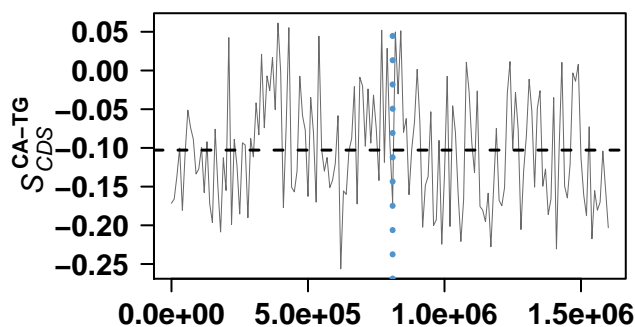
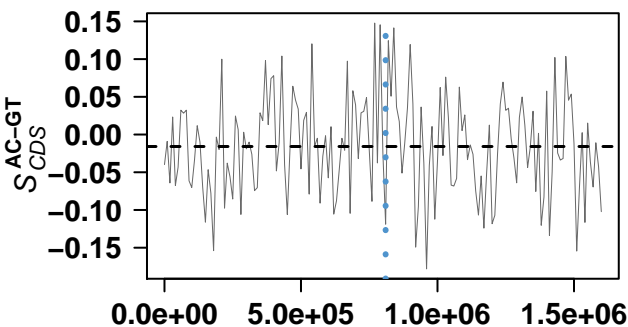
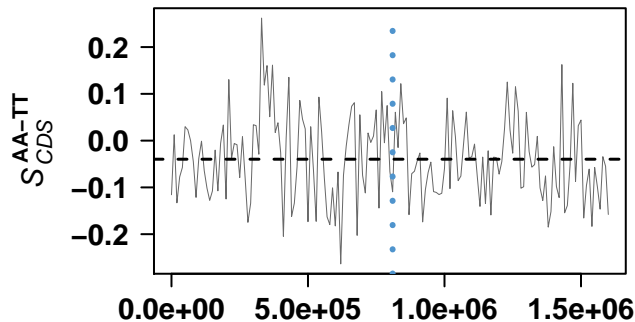
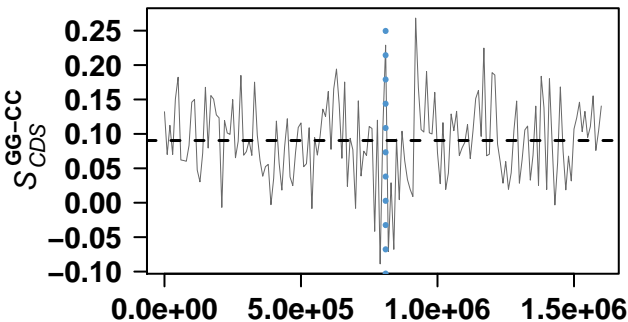
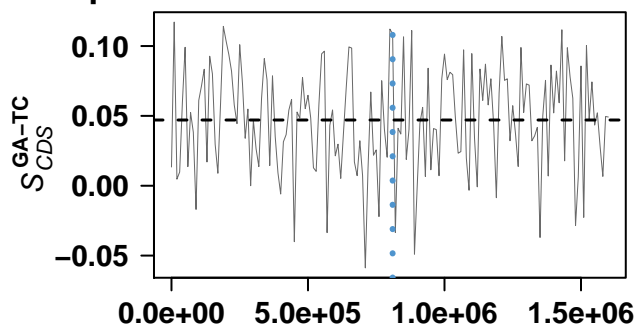
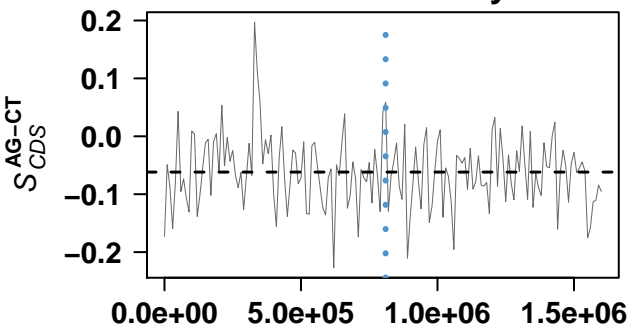
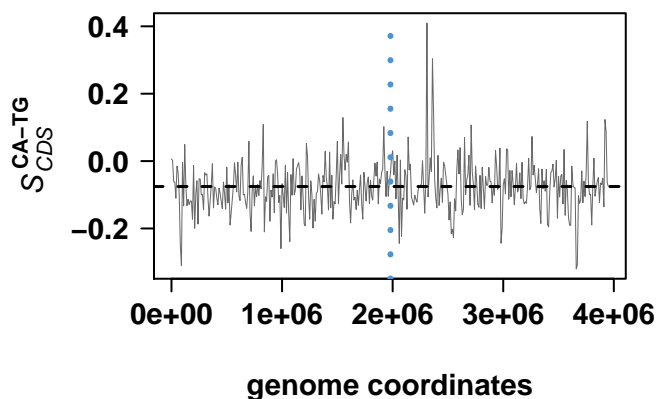
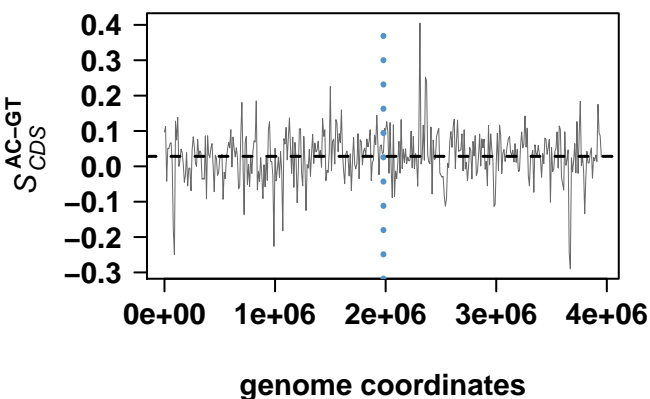
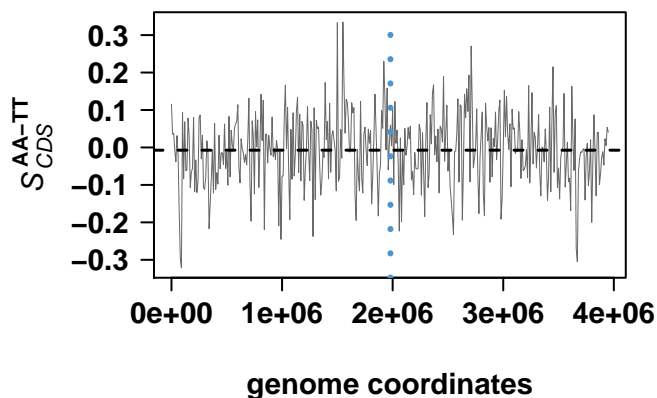
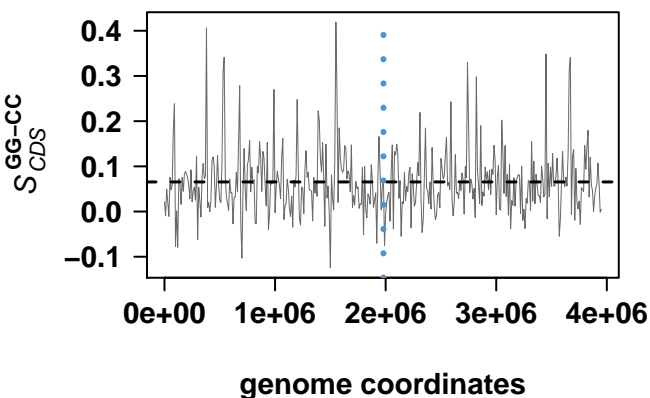
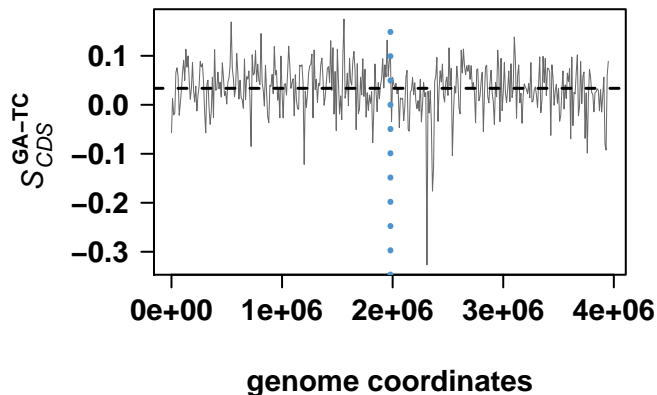
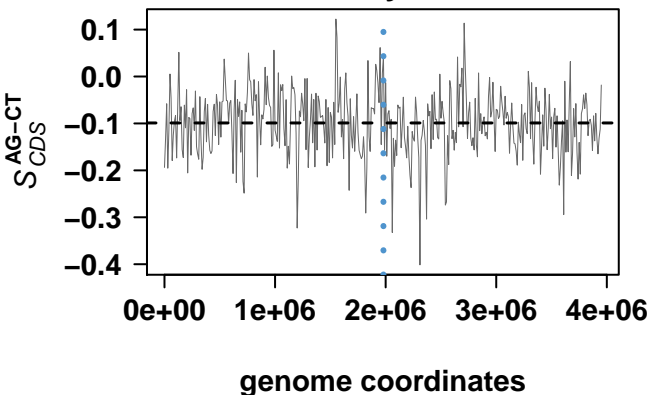


Diagrams (gray curve) and fitted linear models (red thick line) for dinucleotide skews ($S_{\text{CDS}}^{\text{AG-CT}}$, $S_{\text{CDS}}^{\text{GA-TC}}$, $S_{\text{CDS}}^{\text{GG-CC}}$, $S_{\text{CDS}}^{\text{AA-TT}}$, $S_{\text{CDS}}^{\text{AC-GT}}$ and $S_{\text{CDS}}^{\text{CA-TG}}$) along the CDS 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.

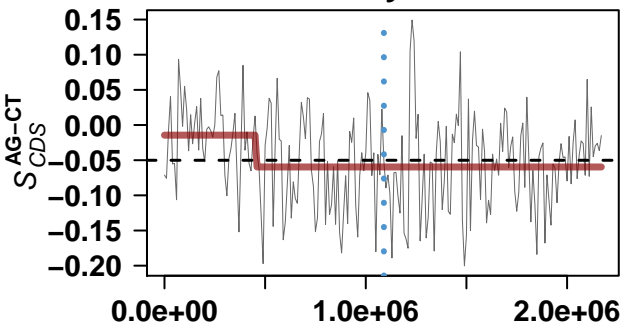
Mycobacterium leprae TN



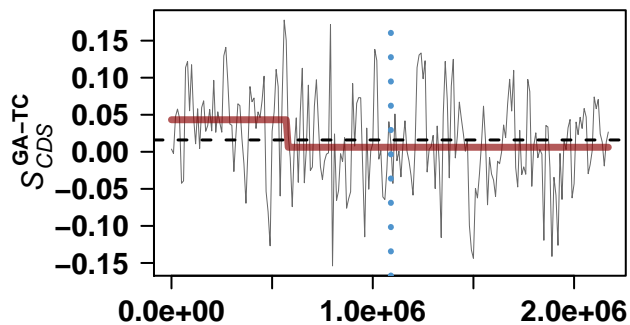
Mycobacterium tuberculosis CDC1551



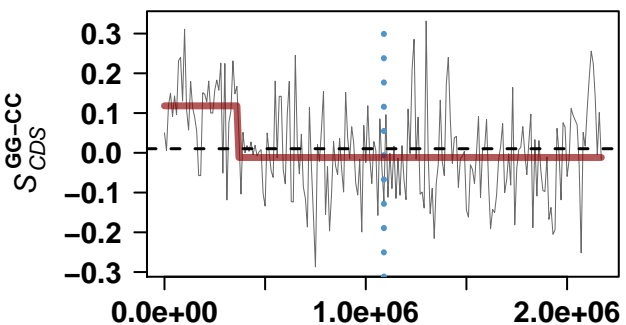
Corynebacterium diphtheriae NCTC 13129



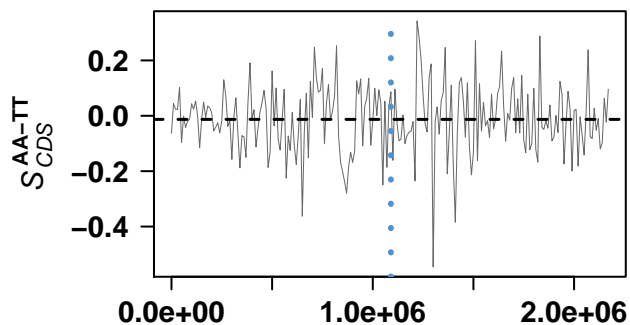
genome coordinates



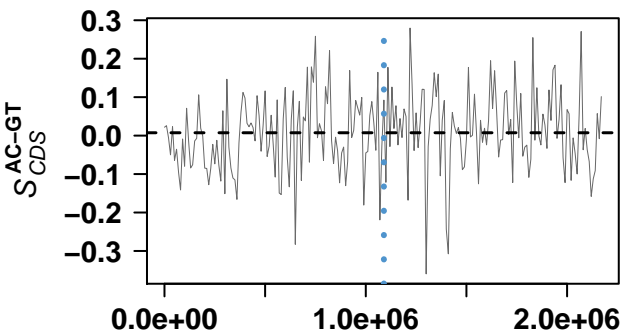
genome coordinates



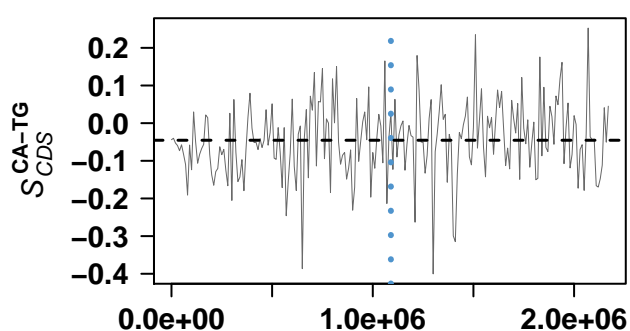
genome coordinates



genome coordinates

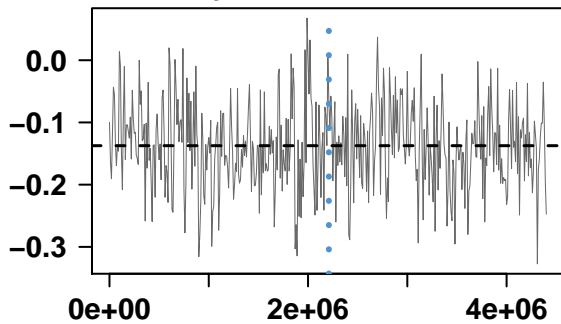


genome coordinates

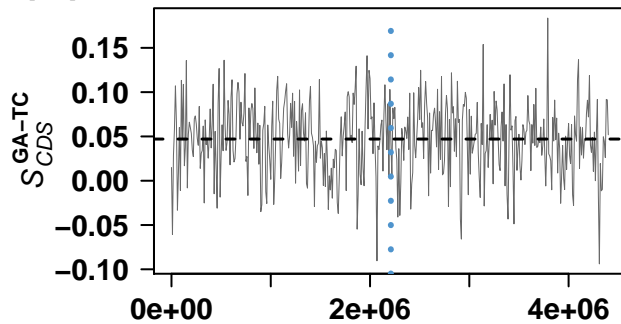


genome coordinates

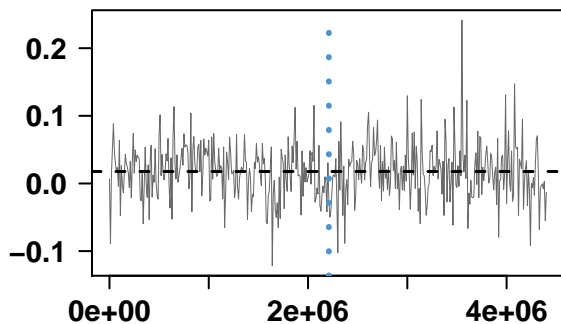
Mycobacterium avium subsp. paratuberculosis K-10



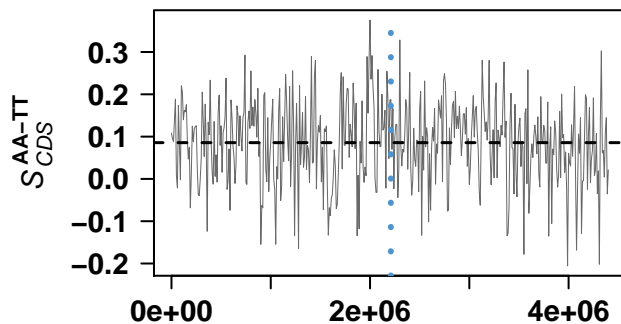
genome coordinates



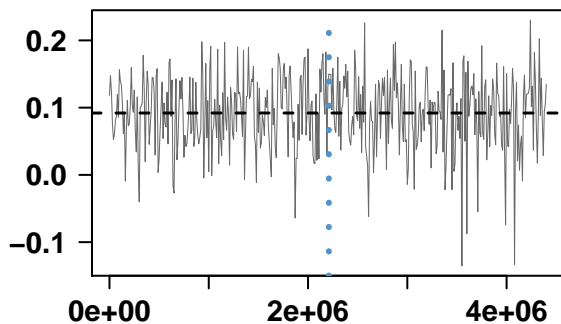
genome coordinates



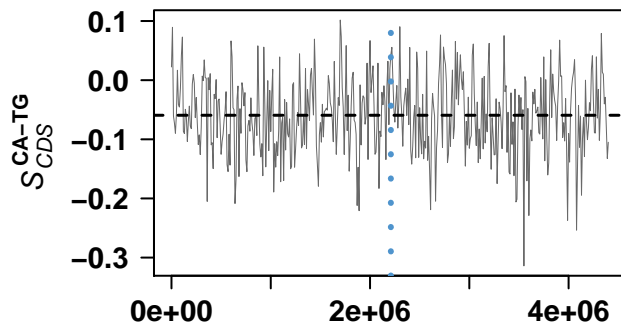
genome coordinates



genome coordinates

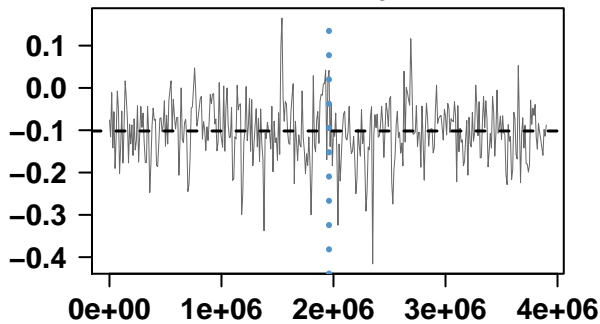


genome coordinates

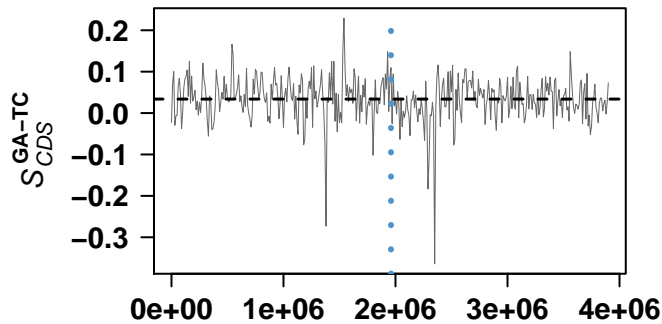


genome coordinates

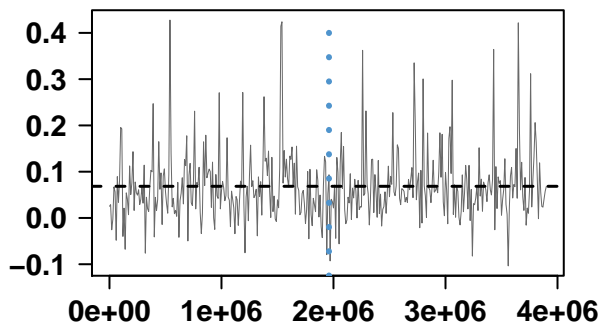
Mycobacterium bovis AF2122/97



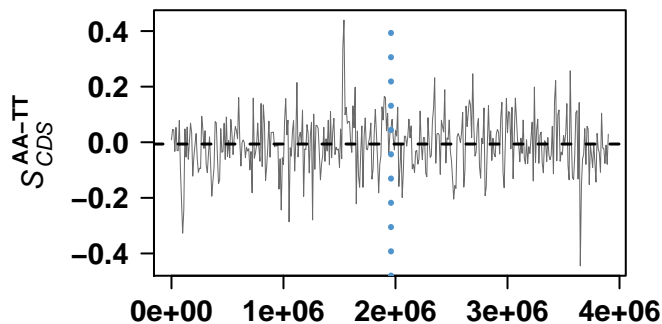
genome coordinates



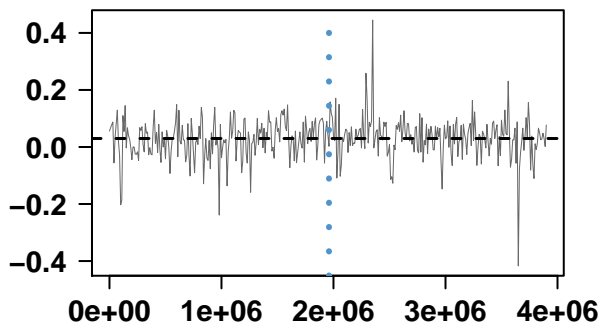
genome coordinates



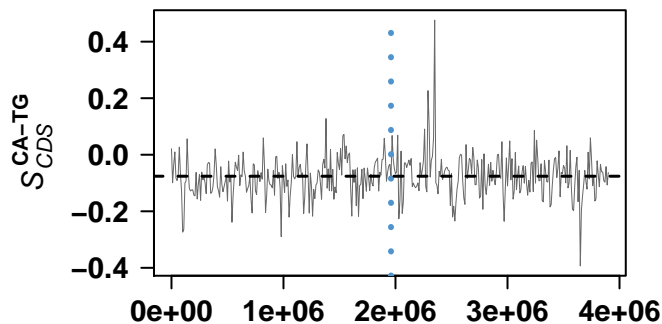
genome coordinates



genome coordinates

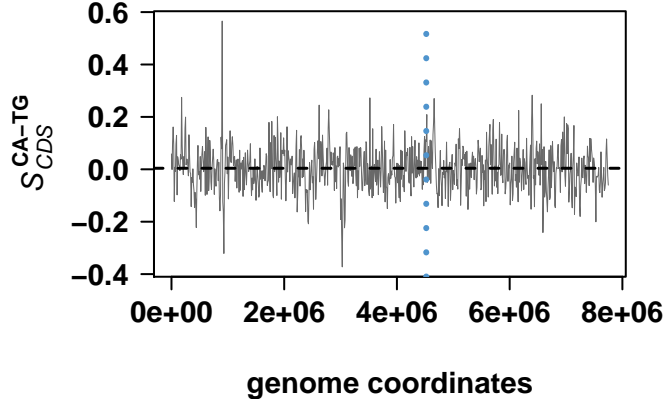
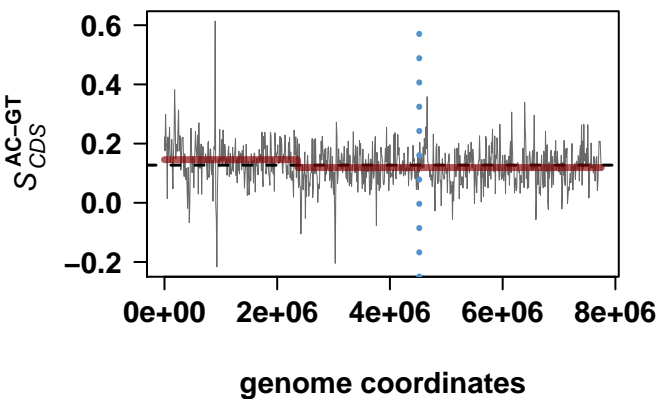
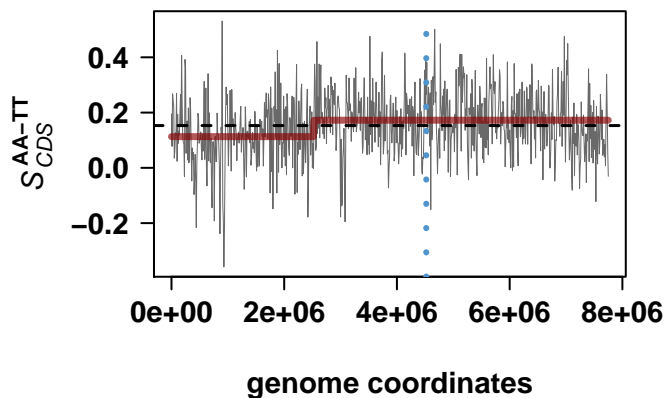
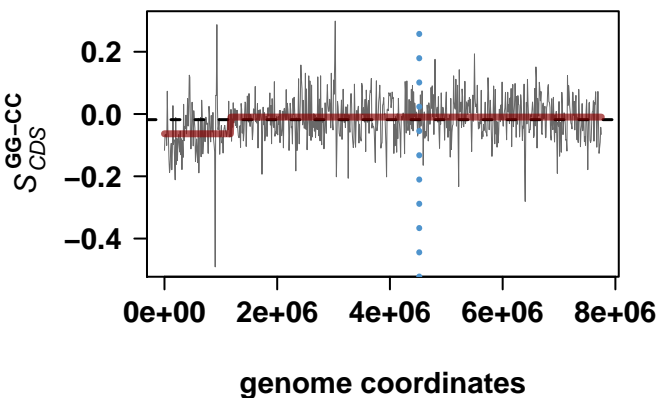
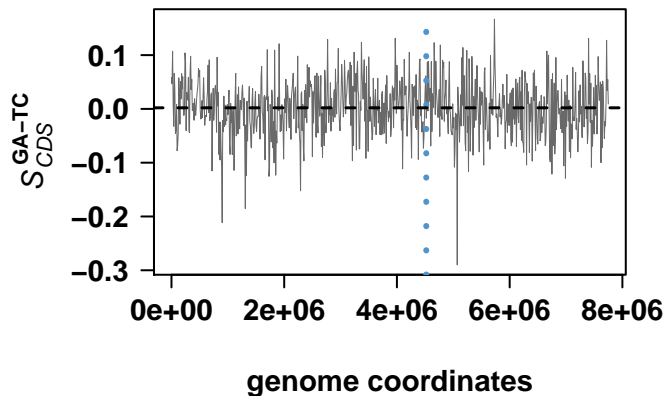
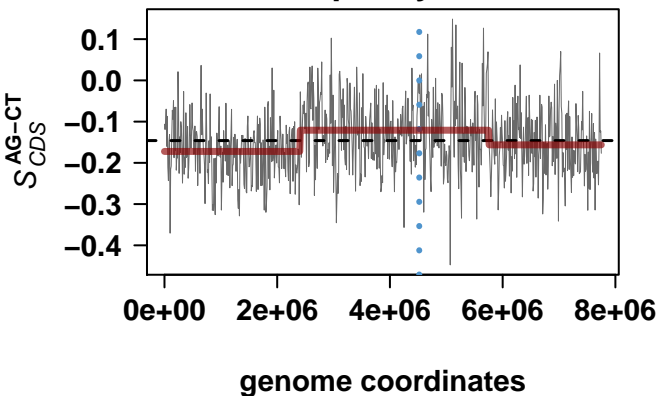


genome coordinates

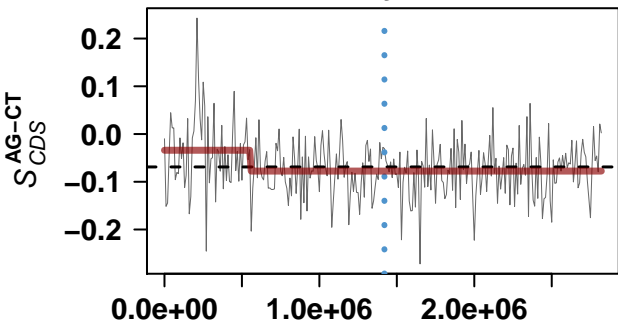


genome coordinates

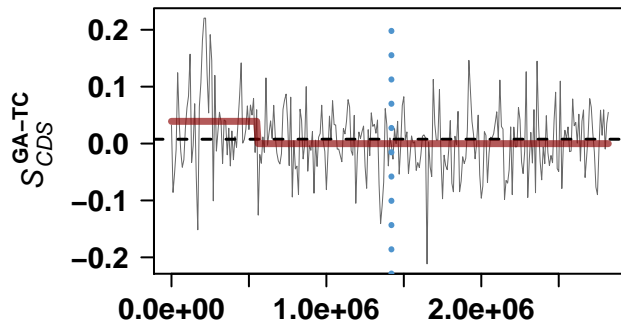
Streptomyces avermitilis MA-4680 = NBRC 14893



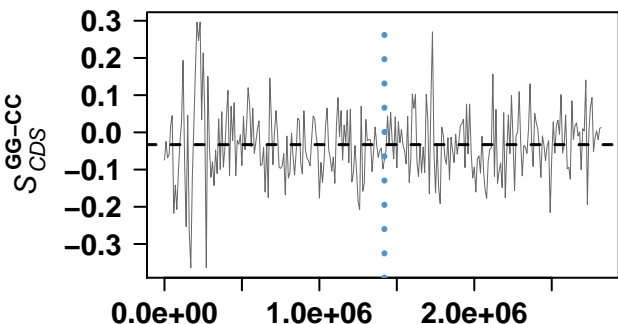
Corynebacterium glutamicum ATCC 13032



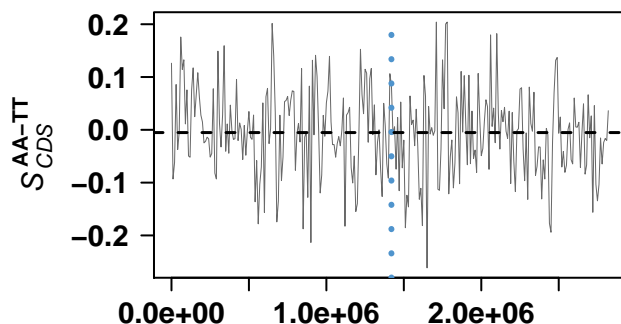
genome coordinates



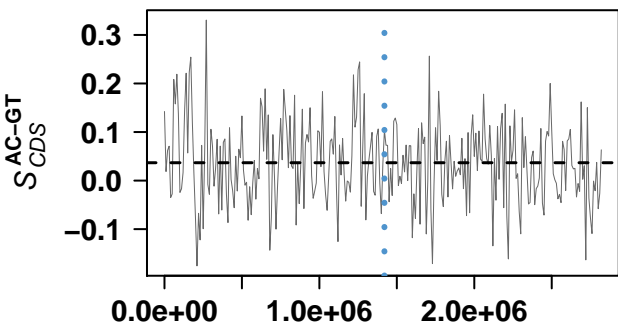
genome coordinates



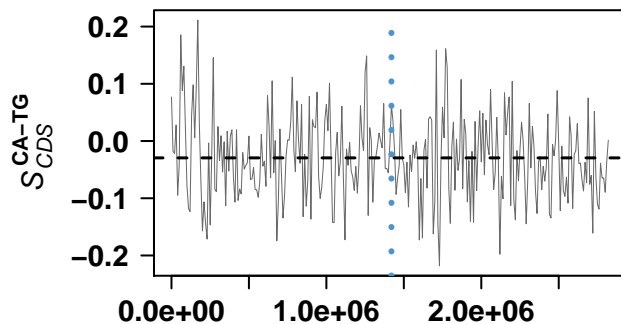
genome coordinates



genome coordinates

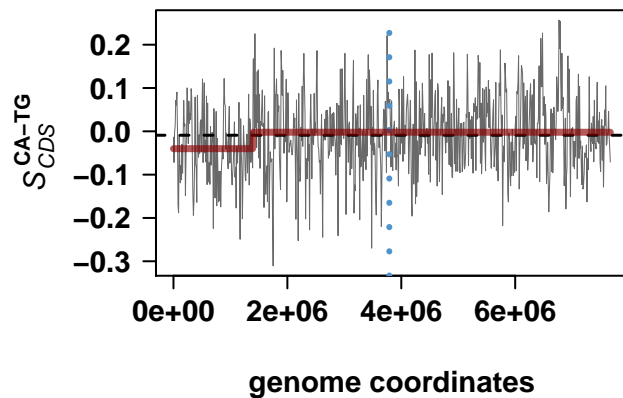
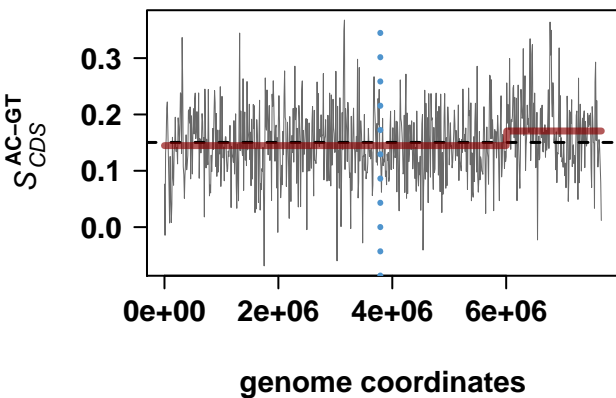
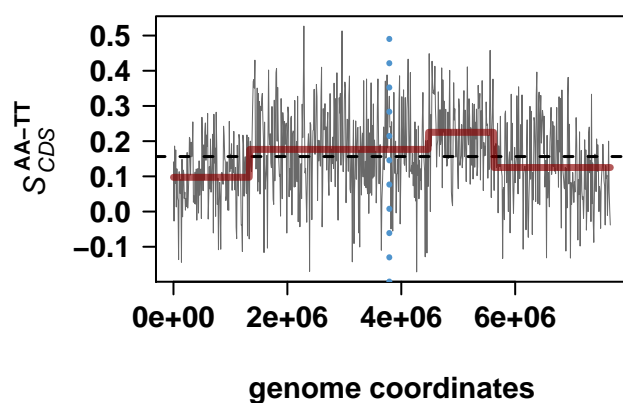
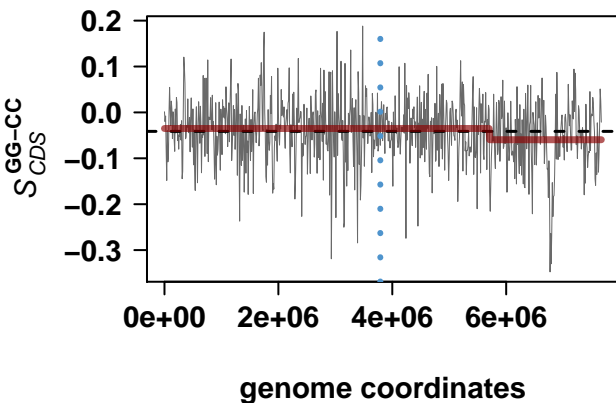
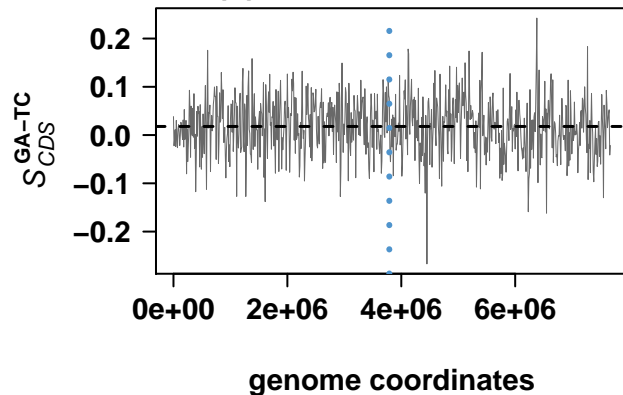
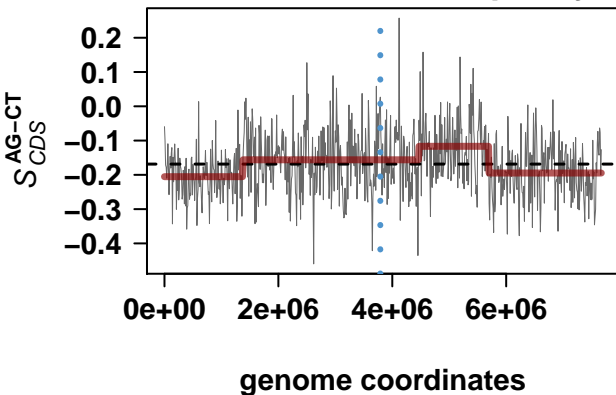


genome coordinates

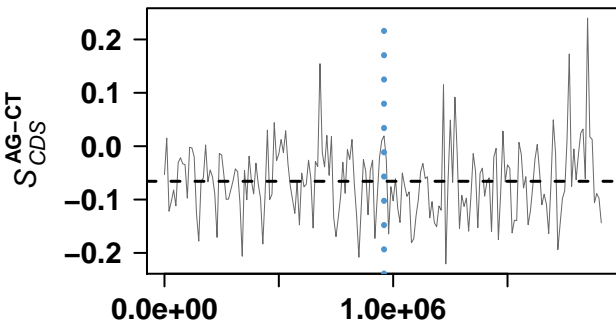


genome coordinates

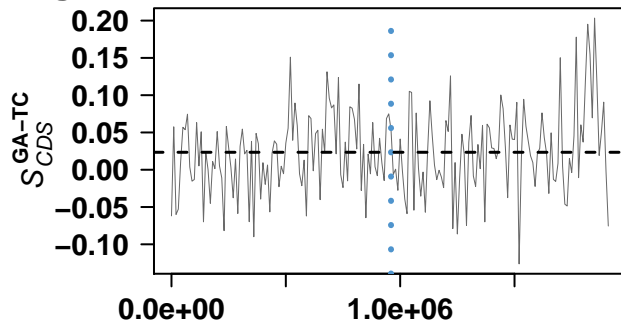
Streptomyces coelicolor A3(2)



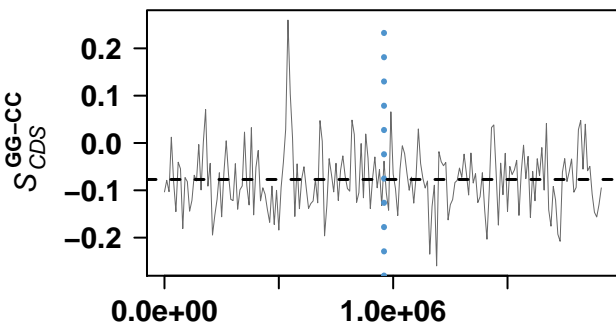
Bifidobacterium longum NCC2705



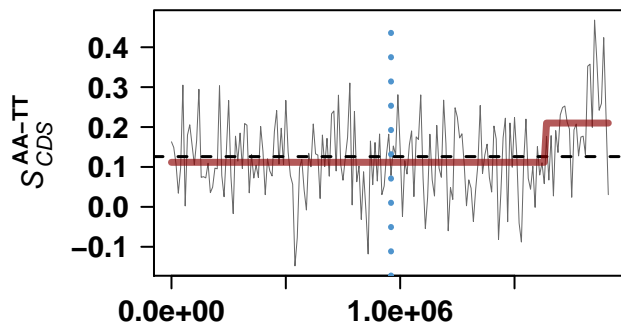
genome coordinates



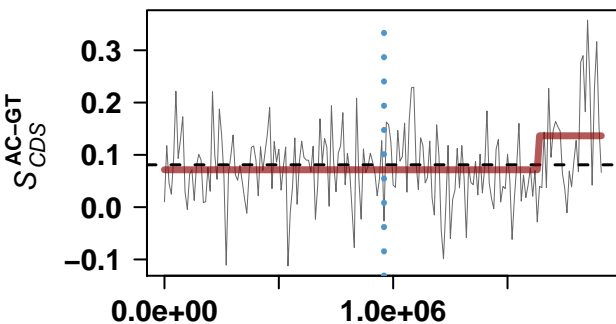
genome coordinates



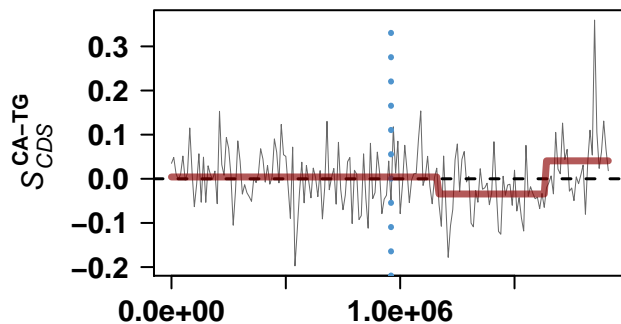
genome coordinates



genome coordinates

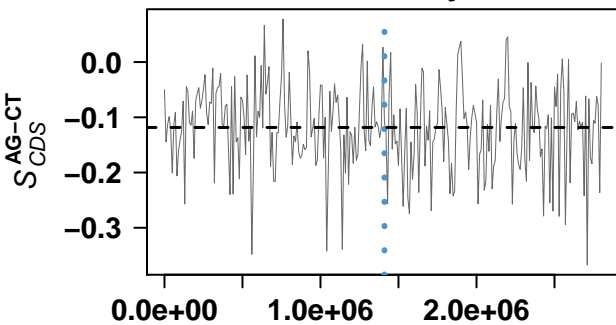


genome coordinates

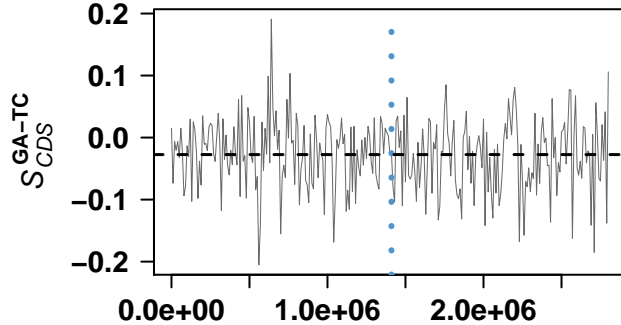


genome coordinates

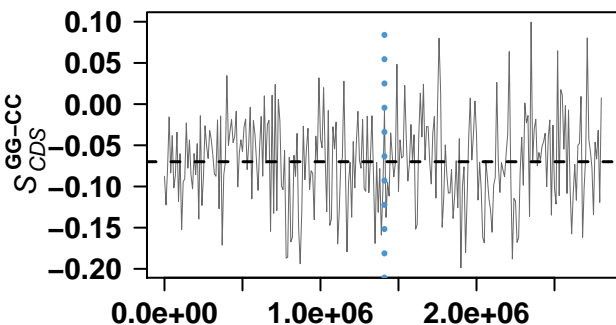
Corynebacterium efficiens YS-314



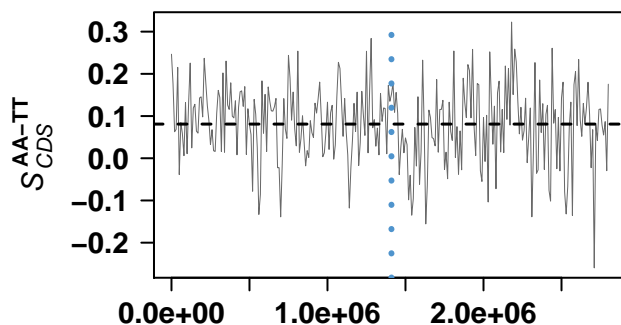
genome coordinates



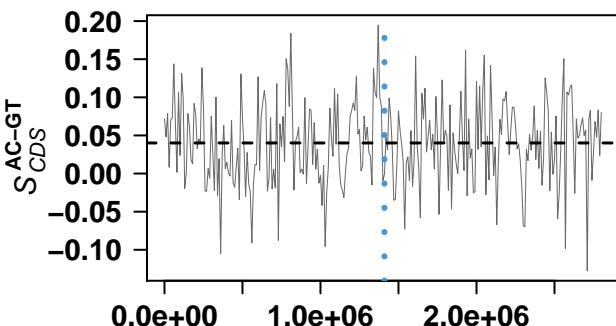
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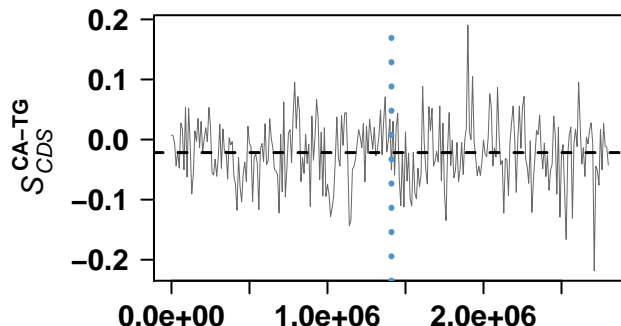
genome coordinates



genome coordinates

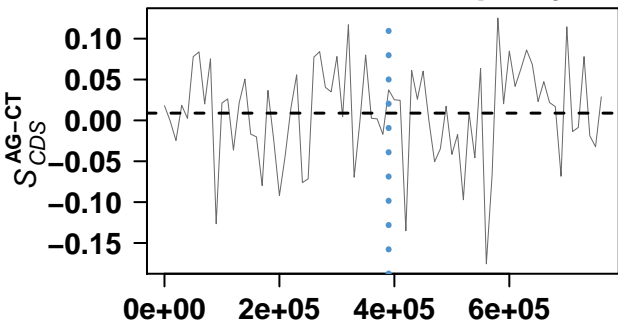


genome coordinates

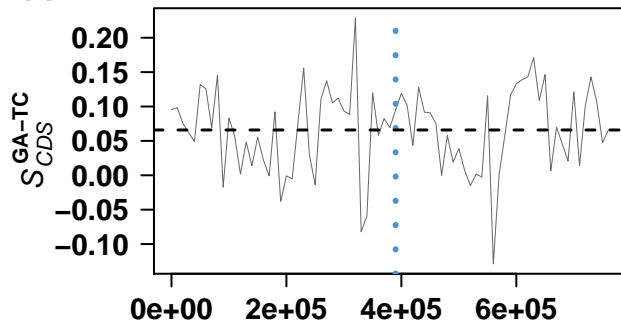


genome coordinates

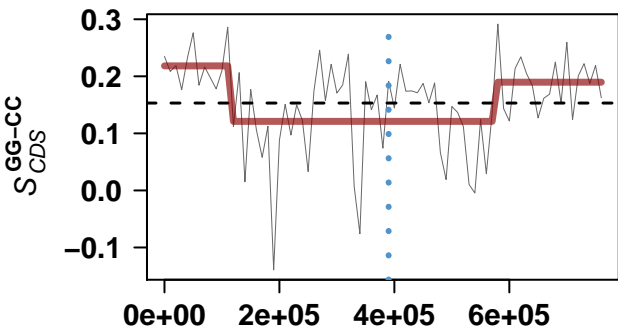
Tropheryma whipplei TW08/27



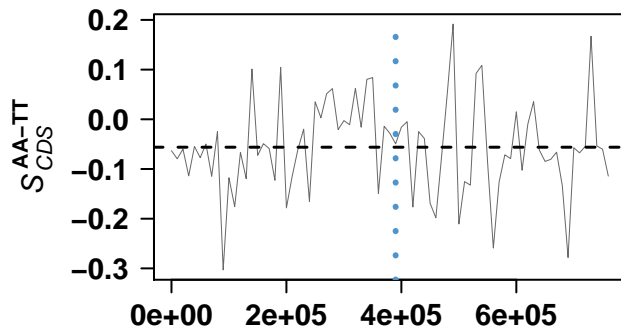
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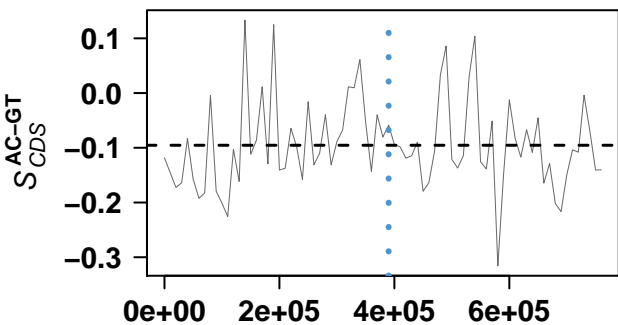
genome coordinates



