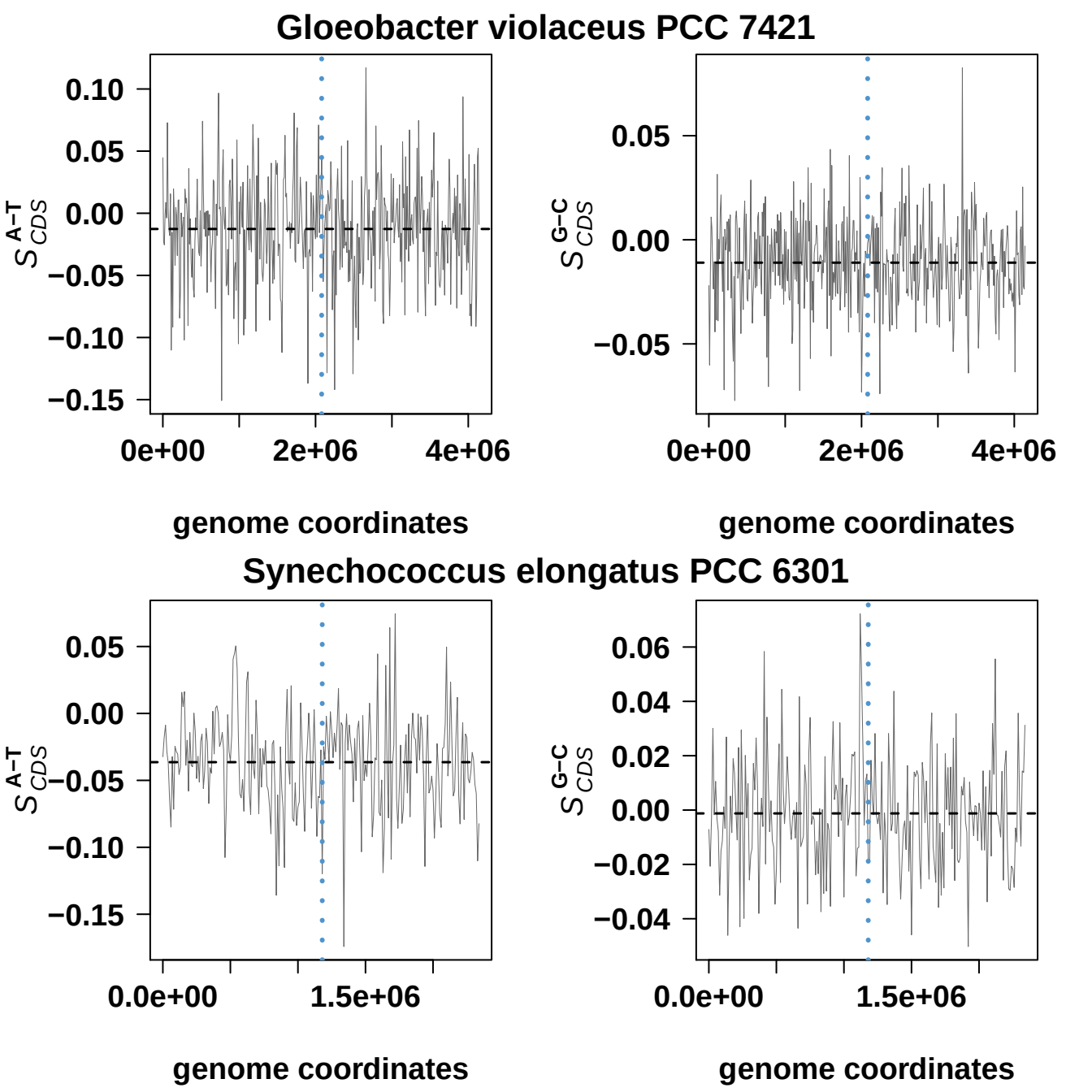

Candidatus Protochlamydia amoebophila UWE25
S^{A-T}_{CDS}
0.10
0.05
0.00
−0.05
−0.10
0.0e+00
1.0e+06
2.0e+06
genome coordinates
S^{G-C}_{CDS}
0.10
0.05
0.00
−0.05
0.0e+00
1.0e+06
2.0e+06
genome coordinates
Chlamydia trachomatis A/HAR−13
S^{A-T}_{CDS}
0.05
0.00
−0.05
−0.10
0e+00
4e+05
8e+05
genome coordinates
S^{G-C}_{CDS}
0.20
0.15
0.10
0.05
0.00
−0.05
−0.10
−0.15
0e+00
4e+05
8e+05
genome coordinates

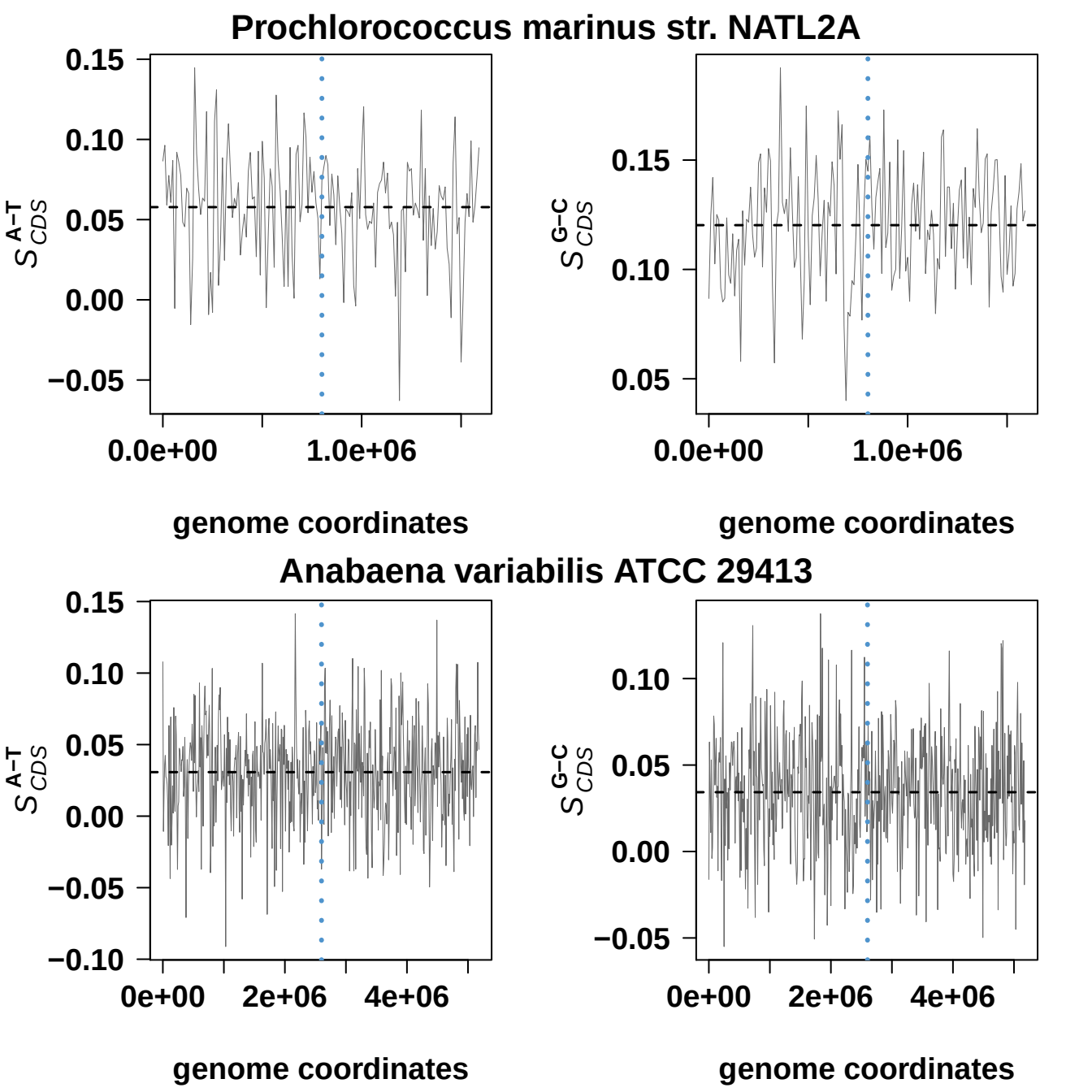

Chlamydophila felis Fe/C−56
0.10
0.05
0.00
−0.05
−0.10
S^{A-T}_{CDS}
0e+00
4e+05
8e+05
genome coordinates
0.15
0.10
0.05
0.00
−0.05
−0.10
−0.15
S^{G-C}_{CDS}
0e+00
4e+05
8e+05
genome coordinates
Synechocystis sp. PCC 6803
0.10
0.05
0.00
−0.05
−0.10
−0.15
S^{A-T}_{CDS}
0.0e+00
1.5e+06
3.0e+06
genome coordinates
0.20
0.15
0.10
0.05
0.00
−0.05
S^{G-C}_{CDS}
0.0e+00
1.5e+06
3.0e+06
genome coordinates

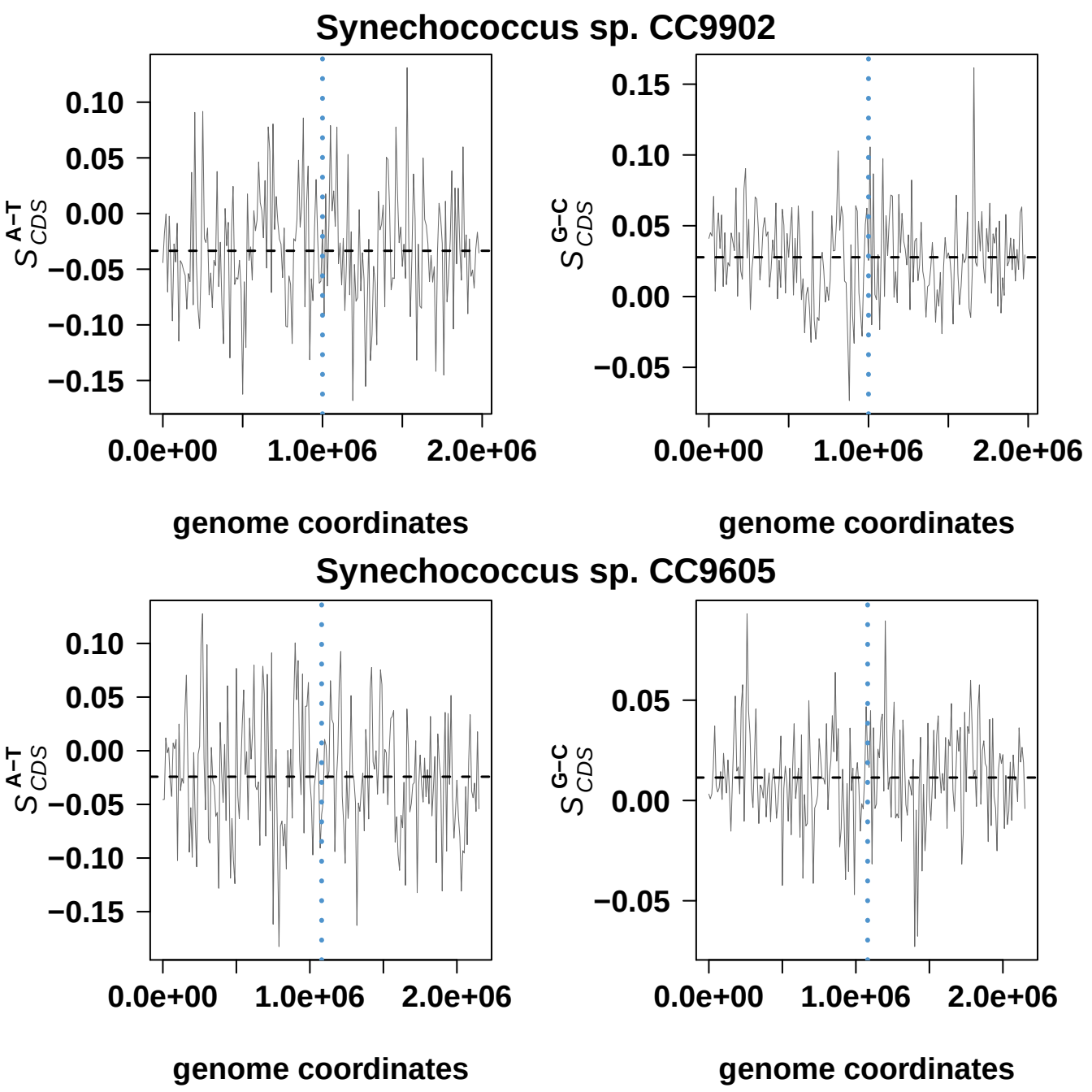

Nostoc sp. PCC 7120
0.15
0.10
0.05
0.00
−0.05
S^{A-T}_{CDS}
0e+00
2e+06
4e+06
genome coordinates
0.10
0.05
0.00
−0.05
−0.10
−0.15
S^{G-C}_{CDS}
0e+00
2e+06
4e+06
genome coordinates
Thermosynechococcus elongatus BP−1
0.10
0.05
0.00
−0.05
−0.10
−0.15
S^{A-T}_{CDS}
0.0e+00
1.0e+06
2.0e+06
genome coordinates
0.04
0.02
0.00
−0.02
−0.04
−0.06
S^{G-C}_{CDS}
0.0e+00
1.0e+06
2.0e+06
genome coordinates

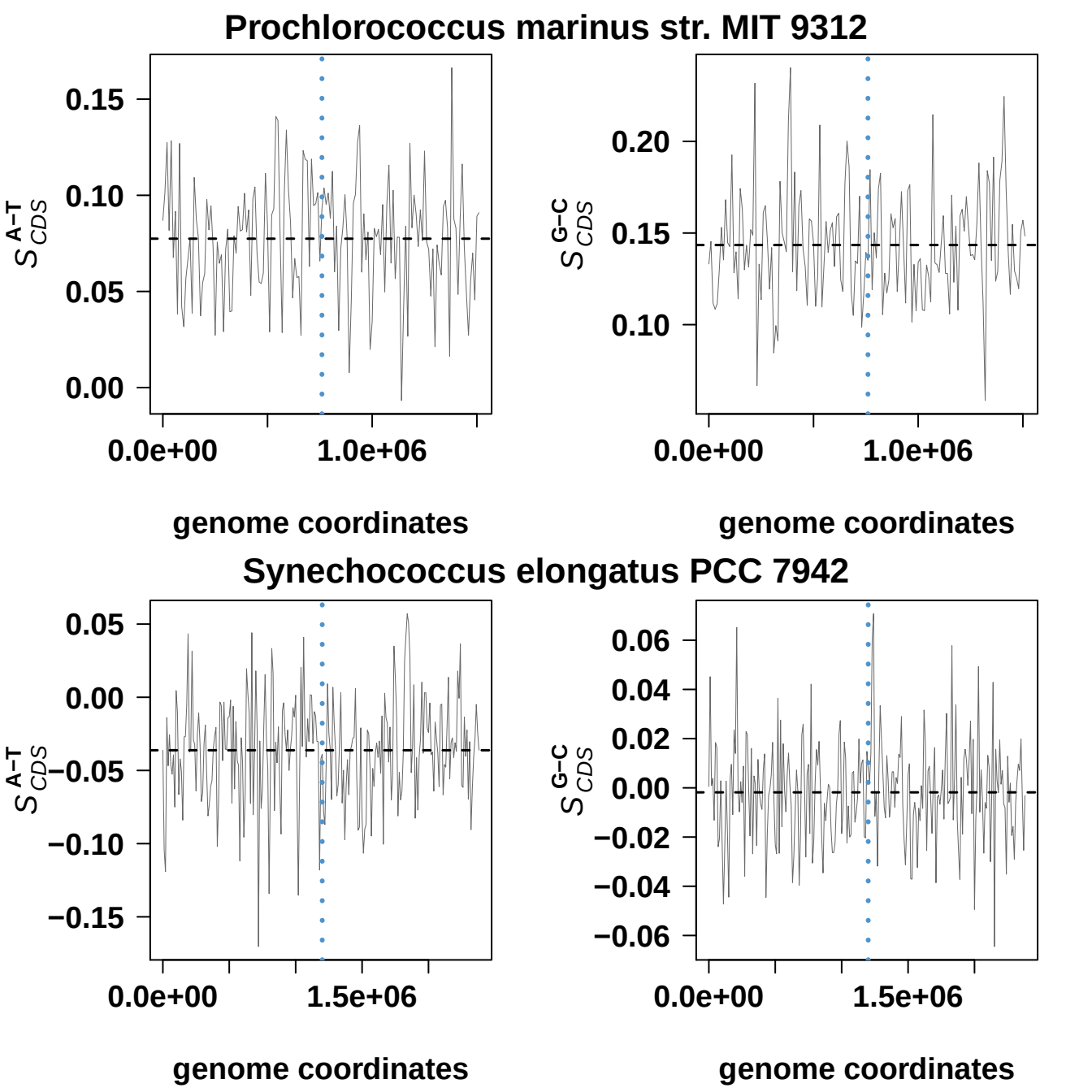

Prochlorococcus marinus subsp. marinus str. CCMP1375
0.15
0.10
0.05
0.00
−0.05
S^{A-T}_{CDS}
0.0e+00
1.0e+06
genome coordinates
0.20
0.15
0.10
0.05
0.00
S^{G-C}_{CDS}
0.0e+00
1.0e+06
genome coordinates
Synechococcus sp. WH 8102
0.10
0.05
0.00
−0.05
−0.10
−0.15
S^{A-T}_{CDS}
0.0e+00
1.0e+06
2.0e+06
genome coordinates
0.10
0.05
0.00
−0.05
−0.10
−0.15
S^{G-C}_{CDS}
0.0e+00
1.0e+06
2.0e+06
genome coordinates

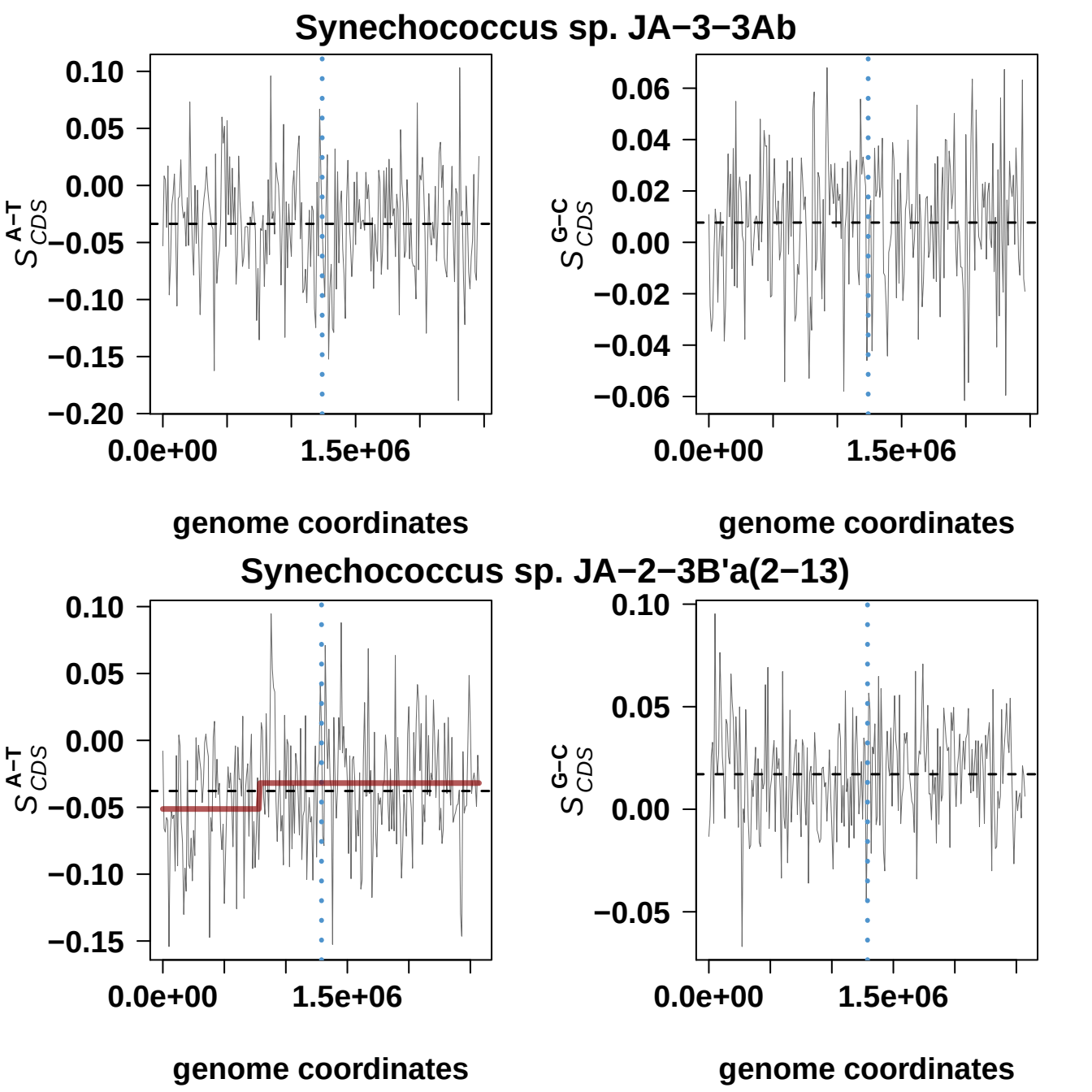

Prochlorococcus marinus str. MIT 9313
0.15
0.10
0.05
0.00
−0.05
−0.10
−0.15
S^{A-T}_{CDS}
0.0e+00
1.0e+06
2.0e+06
genome coordinates
0.15
0.10
0.05
0.00
−0.05
S^{G-C}_{CDS}
0.0e+00
1.0e+06
2.0e+06
genome coordinates
Prochlorococcus marinus subsp. pastoris str. CCMP1986
0.15
0.10
0.05
0.00
S^{A-T}_{CDS}
0.0e+00
8.0e+05
genome coordinates
0.20
0.15
0.10
S^{G-C}_{CDS}
0.0e+00
8.0e+05
genome coordinates


Gloeobacter violaceus PCC 7421
S^{A-T}_{CDS}
0.10
0.05
0.00
−0.05
−0.10
−0.15
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{CDS}
0.05
0.00
−0.05
0e+00
2e+06
4e+06
genome coordinates
Synechococcus elongatus PCC 6301
S^{A-T}_{CDS}
0.05
0.00
−0.05
−0.10
−0.15
0.0e+00
1.5e+06
genome coordinates
S^{G-C}_{CDS}
0.06
0.04
0.02
0.00
−0.02
−0.04
0.0e+00
1.5e+06
genome coordinates

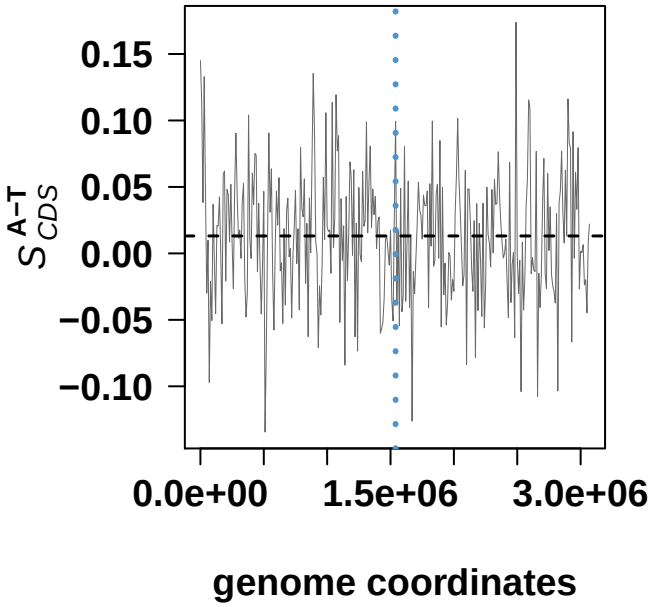

Prochlorococcus marinus str. NATL2A
0.15
0.10
0.05
0.00
−0.05
S^{A-T}_{CDS}
0.0e+00
1.0e+06
genome coordinates
0.15
0.10
0.05
S^{G-C}_{CDS}
0.0e+00
1.0e+06
genome coordinates
Anabaena variabilis ATCC 29413
0.15
0.10
0.05
0.00
−0.05
−0.10
S^{A-T}_{CDS}
0e+00
2e+06
4e+06
genome coordinates
0.10
0.05
0.00
−0.05
S^{G-C}_{CDS}
0e+00
2e+06
4e+06
genome coordinates

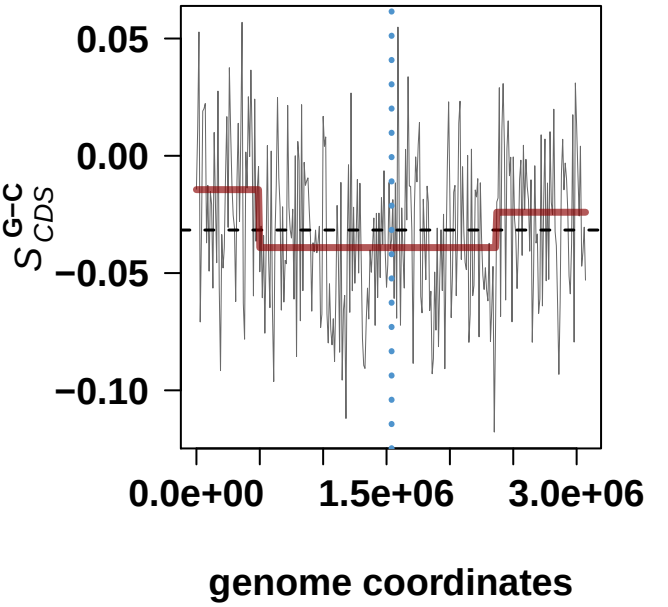

Synechococcus sp. CC9902
0.10
0.05
0.00
−0.05
−0.10
−0.15
S^{A-T}_{CDS}
0.0e+00
1.0e+06
2.0e+06
genome coordinates
0.15
0.10
0.05
0.00
−0.05
S^{G-C}_{CDS}
0.0e+00
1.0e+06
2.0e+06
genome coordinates
Synechococcus sp. CC9605
0.10
0.05
0.00
−0.05
−0.10
−0.15
S^{A-T}_{CDS}
0.0e+00
1.0e+06
2.0e+06
genome coordinates
0.05
0.00
−0.05
S^{G-C}_{CDS}
0.0e+00
1.0e+06
2.0e+06
genome coordinates


Prochlorococcus marinus str. MIT 9312
0.15
0.10
0.05
0.00
S^{A-T}_{CDS}
0.0e+00
1.0e+06
genome coordinates
0.20
0.15
0.10
S^{G-C}_{CDS}
0.0e+00
1.0e+06
genome coordinates
Synechococcus elongatus PCC 7942
0.05
0.00
−0.05
−0.10
−0.15
S^{A-T}_{CDS}
0.0e+00
1.5e+06
genome coordinates
0.06
0.04
0.02
0.00
−0.02
−0.04
−0.06
S^{G-C}_{CDS}
0.0e+00
1.5e+06
genome coordinates

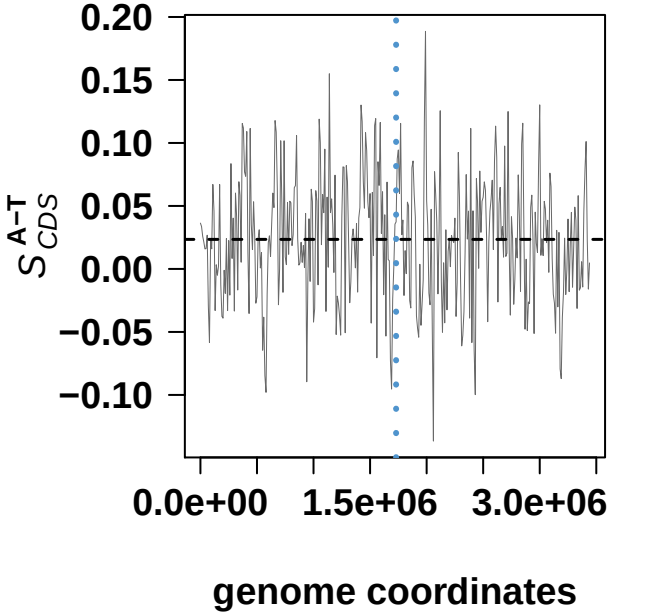

Synechococcus sp. JA−3−3Ab
0.10
0.05
0.00
−0.05
−0.10
−0.15
−0.20
S^{A-T}_{CDS}
0.0e+00
1.5e+06
genome coordinates
0.06
0.04
0.02
0.00
−0.02
−0.04
−0.06
S^{G-C}_{CDS}
0.0e+00
1.5e+06
genome coordinates
Synechococcus sp. JA−2−3B'a(2−13)
0.10
0.05
0.00
−0.05
−0.10
−0.15
S^{A-T}_{CDS}
0.0e+00
1.5e+06
genome coordinates
0.10
0.05
0.00
−0.05
S^{G-C}_{CDS}
0.0e+00
1.5e+06
genome coordinates

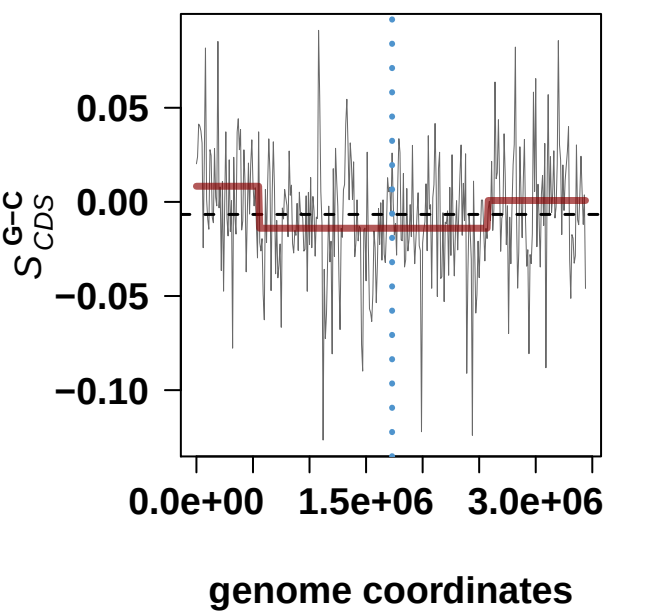
Desulfovibrio vulgaris str. Hildenborough

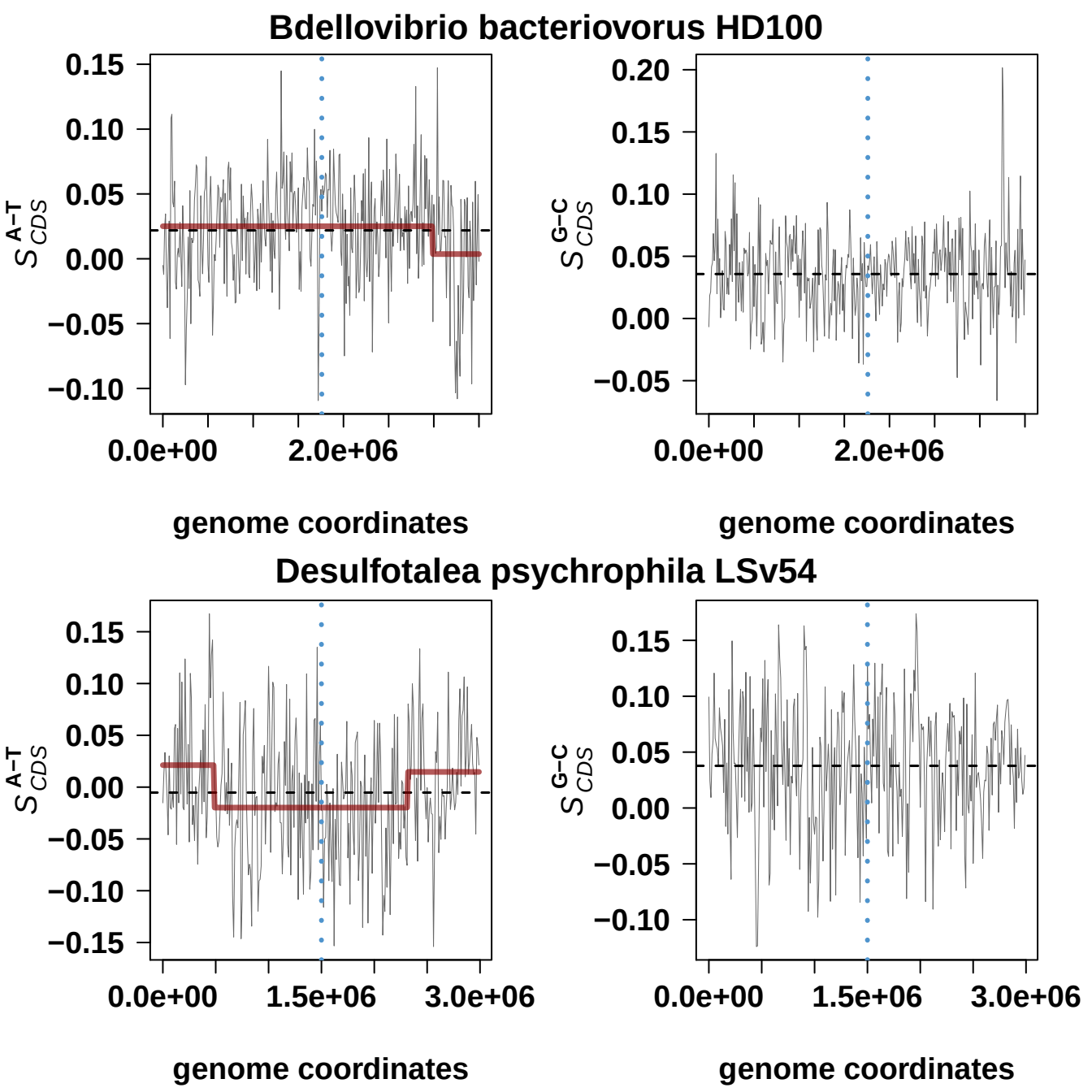


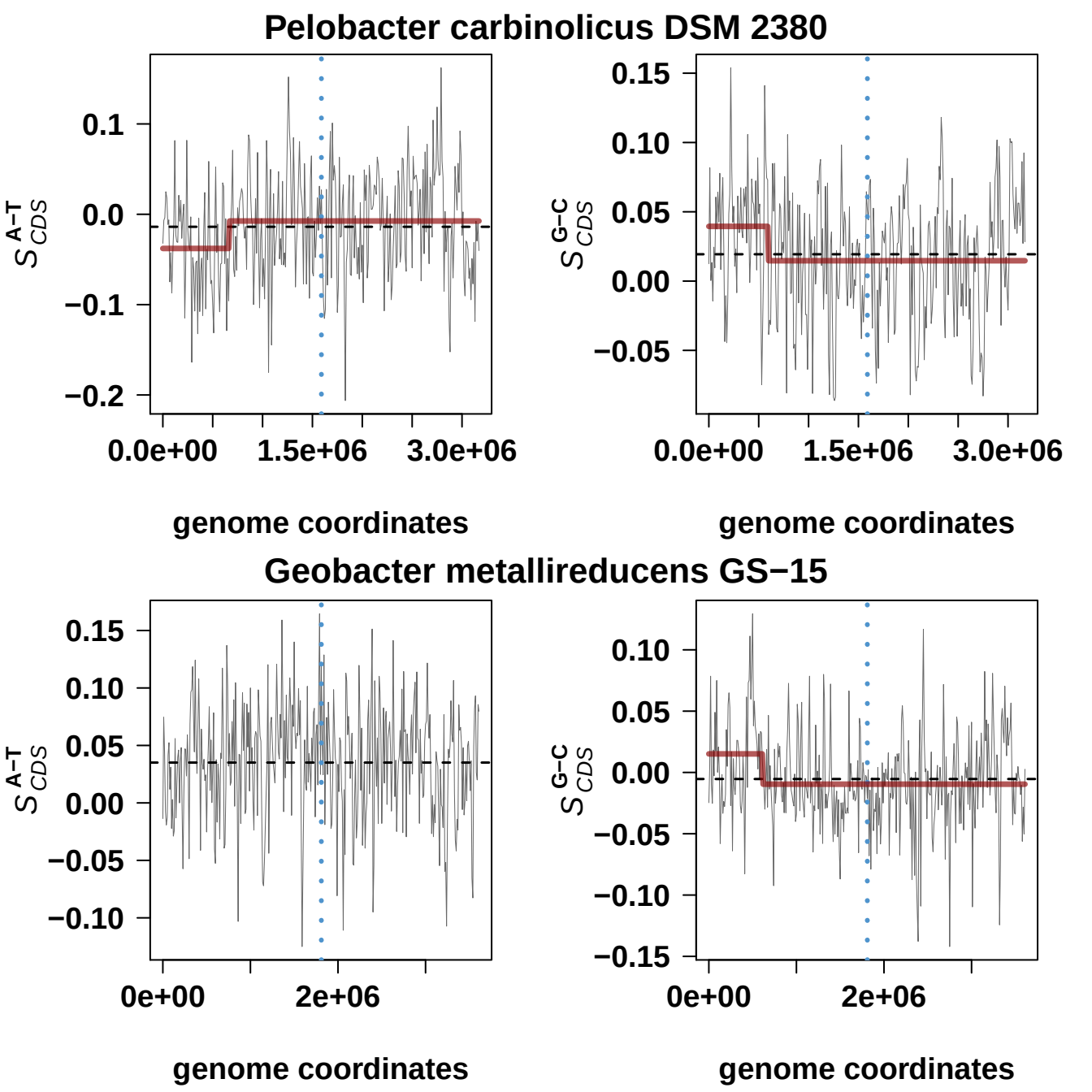


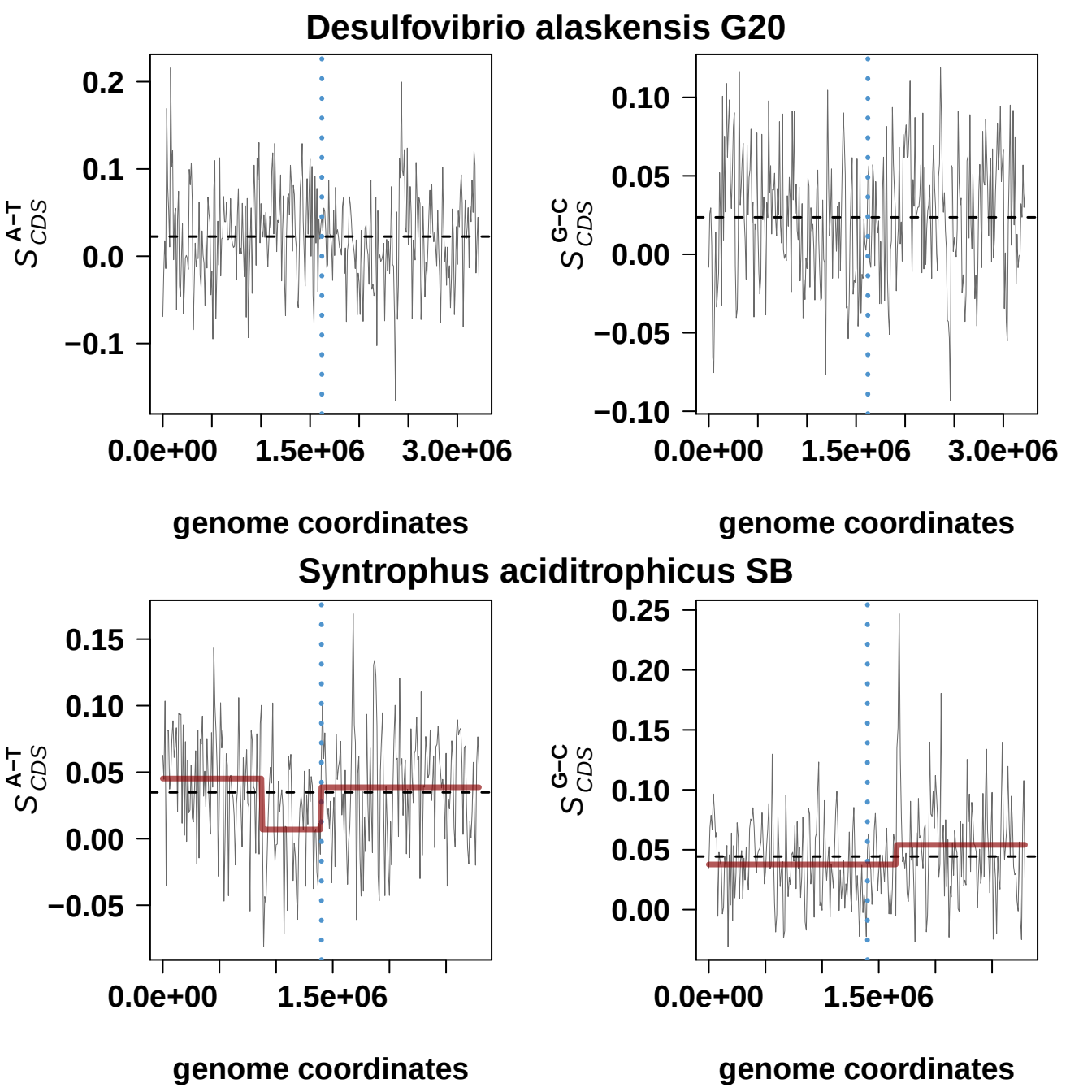
Geobacter sulfurreducens PCA

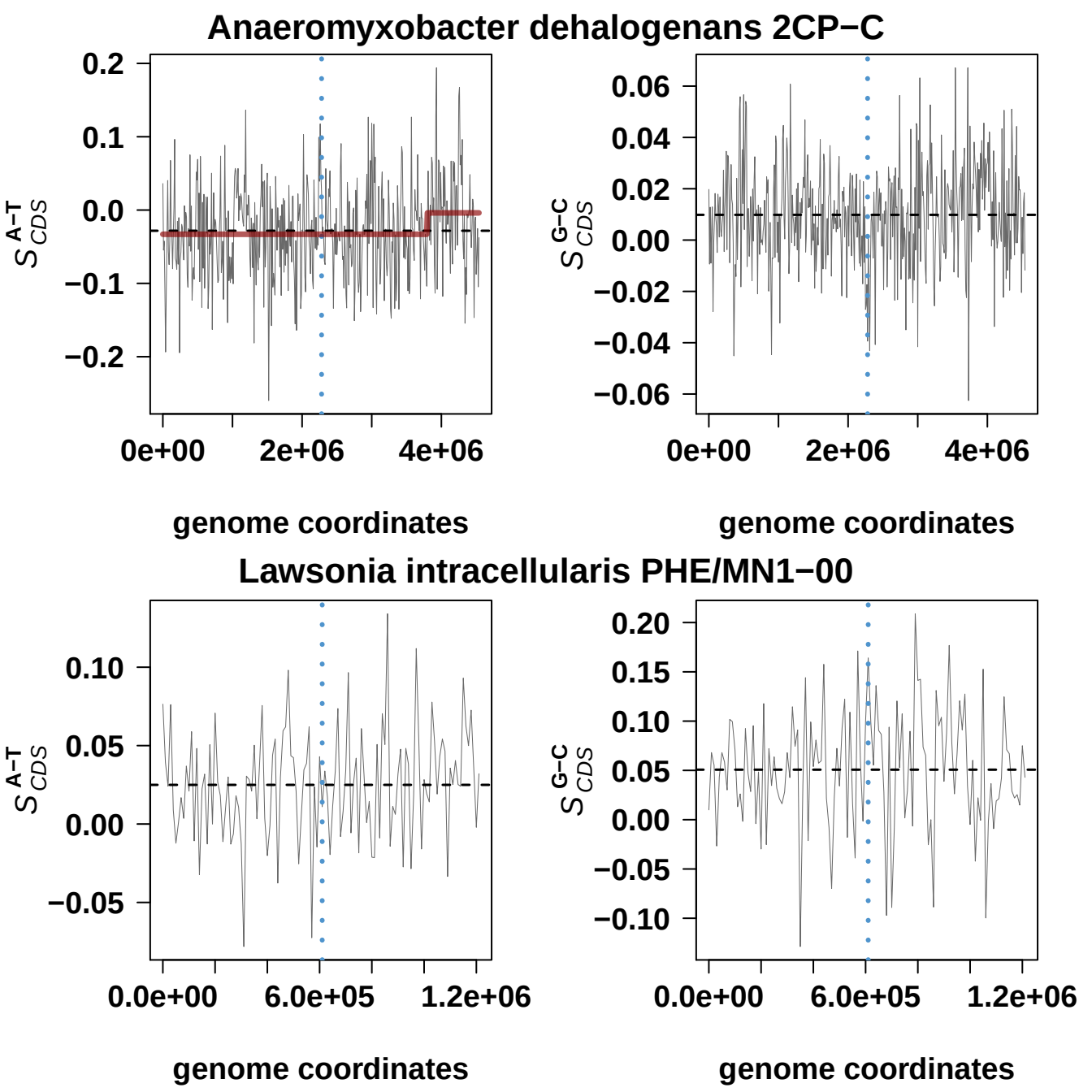


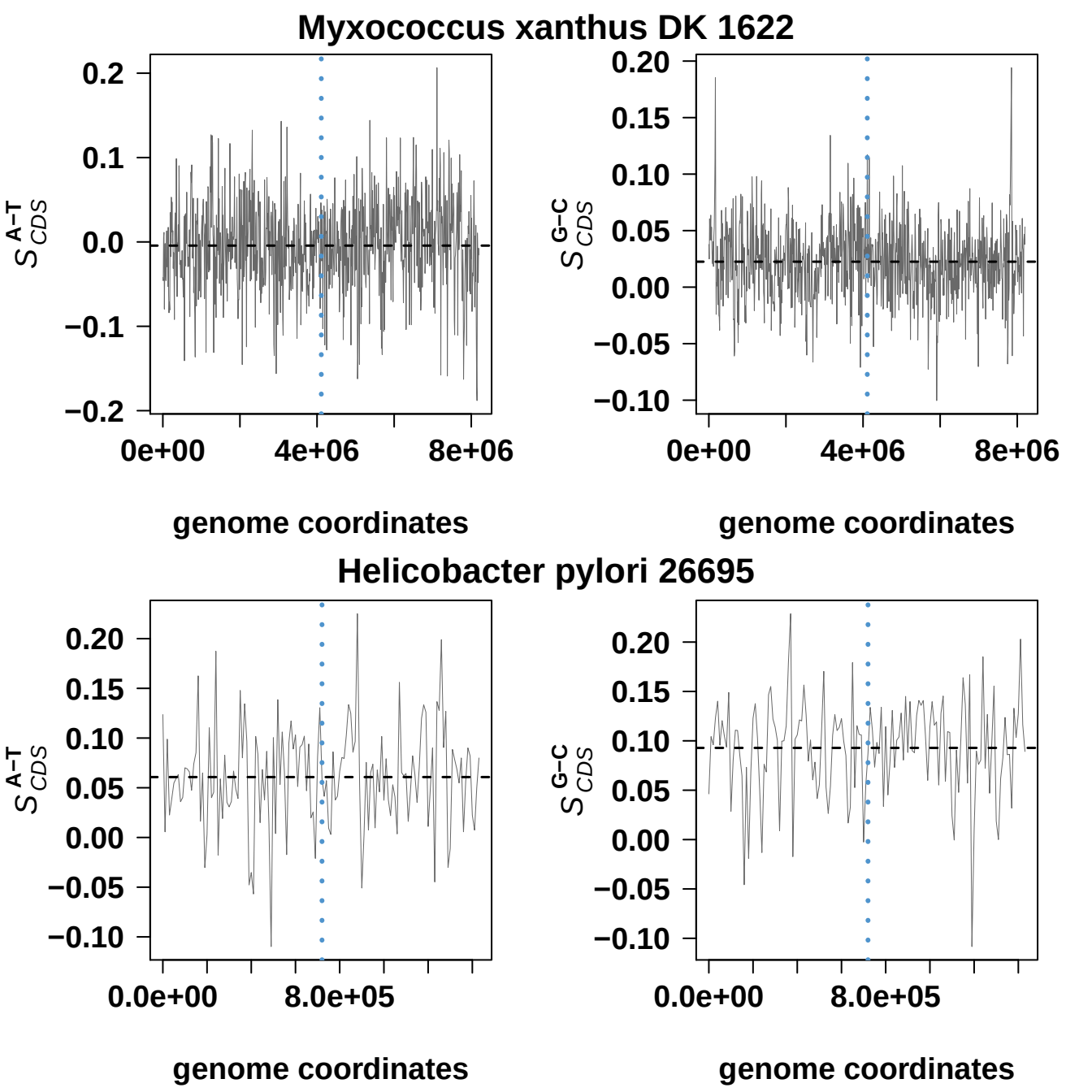


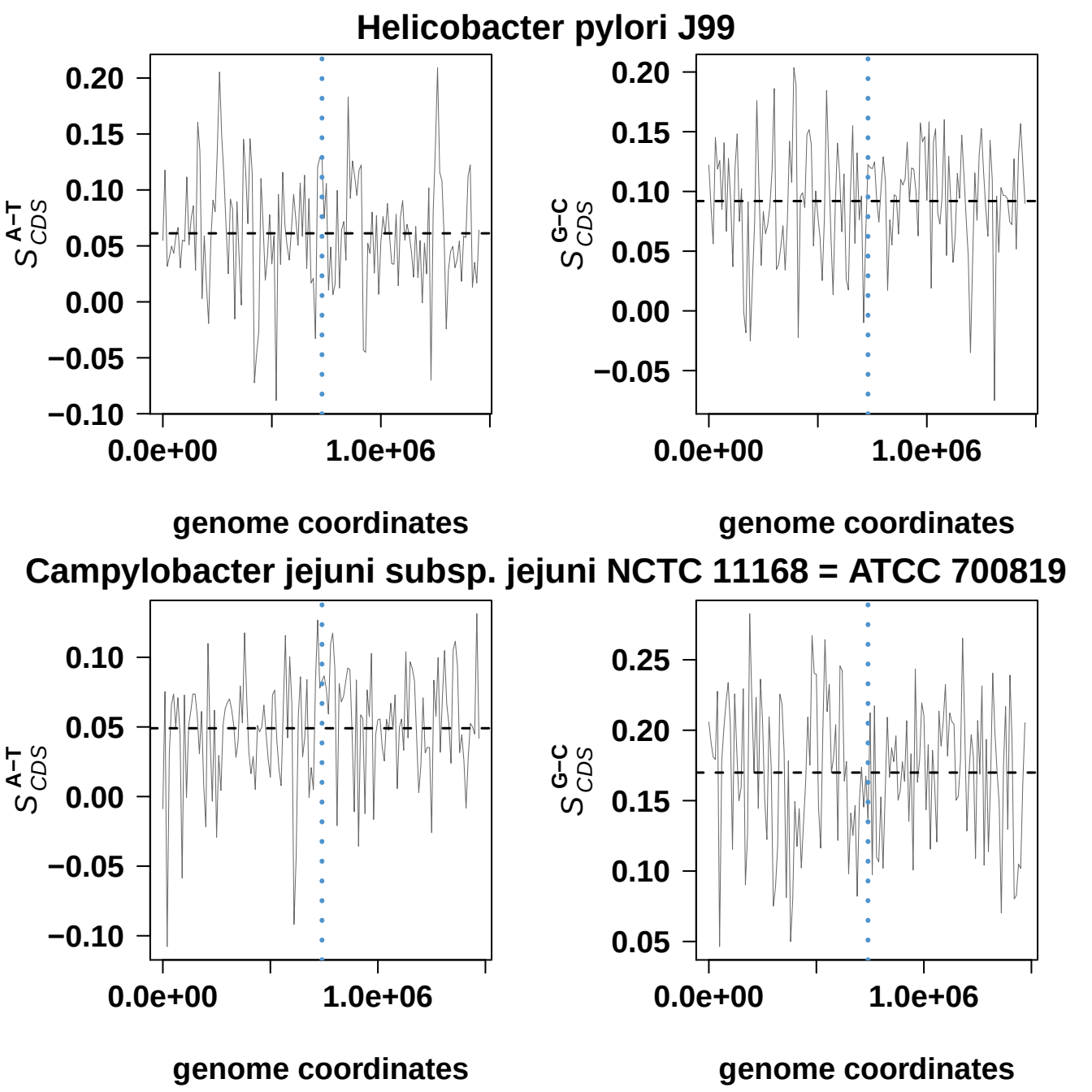

Bdellovibrio bacteriovorus HD100
0.15
0.10
0.05
0.00
−0.05
−0.10
S^{A-T}_{CDS}
0.0e+00
2.0e+06
genome coordinates
0.20
0.15
0.10
0.05
0.00
−0.05
S^{G-C}_{CDS}
0.0e+00
2.0e+06
genome coordinates
Desulfotalea psychrophila LSv54
0.15
0.10
0.05
0.00
−0.05
−0.10
−0.15
S^{A-T}_{CDS}
0.0e+00
1.5e+06
3.0e+06
genome coordinates
0.15
0.10
0.05
0.00
−0.05
−0.10
S^{G-C}_{CDS}
0.0e+00
1.5e+06
3.0e+06
genome coordinates

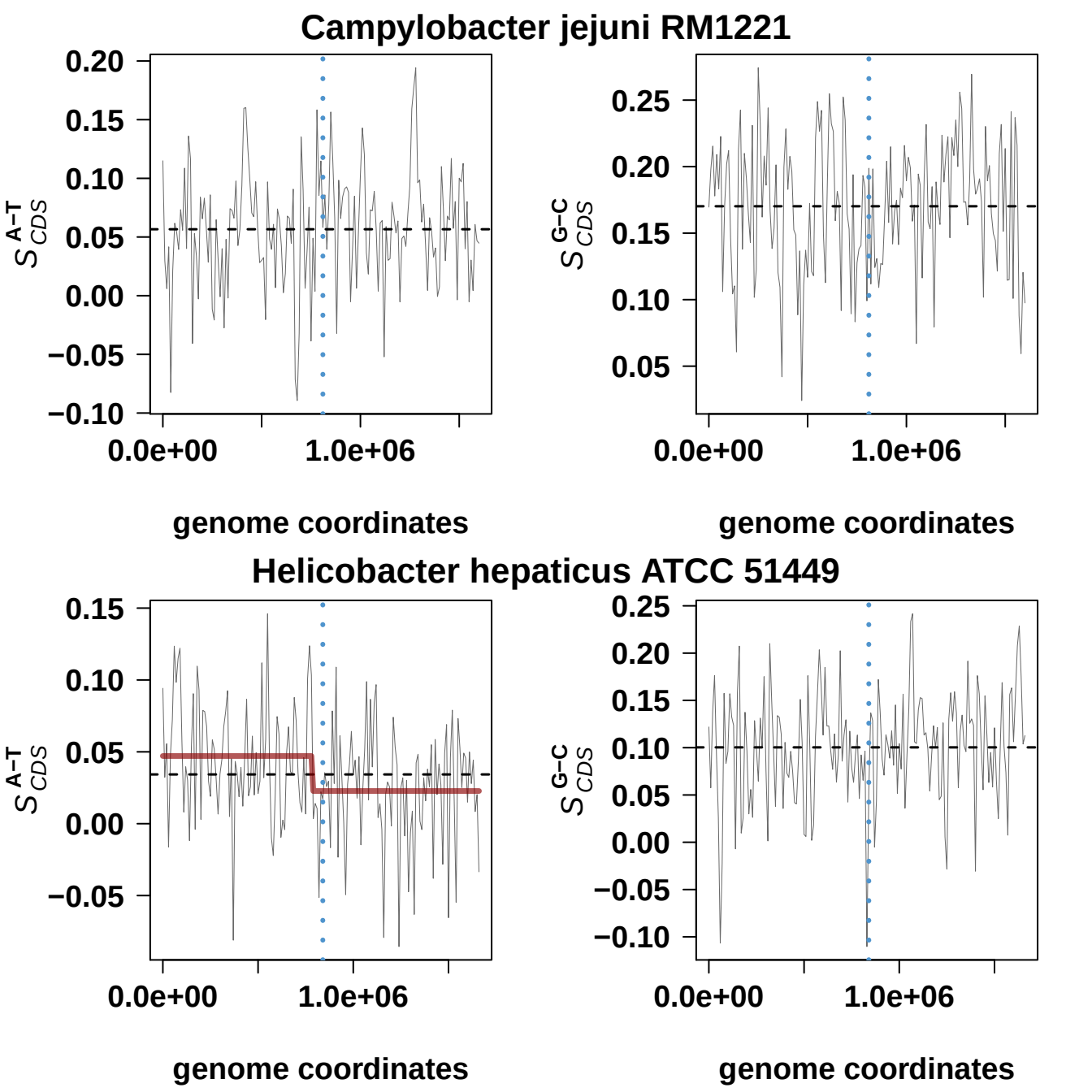

Pelobacter carbinolicus DSM 2380
S^{A-T}_{CDS}
0.1
0.0
−0.1
−0.2
0.0e+00
1.5e+06
3.0e+06
genome coordinates
S^{G-C}_{CDS}
0.15
0.10
0.05
0.00
−0.05
0.0e+00
1.5e+06
3.0e+06
genome coordinates
Geobacter metallireducens GS−15
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
−0.05
−0.10
0e+00
2e+06
genome coordinates
S^{G-C}_{CDS}
0.10
0.05
0.00
−0.05
−0.10
−0.15
0e+00
2e+06
genome coordinates