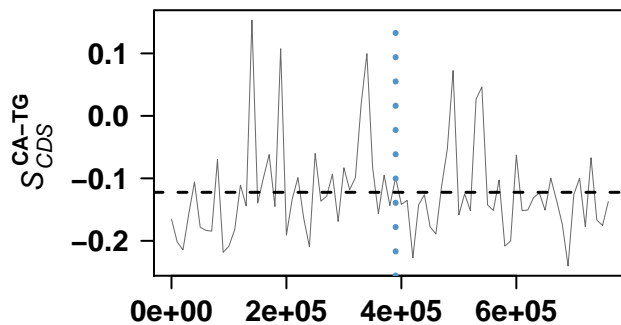
genome coordinates



genome coordinates

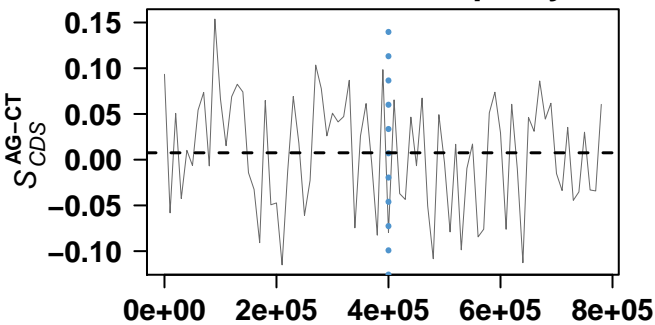


genome coordinates

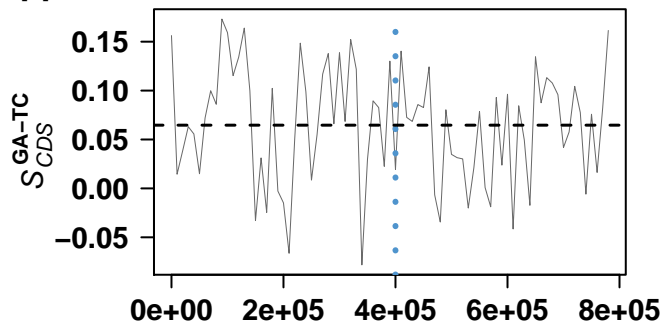


genome coordinates

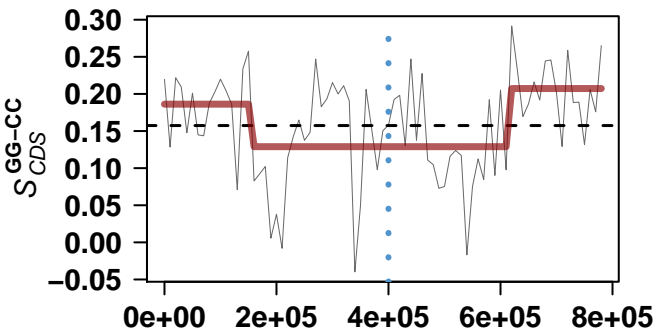
Tropheryma whipplei str. Twist



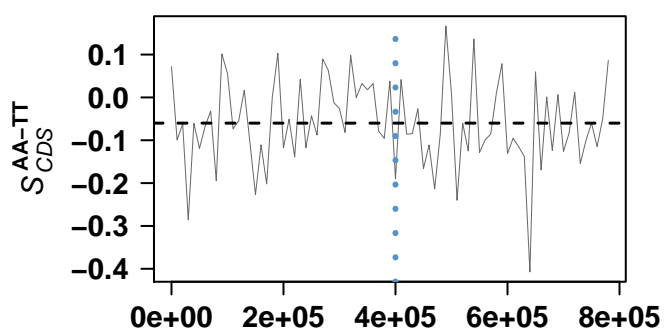
genome coordinates



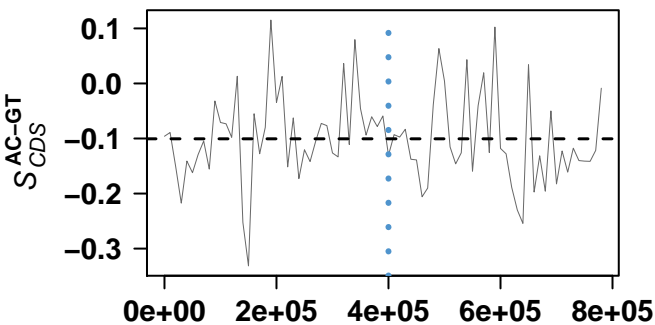
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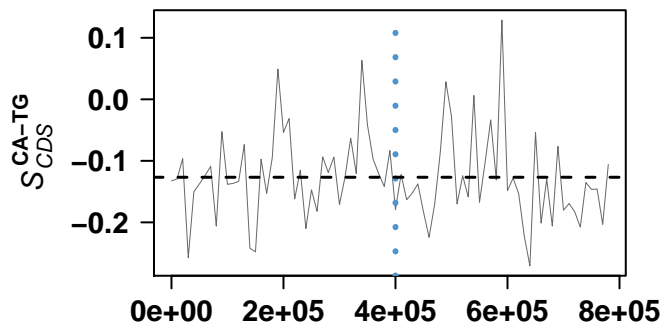
genome coordinates



genome coordinates

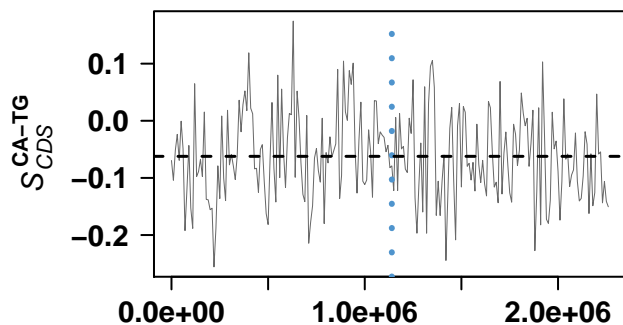
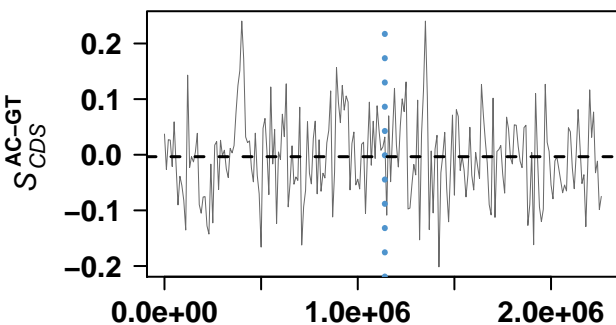
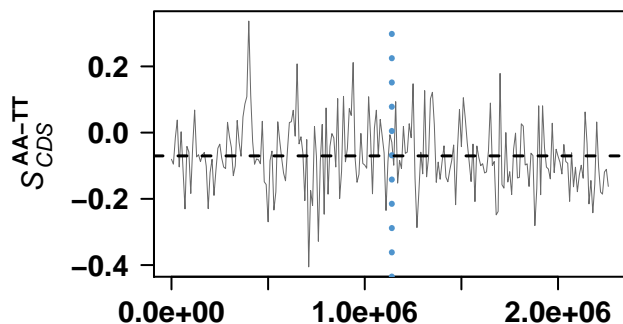
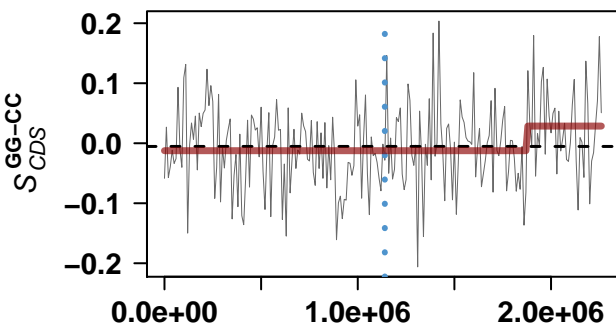
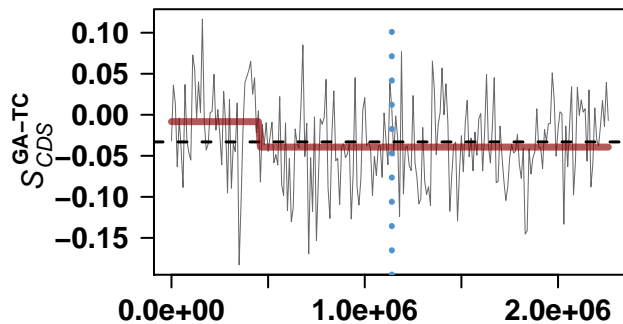
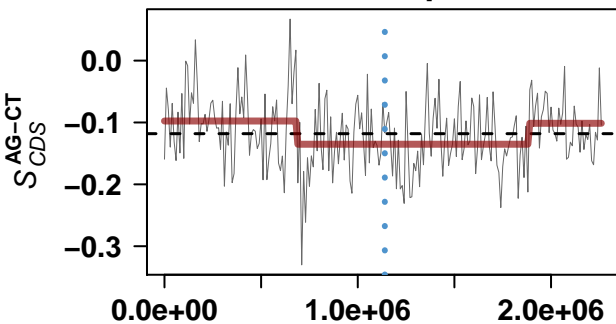


genome coordinates

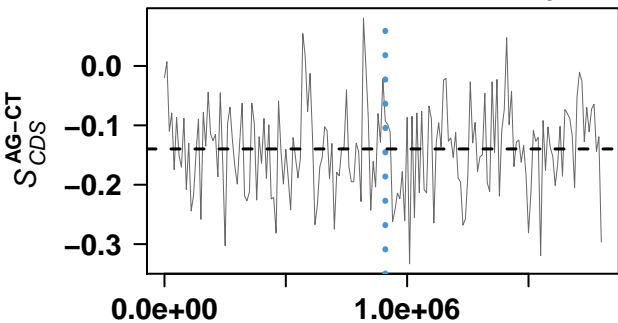


genome coordinates

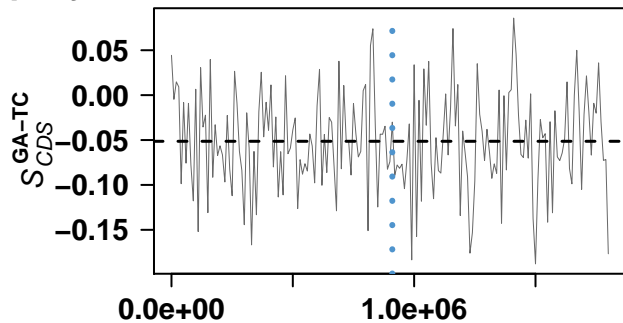
Propionibacterium acnes KPA171202



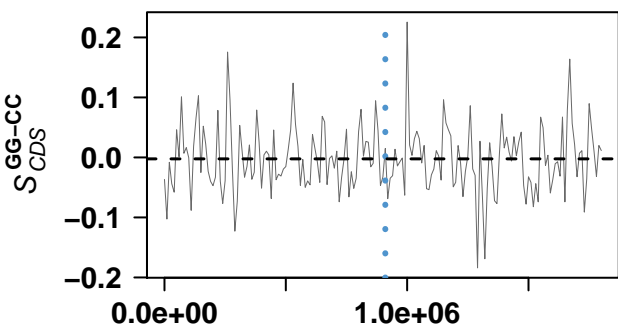
Leifsonia xyli subsp. xyli str. CTCB07



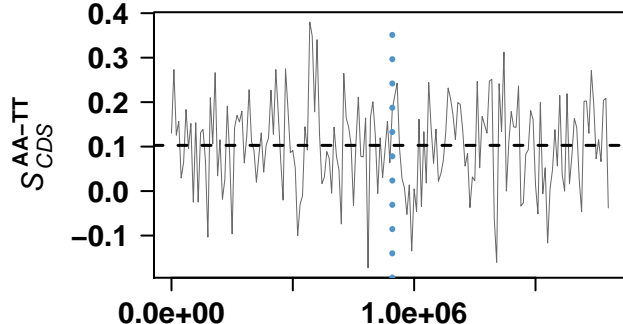
genome coordinates



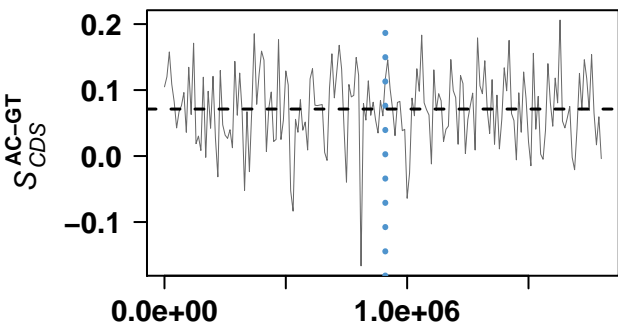
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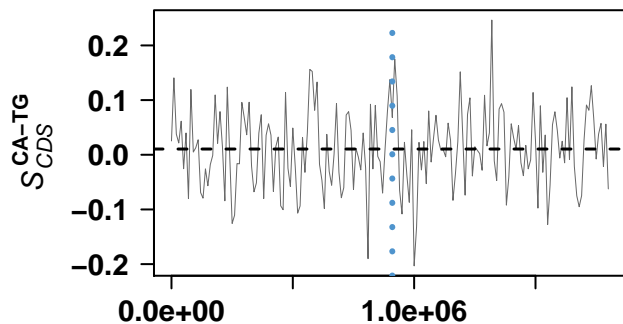
genome coordinates



genome coordinates

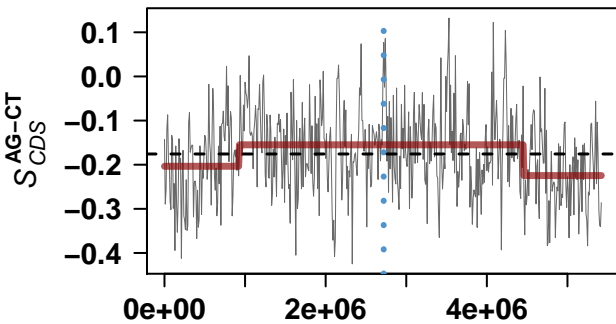


genome coordinates

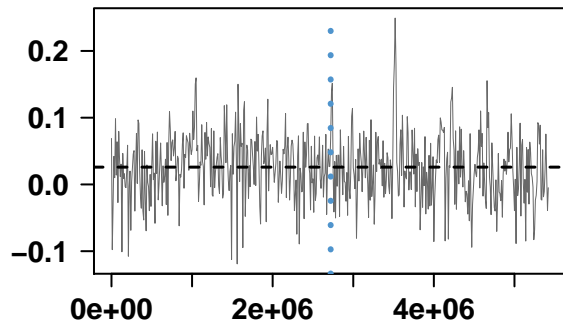


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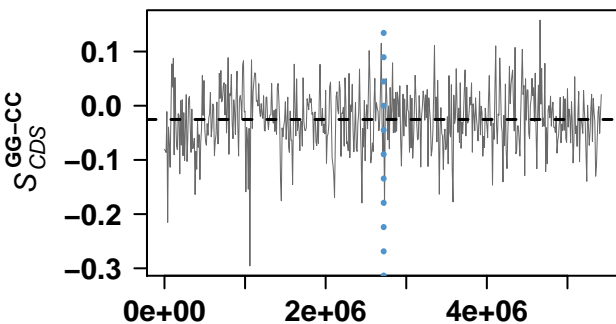
Nocardia farcinica IFM 10152



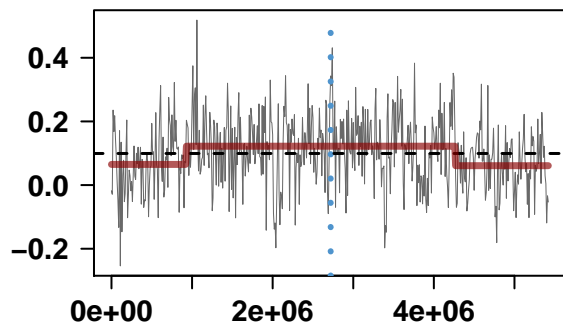
genome coordinates



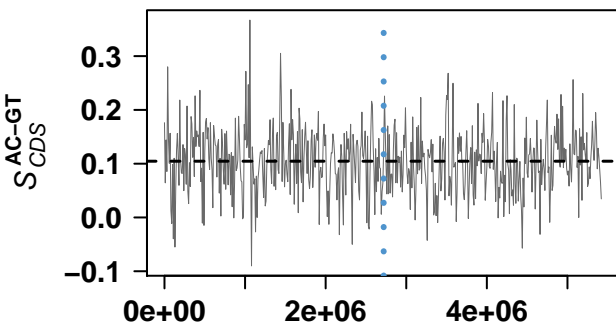
genome coordinates



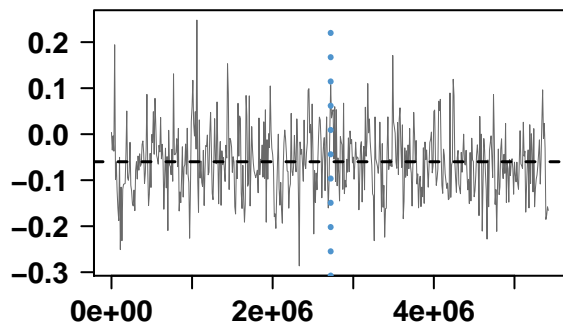
genome coordinates



genome coordinates

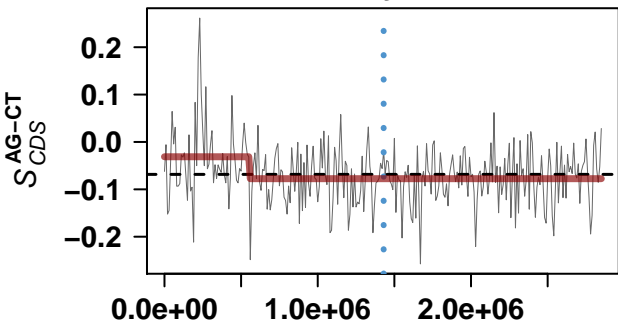


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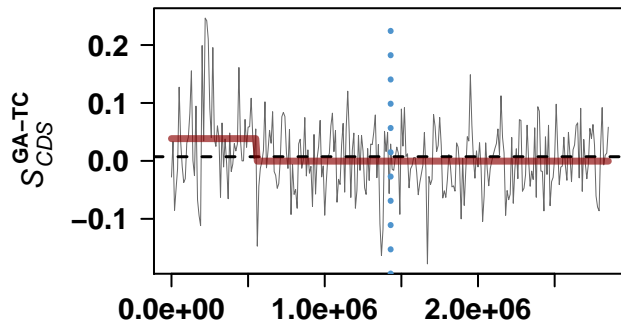


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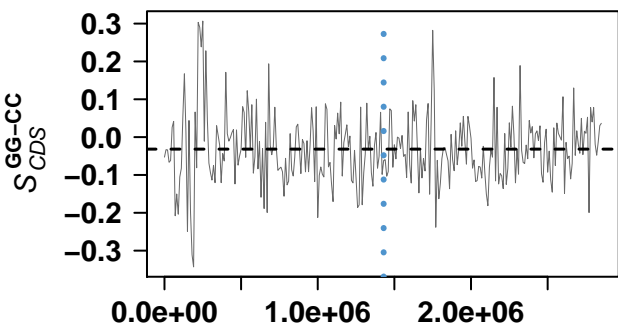
Corynebacterium glutamicum ATCC 13032



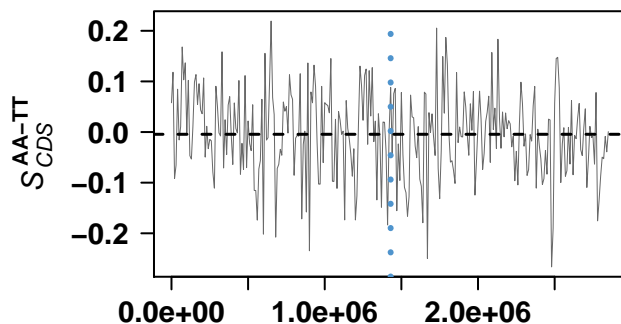
genome coordinates



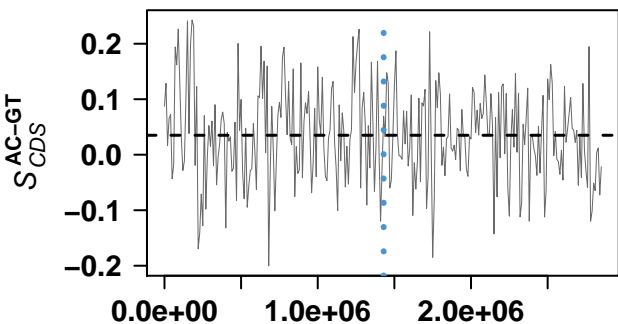
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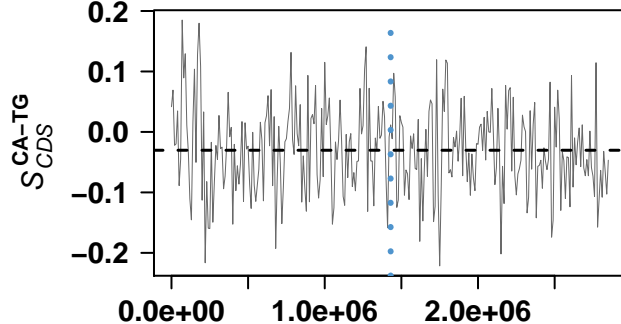
genome coordinates



genome coordinates

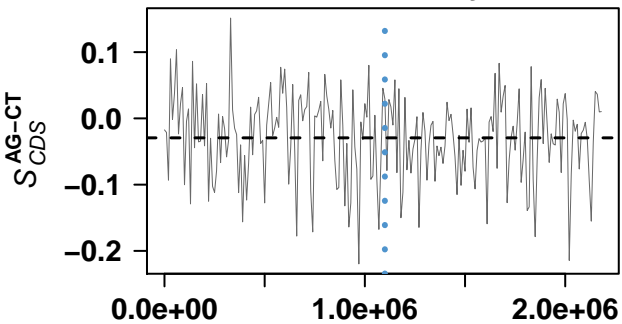


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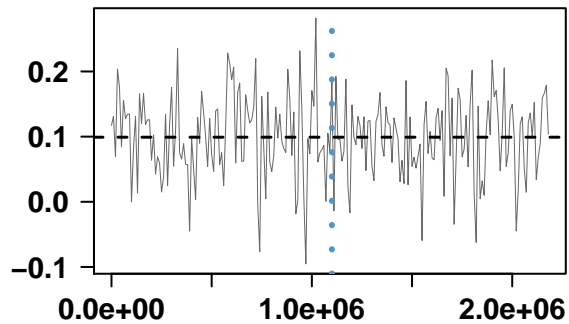


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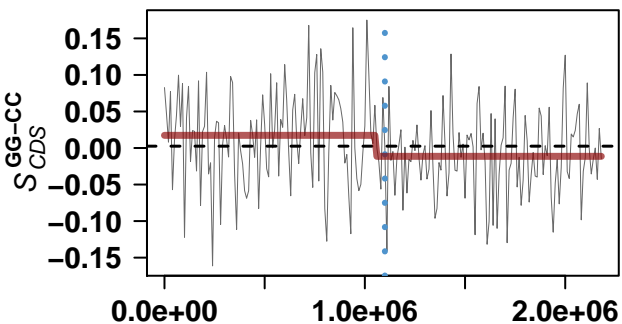
Corynebacterium jeikeium K411



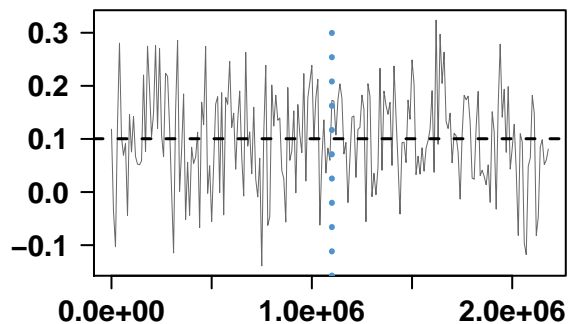
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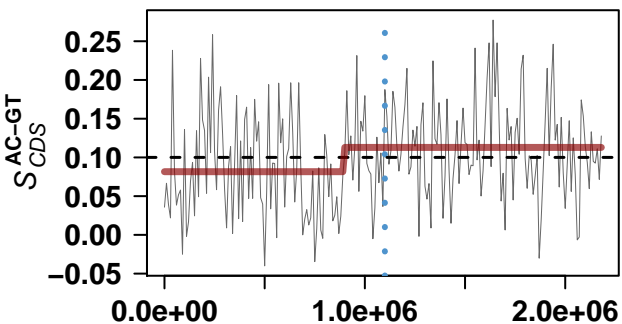
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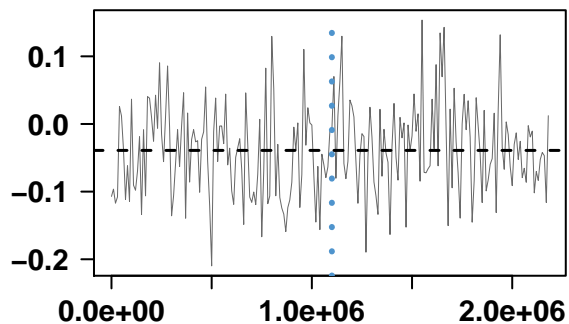
genome coordinates



genome coordinates

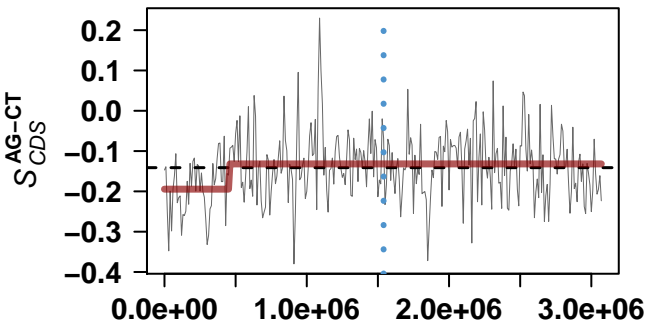


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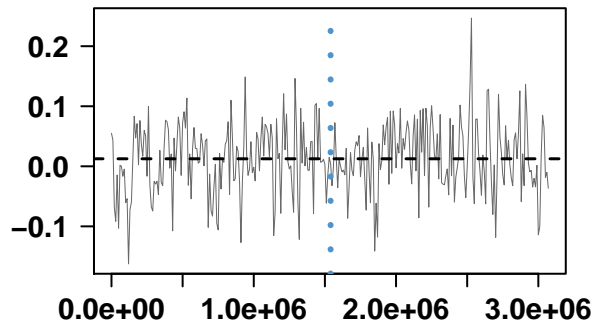


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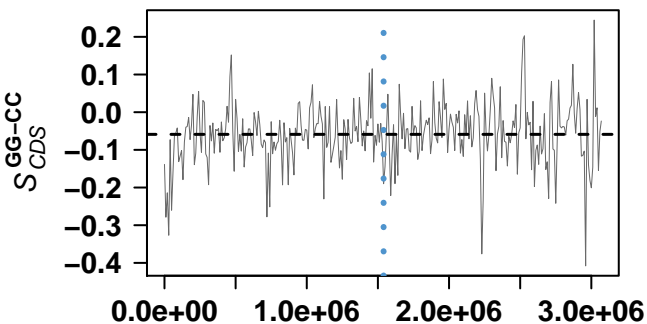
Thermobifida fusca YX



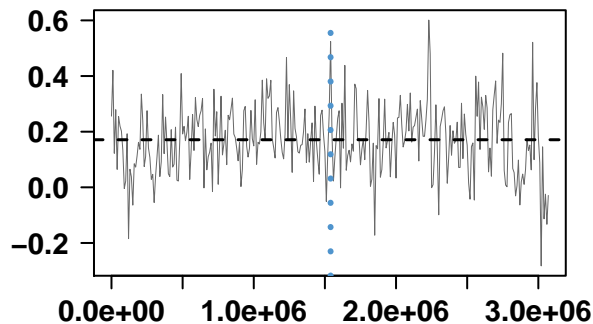
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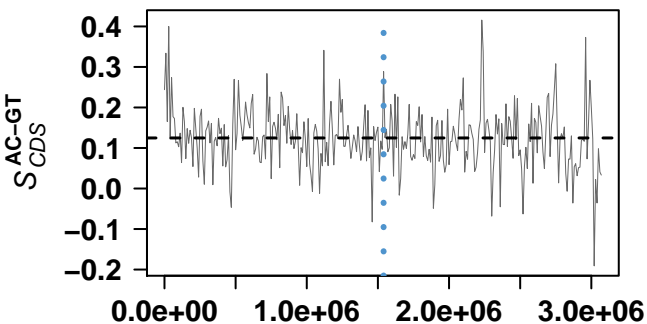
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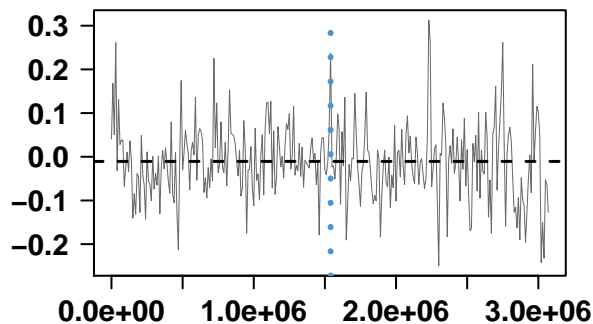
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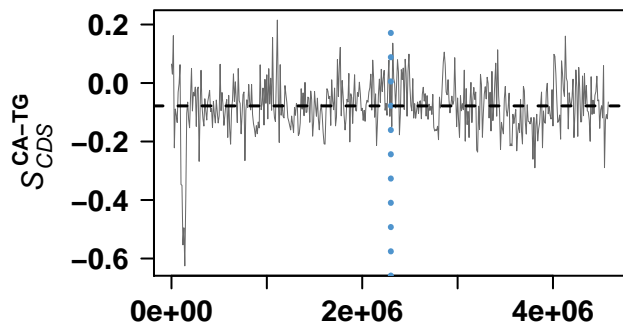
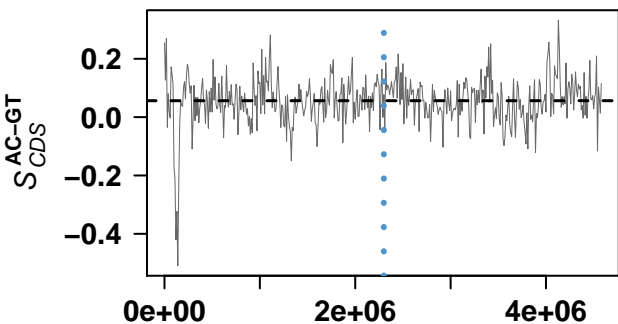
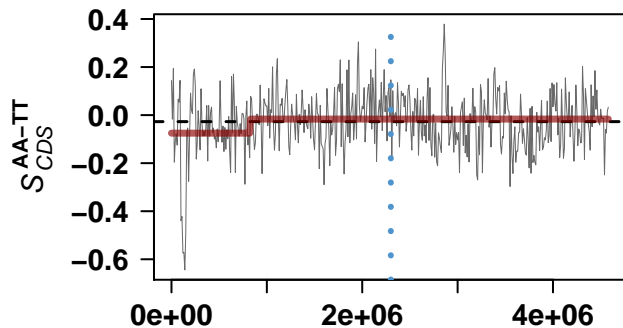
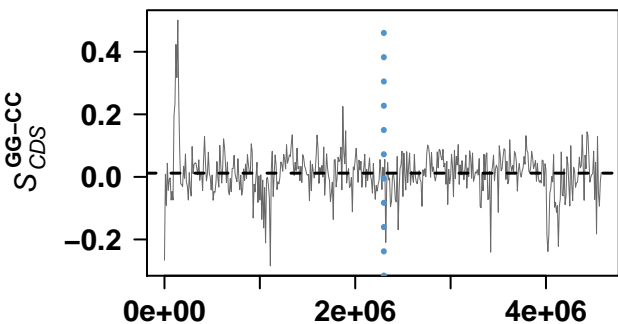
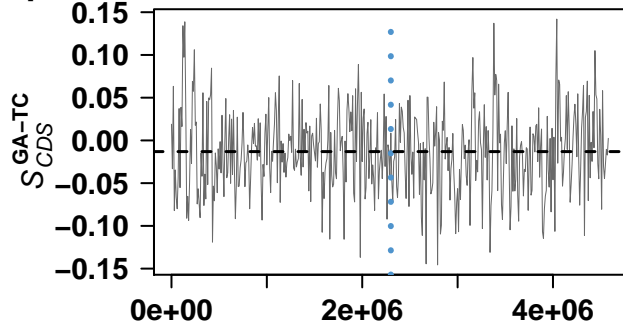
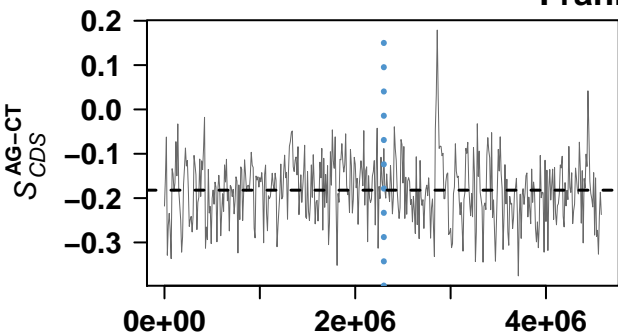


genome coordinates

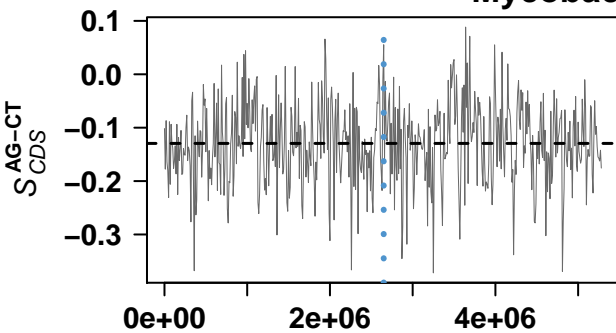


genome coordinates

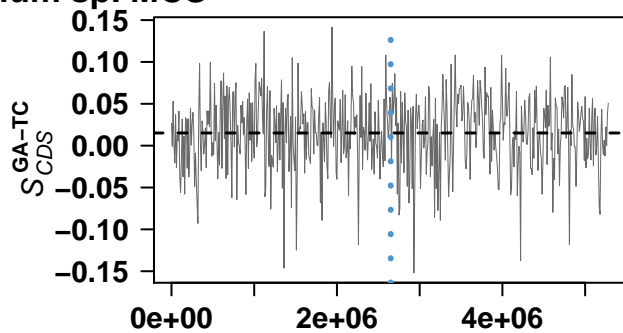
Frankia sp. Ccl3



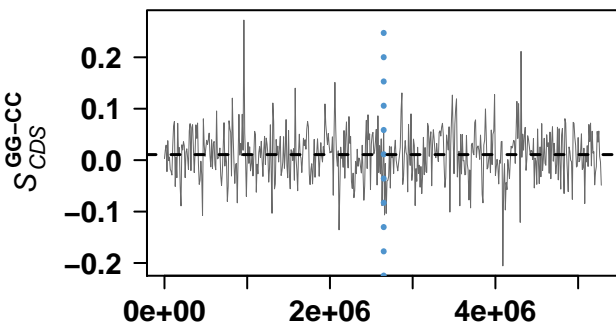
Mycobacterium sp. MCS



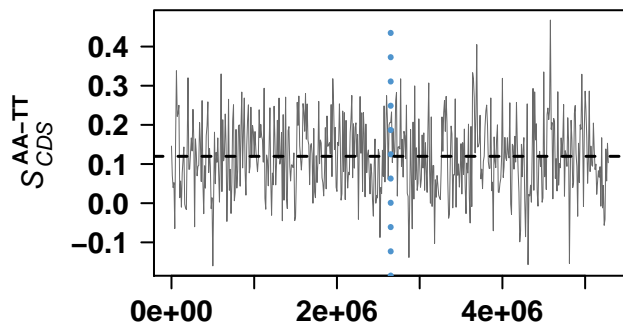
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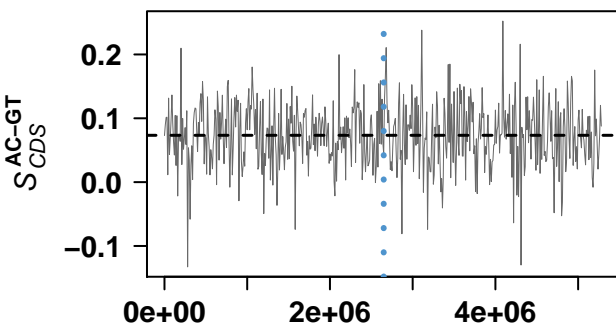
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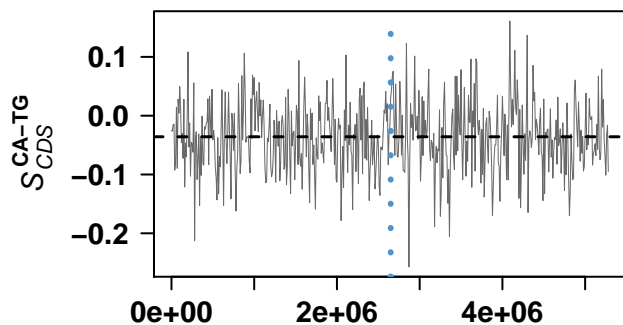
genome coordinates



genome coordinates

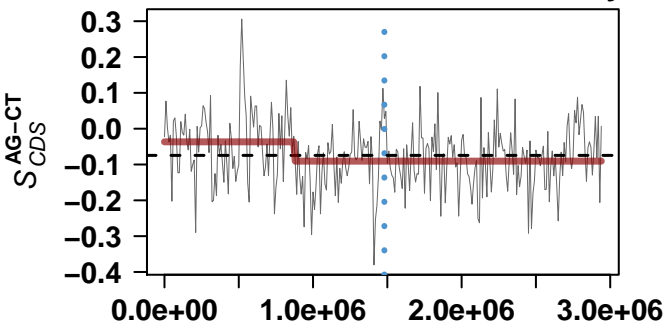


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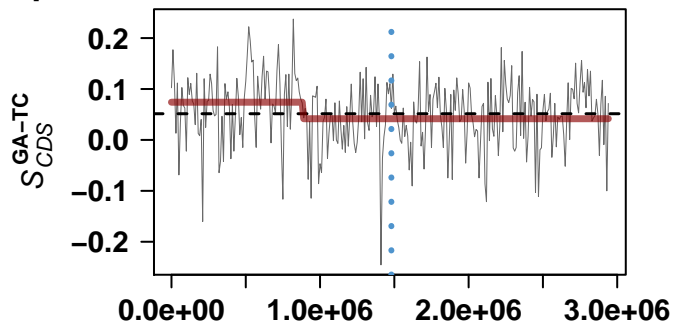


genome coordinates

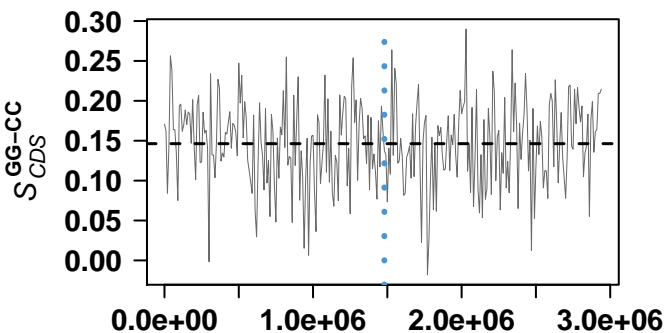
Rubrobacter xylanophilus DSM 9941



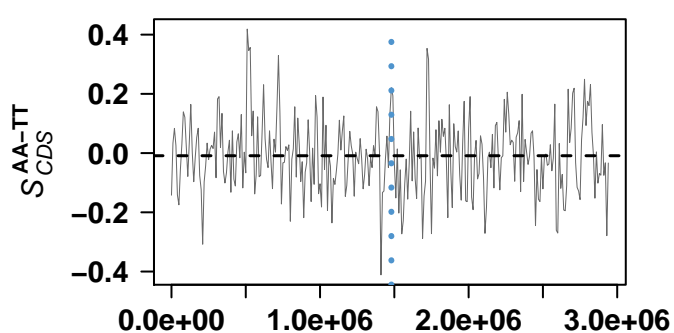
genome coordinates



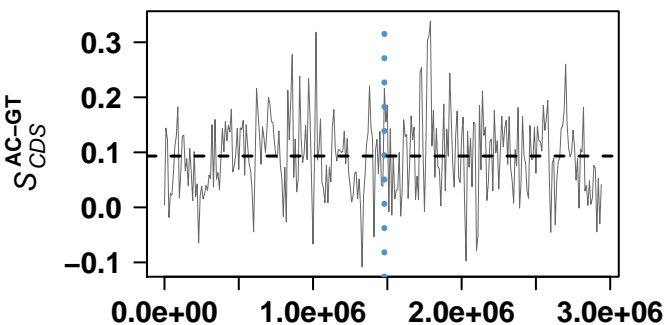
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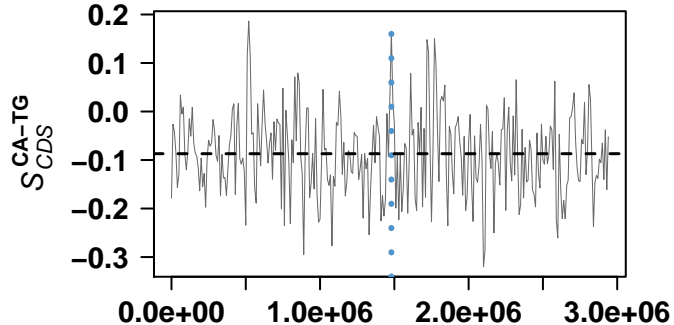
genome coordinates



genome coordinates

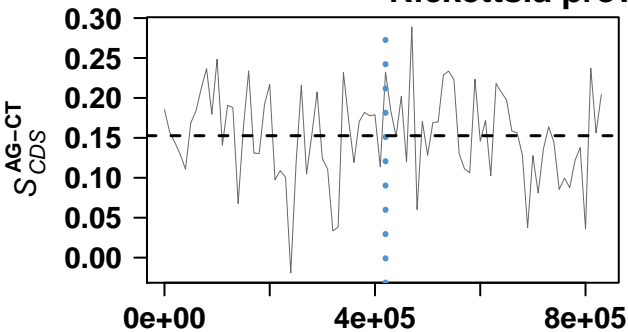


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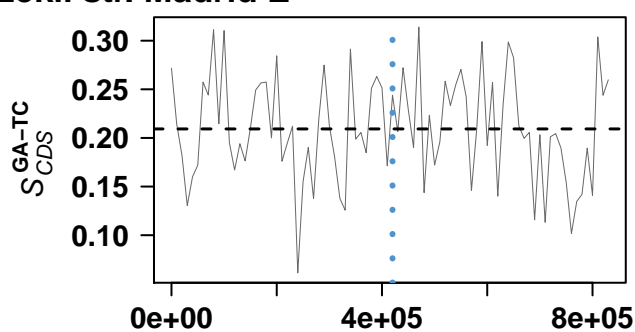


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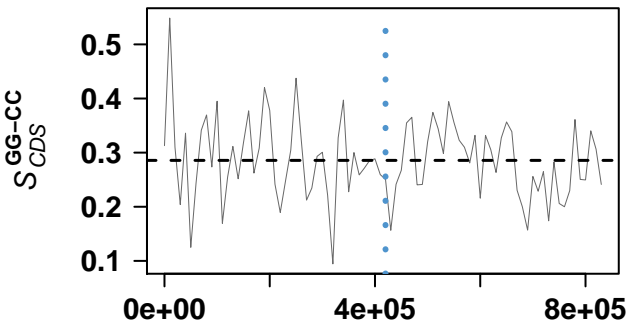
Rickettsia prowazekii str. Madrid E



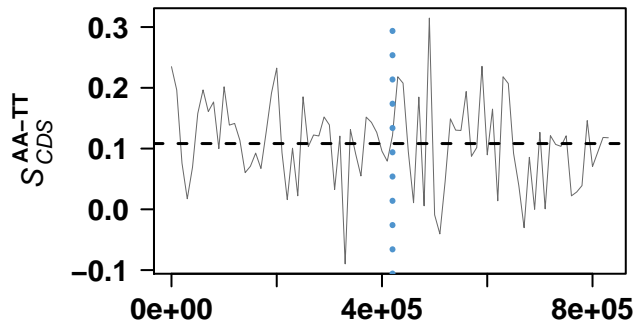
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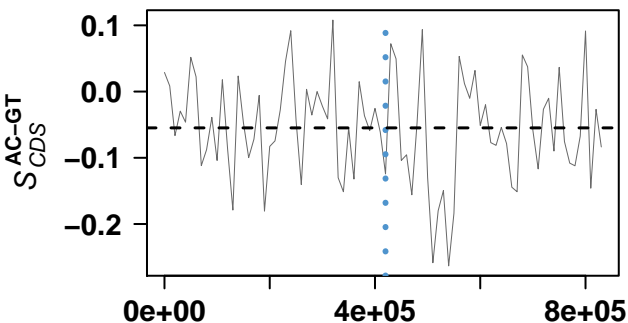
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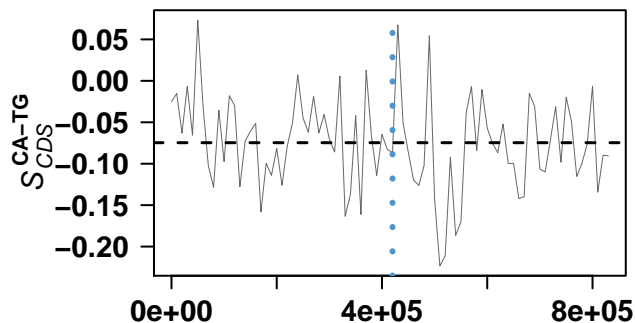
genome coordinates



genome coordinates

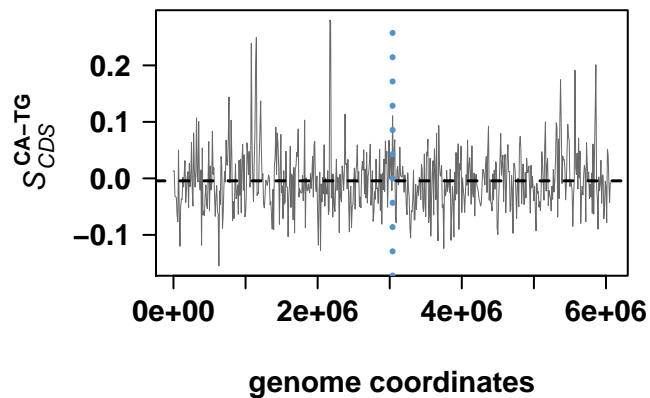
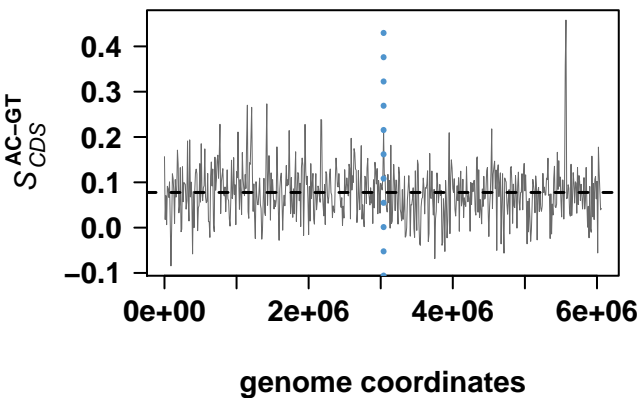
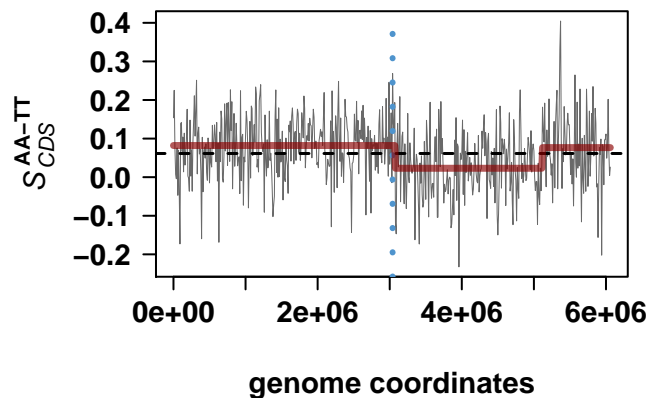
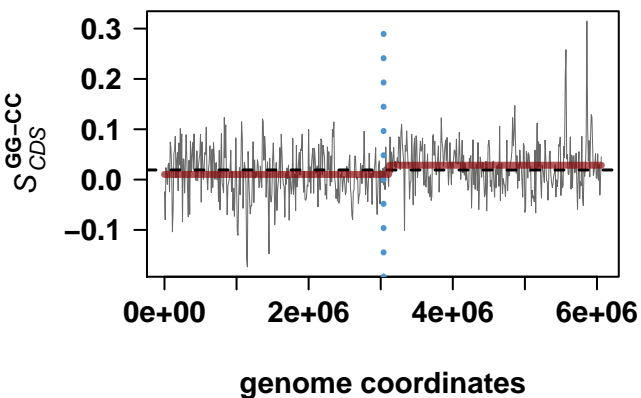
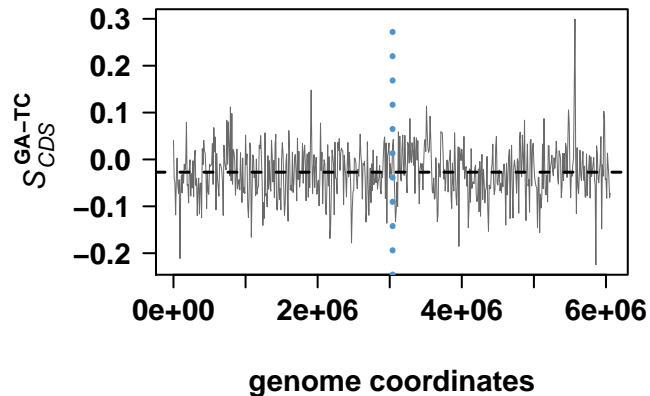
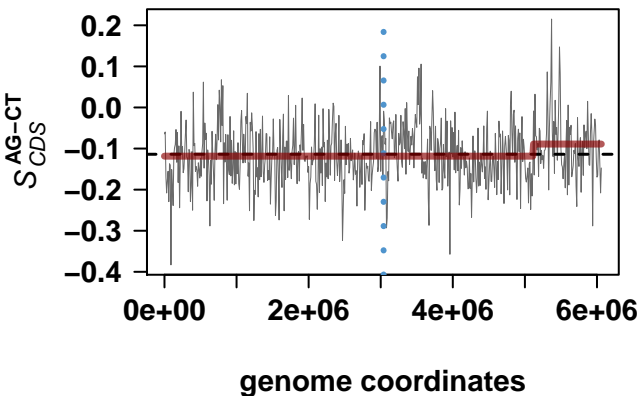