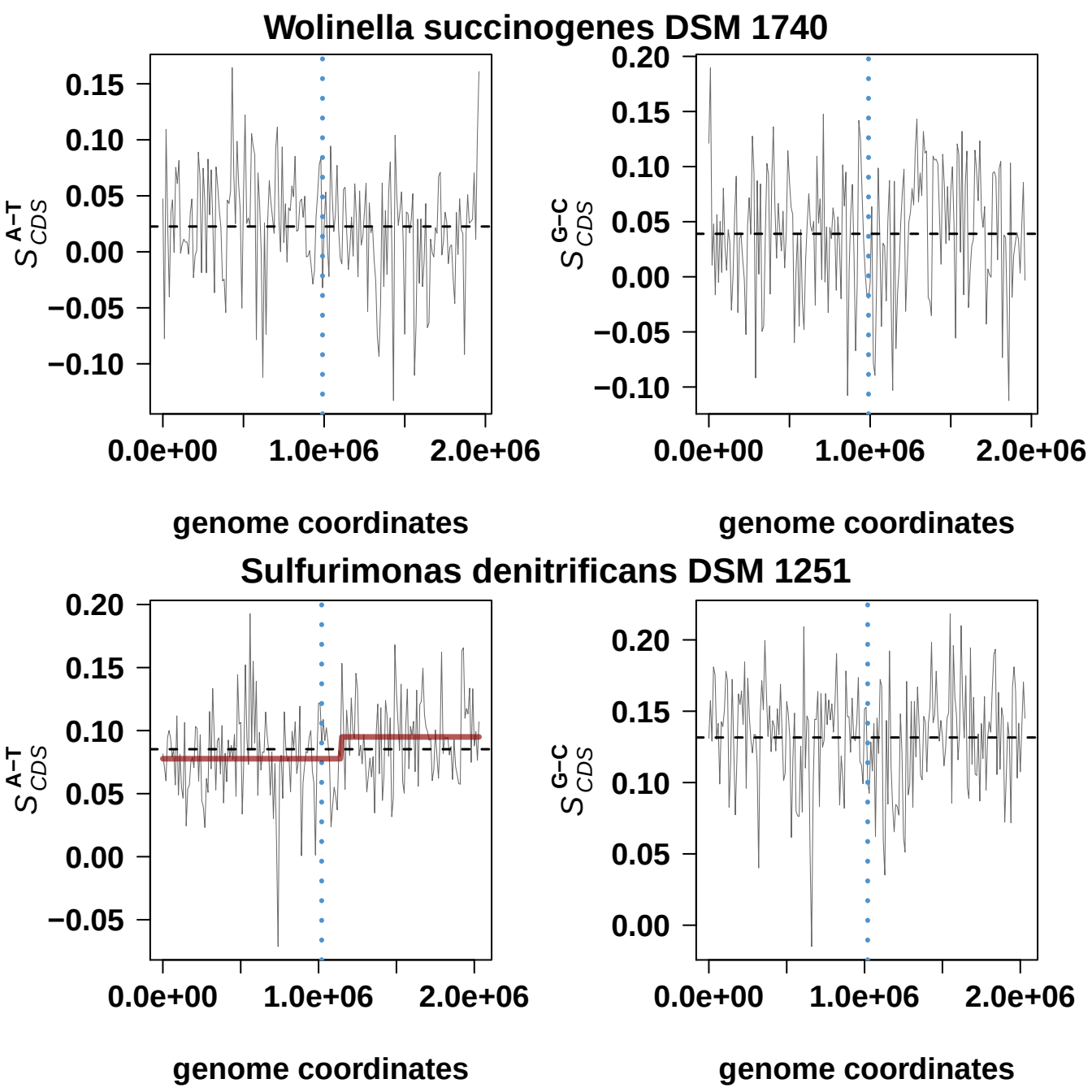

Desulfovibrio alaskensis G20
S^{A-T}_{CDS}
0.2
0.1
0.0
−0.1
0.0e+00
1.5e+06
3.0e+06
genome coordinates
S^{G-C}_{CDS}
0.10
0.05
0.00
−0.05
−0.10
0.0e+00
1.5e+06
3.0e+06
genome coordinates
Syntrophus aciditrophicus SB
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
−0.05
0.0e+00
1.5e+06
genome coordinates
S^{G-C}_{CDS}
0.25
0.20
0.15
0.10
0.05
0.00
0.0e+00
1.5e+06
genome coordinates


Anaeromyxobacter dehalogenans 2CP−C
S^{A-T}_{CDS}
0.2
0.1
0.0
−0.1
−0.2
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{CDS}
0.06
0.04
0.02
0.00
−0.02
−0.04
−0.06
0e+00
2e+06
4e+06
genome coordinates
Lawsonia intracellularis PHE/MN1−00
S^{A-T}_{CDS}
0.10
0.05
0.00
−0.05
0.0e+00
6.0e+05
1.2e+06
genome coordinates
S^{G-C}_{CDS}
0.20
0.15
0.10
0.05
0.00
−0.05
−0.10
0.0e+00
6.0e+05
1.2e+06
genome coordinates


Myxococcus xanthus DK 1622
S^{A-T}_{CDS}
0.2
0.1
0.0
−0.1
−0.2
0e+00
4e+06
8e+06
genome coordinates
S^{G-C}_{CDS}
0.20
0.15
0.10
0.05
0.00
−0.05
−0.10
0e+00
4e+06
8e+06
genome coordinates
Helicobacter pylori 26695
S^{A-T}_{CDS}
0.20
0.15
0.10
0.05
0.00
−0.05
−0.10
0.0e+00
8.0e+05
genome coordinates
S^{G-C}_{CDS}
0.20
0.15
0.10
0.05
0.00
−0.05
−0.10
0.0e+00
8.0e+05
genome coordinates


Helicobacter pylori J99
S^{A-T}_{CDS}
0.20
0.15
0.10
0.05
0.00
−0.05
−0.10
0.0e+00
1.0e+06
genome coordinates
S^{G-C}_{CDS}
0.20
0.15
0.10
0.05
0.00
−0.05
0.0e+00
1.0e+06
genome coordinates
Campylobacter jejuni subsp. jejuni NCTC 11168 = ATCC 700819
S^{A-T}_{CDS}
0.10
0.05
0.00
−0.05
−0.10
0.0e+00
1.0e+06
genome coordinates
S^{G-C}_{CDS}
0.25
0.20
0.15
0.10
0.05
0.0e+00
1.0e+06
genome coordinates


Campylobacter jejuni RM1221
S^{A-T}_{CDS}
0.20
0.15
0.10
0.05
0.00
−0.05
−0.10
0.0e+00
1.0e+06
genome coordinates
S^{G-C}_{CDS}
0.25
0.20
0.15
0.10
0.05
0.0e+00
1.0e+06
genome coordinates
Helicobacter hepaticus ATCC 51449
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
−0.05
0.0e+00
1.0e+06
genome coordinates
S^{G-C}_{CDS}
0.25
0.20
0.15
0.10
0.05
0.00
−0.05
−0.10
0.0e+00
1.0e+06
genome coordinates


Wolinella succinogenes DSM 1740
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
−0.05
−0.10
0.0e+00
1.0e+06
2.0e+06
genome coordinates
S^{G-C}_{CDS}
0.20
0.15
0.10
0.05
0.00
−0.05
−0.10
0.0e+00
1.0e+06
2.0e+06
genome coordinates
Sulfurimonas denitrificans DSM 1251
S^{A-T}_{CDS}
0.20
0.15
0.10
0.05
0.00
−0.05
0.0e+00
1.0e+06
2.0e+06
genome coordinates
S^{G-C}_{CDS}
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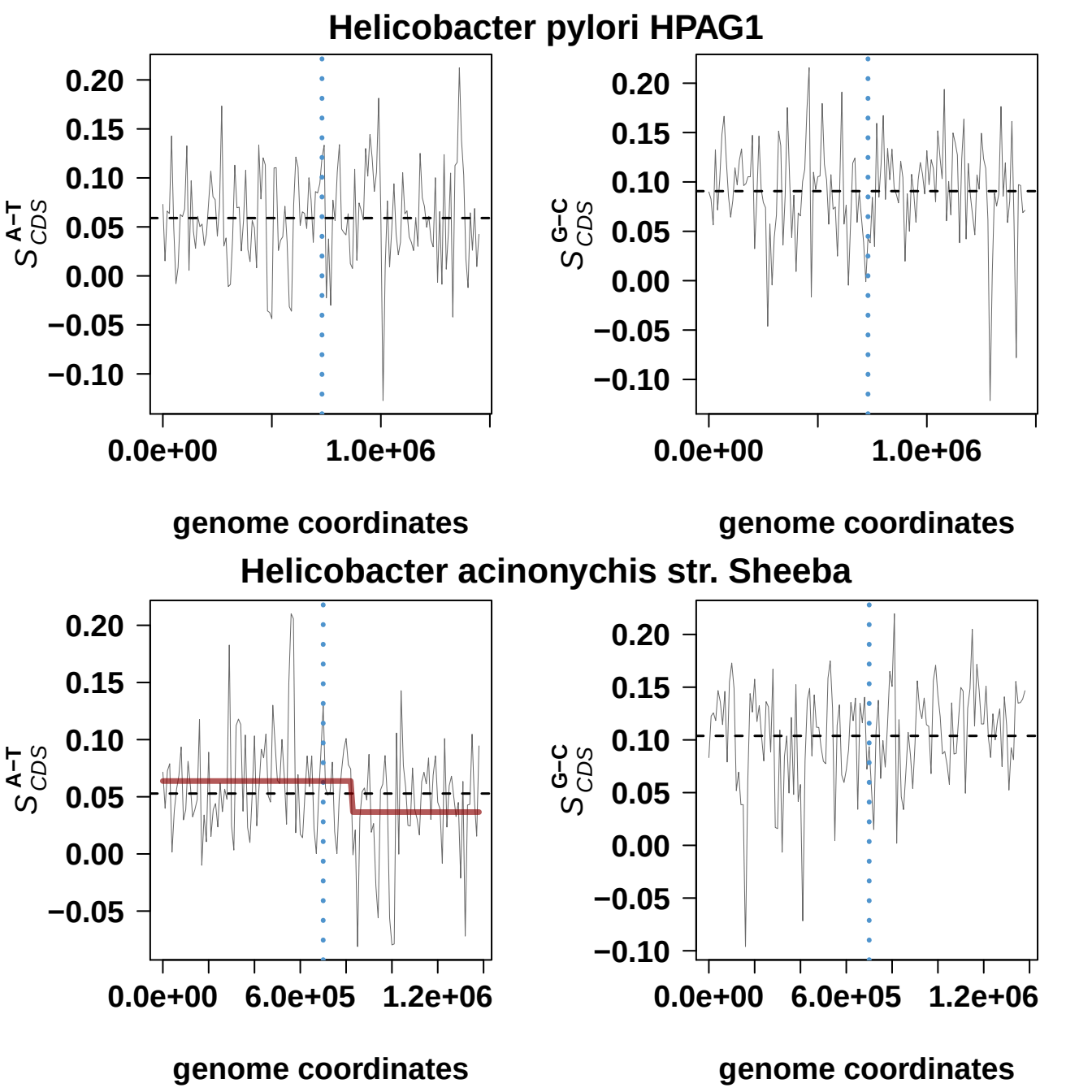
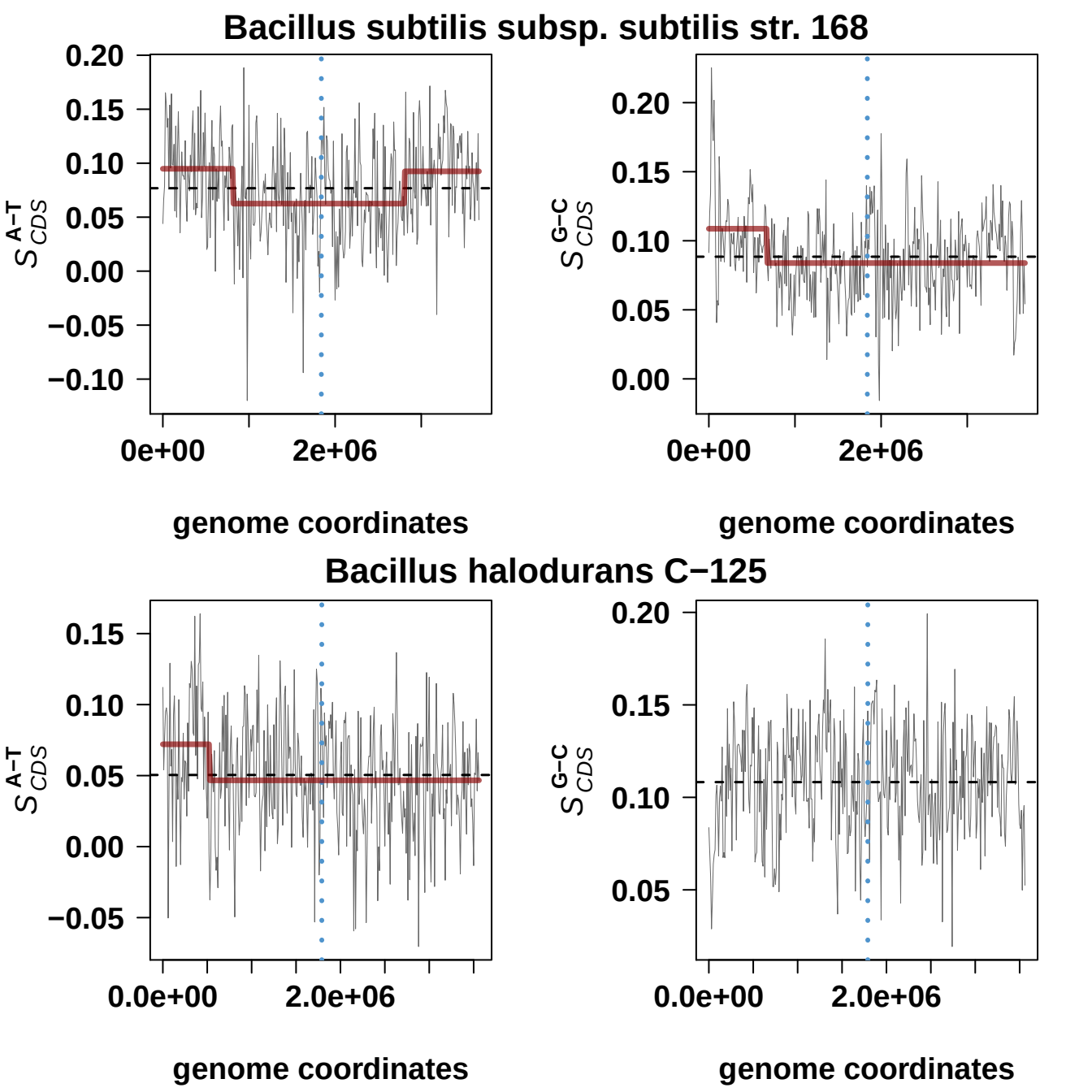
0.15
0.10
0.05
0.00
0.0e+00
1.0e+06
2.0e+06
genome coordinates


Helicobacter pylori HPAG1
S^{A-T}_{CDS}
0.20
0.15
0.10
0.05
0.00
−0.05
−0.10
0.0e+00
1.0e+06
genome coordinates
S^{G-C}_{CDS}
0.20
0.15
0.10
0.05
0.00
−0.05
−0.10
0.0e+00
1.0e+06
genome coordinates
Helicobacter acinonychis str. Sheeba
S^{A-T}_{CDS}
0.20
0.15
0.10
0.05
0.00
−0.05
0.0e+00
6.0e+05
1.2e+06
genome coordinates
S^{G-C}_{CDS}
0.20
0.15
0.10
0.05
0.00
−0.05
−0.10
0.0e+00
6.0e+05
1.2e+06
genome coordinates


Bacillus subtilis subsp. subtilis str. 168
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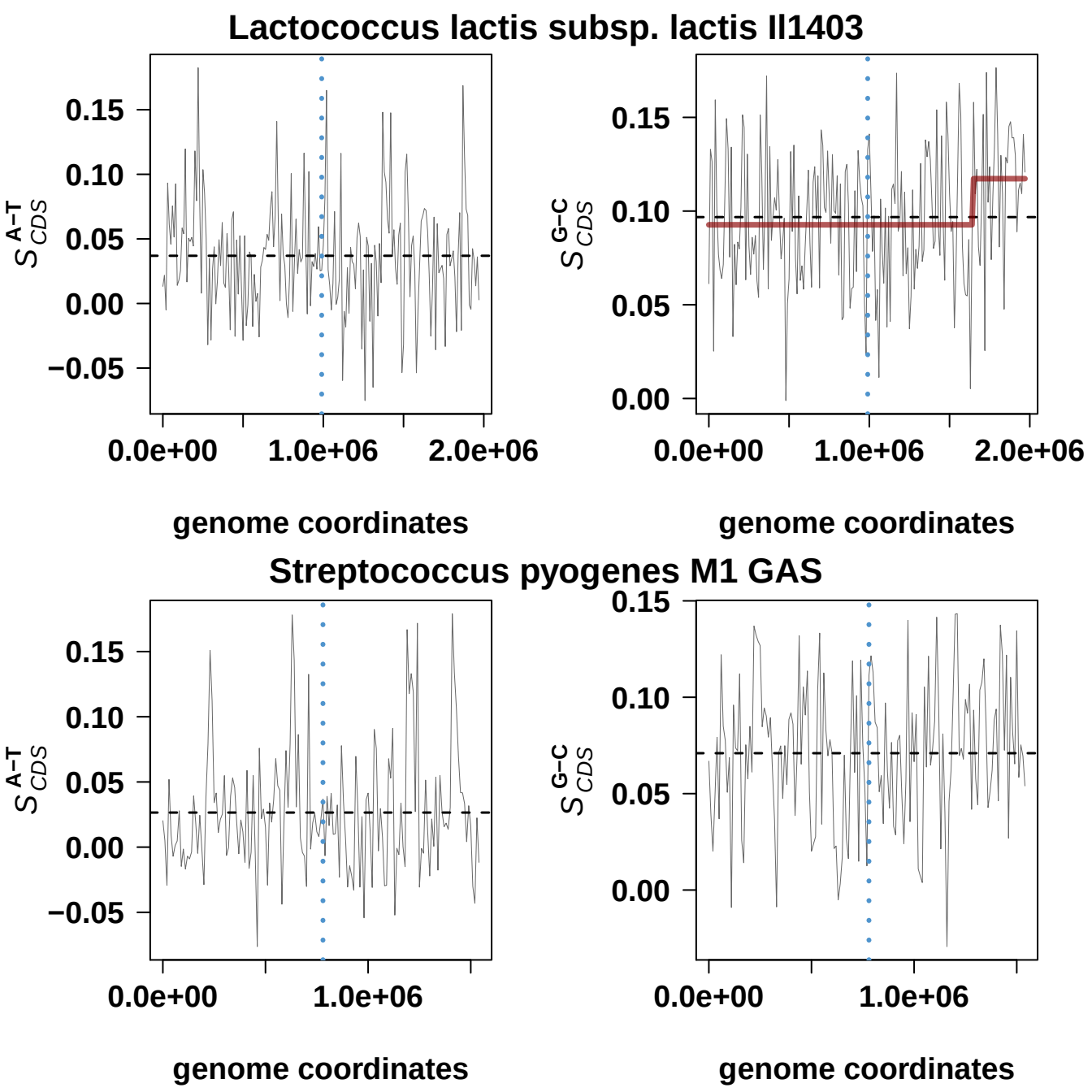
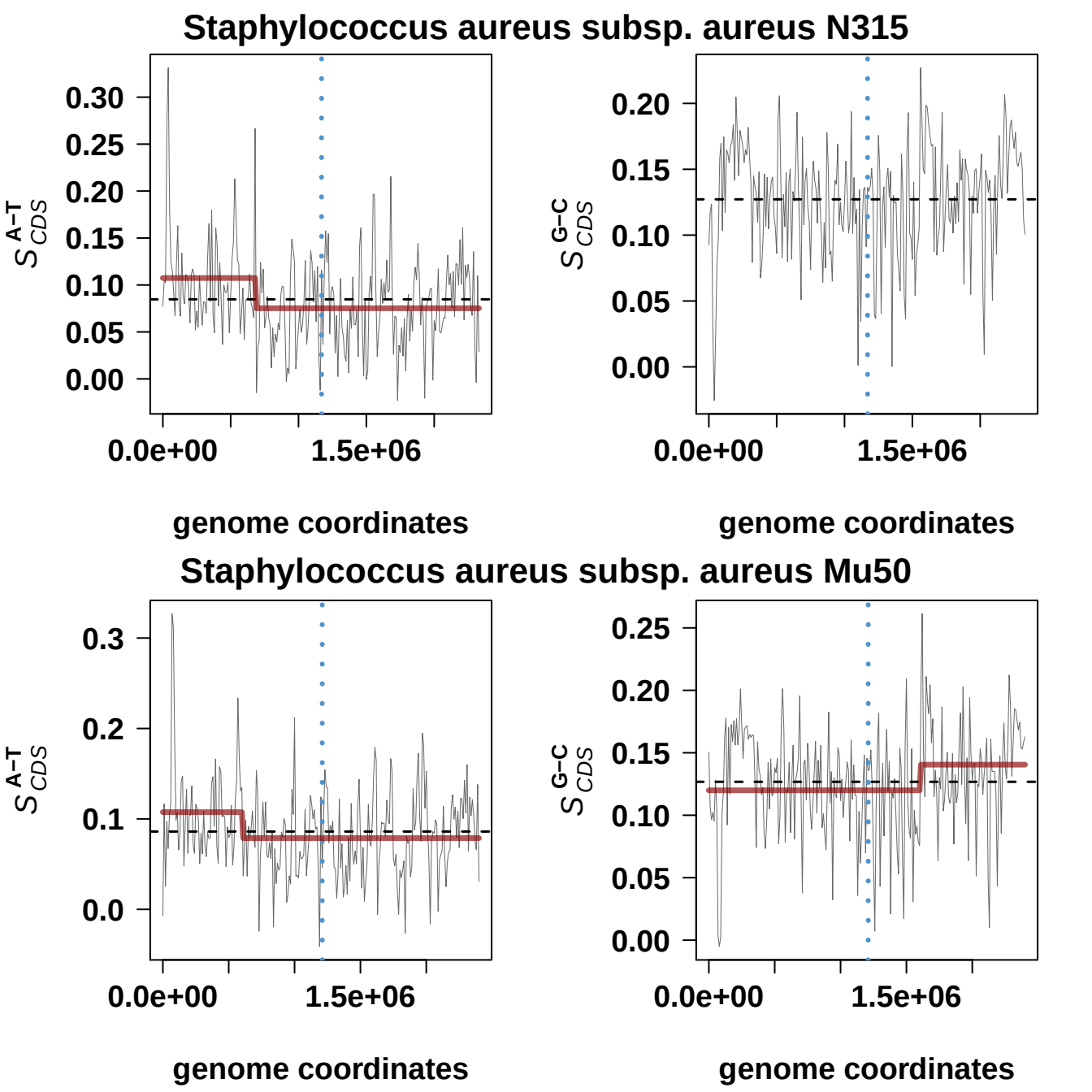
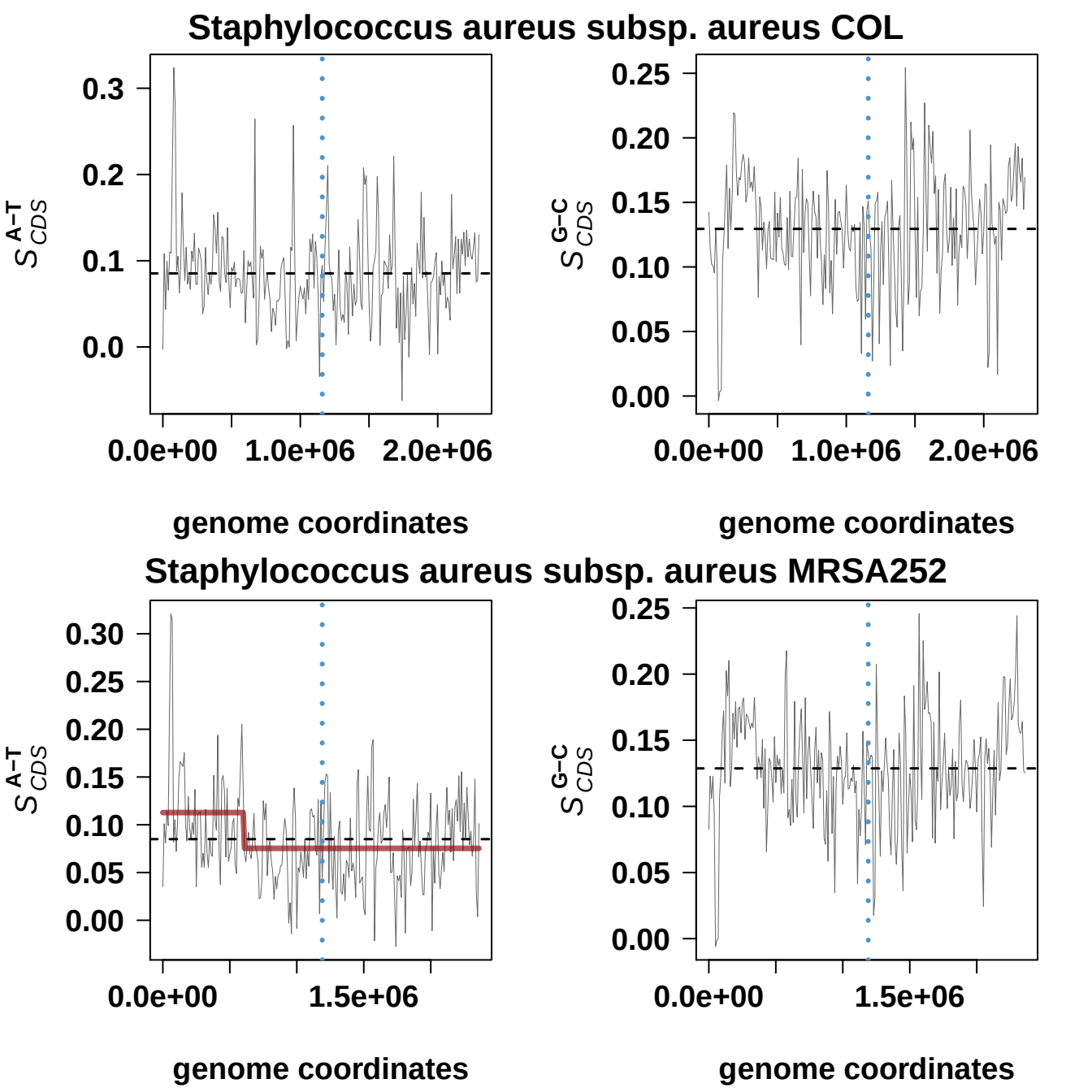
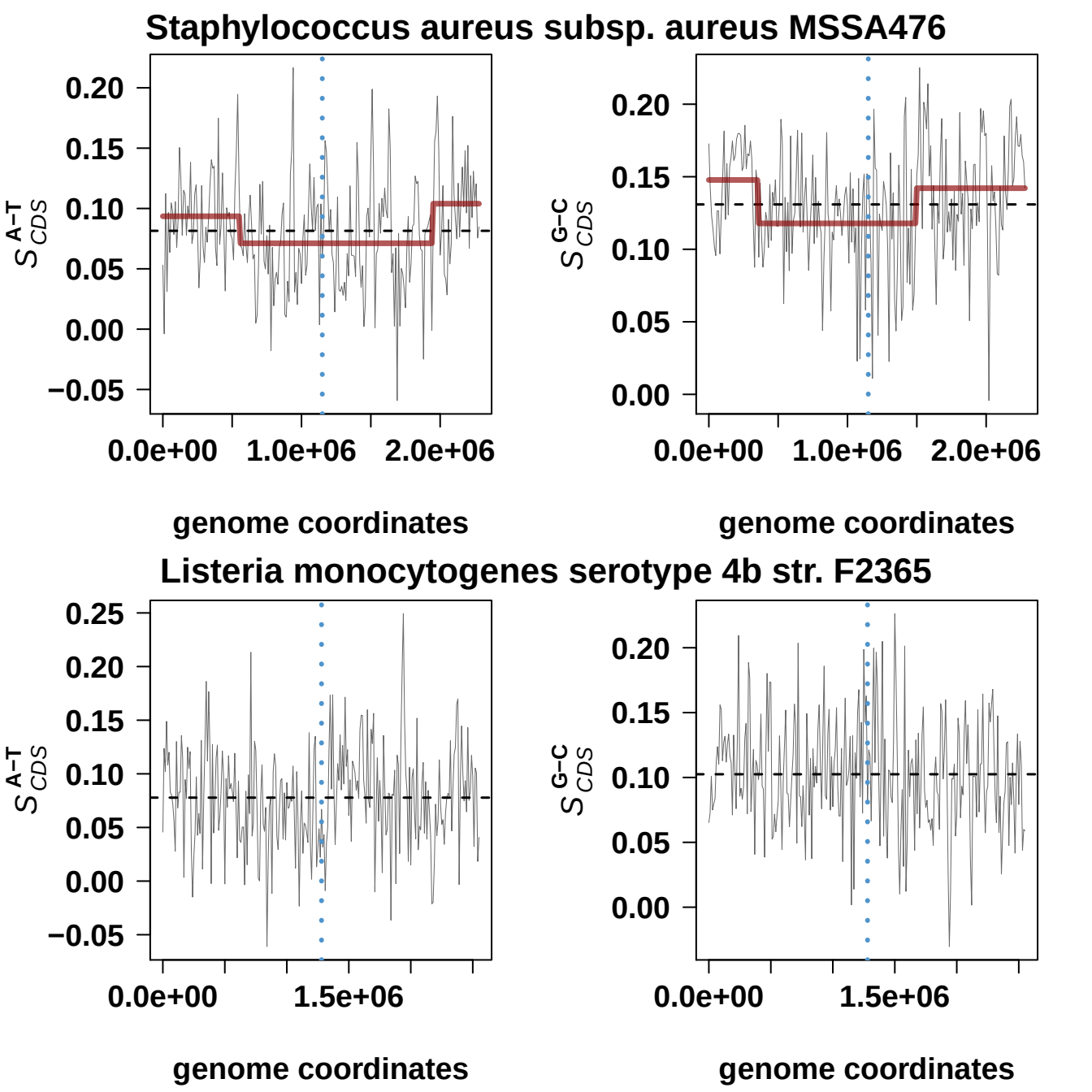
0.15
0.10
0.05
0.00
−0.05
−0.10
S^{A-T}_{CDS}
0e+00
2e+06
genome coordinates
0.20
0.15
0.10
0.05
0.00
S^{G-C}_{CDS}
0e+00
2e+06
genome coordinates
Bacillus halodurans C−125
0.15
0.10
0.05
0.00
−0.05
S^{A-T}_{CDS}
0.0e+00
2.0e+06
genome coordinates
0.20
0.15
0.10
0.05
S^{G-C}_{CDS}
0.0e+00
2.0e+06
genome coordinates


Lactococcus lactis subsp. lactis Il1403
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
−0.05
0.0e+00
1.0e+06
2.0e+06
genome coordinates
S^{G-C}_{CDS}
0.15
0.10
0.05
0.00
0.0e+00
1.0e+06
2.0e+06
genome coordinates
Streptococcus pyogenes M1 GAS
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
−0.05
0.0e+00
1.0e+06
genome coordinates
S^{G-C}_{CDS}
0.15
0.10
0.05
0.00
0.0e+00
1.0e+06
genome coordinates


Staphylococcus aureus subsp. aureus N315
S^{A-T}_{CDS}
0.30
0.25
0.20
0.15
0.10
0.05
0.00
0.0e+00
1.5e+06
genome coordinates
S^{G-C}_{CDS}
0.20
0.15
0.10
0.05
0.00
0.0e+00
1.5e+06
genome coordinates
Staphylococcus aureus subsp. aureus Mu50
S^{A-T}_{CDS}
0.3
0.2
0.1
0.0
0.0e+00
1.5e+06
genome coordinates
S^{G-C}_{CDS}
0.25
0.20
0.15
0.10
0.05
0.00
0.0e+00
1.5e+06
genome coordinates


Staphylococcus aureus subsp. aureus COL
S^{A-T}_{CDS}
0.3
0.2
0.1
0.0
0.0e+00
1.0e+06
2.0e+06
genome coordinates
S^{G-C}_{CDS}
0.25
0.20
0.15
0.10
0.05
0.00
0.0e+00
1.0e+06
2.0e+06
genome coordinates
Staphylococcus aureus subsp. aureus MRSA252
S^{A-T}_{CDS}
0.30
0.25
0.20
0.15
0.10
0.05
0.00
0.0e+00
1.5e+06
genome coordinates
S^{G-C}_{CDS}
0.25
0.20
0.15
0.10
0.05
0.00
0.0e+00
1.5e+06
genome coordinates


Staphylococcus aureus subsp. aureus MSSA476
S^{A-T}_{CDS}
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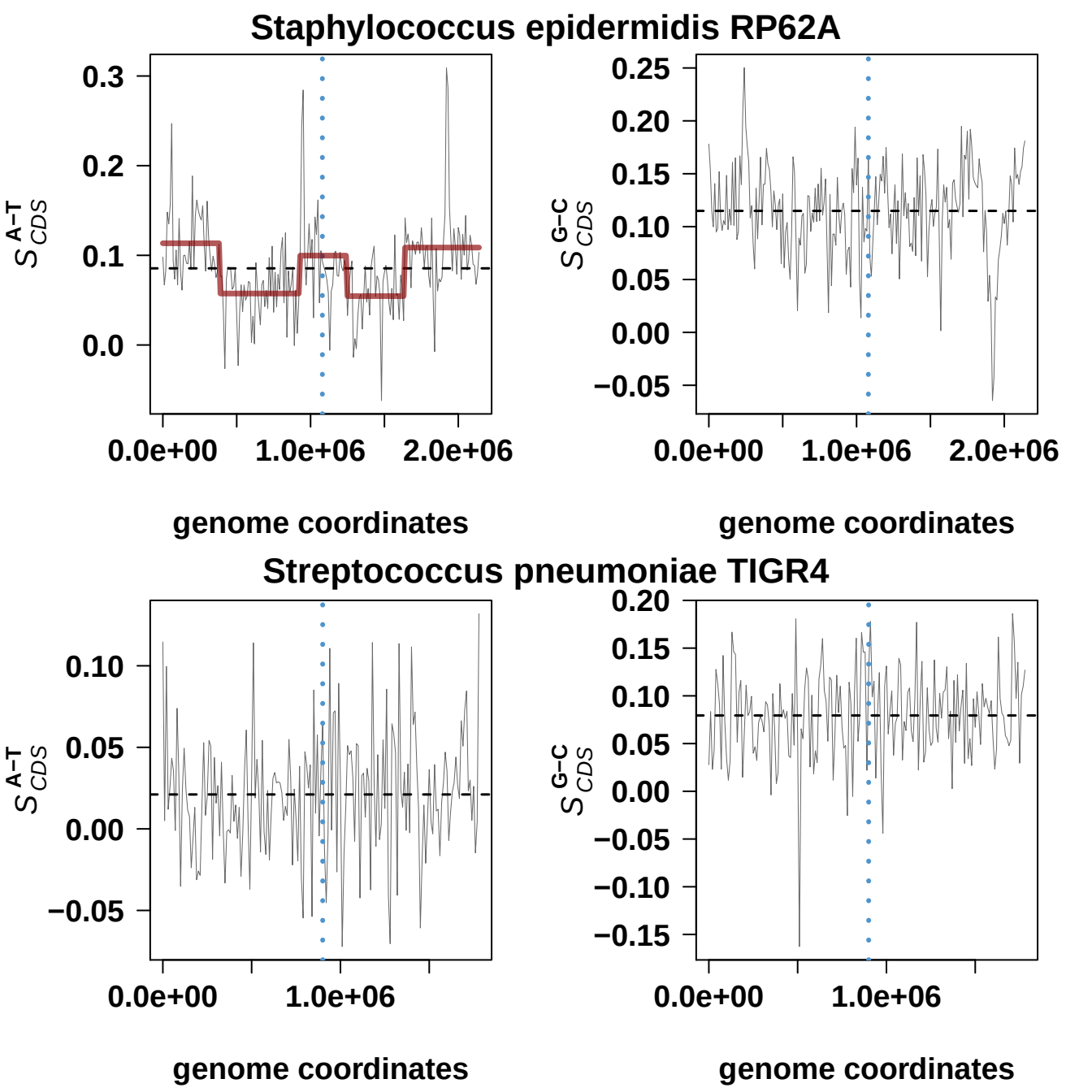
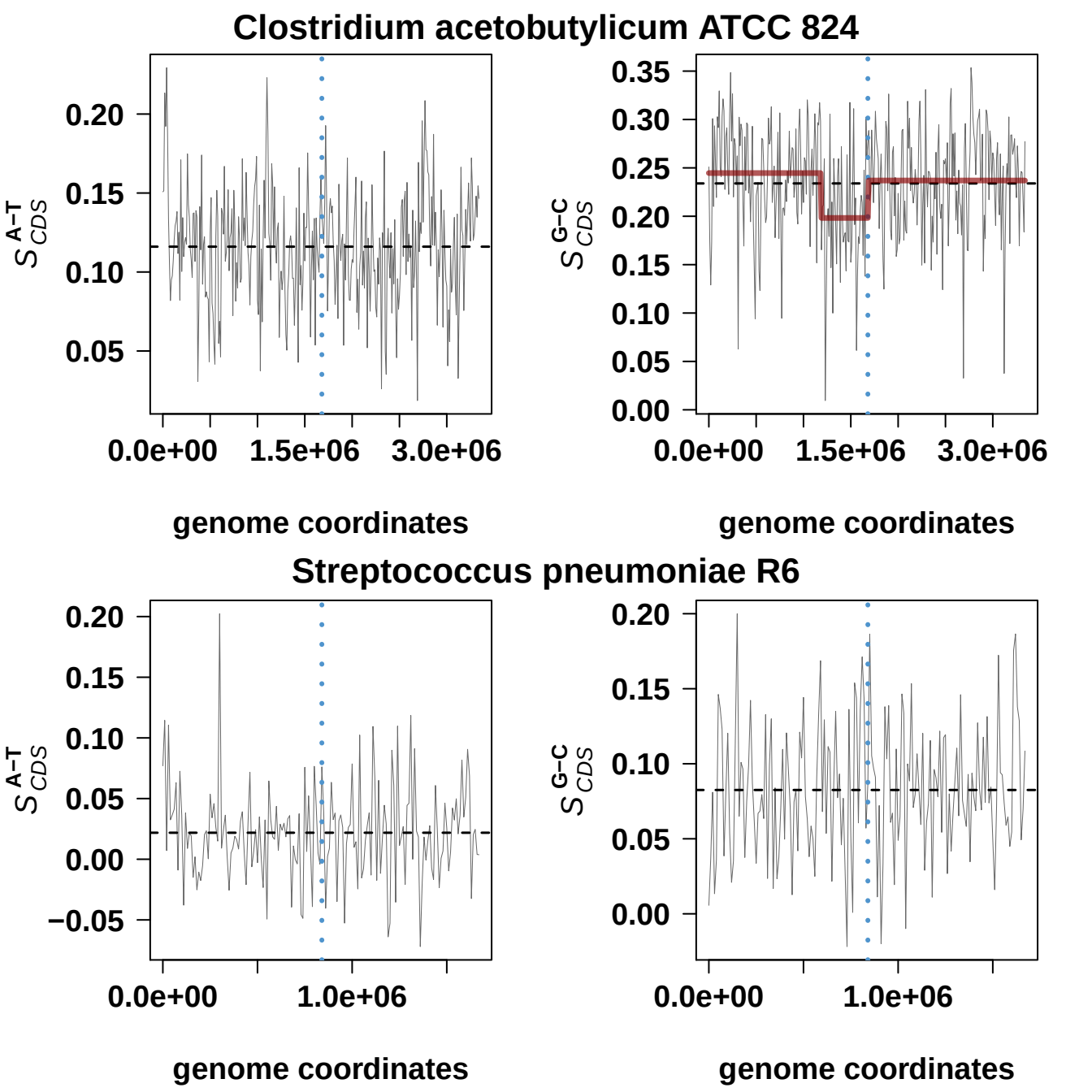
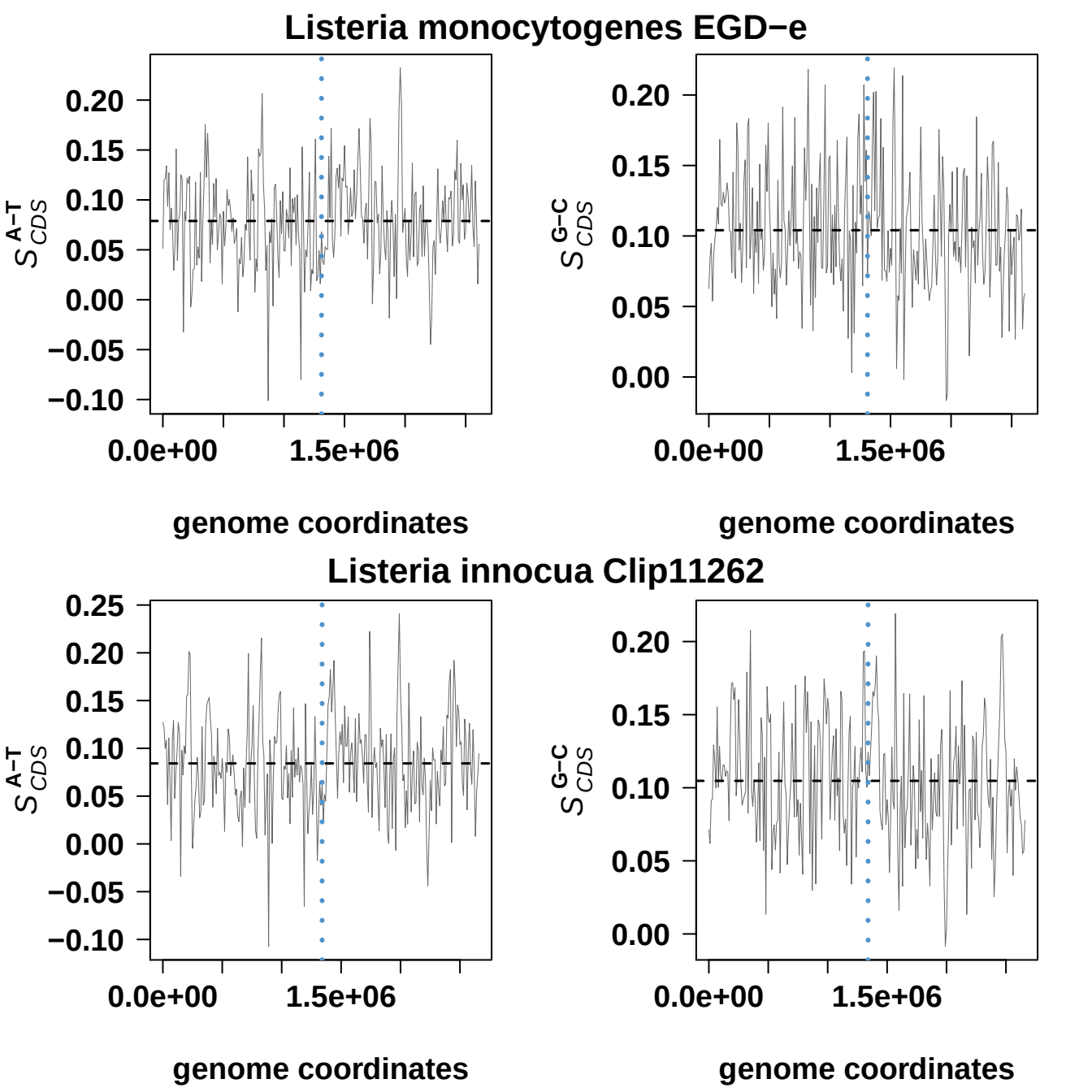
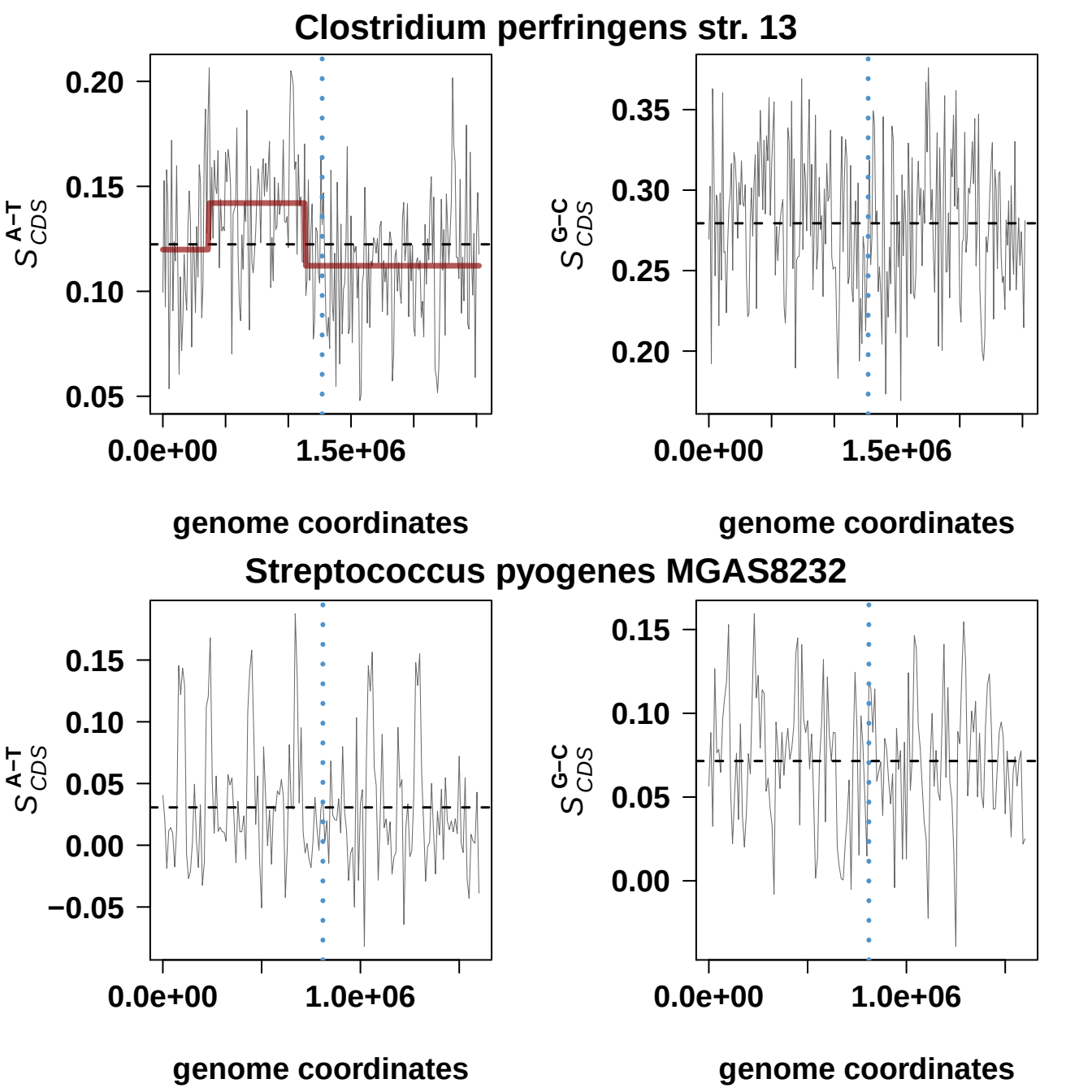
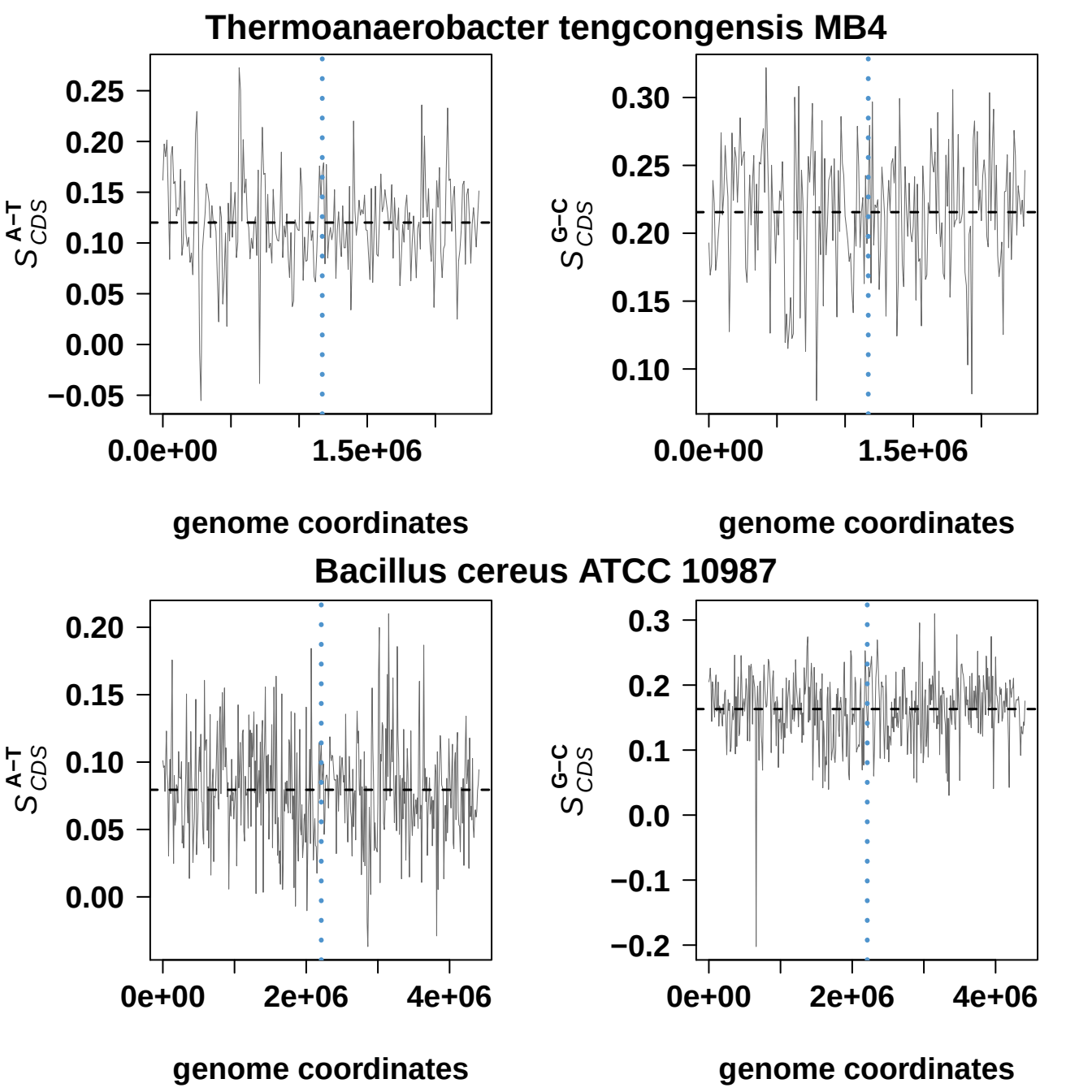
0.15
0.10
0.05
0.00
−0.05
0.0e+00
1.0e+06
2.0e+06
genome coordinates
S^{G-C}_{CDS}
0.20
0.15
0.10
0.05
0.00
0.0e+00
1.0e+06
2.0e+06
genome coordinates
Listeria monocytogenes serotype 4b str. F2365
S^{A-T}_{CDS}
0.25
0.20
0.15
0.10
0.05
0.00
−0.05
0.0e+00
1.5e+06
genome coordinates
S^{G-C}_{CDS}
0.20
0.15
0.10
0.05
0.00
0.0e+00
1.5e+06
genome coordinates

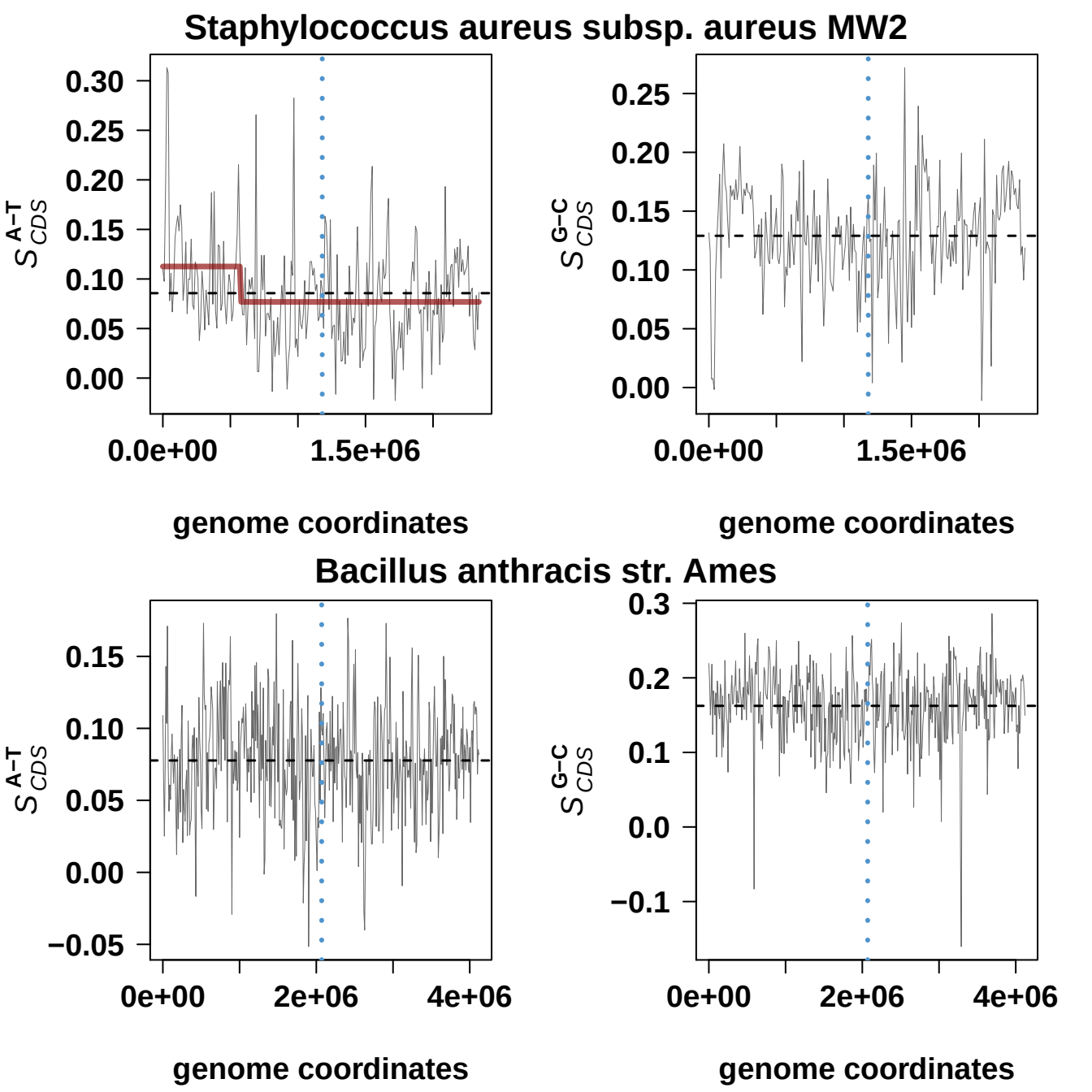

Staphylococcus epidermidis RP62A
S^{A-T}_{CDS}
0.3
0.2
0.1
0.0
0.0e+00
1.0e+06
2.0e+06
genome coordinates
S^{G-C}_{CDS}
0.25
0.20
0.15
0.10
0.05
0.00
−0.05
0.0e+00
1.0e+06
2.0e+06
genome coordinates
Streptococcus pneumoniae TIGR4
S^{A-T}_{CDS}
0.10
0.05
0.00
−0.05
0.0e+00
1.0e+06
genome coordinates
S^{G-C}_{CDS}
0.20
0.15
0.10
0.05
0.00
−0.05
−0.10
−0.15
0.0e+00
1.0e+06
genome coordinates

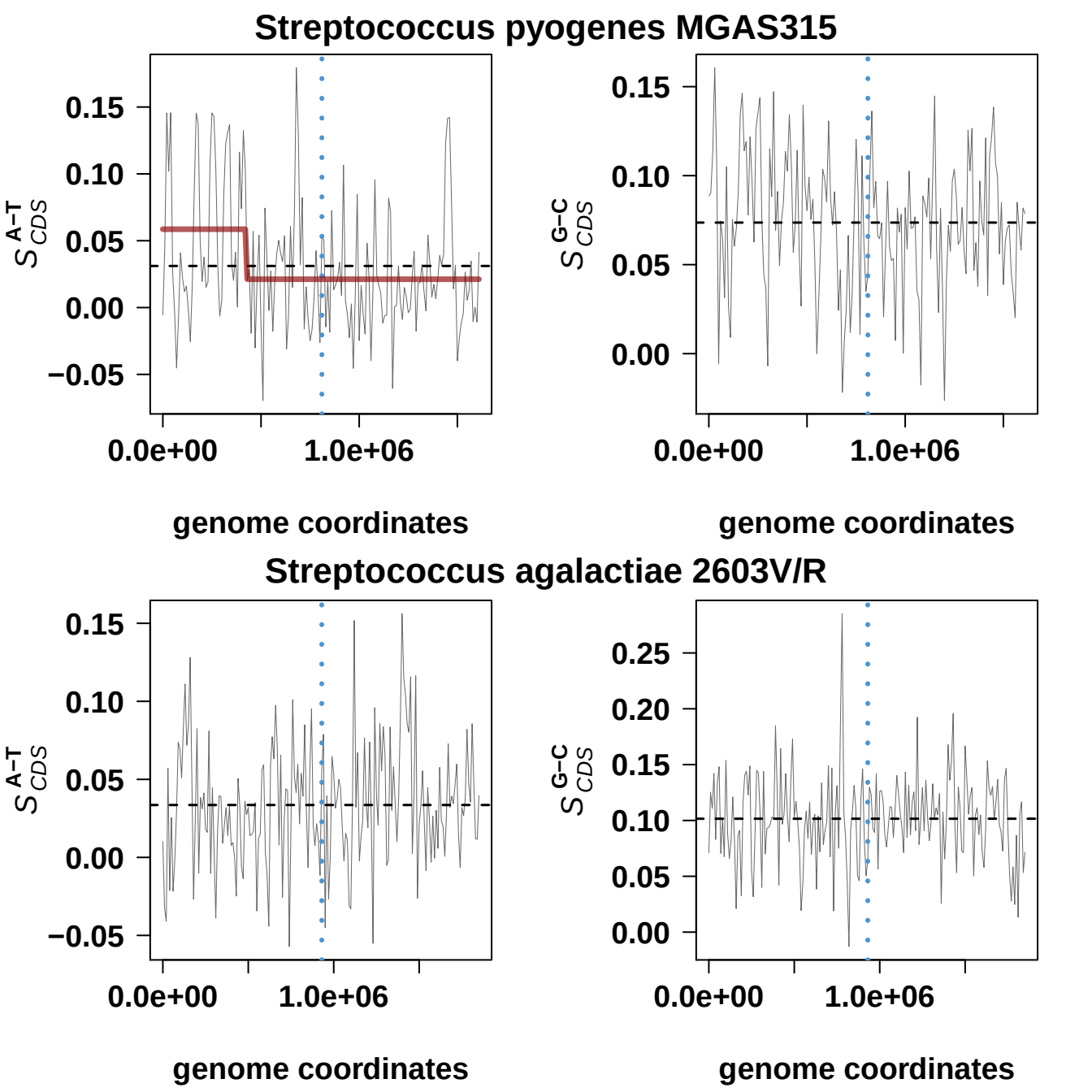

Clostridium acetobutylicum ATCC 824
S^{A-T}_{CDS}
0.20
0.15
0.10
0.05
0.0e+00
1.5e+06
3.0e+06
genome coordinates
S^{G-C}_{CDS}
0.35
0.30
0.25
0.20
0.15
0.10
0.05
0.00
0.0e+00
1.5e+06
3.0e+06
genome coordinates
Streptococcus pneumoniae R6
S^{A-T}_{CDS}
0.20
0.15
0.10
0.05
0.00
−0.05
0.0e+00
1.0e+06
genome coordinates
S^{G-C}_{CDS}
0.20
0.15
0.10
0.05
0.00
0.0e+00
1.0e+06
genome coordinates

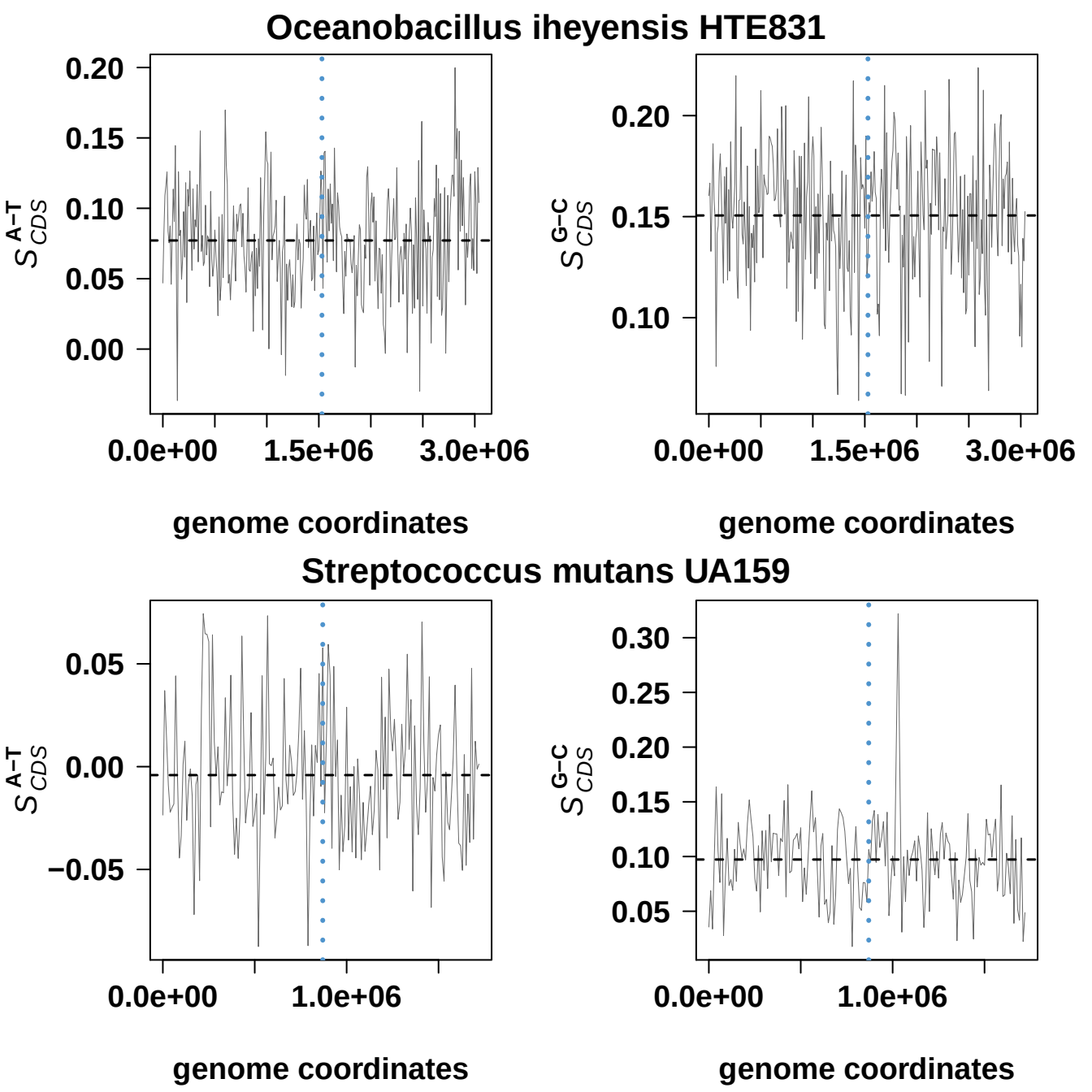

Listeria monocytogenes EGD−e
S^{A-T}_{CDS}
0.20
0.15
0.10
0.05
0.00
−0.05
−0.10
0.0e+00
1.5e+06
genome coordinates
S^{G-C}_{CDS}
0.20
0.15
0.10
0.05
0.00
0.0e+00
1.5e+06
genome coordinates
Listeria innocua Clip11262
S^{A-T}_{CDS}
0.25
0.20
0.15
0.10
0.05
0.00
−0.05
−0.10
0.0e+00
1.5e+06
genome coordinates
S^{G-C}_{CDS}
0.20
0.15
0.10
0.05
0.00
0.0e+00
1.5e+06
genome coordinates

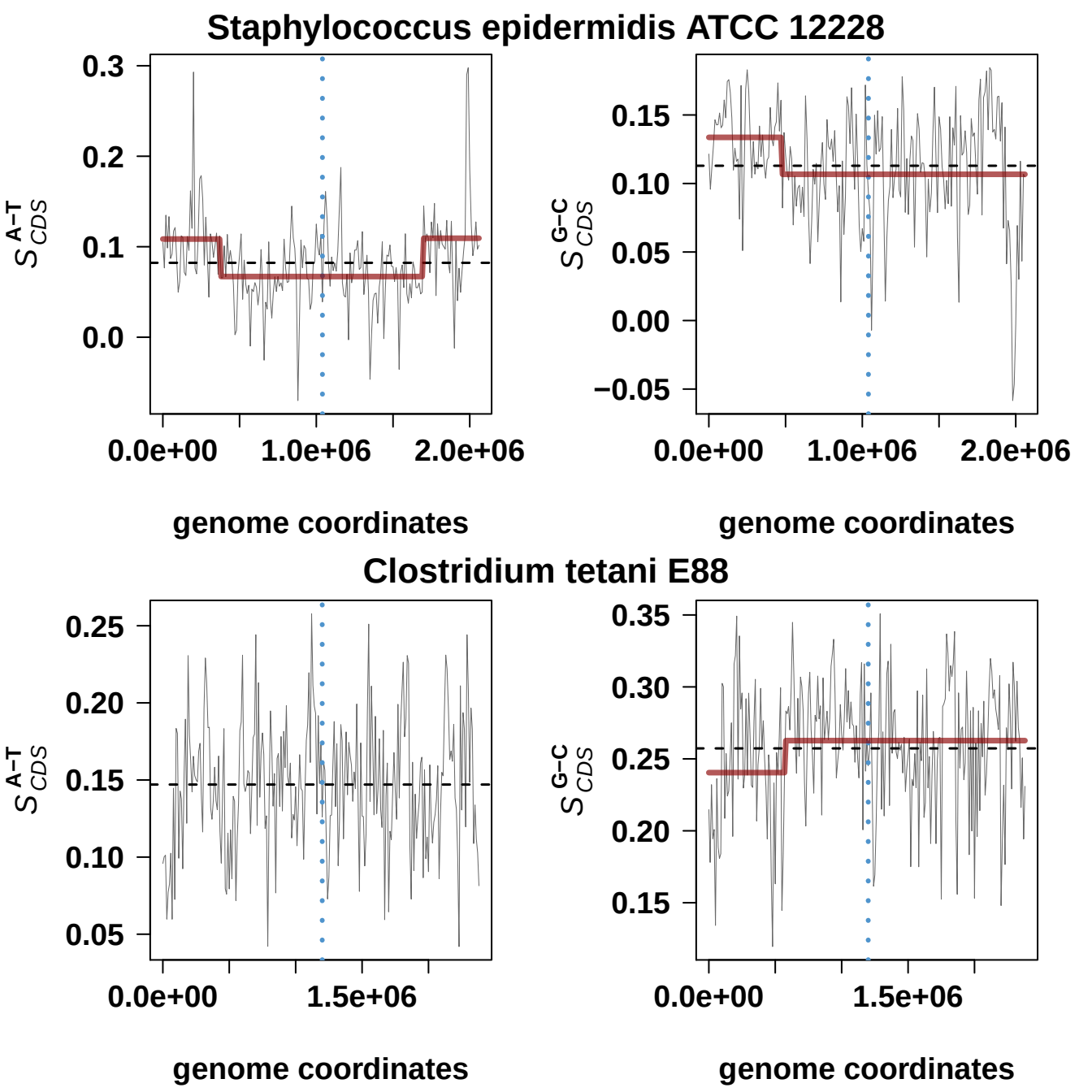

Clostridium perfringens str. 13
0.20
0.15
0.10
0.05
S^{A-T}_{CDS}
0.0e+00
1.5e+06
genome coordinates
0.35
0.30
0.25
0.20
S^{G-C}_{CDS}
0.0e+00
1.5e+06
genome coordinates
Streptococcus pyogenes MGAS8232
0.15
0.10
0.05
0.00
−0.05
S^{A-T}_{CDS}
0.0e+00
1.0e+06
genome coordinates
0.15
0.10
0.05
0.00
S^{G-C}_{CDS}
0.0e+00
1.0e+06
genome coordinates

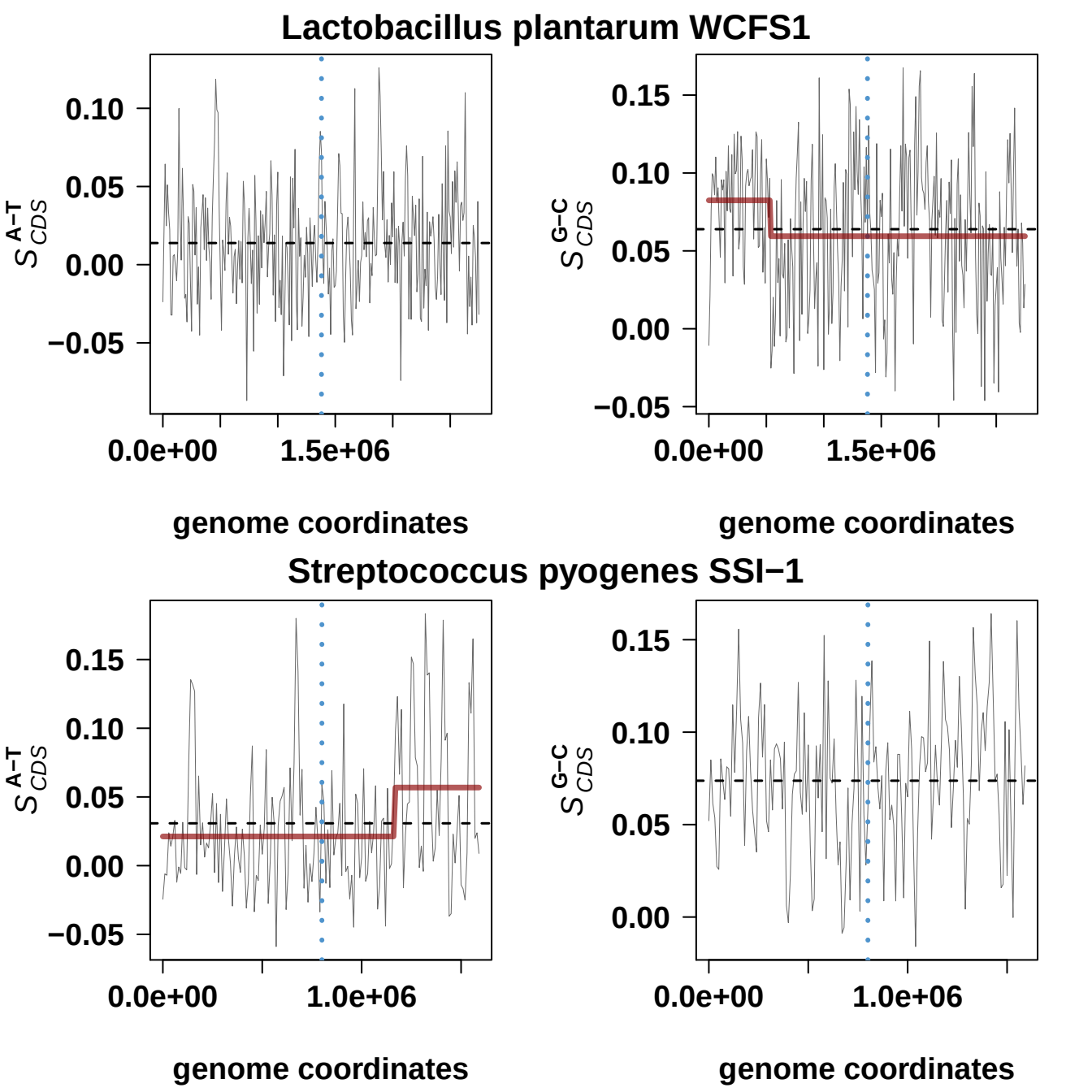

Thermoanaerobacter tengcongensis MB4
S^{A-T}_{CDS}
0.25
0.20
0.15
0.10
0.05
0.00
−0.05
0.0e+00
1.5e+06
genome coordinates
S^{G-C}_{CDS}
0.30
0.25
0.20
0.15
0.10
0.0e+00
1.5e+06
genome coordinates
Bacillus cereus ATCC 10987
S^{A-T}_{CDS}
0.20
0.15
0.10
0.05
0.00
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{CDS}
0.3
0.2
0.1
0.0
−0.1
−0.2
0e+00
2e+06
4e+06
genome coordinates

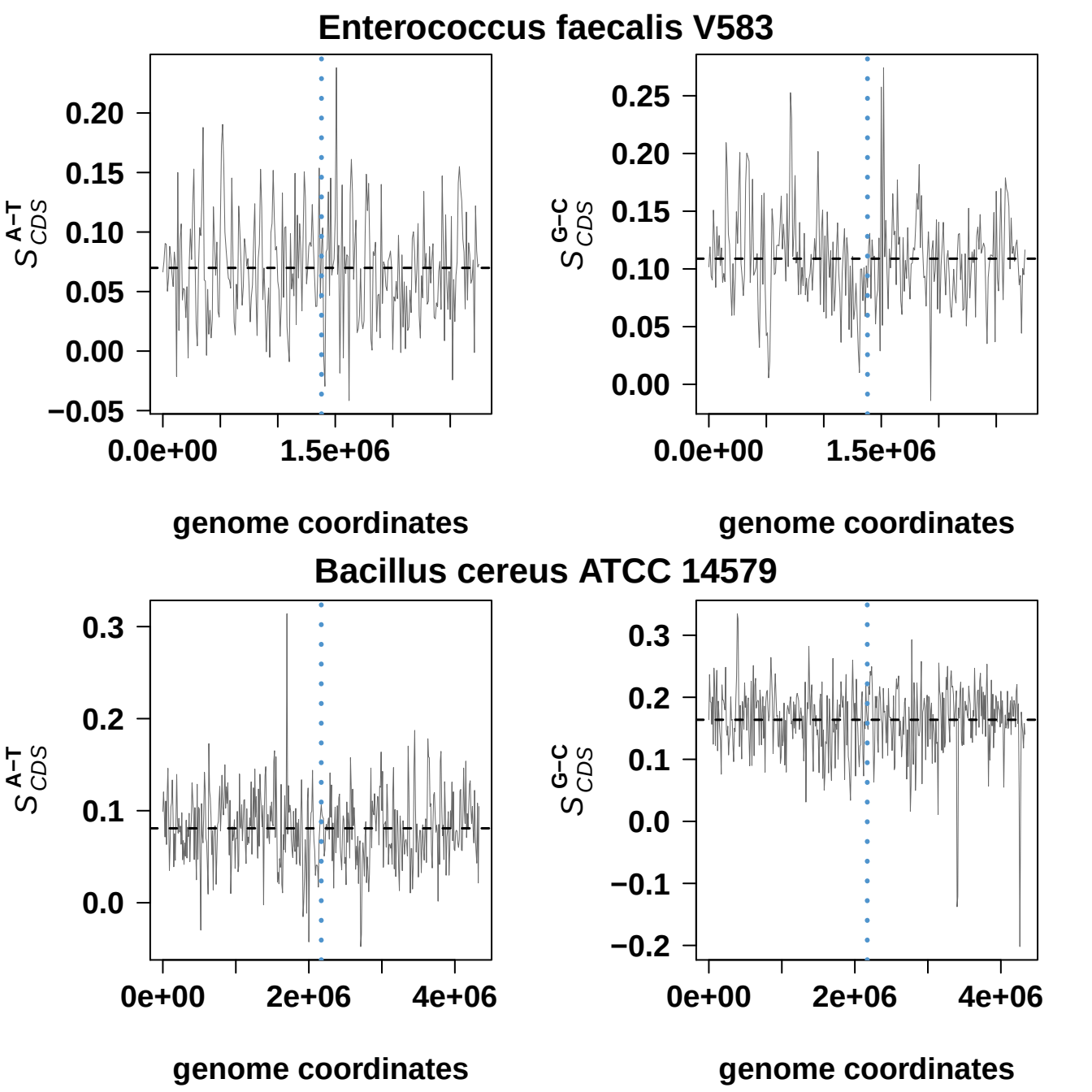

Staphylococcus aureus subsp. aureus MW2
S^{A-T}_{CDS}
0.30
0.25
0.20
0.15
0.10
0.05
0.00
0.0e+00
1.5e+06
genome coordinates
S^{G-C}_{CDS}
0.25
0.20
0.15
0.10
0.05
0.00
0.0e+00
1.5e+06
genome coordinates
Bacillus anthracis str. Ames
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
−0.05
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{CDS}
0.3
0.2
0.1
0.0
−0.1
0e+00
2e+06
4e+06
genome coordinates

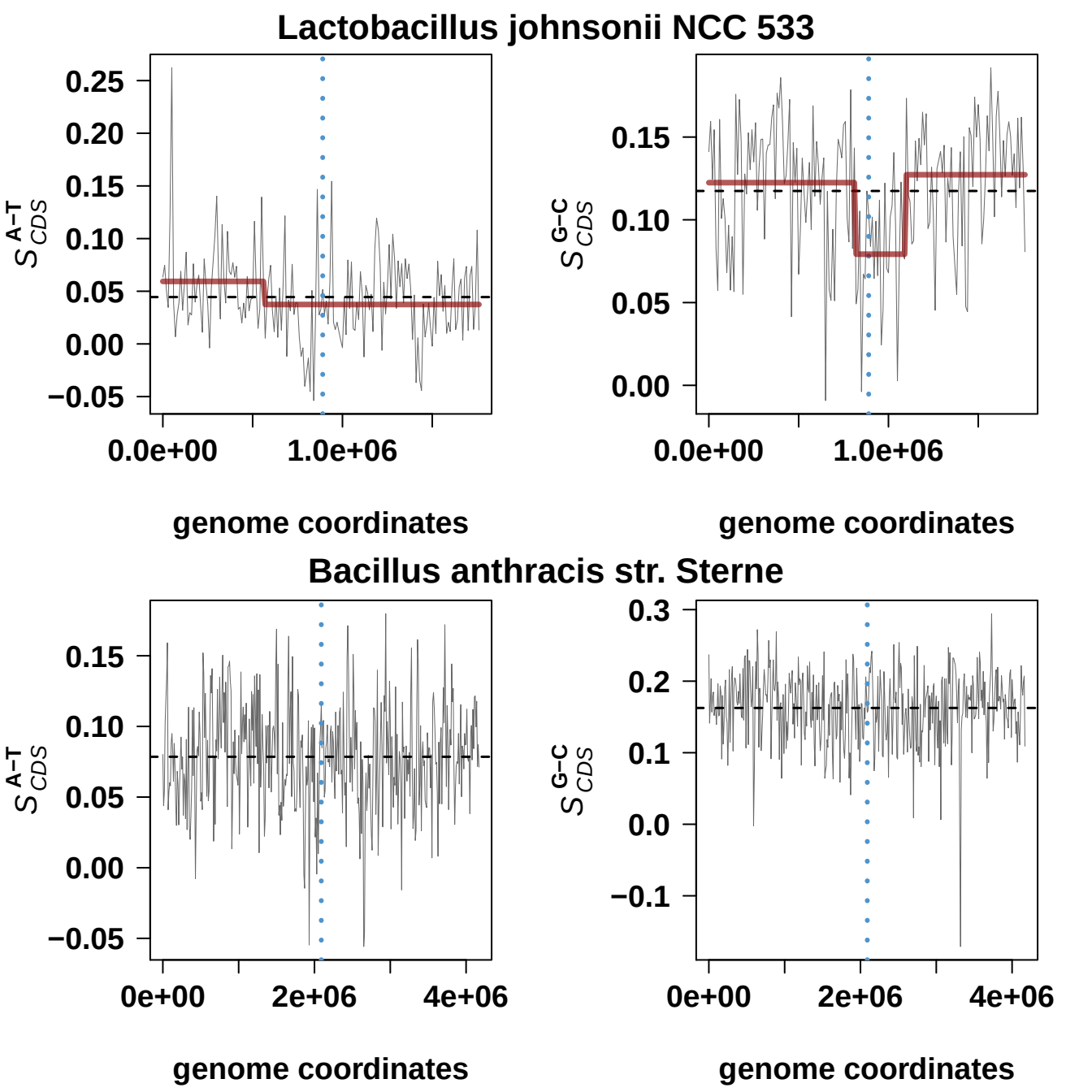

Streptococcus pyogenes MGAS315
0.15
0.10
0.05
0.00
−0.05
S^{A-T}_{CDS}
0.0e+00
1.0e+06
genome coordinates
0.15
0.10
0.05
0.00
S^{G-C}_{CDS}
0.0e+00
1.0e+06
genome coordinates
Streptococcus agalactiae 2603V/R
0.15
0.10
0.05
0.00
−0.05
S^{A-T}_{CDS}
0.0e+00
1.0e+06
genome coordinates
0.25
0.20
0.15
0.10
0.05
0.00
S^{G-C}_{CDS}
0.0e+00
1.0e+06
genome coordinates

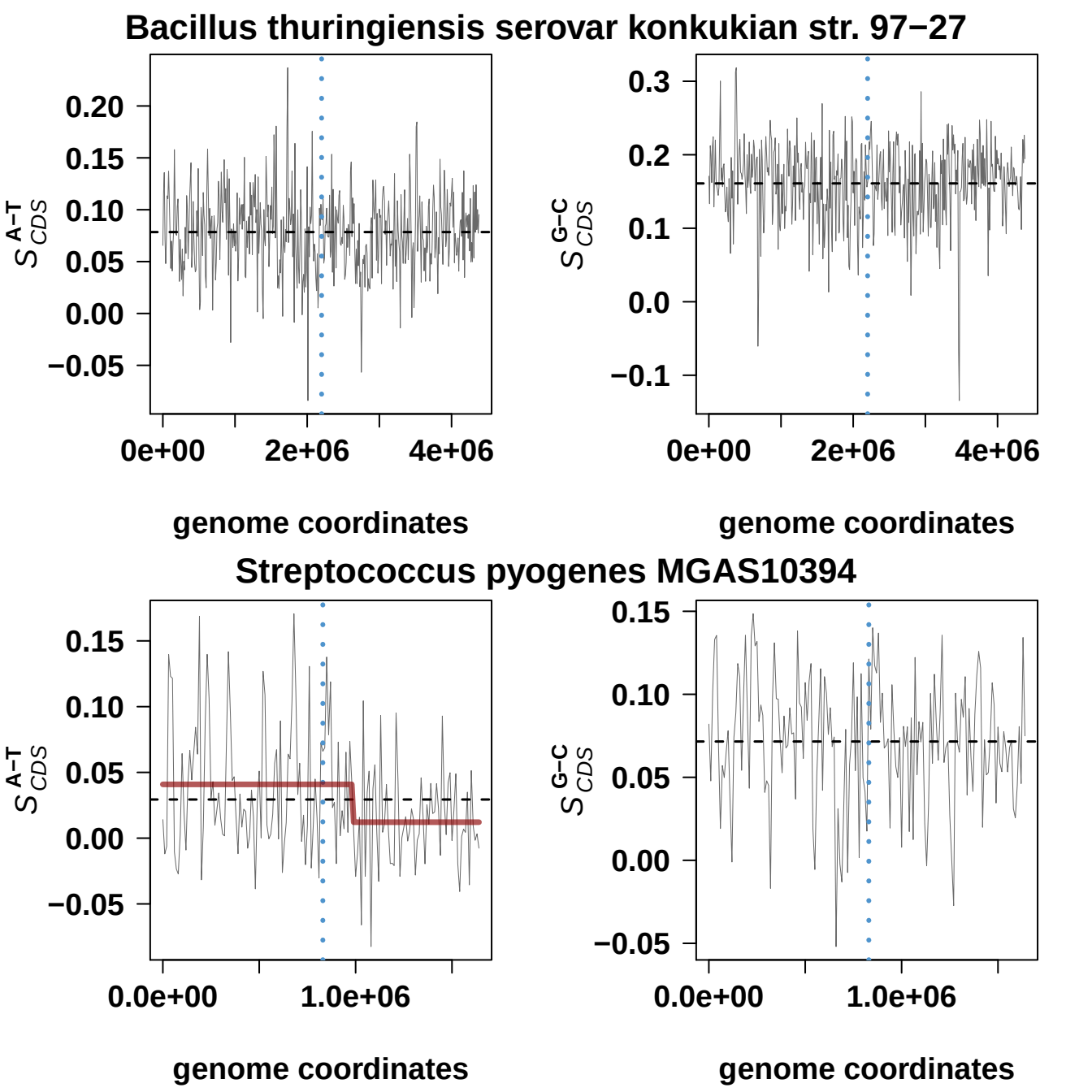

Oceanobacillus iheyensis HTE831
S^{A-T}_{CDS}
0.20
0.15
0.10
0.05
0.00
0.0e+00
1.5e+06
3.0e+06
genome coordinates
S^{G-C}_{CDS}
0.20
0.15
0.10
0.0e+00
1.5e+06
3.0e+06
genome coordinates
Streptococcus mutans UA159
S^{A-T}_{CDS}
0.05
0.00
−0.05
0.0e+00
1.0e+06
genome coordinates
S^{G-C}_{CDS}
0.30
0.25
0.20
0.15
0.10
0.05
0.0e+00
1.0e+06
genome coordinates

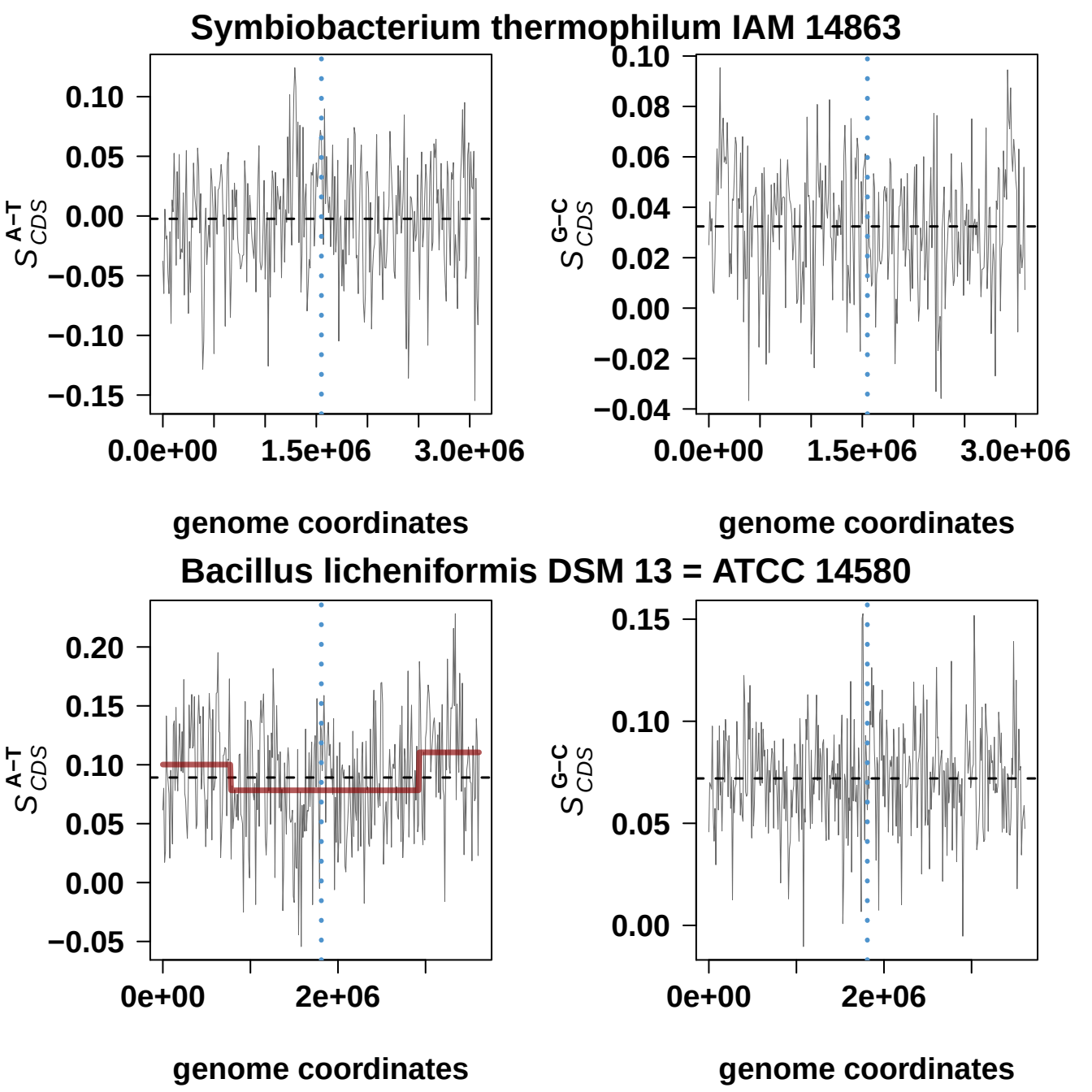

Staphylococcus epidermidis ATCC 12228
S^{A-T}_{CDS}
0.3
0.2
0.1
0.0
0.0e+00
1.0e+06
2.0e+06
genome coordinates
S^{G-C}_{CDS}
0.15
0.10
0.05
0.00
−0.05
0.0e+00
1.0e+06
2.0e+06
genome coordinates
Clostridium tetani E88
S^{A-T}_{CDS}
0.25
0.20
0.15
0.10
0.05
0.0e+00
1.5e+06
genome coordinates
S^{G-C}_{CDS}
0.35
0.30
0.25
0.20
0.15
0.0e+00
1.5e+06
genome coordinates

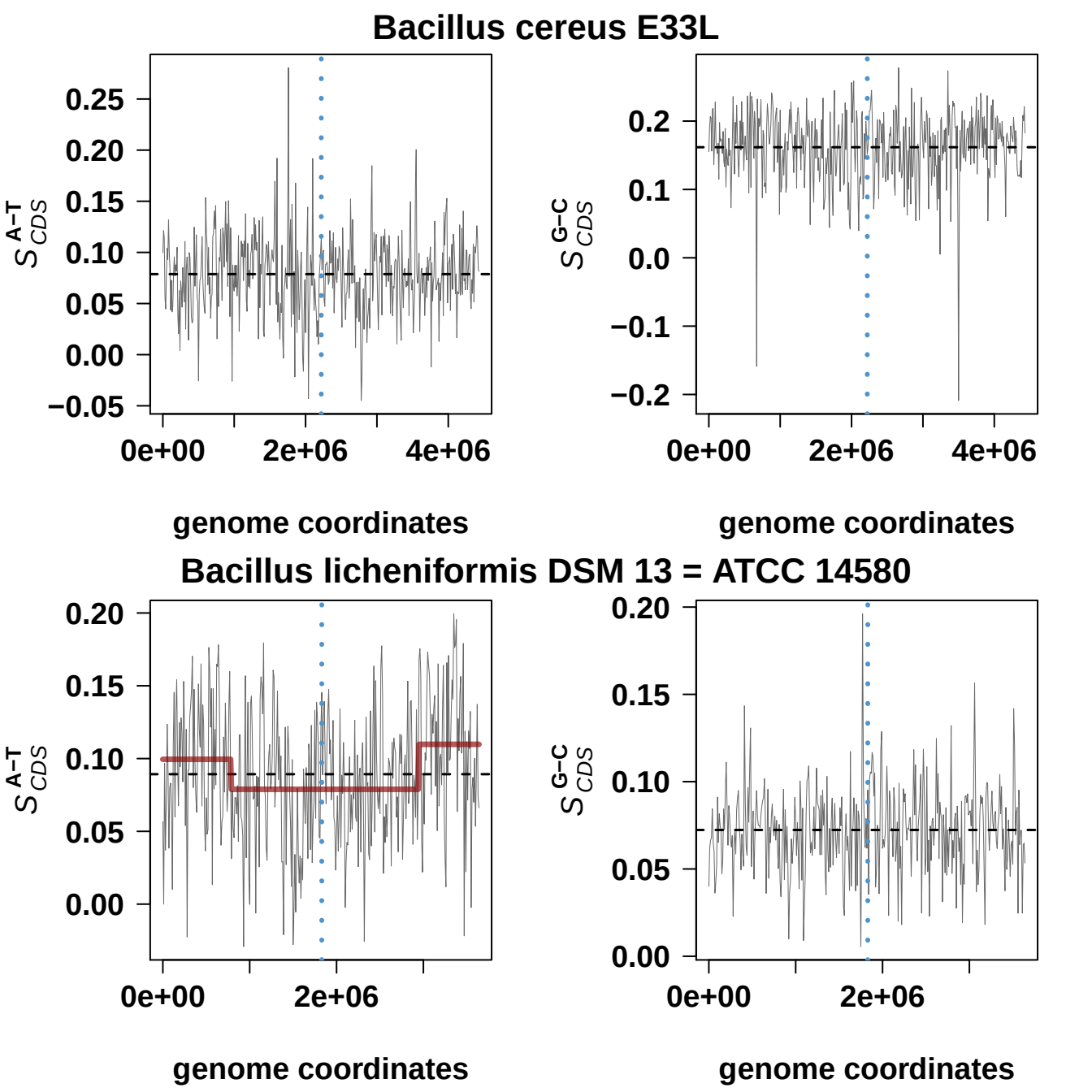

Lactobacillus plantarum WCFS1
0.10
0.05
0.00
−0.05
S^{A-T}_{CDS}
0.0e+00
1.5e+06
genome coordinates
0.15
0.10
0.05
0.00
−0.05
S^{G-C}_{CDS}
0.0e+00
1.5e+06
genome coordinates
Streptococcus pyogenes SSI−1
0.15
0.10
0.05
0.00
−0.05
S^{A-T}_{CDS}
0.0e+00
1.0e+06
genome coordinates
0.15
0.10
0.05
0.00
S^{G-C}_{CDS}
0.0e+00
1.0e+06
genome coordinates

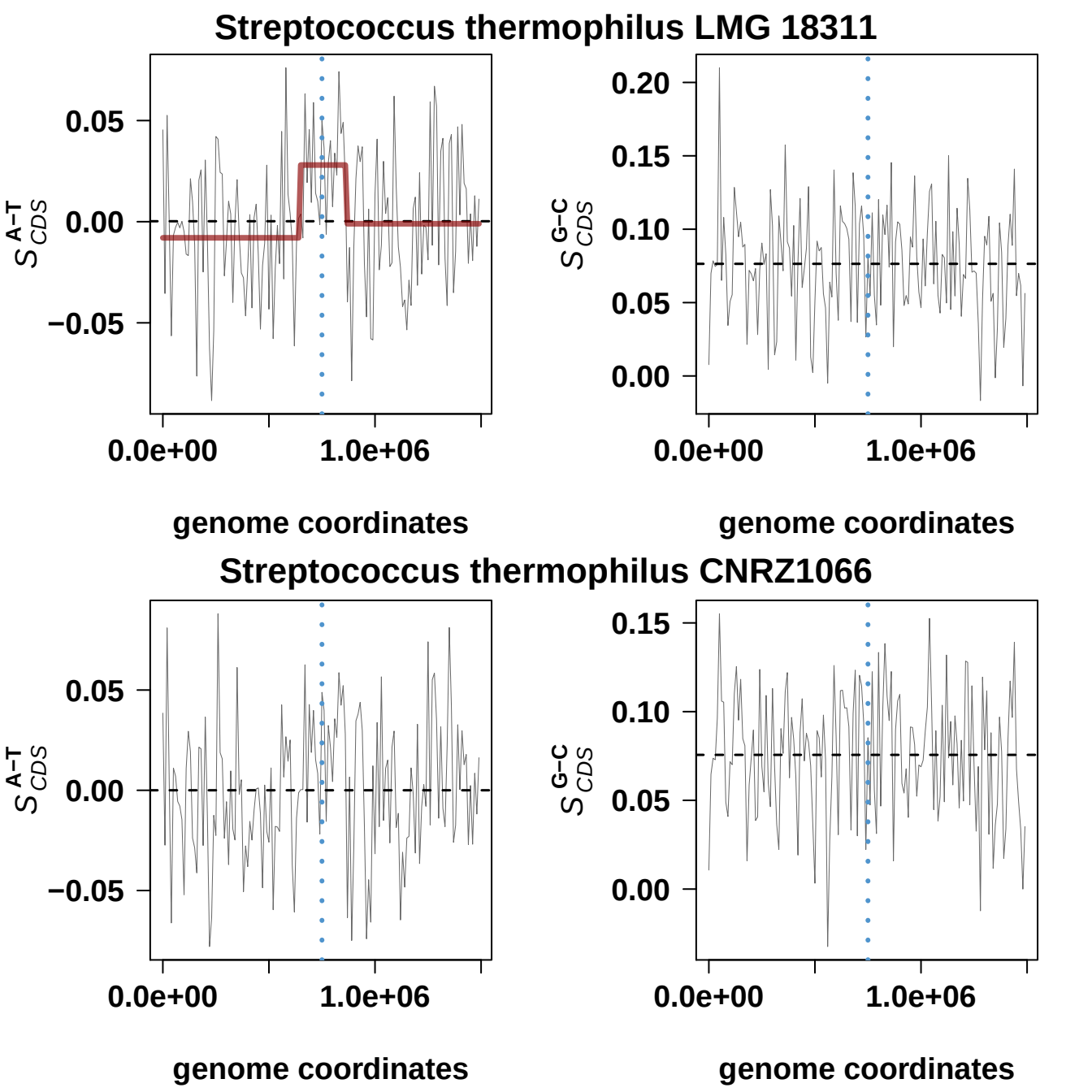

Enterococcus faecalis V583
S^{A-T}_{CDS}
0.20
0.15
0.10
0.05
0.00
−0.05
0.0e+00
1.5e+06
genome coordinates
S^{G-C}_{CDS}
0.25
0.20
0.15
0.10
0.05
0.00
0.0e+00
1.5e+06
genome coordinates
Bacillus cereus ATCC 14579
S^{A-T}_{CDS}
0.3
0.2
0.1
0.0
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{CDS}
0.3
0.2
0.1
0.0
−0.1
−0.2
0e+00
2e+06
4e+06
genome coordinates

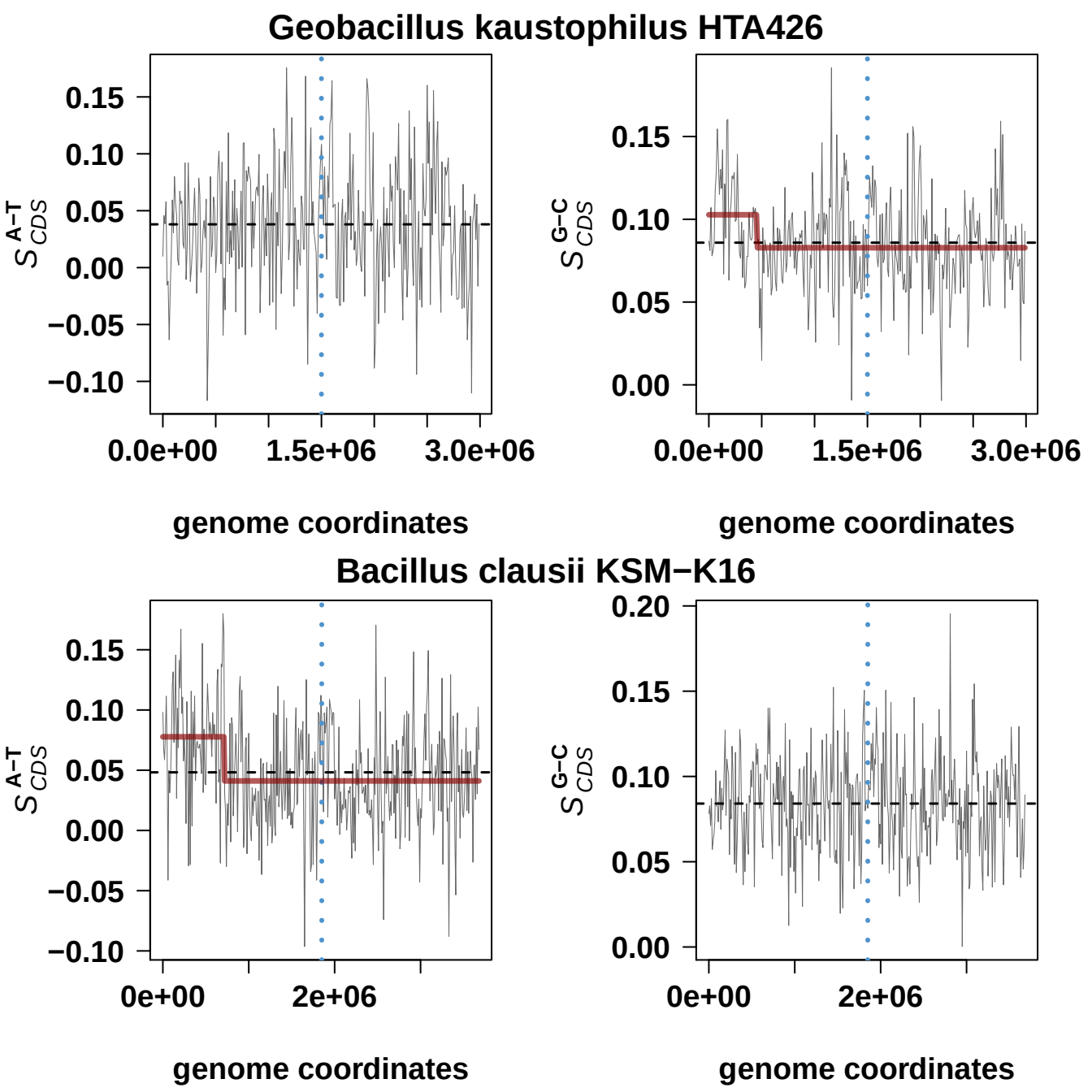

Lactobacillus johnsonii NCC 533
0.25
0.20
0.15
0.10
0.05
0.00
−0.05
S^{A-T}_{CDS}
0.0e+00
1.0e+06
genome coordinates
0.15
0.10
0.05
0.00
S^{G-C}_{CDS}
0.0e+00
1.0e+06
genome coordinates
Bacillus anthracis str. Sterne
0.15
0.10
0.05
0.00
−0.05
S^{A-T}_{CDS}
0e+00
2e+06
4e+06
genome coordinates
0.3
0.2
0.1
0.0
−0.1
S^{G-C}_{CDS}
0e+00
2e+06
4e+06
genome coordinates

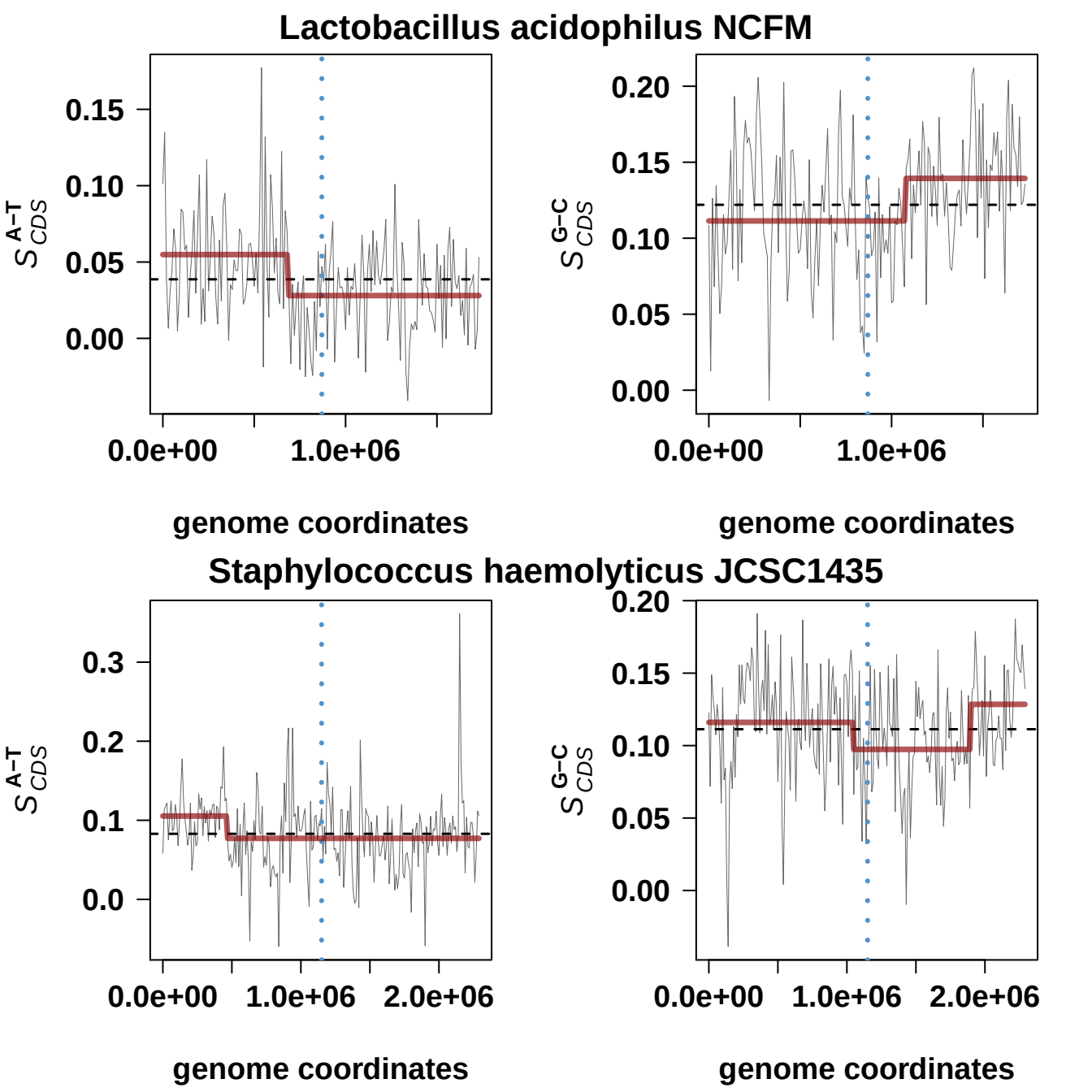

Bacillus thuringiensis serovar konkukian str. 97−27
S^{A-T}_{CDS}
0.20
0.15
0.10
0.05
0.00
−0.05
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{CDS}
0.3
0.2
0.1
0.0
−0.1
0e+00
2e+06
4e+06
genome coordinates
Streptococcus pyogenes MGAS10394
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
−0.05
0.0e+00
1.0e+06
genome coordinates
S^{G-C}_{CDS}
0.15
0.10
0.05
0.00
−0.05
0.0e+00
1.0e+06
genome coordinates