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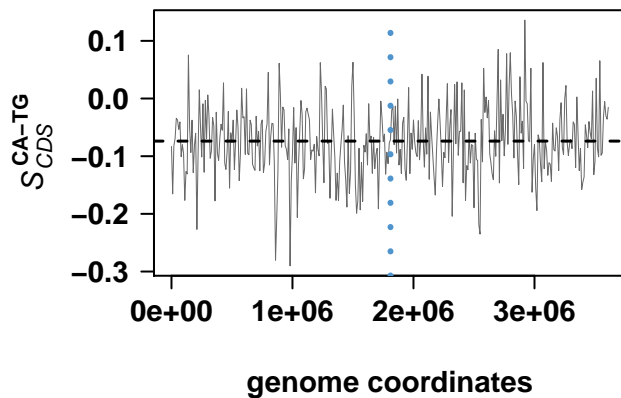
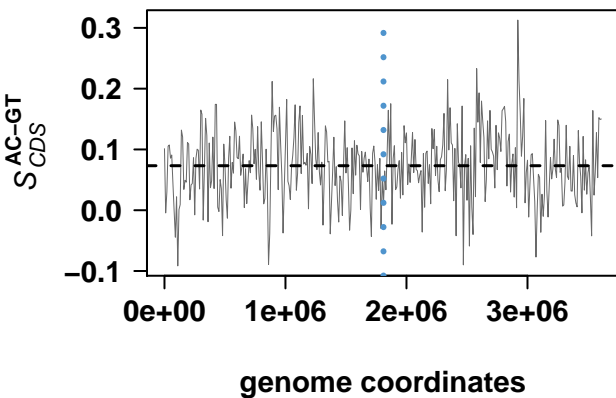
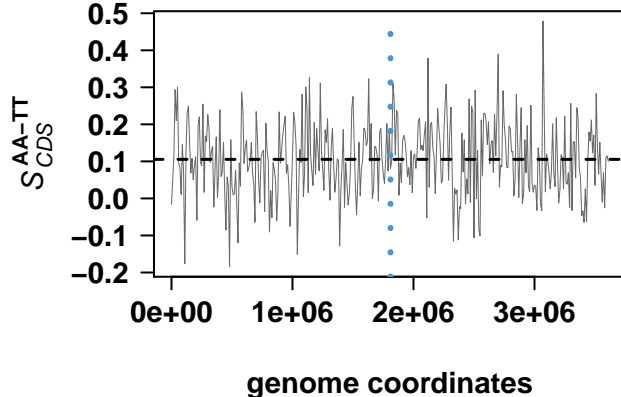
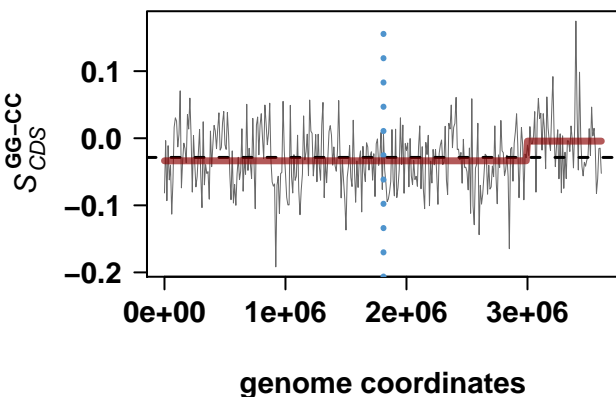
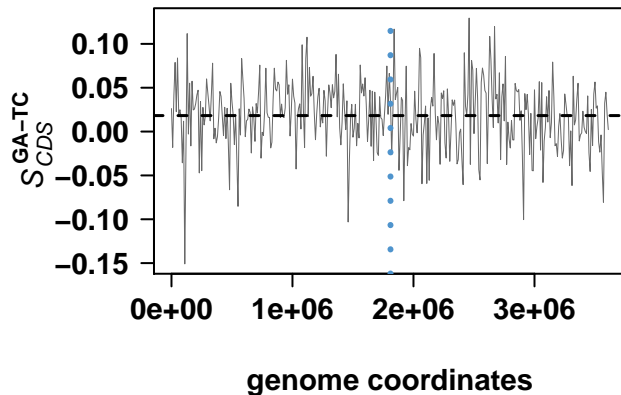
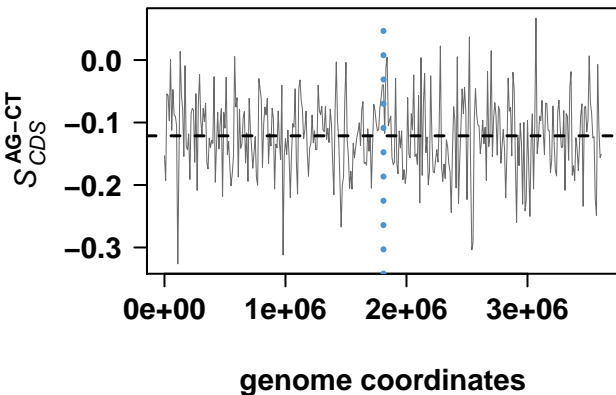


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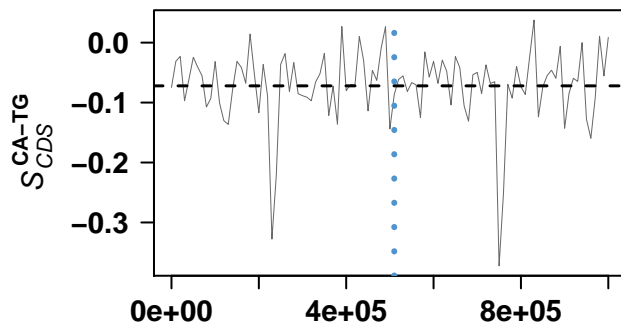
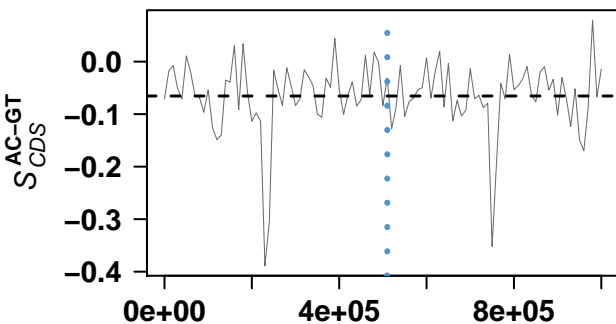
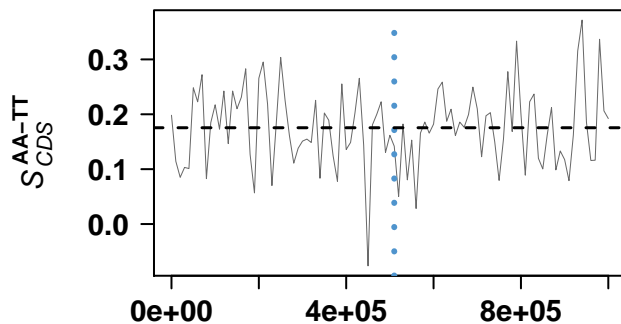
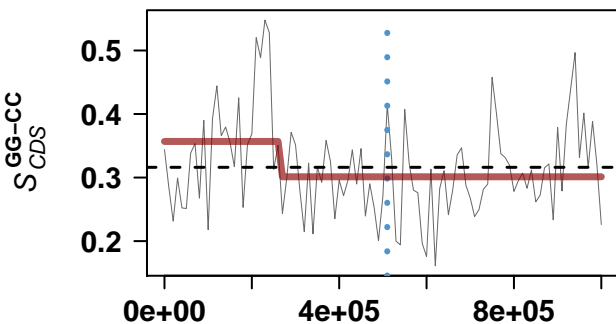
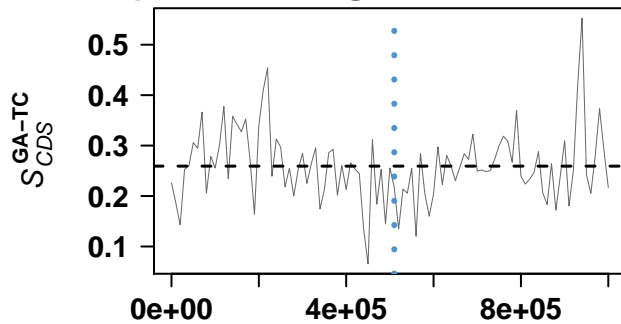
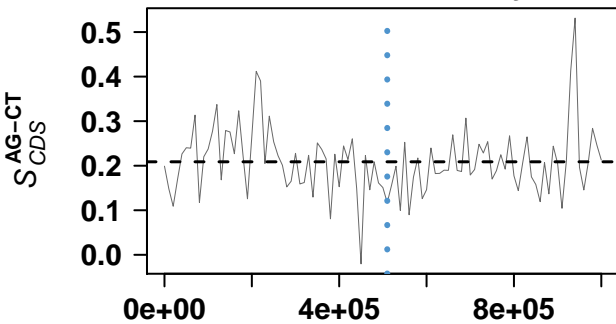
Mesorhizobium loti MAFF303099



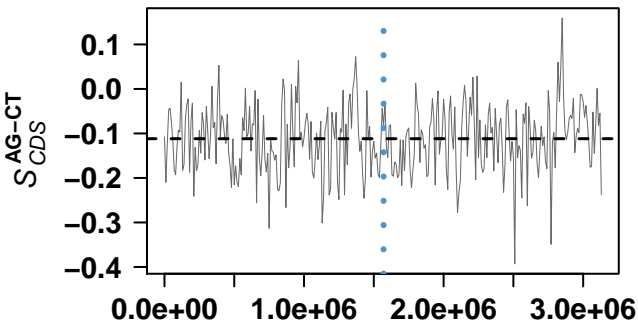
Caulobacter crescentus CB15



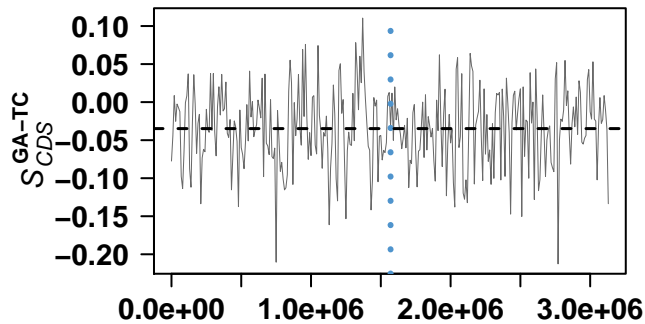
Wolbachia endosymbiont of *Drosophila melanogaster*



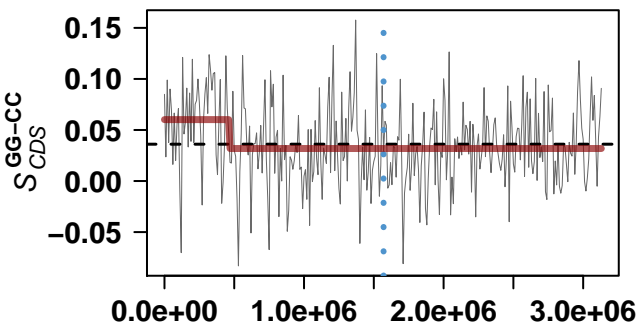
Sinorhizobium meliloti 1021



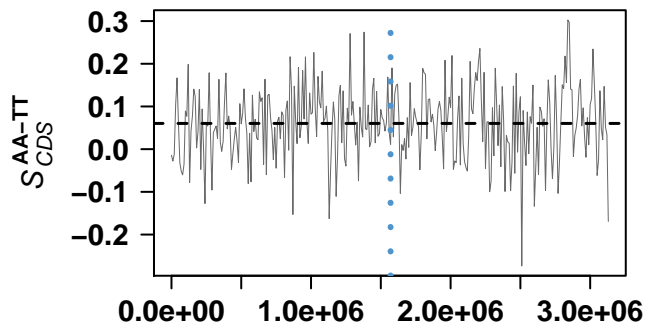
genome coordinates



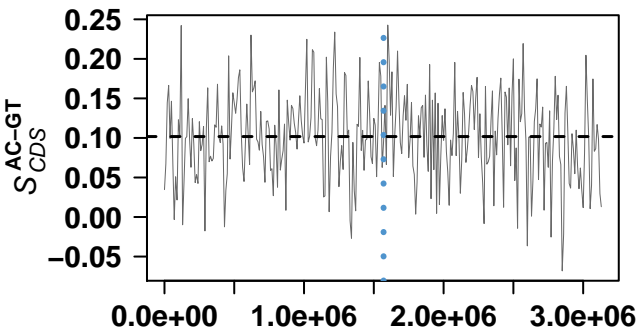
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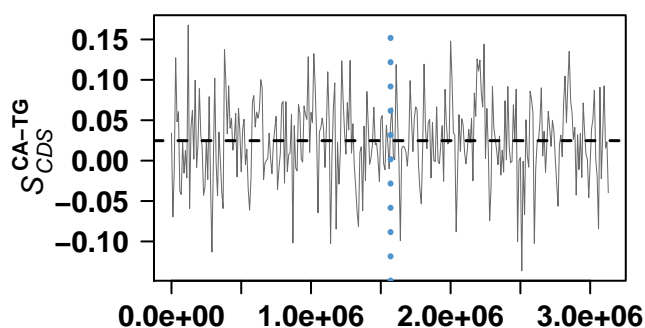
genome coordinates



genome coordinates

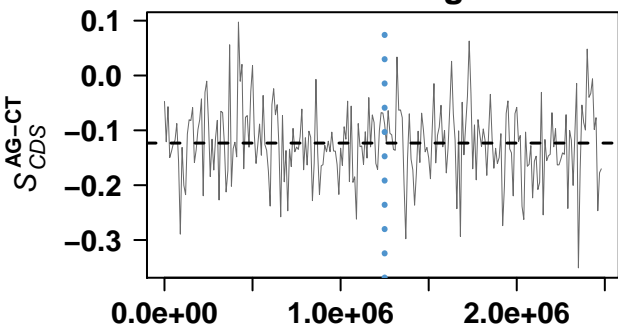


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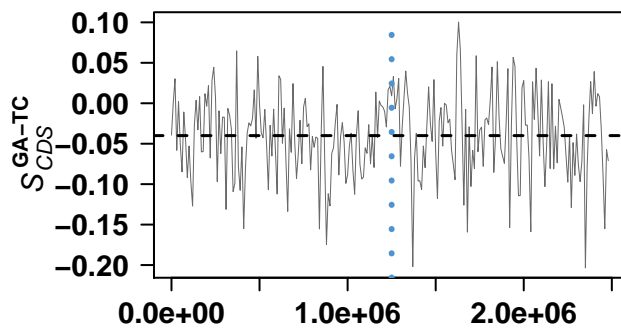


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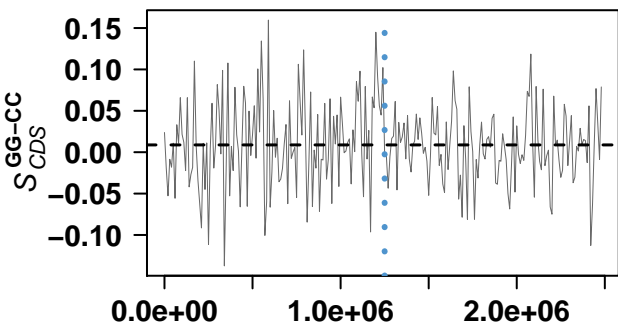
Agrobacterium fabrum str. C58



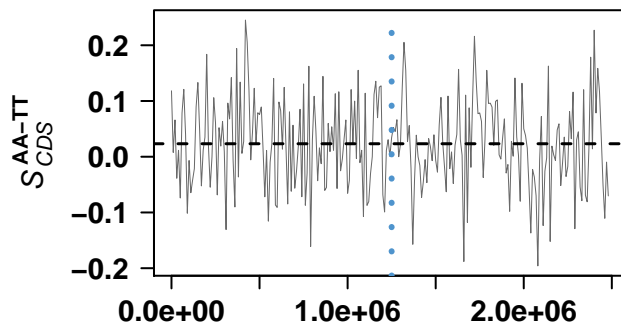
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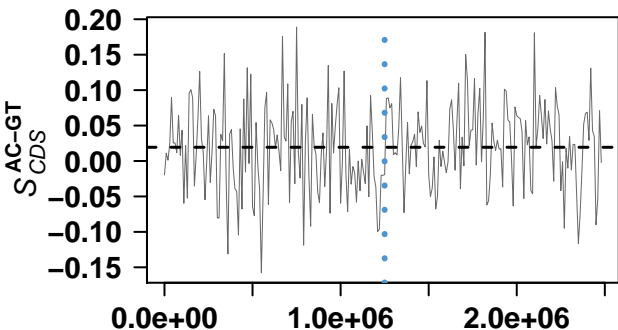
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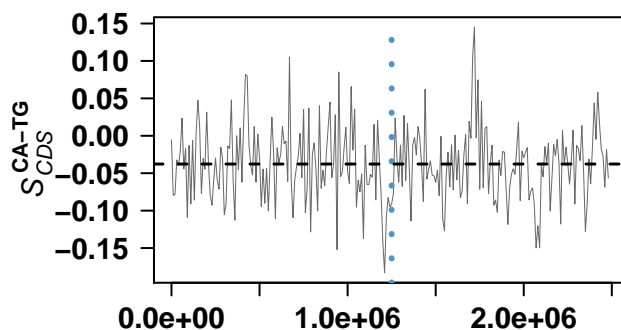
genome coordinates



genome coordinates

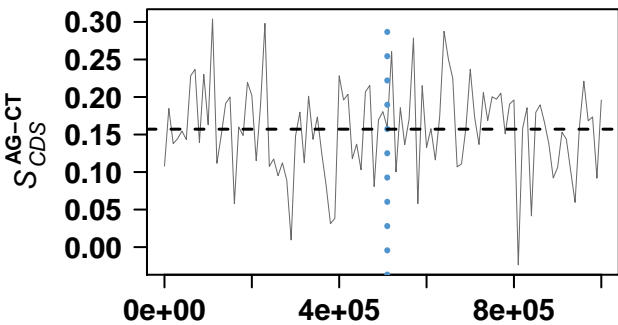


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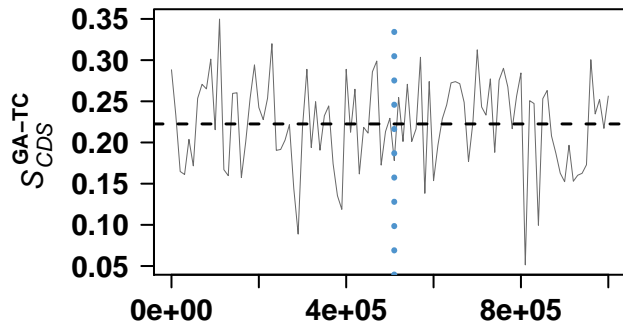


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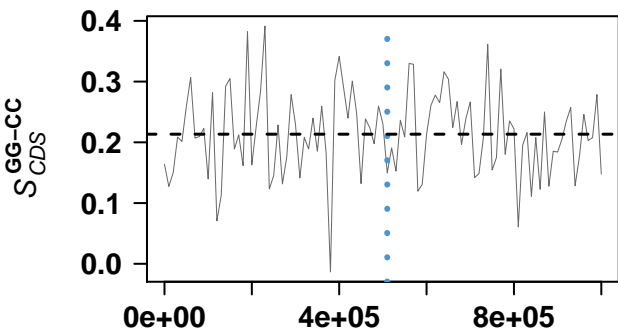
Rickettsia conorii str. Malish 7



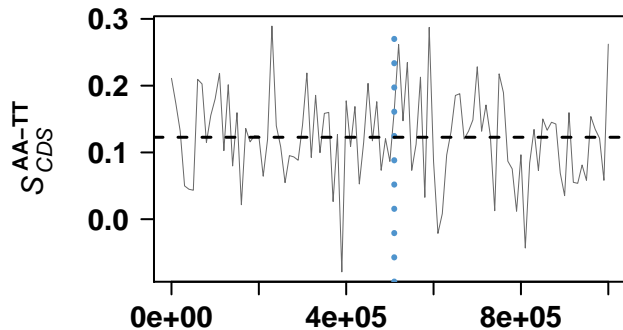
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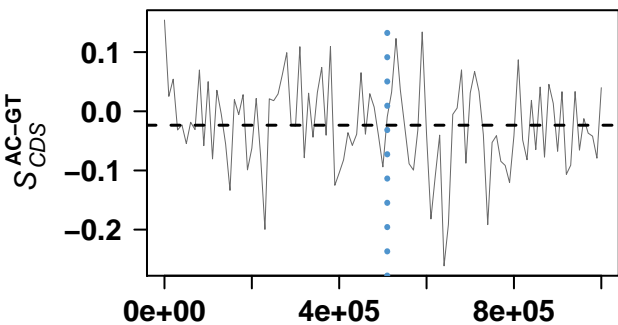
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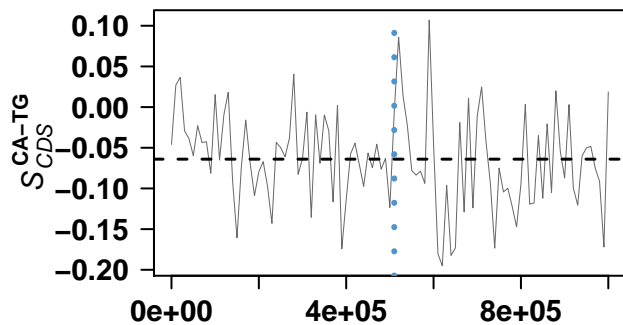
genome coordinates



genome coordinates

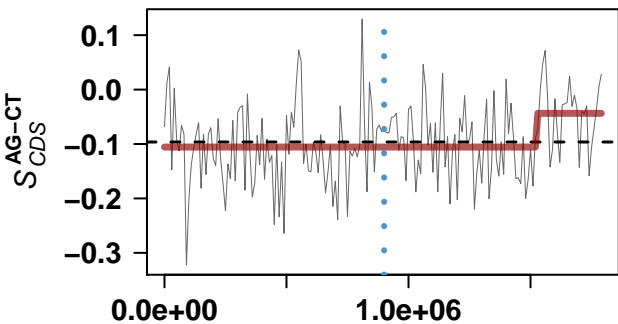


genome coordinates

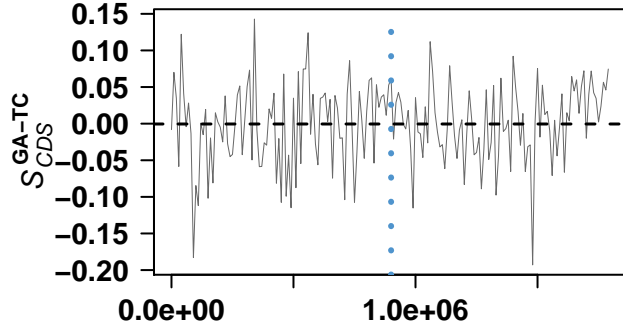


genome coordinates

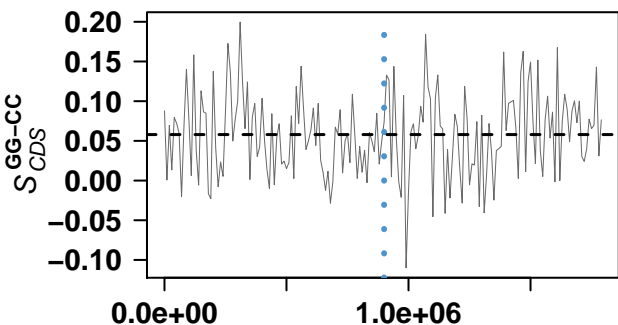
Brucella melitensis bv. 1 str. 16M



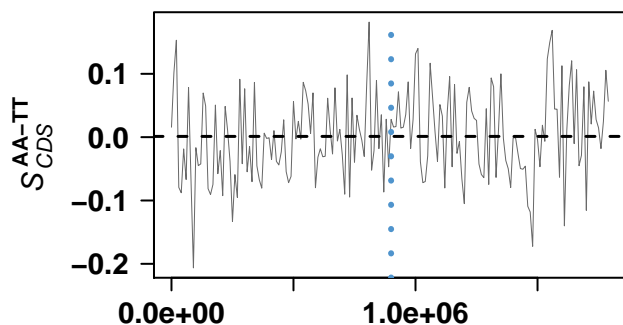
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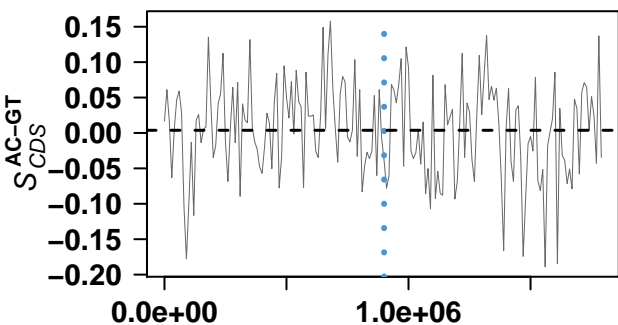
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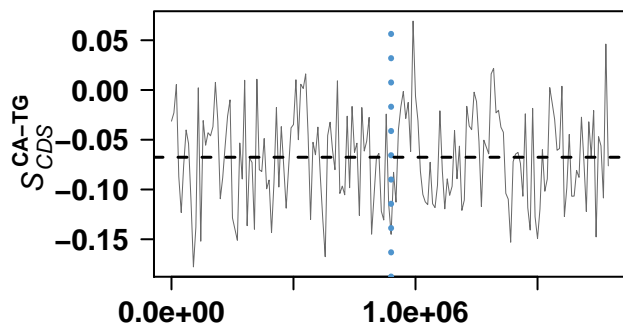
genome coordinates



genome coordinates

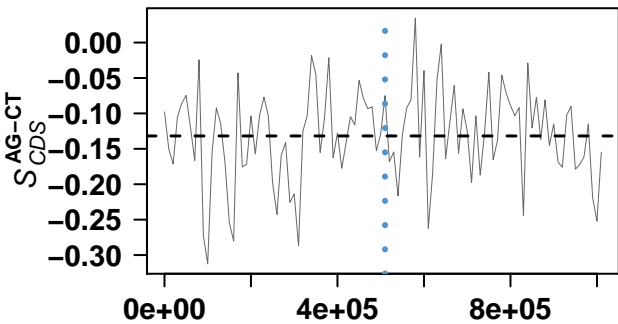


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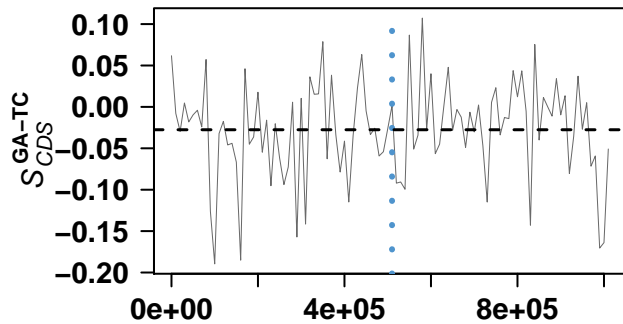


genome coordinates

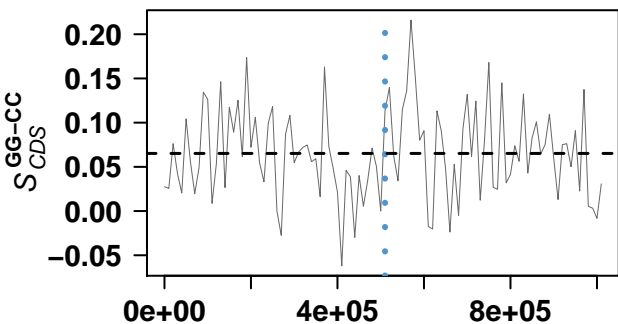
Brucella melitensis bv. 1 str. 16M



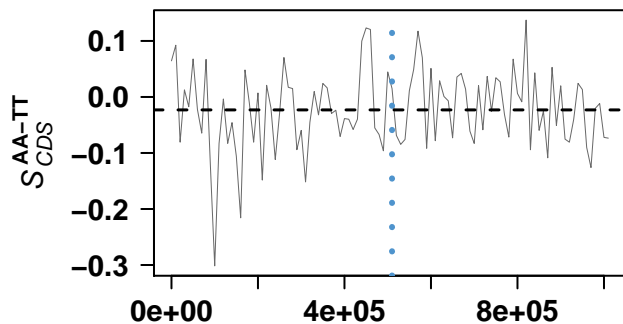
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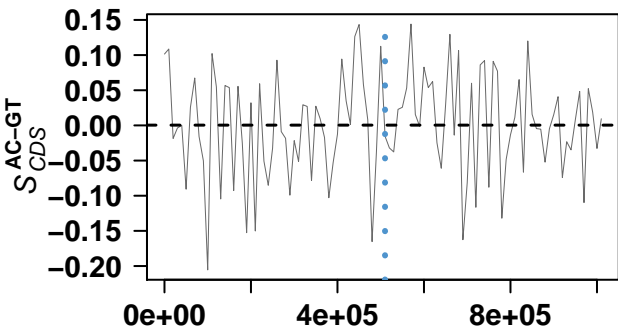
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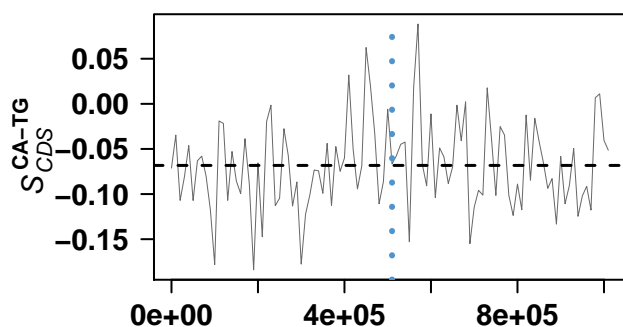
genome coordinates



genome coordinates

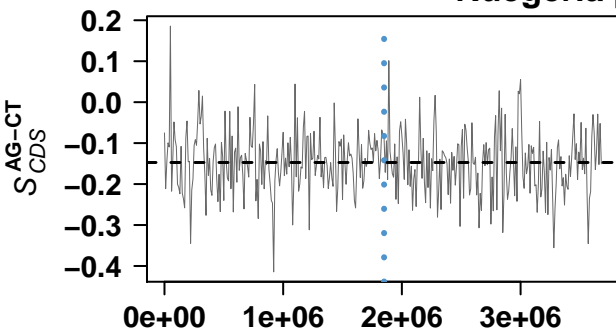


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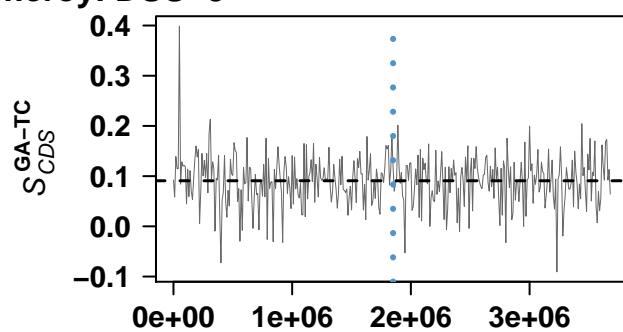


genome coordinates

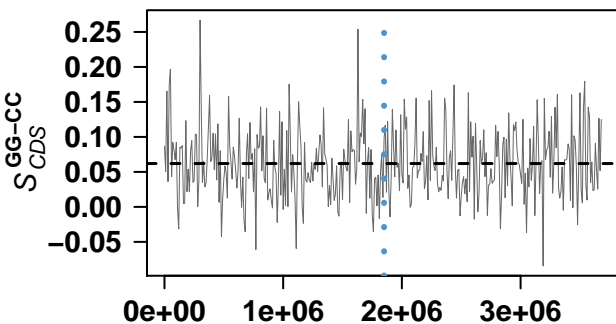
Ruegeria pomeroyi DSS-3



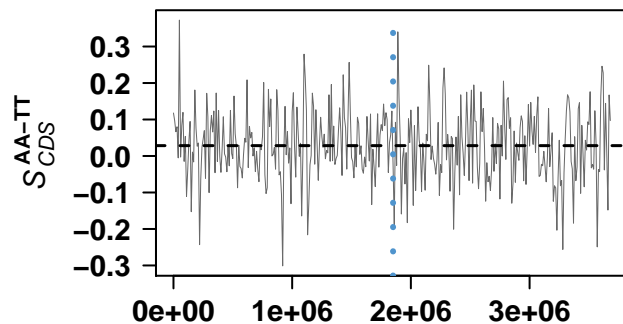
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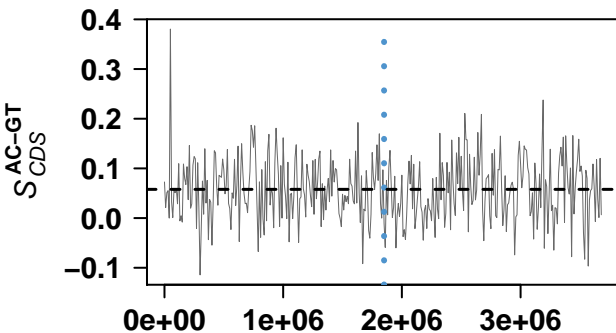
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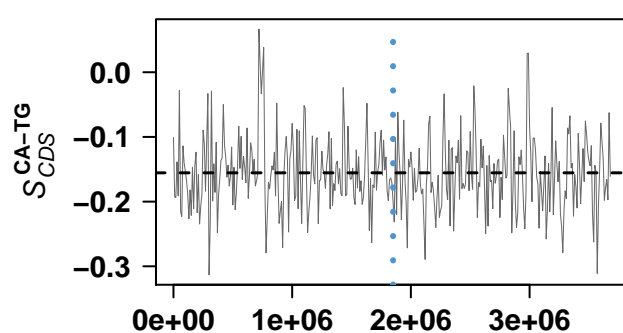
genome coordinates



genome coordinates

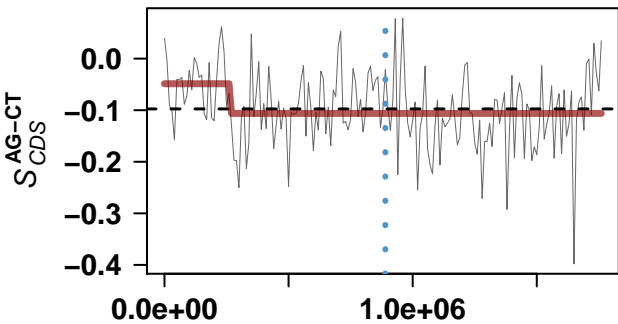


genome coordinates

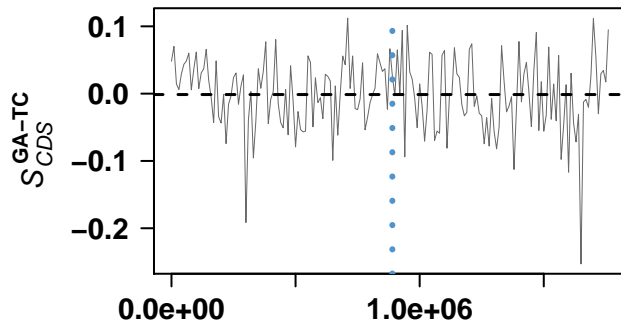


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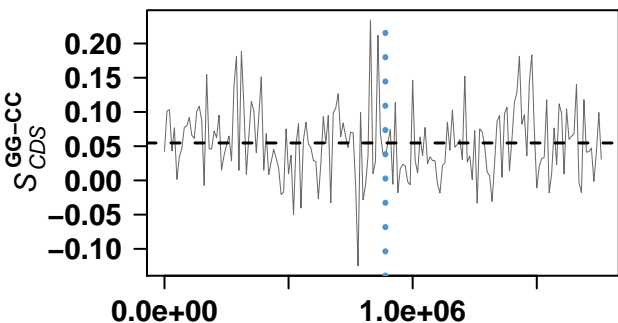
Brucella suis 1330



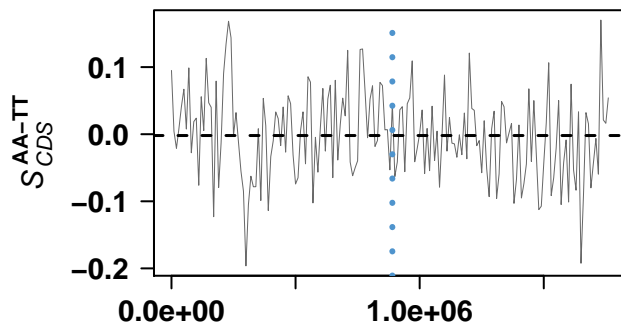
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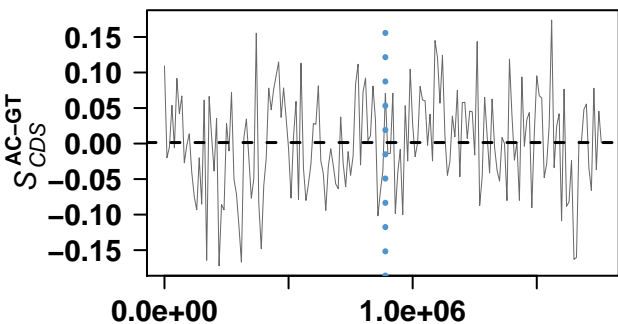
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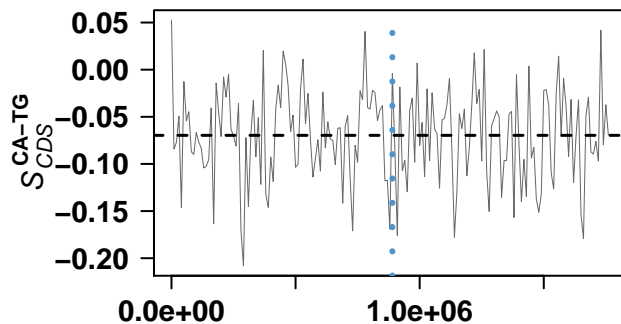
genome coordinates



genome coordinates

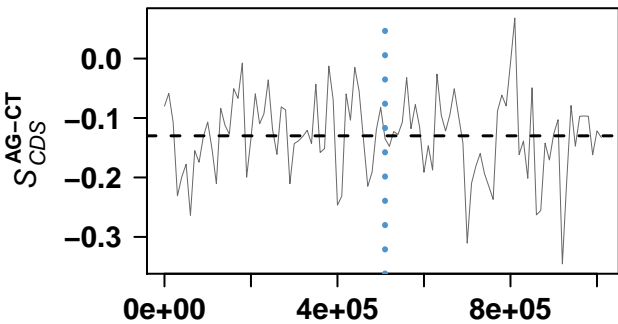


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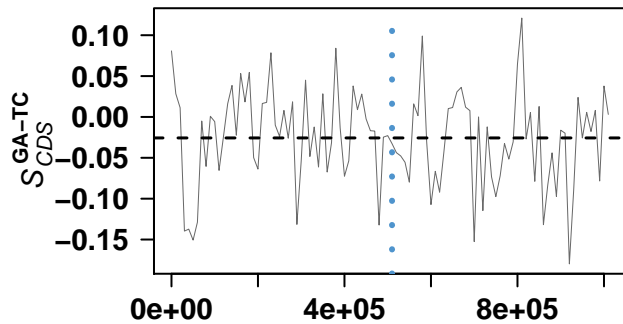


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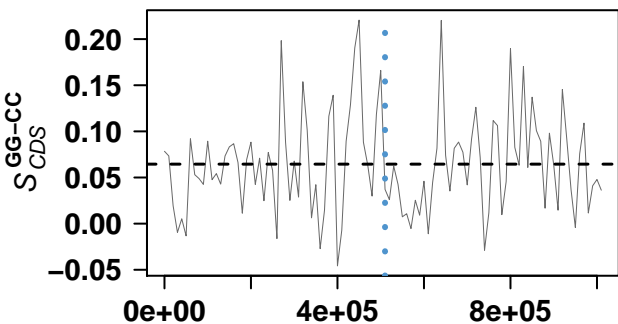
Brucella suis 1330



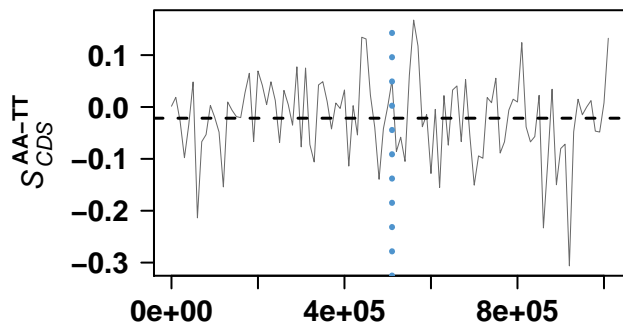
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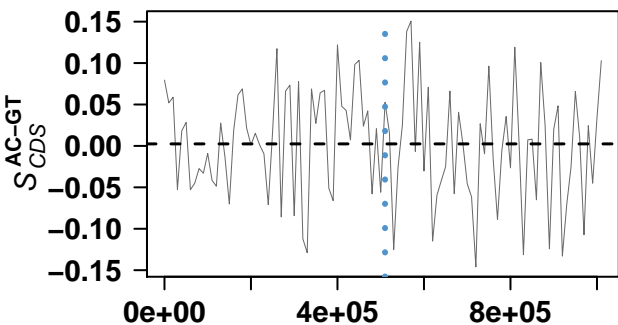
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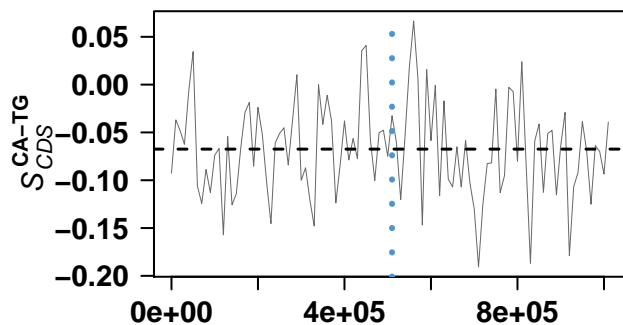
genome coordinates



genome coordinates

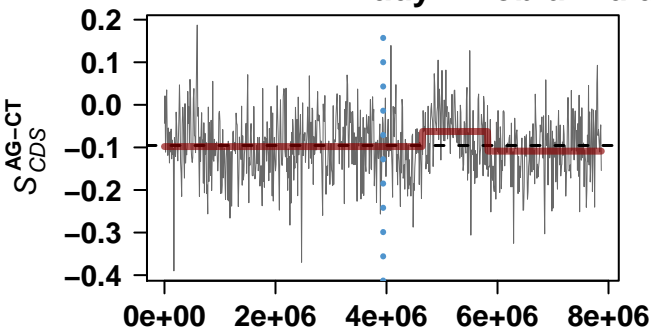


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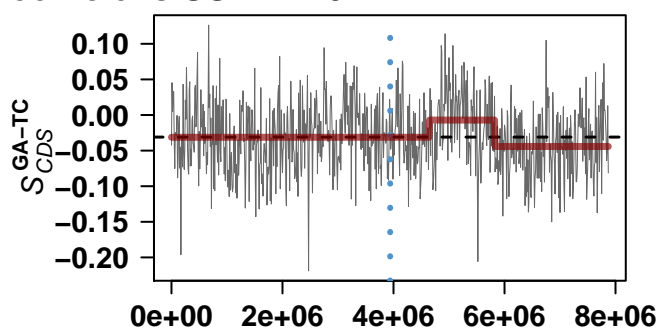


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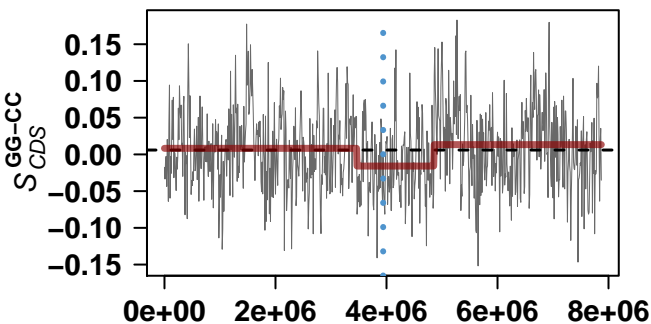
Bradyrhizobium diazoefficiens USDA 110



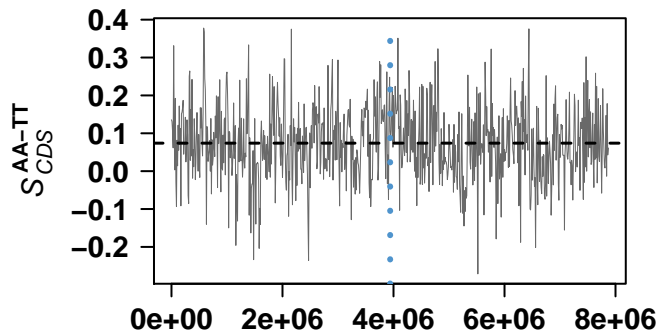
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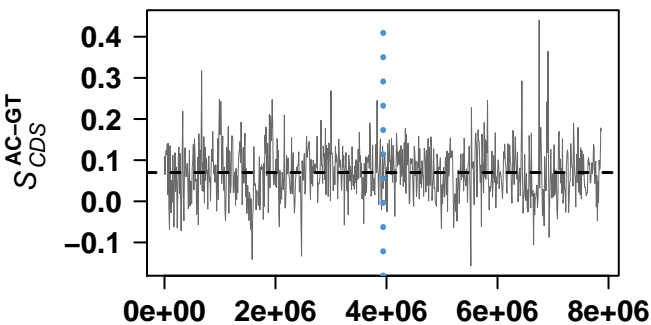
genome coordinates