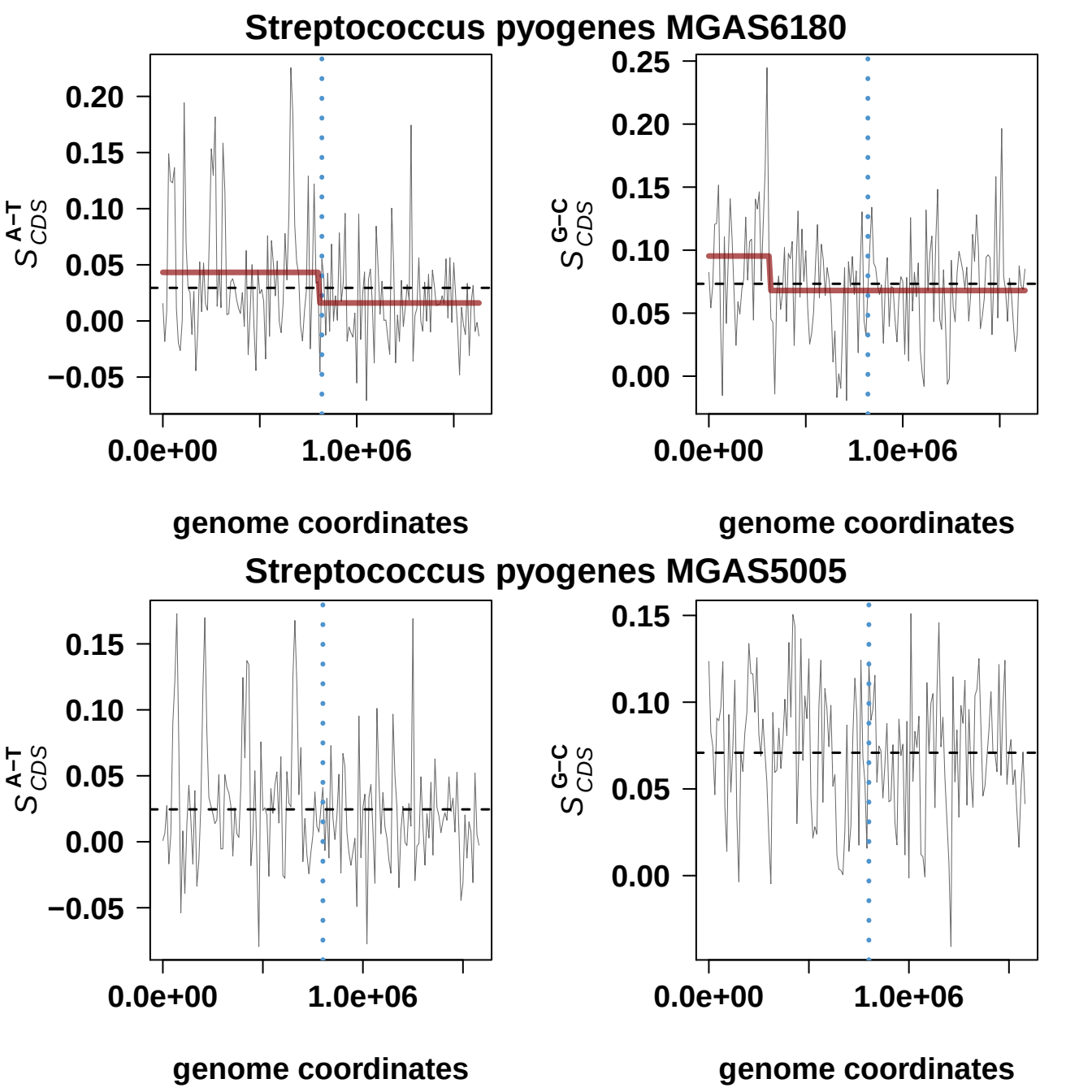

Symbiobacterium thermophilum IAM 14863
S^{A-T}_{CDS}
0.10
0.05
0.00
−0.05
−0.10
−0.15
0.0e+00
1.5e+06
3.0e+06
genome coordinates
S^{G-C}_{CDS}
0.10
0.08
0.06
0.04
0.02
0.00
−0.02
−0.04
0.0e+00
1.5e+06
3.0e+06
genome coordinates
Bacillus licheniformis DSM 13 = ATCC 14580
S^{A-T}_{CDS}
0.20
0.15
0.10
0.05
0.00
−0.05
0e+00
2e+06
genome coordinates
S^{G-C}_{CDS}
0.15
0.10
0.05
0.00
0e+00
2e+06
genome coordinates

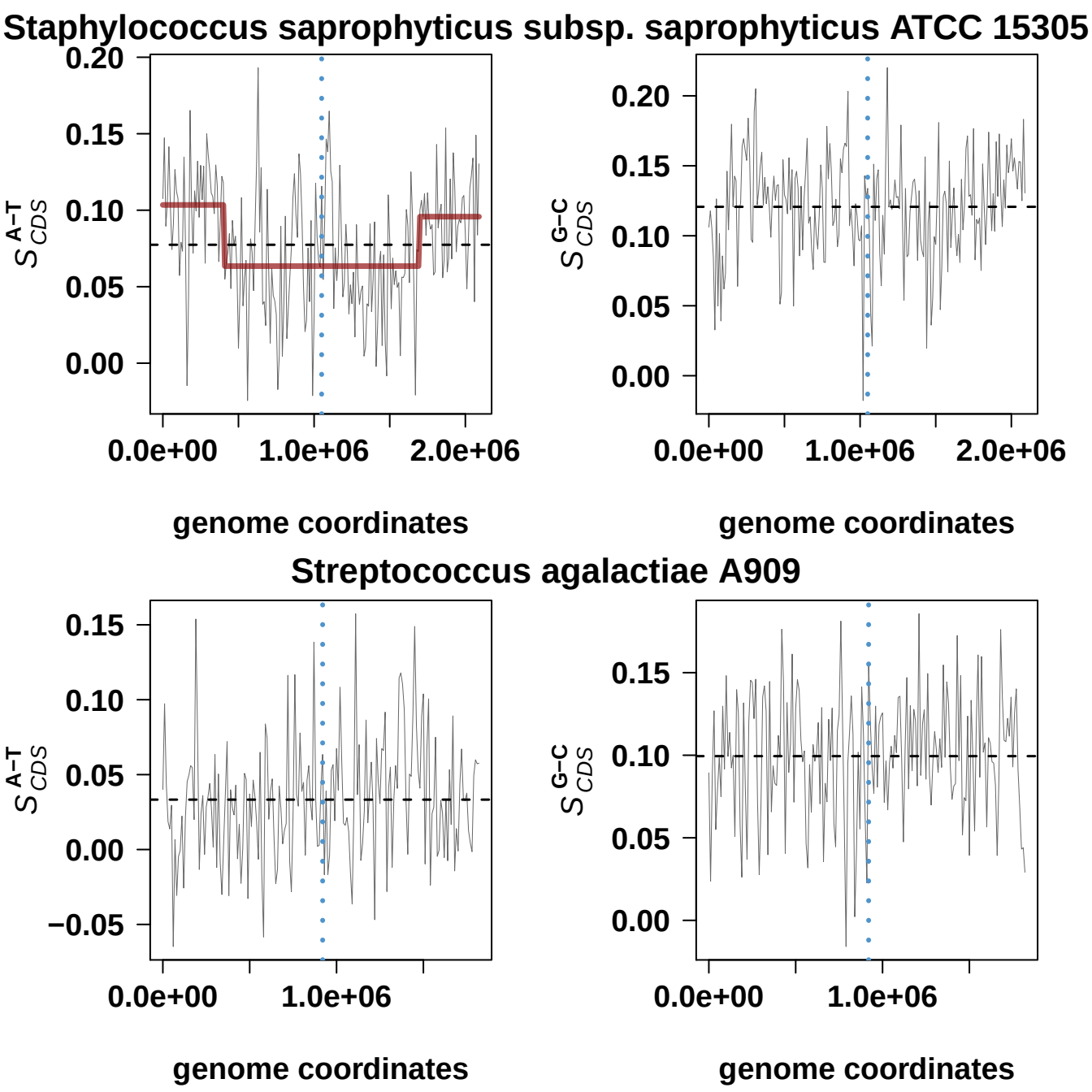

Bacillus cereus E33L
S^{A-T}_{CDS}
0.25
0.20
0.15
0.10
0.05
0.00
−0.05
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{CDS}
0.2
0.1
0.0
−0.1
−0.2
0e+00
2e+06
4e+06
genome coordinates
Bacillus licheniformis DSM 13 = ATCC 14580
S^{A-T}_{CDS}
0.20
0.15
0.10
0.05
0.00
0e+00
2e+06
genome coordinates
S^{G-C}_{CDS}
0.20
0.15
0.10
0.05
0.00
0e+00
2e+06
genome coordinates

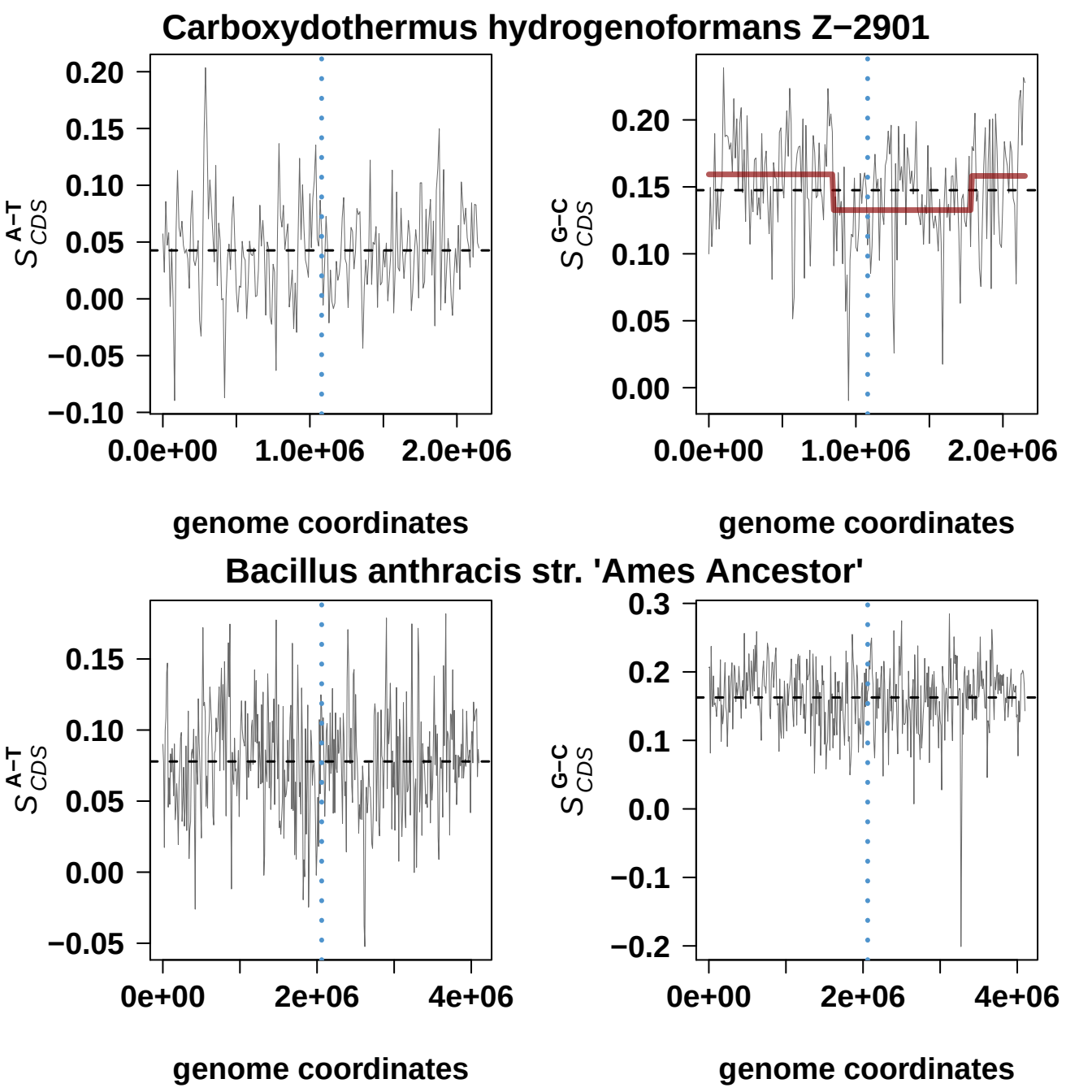

Streptococcus thermophilus LMG 18311
0.05
0.00
−0.05
S^{A-T}_{CDS}
0.0e+00
1.0e+06
genome coordinates
0.20
0.15
0.10
0.05
0.00
S^{G-C}_{CDS}
0.0e+00
1.0e+06
genome coordinates
Streptococcus thermophilus CNRZ1066
0.05
0.00
−0.05
S^{A-T}_{CDS}
0.0e+00
1.0e+06
genome coordinates
0.15
0.10
0.05
0.00
S^{G-C}_{CDS}
0.0e+00
1.0e+06
genome coordinates

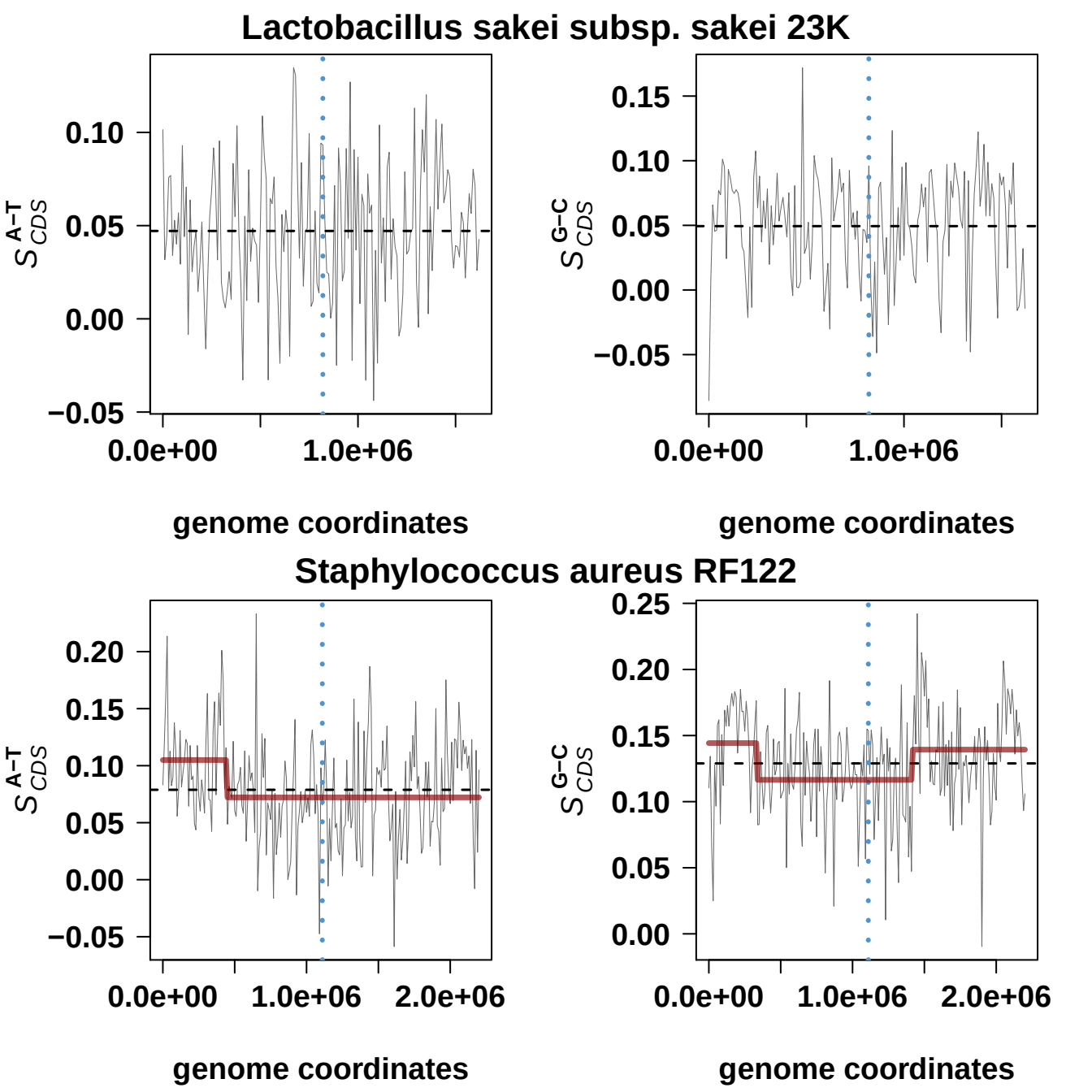

Geobacillus kaustophilus HTA426
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
−0.05
−0.10
0.0e+00
1.5e+06
3.0e+06
genome coordinates
S^{G-C}_{CDS}
0.15
0.10
0.05
0.00
0.0e+00
1.5e+06
3.0e+06
genome coordinates
Bacillus clausii KSM−K16
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
−0.05
−0.10
0e+00
2e+06
genome coordinates
S^{G-C}_{CDS}
0.20
0.15
0.10
0.05
0.00
0e+00
2e+06
genome coordinates

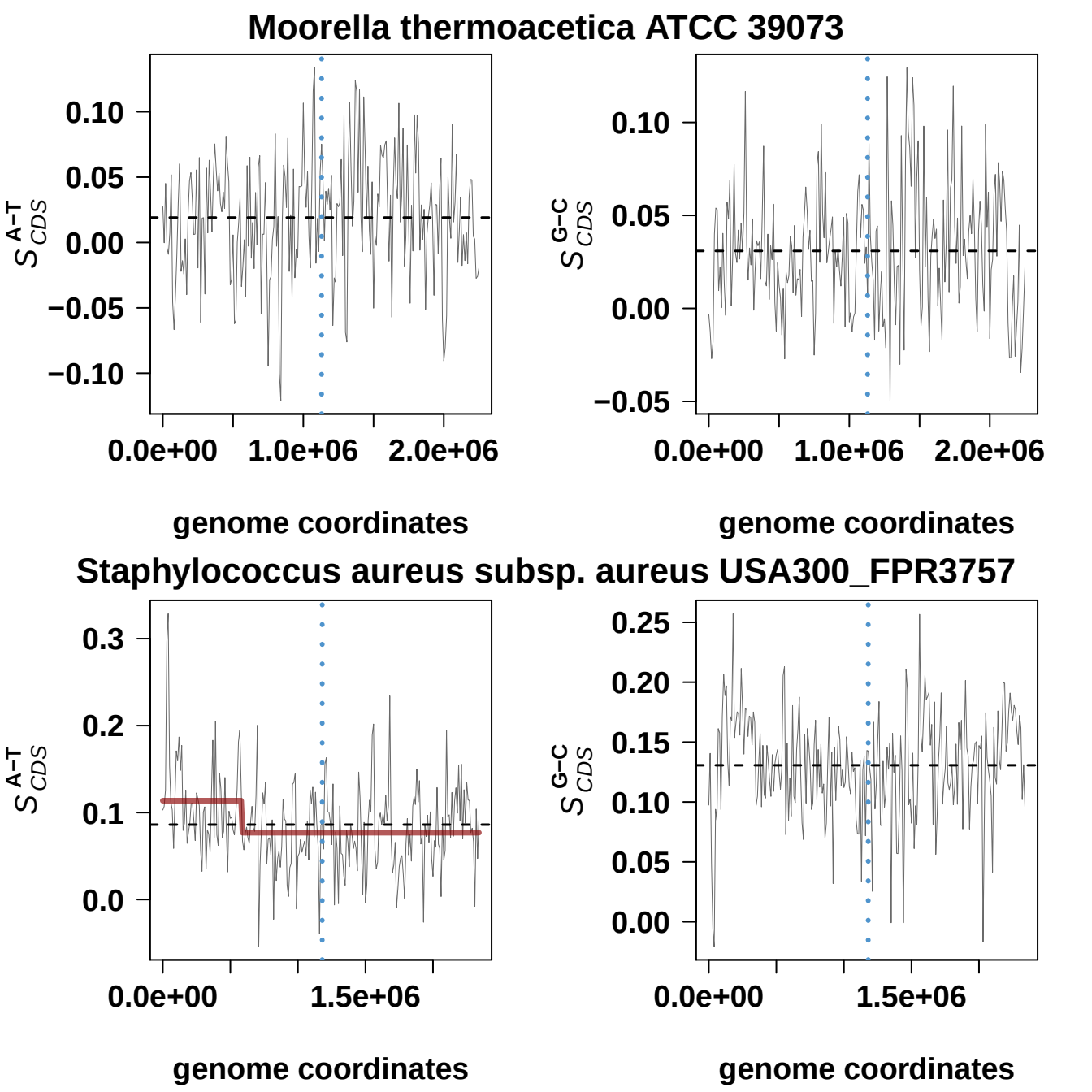

Lactobacillus acidophilus NCFM
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
0.0e+00
1.0e+06
genome coordinates
S^{G-C}_{CDS}
0.20
0.15
0.10
0.05
0.00
0.0e+00
1.0e+06
genome coordinates
Staphylococcus haemolyticus JCSC1435
S^{A-T}_{CDS}
0.3
0.2
0.1
0.0
0.0e+00
1.0e+06
2.0e+06
genome coordinates
S^{G-C}_{CDS}
0.20
0.15
0.10
0.05
0.00
0.0e+00
1.0e+06
2.0e+06
genome coordinates

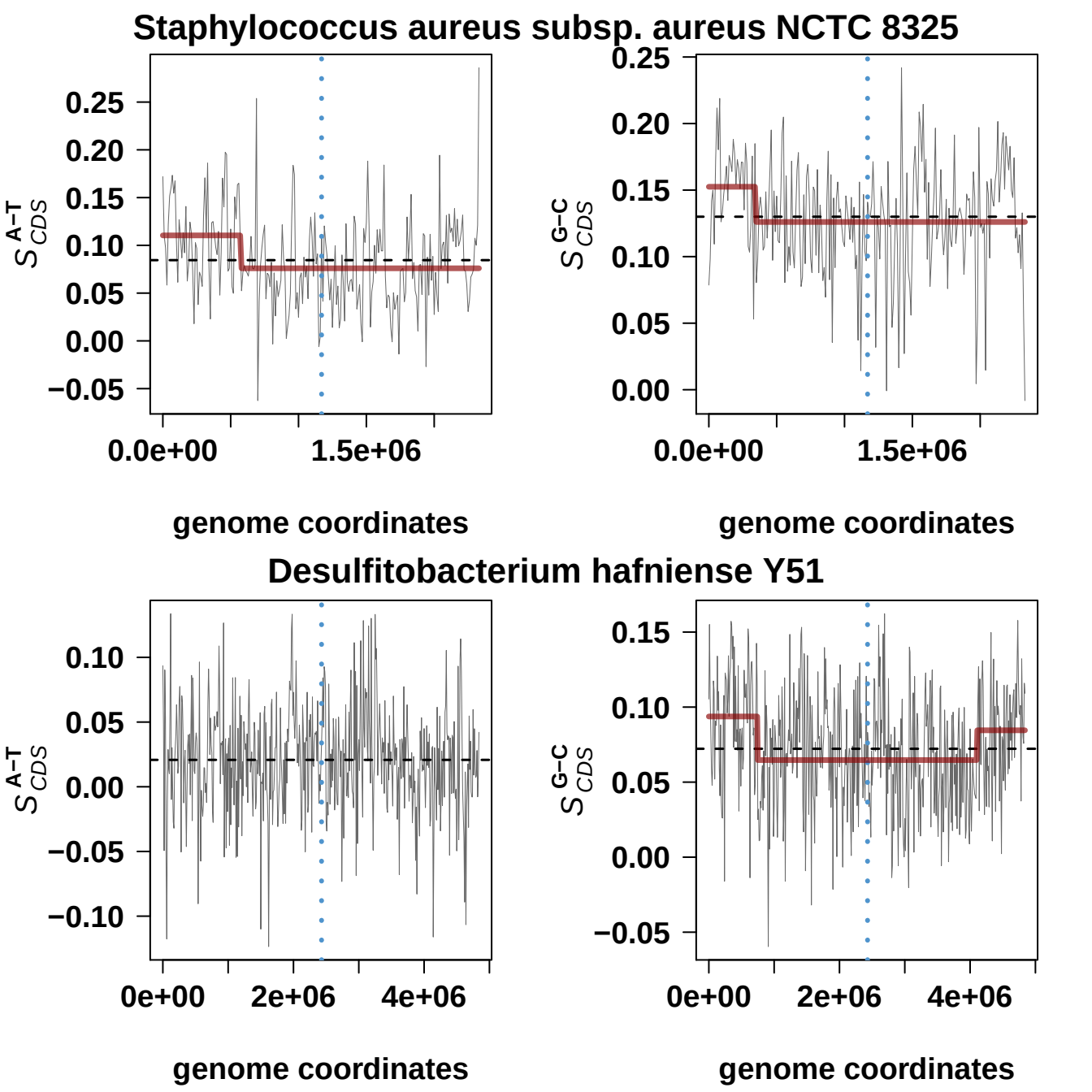

Streptococcus pyogenes MGAS6180
0.20
0.15
0.10
0.05
0.00
−0.05
S^{A-T}_{CDS}
0.0e+00
1.0e+06
genome coordinates
0.25
0.20
0.15
0.10
0.05
0.00
S^{G-C}_{CDS}
0.0e+00
1.0e+06
genome coordinates
Streptococcus pyogenes MGAS5005
0.15
0.10
0.05
0.00
−0.05
S^{A-T}_{CDS}
0.0e+00
1.0e+06
genome coordinates
0.15
0.10
0.05
0.00
S^{G-C}_{CDS}
0.0e+00
1.0e+06
genome coordinates

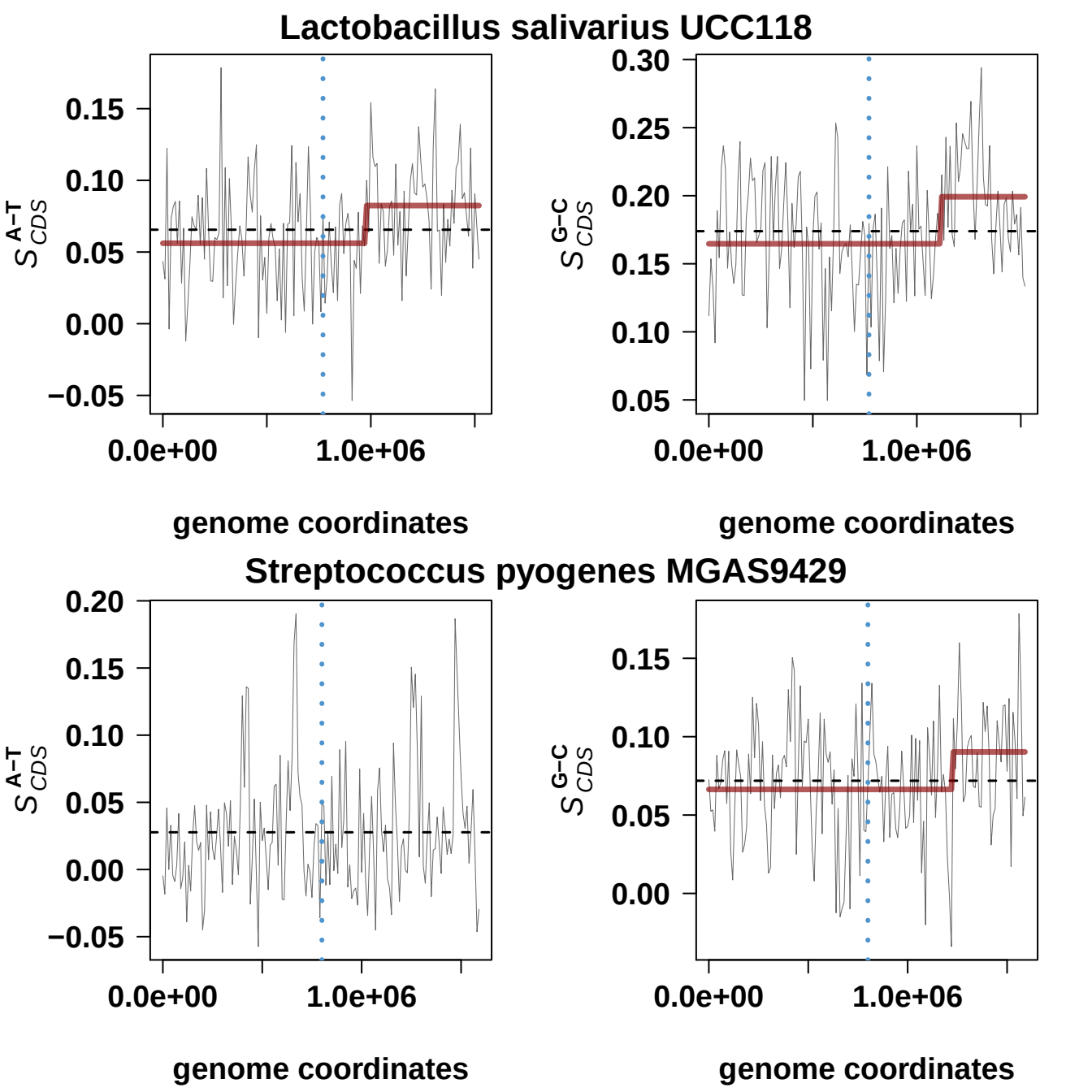

Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305
S^{A-T}_{CDS}
0.20
0.15
0.10
0.05
0.00
0.0e+00
1.0e+06
2.0e+06
genome coordinates
S^{G-C}_{CDS}
0.20
0.15
0.10
0.05
0.00
0.0e+00
1.0e+06
2.0e+06
genome coordinates
Streptococcus agalactiae A909
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
−0.05
0.0e+00
1.0e+06
genome coordinates
S^{G-C}_{CDS}
0.15
0.10
0.05
0.00
0.0e+00
1.0e+06
genome coordinates

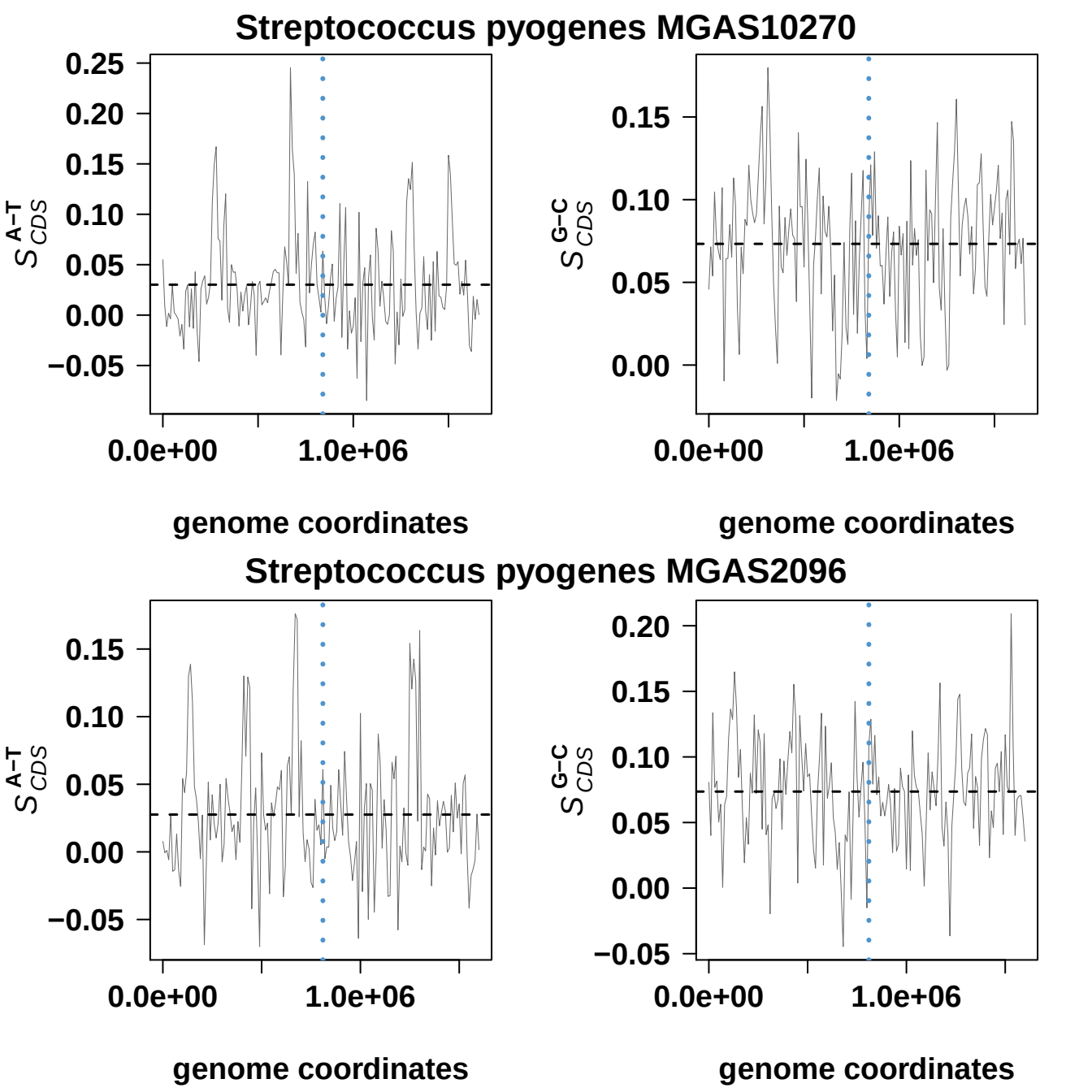

Carboxydothermus hydrogenoformans Z−2901
S^{A-T}_{CDS}
0.20
0.15
0.10
0.05
0.00
−0.05
−0.10
0.0e+00
1.0e+06
2.0e+06
genome coordinates
S^{G-C}_{CDS}
0.20
0.15
0.10
0.05
0.00
0.0e+00
1.0e+06
2.0e+06
genome coordinates
Bacillus anthracis str. 'Ames Ancestor'
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
−0.05
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{CDS}
0.3
0.2
0.1
0.0
−0.1
−0.2
0e+00
2e+06
4e+06
genome coordinates

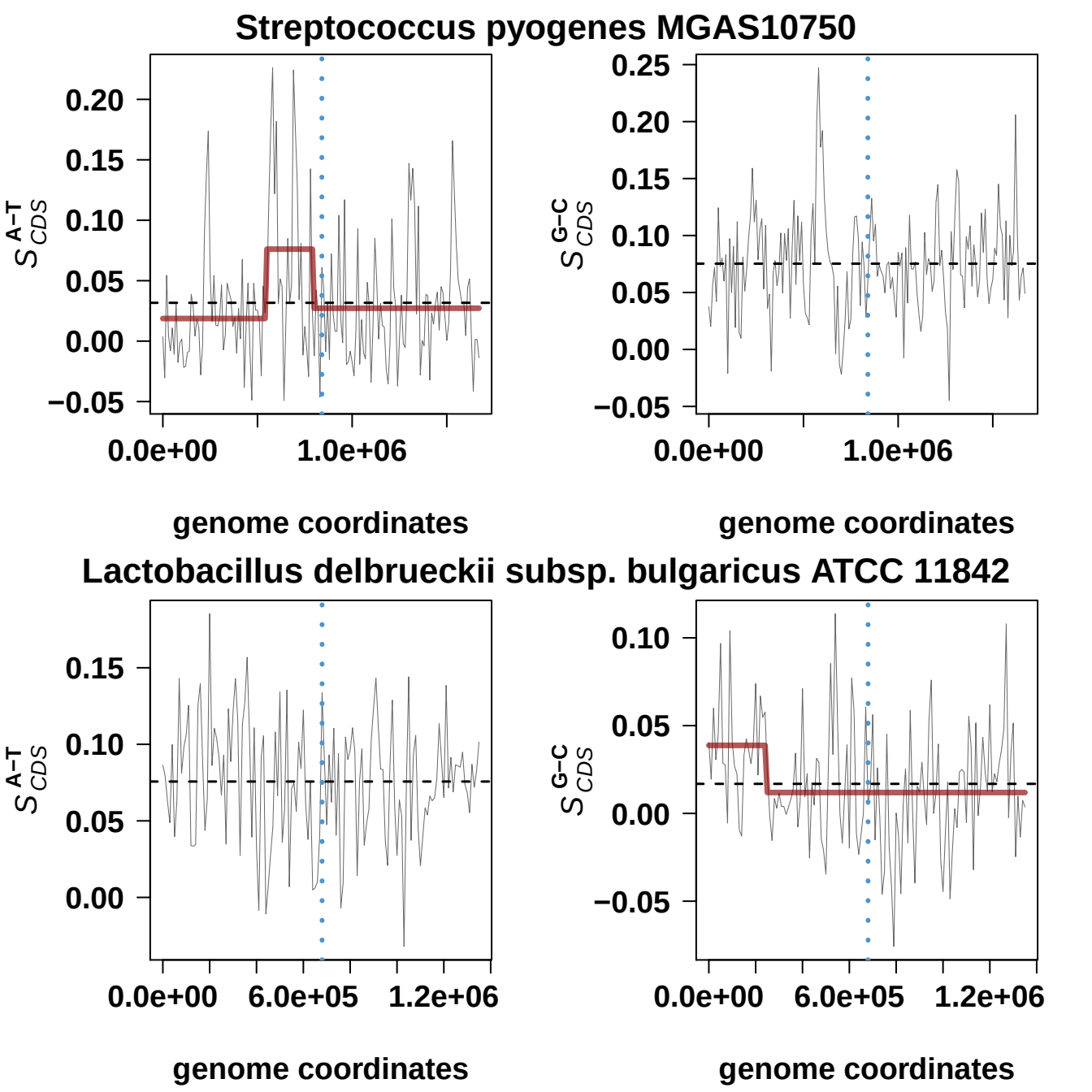

Lactobacillus sakei subsp. sakei 23K
S^{A-T}_{CDS}
0.10
0.05
0.00
−0.05
0.0e+00
1.0e+06
genome coordinates
S^{G-C}_{CDS}
0.15
0.10
0.05
0.00
−0.05
0.0e+00
1.0e+06
genome coordinates
Staphylococcus aureus RF122
S^{A-T}_{CDS}
0.20
0.15
0.10
0.05
0.00
−0.05
0.0e+00
1.0e+06
2.0e+06
genome coordinates
S^{G-C}_{CDS}
0.25
0.20
0.15
0.10
0.05
0.00
0.0e+00
1.0e+06
2.0e+06
genome coordinates


Moorella thermoacetica ATCC 39073
S^{A-T}_{CDS}
0.10
0.05
0.00
−0.05
−0.10
0.0e+00
1.0e+06
2.0e+06
genome coordinates
S^{G-C}_{CDS}
0.10
0.05
0.00
−0.05
0.0e+00
1.0e+06
2.0e+06
genome coordinates
Staphylococcus aureus subsp. aureus USA300_FPR3757
S^{A-T}_{CDS}
0.3
0.2
0.1
0.0
0.0e+00
1.5e+06
genome coordinates
S^{G-C}_{CDS}
0.25
0.20
0.15
0.10
0.05
0.00
0.0e+00
1.5e+06
genome coordinates


Staphylococcus aureus subsp. aureus NCTC 8325
S^{A-T}_{CDS}
0.25
0.20
0.15
0.10
0.05
0.00
−0.05
0.0e+00
1.5e+06
genome coordinates
S^{G-C}_{CDS}
0.25
0.20
0.15
0.10
0.05
0.00
0.0e+00
1.5e+06
genome coordinates
Desulfitobacterium hafniense Y51
S^{A-T}_{CDS}
0.10
0.05
0.00
−0.05
−0.10
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{CDS}
0.15
0.10
0.05
0.00
−0.05
0e+00
2e+06
4e+06
genome coordinates


Lactobacillus salivarius UCC118
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
−0.05
0.0e+00
1.0e+06
genome coordinates
S^{G-C}_{CDS}
0.30
0.25
0.20
0.15
0.10
0.05
0.0e+00
1.0e+06
genome coordinates
Streptococcus pyogenes MGAS9429
S^{A-T}_{CDS}
0.20
0.15
0.10
0.05
0.00
−0.05
0.0e+00
1.0e+06
genome coordinates
S^{G-C}_{CDS}
0.15
0.10
0.05
0.00
0.0e+00
1.0e+06
genome coordinates


Streptococcus pyogenes MGAS10270
0.25
0.20
0.15
0.10
0.05
0.00
−0.05
S^{A-T}_{CDS}
0.0e+00
1.0e+06
genome coordinates
0.15
0.10
0.05
0.00
S^{G-C}_{CDS}
0.0e+00
1.0e+06
genome coordinates
Streptococcus pyogenes MGAS2096
0.15
0.10
0.05
0.00
−0.05
S^{A-T}_{CDS}
0.0e+00
1.0e+06
genome coordinates
0.20
0.15
0.10
0.05
0.00
−0.05
S^{G-C}_{CDS}
0.0e+00
1.0e+06
genome coordinates


Streptococcus pyogenes MGAS10750
S^{A-T}_{CDS}
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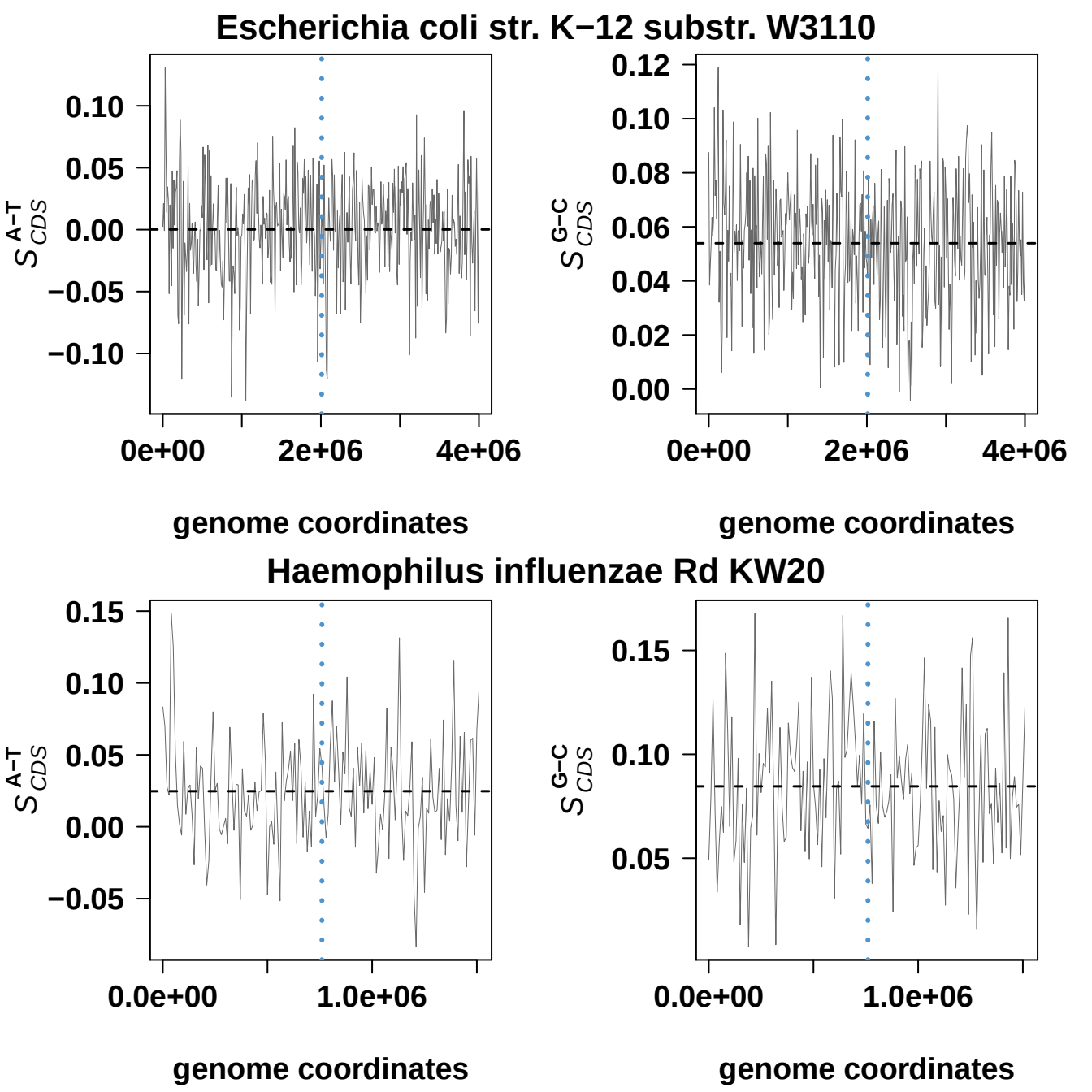
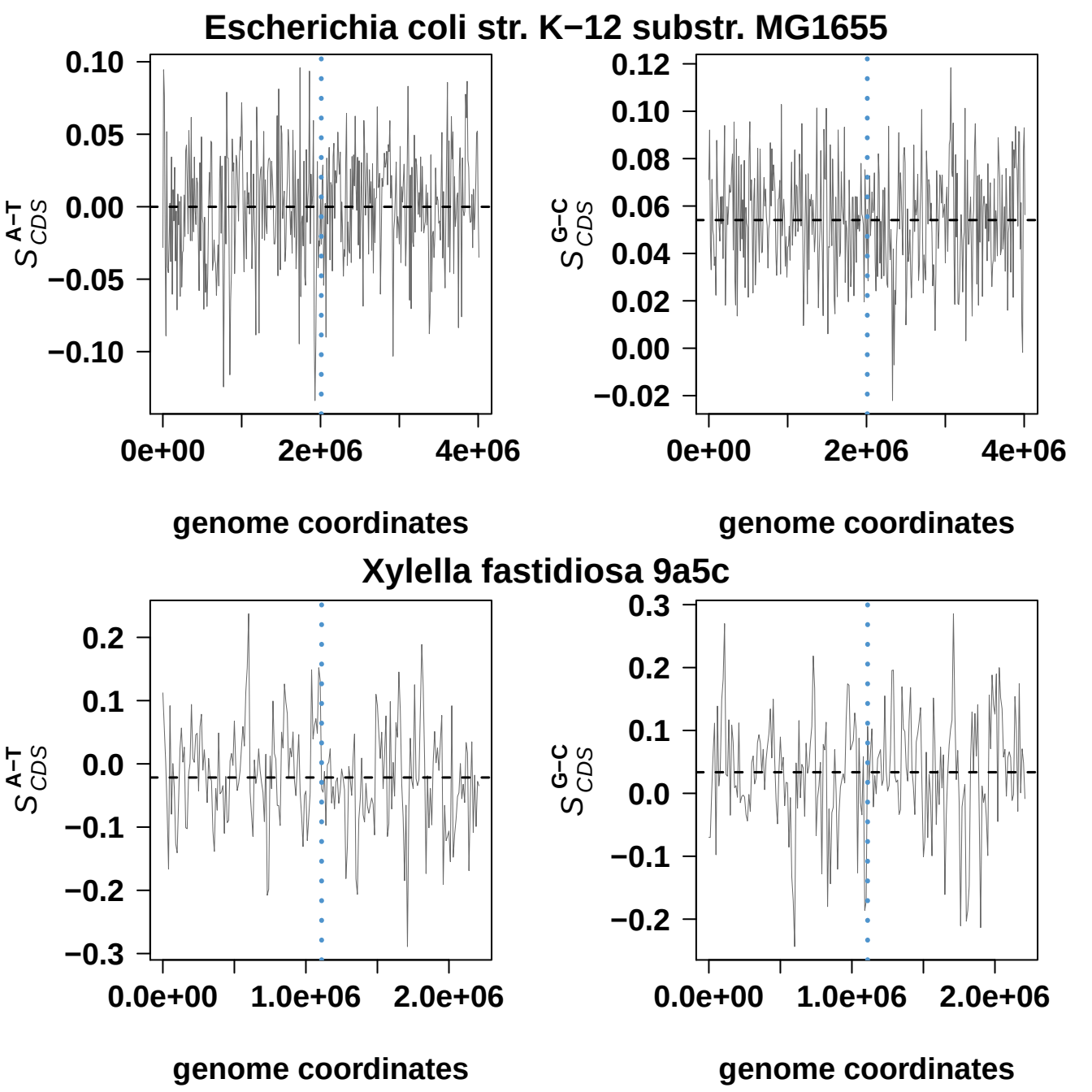
0.15
0.10
0.05
0.00
−0.05
0.0e+00
1.0e+06
genome coordinates
S^{G-C}_{CDS}
0.25
0.20
0.15
0.10
0.05
0.00
−0.05
0.0e+00
1.0e+06
genome coordinates
Lactobacillus delbrueckii subsp. bulgaricus ATCC 11842
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
0.0e+00
6.0e+05
1.2e+06
genome coordinates
S^{G-C}_{CDS}
0.10
0.05
0.00
−0.05
0.0e+00
6.0e+05
1.2e+06
genome coordinates


Escherichia coli str. K−12 substr. W3110
S^{A-T}_{CDS}
0.10
0.05
0.00
−0.05
−0.10
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{CDS}
0.12
0.10
0.08
0.06
0.04
0.02
0.00
0e+00
2e+06
4e+06
genome coordinates
Haemophilus influenzae Rd KW20
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
−0.05
0.0e+00
1.0e+06
genome coordinates
S^{G-C}_{CDS}
0.15
0.10
0.05
0.0e+00
1.0e+06
genome coordinates