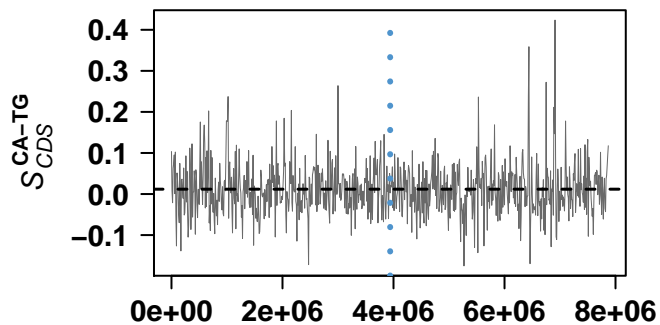
genome coordinates



genome coordinates

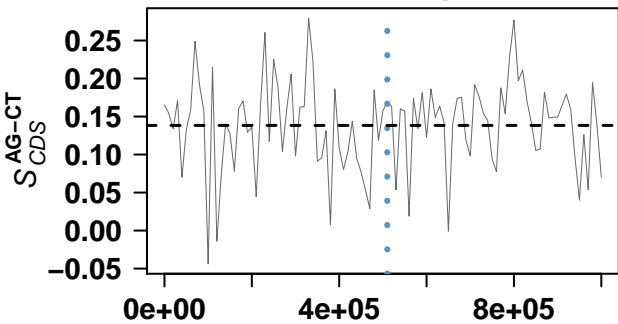


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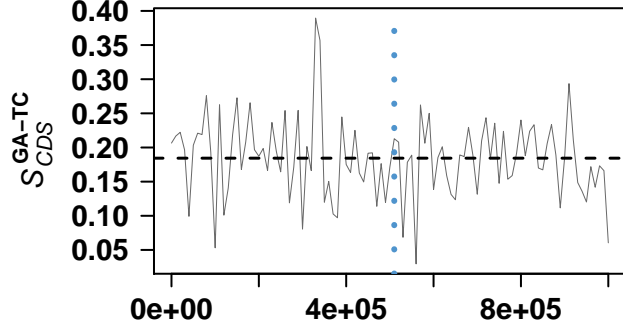


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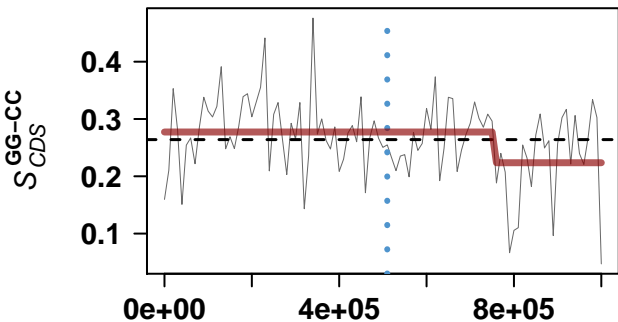
Anaplasma marginale str. St. Maries



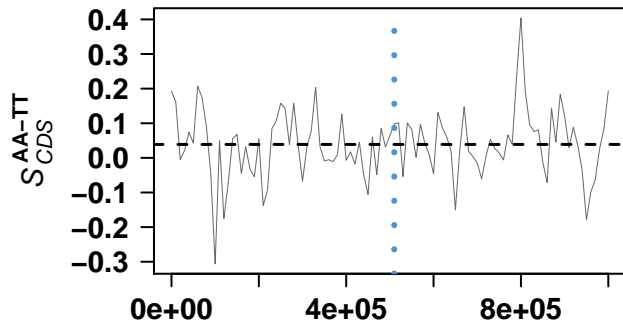
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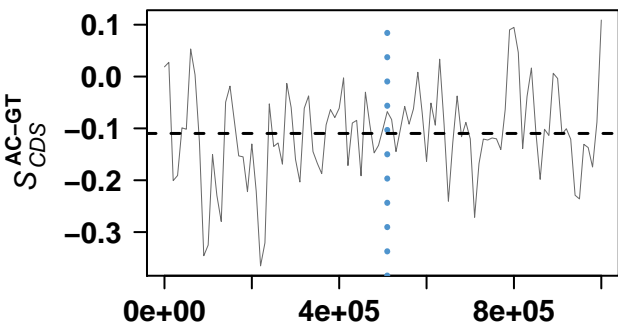
genome coordinates



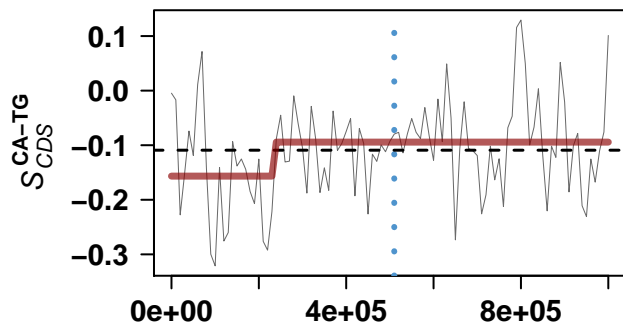
genome coordinates



genome coordinates

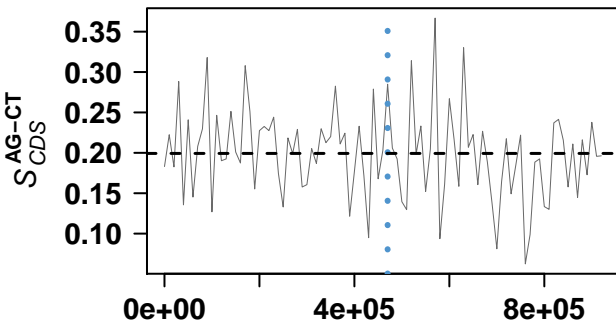


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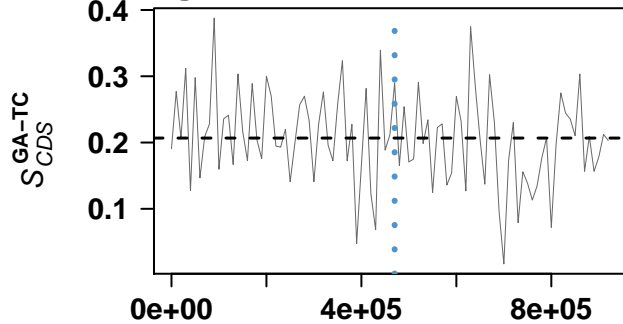


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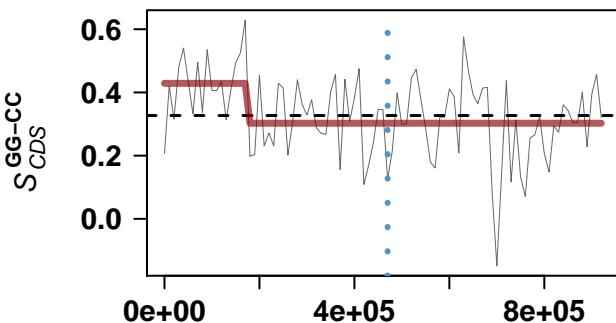
Ehrlichia ruminantium str. Welgevonden



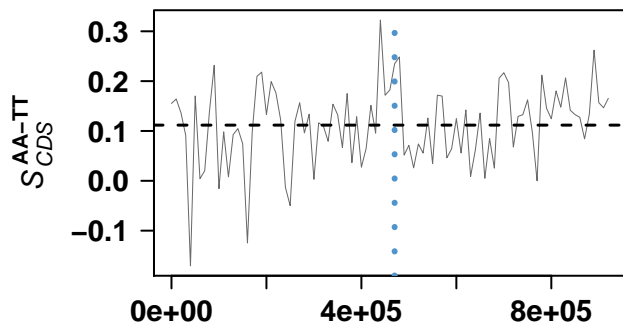
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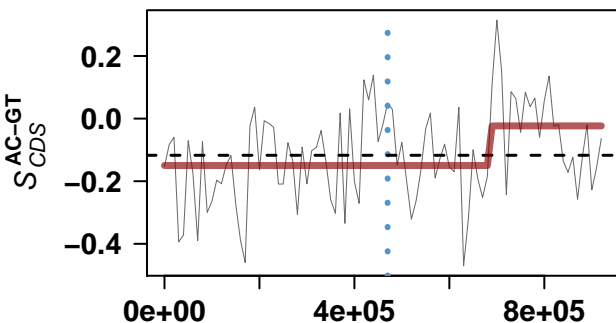
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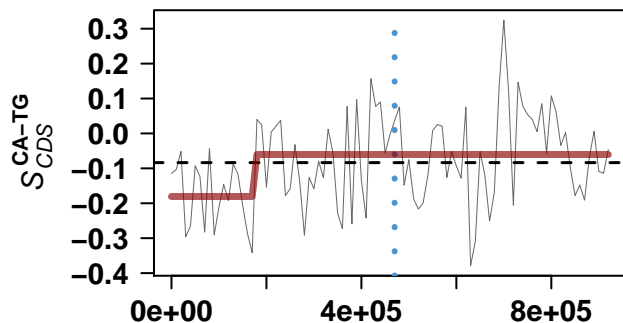
genome coordinates



genome coordinates

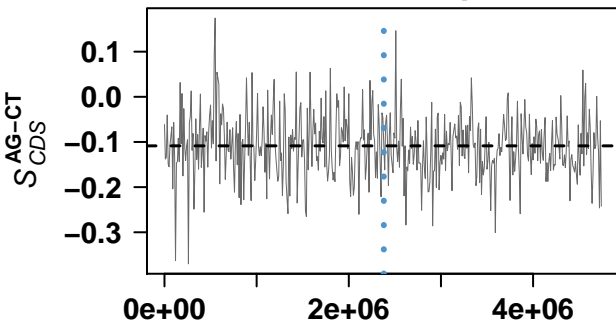


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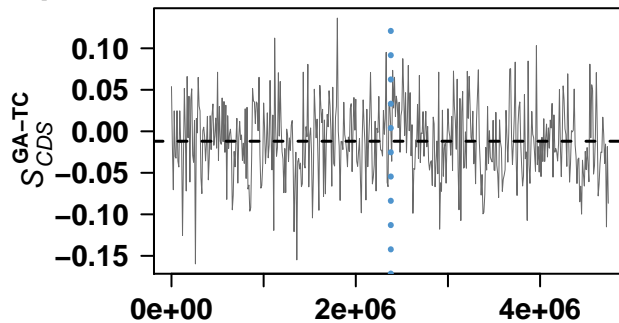


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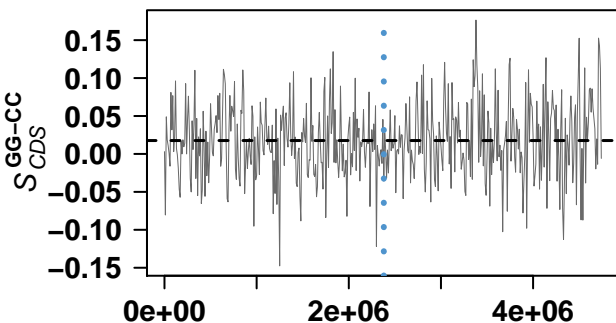
Rhodopseudomonas palustris CGA009



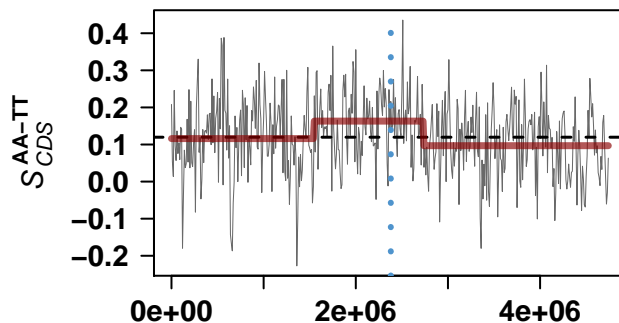
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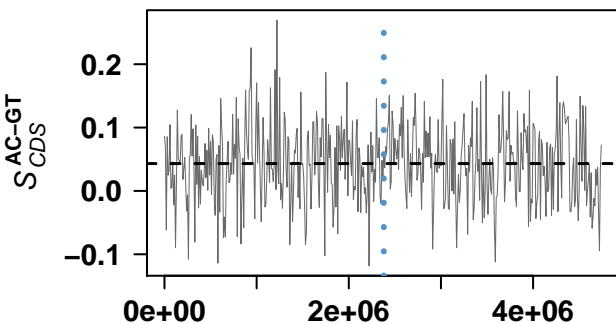
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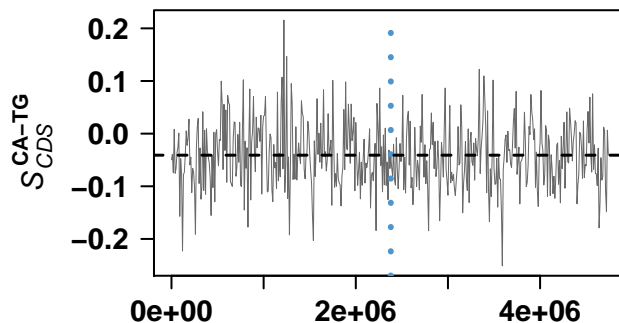
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genome coordinates

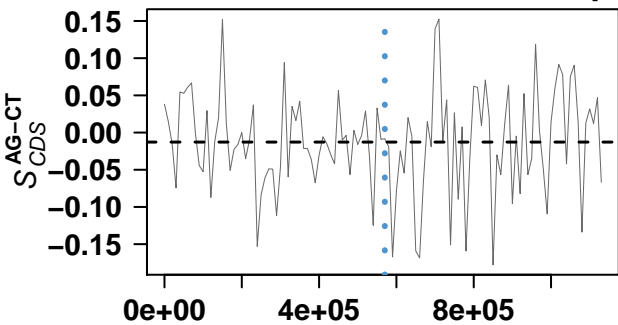


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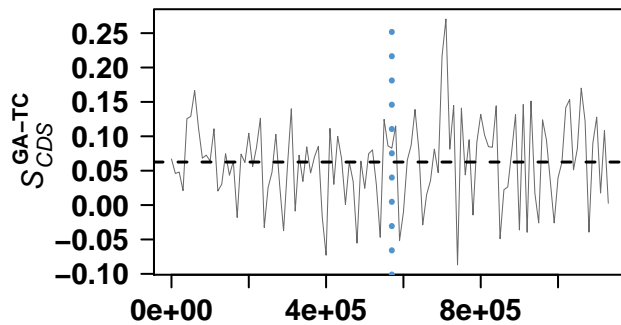


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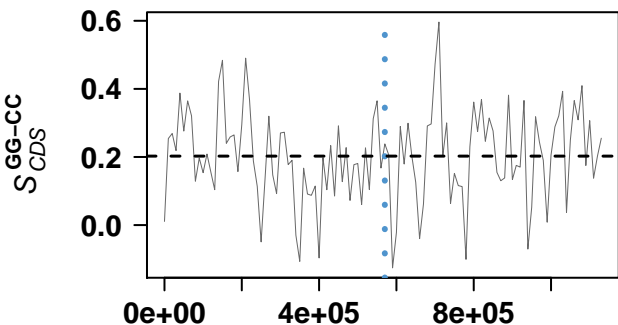
Bartonella quintana str. Toulouse



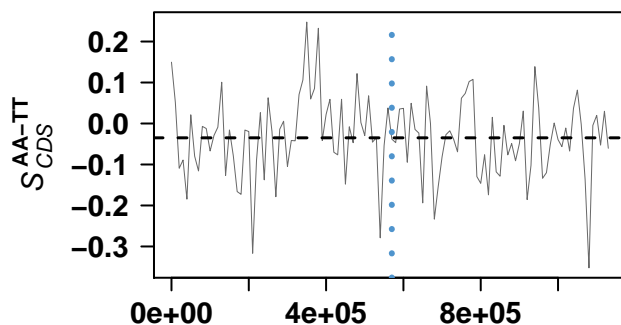
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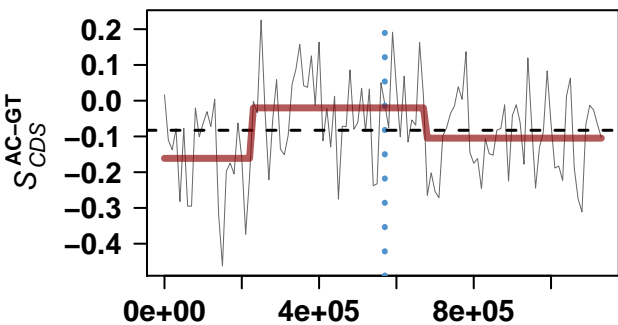
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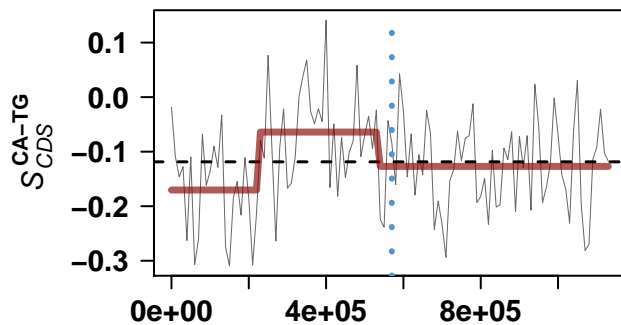
genome coordinates



genome coordinates

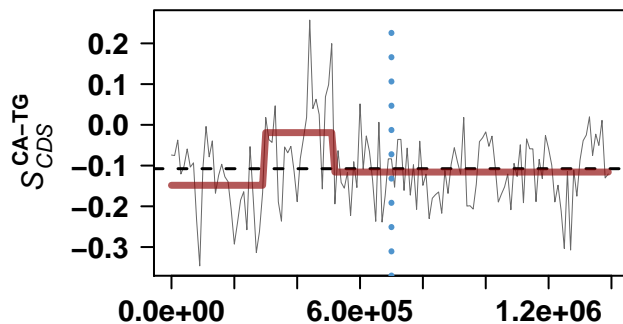
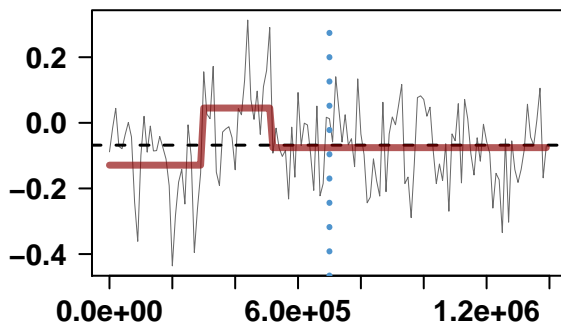
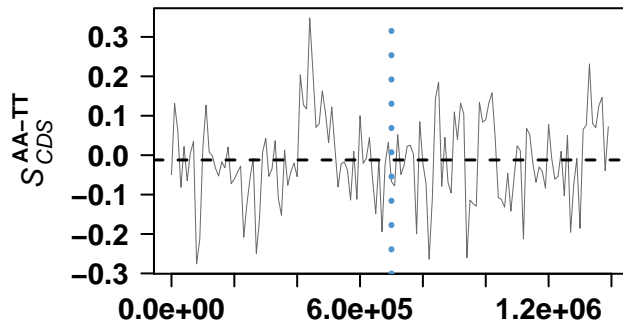
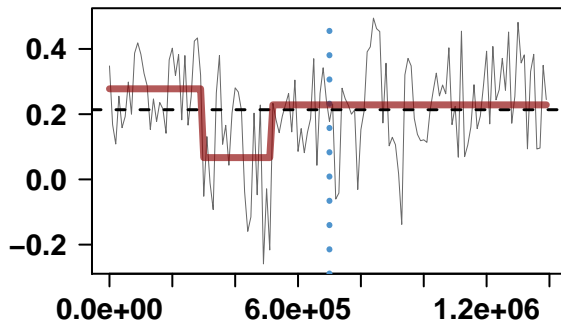
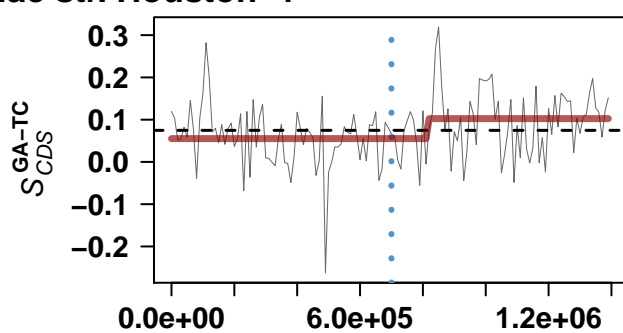
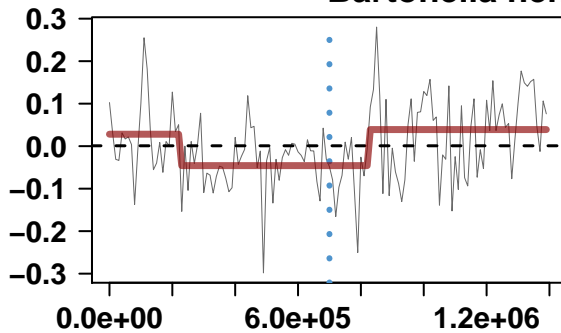


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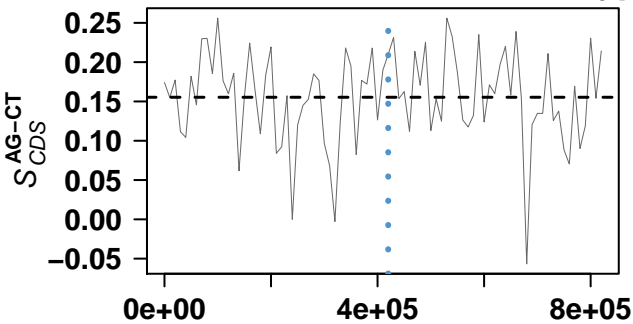


genome coordinates

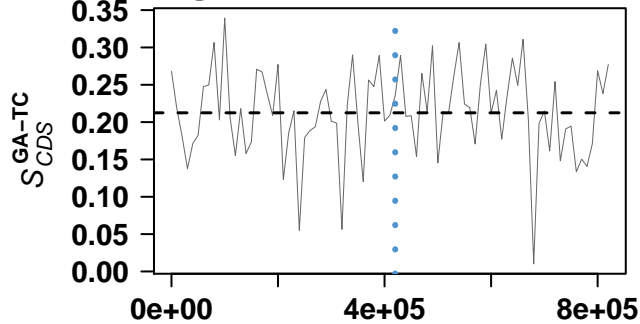
Bartonella henselae str. Houston-1



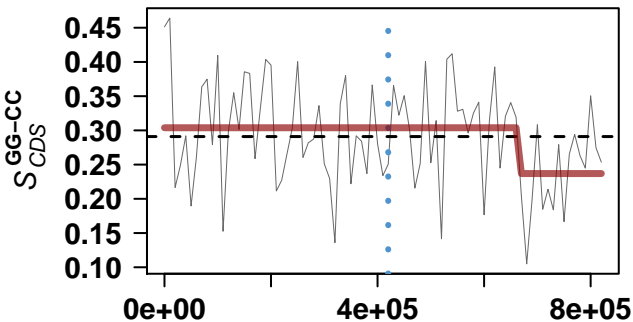
Rickettsia typhi str. Wilmington



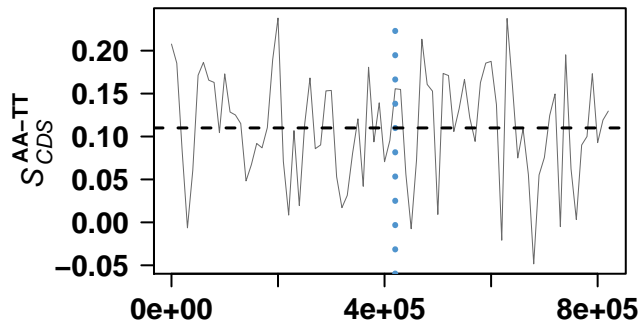
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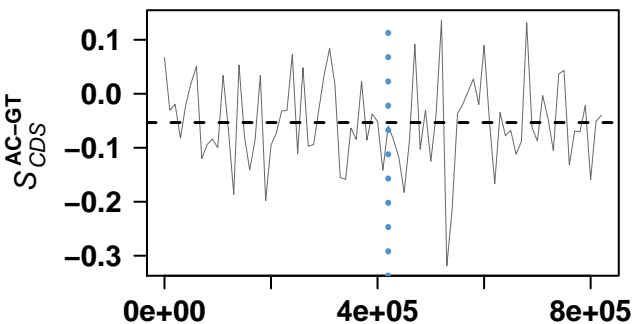
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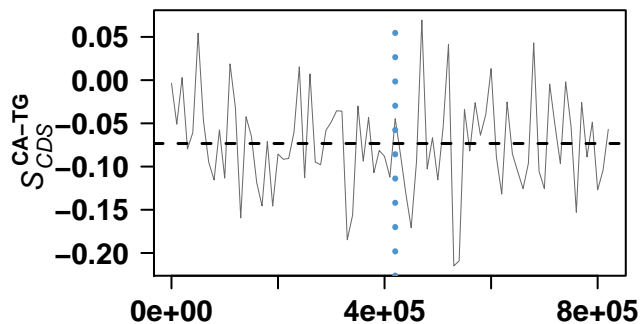
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genome coordinates

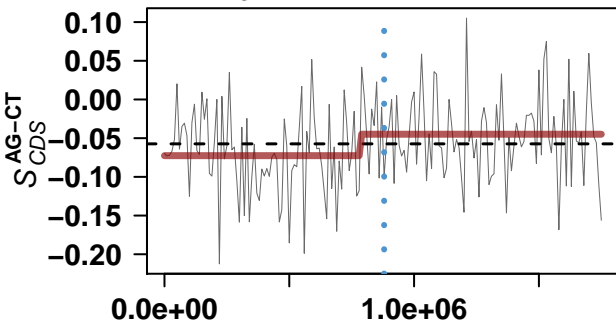


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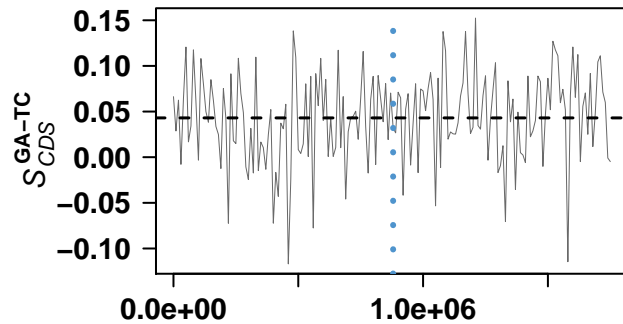


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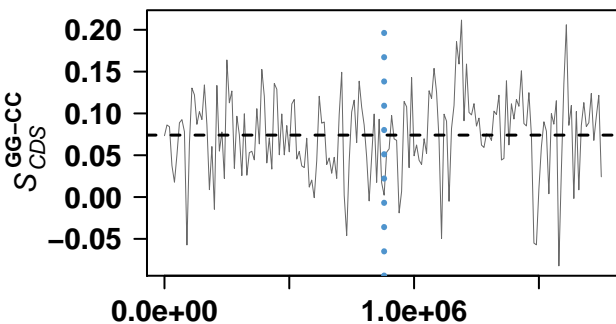
Zymomonas mobilis subsp. mobilis ZM4 = ATCC 31821



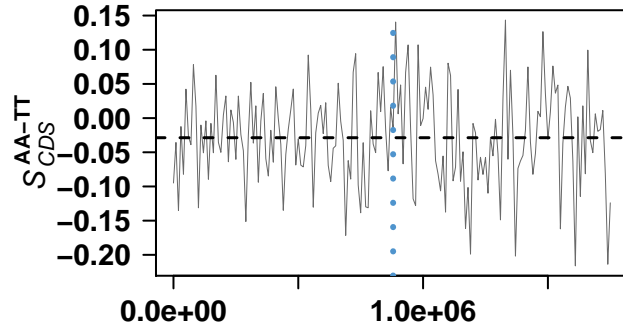
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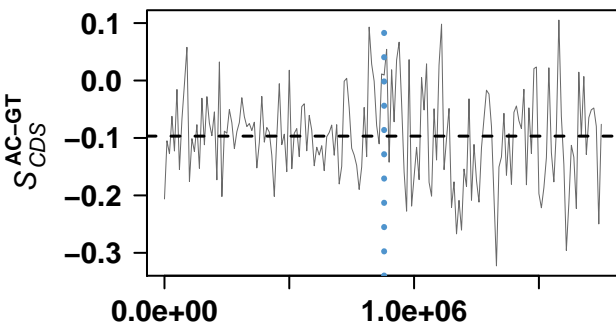
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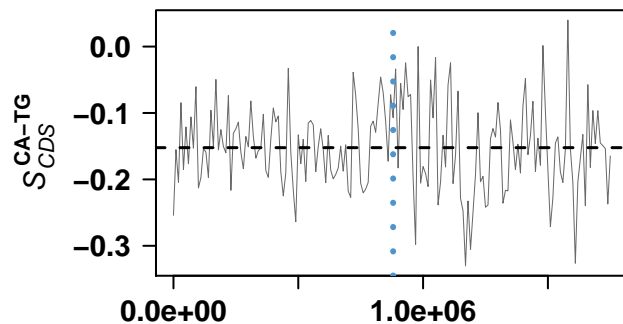
genome coordinates



genome coordinates

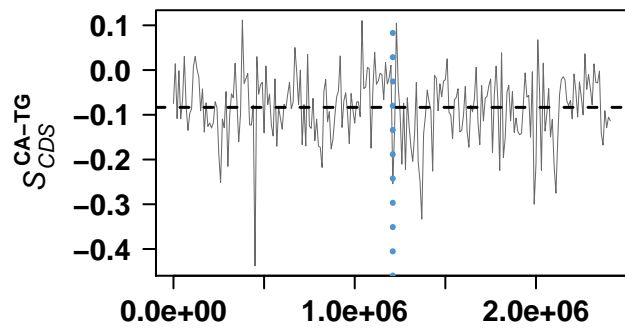
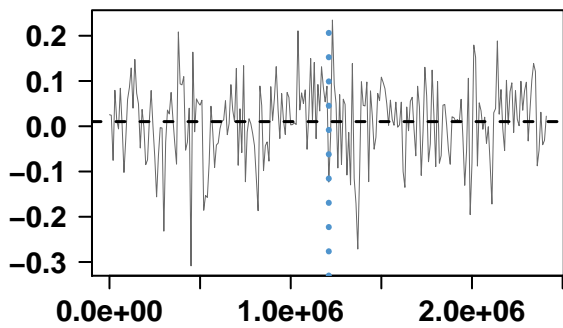
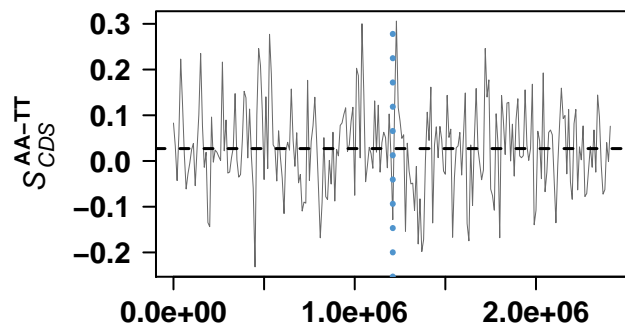
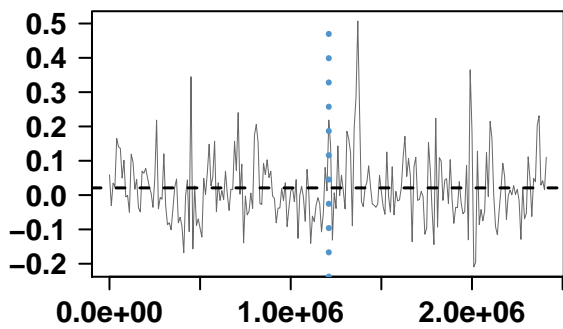
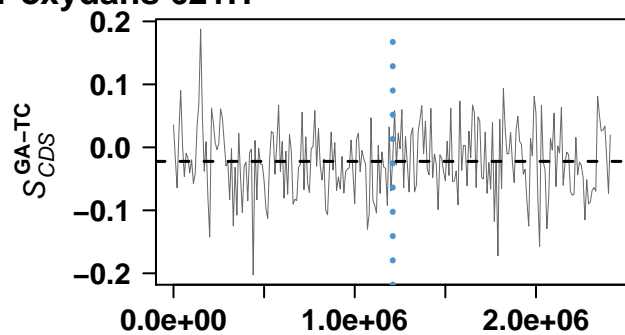
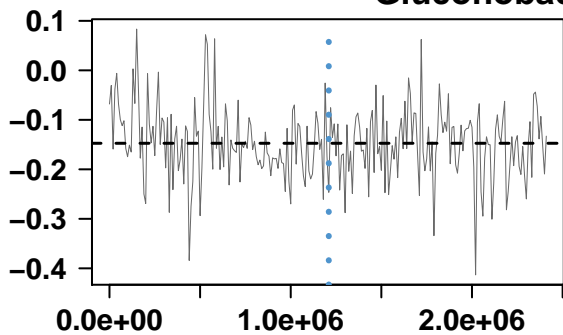


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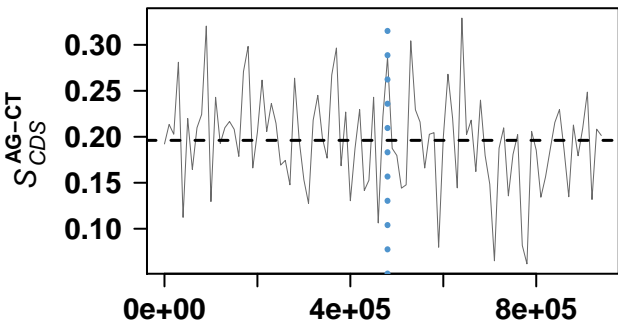


genome coordinates

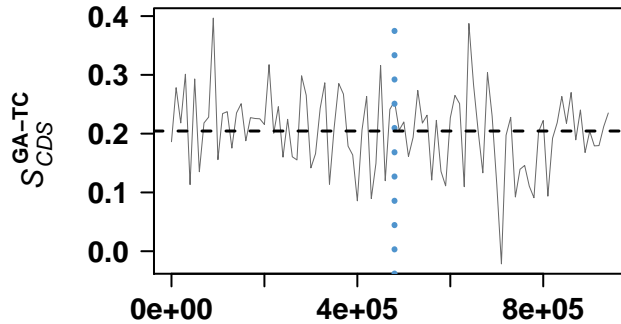
Gluconobacter oxydans 621H



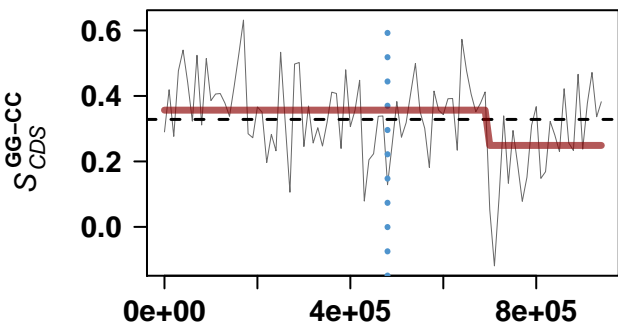
Ehrlichia ruminantium str. Gardel



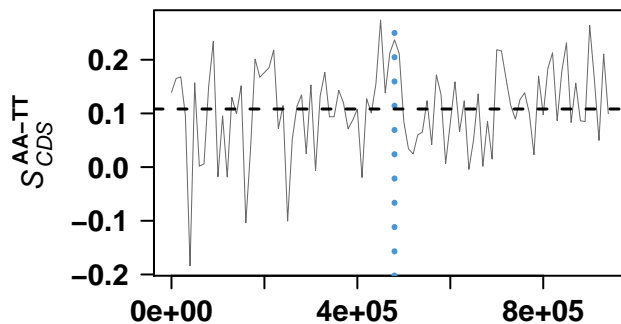
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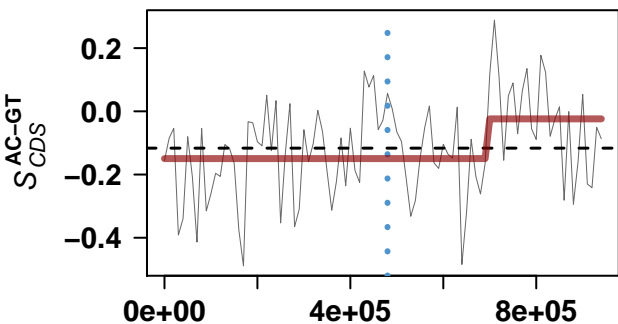
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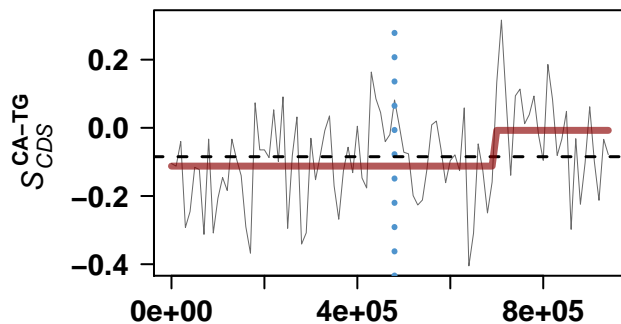
genome coordinates



genome coordinates

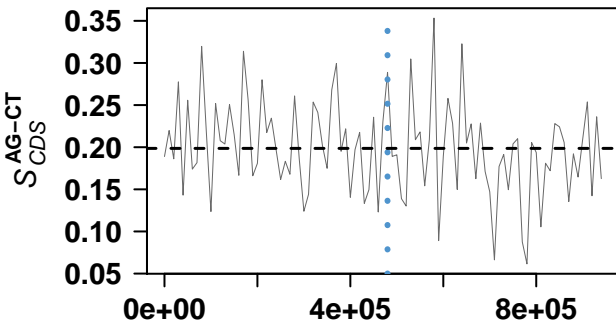


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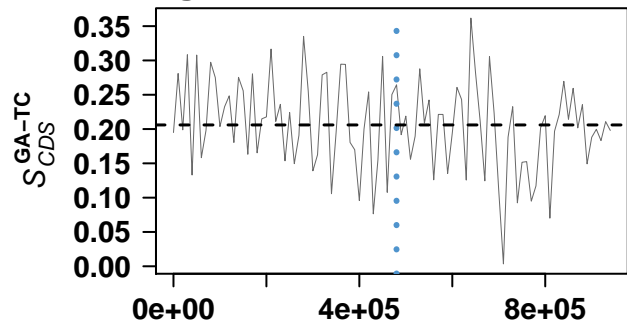


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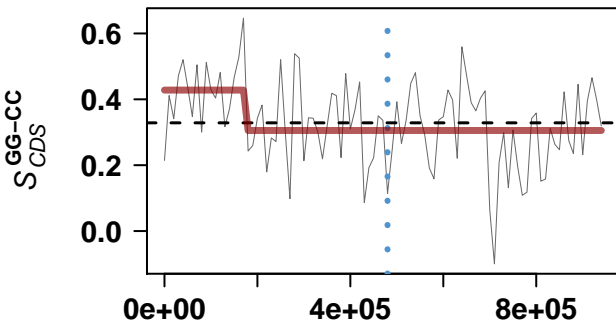
Ehrlichia ruminantium str. Welgevonden



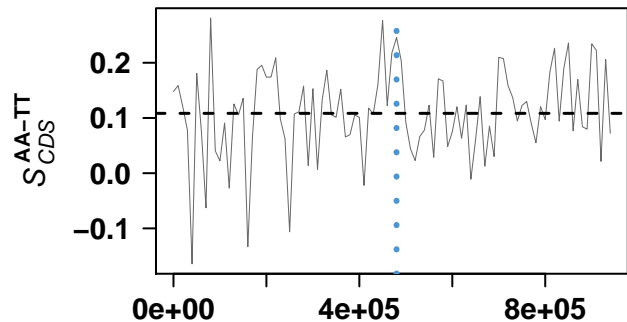
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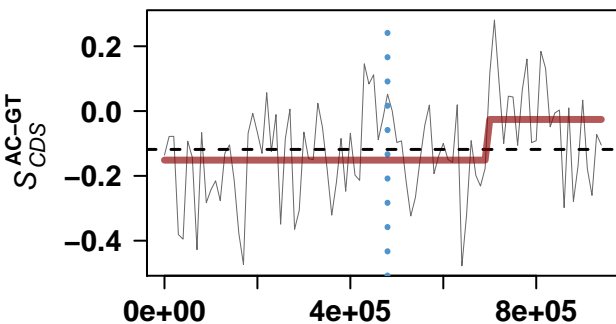
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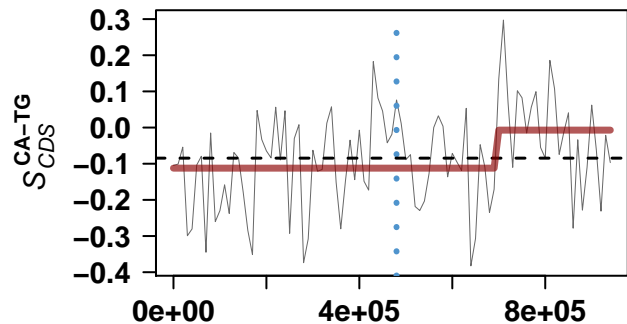
genome coordinates



genome coordinates

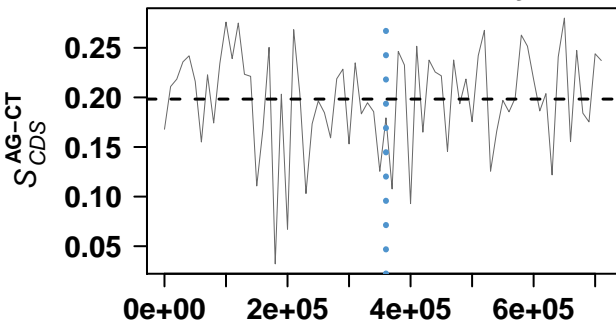


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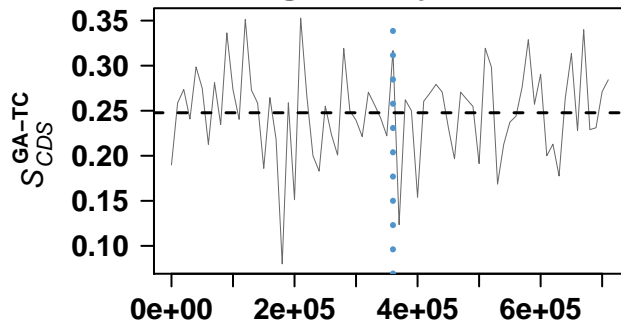


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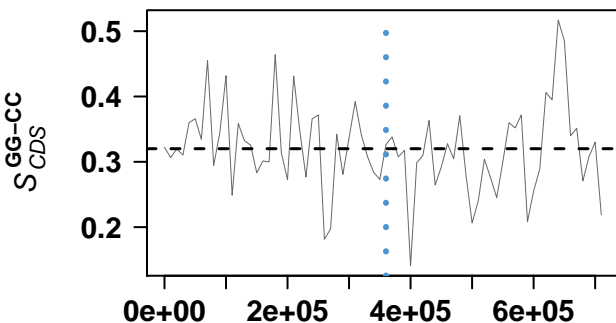
Wolbachia endosymbiont strain TRS of *Brugia malayi*



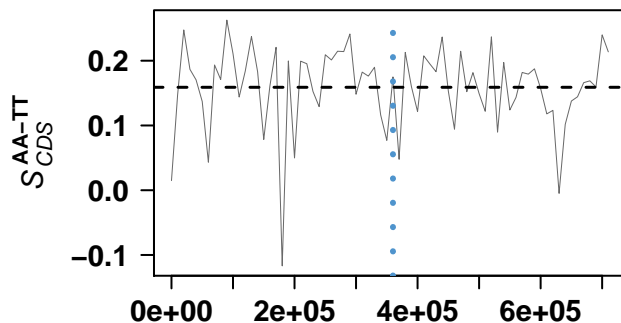
genome coordinates



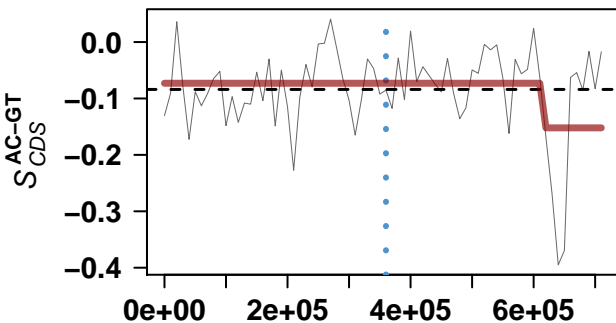
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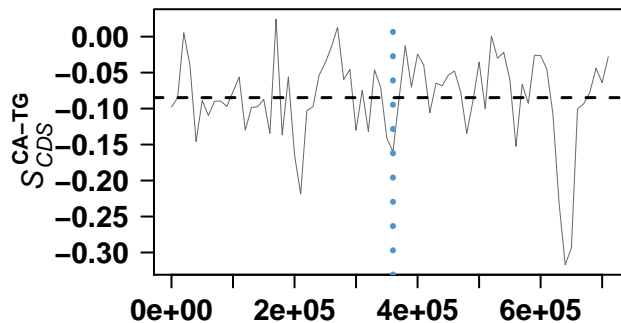
genome coordinates



genome coordinates

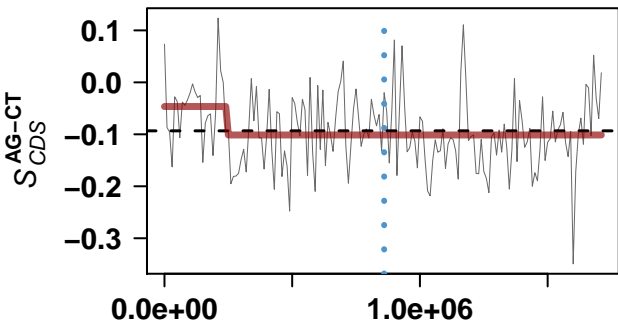


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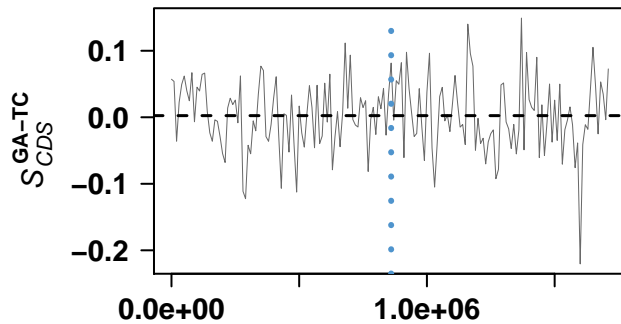


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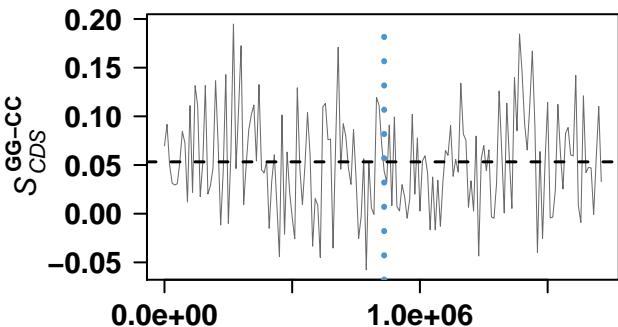
Brucella abortus bv. 1 str. 9-941



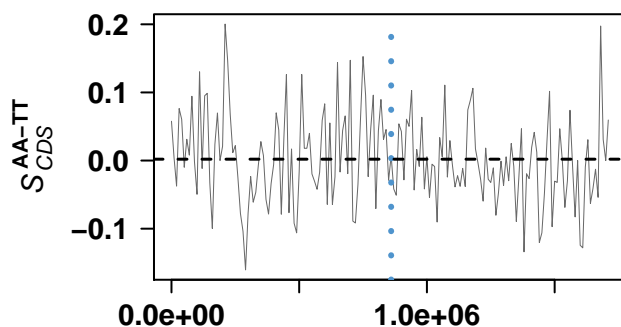
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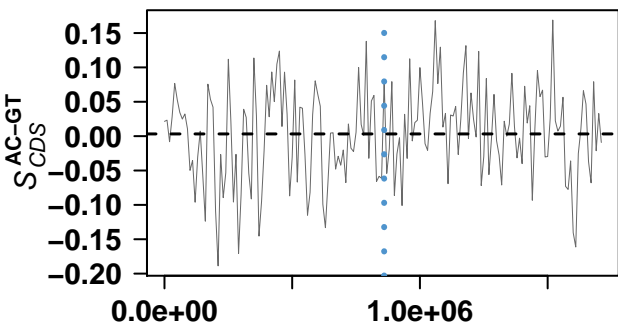
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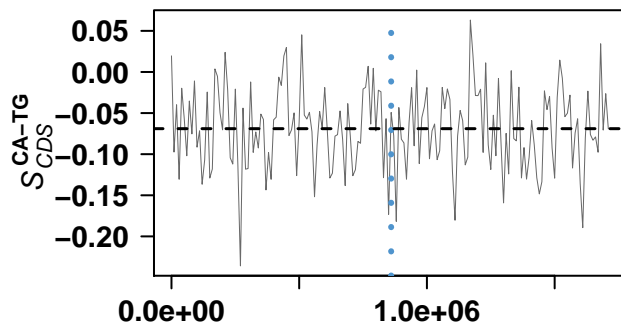
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genome coordinates

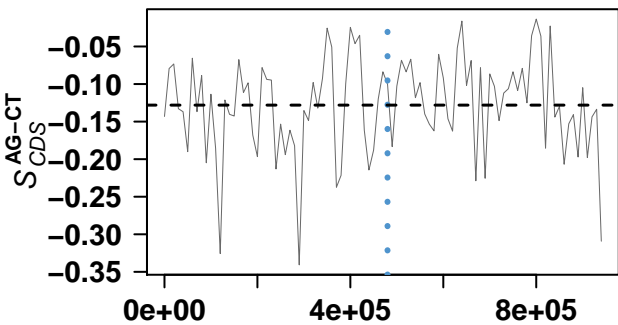


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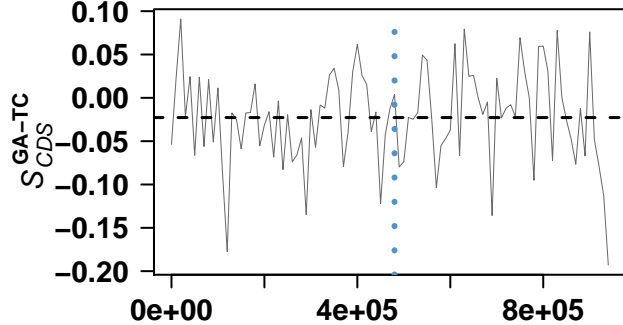


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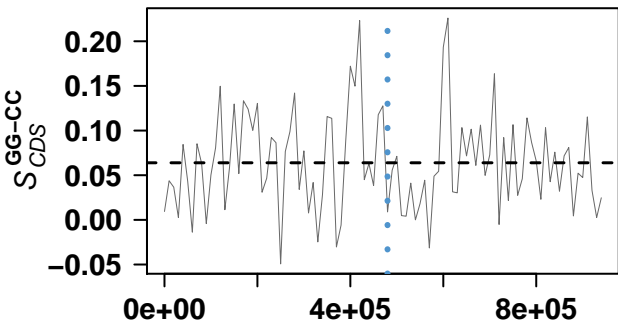
Brucella abortus bv. 1 str. 9-941



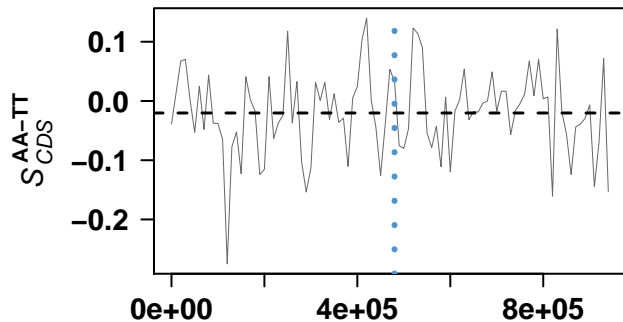
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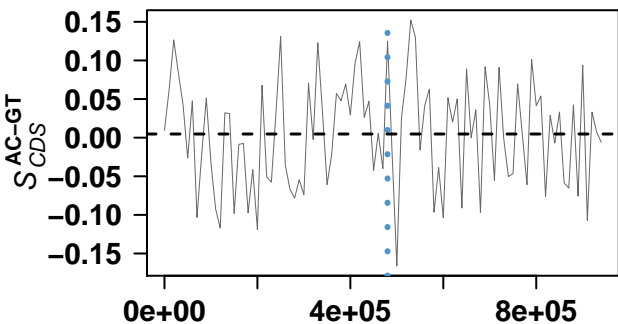
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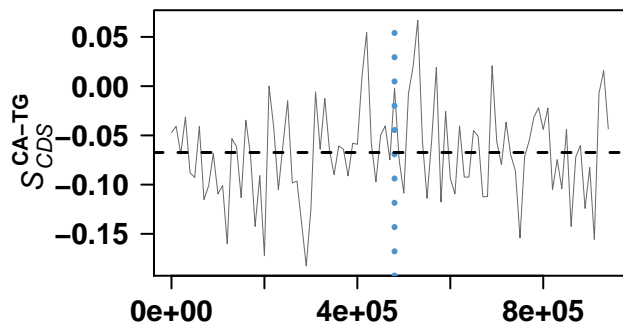
genome coordinates



genome coordinates

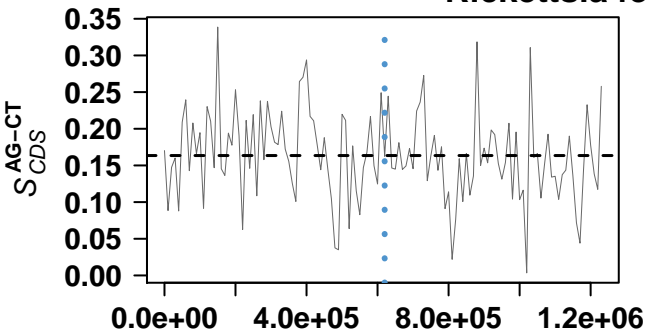


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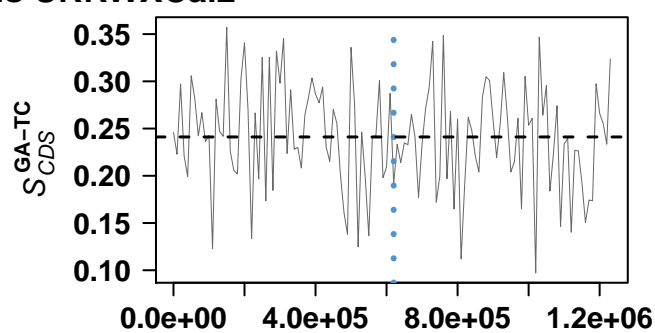


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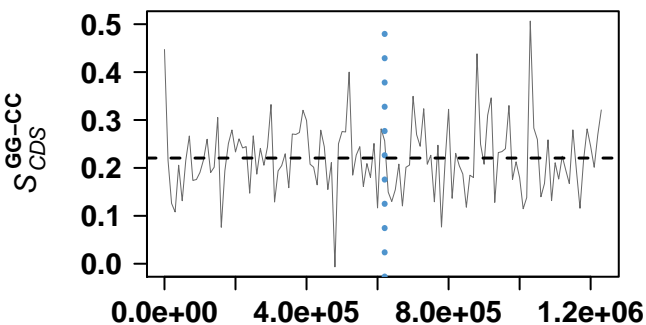
Rickettsia felis URRWXCa2



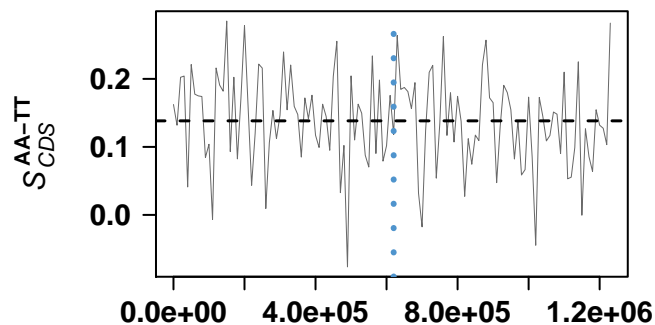
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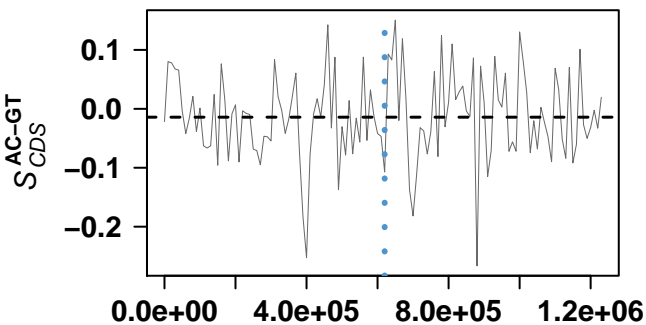
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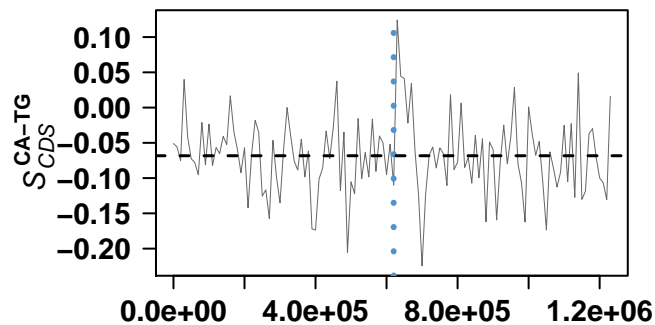
genome coordinates



genome coordinates

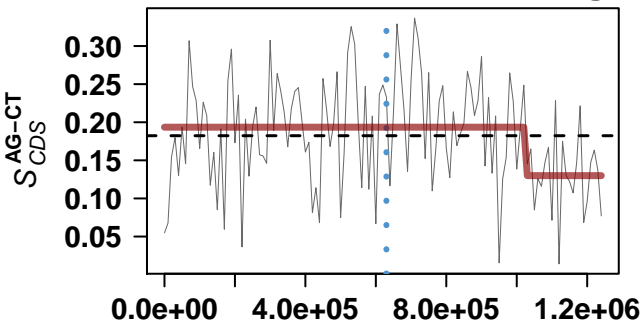


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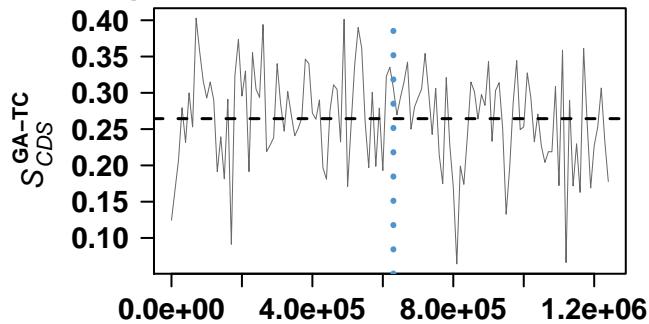


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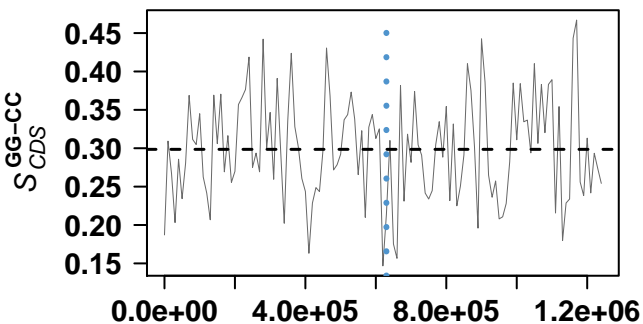
Candidatus Pelagibacter ubique HTCC1062



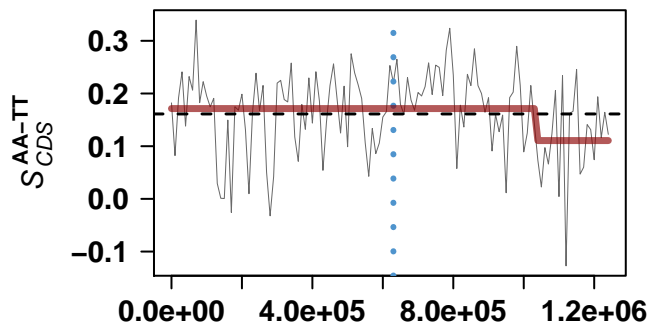
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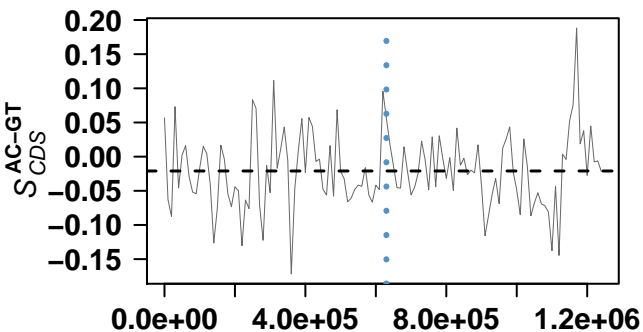
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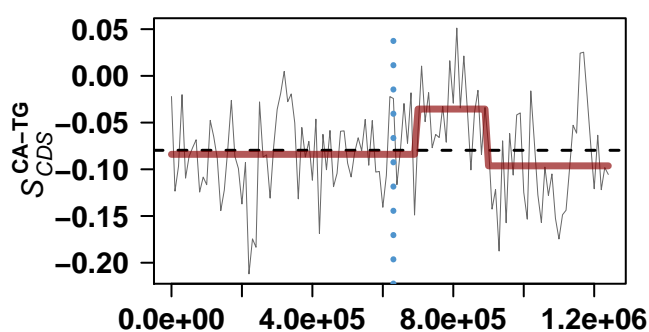
genome coordinates



genome coordinates

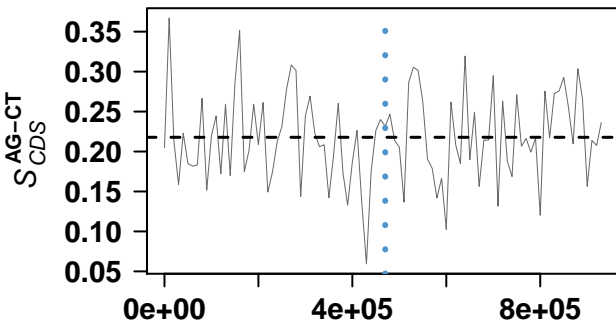


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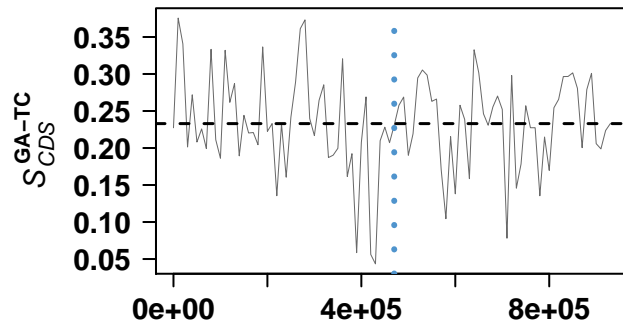


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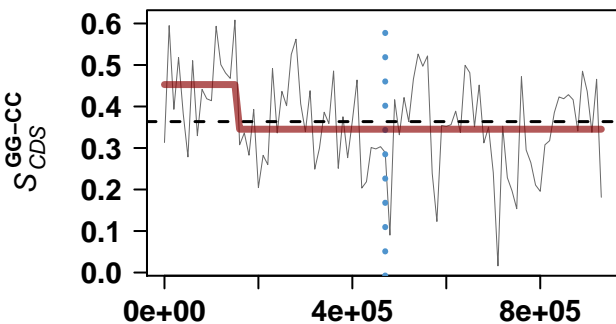
Ehrlichia canis str. Jake



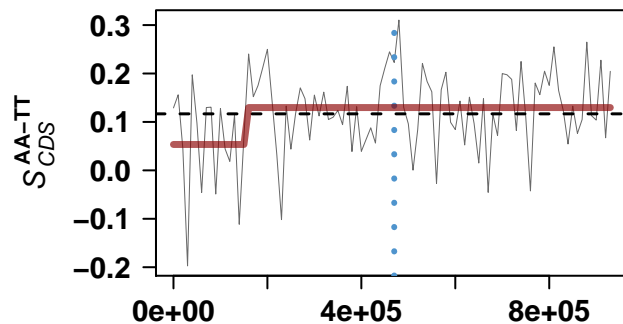
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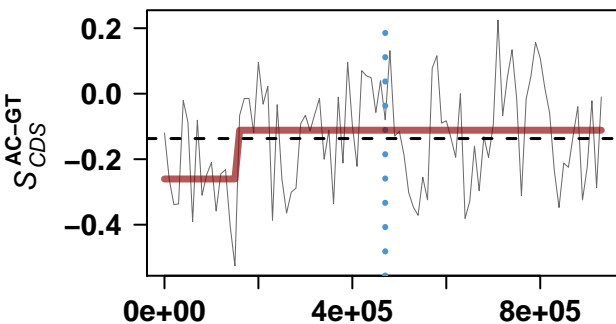
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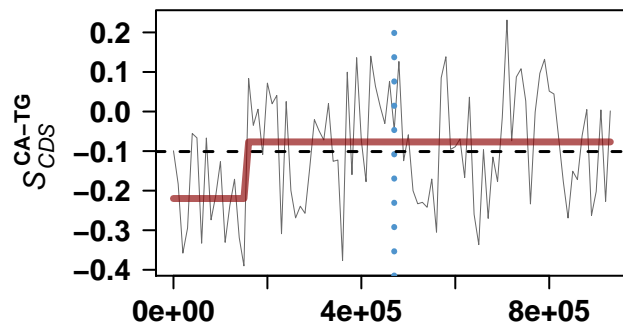
genome coordinates



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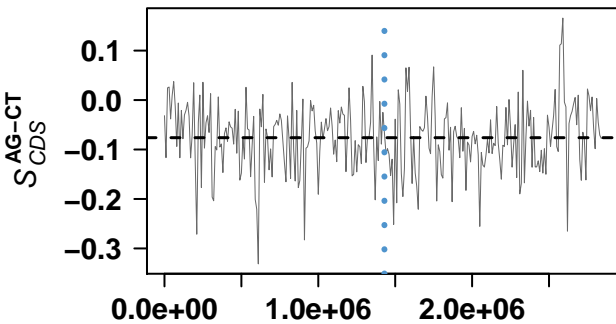


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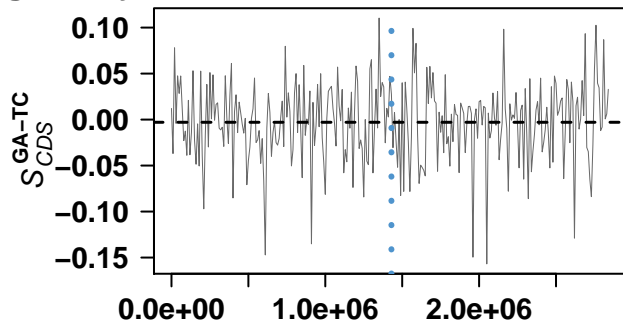


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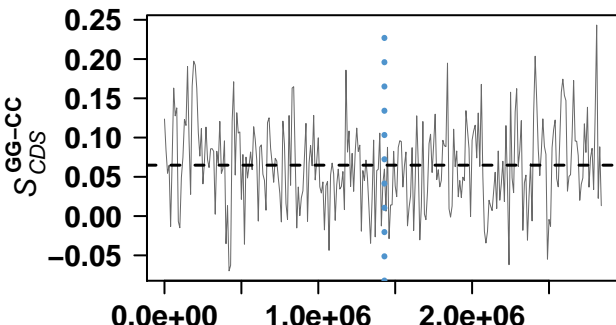
Nitrobacter winogradskyi Nb-255



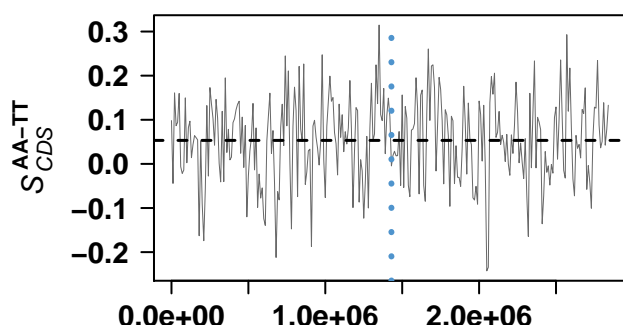
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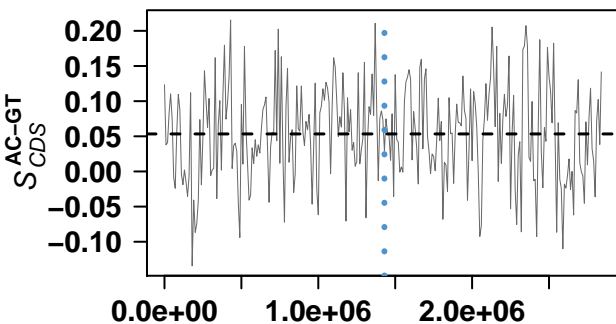
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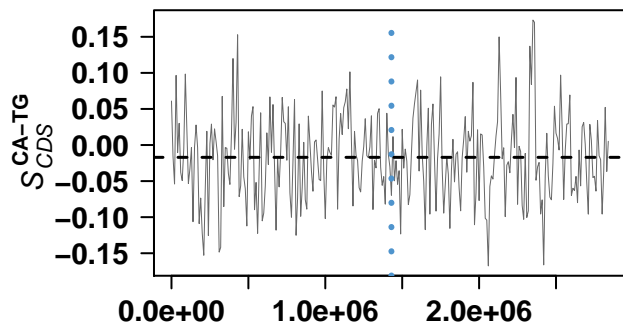
genome coordinates



genome coordinates

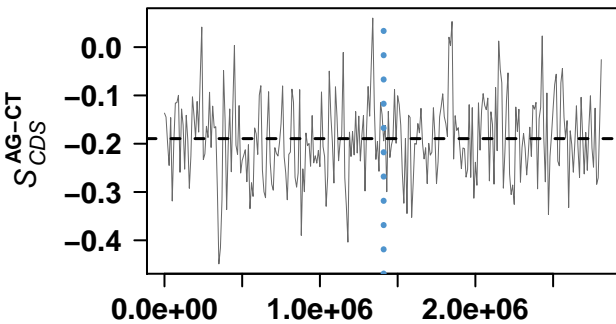


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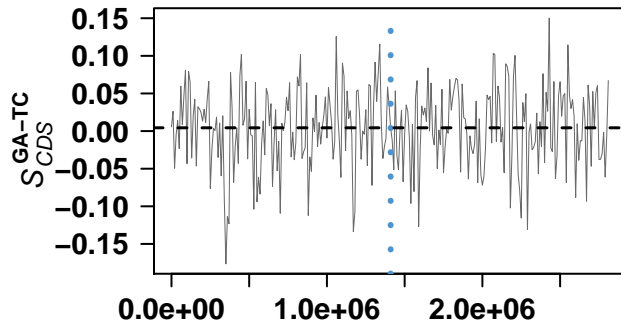


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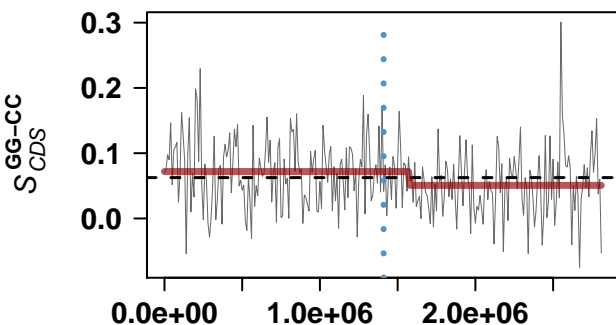
Rhodobacter sphaeroides 2.4.1



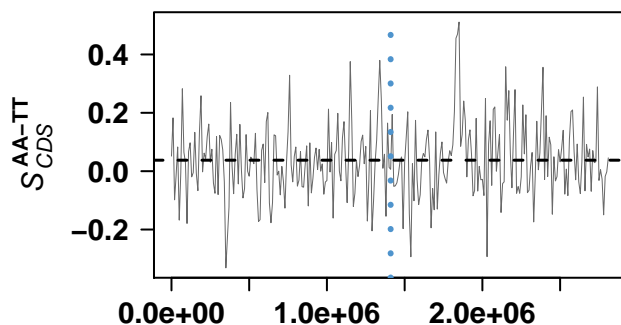
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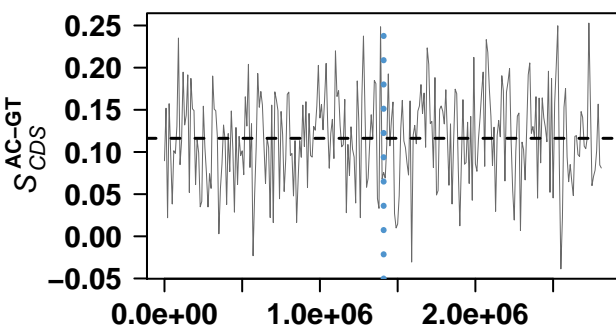
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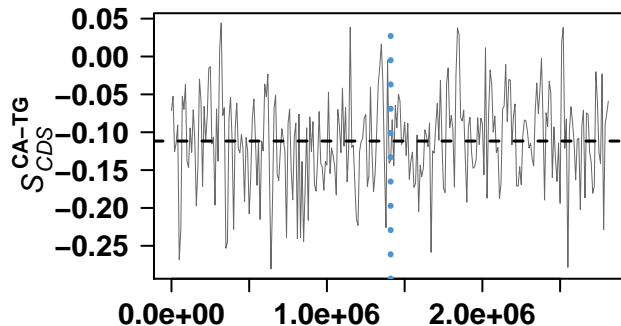
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genome coordinates

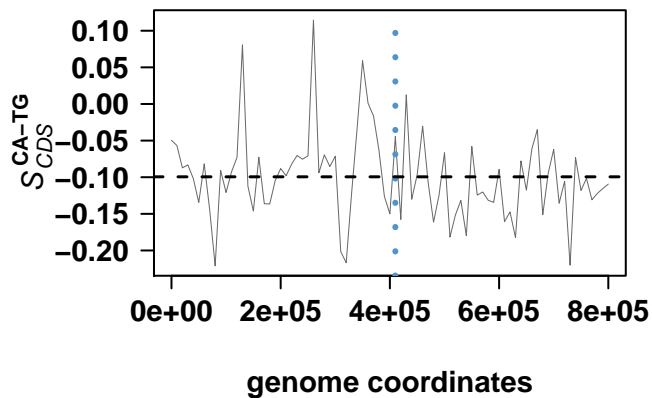
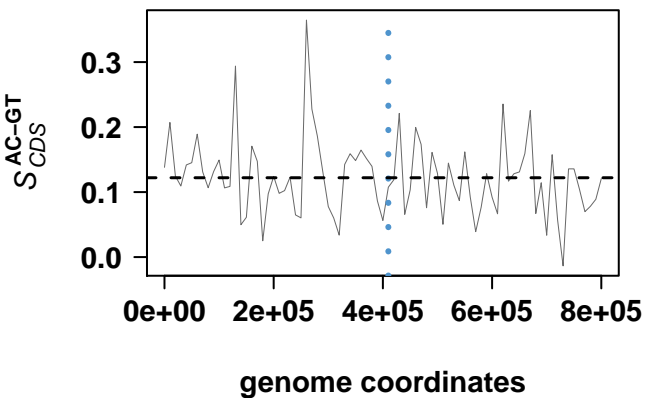
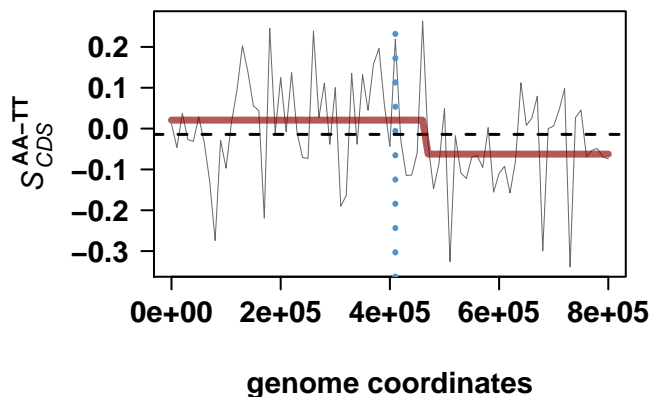
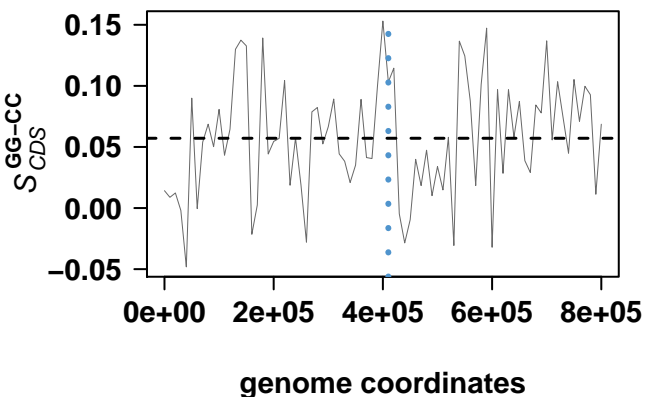
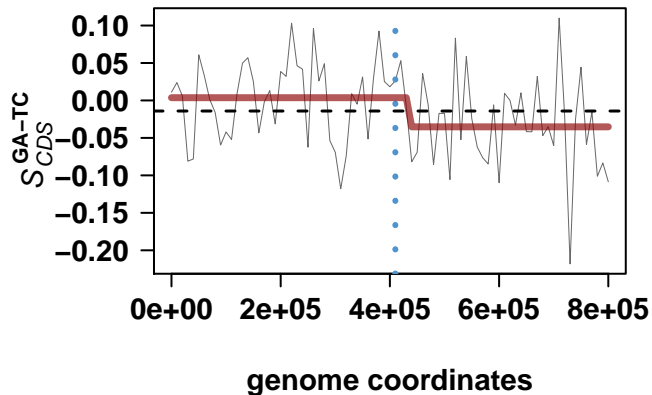
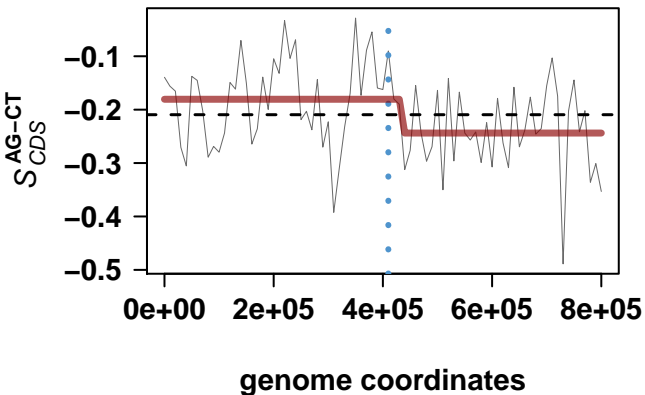


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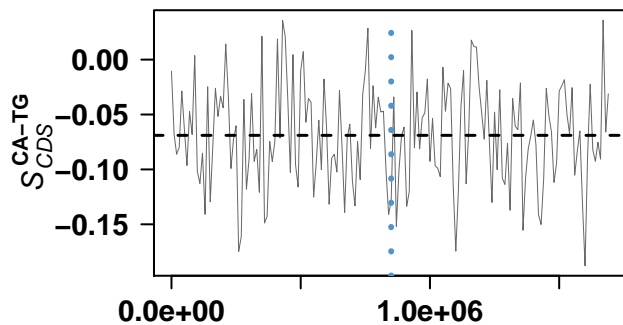
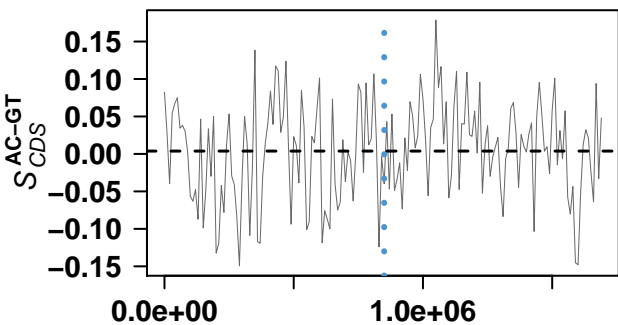
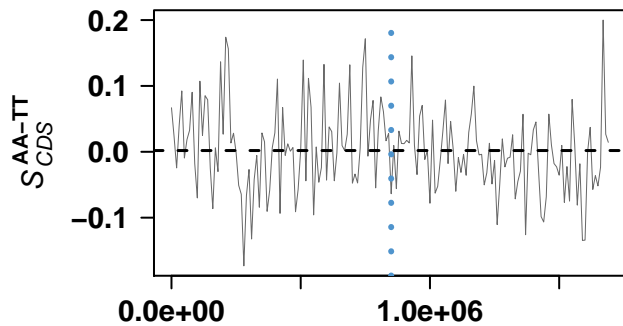
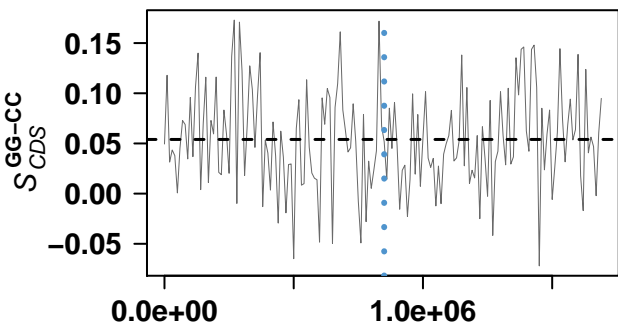
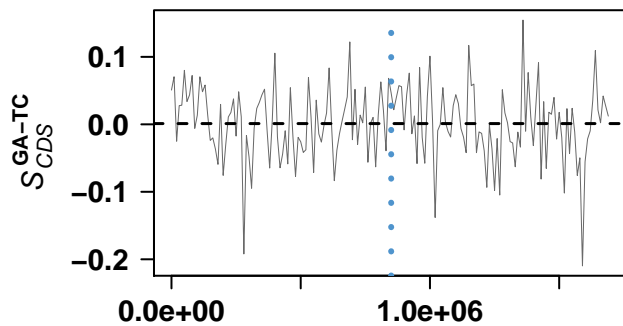
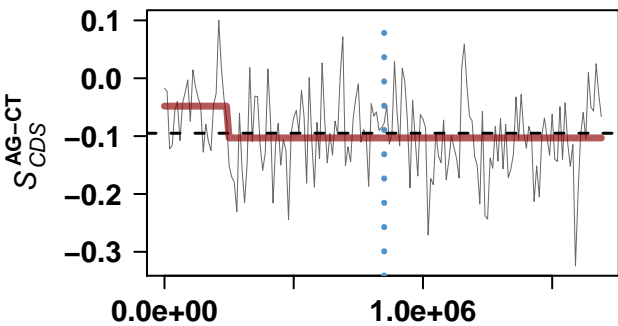


genome coordinates

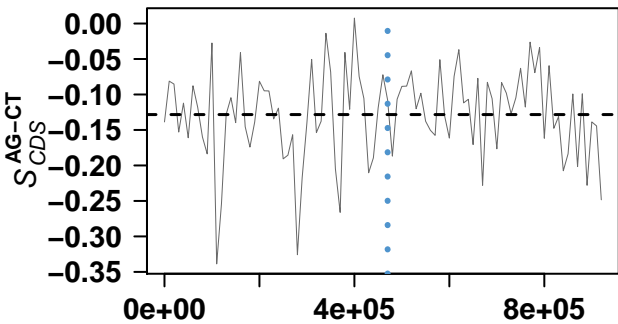
Rhodobacter sphaeroides 2.4.1



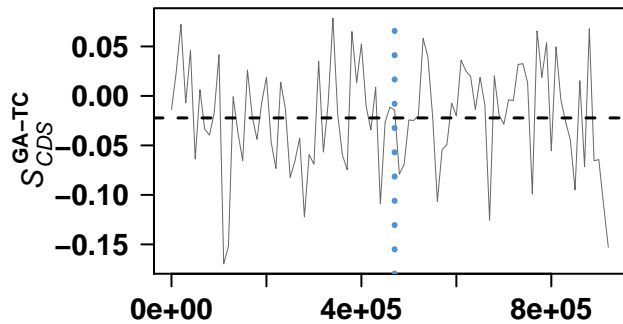
Brucella abortus 2308



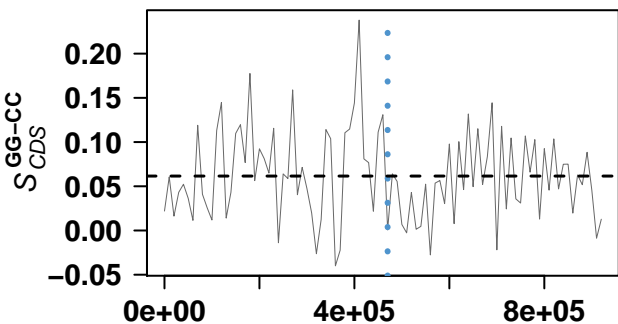
Brucella abortus 2308



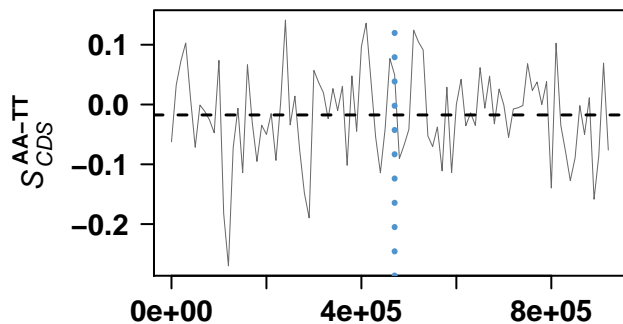
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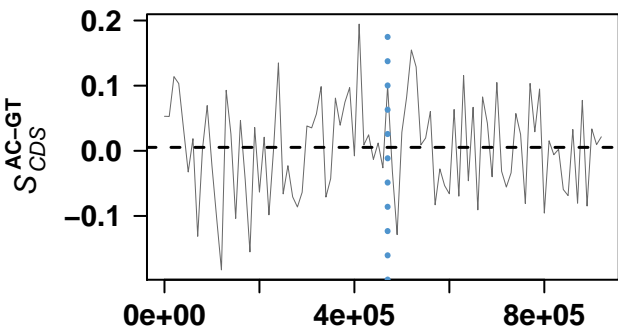
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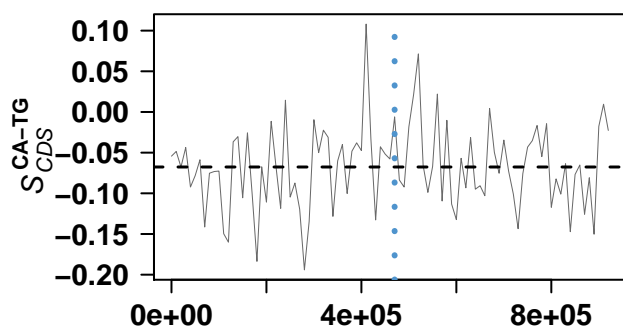
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genome coordinates

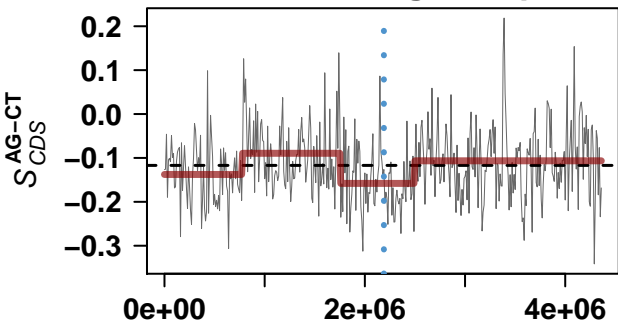


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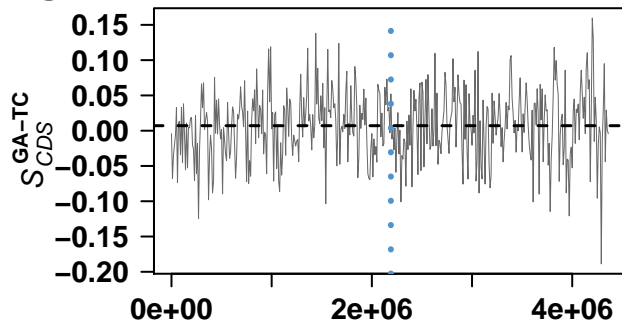


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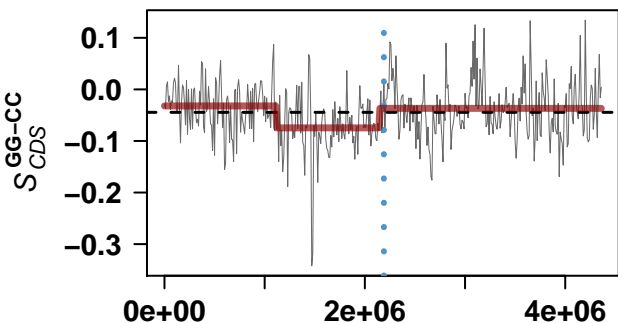
Magnetospirillum magneticum AMB-1



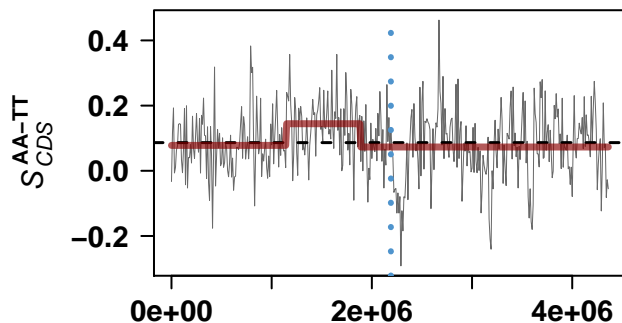
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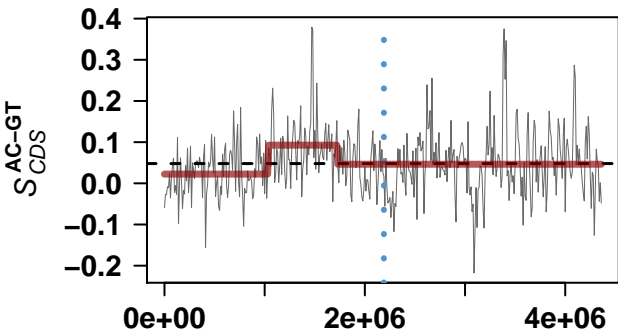
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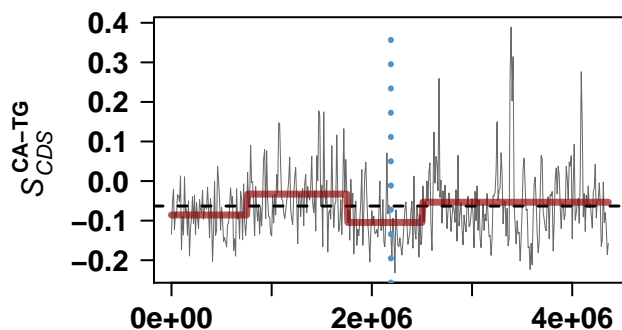
genome coordinates



genome coordinates

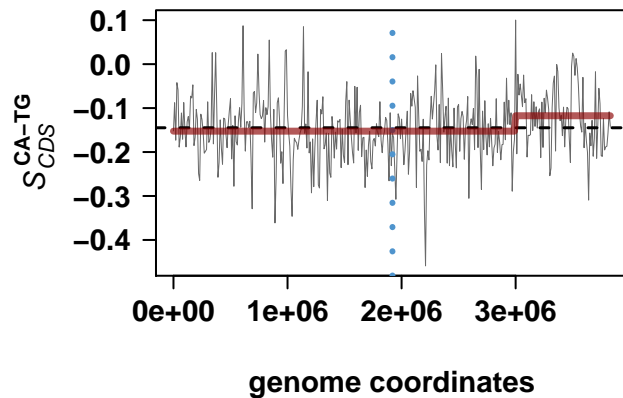
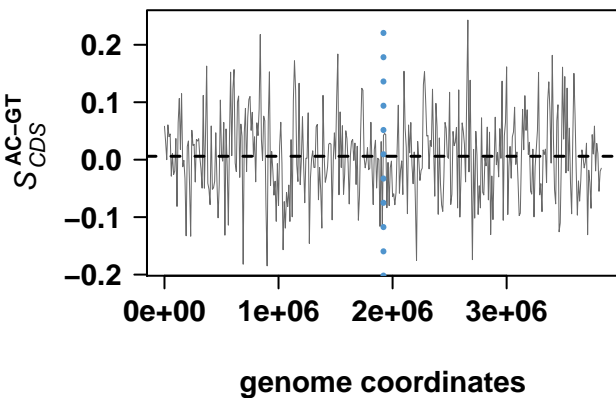
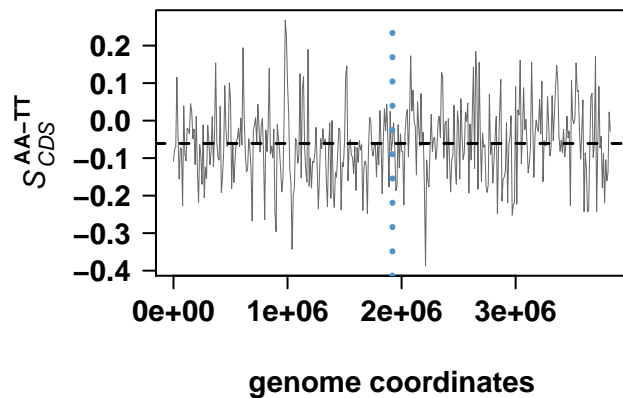
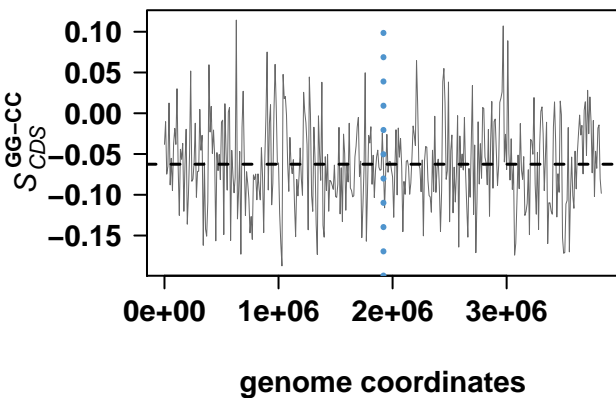
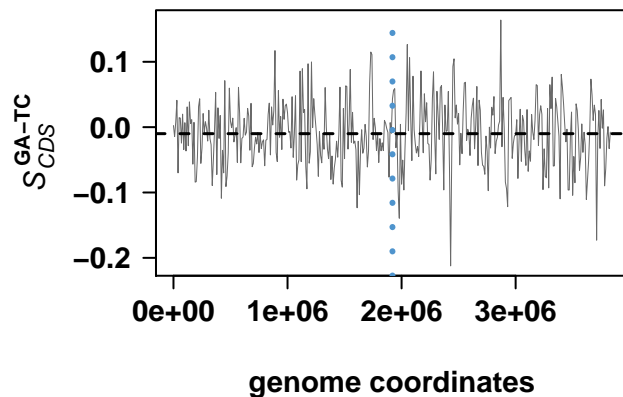
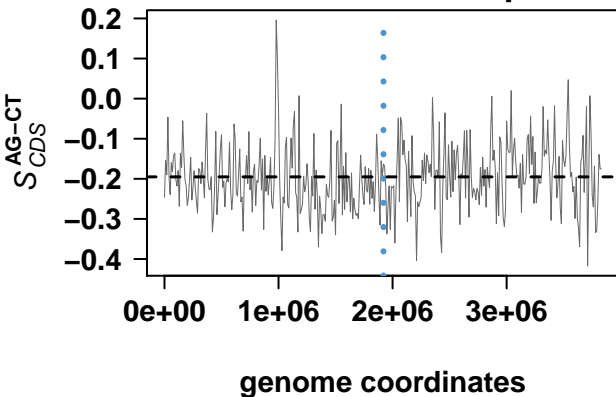


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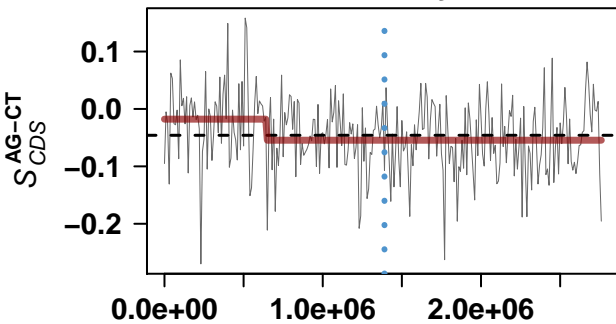