Escherichia coli str. K−12 substr. MG1655
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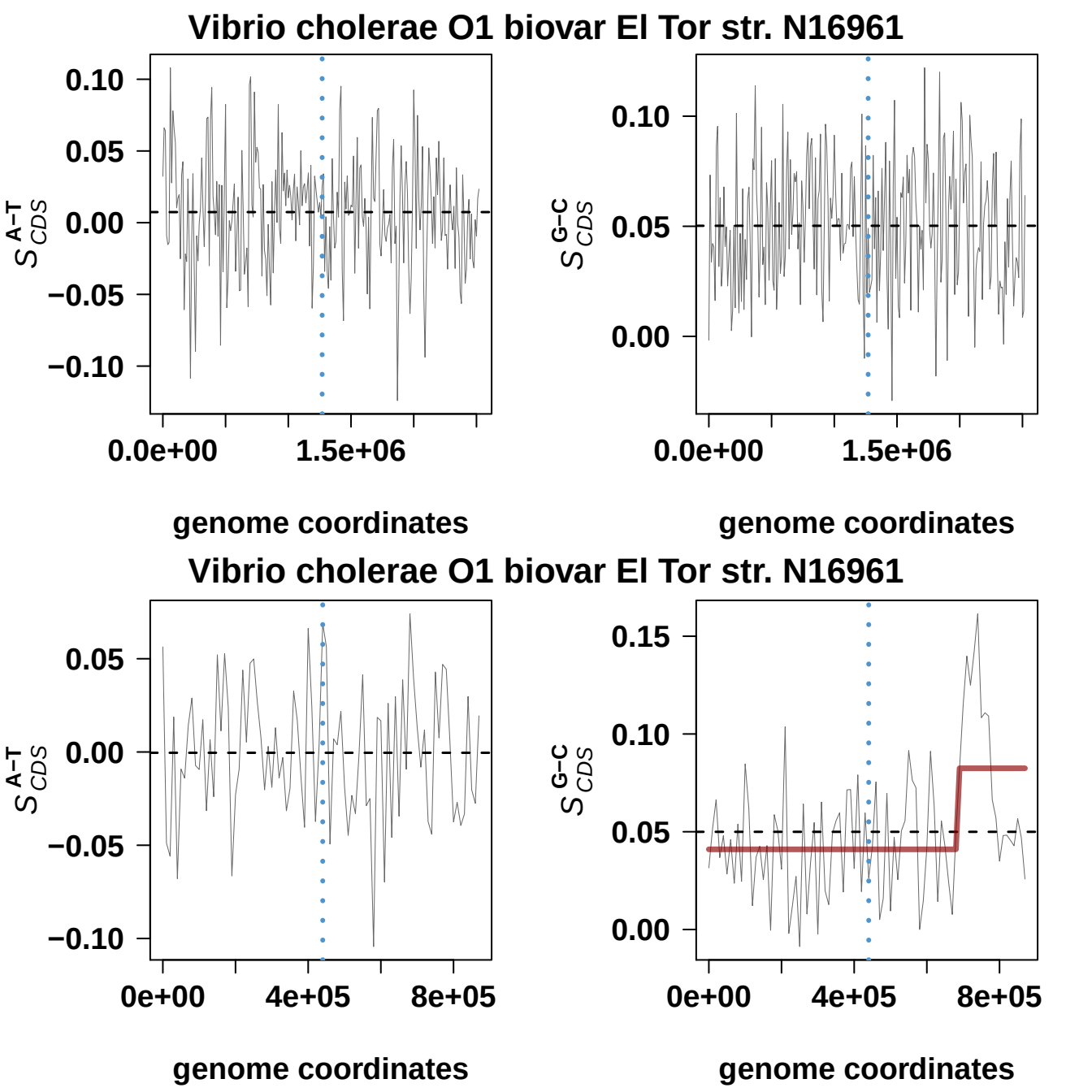
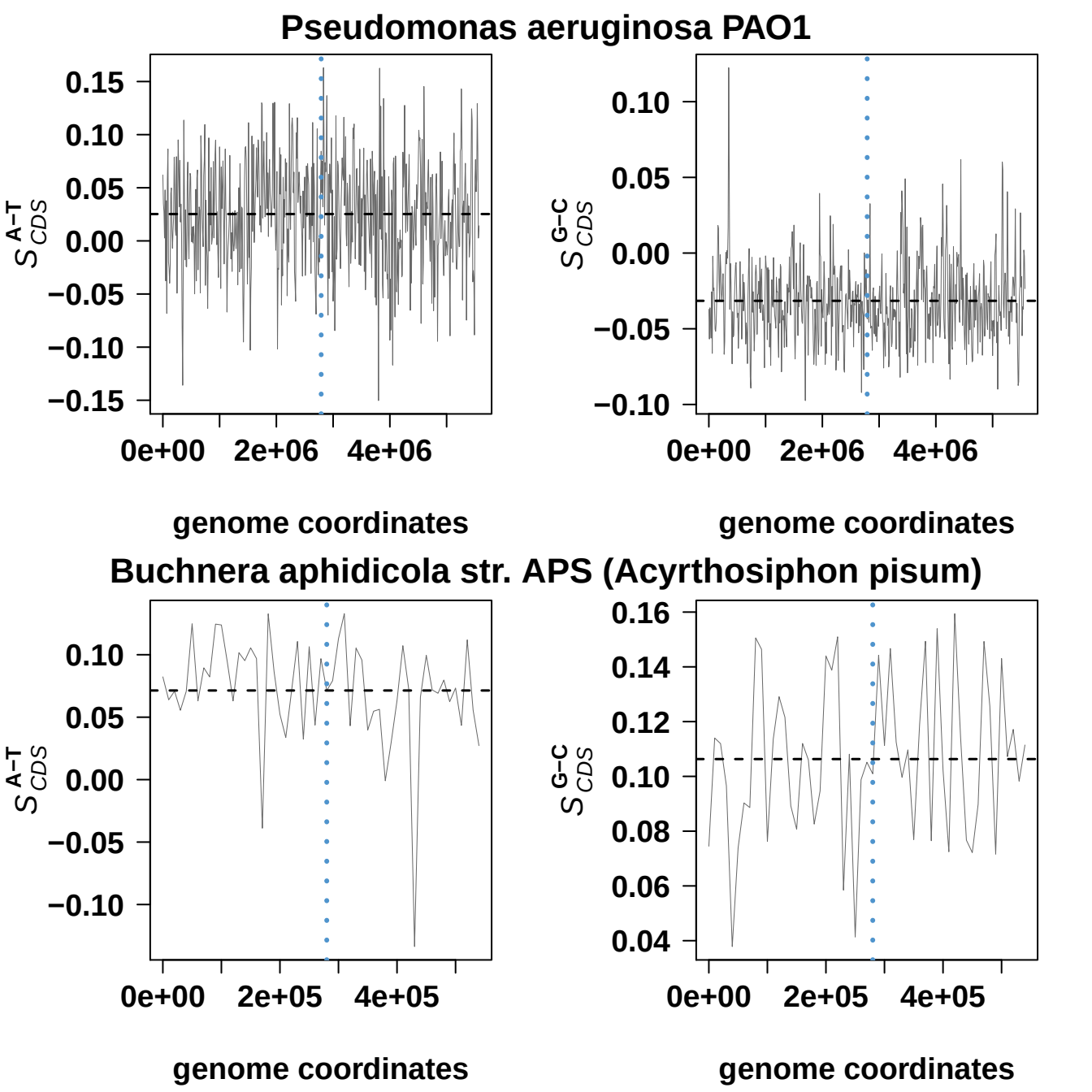
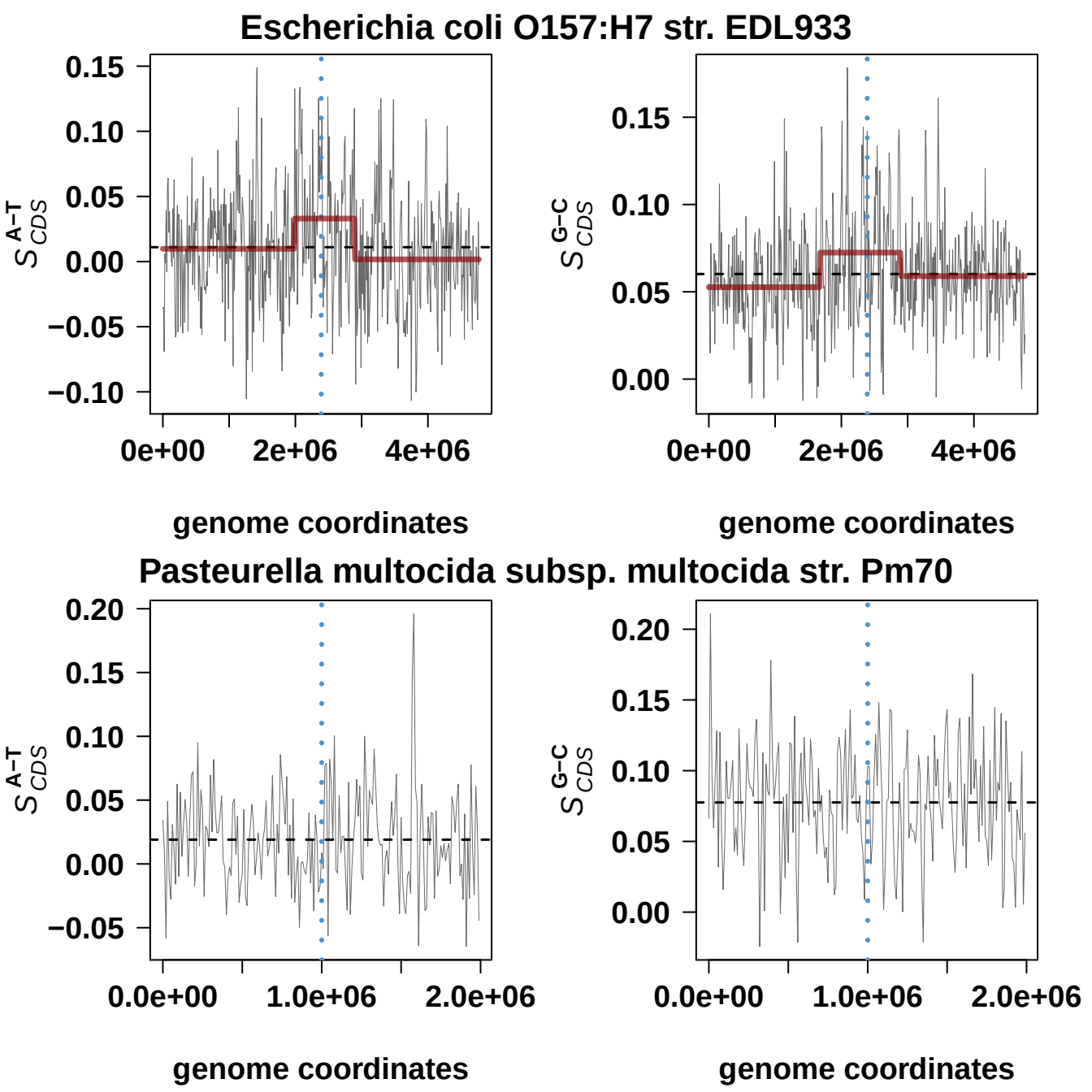
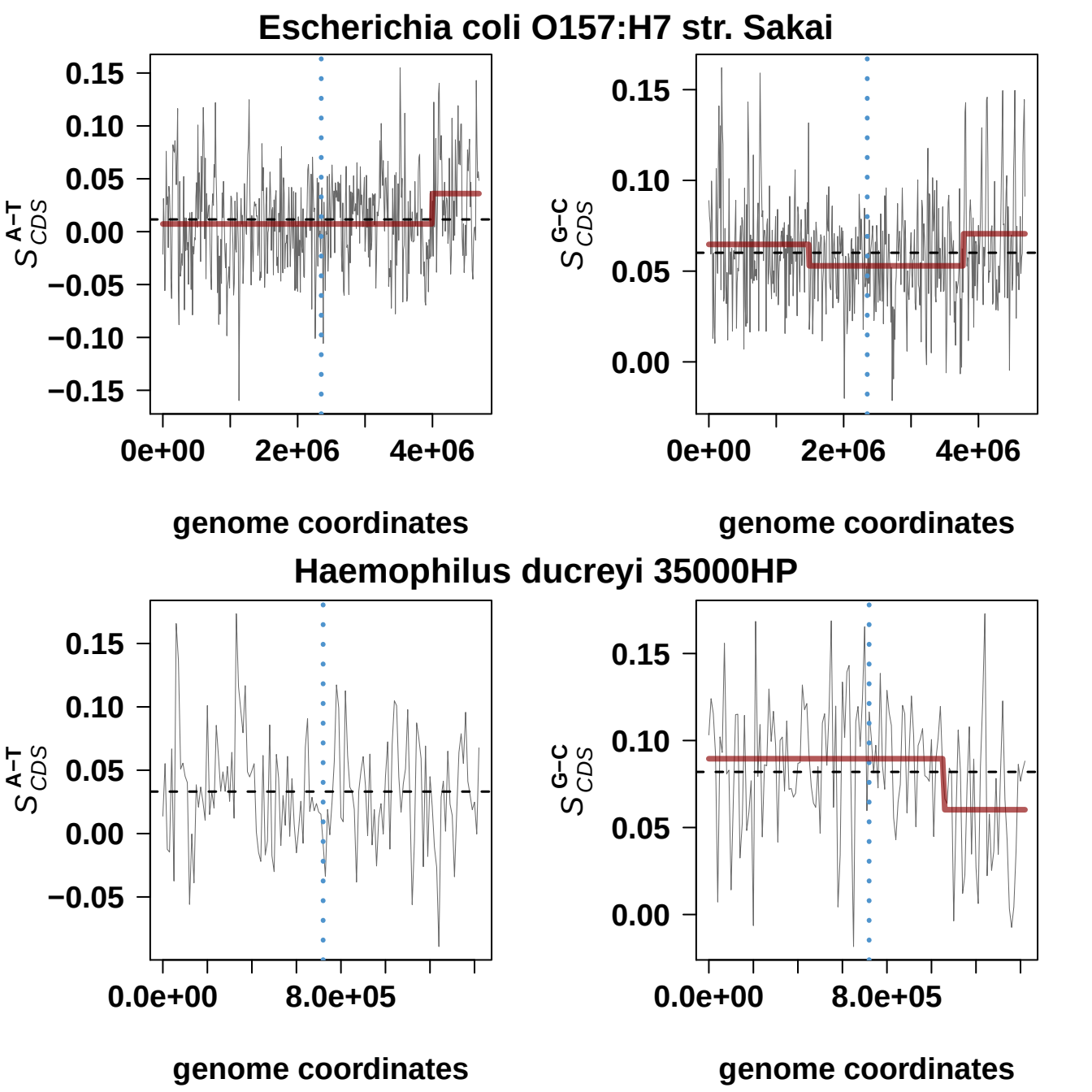
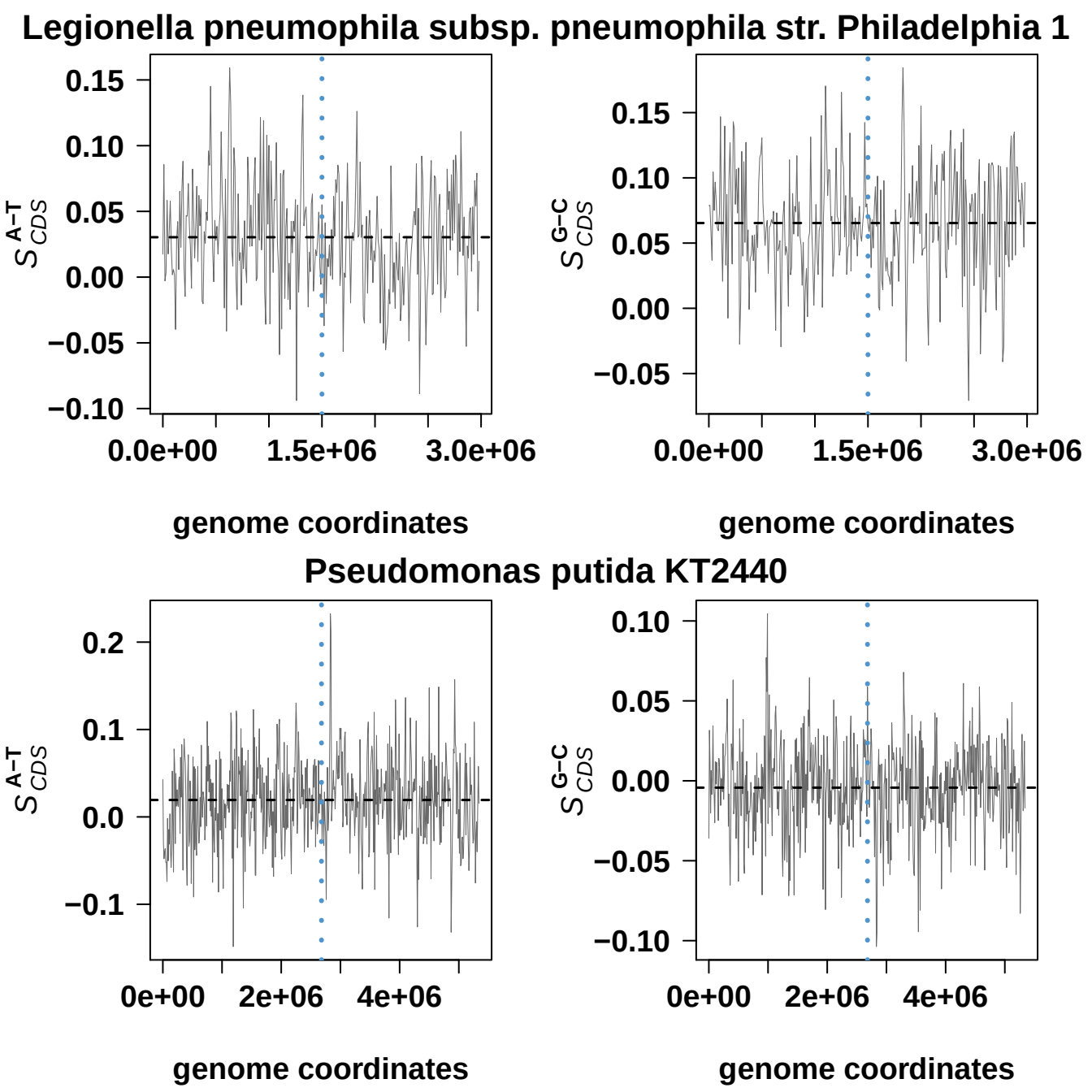
0.05
0.00
−0.05
−0.10
S^{A-T}_{CDS}
0e+00
2e+06
4e+06
genome coordinates
0.12
0.10
0.08
0.06
0.04
0.02
0.00
−0.02
S^{G-C}_{CDS}
0e+00
2e+06
4e+06
genome coordinates
Xylella fastidiosa 9a5c
0.2
0.1
0.0
−0.1
−0.2
−0.3
S^{A-T}_{CDS}
0.0e+00
1.0e+06
2.0e+06
genome coordinates
0.3
0.2
0.1
0.0
−0.1
−0.2
S^{G-C}_{CDS}
0.0e+00
1.0e+06
2.0e+06
genome coordinates

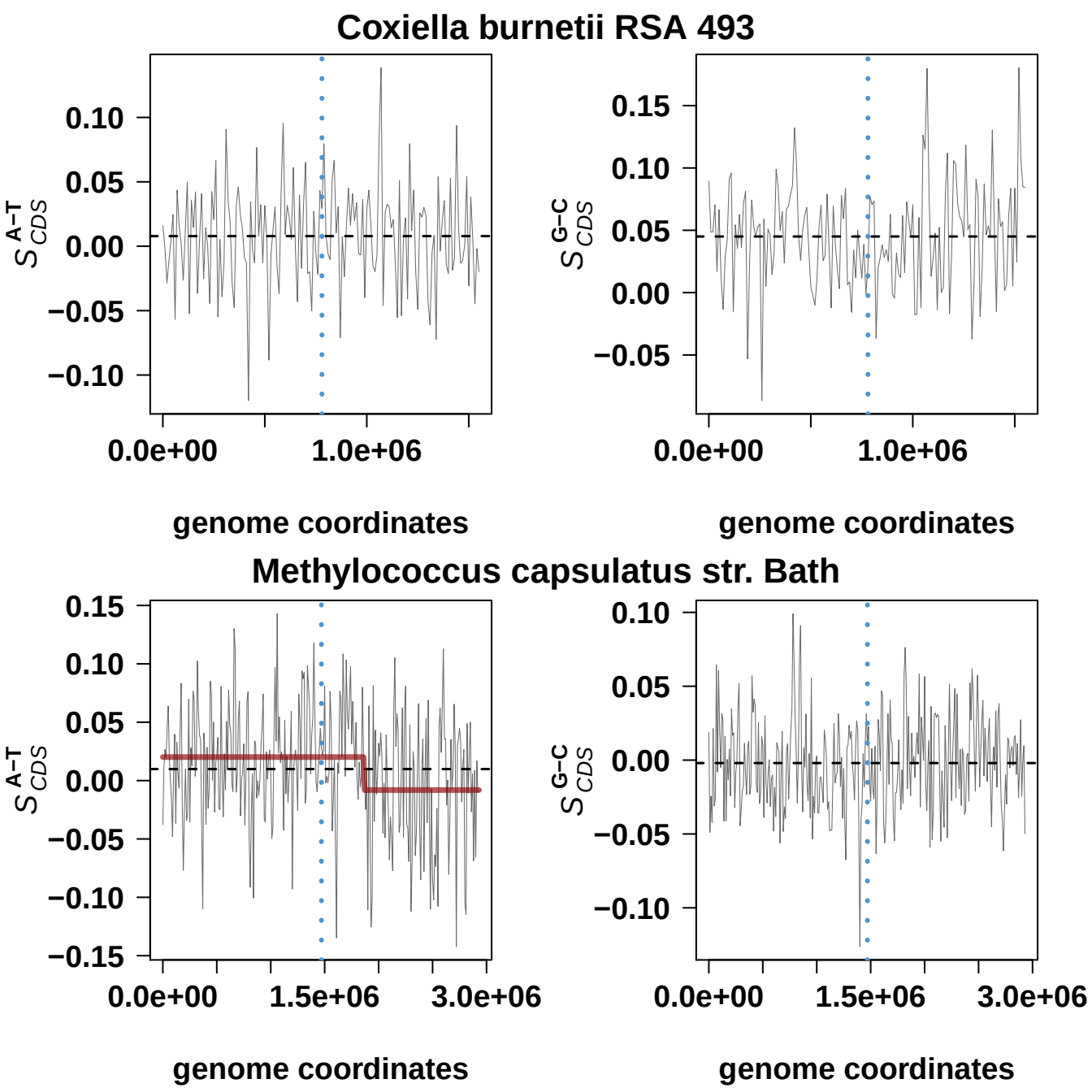

Vibrio cholerae O1 biovar El Tor str. N16961
0.10
0.05
0.00
−0.05
−0.10
S^{A-T}_{CDS}
0.0e+00
1.5e+06
genome coordinates
0.10
0.05
0.00
S^{G-C}_{CDS}
0.0e+00
1.5e+06
genome coordinates
Vibrio cholerae O1 biovar El Tor str. N16961
0.05
0.00
−0.05
−0.10
S^{A-T}_{CDS}
0e+00
4e+05
8e+05
genome coordinates
0.15
0.10
0.05
0.00
S^{G-C}_{CDS}
0e+00
4e+05
8e+05
genome coordinates


Pseudomonas aeruginosa PAO1
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
−0.05
−0.10
−0.15
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{CDS}
0.10
0.05
0.00
−0.05
−0.10
0e+00
2e+06
4e+06
genome coordinates
Buchnera aphidicola str. APS (Acyrthosiphon pisum)
S^{A-T}_{CDS}
0.10
0.05
0.00
−0.05
−0.10
0e+00
2e+05
4e+05
genome coordinates
S^{G-C}_{CDS}
0.16
0.14
0.12
0.10
0.08
0.06
0.04
0e+00
2e+05
4e+05
genome coordinates


Escherichia coli O157:H7 str. EDL933
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
−0.05
−0.10
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{CDS}
0.15
0.10
0.05
0.00
0e+00
2e+06
4e+06
genome coordinates
Pasteurella multocida subsp. multocida str. Pm70
S^{A-T}_{CDS}
0.20
0.15
0.10
0.05
0.00
−0.05
0.0e+00
1.0e+06
2.0e+06
genome coordinates
S^{G-C}_{CDS}
0.20
0.15
0.10
0.05
0.00
0.0e+00
1.0e+06
2.0e+06
genome coordinates


Escherichia coli O157:H7 str. Sakai
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
−0.05
−0.10
−0.15
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{CDS}
0.15
0.10
0.05
0.00
0e+00
2e+06
4e+06
genome coordinates
Haemophilus ducreyi 35000HP
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
−0.05
0.0e+00
8.0e+05
genome coordinates
S^{G-C}_{CDS}
0.15
0.10
0.05
0.00
0.0e+00
8.0e+05
genome coordinates


Legionella pneumophila subsp. pneumophila str. Philadelphia 1
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
−0.05
−0.10
0.0e+00
1.5e+06
3.0e+06
genome coordinates
S^{G-C}_{CDS}
0.15
0.10
0.05
0.00
−0.05
0.0e+00
1.5e+06
3.0e+06
genome coordinates
Pseudomonas putida KT2440
S^{A-T}_{CDS}
0.2
0.1
0.0
−0.1
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{CDS}
0.10
0.05
0.00
−0.05
−0.10
0e+00
2e+06
4e+06
genome coordinates


Coxiella burnetii RSA 493
S^{A-T}_{CDS}
0.10
0.05
0.00
−0.05
−0.10
0.0e+00
1.0e+06
genome coordinates
S^{G-C}_{CDS}
0.15
0.10
0.05
0.00
−0.05
0.0e+00
1.0e+06
genome coordinates
Methylococcus capsulatus str. Bath
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
−0.05
−0.10
−0.15
0.0e+00
1.5e+06
3.0e+06
genome coordinates
S^{G-C}_{CDS}
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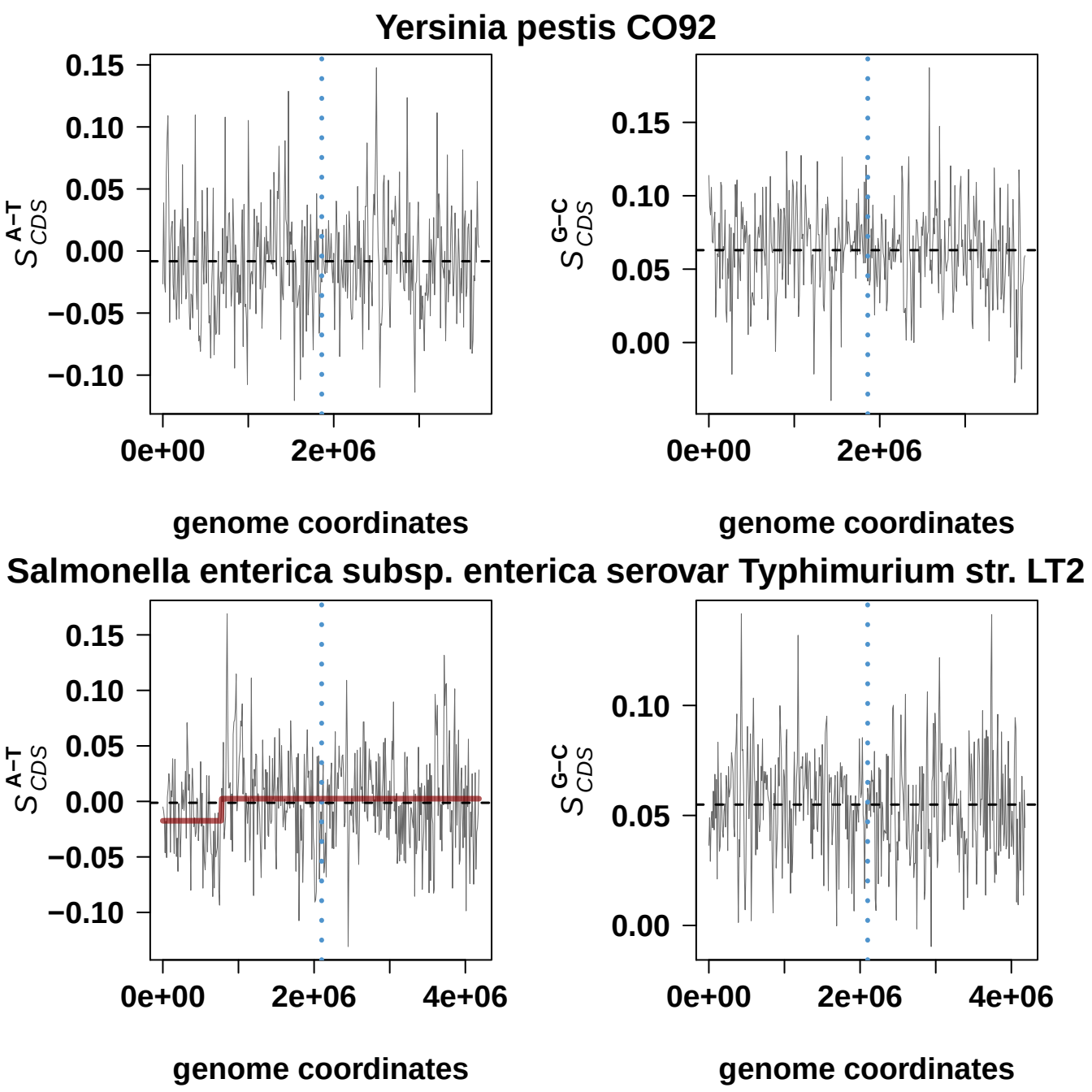
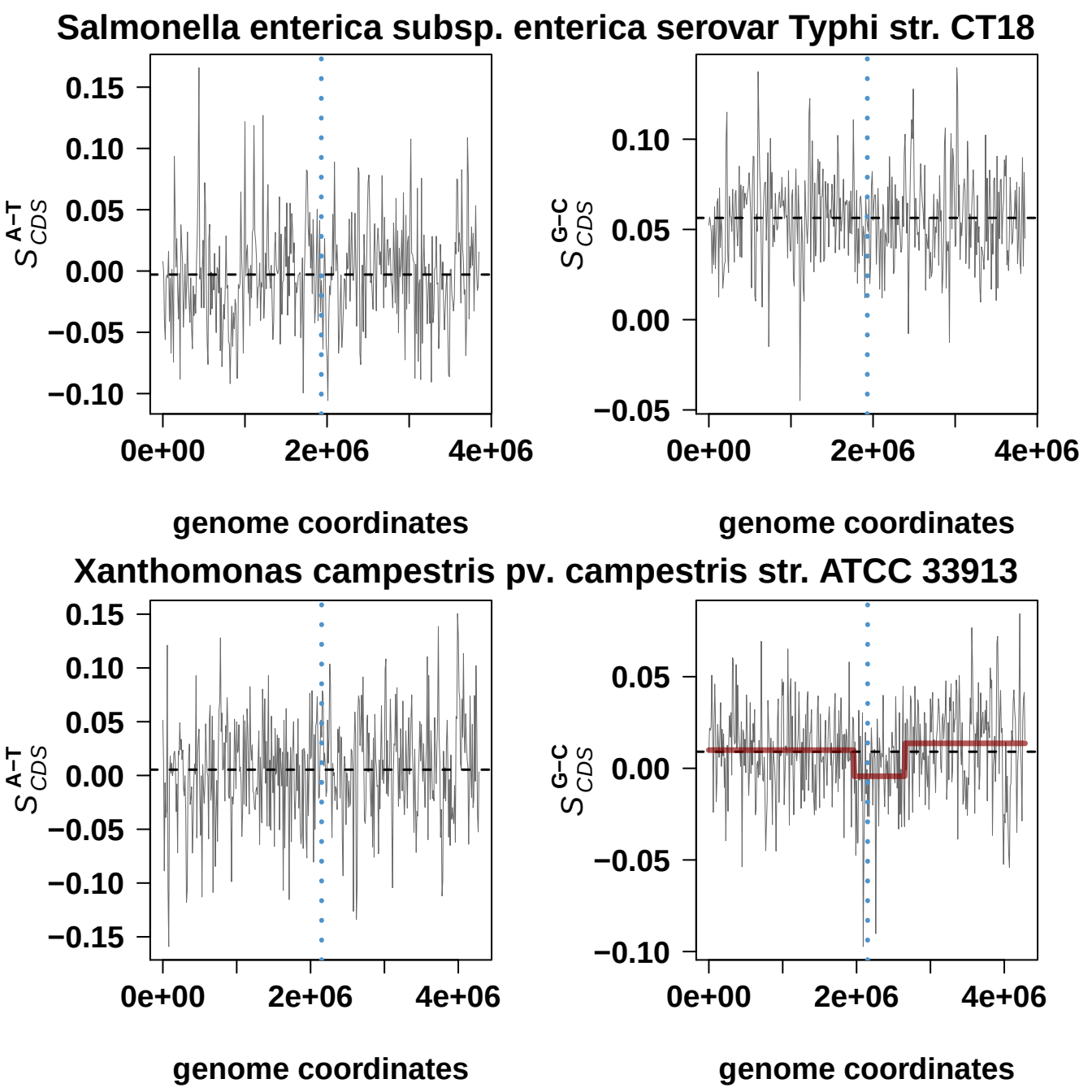
0.05
0.00
−0.05
−0.10
0.0e+00
1.5e+06
3.0e+06
genome coordinates


Yersinia pestis CO92
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
−0.05
−0.10
0e+00
2e+06
genome coordinates
S^{G-C}_{CDS}
0.15
0.10
0.05
0.00
0e+00
2e+06
genome coordinates
Salmonella enterica subsp. enterica serovar Typhimurium str. LT2
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
−0.05
−0.10
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{CDS}
0.10
0.05
0.00
0e+00
2e+06
4e+06
genome coordinates


Salmonella enterica subsp. enterica serovar Typhi str. CT18
S^{A-T}_{CDS}
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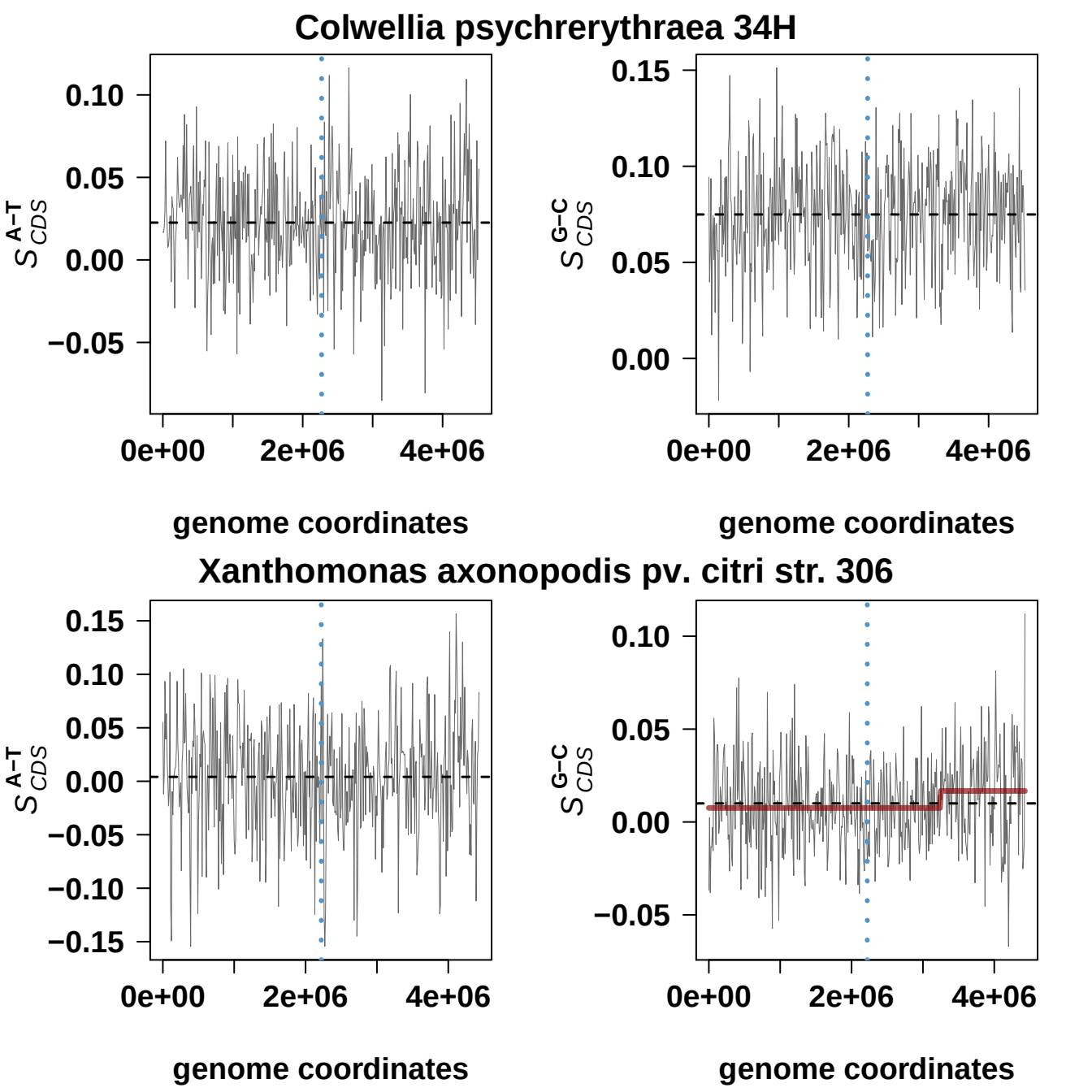
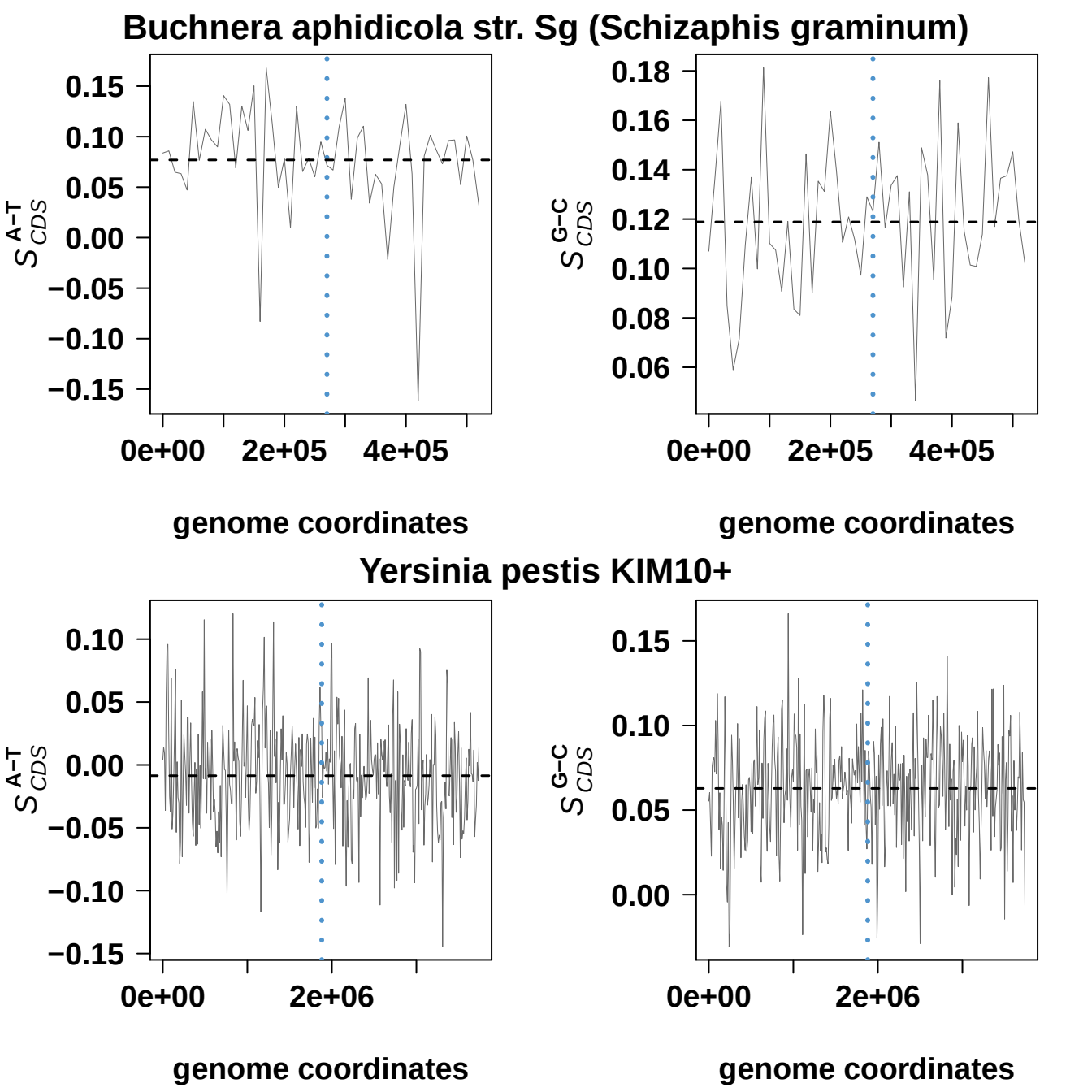
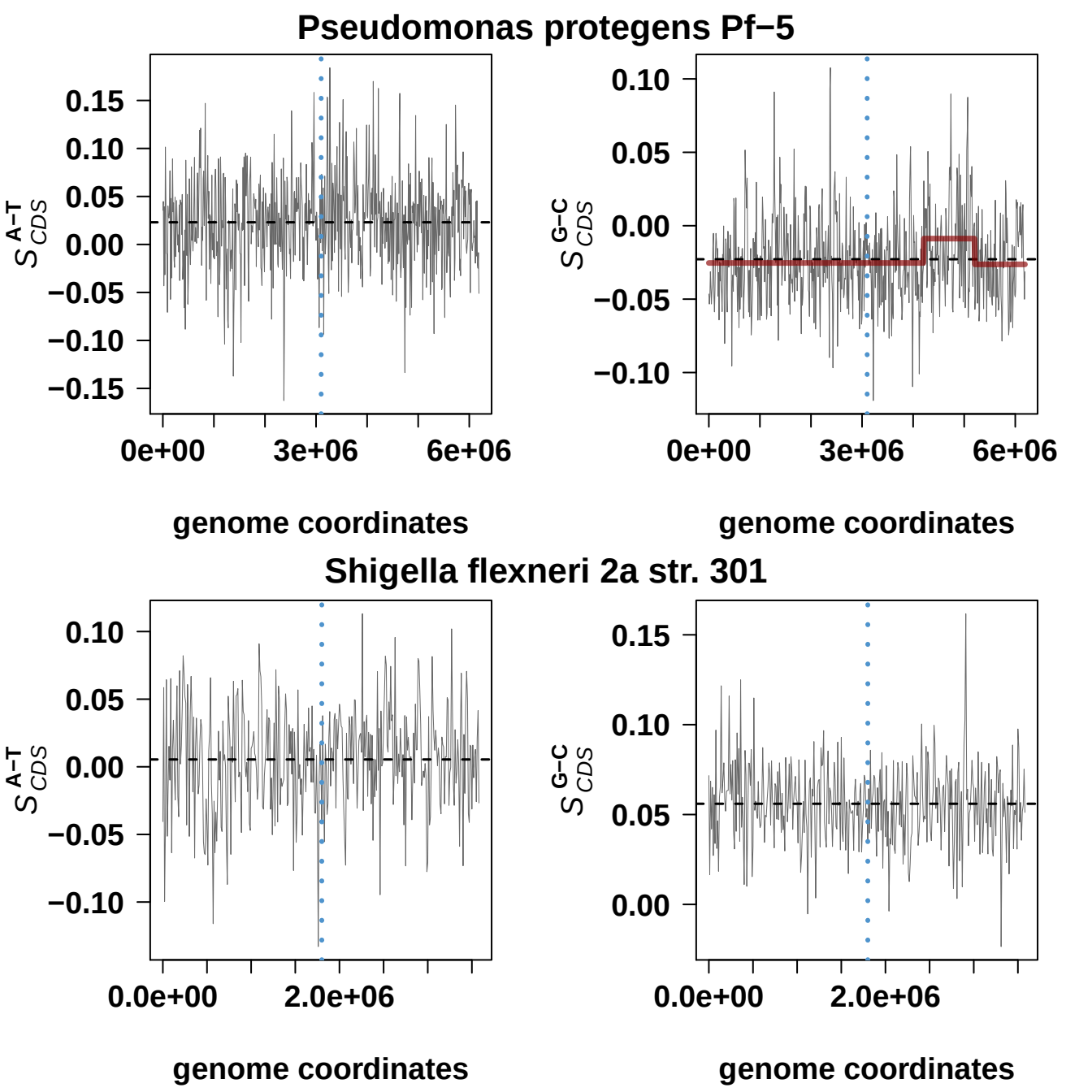
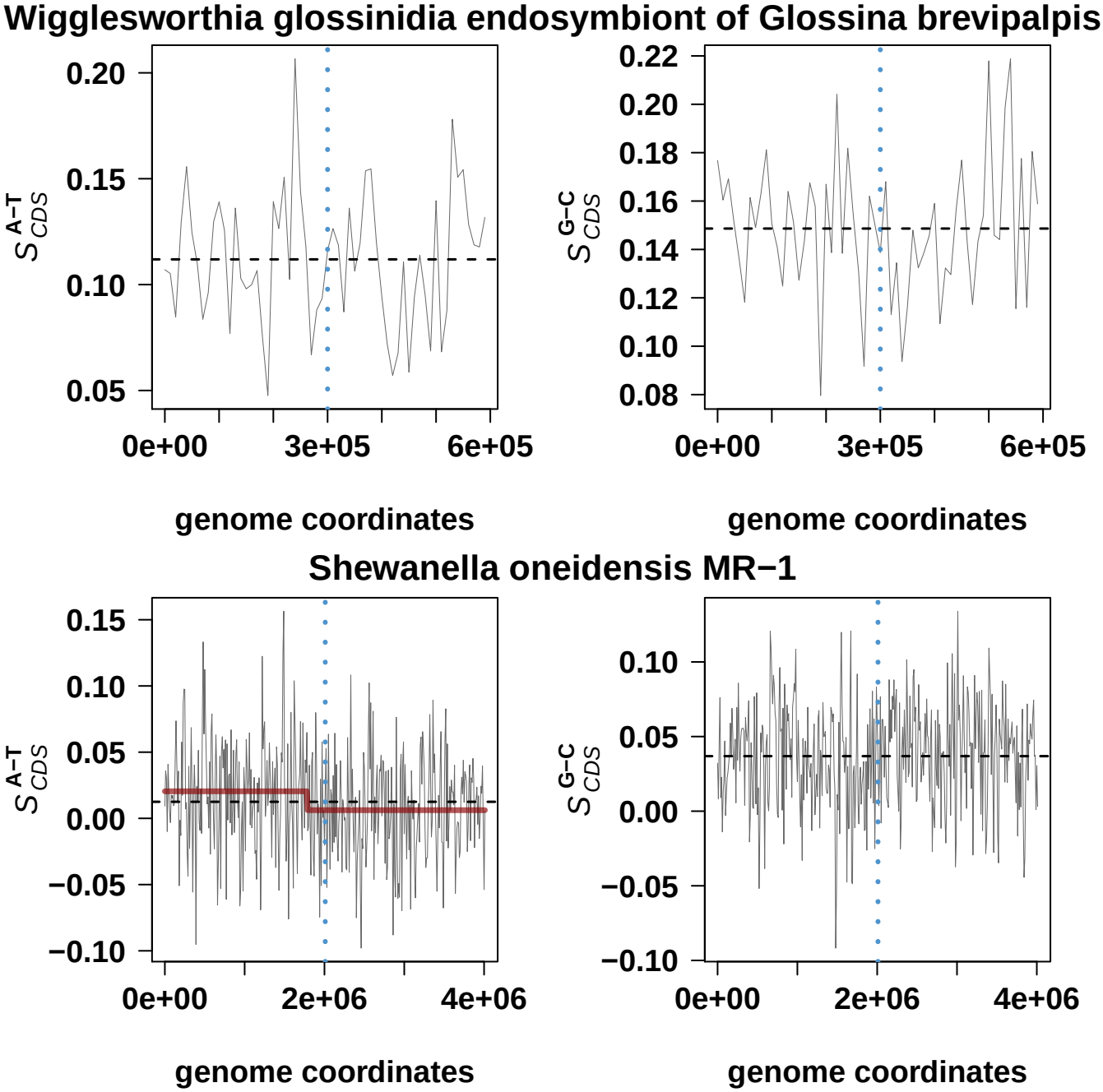
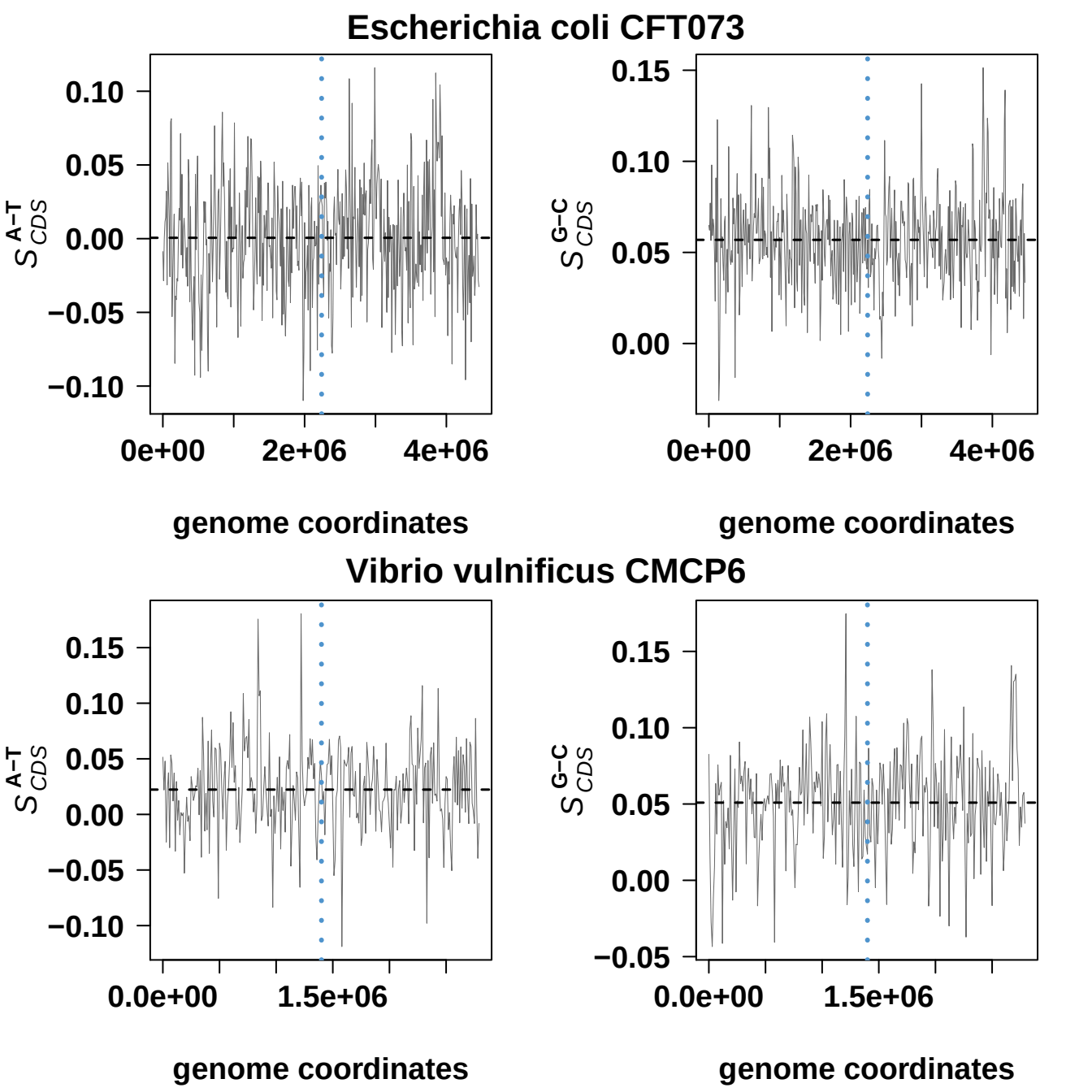
0.10
0.05
0.00
−0.05
−0.10
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{CDS}
0.10
0.05
0.00
−0.05
0e+00
2e+06
4e+06
genome coordinates
Xanthomonas campestris pv. campestris str. ATCC 33913
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
−0.05
−0.10
−0.15
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{CDS}
0.05
0.00
−0.05
−0.10
0e+00
2e+06
4e+06
genome coordinates

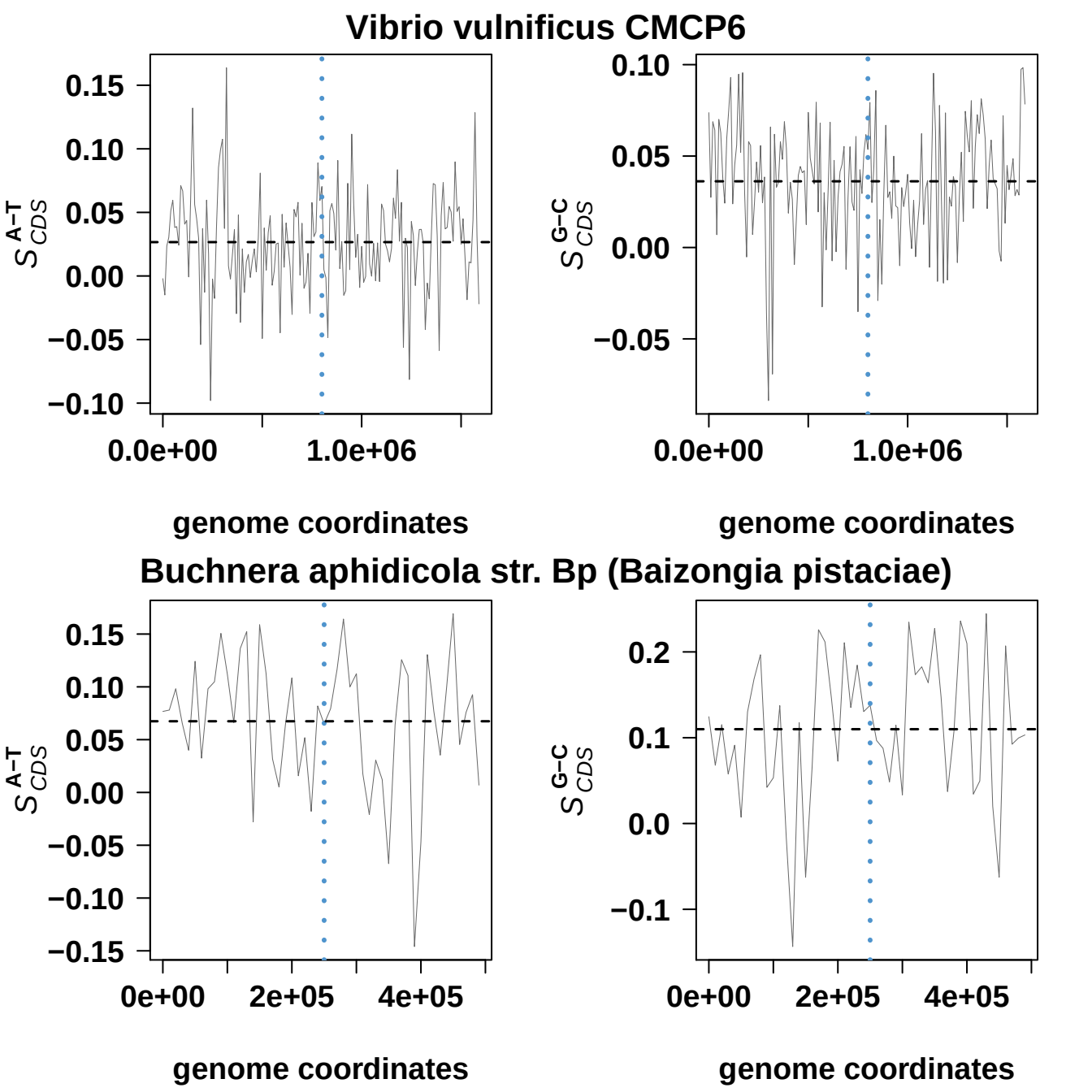

Colwellia psychrerythraea 34H
S^{A-T}_{CDS}
0.10
0.05
0.00
−0.05
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{CDS}
0.15
0.10
0.05
0.00
0e+00
2e+06
4e+06
genome coordinates
Xanthomonas axonopodis pv. citri str. 306
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
−0.05
−0.10
−0.15
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{CDS}
0.10
0.05
0.00
−0.05
0e+00
2e+06
4e+06
genome coordinates

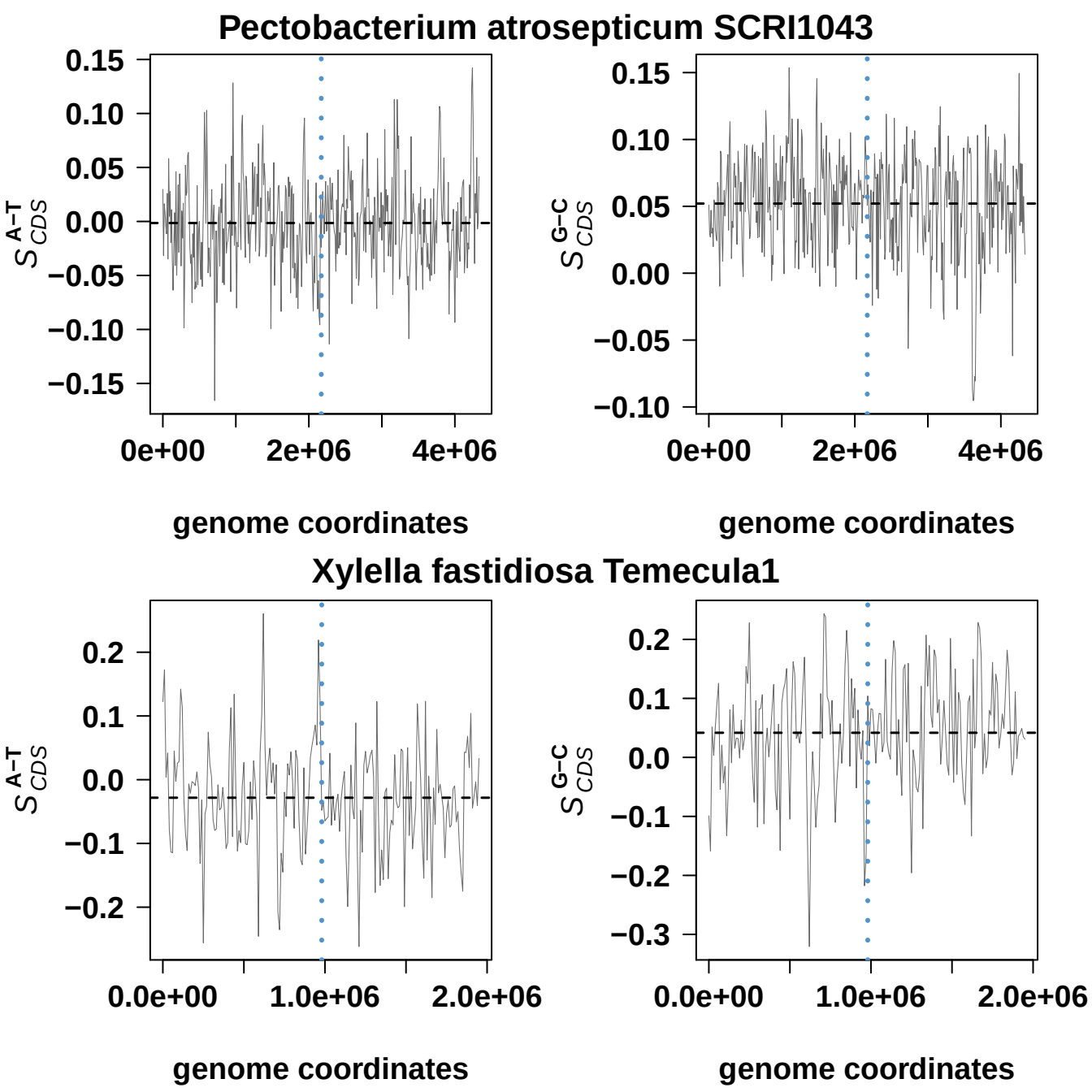

Buchnera aphidicola str. Sg (Schizaphis graminum)
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
−0.05
−0.10
−0.15
0e+00
2e+05
4e+05
genome coordinates
S^{G-C}_{CDS}
0.18
0.16
0.14
0.12
0.10
0.08
0.06
0e+00
2e+05
4e+05
genome coordinates
Yersinia pestis KIM10+
S^{A-T}_{CDS}
0.10
0.05
0.00
−0.05
−0.10
−0.15
0e+00
2e+06
genome coordinates
S^{G-C}_{CDS}
0.15
0.10
0.05
0.00
0e+00
2e+06
genome coordinates


Pseudomonas protegens Pf−5
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
−0.05
−0.10
−0.15
0e+00
3e+06
6e+06
genome coordinates
S^{G-C}_{CDS}
0.10
0.05
0.00
−0.05
−0.10
0e+00
3e+06
6e+06
genome coordinates
Shigella flexneri 2a str. 301
S^{A-T}_{CDS}
0.10
0.05
0.00
−0.05
−0.10
0.0e+00
2.0e+06
genome coordinates
S^{G-C}_{CDS}
0.15
0.10
0.05
0.00
0.0e+00
2.0e+06
genome coordinates


Wigglesworthia glossinidia endosymbiont of Glossina brevipalpis
S^{A-T}_{CDS}
0.20
0.15
0.10
0.05
0e+00
3e+05
6e+05
genome coordinates
S^{G-C}_{CDS}
0.22
0.20
0.18
0.16
0.14
0.12
0.10
0.08
0e+00
3e+05
6e+05
genome coordinates
Shewanella oneidensis MR−1
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
−0.05
−0.10
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{CDS}
0.10
0.05
0.00
−0.05
−0.10
0e+00
2e+06
4e+06
genome coordinates


Escherichia coli CFT073
S^{A-T}_{CDS}
0.10
0.05
0.00
−0.05
−0.10
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{CDS}
0.15
0.10
0.05
0.00
0e+00
2e+06
4e+06
genome coordinates
Vibrio vulnificus CMCP6
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
−0.05
−0.10
0.0e+00
1.5e+06
genome coordinates
S^{G-C}_{CDS}
0.15
0.10
0.05
0.00
−0.05
0.0e+00
1.5e+06
genome coordinates


Vibrio vulnificus CMCP6
0.15
0.10
0.05
0.00
−0.05
−0.10
S^{A-T}_{CDS}
0.0e+00
1.0e+06
genome coordinates
0.10
0.05
0.00
−0.05
S^{G-C}_{CDS}
0.0e+00
1.0e+06
genome coordinates
Buchnera aphidicola str. Bp (Baizongia pistaciae)
0.15
0.10
0.05
0.00
−0.05
−0.10
−0.15
S^{A-T}_{CDS}
0e+00
2e+05
4e+05
genome coordinates
0.2
0.1
0.0
−0.1
S^{G-C}_{CDS}
0e+00
2e+05
4e+05
genome coordinates


Pectobacterium atrosepticum SCRI1043
S^{A-T}_{CDS}
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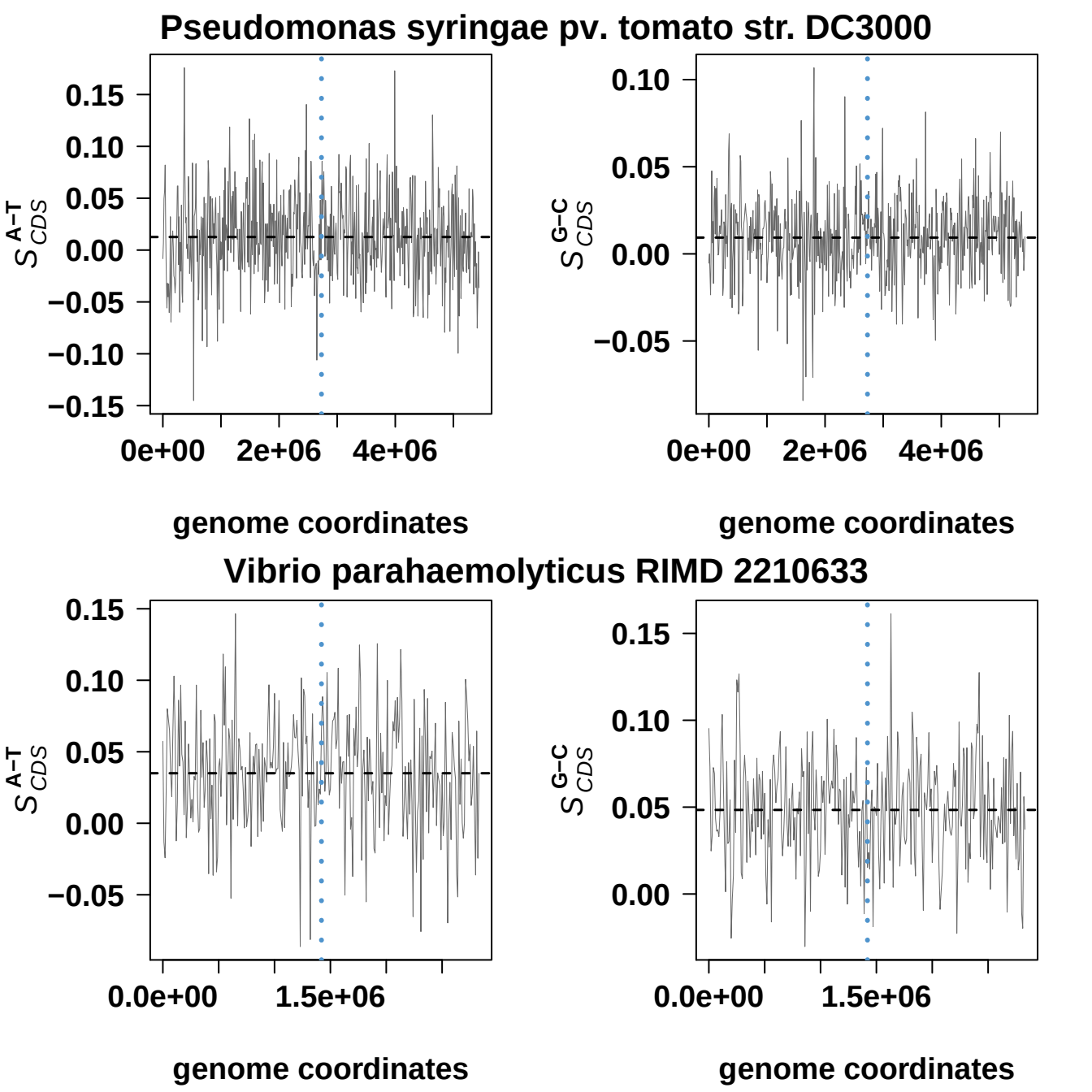
0.10
0.05
0.00
−0.05
−0.10
−0.15
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{CDS}
0.15
0.10
0.05
0.00
−0.05
−0.10
0e+00
2e+06
4e+06
genome coordinates
Xylella fastidiosa Temecula1
S^{A-T}_{CDS}
0.2
0.1
0.0
−0.1
−0.2
0.0e+00
1.0e+06
2.0e+06
genome coordinates
S^{G-C}_{CDS}
0.2
0.1
0.0
−0.1
−0.2
−0.3
0.0e+00
1.0e+06
2.0e+06
genome coordinates


Pseudomonas syringae pv. tomato str. DC3000
S^{A-T}_{CDS}
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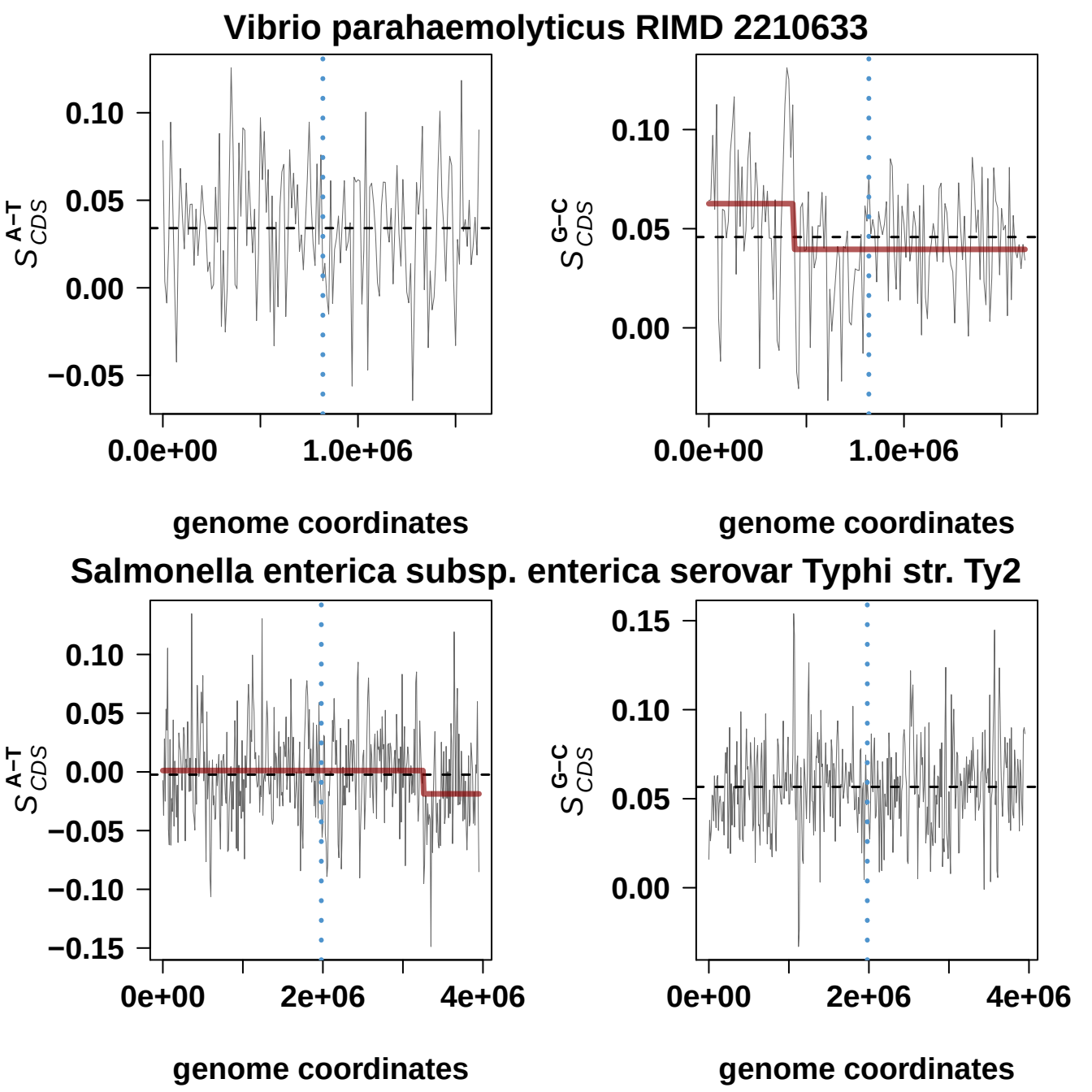
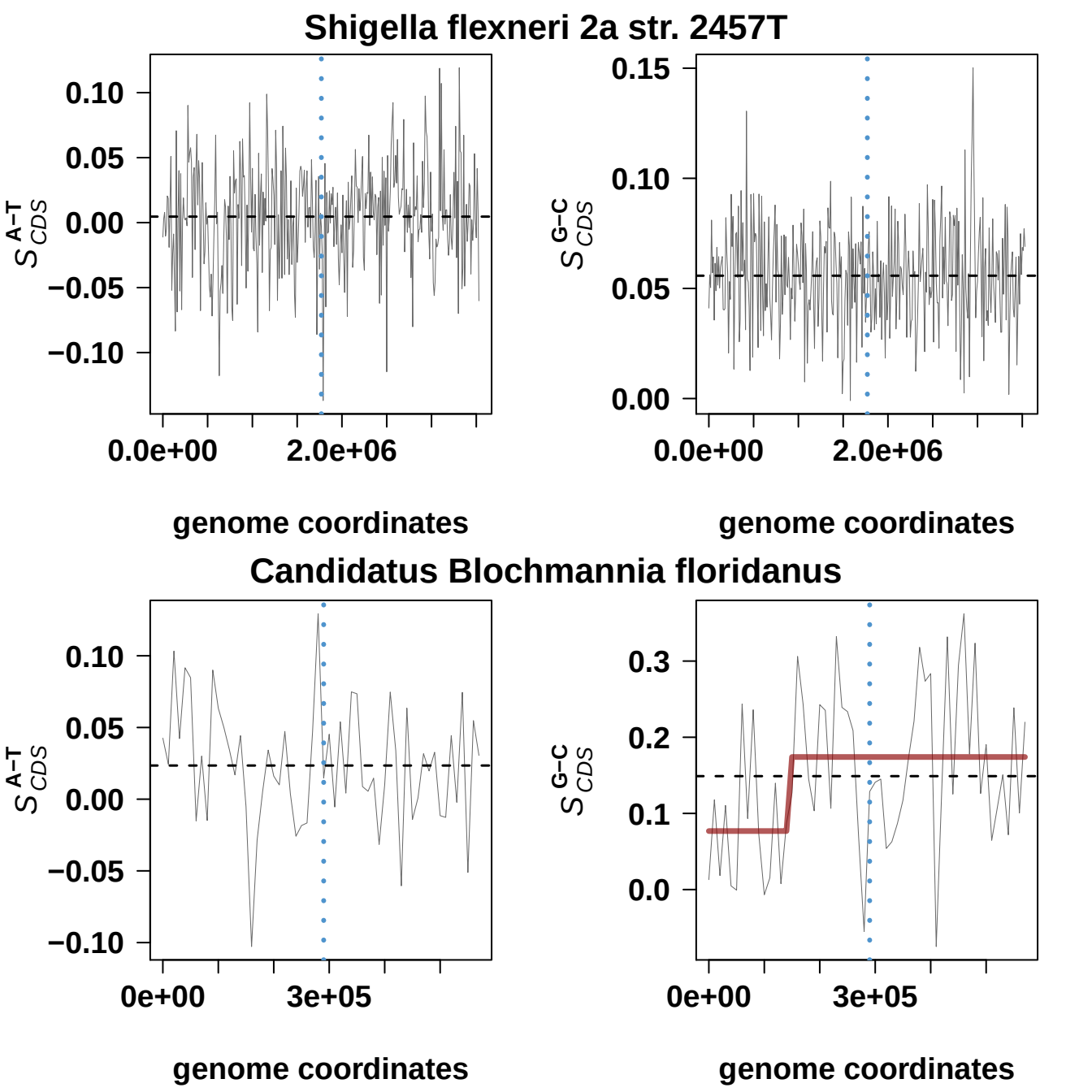
0.10
0.05
0.00
−0.05
−0.10
−0.15
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{CDS}
0.10
0.05
0.00
−0.05
0e+00
2e+06
4e+06
genome coordinates
Vibrio parahaemolyticus RIMD 2210633
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
−0.05
0.0e+00
1.5e+06
genome coordinates
S^{G-C}_{CDS}
0.15
0.10
0.05
0.00
0.0e+00
1.5e+06
genome coordinates


Vibrio parahaemolyticus RIMD 2210633
S^{A-T}_{CDS}
0.10
0.05
0.00
−0.05
0.0e+00
1.0e+06
genome coordinates
S^{G-C}_{CDS}
0.10
0.05
0.00
0.0e+00
1.0e+06
genome coordinates
Salmonella enterica subsp. enterica serovar Typhi str. Ty2
S^{A-T}_{CDS}
0.10
0.05
0.00
−0.05
−0.10
−0.15
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{CDS}
0.15
0.10
0.05
0.00
0e+00
2e+06
4e+06
genome coordinates


Shigella flexneri 2a str. 2457T
S^{A-T}_{CDS}
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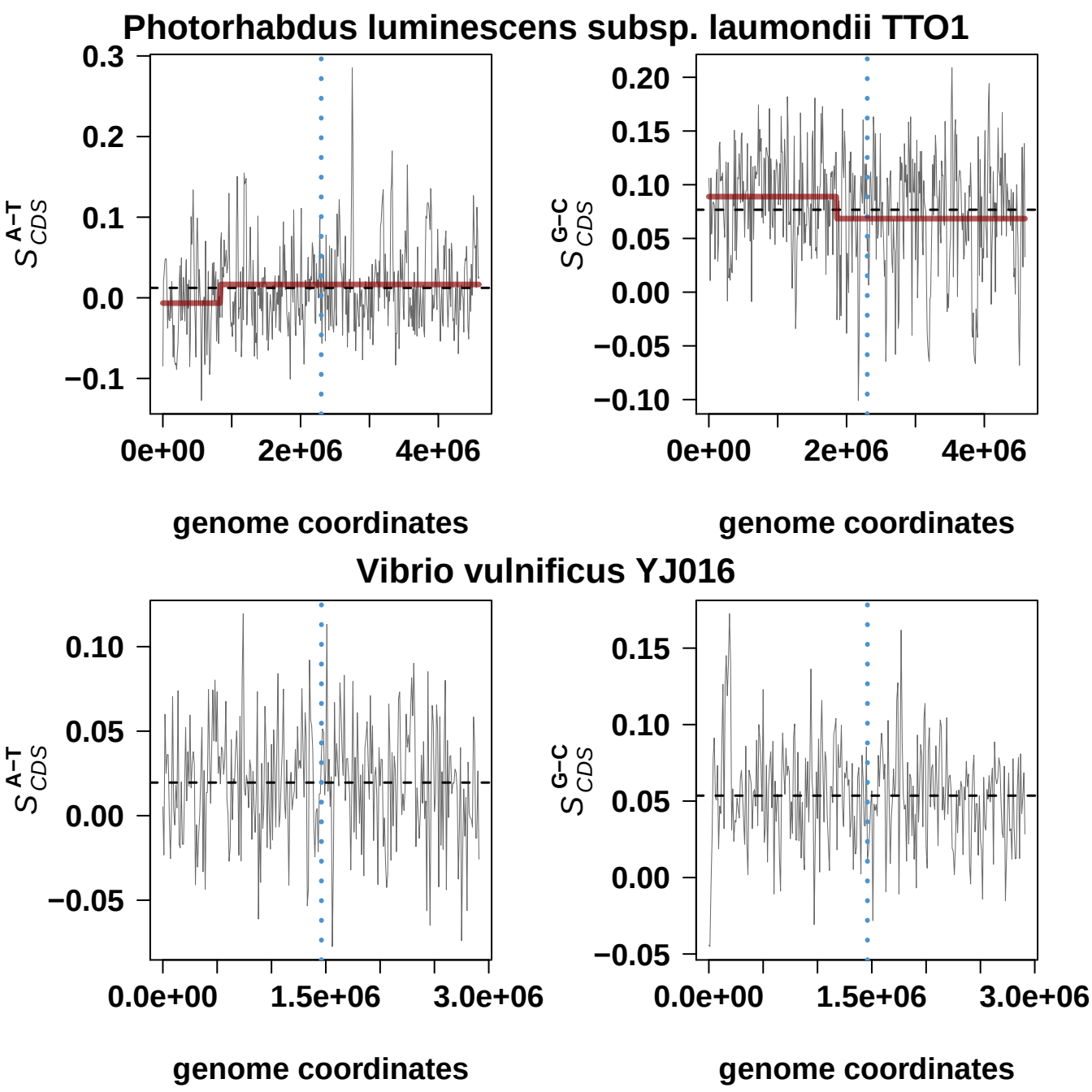
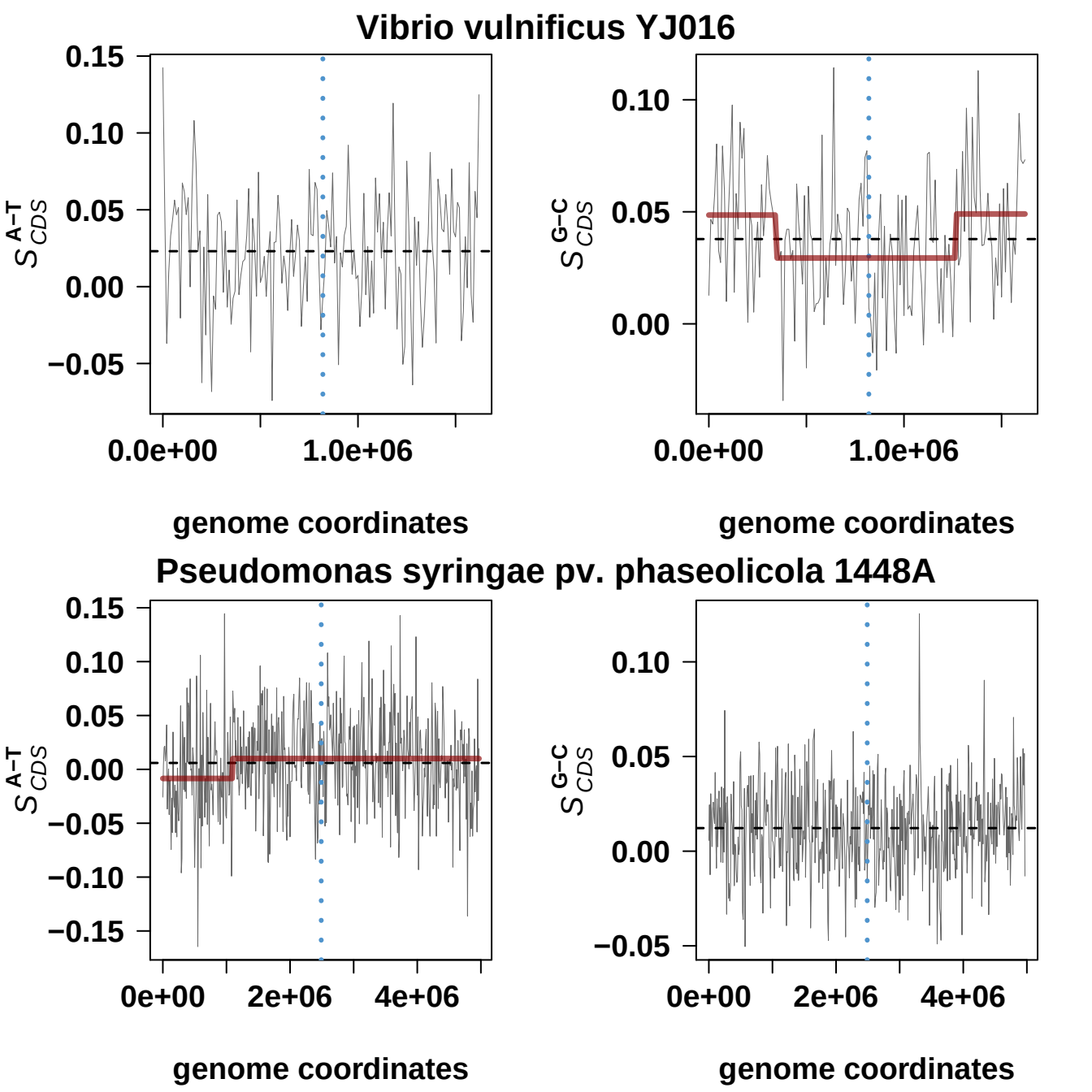
0.05
0.00
−0.05
−0.10
0.0e+00
2.0e+06
genome coordinates
S^{G-C}_{CDS}
0.15
0.10
0.05
0.00
0.0e+00
2.0e+06
genome coordinates
Candidatus Blochmannia floridanus
S^{A-T}_{CDS}
0.10
0.05
0.00
−0.05
−0.10
0e+00
3e+05
genome coordinates
S^{G-C}_{CDS}
0.3
0.2
0.1
0.0
0e+00
3e+05
genome coordinates


Photorhabdus luminescens subsp. laumondii TTO1
0.3
0.2
0.1
0.0
−0.1
S^{A-T}_{CDS}
0e+00
2e+06
4e+06
genome coordinates
0.20
0.15
0.10
0.05
0.00
−0.05
−0.10
S^{G-C}_{CDS}
0e+00
2e+06
4e+06
genome coordinates
Vibrio vulnificus YJ016
0.10
0.05
0.00
−0.05
S^{A-T}_{CDS}
0.0e+00
1.5e+06
3.0e+06
genome coordinates
0.15
0.10
0.05
0.00
−0.05
S^{G-C}_{CDS}
0.0e+00
1.5e+06
3.0e+06
genome coordinates


Vibrio vulnificus YJ016
S^{A-T}_{CDS}
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0.10
0.05
0.00
−0.05
0.0e+00
1.0e+06
genome coordinates
S^{G-C}_{CDS}
0.10
0.05
0.00
0.0e+00
1.0e+06
genome coordinates
Pseudomonas syringae pv. phaseolicola 1448A
S^{A-T}_{CDS}
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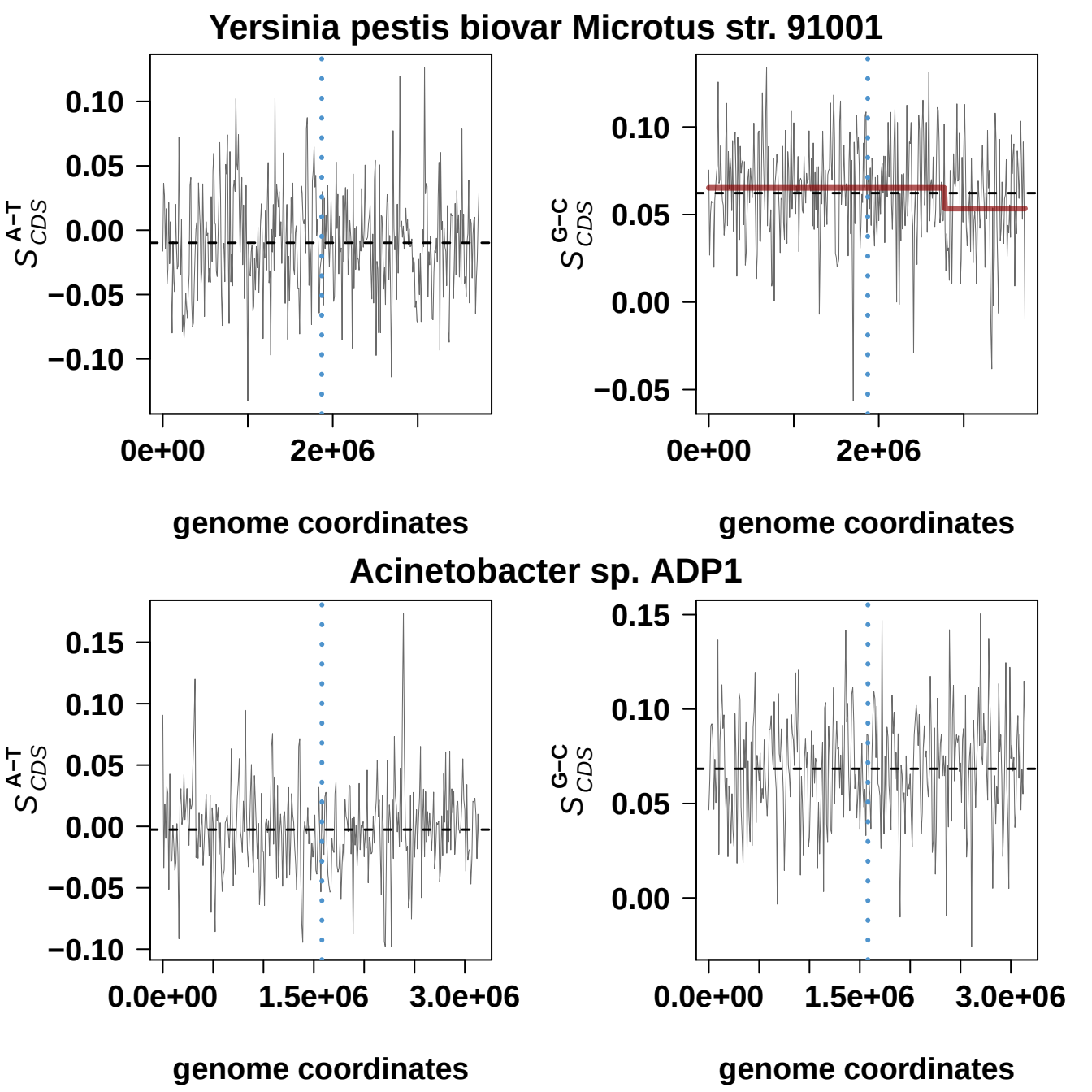
0.10
0.05
0.00
−0.05
−0.10
−0.15
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{CDS}
0.10
0.05
0.00
−0.05
0e+00
2e+06
4e+06
genome coordinates


Yersinia pestis biovar Microtus str. 91001
S^{A-T}_{CDS}
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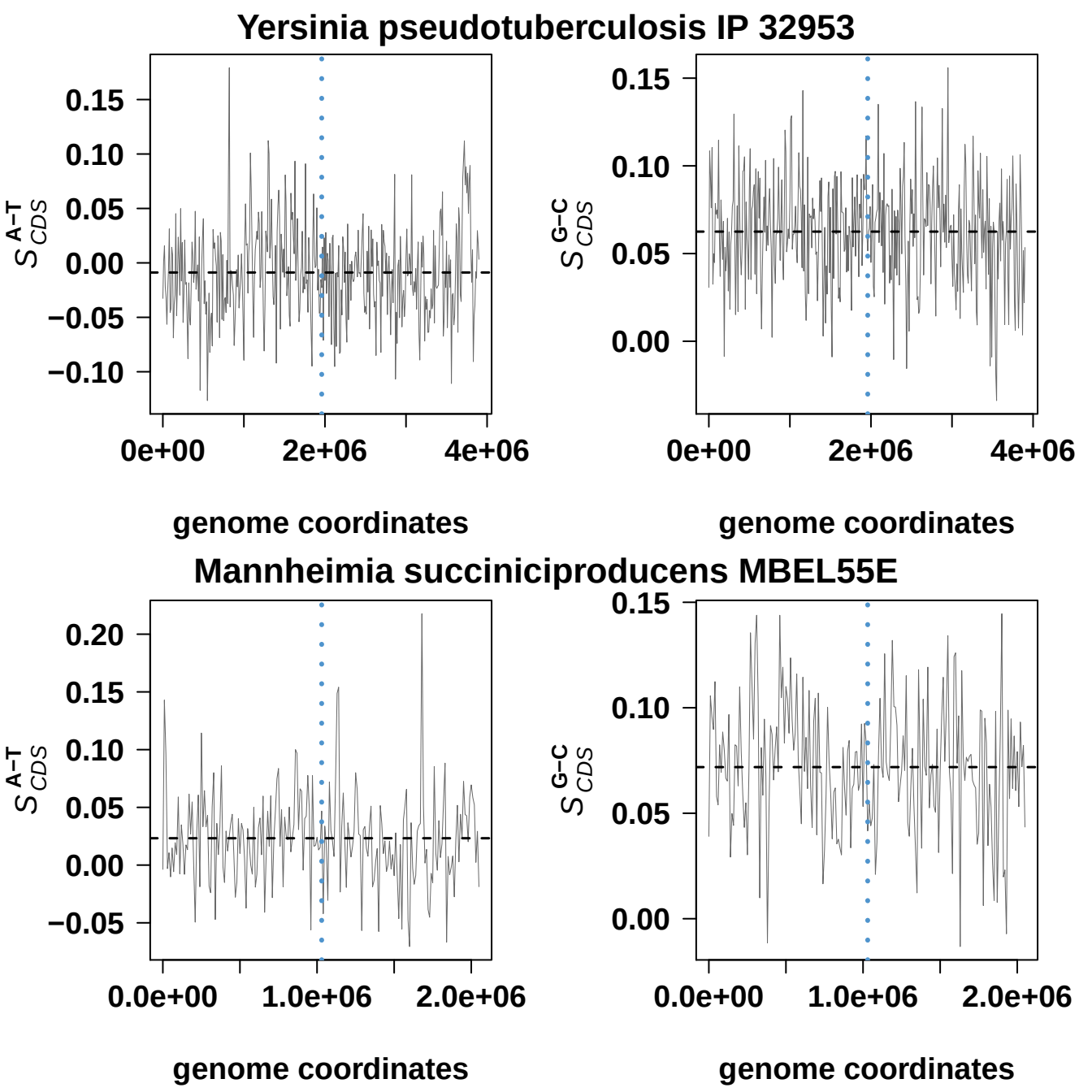
0.05
0.00
−0.05
−0.10
0e+00
2e+06
genome coordinates
S^{G-C}_{CDS}
0.10
0.05
0.00
−0.05
0e+00
2e+06
genome coordinates
Acinetobacter sp. ADP1
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
−0.05
−0.10
0.0e+00
1.5e+06
3.0e+06
genome coordinates
S^{G-C}_{CDS}
0.15
0.10
0.05
0.00
0.0e+00
1.5e+06
3.0e+06
genome coordinates


Yersinia pseudotuberculosis IP 32953
S^{A-T}_{CDS}
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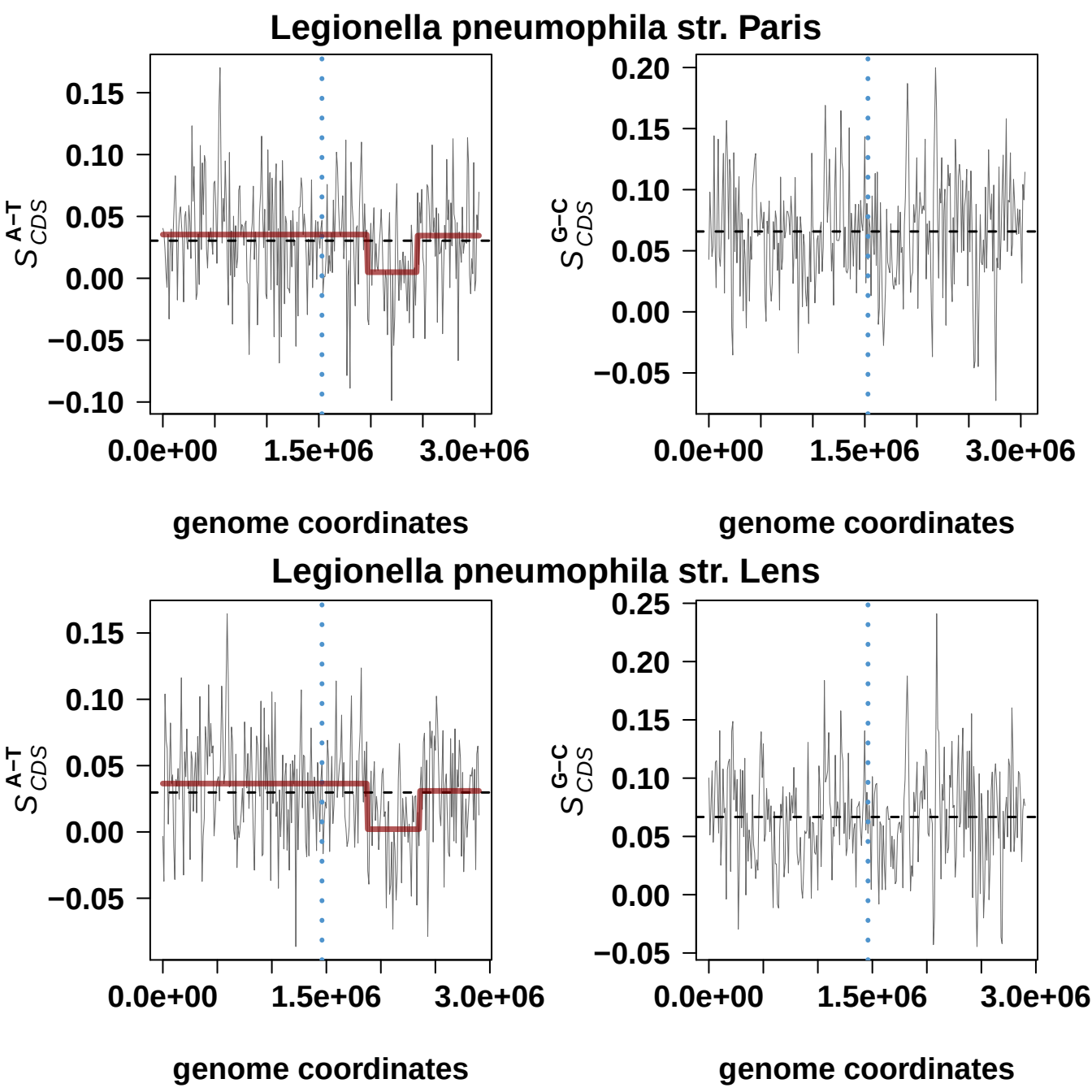
0.10
0.05
0.00
−0.05
−0.10
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{CDS}
0.15
0.10
0.05
0.00
0e+00
2e+06
4e+06
genome coordinates
Mannheimia succiniciproducens MBEL55E
S^{A-T}_{CDS}
0.20
0.15
0.10
0.05
0.00
−0.05
0.0e+00
1.0e+06
2.0e+06
genome coordinates
S^{G-C}_{CDS}
0.15
0.10
0.05
0.00
0.0e+00
1.0e+06
2.0e+06
genome coordinates


Legionella pneumophila str. Paris
S^{A-T}_{CDS}
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0.10
0.05
0.00
−0.05
−0.10
0.0e+00
1.5e+06
3.0e+06
genome coordinates
S^{G-C}_{CDS}
0.20
0.15
0.10
0.05
0.00
−0.05
0.0e+00
1.5e+06
3.0e+06
genome coordinates
Legionella pneumophila str. Lens
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
−0.05
0.0e+00
1.5e+06
3.0e+06
genome coordinates
S^{G-C}_{CDS}
0.25
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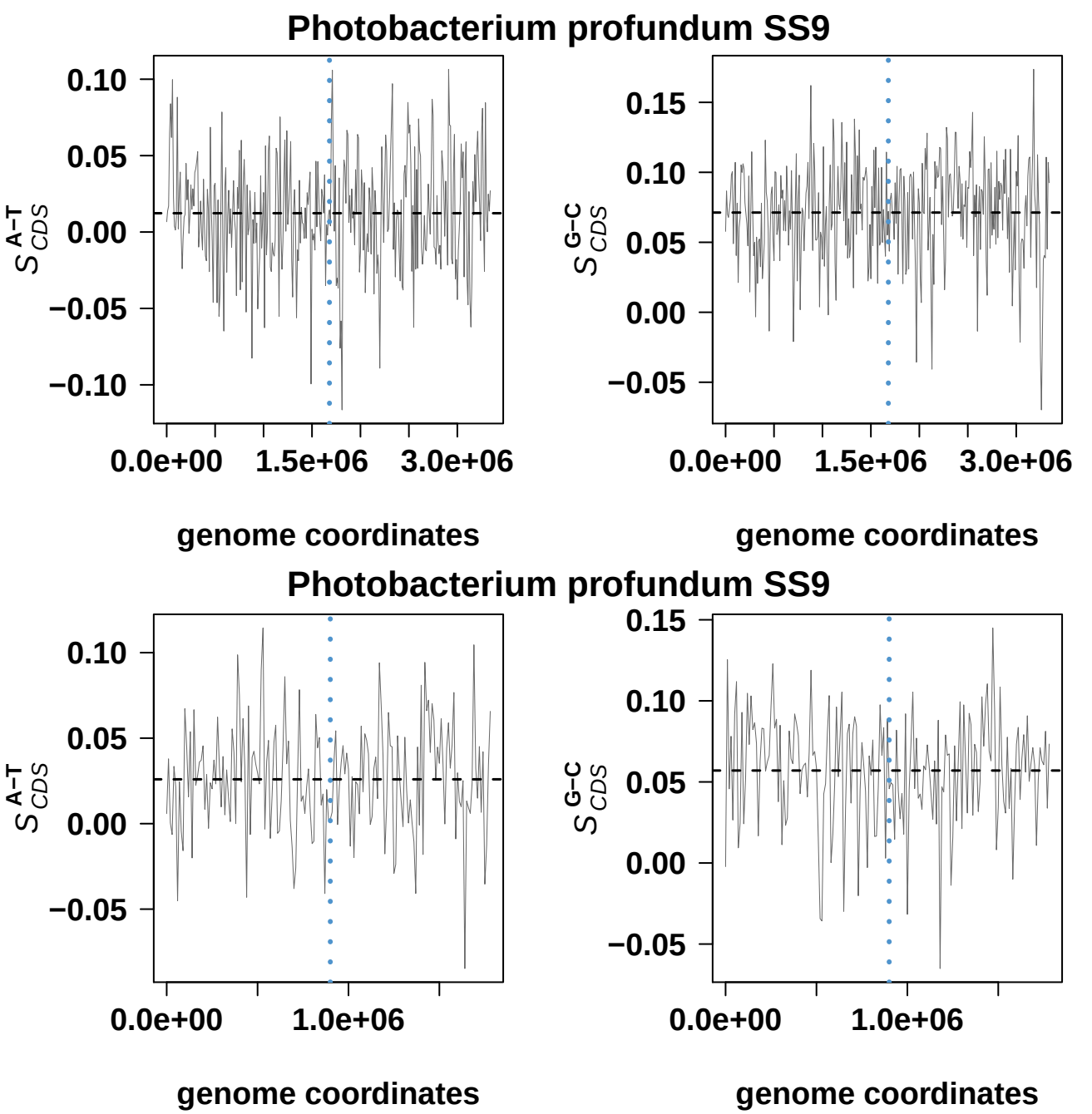
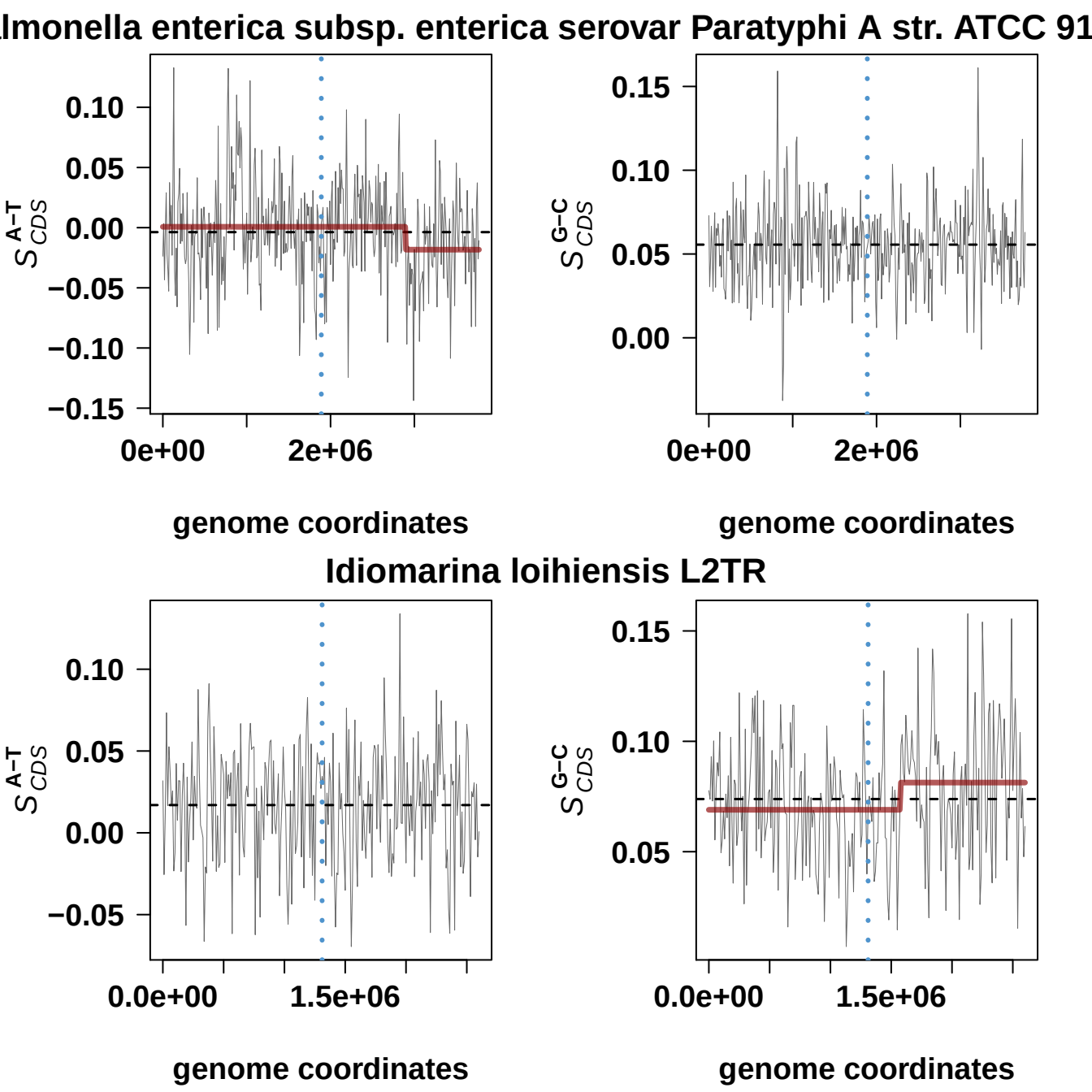
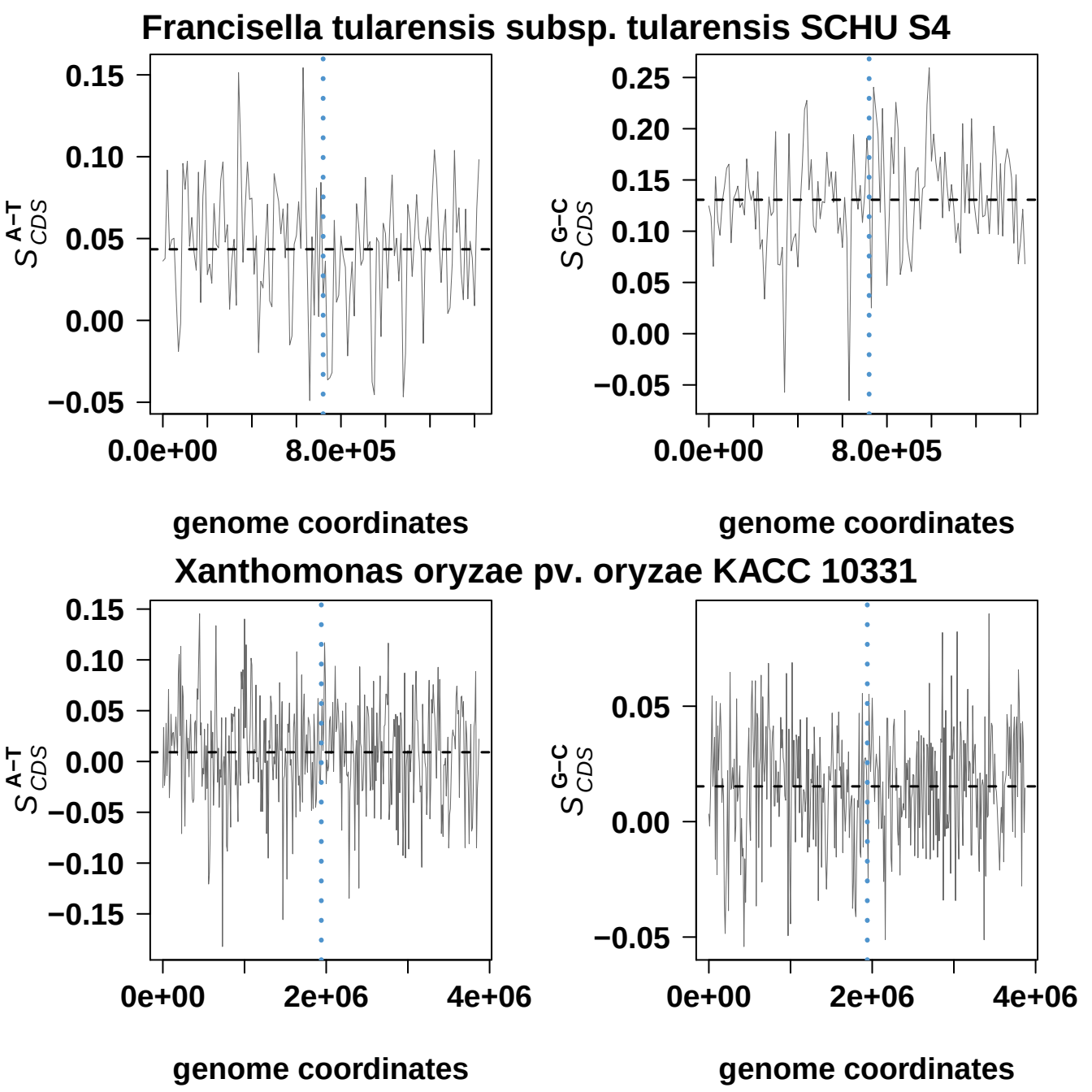
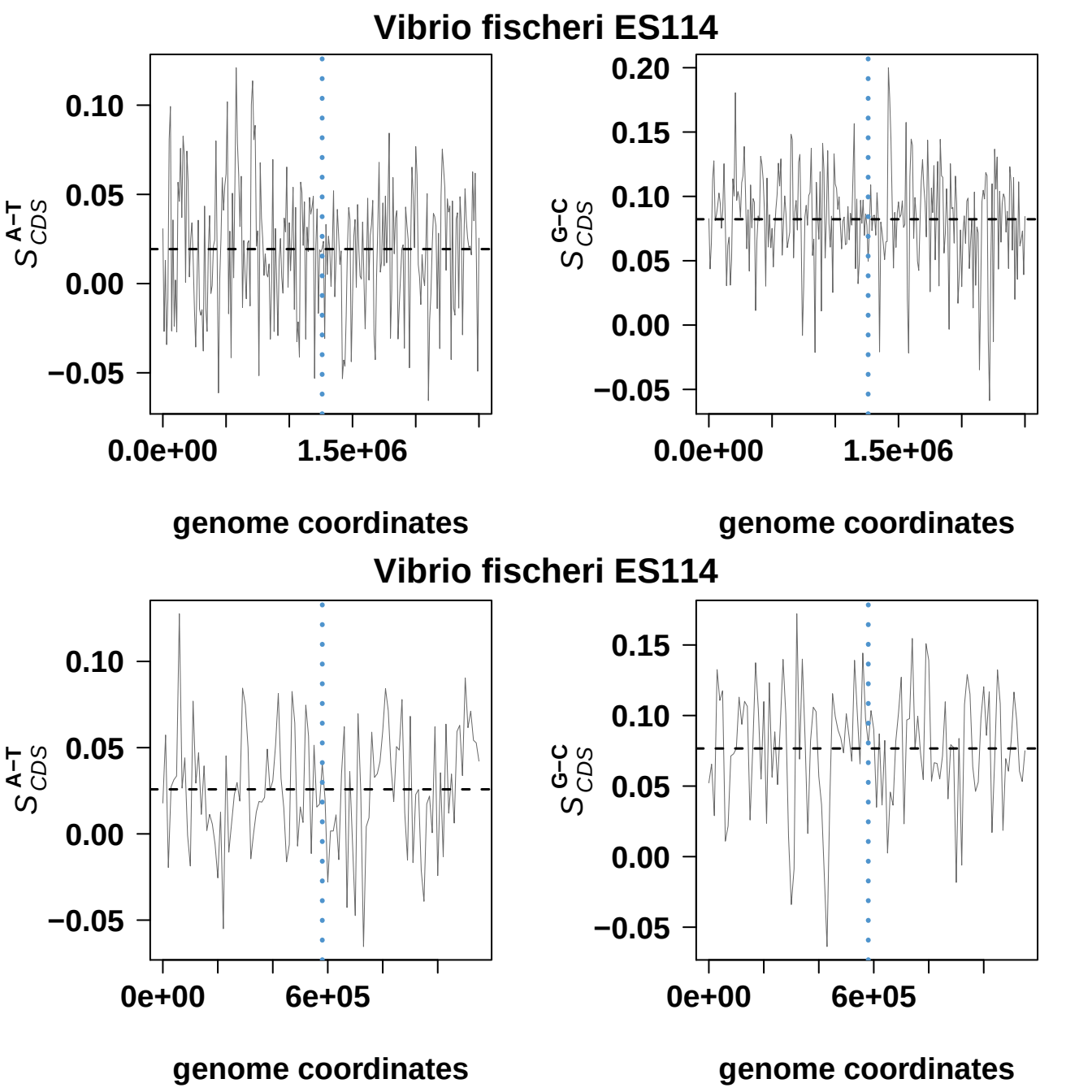
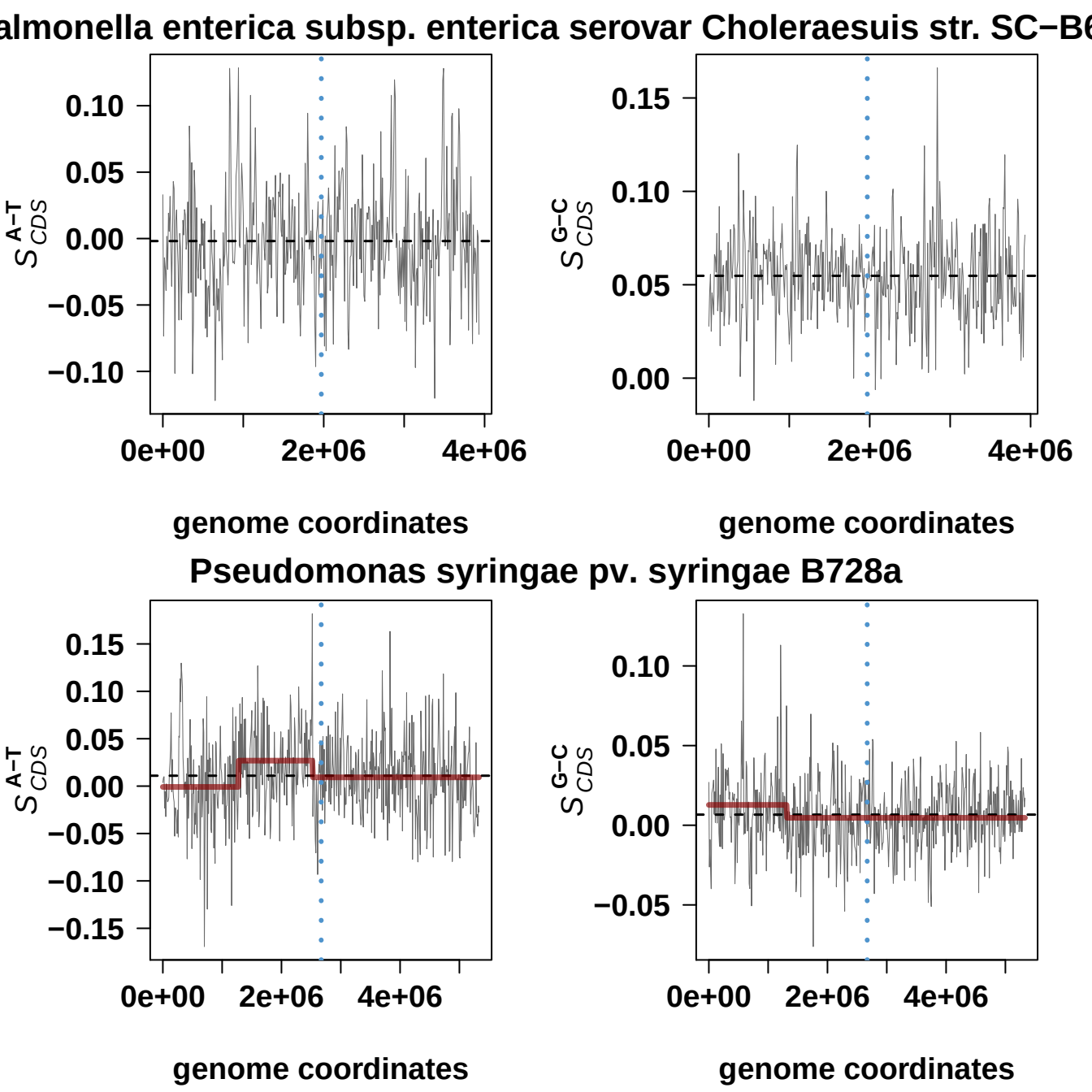
0.10
0.05
0.00
−0.05
0.0e+00
1.5e+06
3.0e+06
genome coordinates

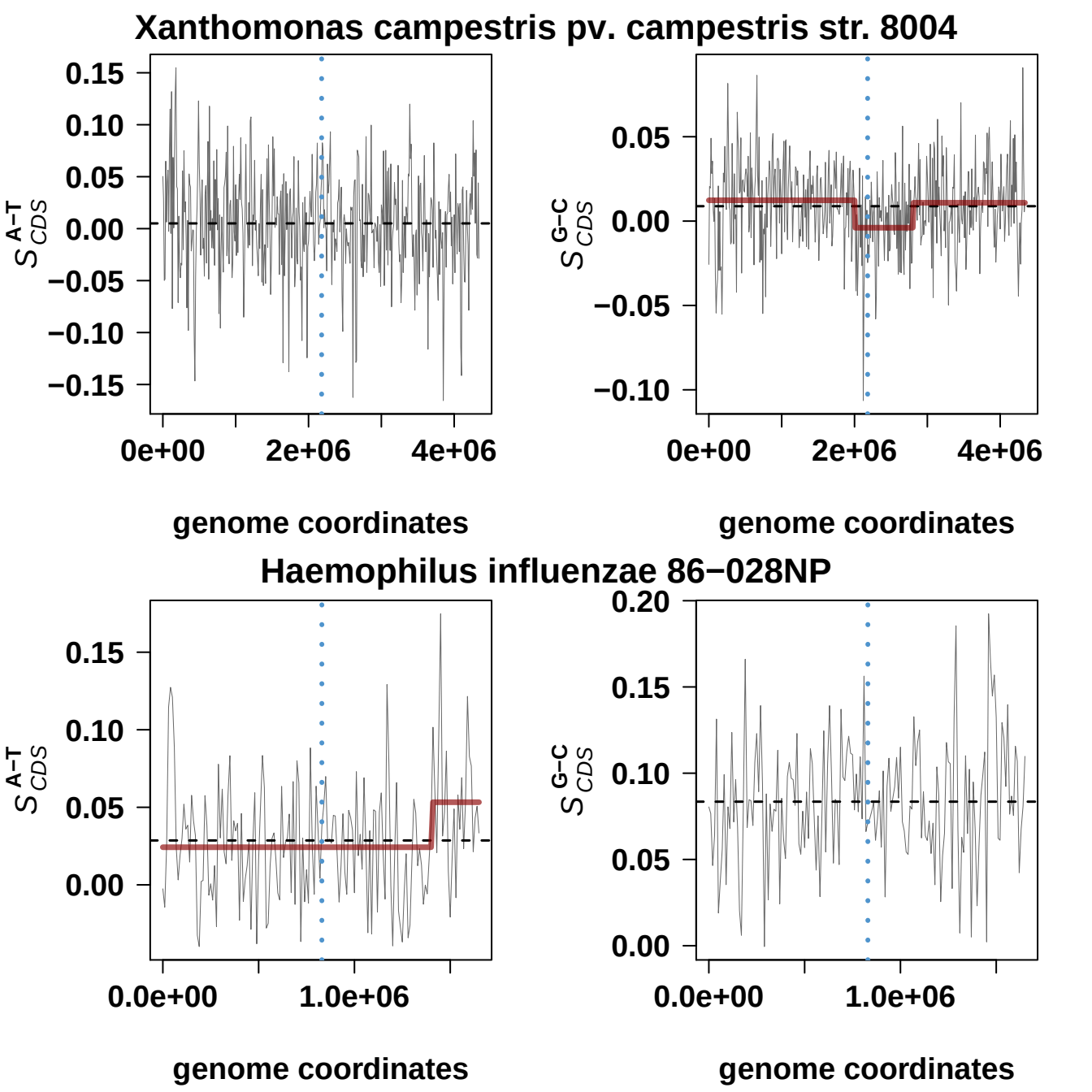

Photobacterium profundum SS9
0.10
0.05
0.00
−0.05
−0.10
S^{A-T}_{CDS}
0.0e+00
1.5e+06
3.0e+06
genome coordinates
0.15
0.10
0.05
0.00
−0.05
S^{G-C}_{CDS}
0.0e+00
1.5e+06
3.0e+06
genome coordinates
Photobacterium profundum SS9
0.10
0.05
0.00
−0.05
S^{A-T}_{CDS}
0.0e+00
1.0e+06
genome coordinates
0.15
0.10
0.05
0.00
−0.05
S^{G-C}_{CDS}
0.0e+00
1.0e+06
genome coordinates


lmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 91
0.10
0.05
0.00
−0.05
−0.10
−0.15
S^{A-T}_{CDS}
0e+00
2e+06
genome coordinates
0.15
0.10
0.05
0.00
S^{G-C}_{CDS}
0e+00
2e+06
genome coordinates
Idiomarina loihiensis L2TR
0.10
0.05
0.00
−0.05
S^{A-T}_{CDS}
0.0e+00
1.5e+06
genome coordinates
0.15
0.10
0.05
S^{G-C}_{CDS}
0.0e+00
1.5e+06
genome coordinates