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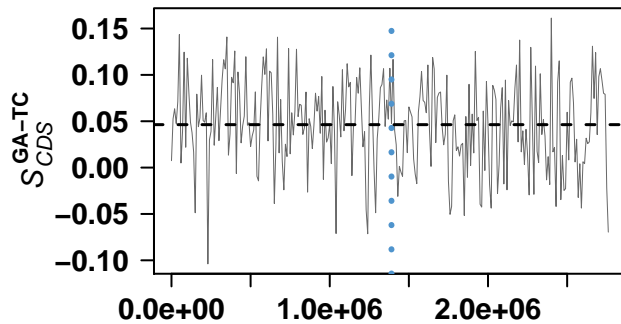
Rhodospirillum rubrum ATCC 11170



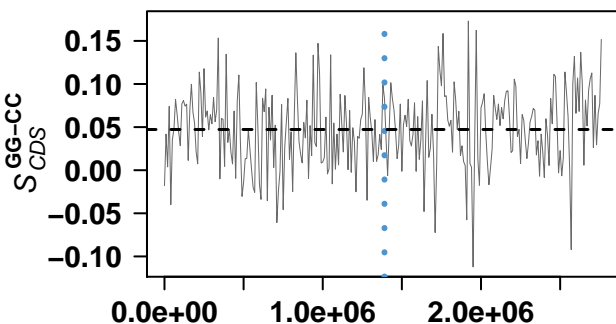
Erythrobacter litoralis HTCC2594



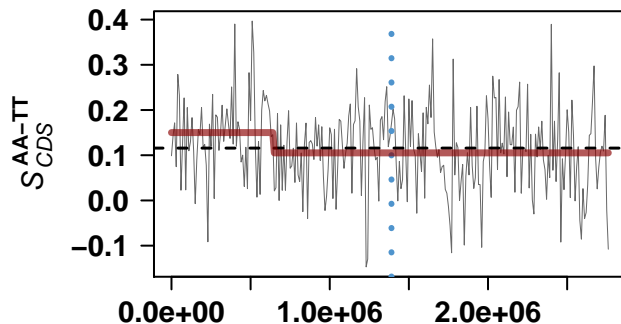
genome coordinates



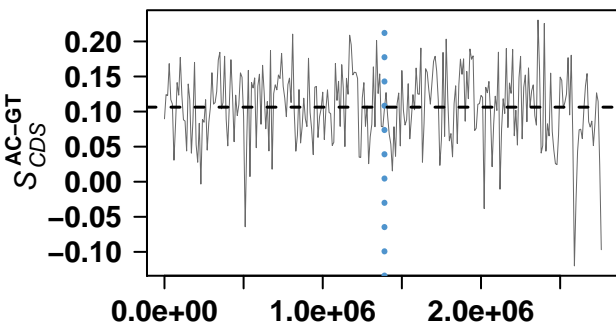
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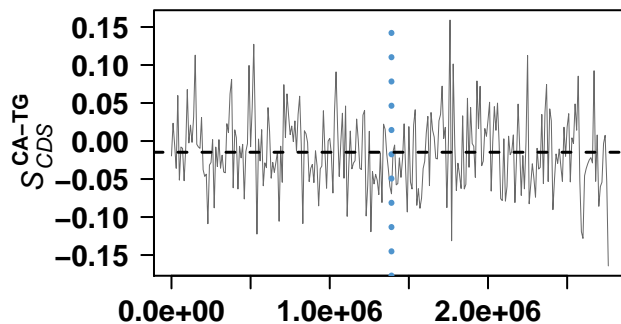
genome coordinates



genome coordinates

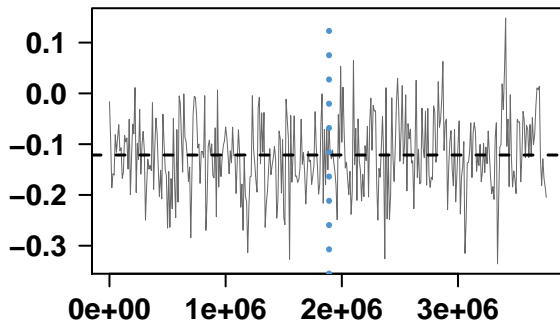


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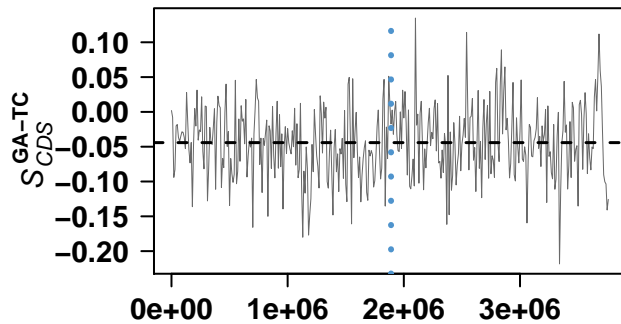


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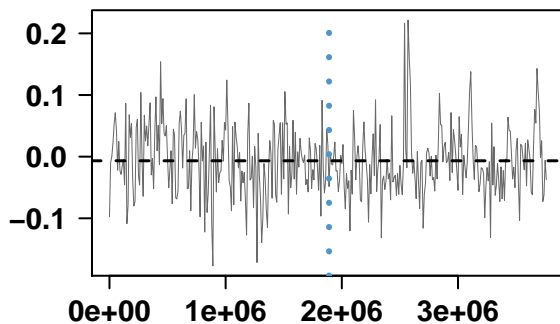
Rhizobium etli CFN 42



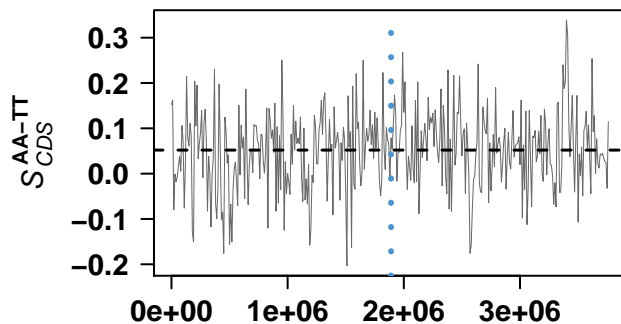
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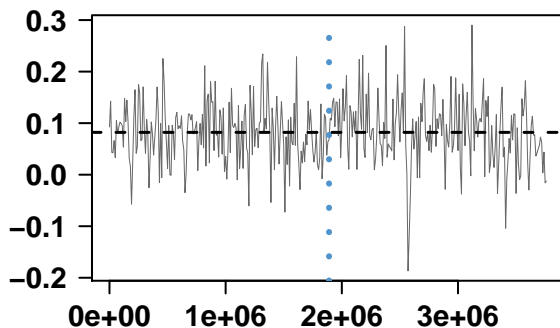
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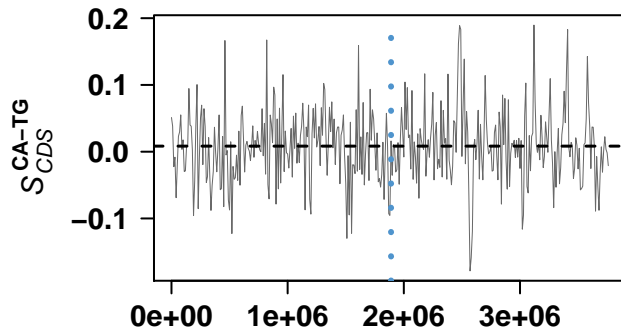
genome coordinates



genome coordinates

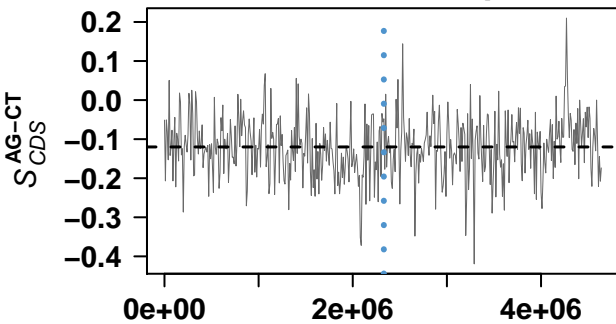


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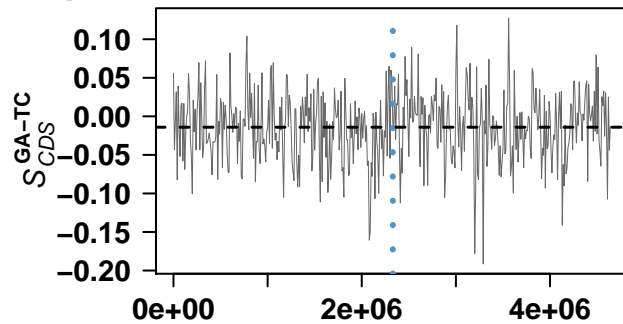


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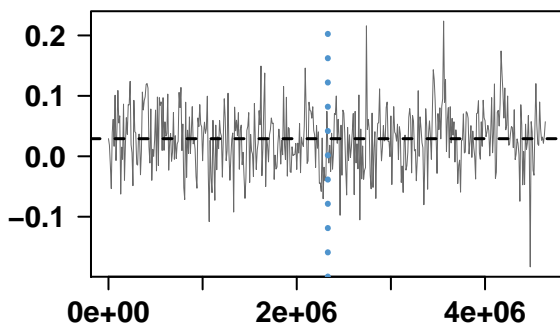
Rhodospseudomonas palustris HaA2



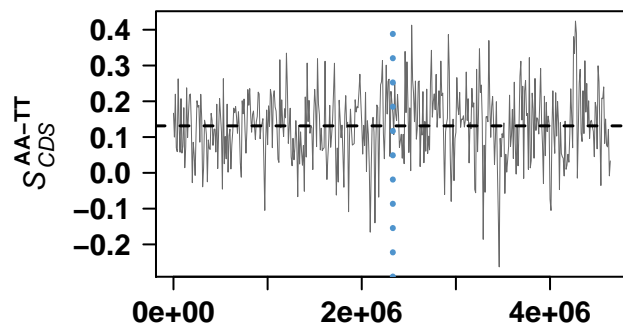
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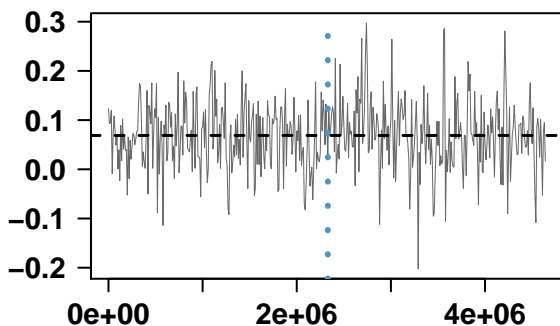
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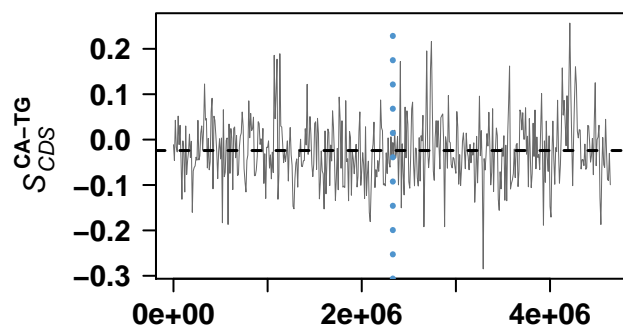
genome coordinates



genome coordinates

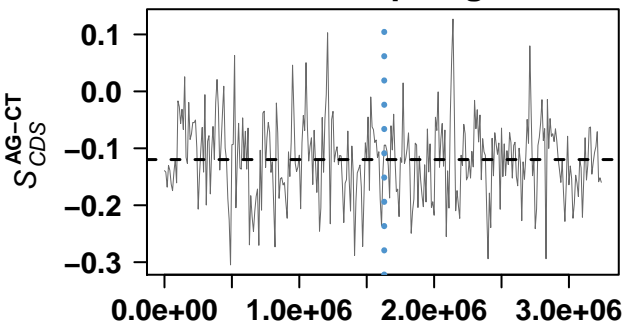


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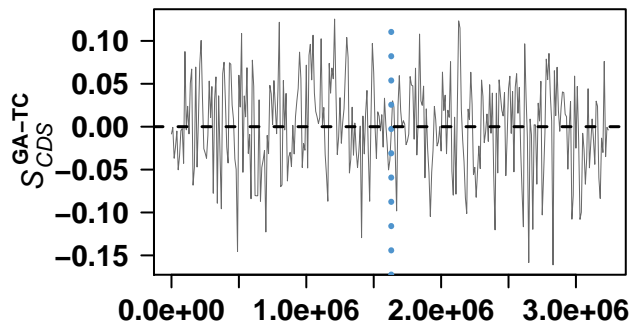


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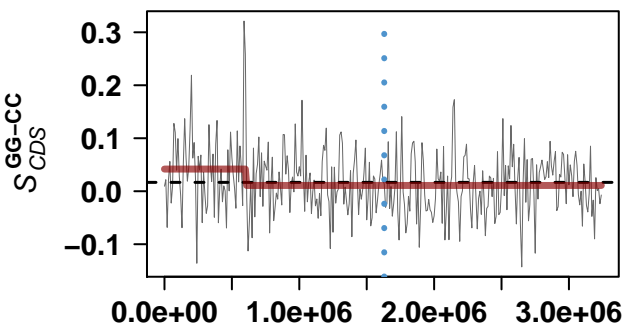
Novosphingobium aromaticivorans DSM 12444



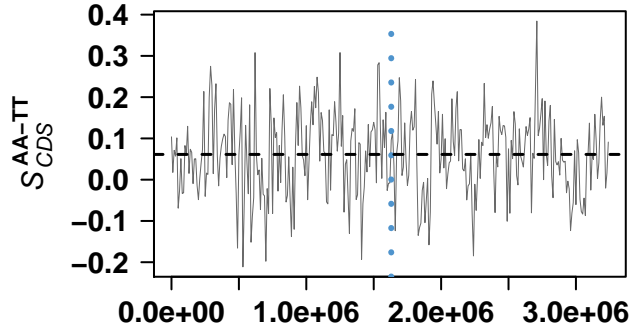
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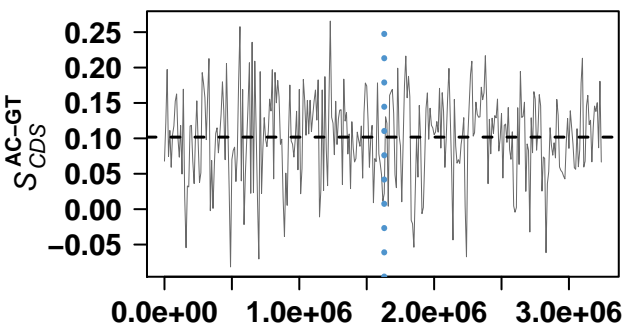
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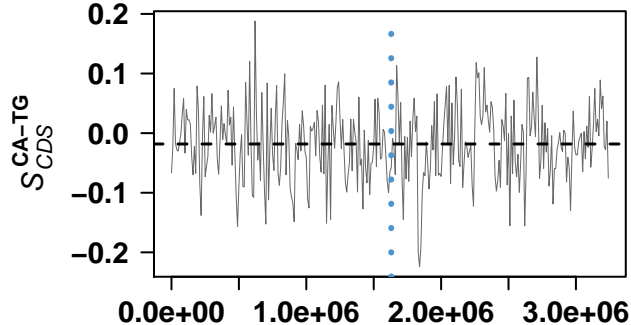
genome coordinates



genome coordinates

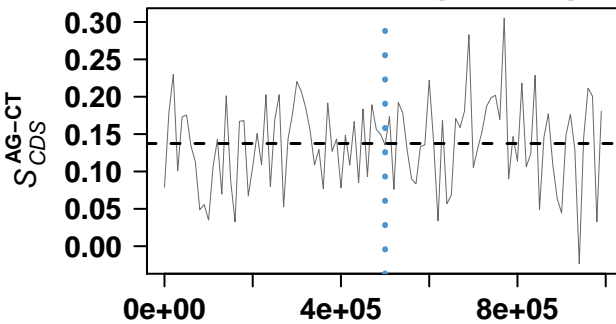


genome coordinates

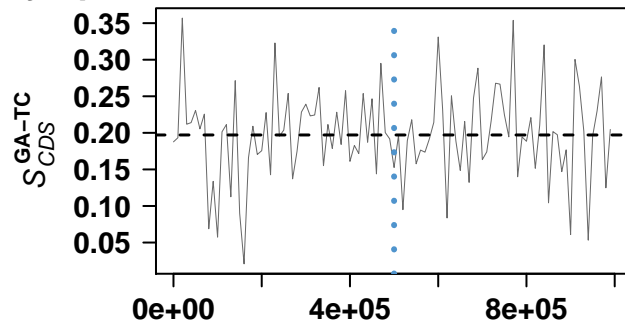


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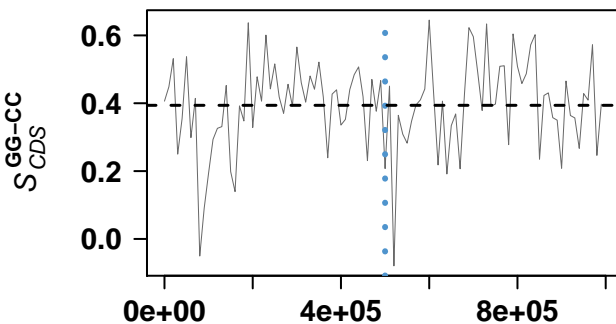
Anaplasma phagocytophilum str. HZ



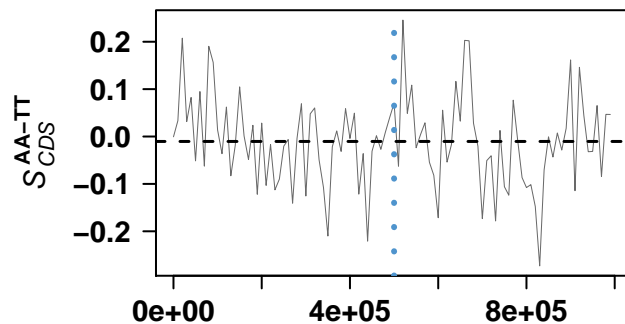
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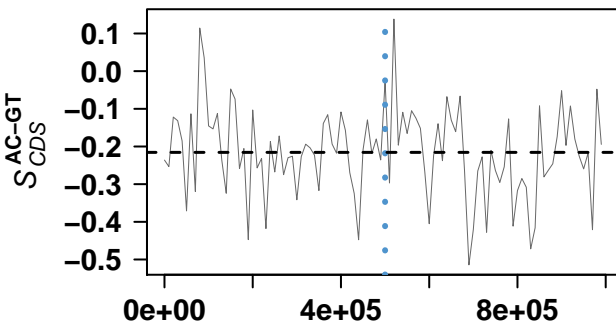
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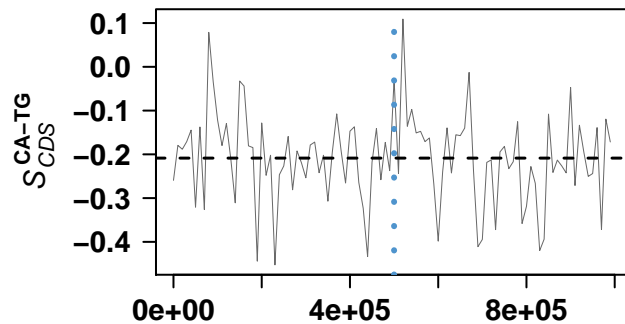
genome coordinates



genome coordinates

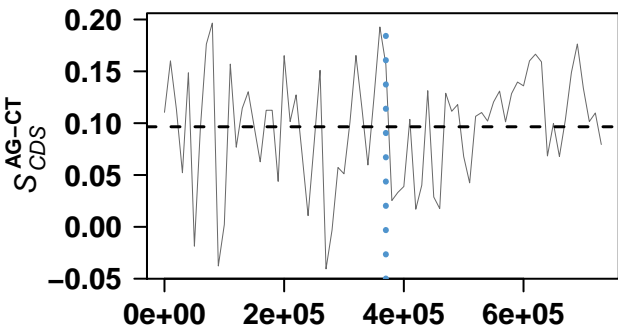


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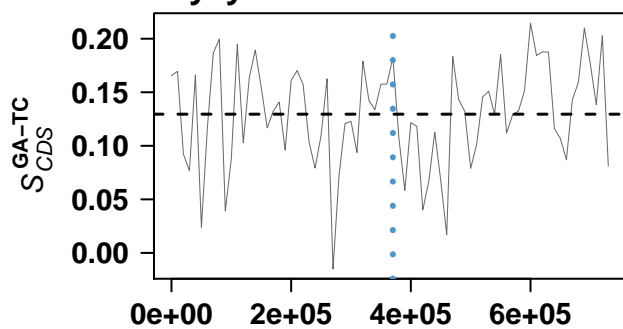


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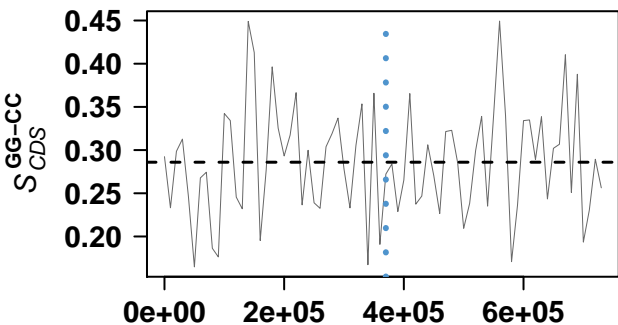
Neorickettsia sennetsu str. Miyayama



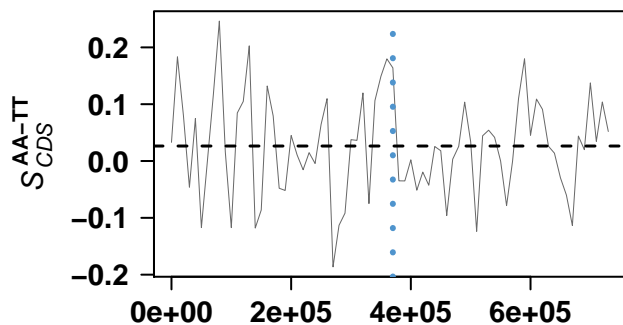
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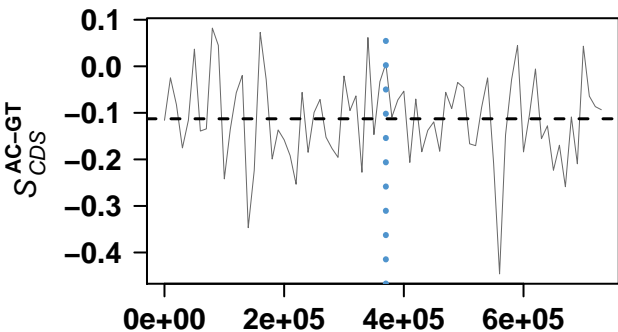
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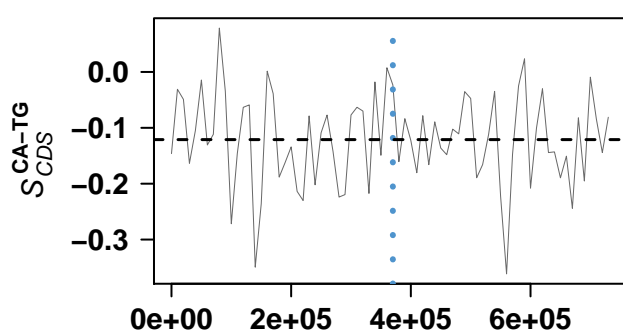
genome coordinates



genome coordinates

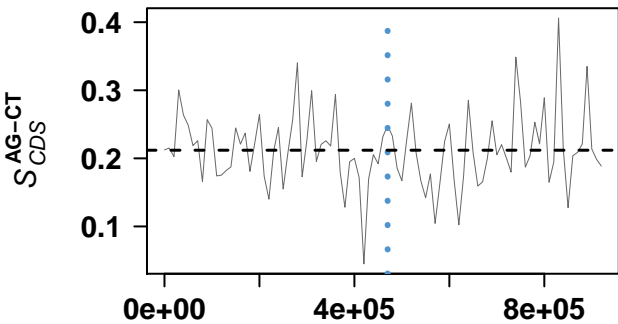


genome coordinates

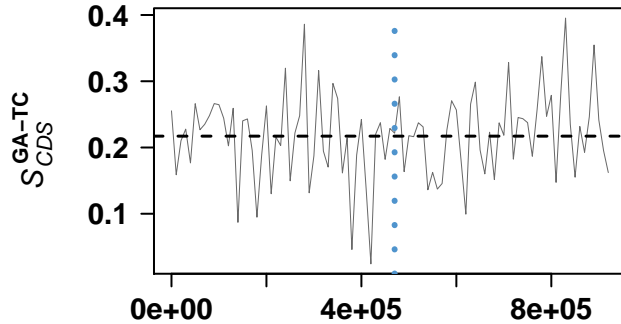


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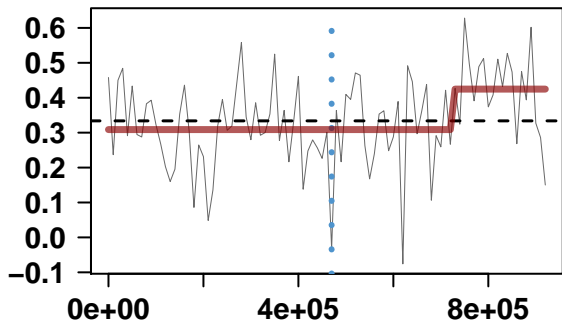
Ehrlichia chaffeensis str. Arkansas



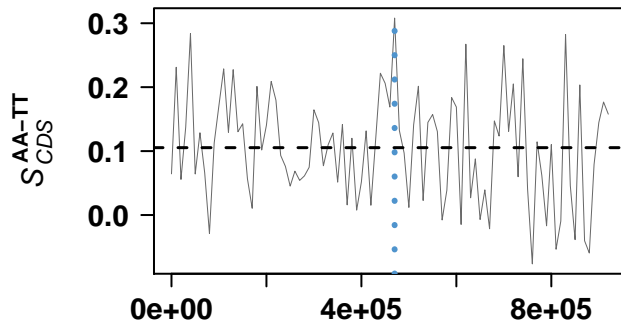
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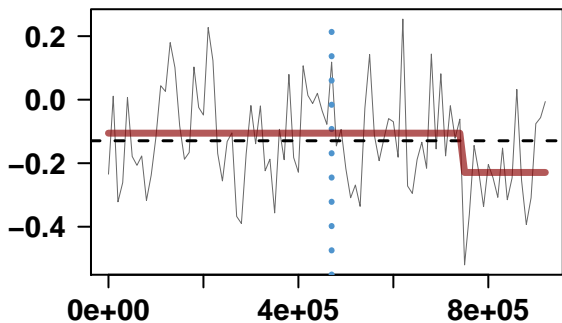
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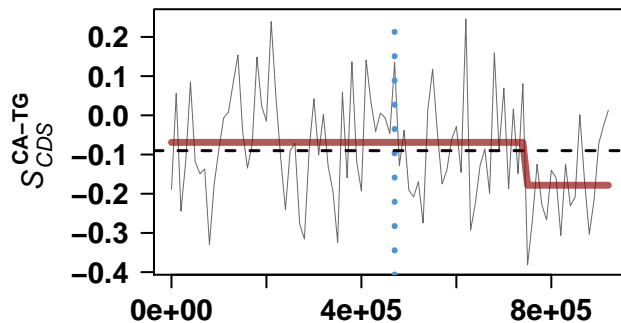
genome coordinates



genome coordinates

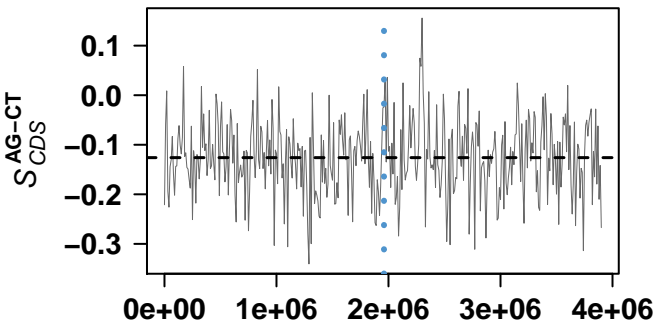


genome coordinates

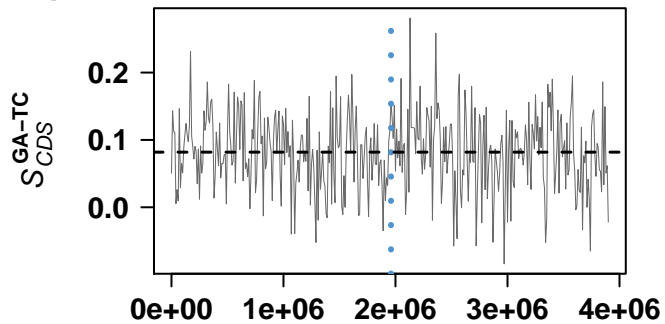


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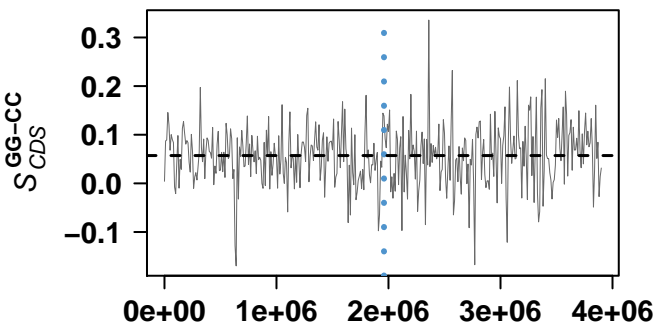
Jannaschia sp. CCS1



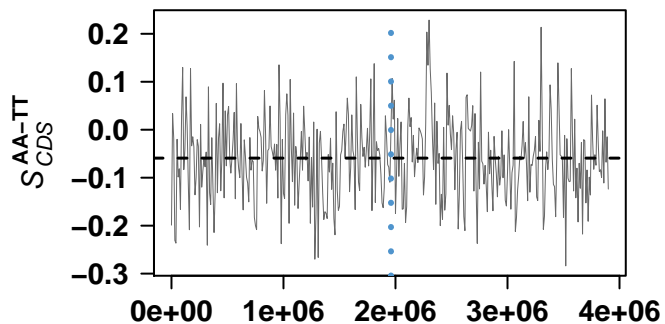
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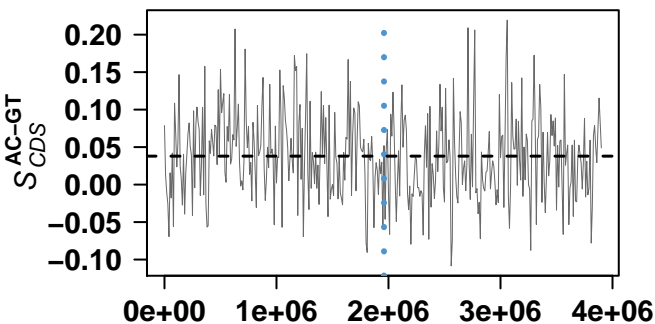
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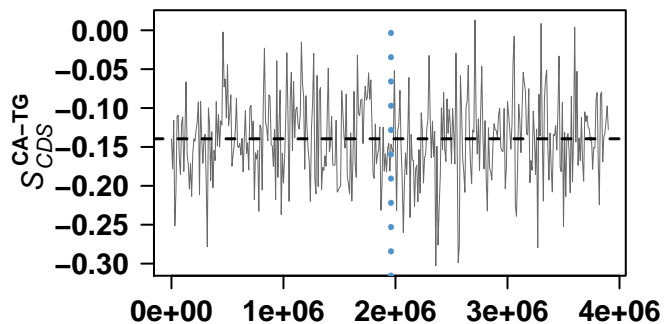
genome coordinates



genome coordinates

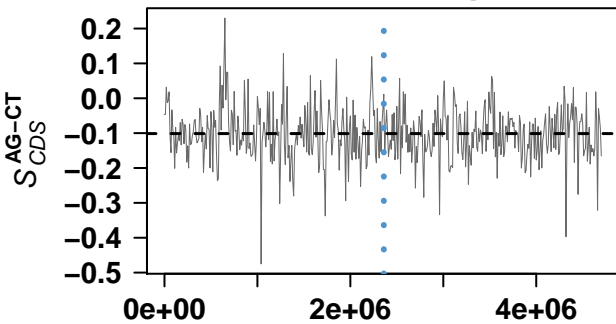


genome coordinates

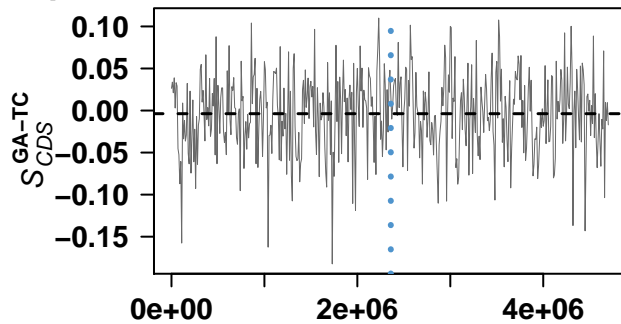


genome coordinates

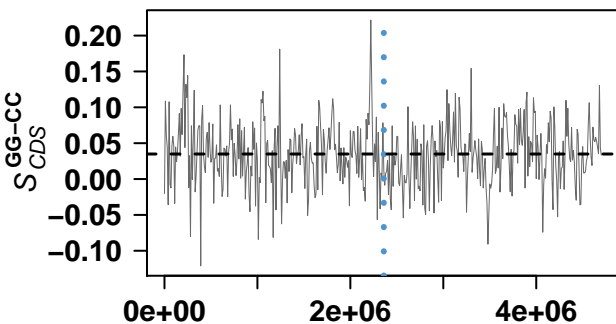
Rhodopseudomonas palustris BisB18



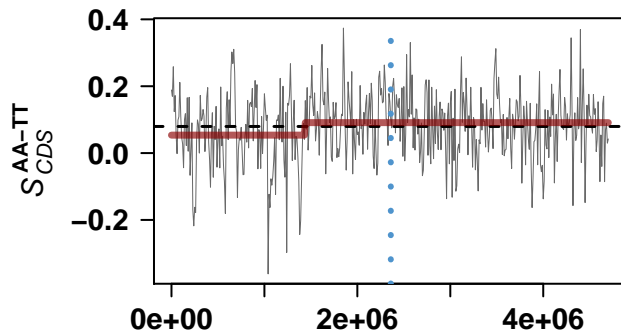
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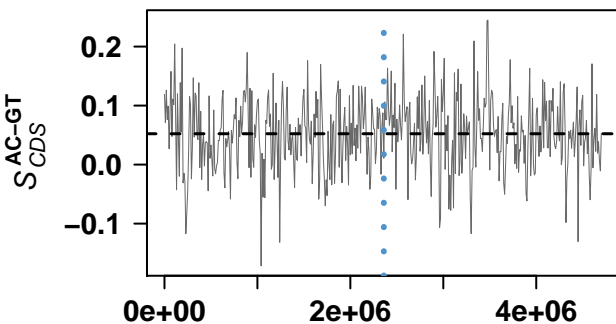
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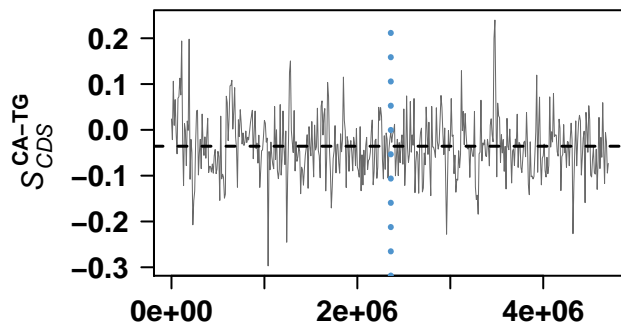
genome coordinates



genome coordinates

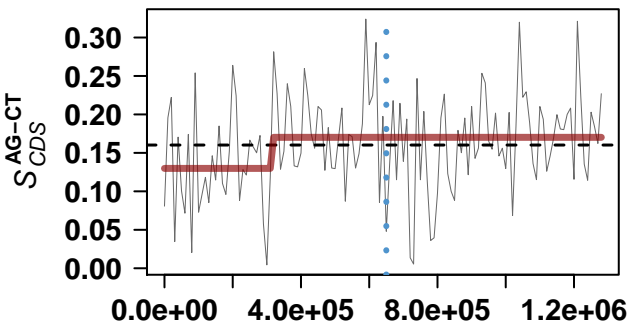


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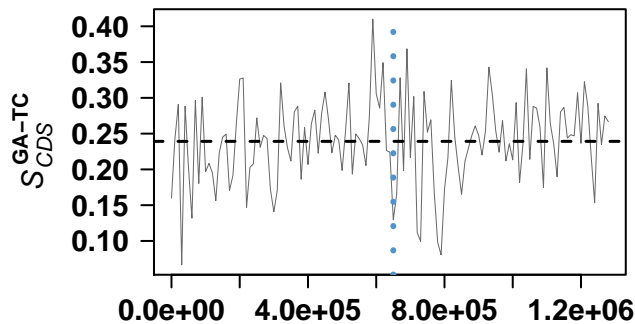


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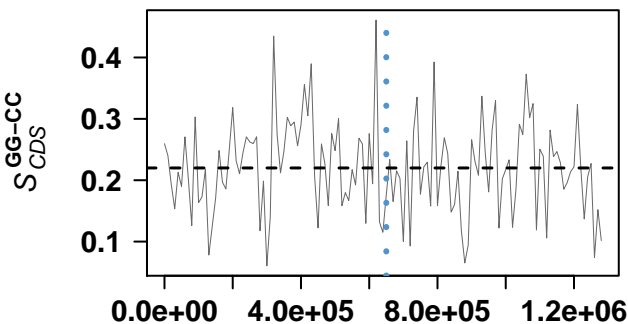
Rickettsia bellii RML369-C



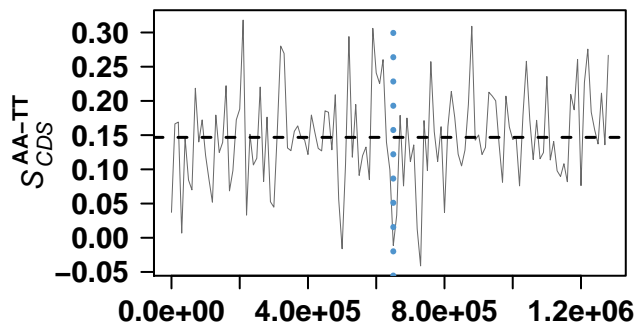
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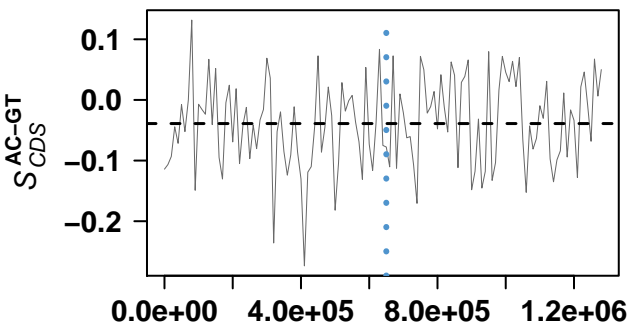
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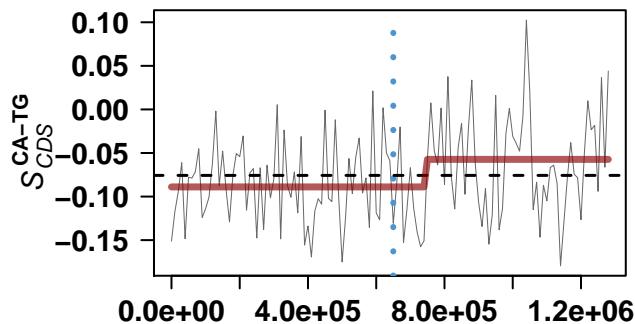
genome coordinates



genome coordinates

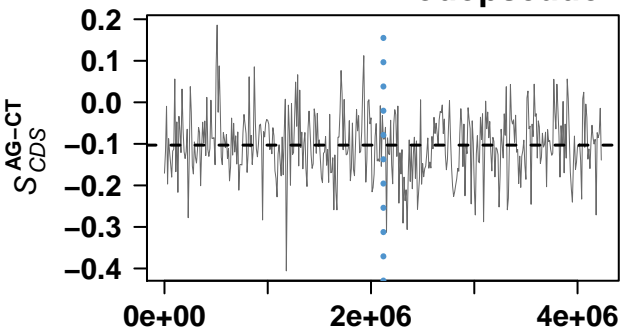


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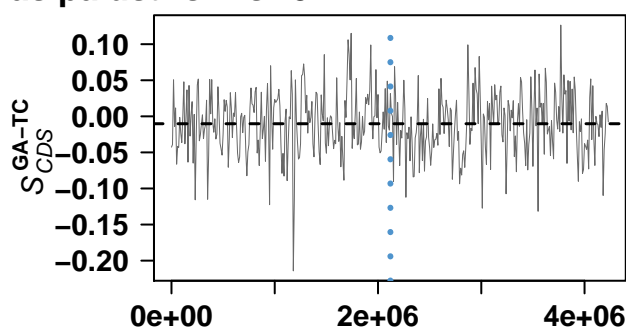


genome coordinates

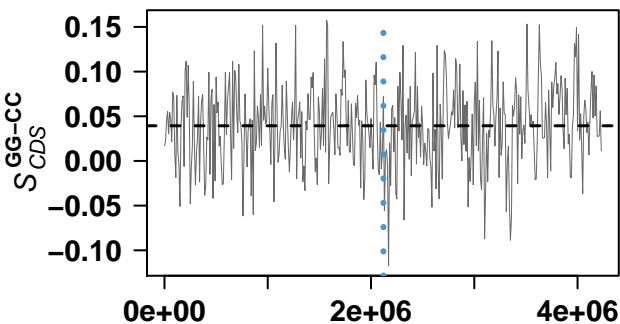
Rhodopseudomonas palustris BisB5



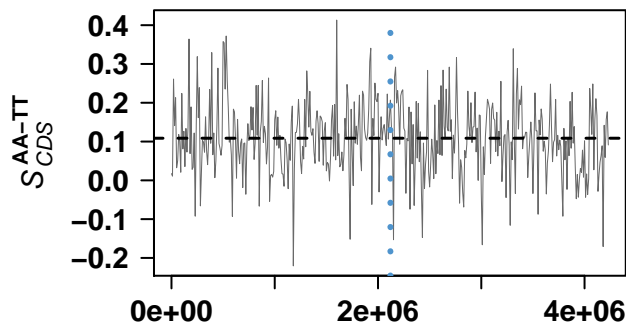
genome coordinates



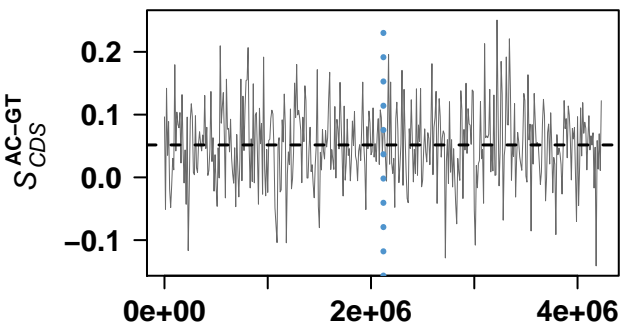
genome coordinates



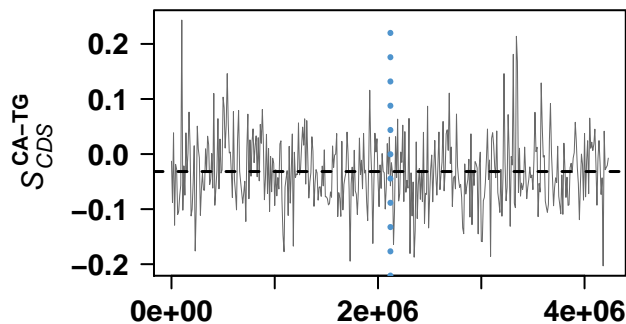
genome coordinates



genome coordinates

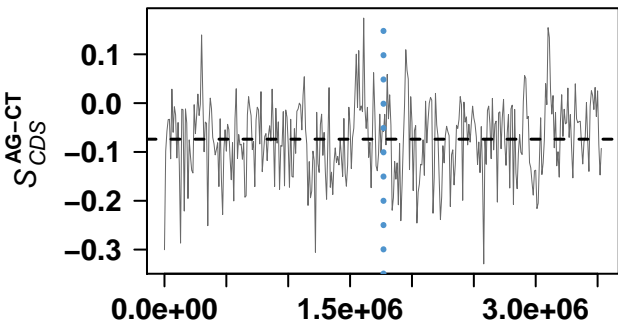


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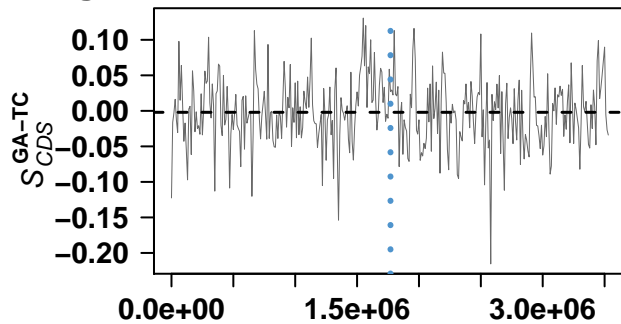


genome coordinates

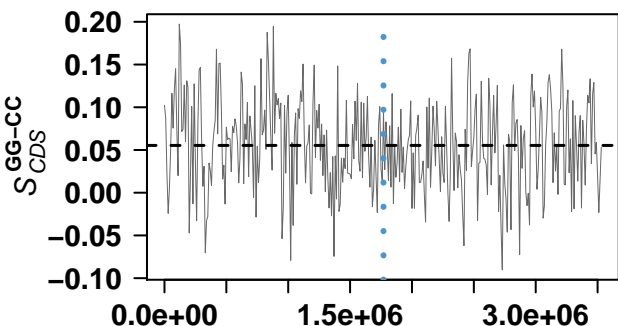
Nitrobacter hamburgensis X14



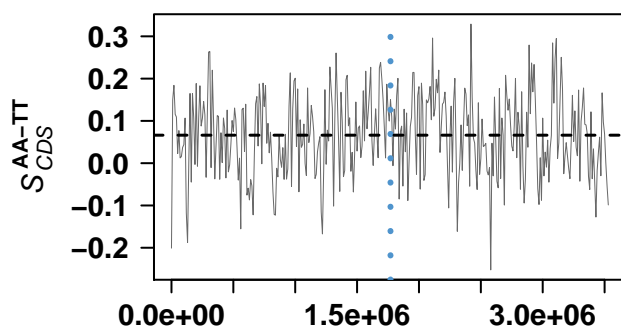
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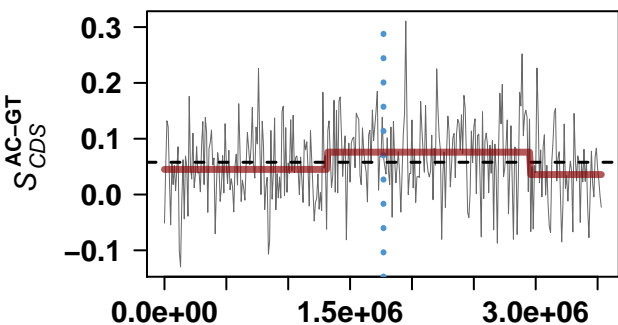
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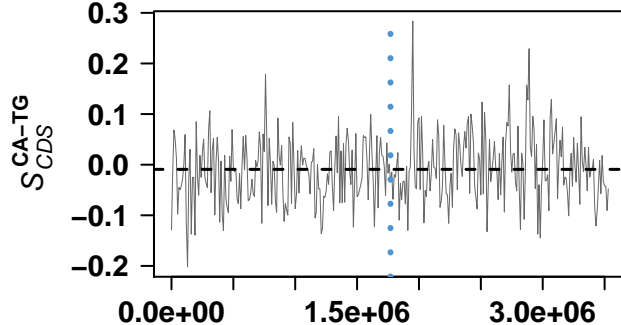
genome coordinates



genome coordinates

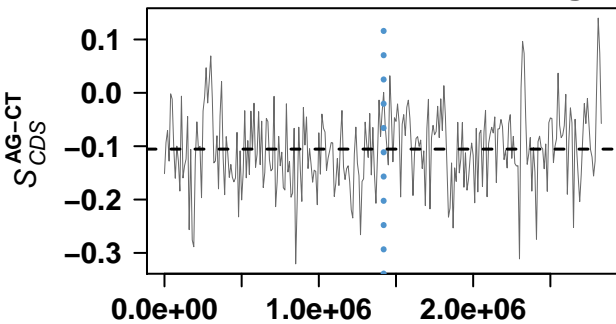


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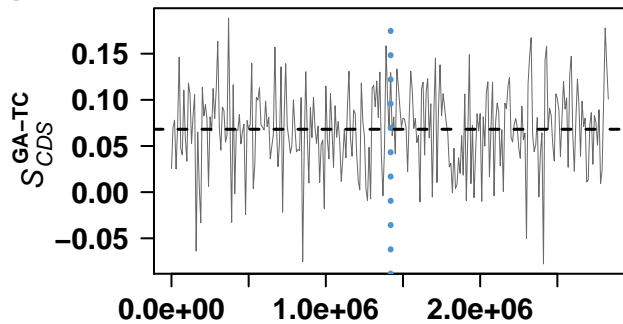