Francisella tularensis subsp. tularensis SCHU S4
0.15
0.10
0.05
0.00
−0.05
S^{A-T}_{CDS}
0.0e+00
8.0e+05
genome coordinates
0.25
0.20
0.15
0.10
0.05
0.00
−0.05
S^{G-C}_{CDS}
0.0e+00
8.0e+05
genome coordinates
Xanthomonas oryzae pv. oryzae KACC 10331
0.15
0.10
0.05
0.00
−0.05
−0.10
−0.15
S^{A-T}_{CDS}
0e+00
2e+06
4e+06
genome coordinates
0.05
0.00
−0.05
S^{G-C}_{CDS}
0e+00
2e+06
4e+06
genome coordinates


Vibrio fischeri ES114
S^{A-T}_{CDS}
0.10
0.05
0.00
−0.05
0.0e+00
1.5e+06
genome coordinates
S^{G-C}_{CDS}
0.20
0.15
0.10
0.05
0.00
−0.05
0.0e+00
1.5e+06
genome coordinates
Vibrio fischeri ES114
S^{A-T}_{CDS}
0.10
0.05
0.00
−0.05
0e+00
6e+05
genome coordinates
S^{G-C}_{CDS}
0.15
0.10
0.05
0.00
−0.05
0e+00
6e+05
genome coordinates


almonella enterica subsp. enterica serovar Choleraesuis str. SC−B6
0.10
0.05
0.00
−0.05
−0.10
S^{A-T}_{CDS}
0e+00
2e+06
4e+06
genome coordinates
0.15
0.10
0.05
0.00
S^{G-C}_{CDS}
0e+00
2e+06
4e+06
genome coordinates
Pseudomonas syringae pv. syringae B728a
0.15
0.10
0.05
0.00
−0.05
−0.10
−0.15
S^{A-T}_{CDS}
0e+00
2e+06
4e+06
genome coordinates
0.10
0.05
0.00
−0.05
S^{G-C}_{CDS}
0e+00
2e+06
4e+06
genome coordinates


Xanthomonas campestris pv. campestris str. 8004
S^{A-T}_{CDS}
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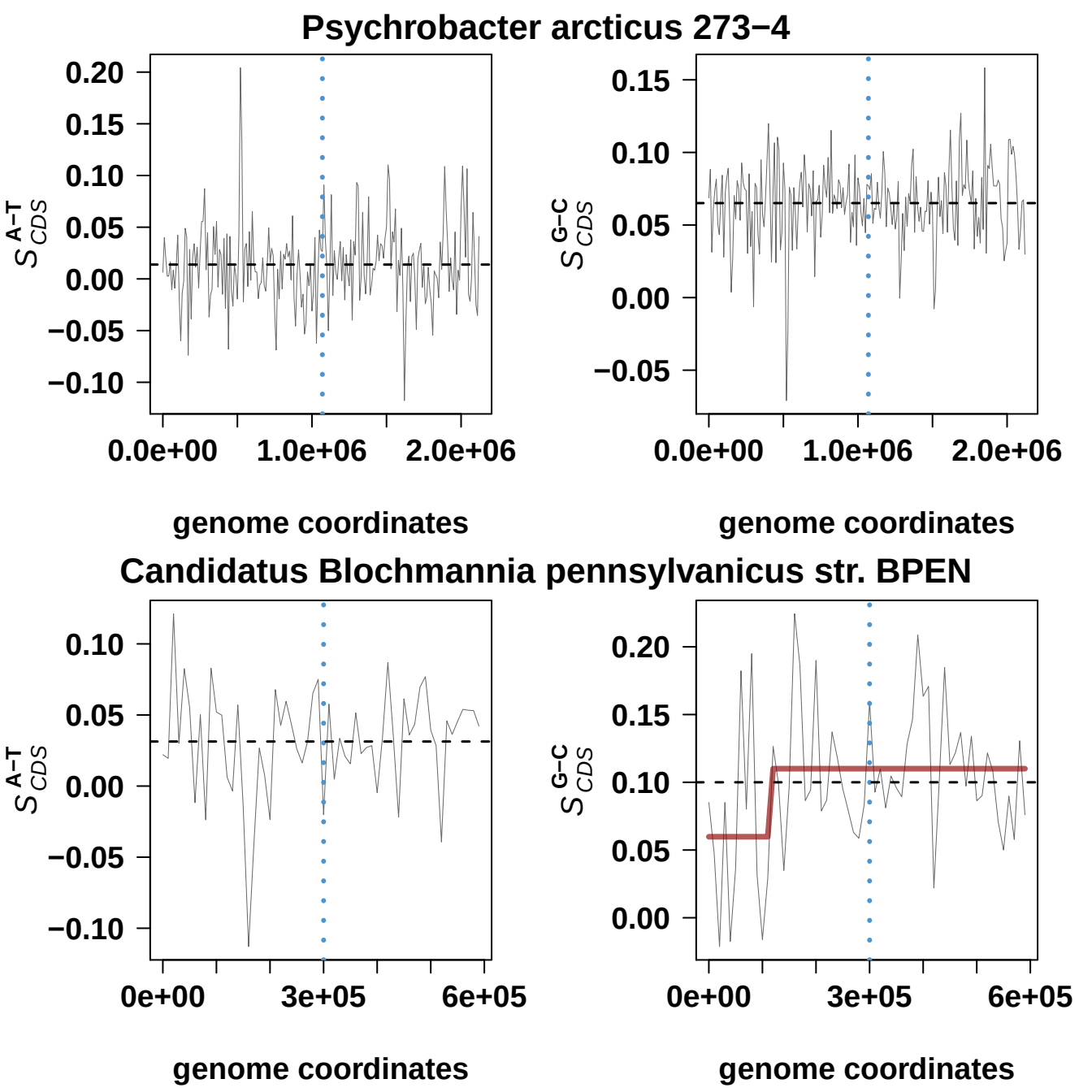
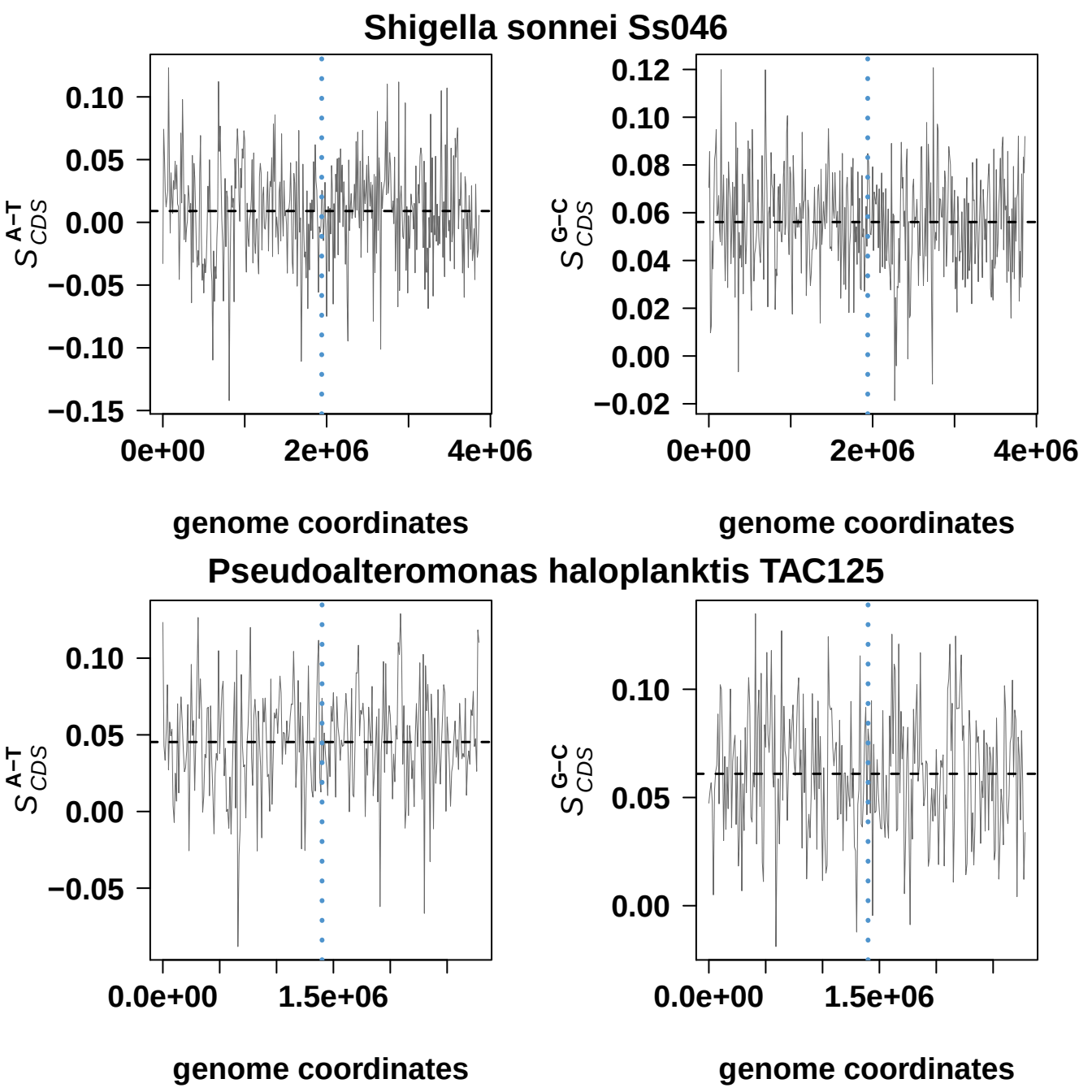
0.10
0.05
0.00
−0.05
−0.10
−0.15
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{CDS}
0.05
0.00
−0.05
−0.10
0e+00
2e+06
4e+06
genome coordinates
Haemophilus influenzae 86−028NP
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
0.0e+00
1.0e+06
genome coordinates
S^{G-C}_{CDS}
0.20
0.15
0.10
0.05
0.00
0.0e+00
1.0e+06
genome coordinates


Psychrobacter arcticus 273−4
0.20
0.15
0.10
0.05
0.00
−0.05
−0.10
S^{A-T}_{CDS}
0.0e+00
1.0e+06
2.0e+06
genome coordinates
0.15
0.10
0.05
0.00
−0.05
S^{G-C}_{CDS}
0.0e+00
1.0e+06
2.0e+06
genome coordinates
Candidatus Blochmannia pennsylvanicus str. BPEN
0.10
0.05
0.00
−0.05
−0.10
S^{A-T}_{CDS}
0e+00
3e+05
6e+05
genome coordinates
0.20
0.15
0.10
0.05
0.00
S^{G-C}_{CDS}
0e+00
3e+05
6e+05
genome coordinates


Shigella sonnei Ss046
S^{A-T}_{CDS}
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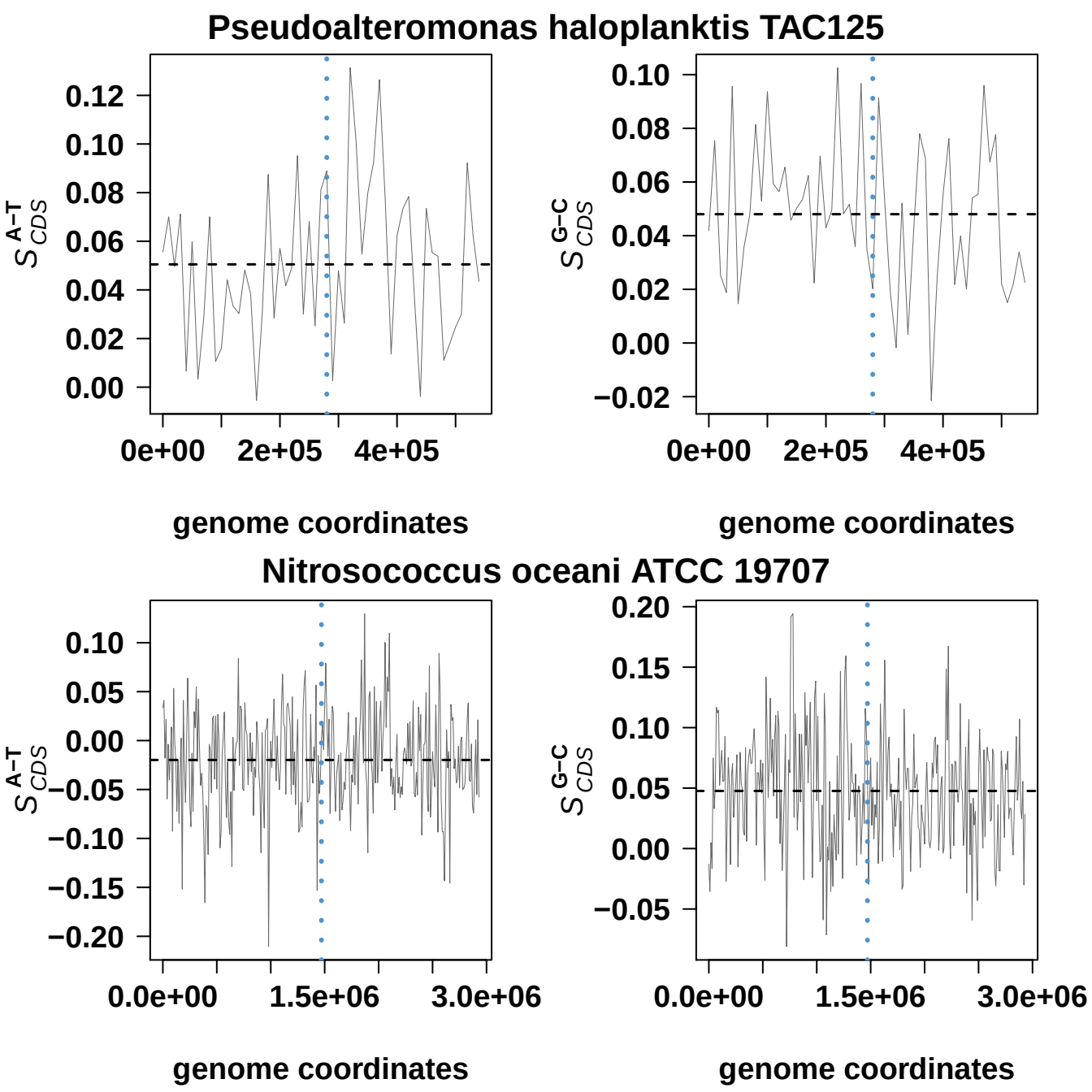
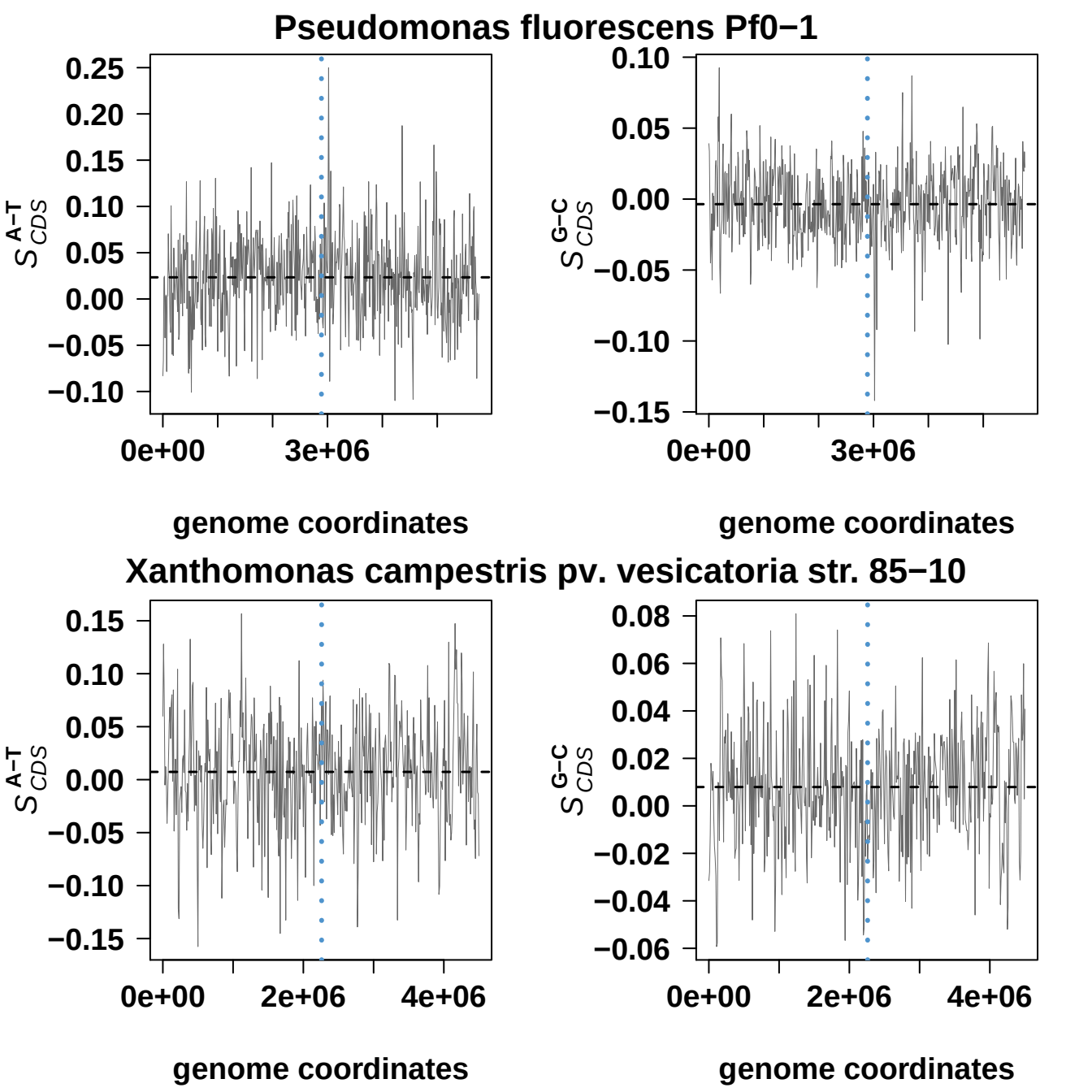
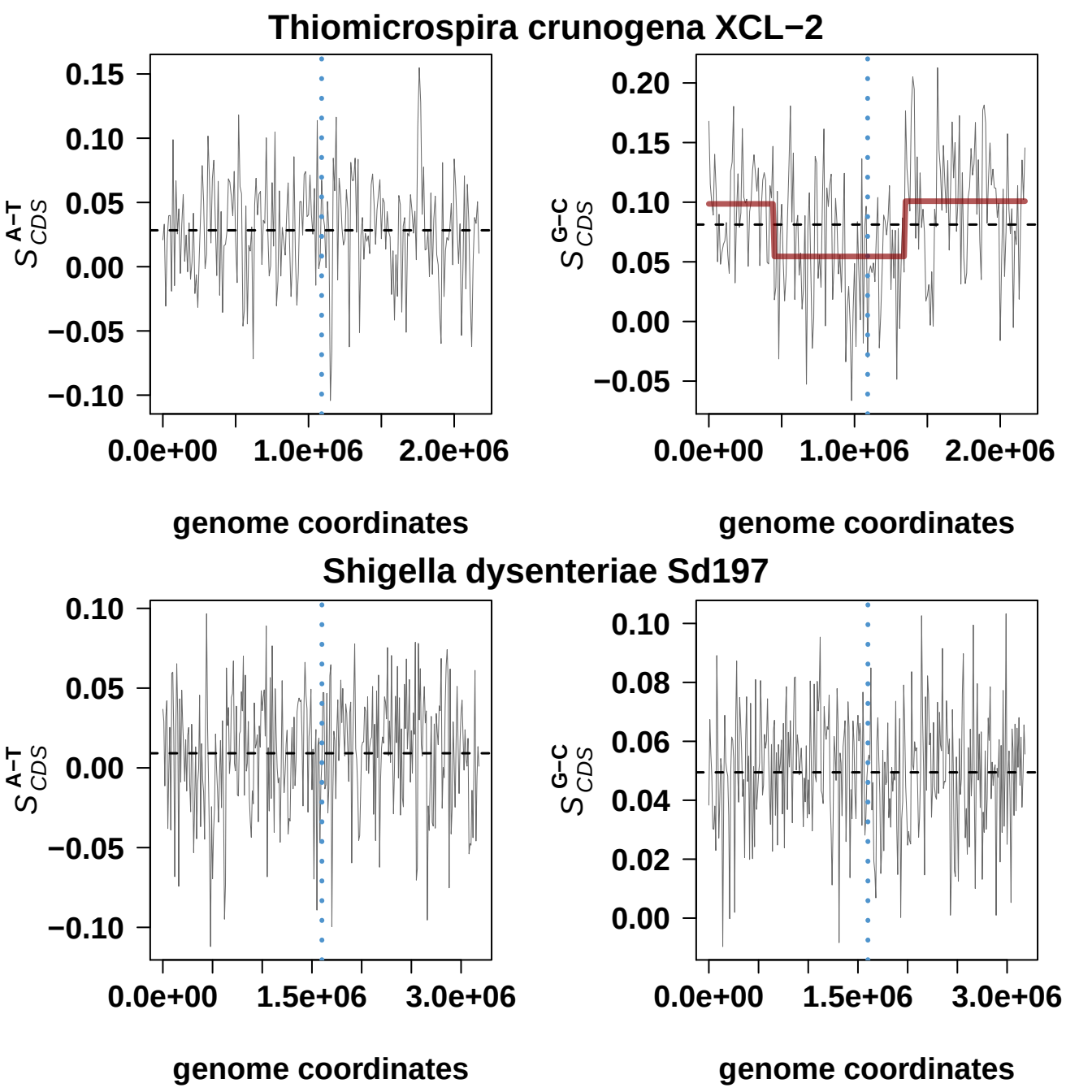
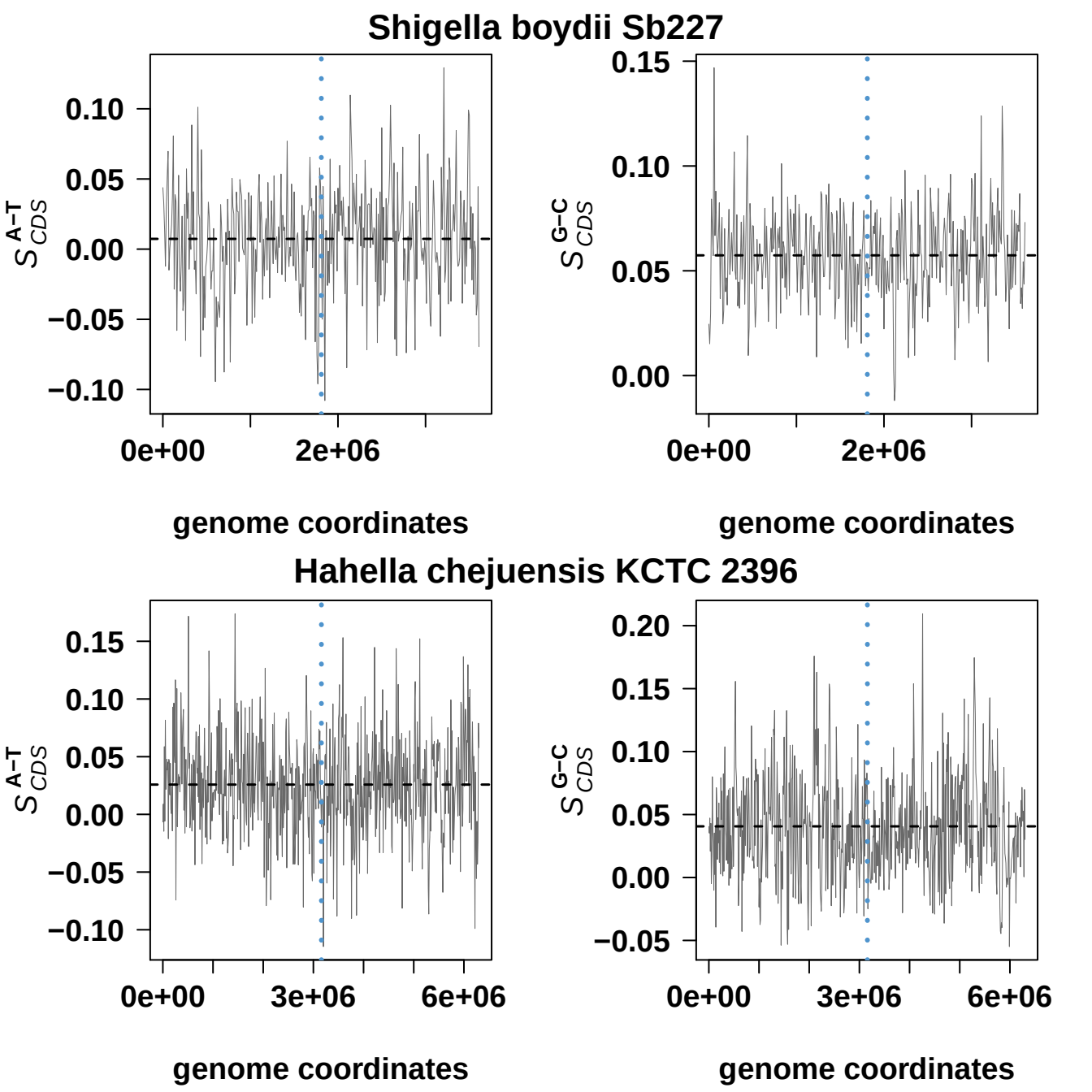
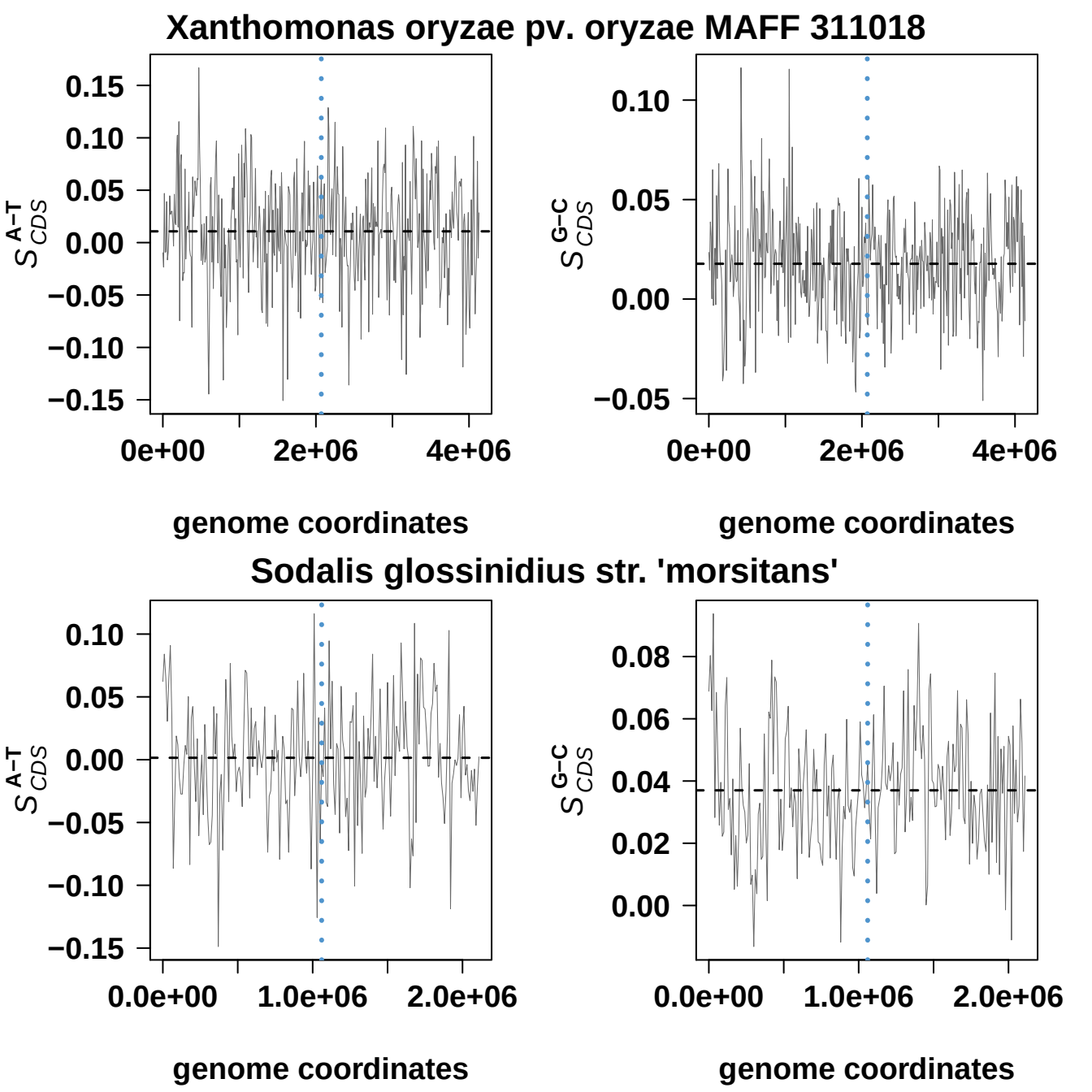
0.05
0.00
−0.05
−0.10
−0.15
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{CDS}
0.12
0.10
0.08
0.06
0.04
0.02
0.00
−0.02
0e+00
2e+06
4e+06
genome coordinates
Pseudoalteromonas haloplanktis TAC125
S^{A-T}_{CDS}
0.10
0.05
0.00
−0.05
0.0e+00
1.5e+06
genome coordinates
S^{G-C}_{CDS}
0.10
0.05
0.00
0.0e+00
1.5e+06
genome coordinates

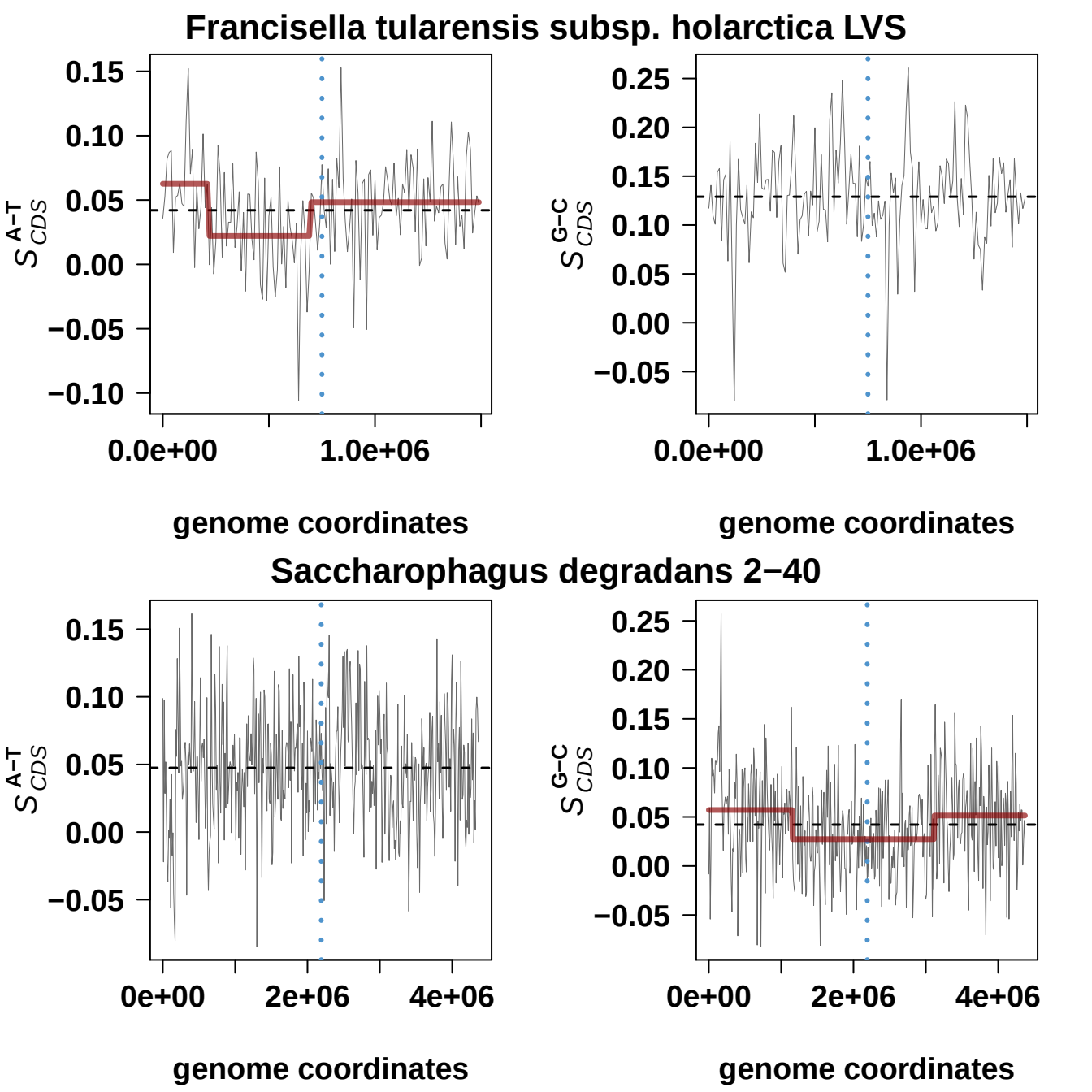

Pseudoalteromonas haloplanktis TAC125
S^{A-T}_{CDS}
0.12
0.10
0.08
0.06
0.04
0.02
0.00
0e+00
2e+05
4e+05
genome coordinates
S^{G-C}_{CDS}
0.10
0.08
0.06
0.04
0.02
0.00
−0.02
0e+00
2e+05
4e+05
genome coordinates
Nitrosococcus oceani ATCC 19707
S^{A-T}_{CDS}
0.10
0.05
0.00
−0.05
−0.10
−0.15
−0.20
0.0e+00
1.5e+06
3.0e+06
genome coordinates
S^{G-C}_{CDS}
0.20
0.15
0.10
0.05
0.00
−0.05
0.0e+00
1.5e+06
3.0e+06
genome coordinates

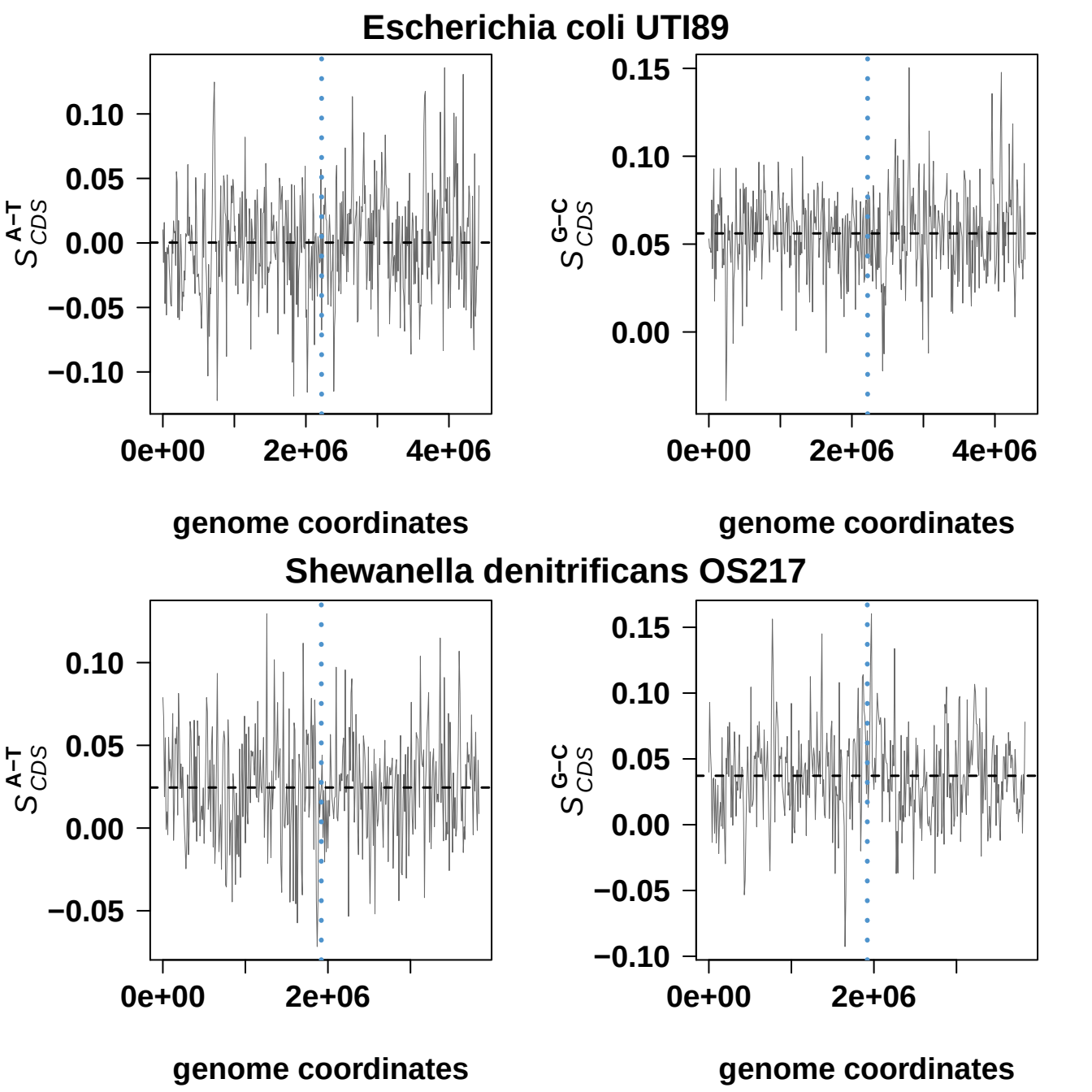

Pseudomonas fluorescens Pf0−1
S^{A-T}_{CDS}
0.25
0.20
0.15
0.10
0.05
0.00
−0.05
−0.10
0e+00
3e+06
genome coordinates
S^{G-C}_{CDS}
0.10
0.05
0.00
−0.05
−0.10
−0.15
0e+00
3e+06
genome coordinates
Xanthomonas campestris pv. vesicatoria str. 85−10
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
−0.05
−0.10
−0.15
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{CDS}
0.08
0.06
0.04
0.02
0.00
−0.02
−0.04
−0.06
0e+00
2e+06
4e+06
genome coordinates

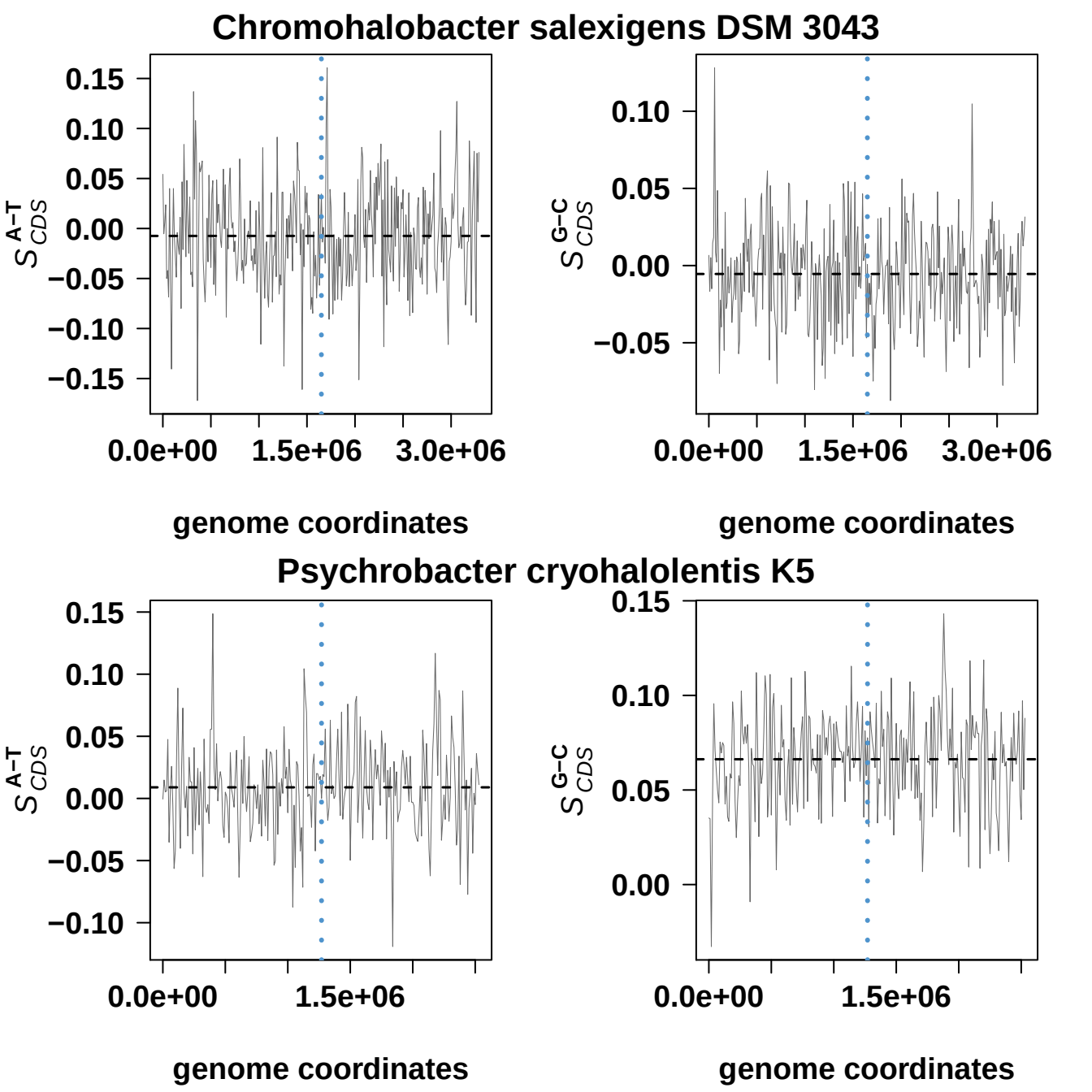

Thiomicrospira crunogena XCL−2
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
−0.05
−0.10
0.0e+00
1.0e+06
2.0e+06
genome coordinates
S^{G-C}_{CDS}
0.20
0.15
0.10
0.05
0.00
−0.05
0.0e+00
1.0e+06
2.0e+06
genome coordinates
Shigella dysenteriae Sd197
S^{A-T}_{CDS}
0.10
0.05
0.00
−0.05
−0.10
0.0e+00
1.5e+06
3.0e+06
genome coordinates
S^{G-C}_{CDS}
0.10
0.08
0.06
0.04
0.02
0.00
0.0e+00
1.5e+06
3.0e+06
genome coordinates

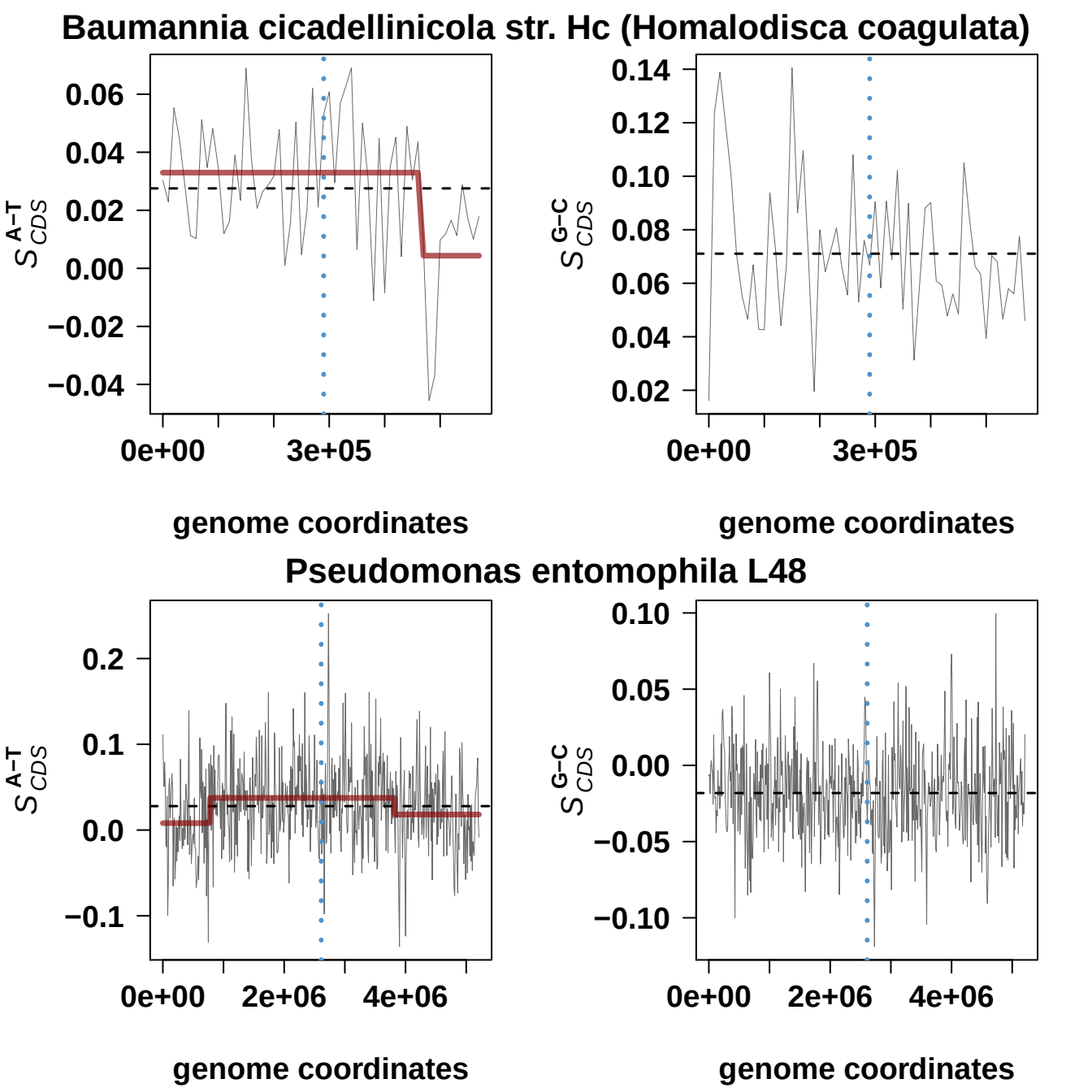

Shigella boydii Sb227
S^{A-T}_{CDS}
0.10
0.05
0.00
−0.05
−0.10
0e+00
2e+06
genome coordinates
S^{G-C}_{CDS}
0.15
0.10
0.05
0.00
0e+00
2e+06
genome coordinates
Hahella chejuensis KCTC 2396
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
−0.05
−0.10
0e+00
3e+06
6e+06
genome coordinates
S^{G-C}_{CDS}
0.20
0.15
0.10
0.05
0.00
−0.05
0e+00
3e+06
6e+06
genome coordinates

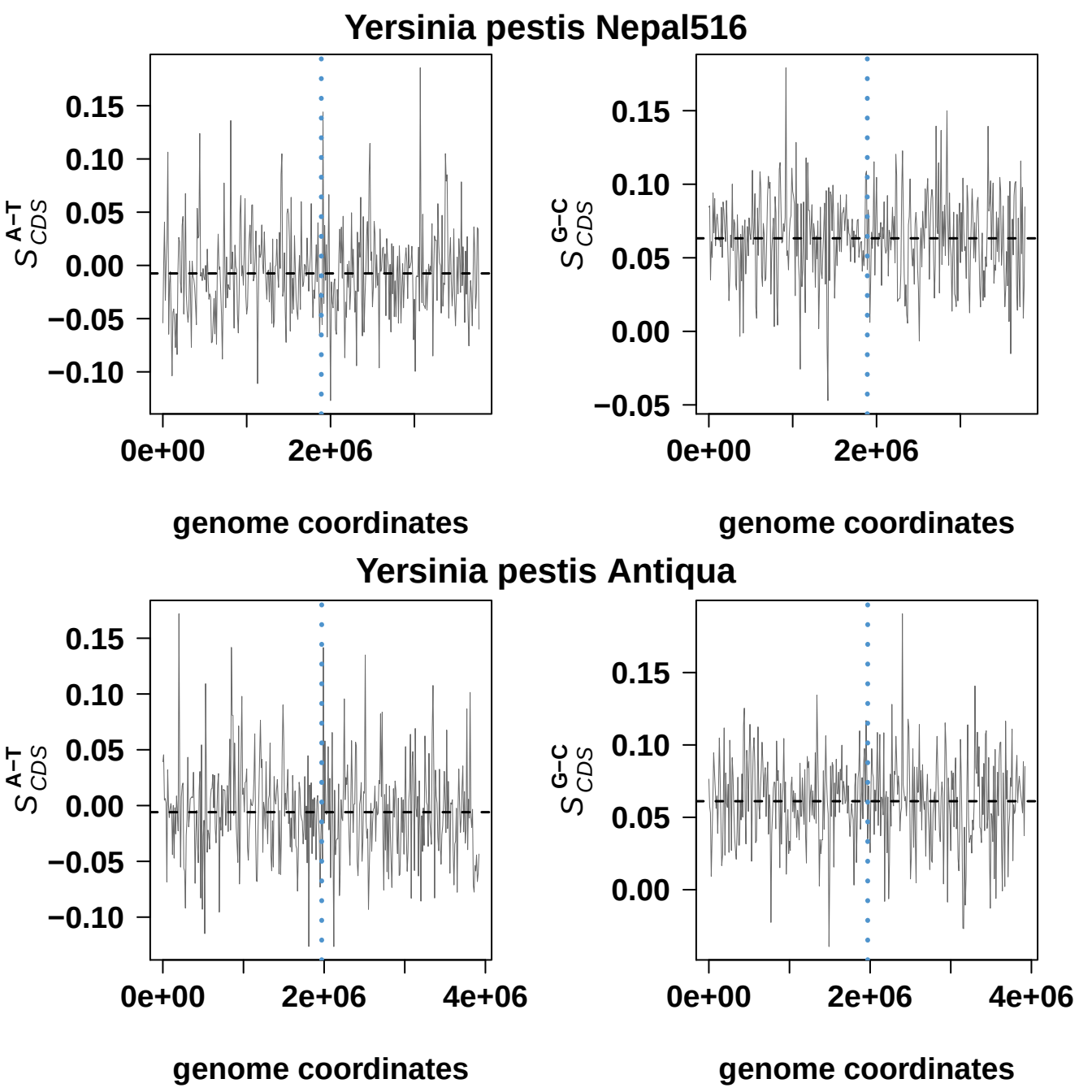

Xanthomonas oryzae pv. oryzae MAFF 311018
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
−0.05
−0.10
−0.15
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{CDS}
0.10
0.05
0.00
−0.05
0e+00
2e+06
4e+06
genome coordinates
Sodalis glossinidius str. 'morsitans'
S^{A-T}_{CDS}
0.10
0.05
0.00
−0.05
−0.10
−0.15
0.0e+00
1.0e+06
2.0e+06
genome coordinates
S^{G-C}_{CDS}
0.08
0.06
0.04
0.02
0.00
0.0e+00
1.0e+06
2.0e+06
genome coordinates


Francisella tularensis subsp. holarctica LVS
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
−0.05
−0.10
0.0e+00
1.0e+06
genome coordinates
S^{G-C}_{CDS}
0.25
0.20
0.15
0.10
0.05
0.00
−0.05
0.0e+00
1.0e+06
genome coordinates
Saccharophagus degradans 2−40
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
−0.05
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{CDS}
0.25
0.20
0.15
0.10
0.05
0.00
−0.05
0e+00
2e+06
4e+06
genome coordinates


Escherichia coli UTI89
S^{A-T}_{CDS}
0.10
0.05
0.00
−0.05
−0.10
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{CDS}
0.15
0.10
0.05
0.00
0e+00
2e+06
4e+06
genome coordinates
Shewanella denitrificans OS217
S^{A-T}_{CDS}
0.10
0.05
0.00
−0.05
0e+00
2e+06
genome coordinates
S^{G-C}_{CDS}
0.15
0.10
0.05
0.00
−0.05
−0.10
0e+00
2e+06
genome coordinates


Chromohalobacter salexigens DSM 3043
0.15
0.10
0.05
0.00
−0.05
−0.10
−0.15
S^{A-T}_{CDS}
0.0e+00
1.5e+06
3.0e+06
genome coordinates
0.10
0.05
0.00
−0.05
S^{G-C}_{CDS}
0.0e+00
1.5e+06
3.0e+06
genome coordinates
Psychrobacter cryohalolentis K5
0.15
0.10
0.05
0.00
−0.05
−0.10
S^{A-T}_{CDS}
0.0e+00
1.5e+06
genome coordinates
0.15
0.10
0.05
0.00
S^{G-C}_{CDS}
0.0e+00
1.5e+06
genome coordinates


Baumannia cicadellinicola str. Hc (Homalodisca coagulata)
S^{A-T}_{CDS}
0.06
0.04
0.02
0.00
−0.02
−0.04
0e+00
3e+05
genome coordinates
S^{G-C}_{CDS}
0.14
0.12
0.10
0.08
0.06
0.04
0.02
0e+00
3e+05
genome coordinates
Pseudomonas entomophila L48
S^{A-T}_{CDS}
0.2
0.1
0.0
−0.1
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{CDS}
0.10
0.05
0.00
−0.05
−0.10
0e+00
2e+06
4e+06
genome coordinates