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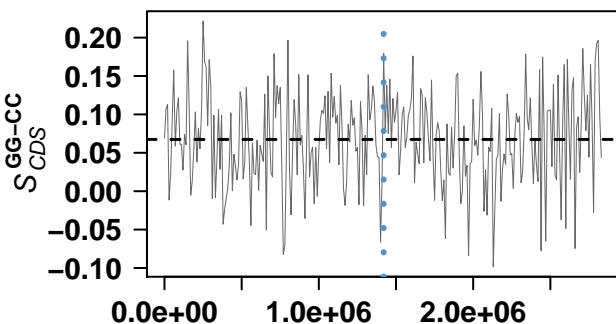
Ruegeria sp. TM1040



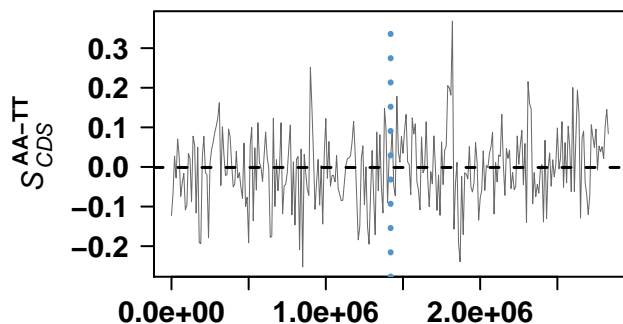
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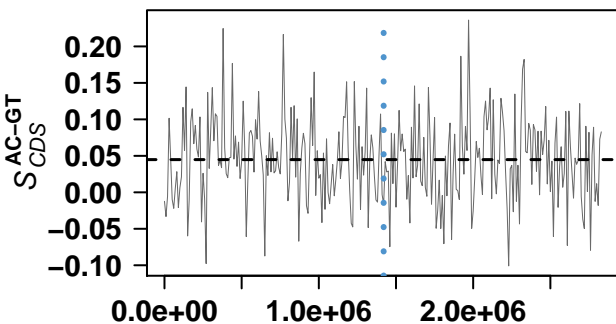
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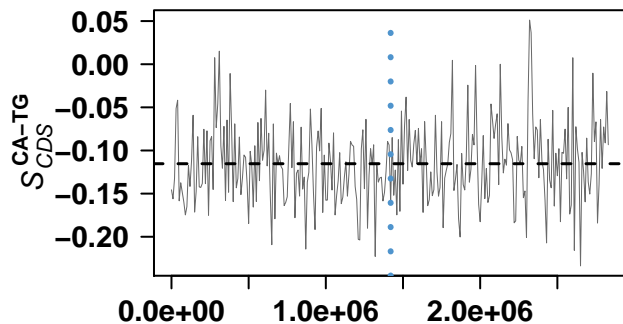
genome coordinates



genome coordinates

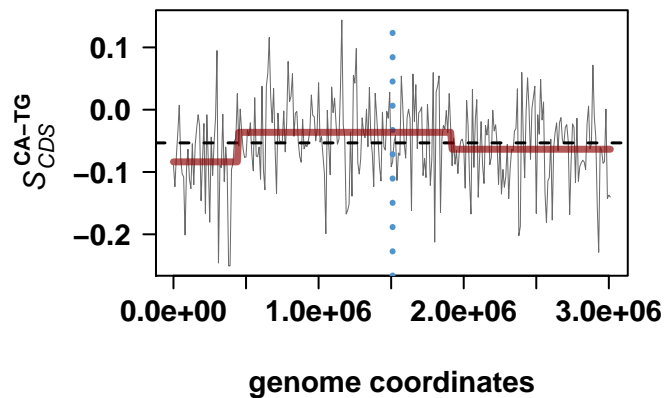
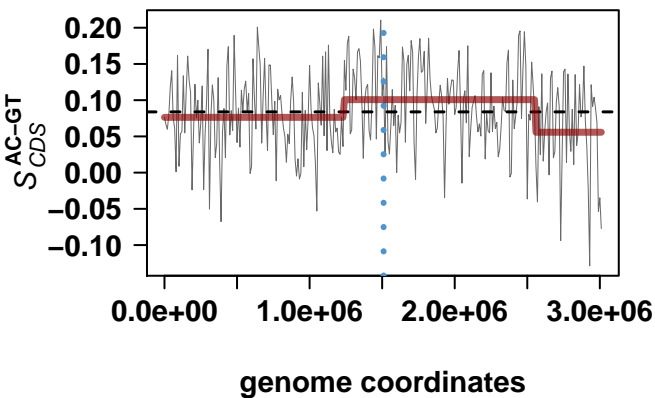
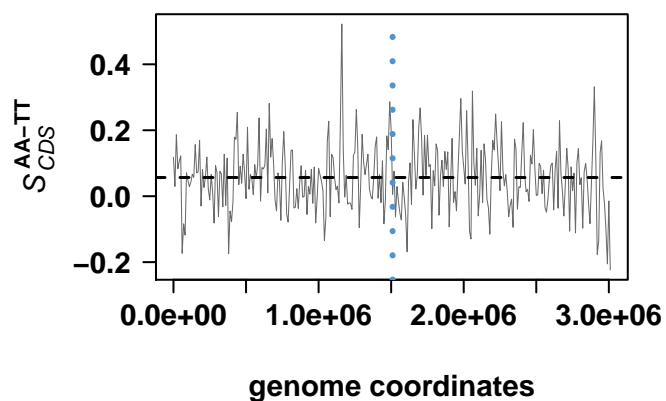
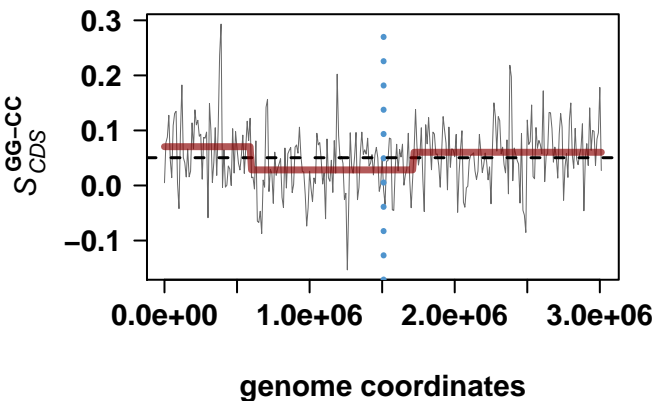
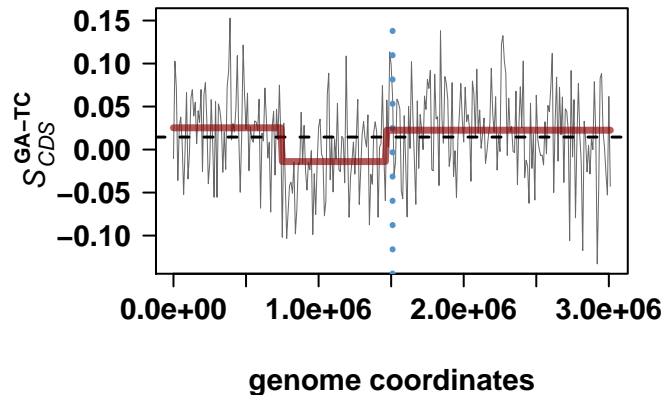
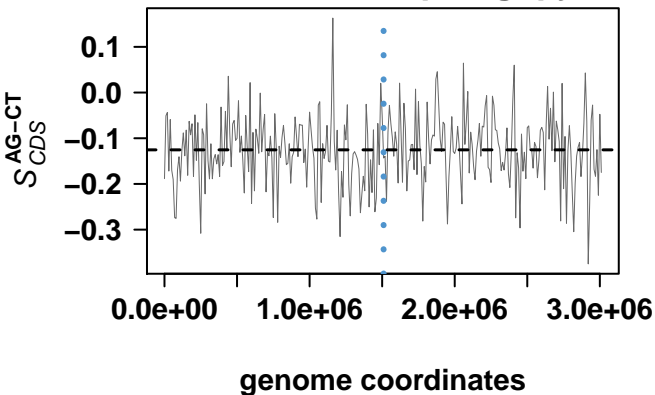


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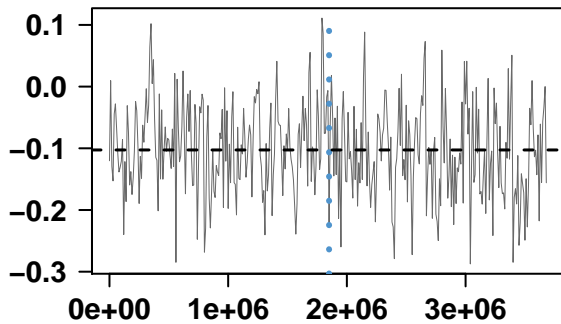


genome coordinates

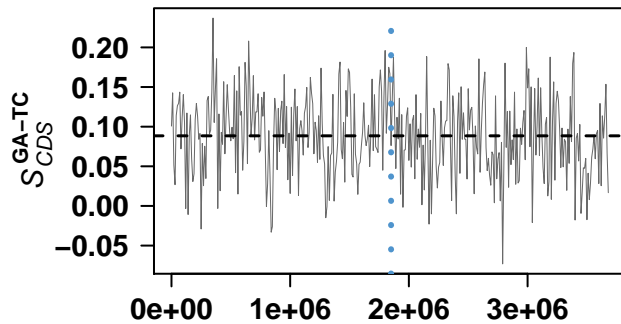
Spingopyxis alaskensis RB2256



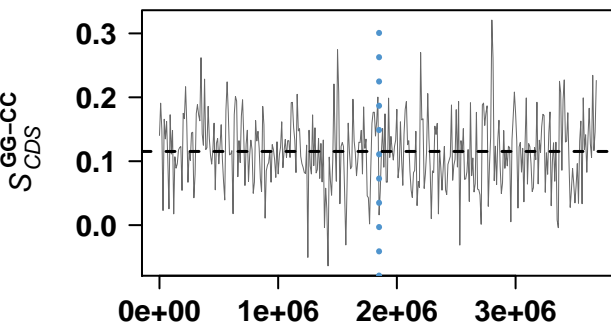
Roseobacter denitrificans OCh 114



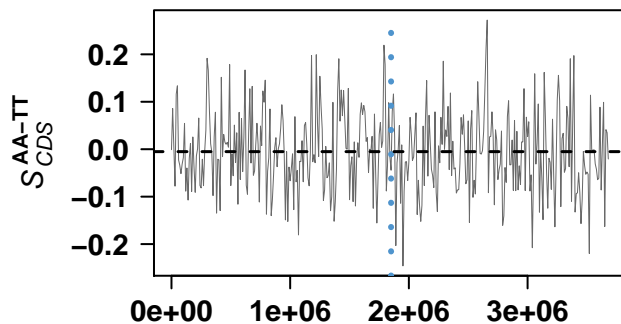
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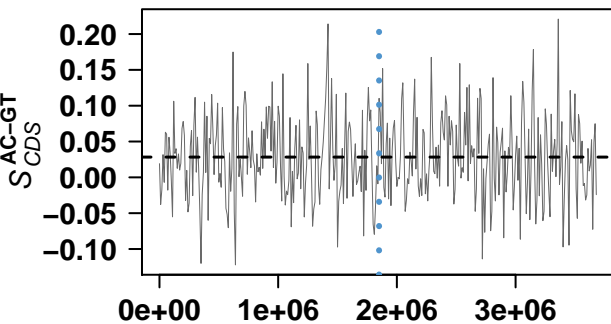
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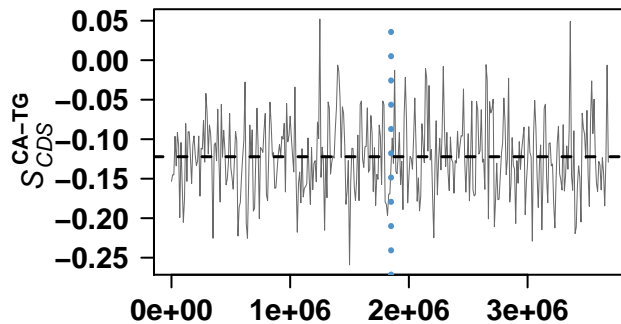
genome coordinates



genome coordinates

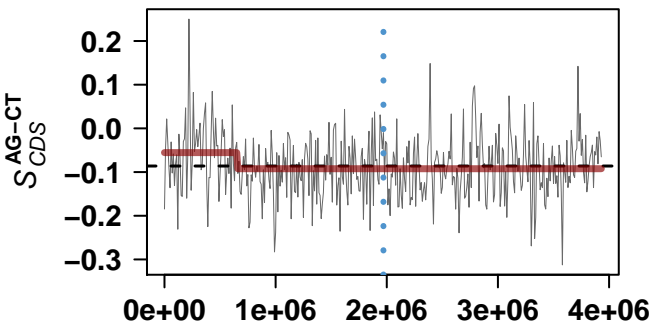


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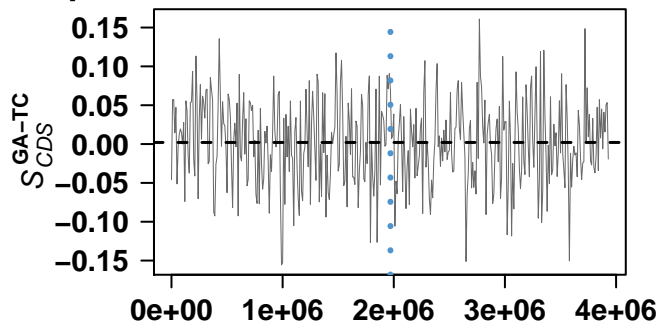


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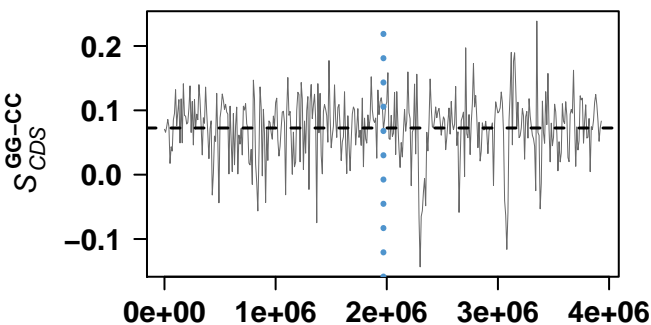
Chelativorans sp. BNC1



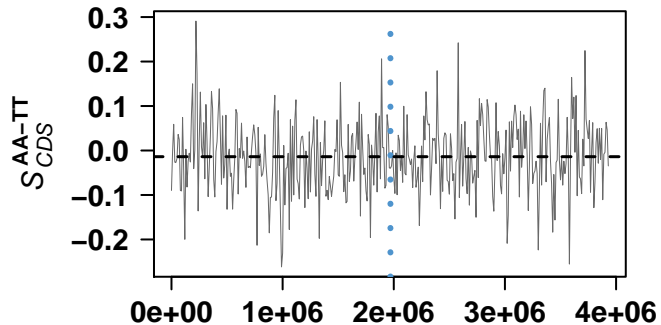
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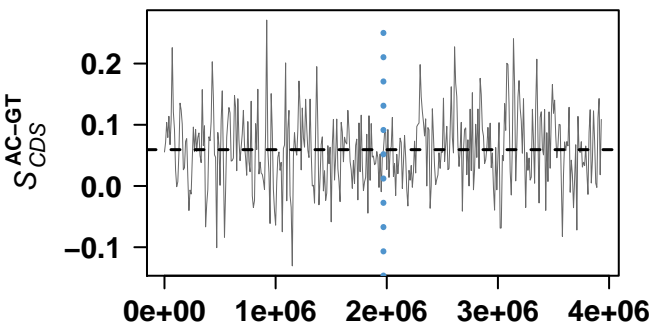
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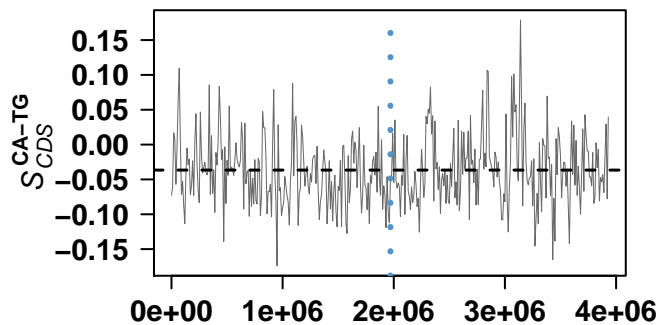
genome coordinates



genome coordinates

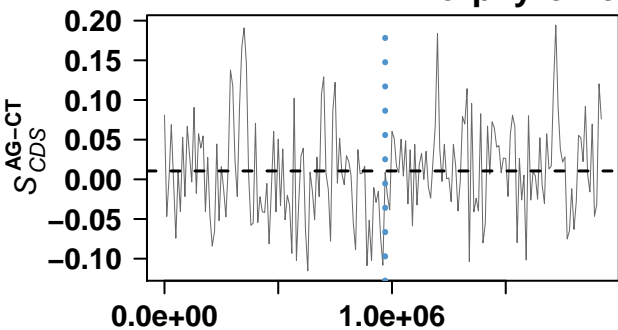


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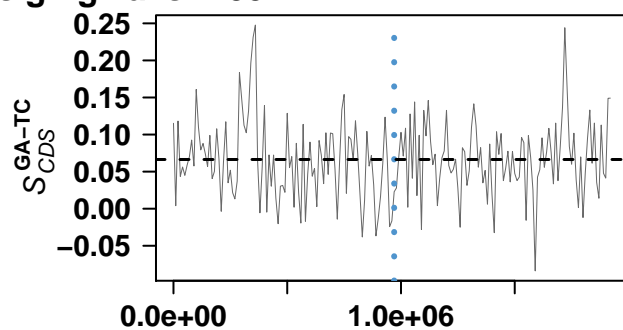


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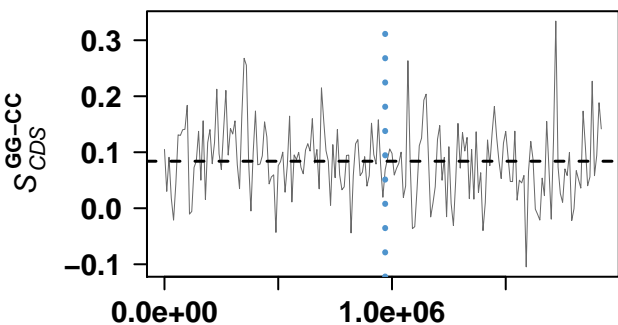
Porphyromonas gingivalis W83



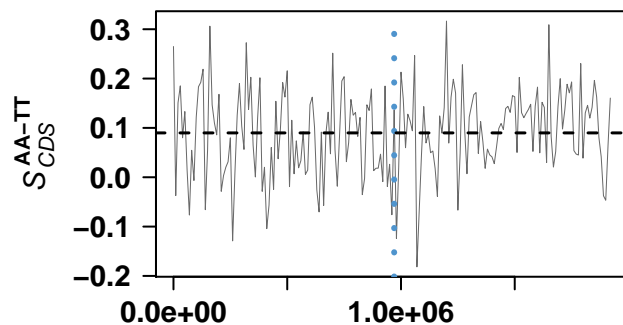
genome coordinates



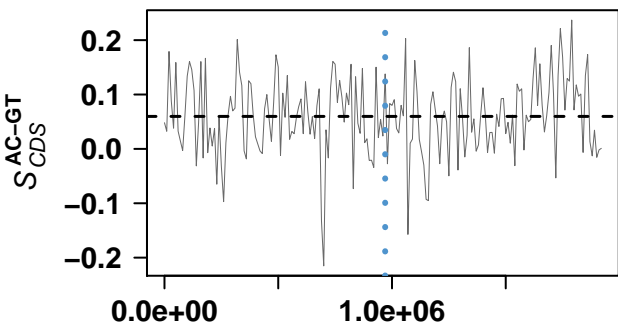
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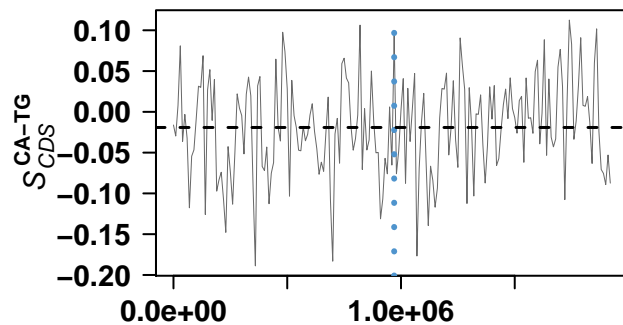
genome coordinates



genome coordinates

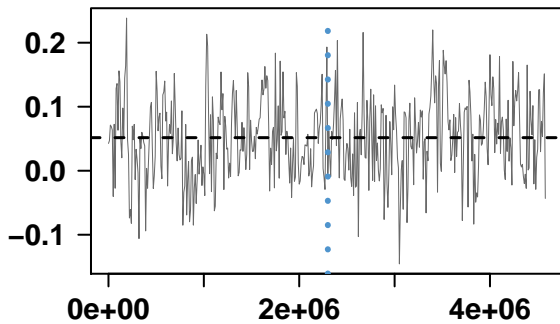


genome coordinates

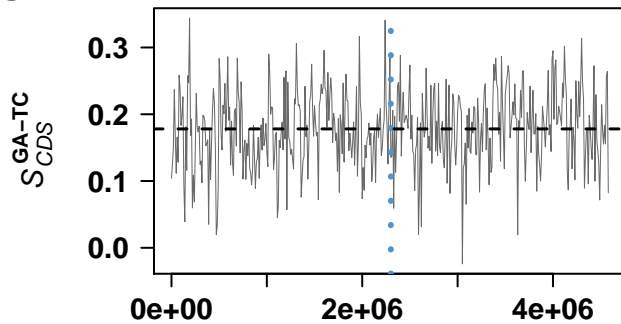


genome coordinates

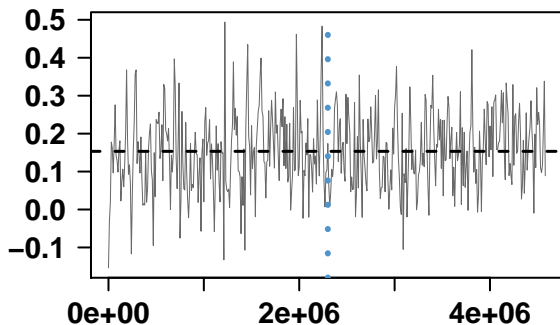
Bacteroides fragilis NCTC 9343



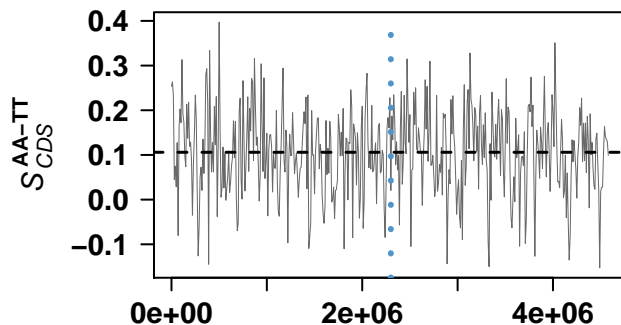
genome coordinates



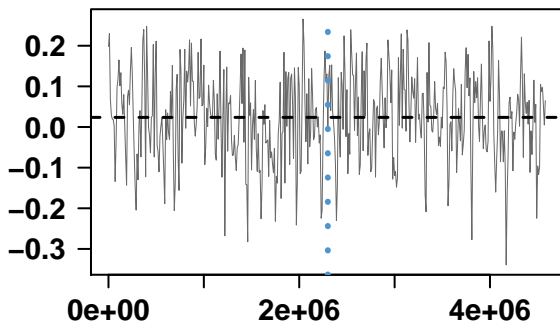
genome coordinates



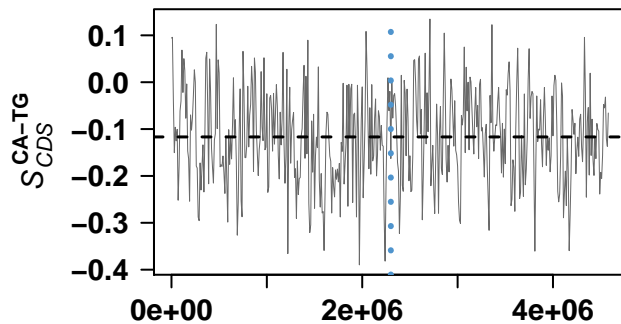
genome coordinates



genome coordinates

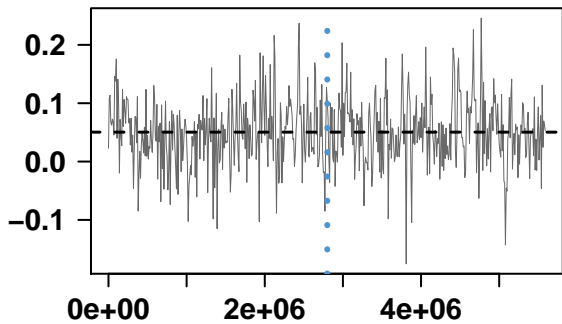


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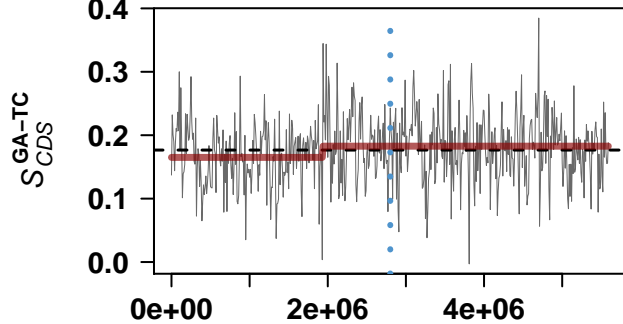


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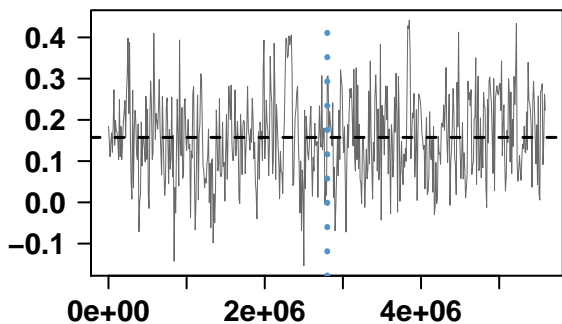
Bacteroides thetaiotaomicron VPI-5482



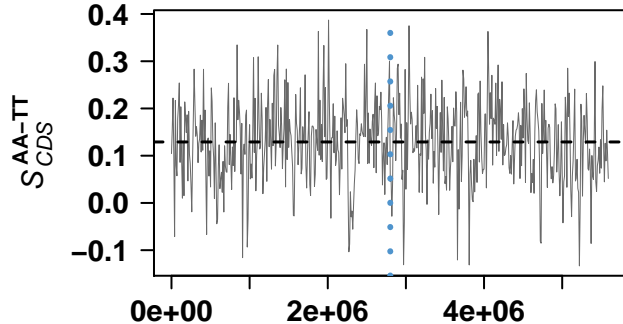
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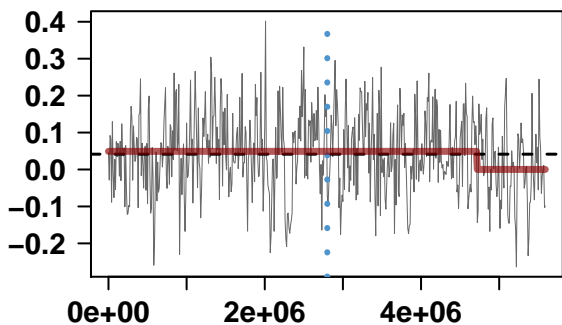
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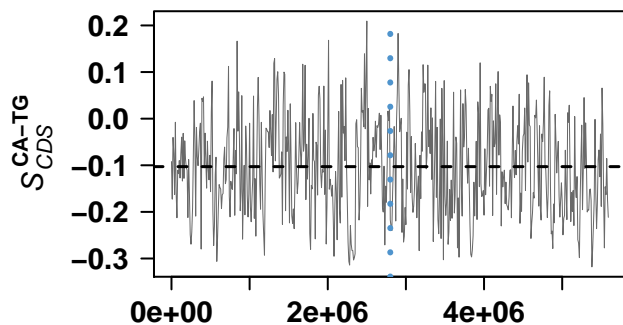
genome coordinates



genome coordinates

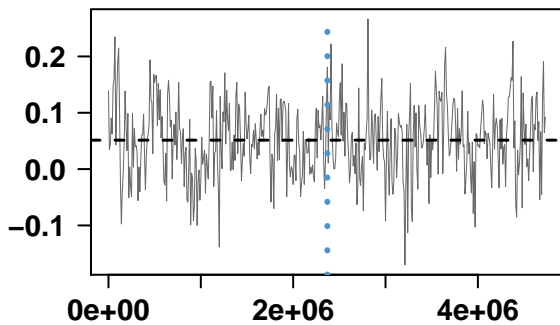


genome coordinates

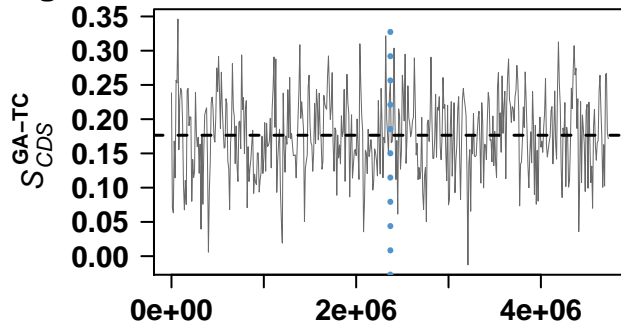


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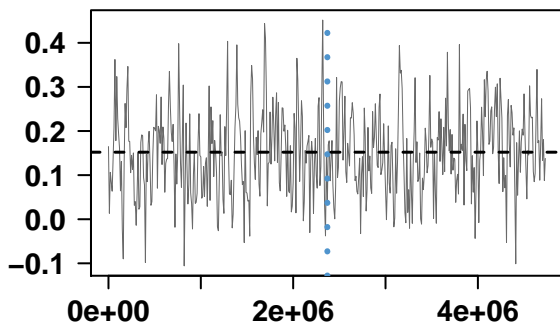
Bacteroides fragilis YCH46



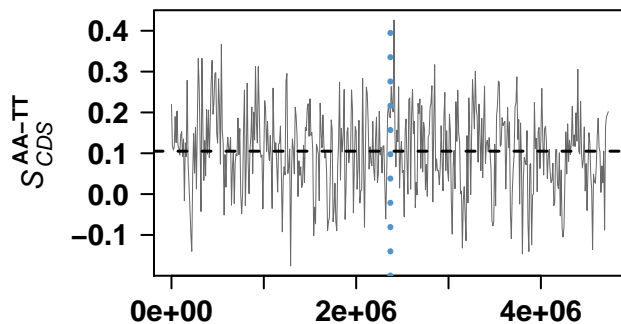
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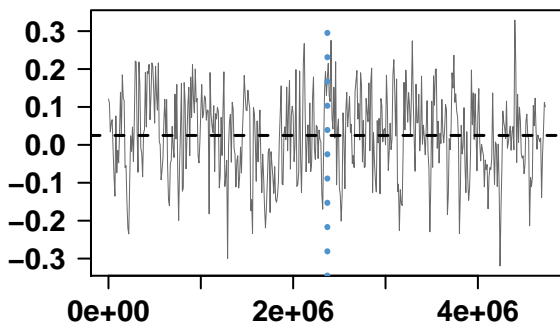
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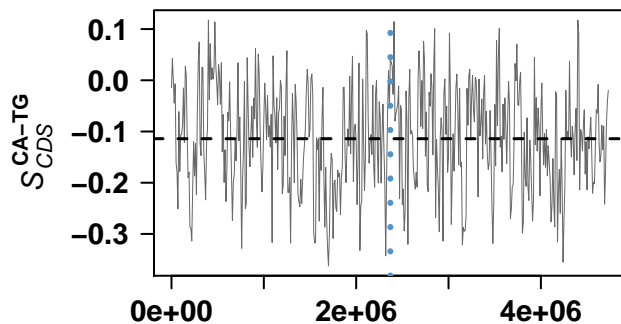
genome coordinates



genome coordinates

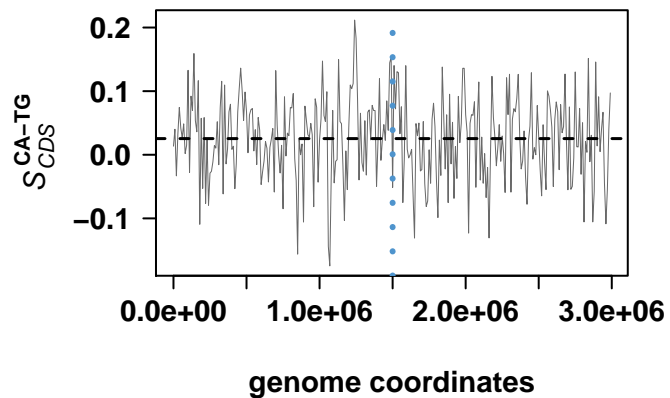
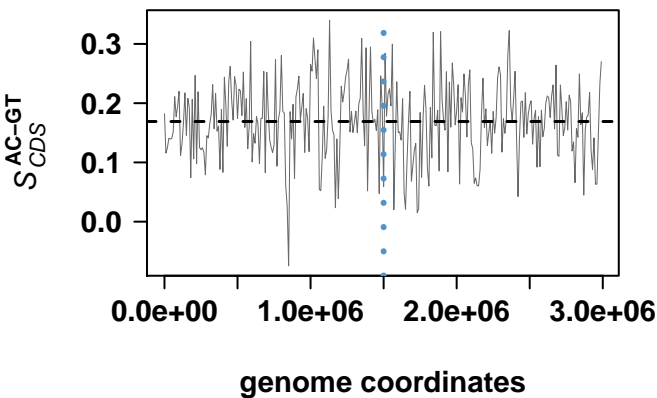
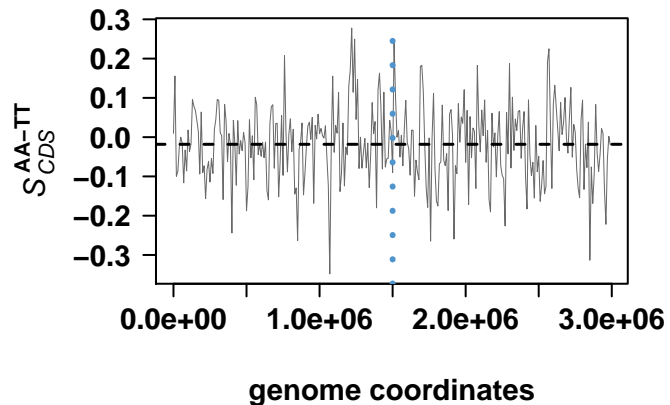
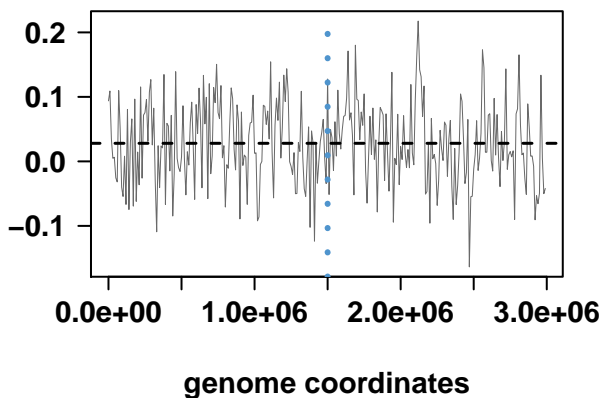
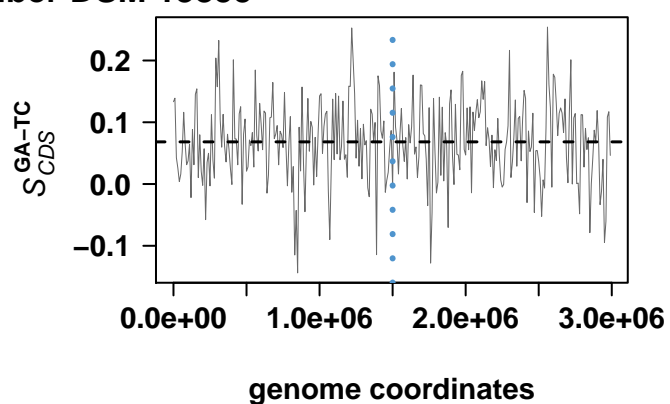
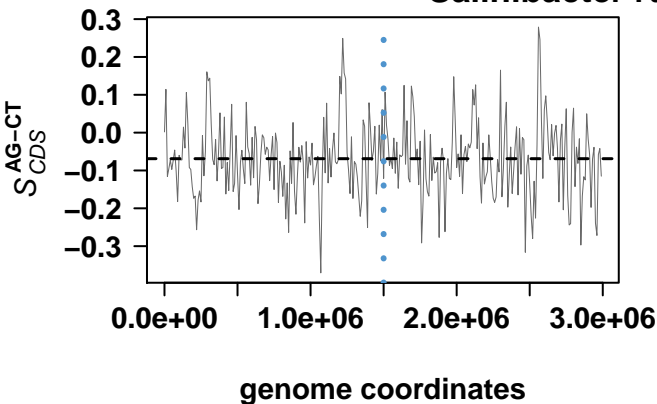


genome coordinates

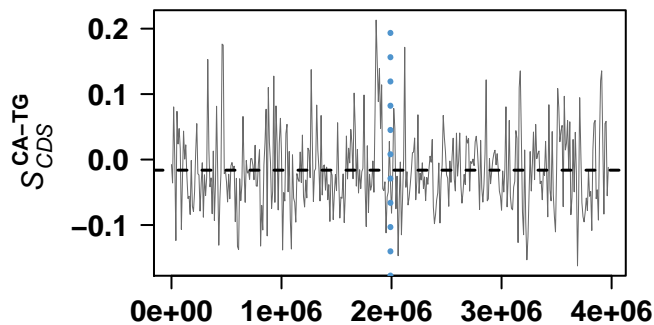
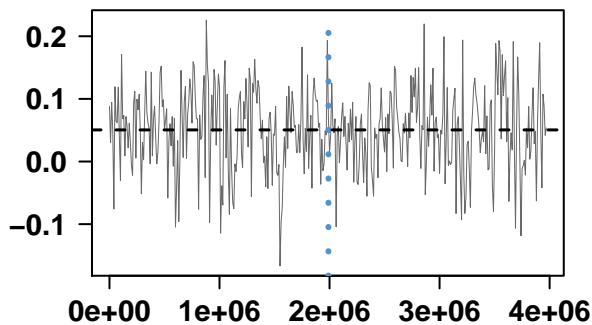
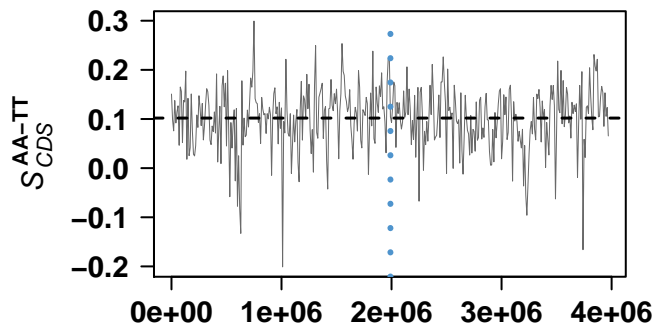
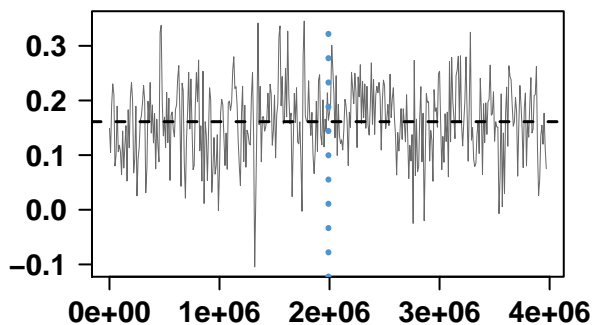
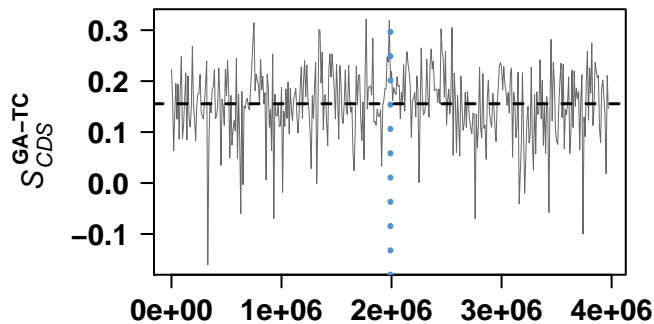
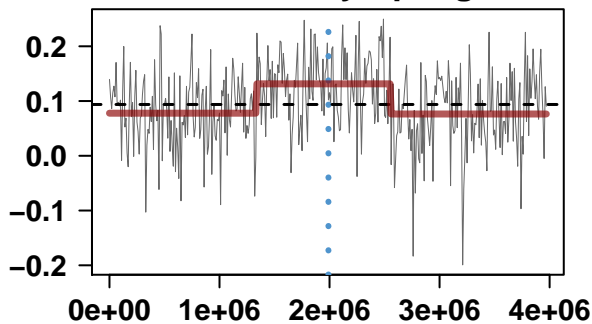


genome coordinates

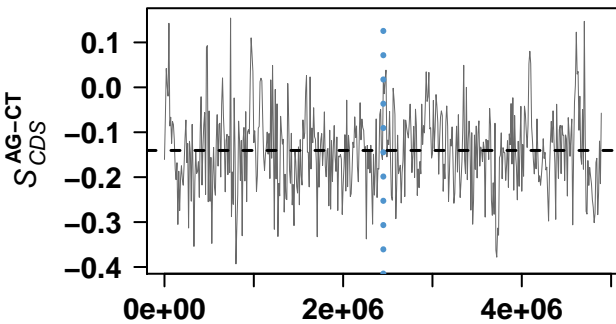
Salinibacter ruber DSM 13855



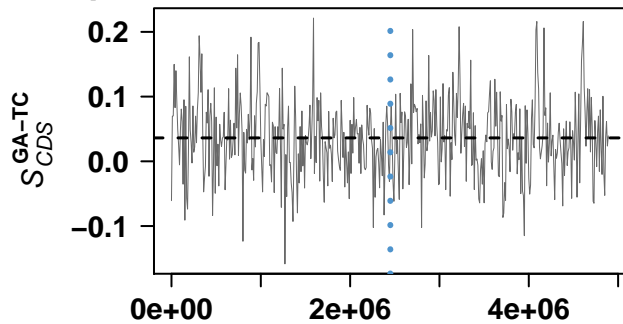
Cytophaga hutchinsonii ATCC 33406



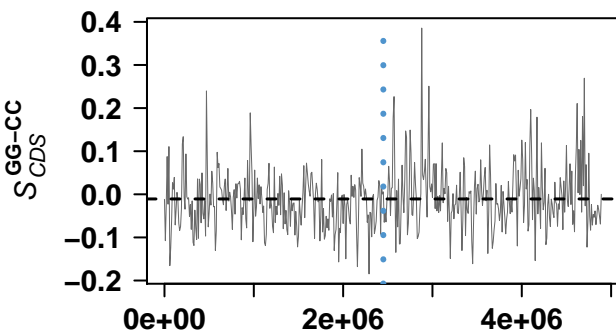
Bordetella bronchiseptica RB50



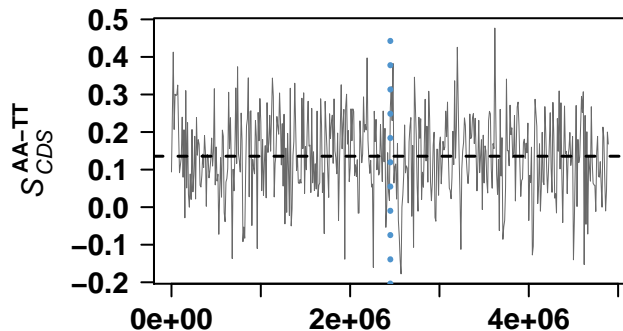
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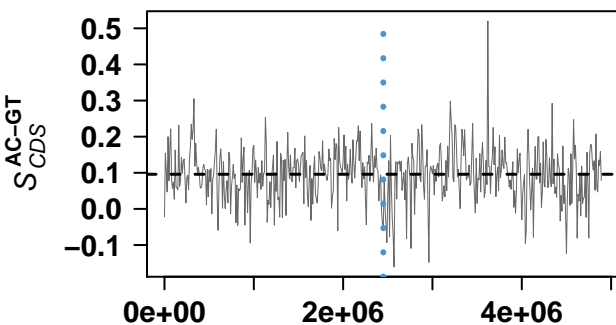
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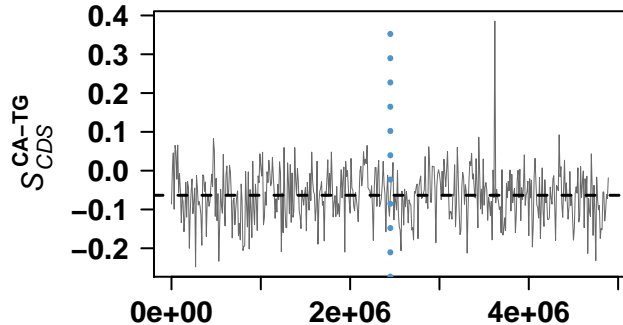
genome coordinates



genome coordinates

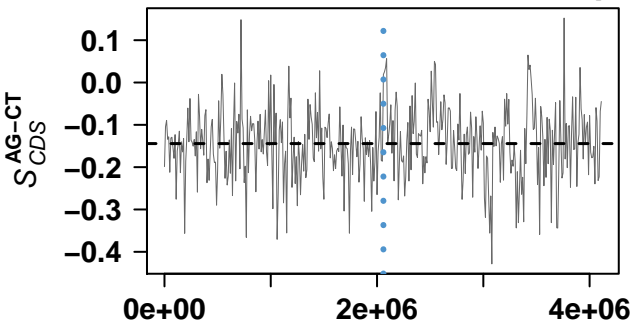


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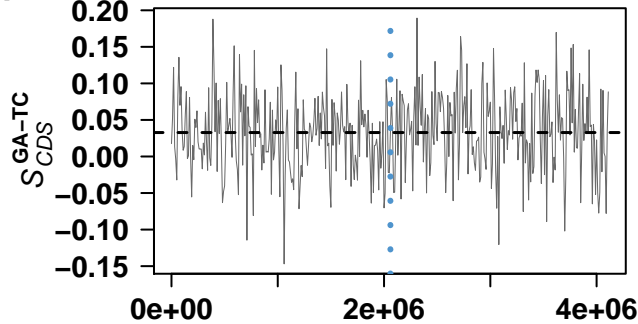