Yersinia pestis Nepal516
S^{A-T}_{CDS}
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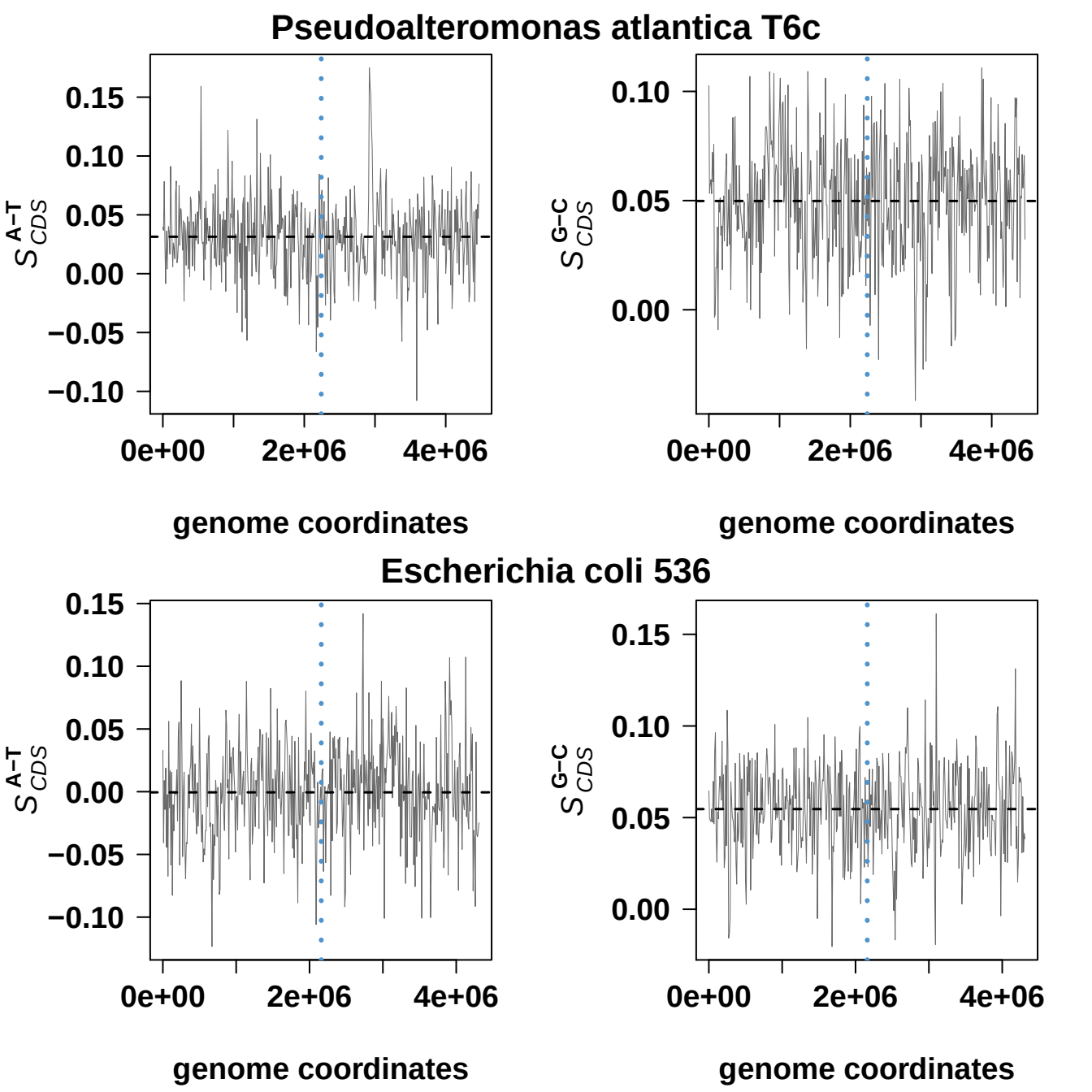
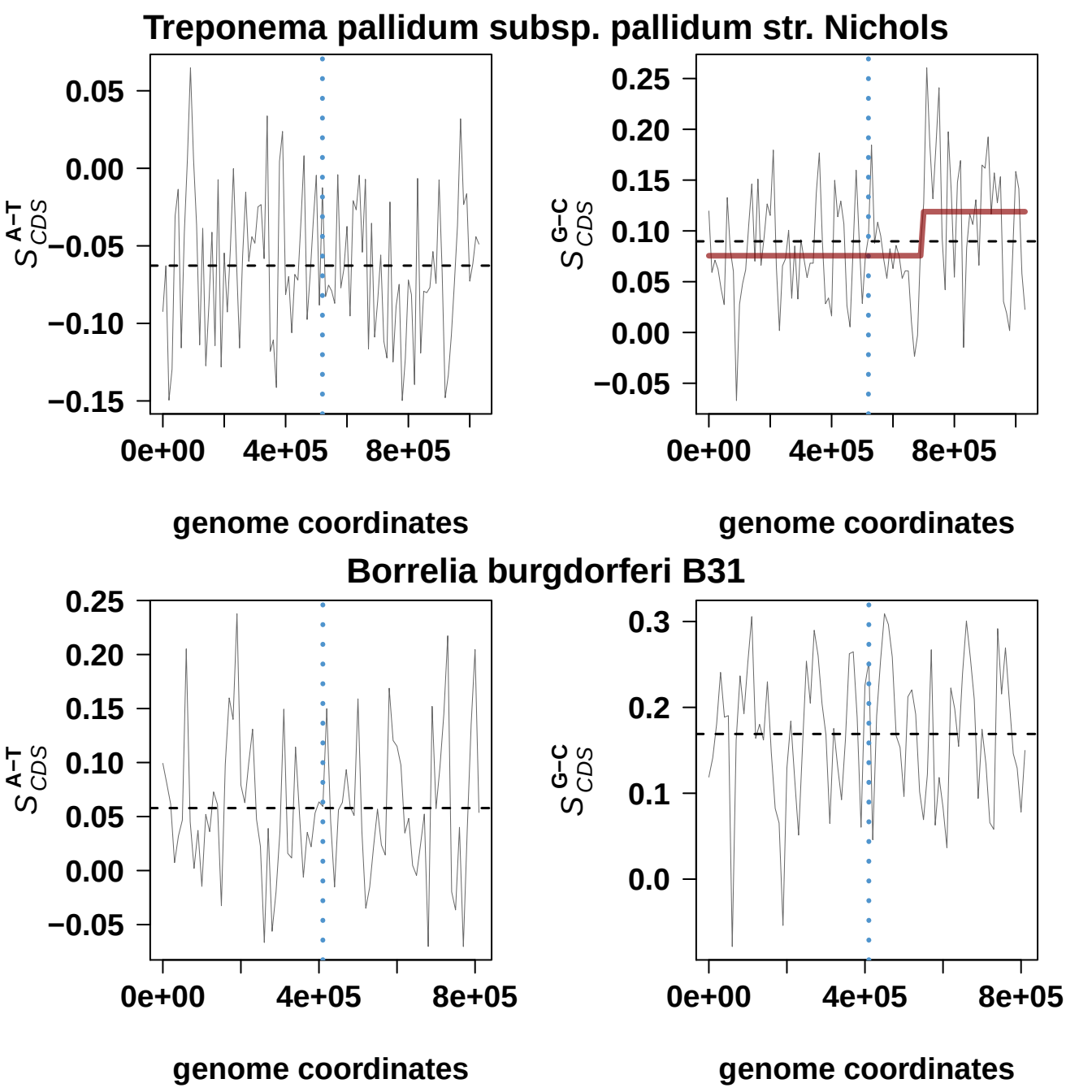
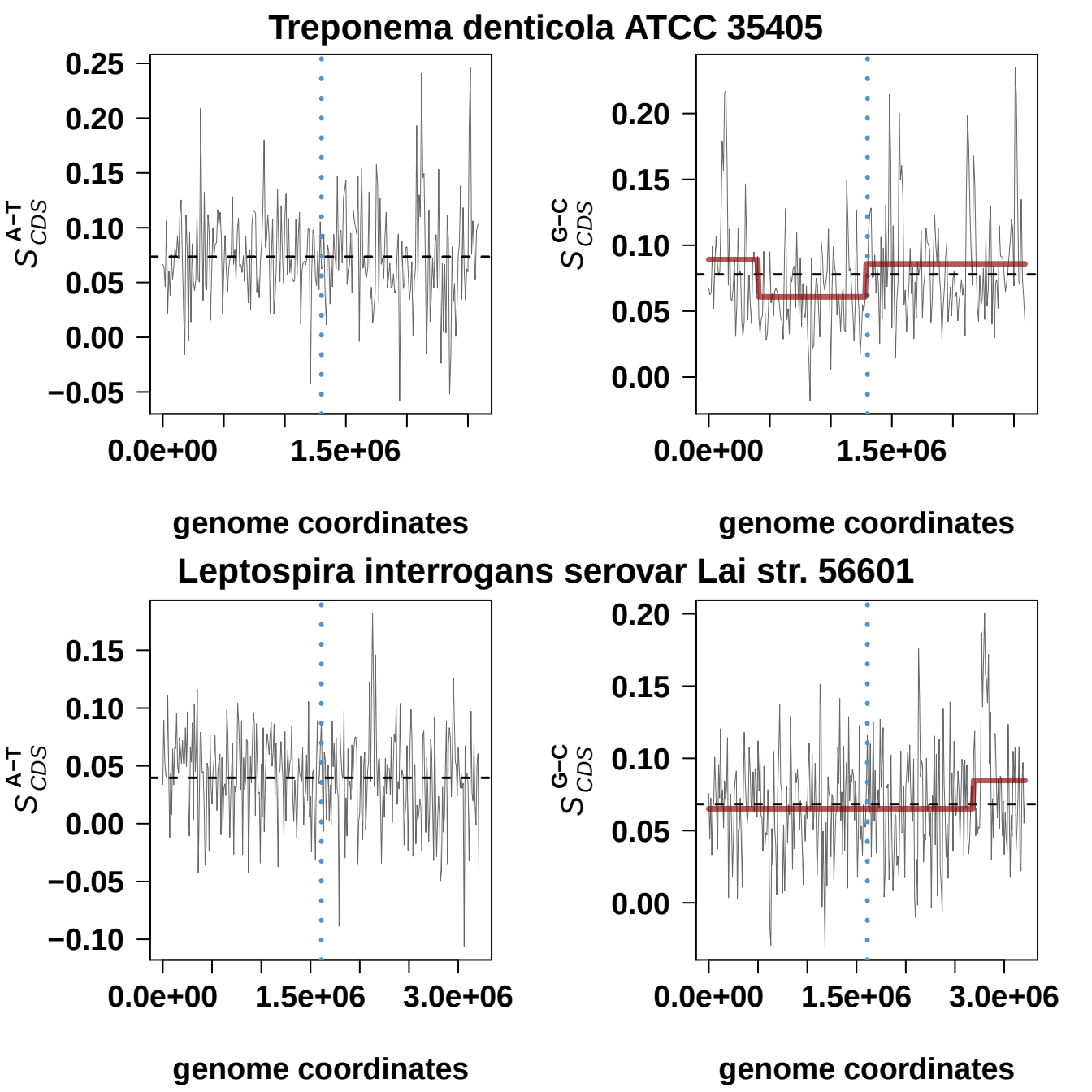
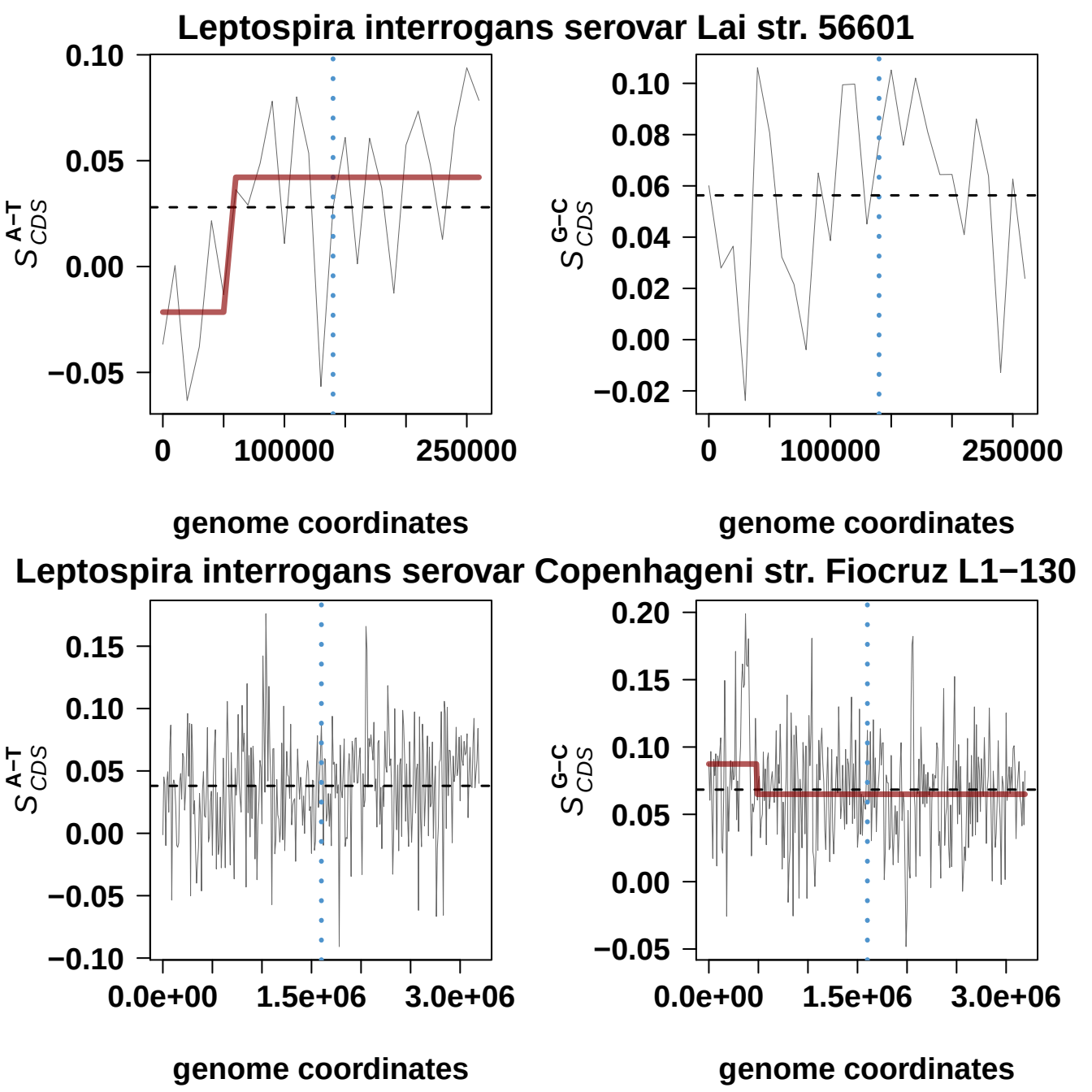
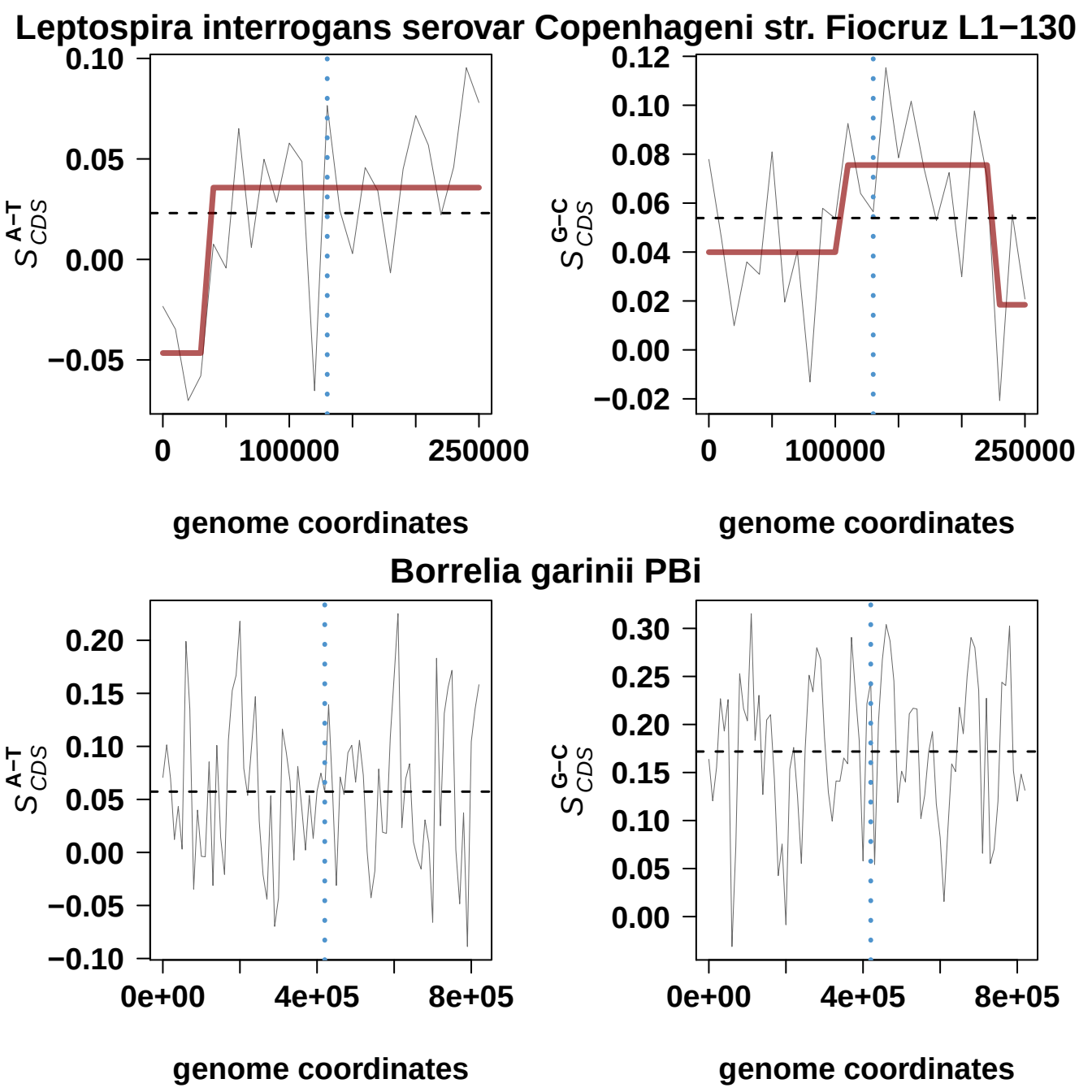
0.10
0.05
0.00
−0.05
−0.10
0e+00
2e+06
genome coordinates
S^{G-C}_{CDS}
0.15
0.10
0.05
0.00
−0.05
0e+00
2e+06
genome coordinates
Yersinia pestis Antiqua
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
−0.05
−0.10
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{CDS}
0.15
0.10
0.05
0.00
0e+00
2e+06
4e+06
genome coordinates

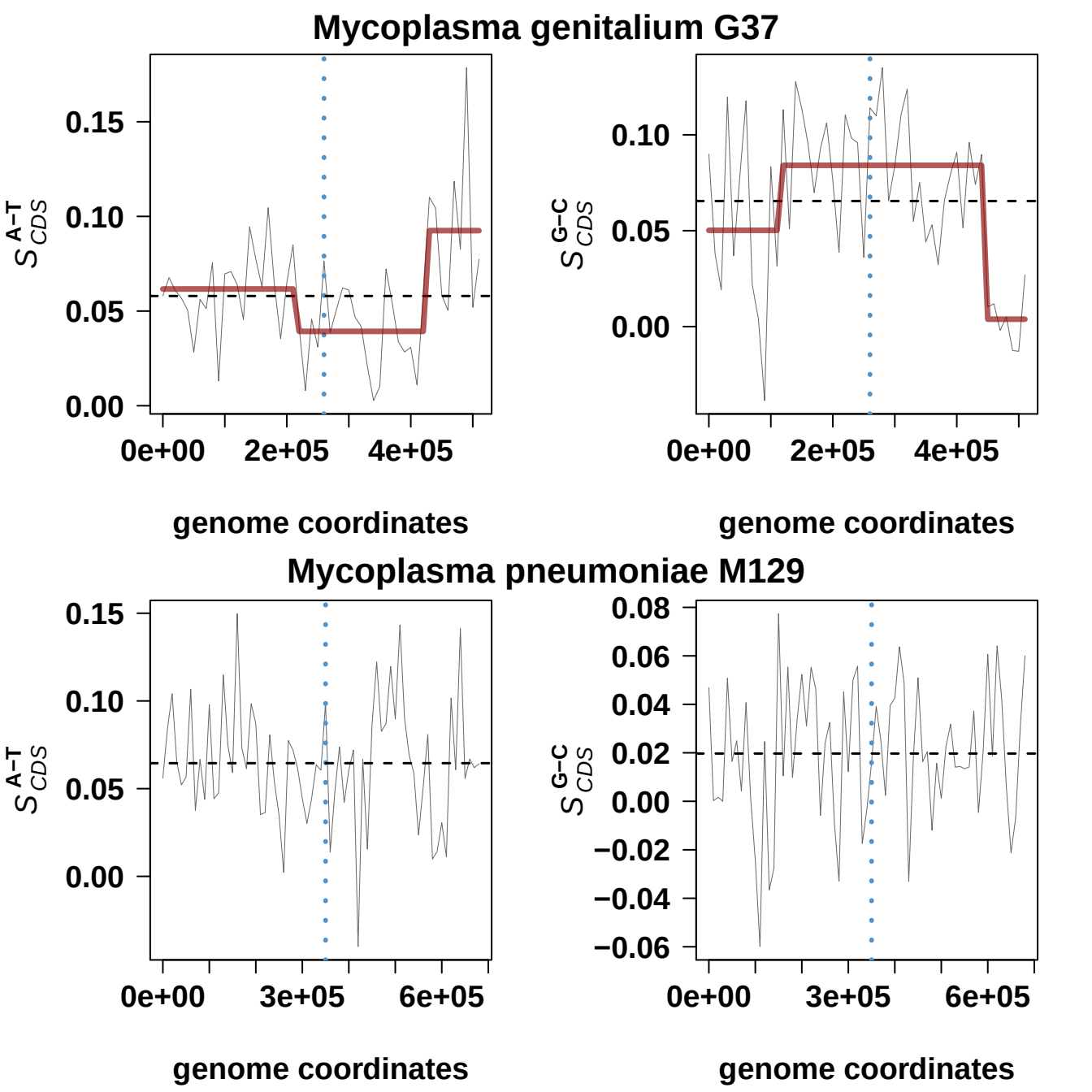

Pseudoalteromonas atlantica T6c
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
−0.05
−0.10
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{CDS}
0.10
0.05
0.00
0e+00
2e+06
4e+06
genome coordinates
Escherichia coli 536
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
−0.05
−0.10
0e+00
2e+06
4e+06
genome coordinates
S^{G-C}_{CDS}
0.15
0.10
0.05
0.00
0e+00
2e+06
4e+06
genome coordinates

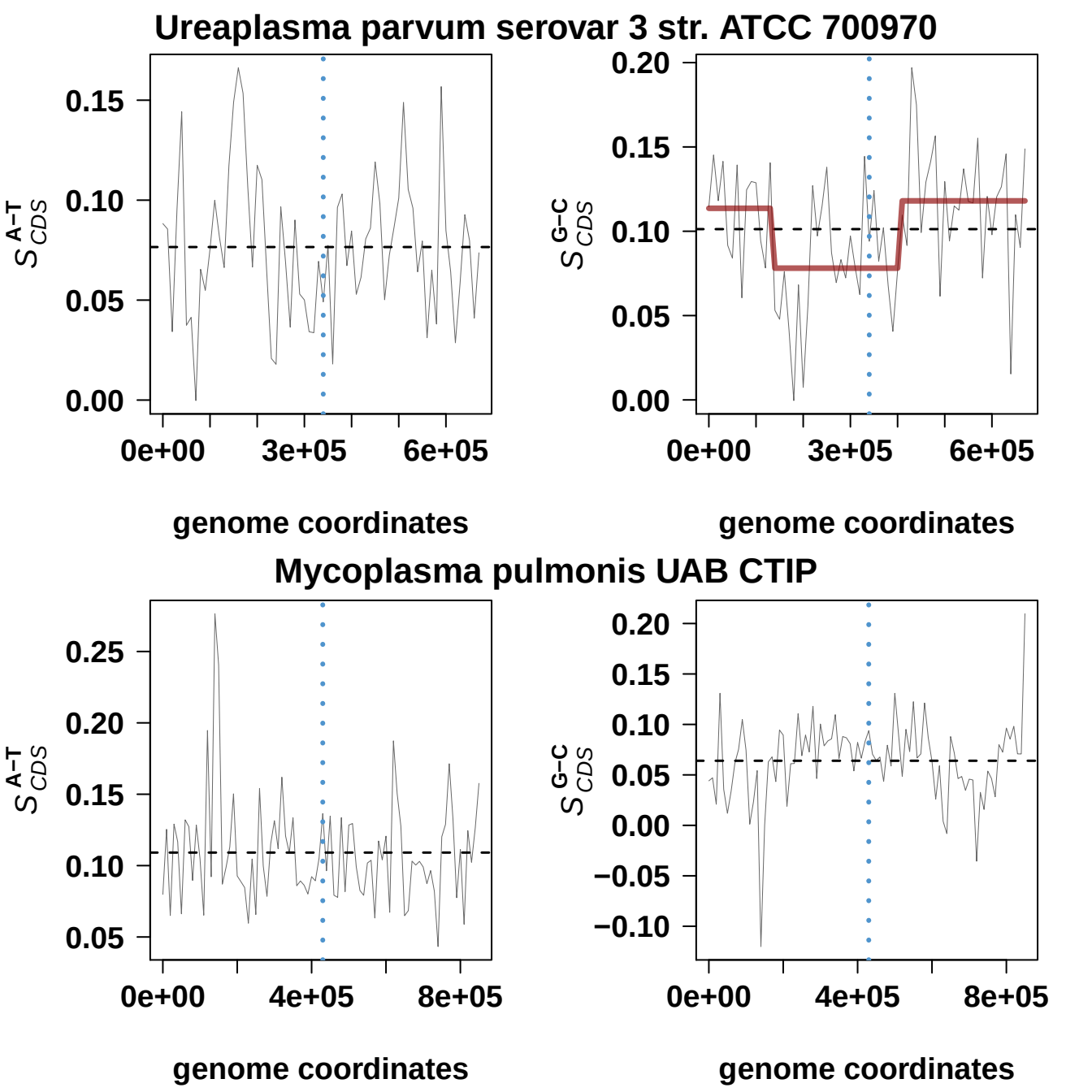

Treponema pallidum subsp. pallidum str. Nichols
S^{A-T}_{CDS}
0.05
0.00
−0.05
−0.10
−0.15
0e+00
4e+05
8e+05
genome coordinates
S^{G-C}_{CDS}
0.25
0.20
0.15
0.10
0.05
0.00
−0.05
0e+00
4e+05
8e+05
genome coordinates
Borrelia burgdorferi B31
S^{A-T}_{CDS}
0.25
0.20
0.15
0.10
0.05
0.00
−0.05
0e+00
4e+05
8e+05
genome coordinates
S^{G-C}_{CDS}
0.3
0.2
0.1
0.0
0e+00
4e+05
8e+05
genome coordinates

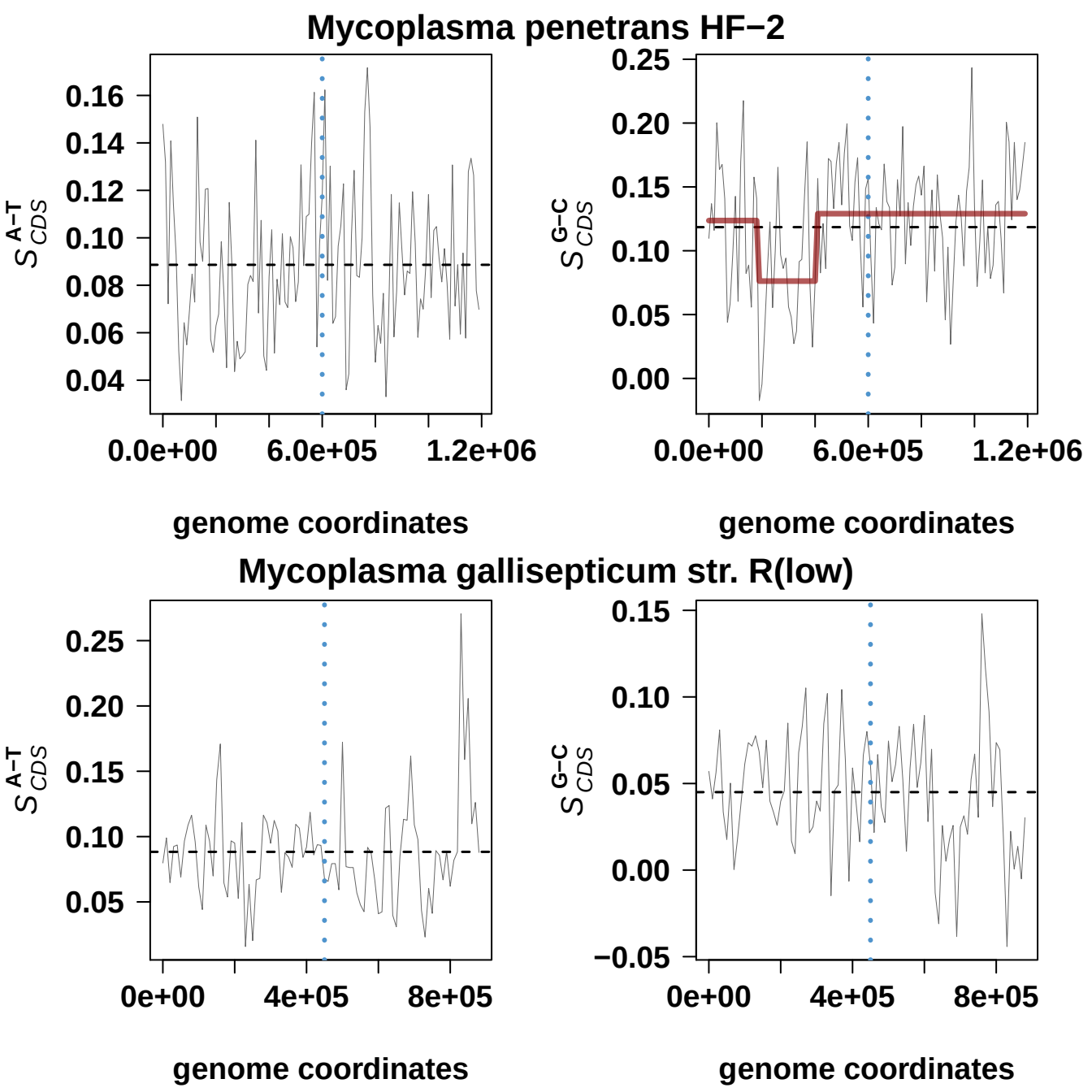

Treponema denticola ATCC 35405
S^{A-T}_{CDS}
0.25
0.20
0.15
0.10
0.05
0.00
−0.05
0.0e+00
1.5e+06
genome coordinates
S^{G-C}_{CDS}
0.20
0.15
0.10
0.05
0.00
0.0e+00
1.5e+06
genome coordinates
Leptospira interrogans serovar Lai str. 56601
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
−0.05
−0.10
0.0e+00
1.5e+06
3.0e+06
genome coordinates
S^{G-C}_{CDS}
0.20
0.15
0.10
0.05
0.00
0.0e+00
1.5e+06
3.0e+06
genome coordinates

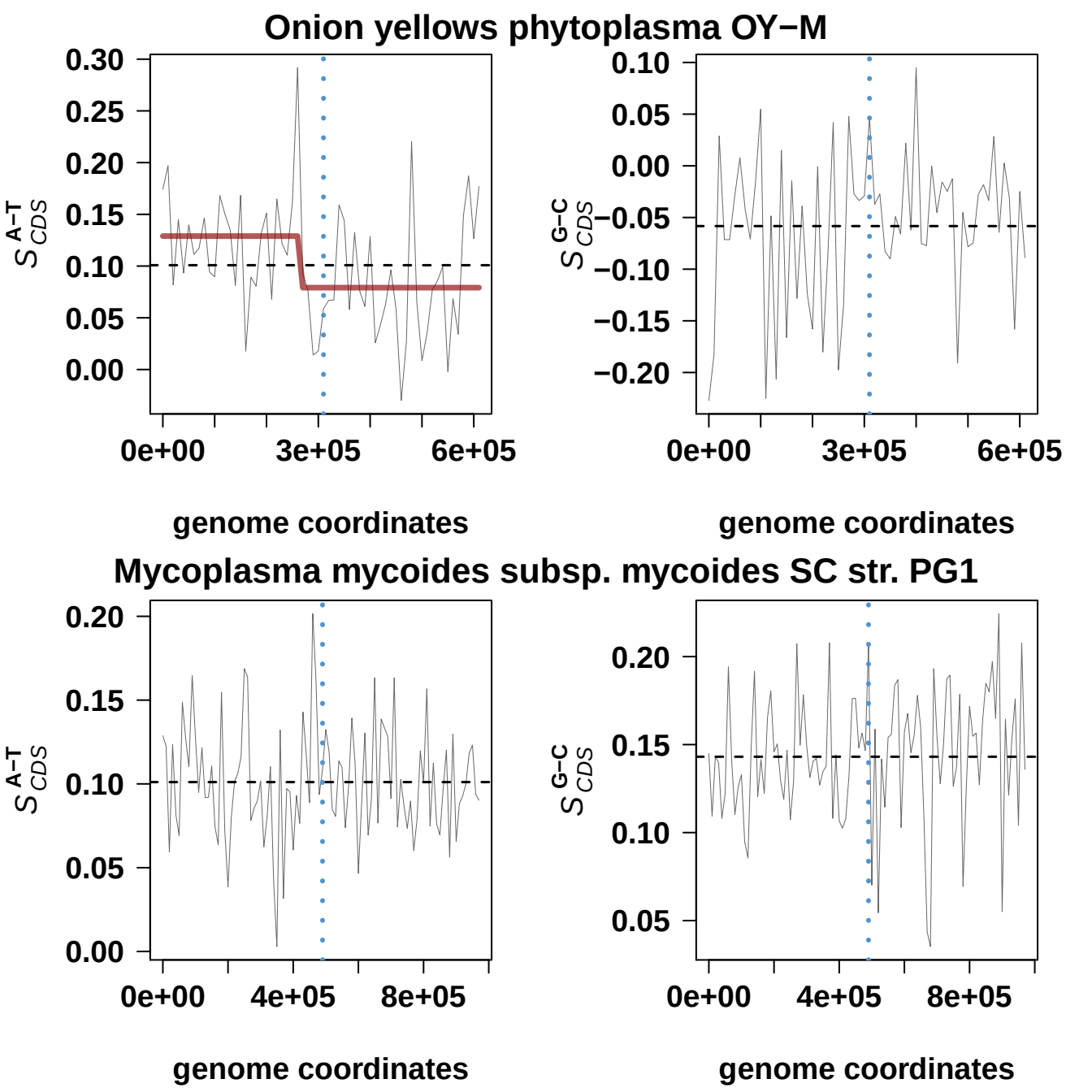

Leptospira interrogans serovar Lai str. 56601
S^{A-T}_{CDS}
0.10
0.05
0.00
−0.05
0
100000
250000
genome coordinates
S^{G-C}_{CDS}
0.10
0.08
0.06
0.04
0.02
0.00
−0.02
0
100000
250000
genome coordinates
Leptospira interrogans serovar Copenhageni str. Fiocruz L1−130
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
−0.05
−0.10
0.0e+00
1.5e+06
3.0e+06
genome coordinates
S^{G-C}_{CDS}
0.20
0.15
0.10
0.05
0.00
−0.05
0.0e+00
1.5e+06
3.0e+06
genome coordinates

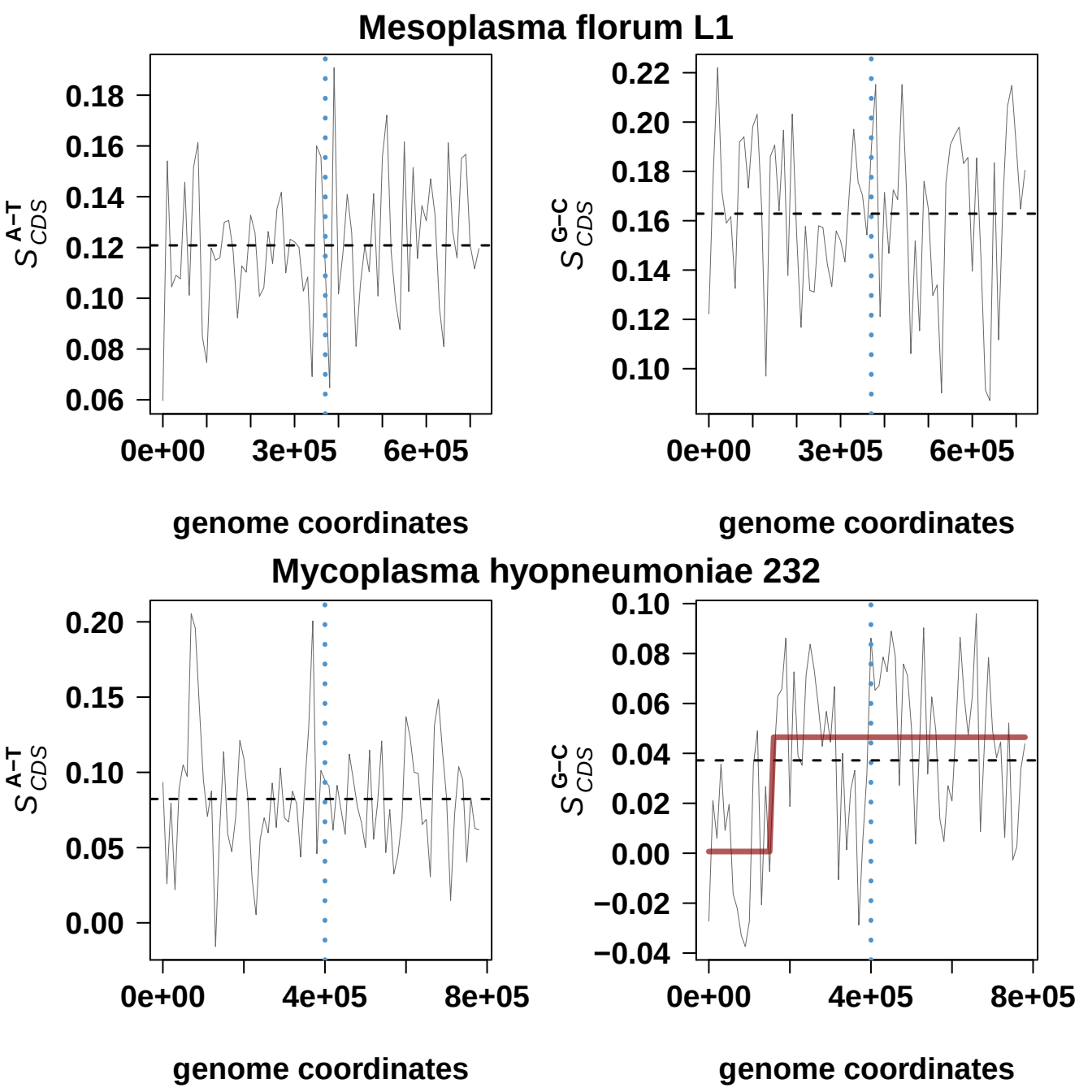

Leptospira interrogans serovar Copenhageni str. Fiocruz L1−130
S^{A-T}_{CDS}
0.10
0.05
0.00
−0.05
0
100000
250000
genome coordinates
S^{G-C}_{CDS}
0.12
0.10
0.08
0.06
0.04
0.02
0.00
−0.02
0
100000
250000
genome coordinates
Borrelia garinii PBi
S^{A-T}_{CDS}
0.20
0.15
0.10
0.05
0.00
−0.05
−0.10
0e+00
4e+05
8e+05
genome coordinates
S^{G-C}_{CDS}
0.30
0.25
0.20
0.15
0.10
0.05
0.00
0e+00
4e+05
8e+05
genome coordinates

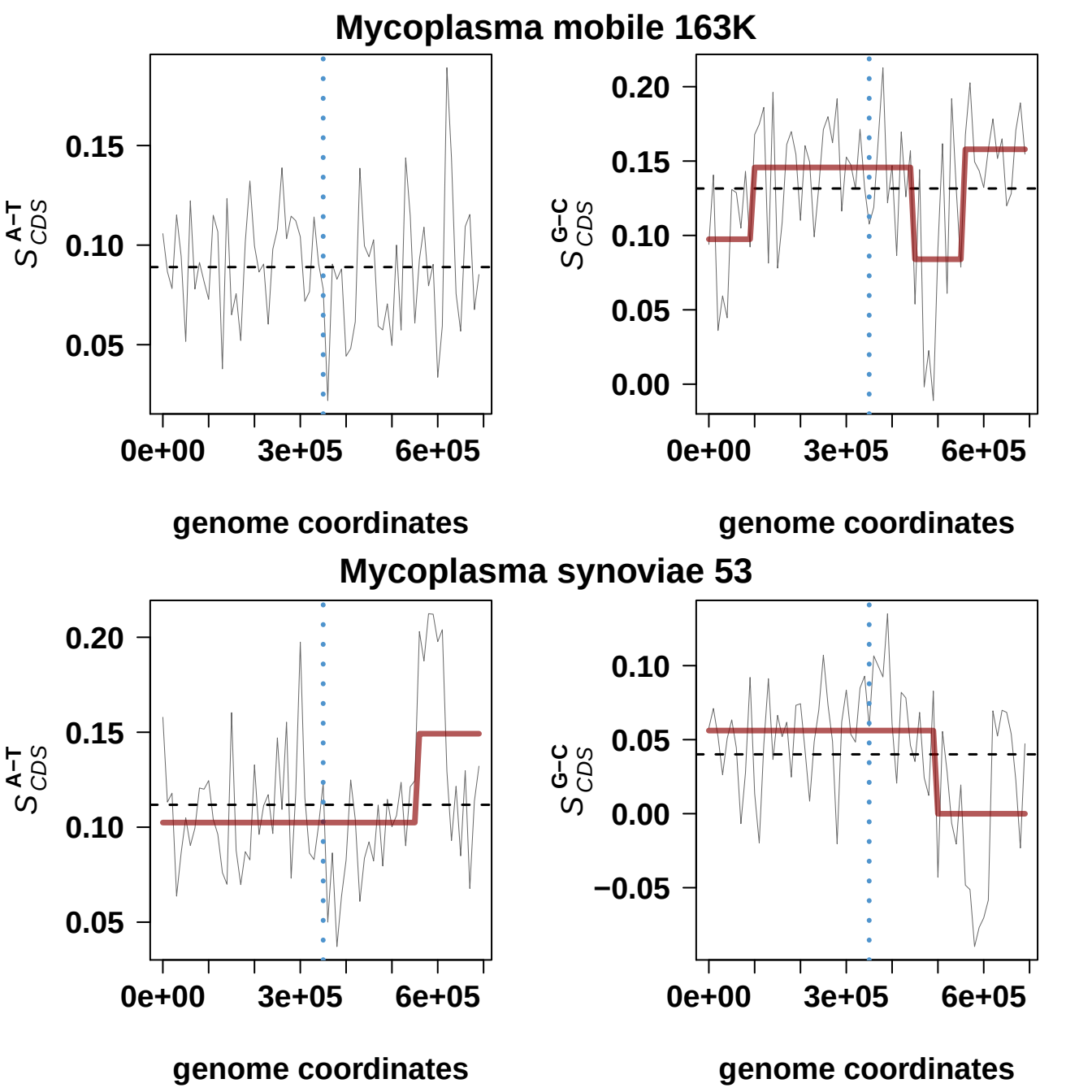

Mycoplasma genitalium G37
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
0e+00
2e+05
4e+05
genome coordinates
S^{G-C}_{CDS}
0.10
0.05
0.00
0e+00
2e+05
4e+05
genome coordinates
Mycoplasma pneumoniae M129
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
0e+00
3e+05
6e+05
genome coordinates
S^{G-C}_{CDS}
0.08
0.06
0.04
0.02
0.00
−0.02
−0.04
−0.06
0e+00
3e+05
6e+05
genome coordinates

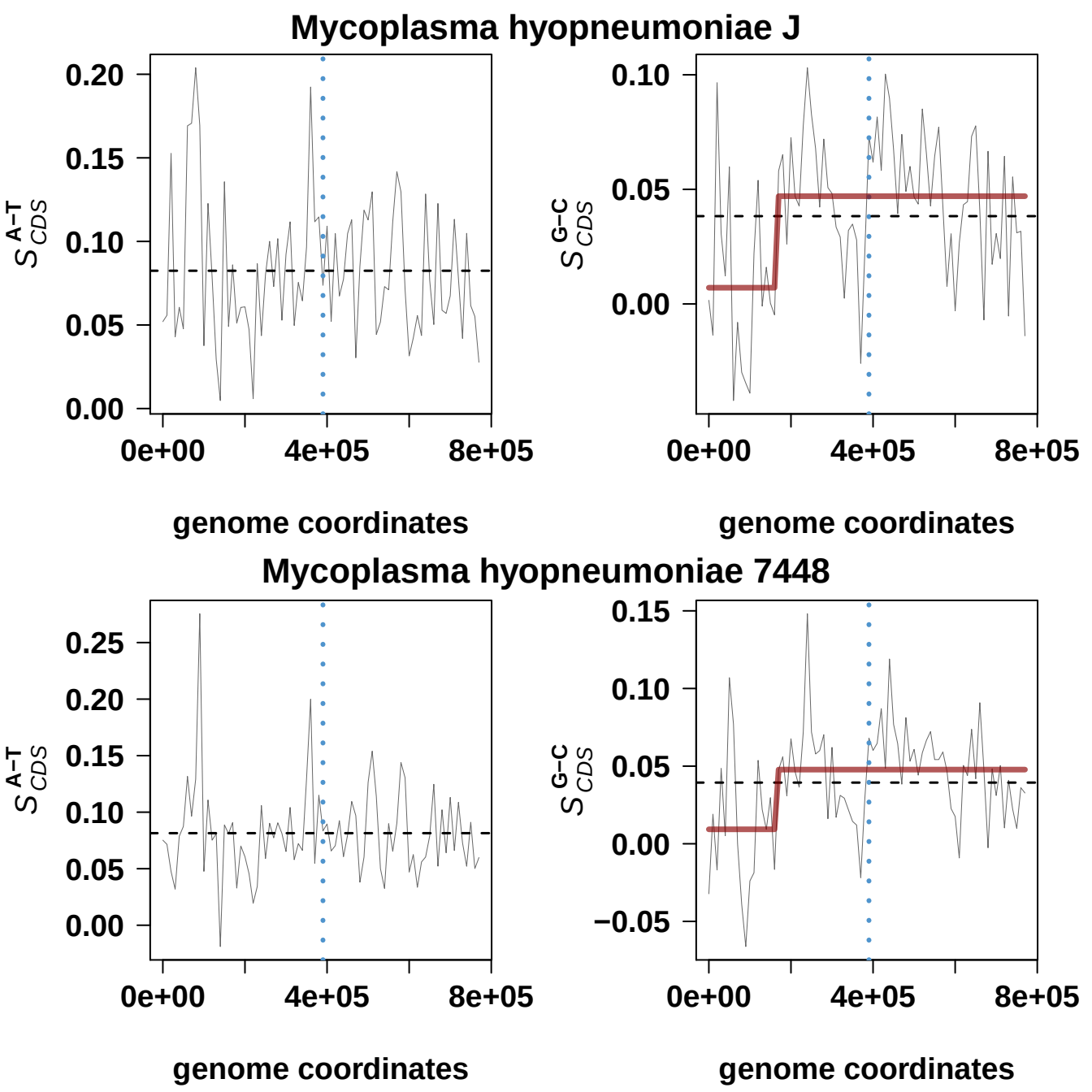

Ureaplasma parvum serovar 3 str. ATCC 700970
S^{A-T}_{CDS}
0.15
0.10
0.05
0.00
0e+00
3e+05
6e+05
genome coordinates
S^{G-C}_{CDS}
0.20
0.15
0.10
0.05
0.00
0e+00
3e+05
6e+05
genome coordinates
Mycoplasma pulmonis UAB CTIP
S^{A-T}_{CDS}
0.25
0.20
0.15
0.10
0.05
0e+00
4e+05
8e+05
genome coordinates
S^{G-C}_{CDS}
0.20
0.15
0.10
0.05
0.00
−0.05
−0.10
0e+00
4e+05
8e+05
genome coordinates

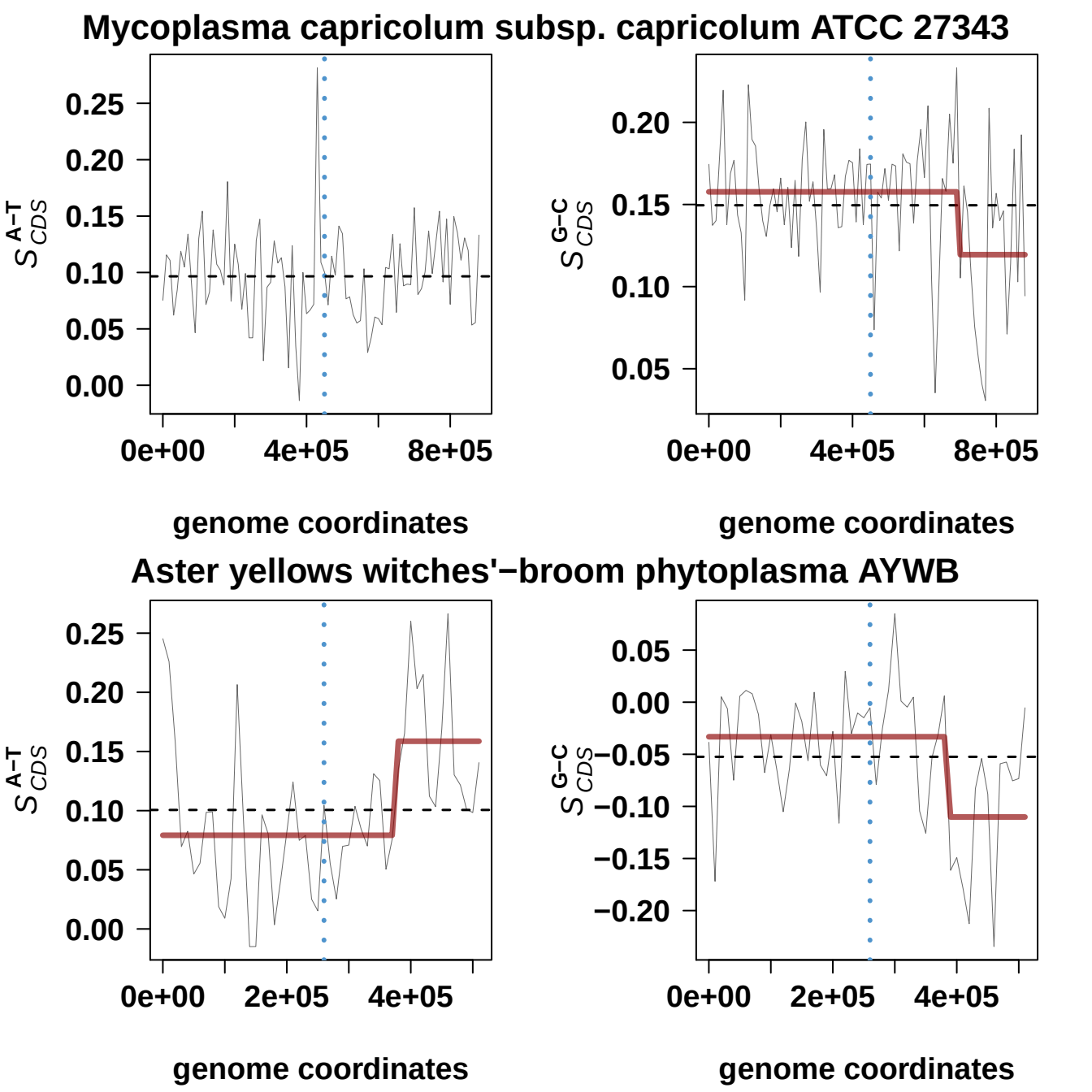

Mycoplasma penetrans HF−2
S^{A-T}_{CDS}
0.16
0.14
0.12
0.10
0.08
0.06
0.04
0.0e+00
6.0e+05
1.2e+06
genome coordinates
S^{G-C}_{CDS}
0.25
0.20
0.15
0.10
0.05
0.00
0.0e+00
6.0e+05
1.2e+06
genome coordinates
Mycoplasma gallisepticum str. R(low)
S^{A-T}_{CDS}
0.25
0.20
0.15
0.10
0.05
0e+00
4e+05
8e+05
genome coordinates
S^{G-C}_{CDS}
0.15
0.10
0.05
0.00
−0.05
0e+00
4e+05
8e+05
genome coordinates


Onion yellows phytoplasma OY−M
S^{A-T}_{CDS}
0.30
0.25
0.20
0.15
0.10
0.05
0.00
0e+00
3e+05
6e+05
genome coordinates
S^{G-C}_{CDS}
0.10
0.05
0.00
−0.05
−0.10
−0.15
−0.20
0e+00
3e+05
6e+05
genome coordinates
Mycoplasma mycoides subsp. mycoides SC str. PG1
S^{A-T}_{CDS}
0.20
0.15
0.10
0.05
0.00
0e+00
4e+05
8e+05
genome coordinates
S^{G-C}_{CDS}
0.20
0.15
0.10
0.05
0e+00
4e+05
8e+05
genome coordinates


Mesoplasma florum L1
S^{A-T}_{CDS}
0.18
0.16
0.14
0.12
0.10
0.08
0.06
0e+00
3e+05
6e+05
genome coordinates
S^{G-C}_{CDS}
0.22
0.20
0.18
0.16
0.14
0.12
0.10
0e+00
3e+05
6e+05
genome coordinates
Mycoplasma hyopneumoniae 232
S^{A-T}_{CDS}
0.20
0.15
0.10
0.05
0.00
0e+00
4e+05
8e+05
genome coordinates
S^{G-C}_{CDS}
0.10
0.08
0.06
0.04
0.02
0.00
−0.02
−0.04
0e+00
4e+05
8e+05
genome coordinates


Mycoplasma mobile 163K
S^{A-T}_{CDS}
0.15
0.10
0.05
0e+00
3e+05
6e+05
genome coordinates
S^{G-C}_{CDS}
0.20
0.15
0.10
0.05
0.00
0e+00
3e+05
6e+05
genome coordinates
Mycoplasma synoviae 53
S^{A-T}_{CDS}
0.20
0.15
0.10
0.05
0e+00
3e+05
6e+05
genome coordinates
S^{G-C}_{CDS}
0.10
0.05
0.00
−0.05
0e+00
3e+05
6e+05
genome coordinates


Mycoplasma hyopneumoniae J
0.20
0.15
0.10
0.05
0.00
S^{A-T}_{CDS}
0e+00
4e+05
8e+05
genome coordinates
0.10
0.05
0.00
S^{G-C}_{CDS}
0e+00
4e+05
8e+05
genome coordinates
Mycoplasma hyopneumoniae 7448
0.25
0.20
0.15
0.10
0.05
0.00
S^{A-T}_{CDS}
0e+00
4e+05
8e+05
genome coordinates
0.15
0.10
0.05
0.00
−0.05
S^{G-C}_{CDS}
0e+00
4e+05
8e+05
genome coordinates


Mycoplasma capricolum subsp. capricolum ATCC 27343
S^{A-T}_{CDS}
0.25
0.20
0.15
0.10
0.05
0.00
0e+00
4e+05
8e+05
genome coordinates
S^{G-C}_{CDS}
0.20
0.15
0.10
0.05
0e+00
4e+05
8e+05
genome coordinates
Aster yellows witches'−broom phytoplasma AYWB
S^{A-T}_{CDS}
0.25
0.20
0.15
0.10
0.05
0.00
0e+00
2e+05
4e+05
genome coordinates
S^{G-C}_{CDS}
0.05
0.00
−0.05
−0.10
−0.15
−0.20
0e+00
2e+05
4e+05
genome coordinates