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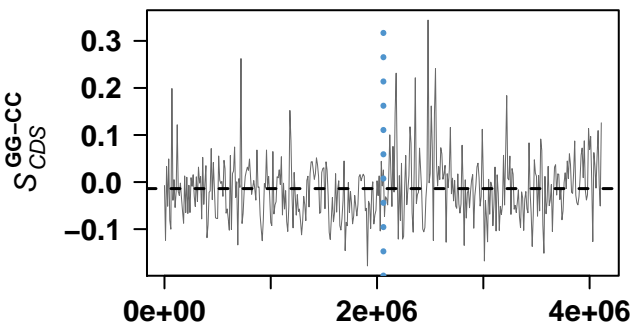
Bordetella parapturtussis 12822



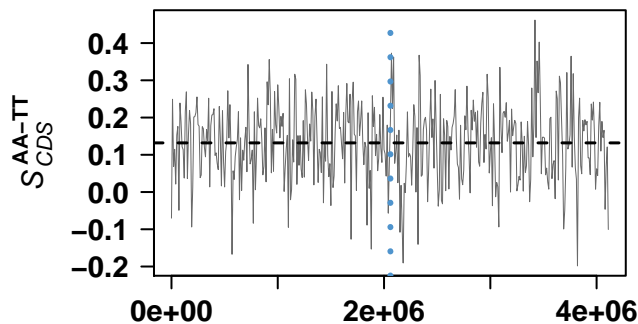
genome coordinates



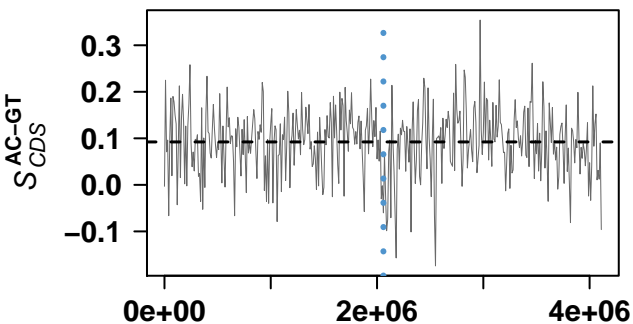
genome coordinates



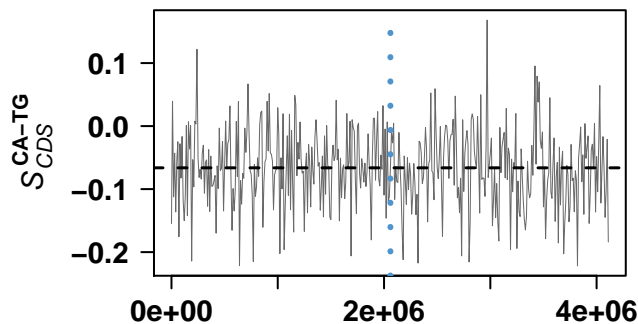
genome coordinates



genome coordinates

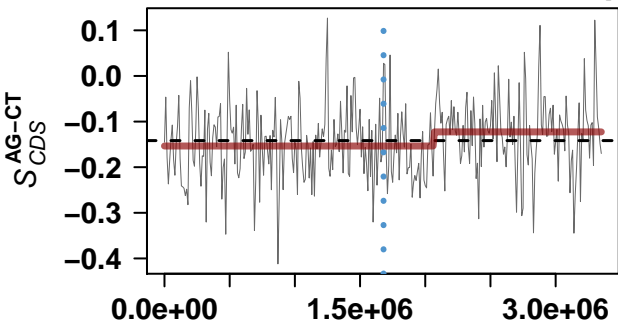


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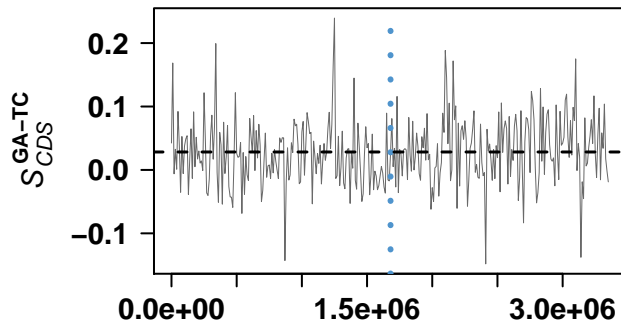


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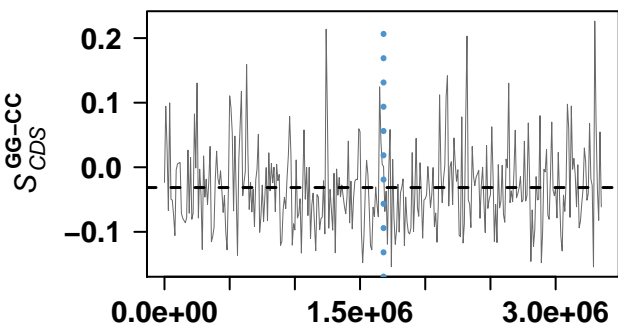
Bordetella pertussis Tohama I



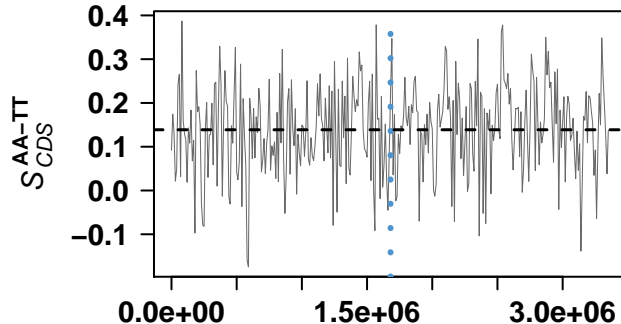
genome coordinates



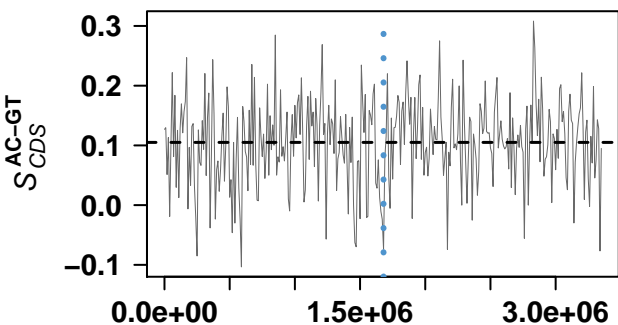
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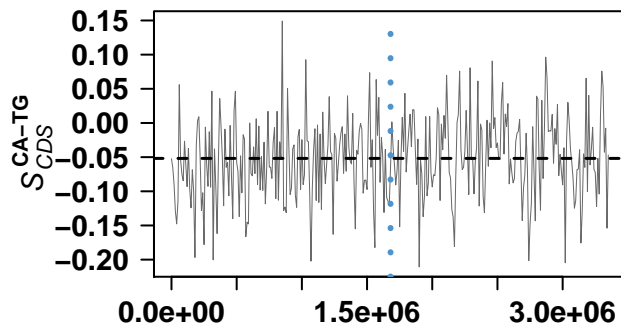
genome coordinates



genome coordinates

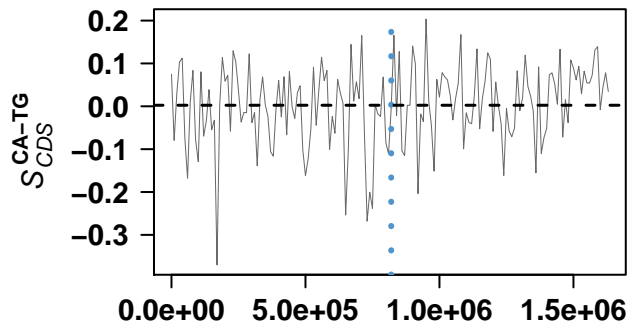
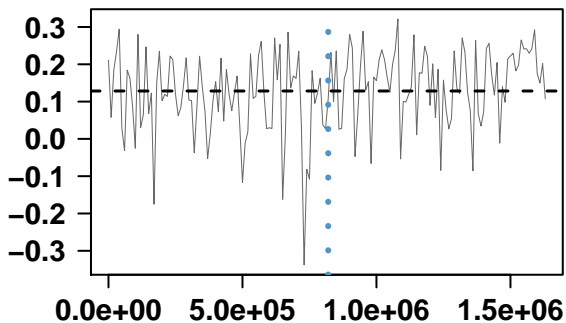
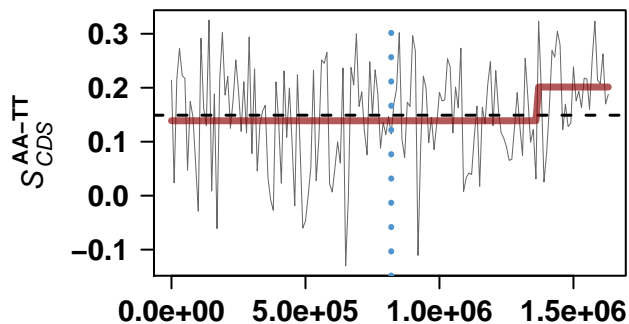
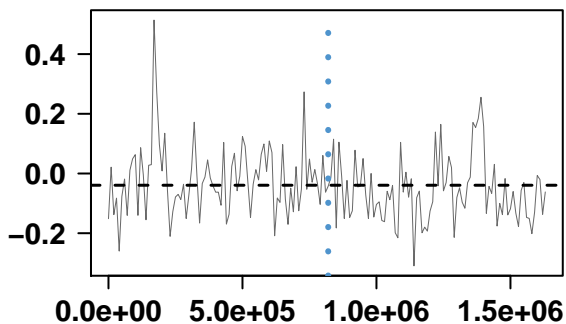
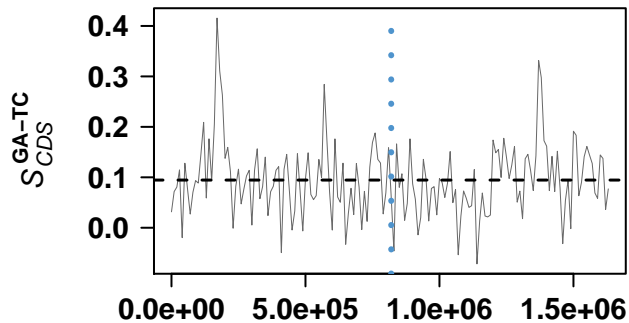
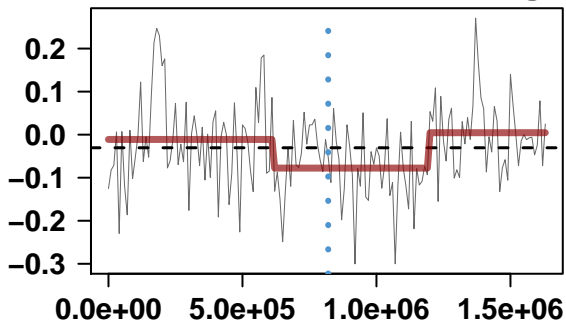


genome coordinates

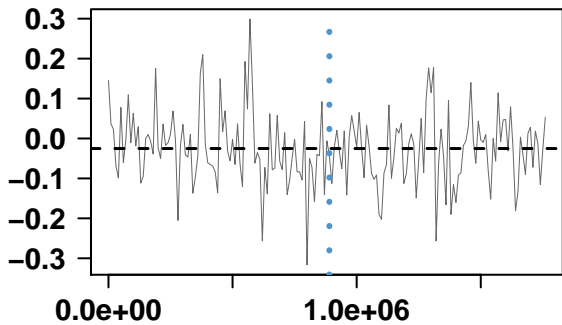


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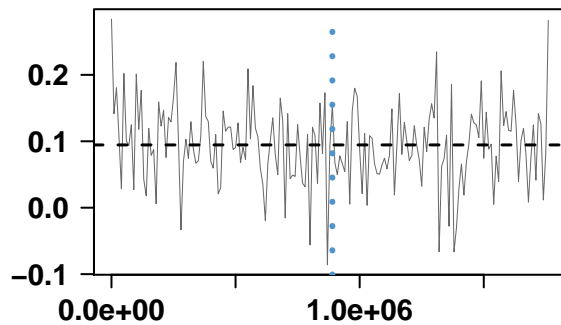
Neisseria gonorrhoeae FA 1090



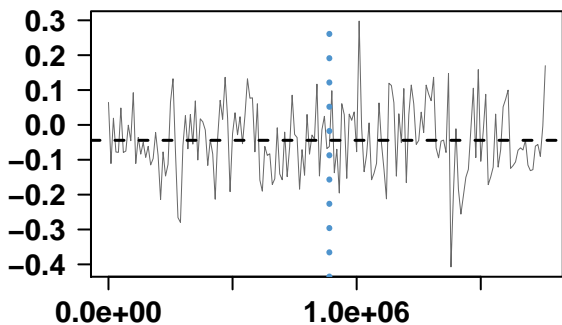
Neisseria meningitidis MC58



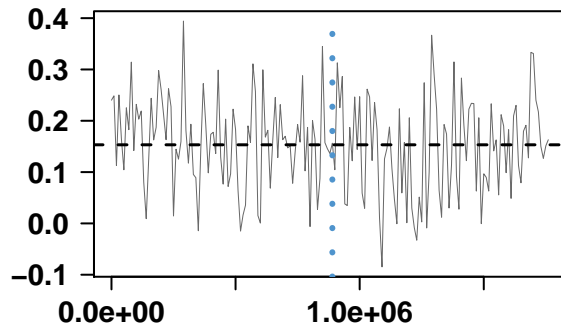
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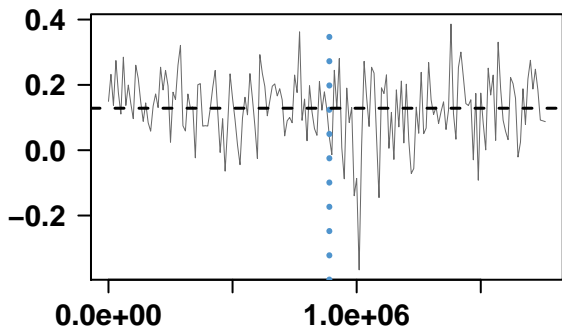
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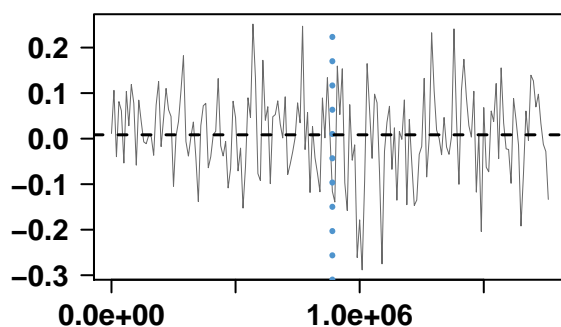
genome coordinates



genome coordinates

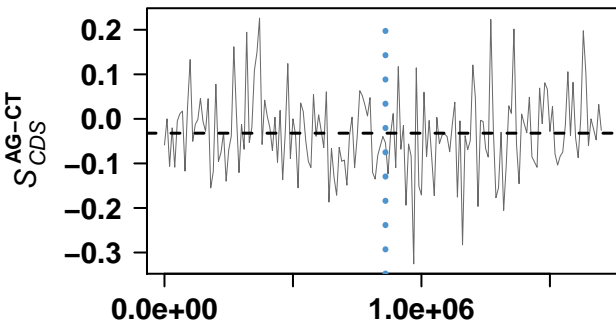


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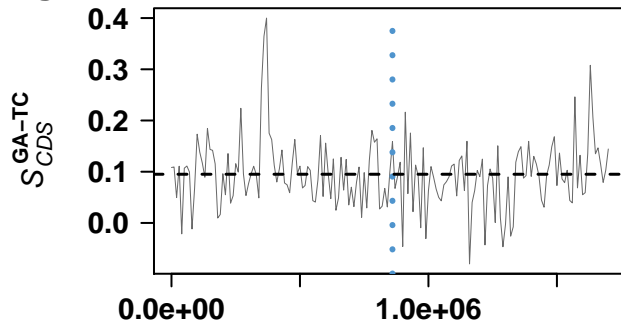


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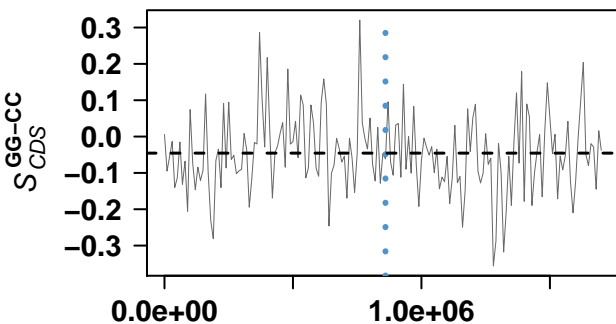
Neisseria meningitidis Z2491



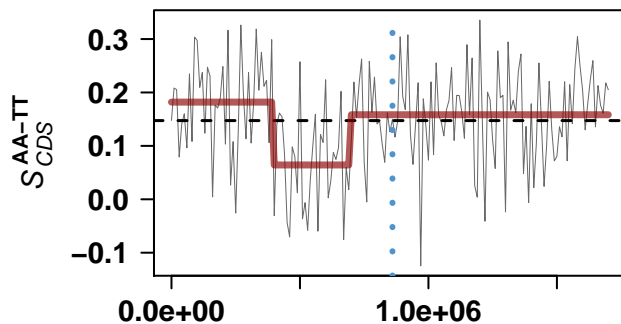
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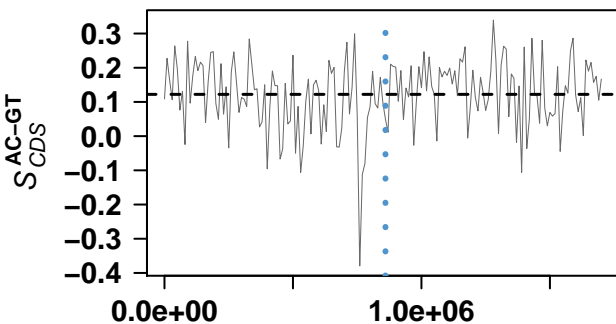
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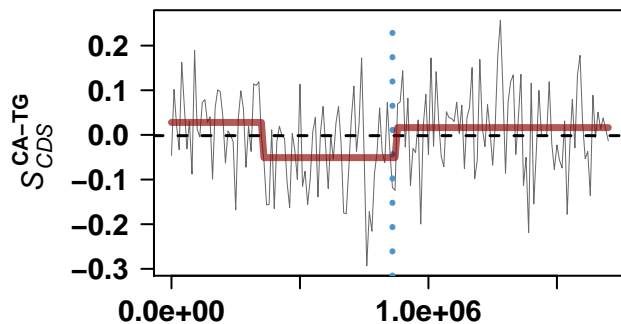
genome coordinates



genome coordinates

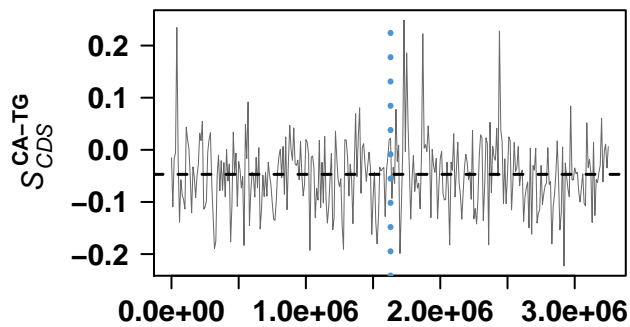
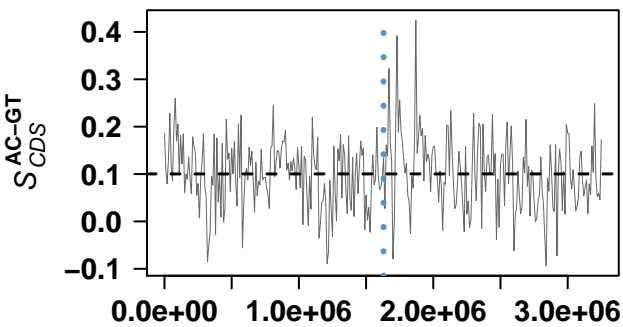
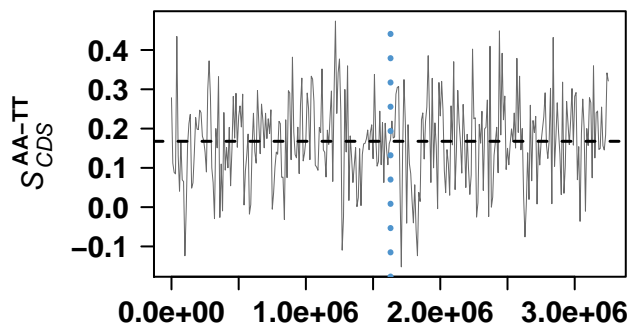
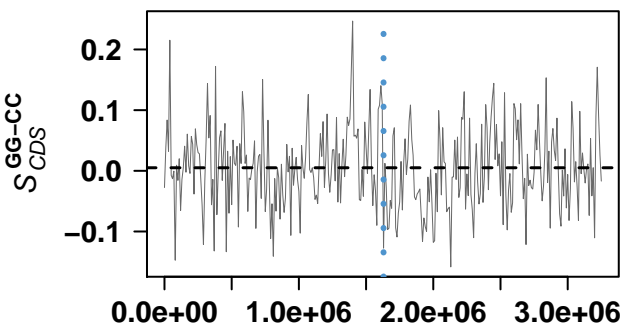
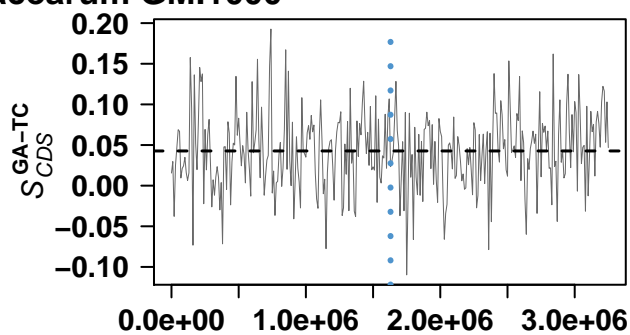
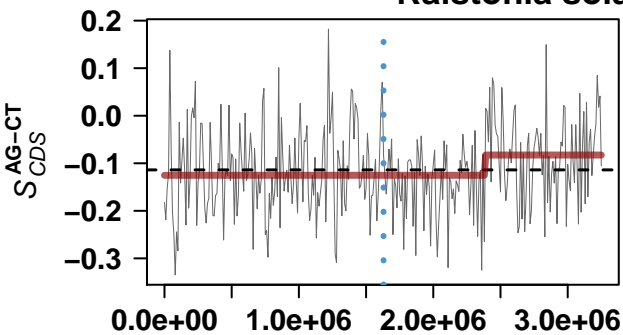


genome coordinates

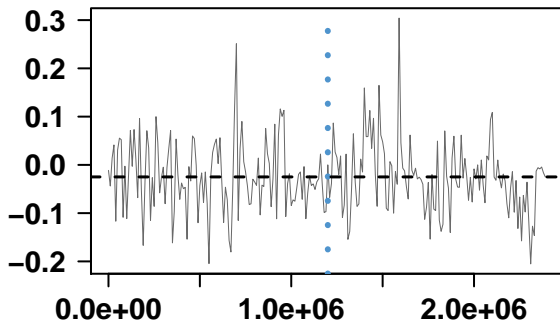


genome coordinates

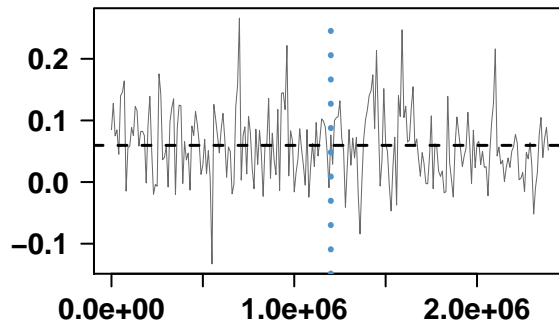
Ralstonia solanacearum GMI1000



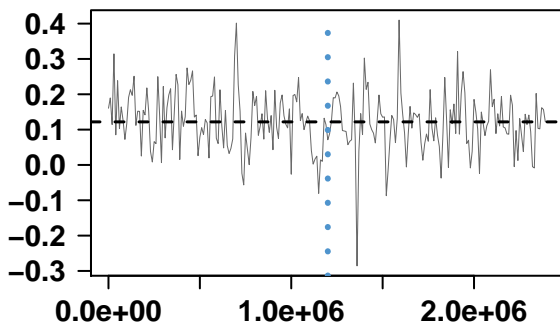
Nitrosomonas europaea ATCC 19718



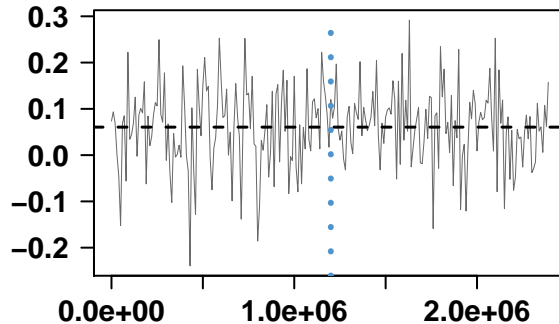
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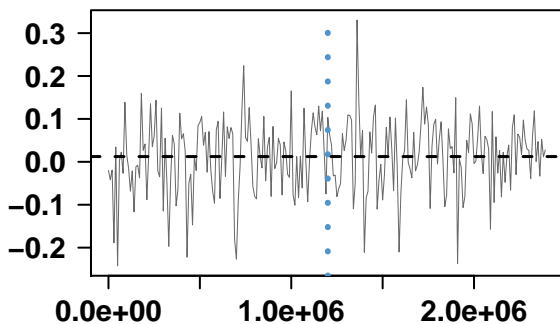
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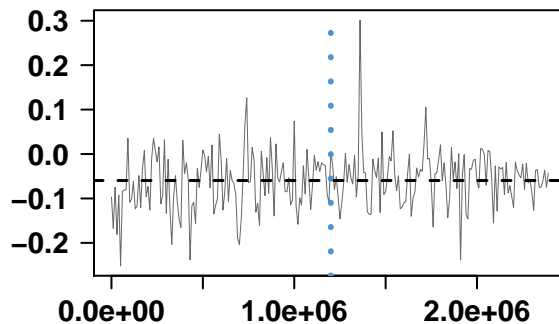
genome coordinates



genome coordinates

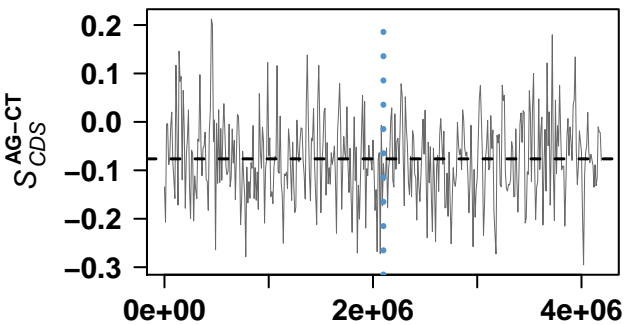


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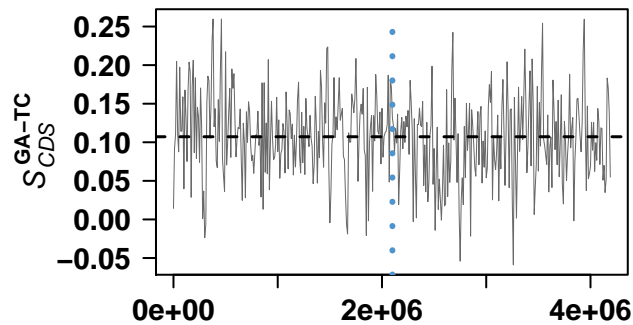


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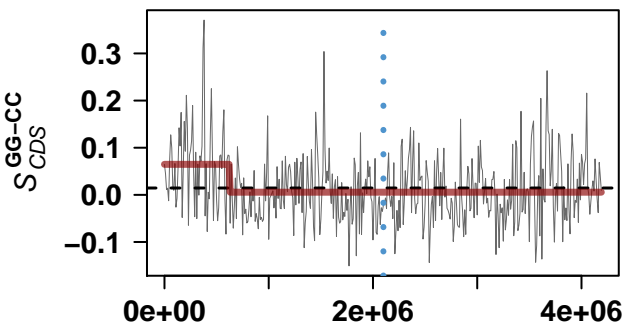
Chromobacterium violaceum ATCC 12472



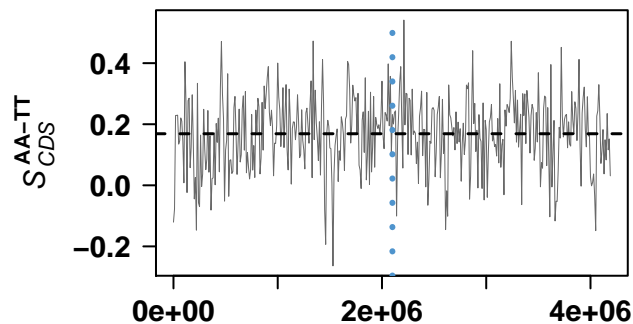
genome coordinates



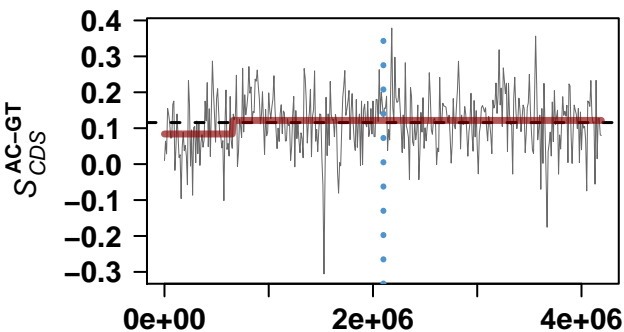
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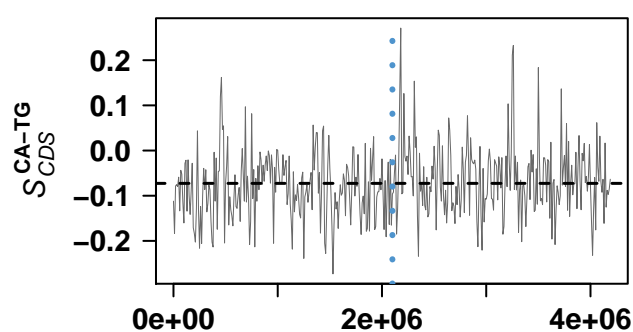
genome coordinates



genome coordinates

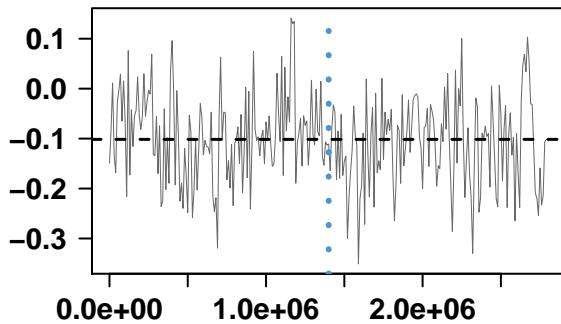


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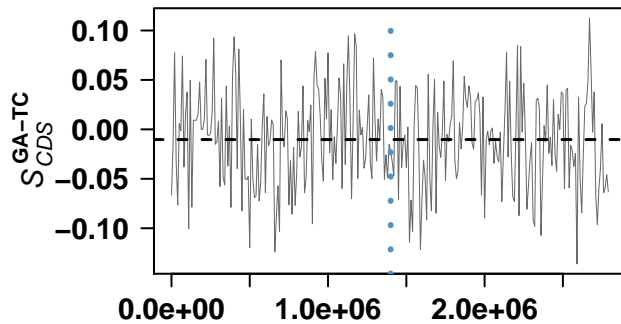


genome coordinates

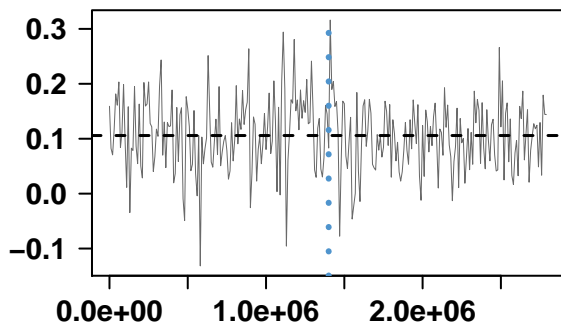
Burkholderia mallei ATCC 23344



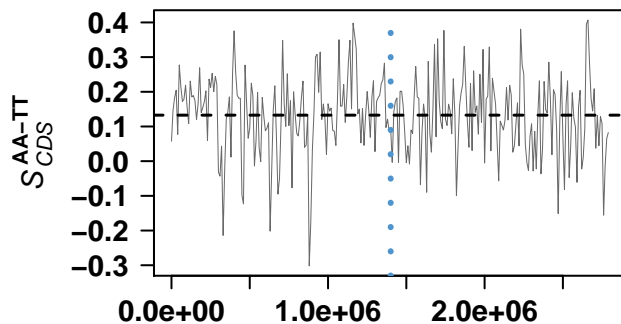
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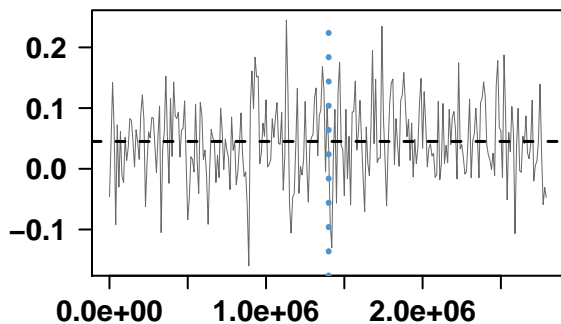
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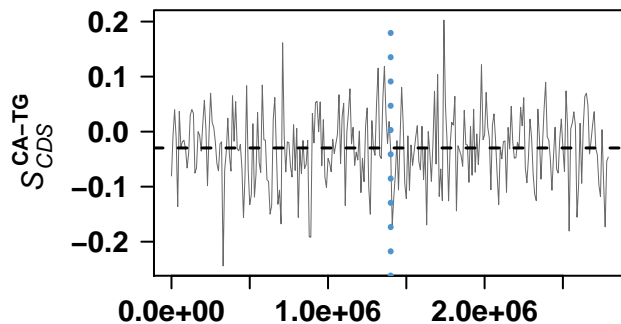
genome coordinates



genome coordinates

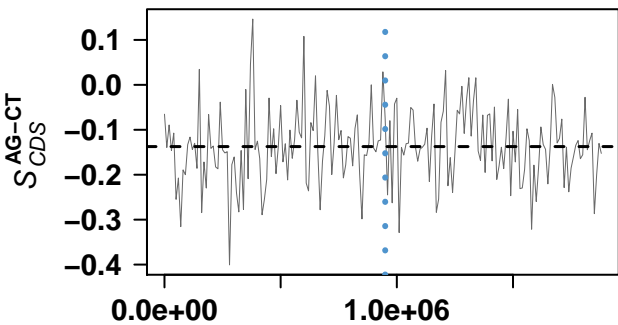


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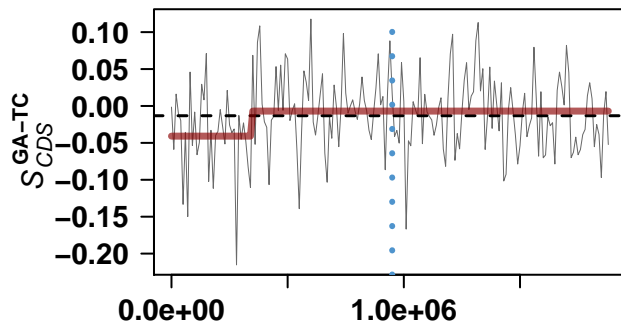


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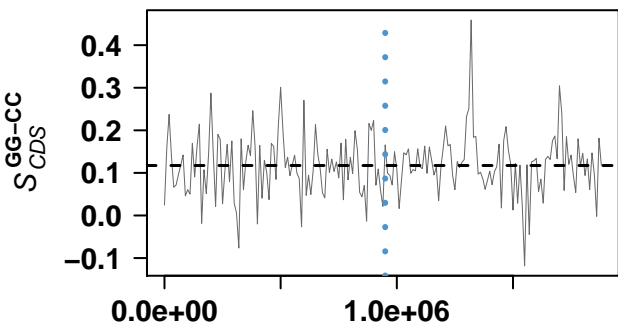
Burkholderia mallei ATCC 23344



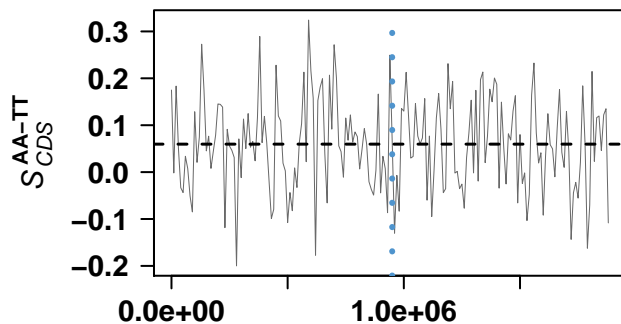
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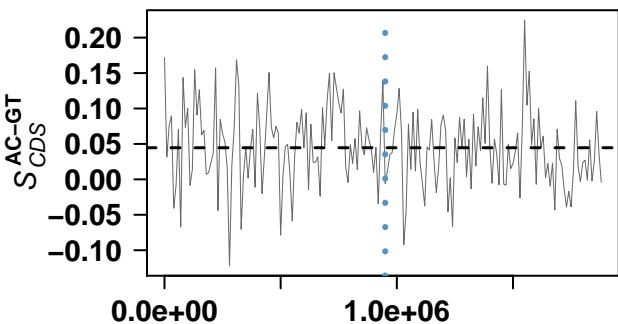
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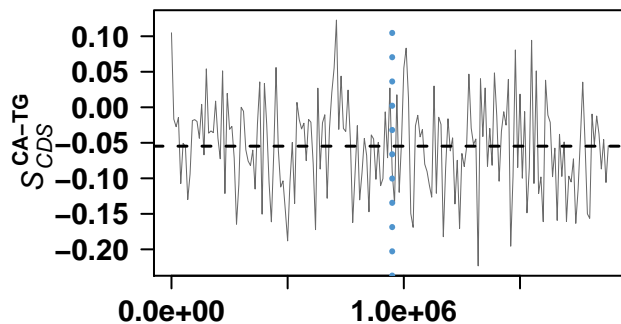
genome coordinates



genome coordinates

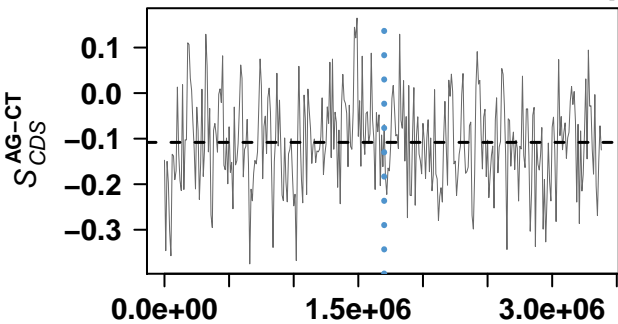


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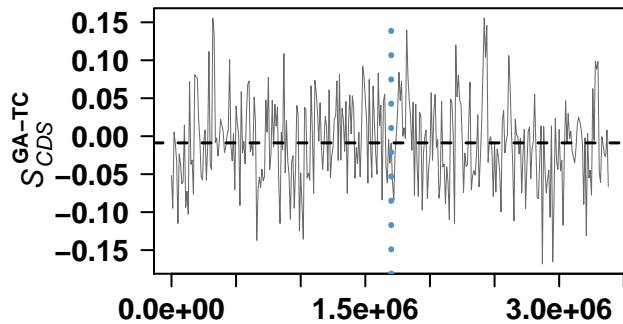


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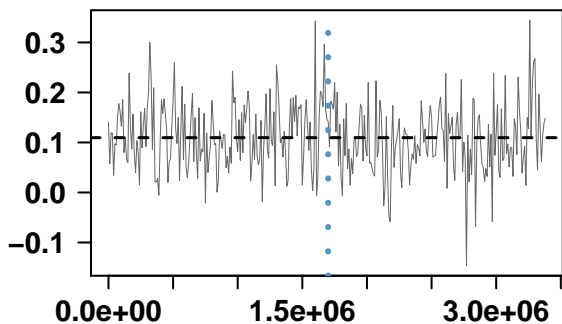
Burkholderia pseudomallei K96243



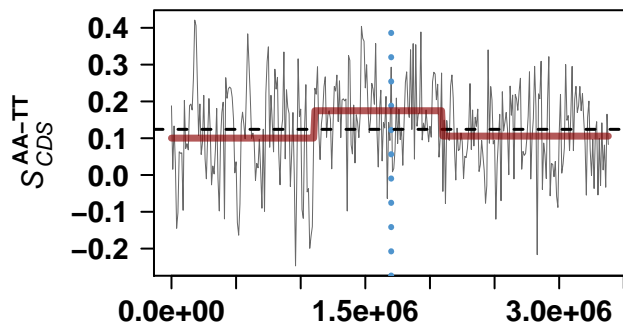
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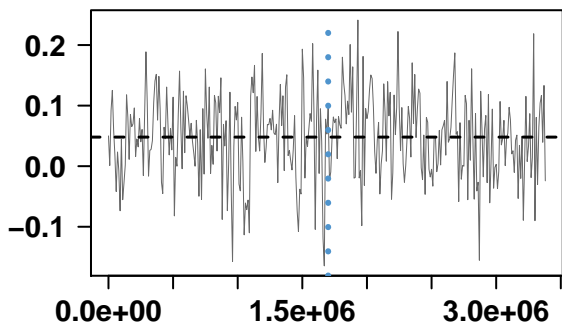
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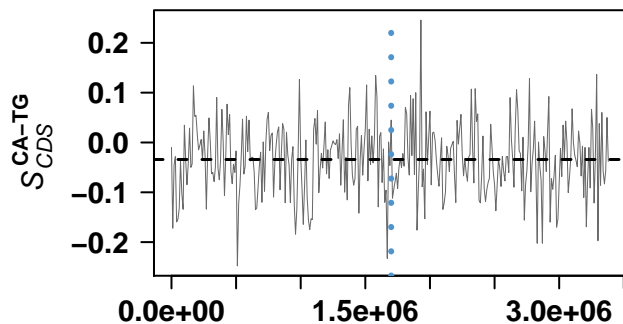
genome coordinates



genome coordinates

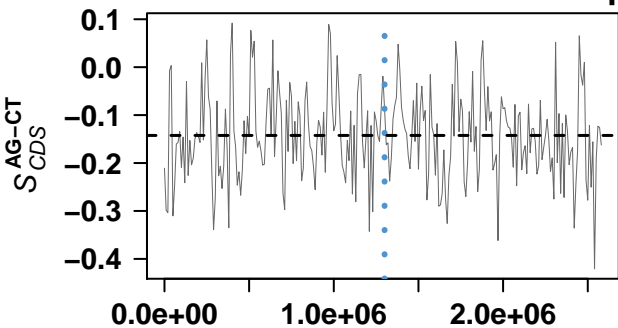


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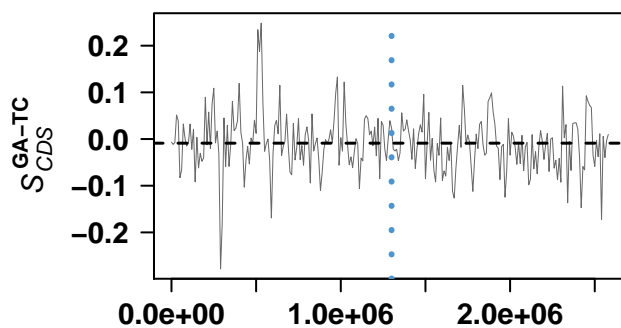


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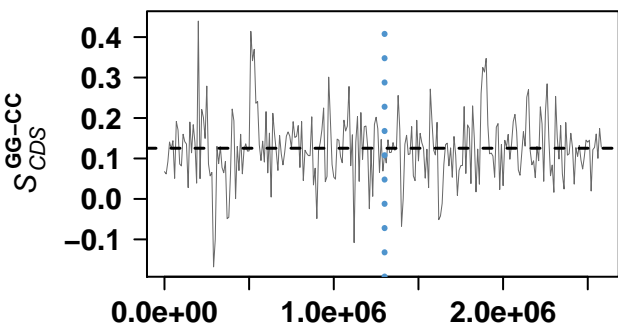
Burkholderia pseudomallei K96243



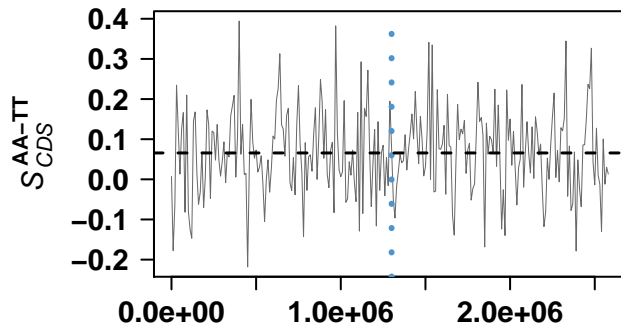
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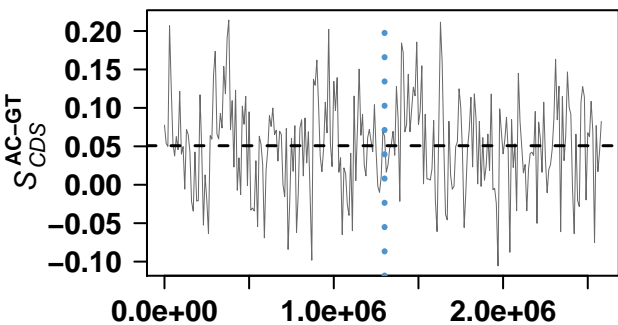
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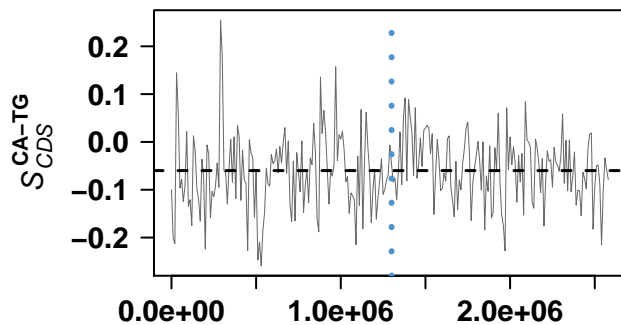
genome coordinates



genome coordinates

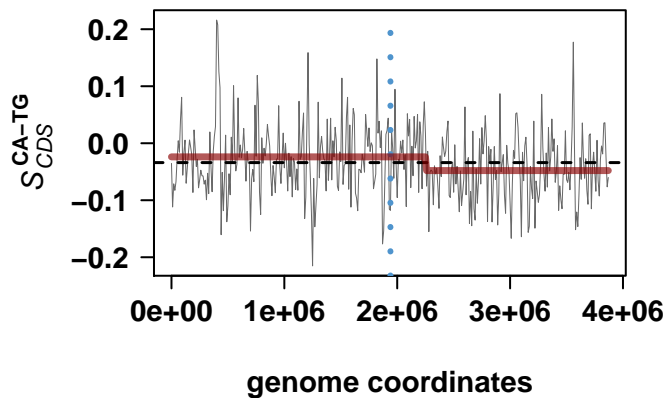
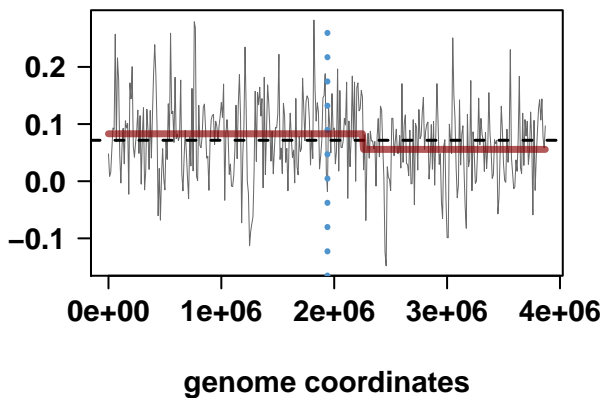
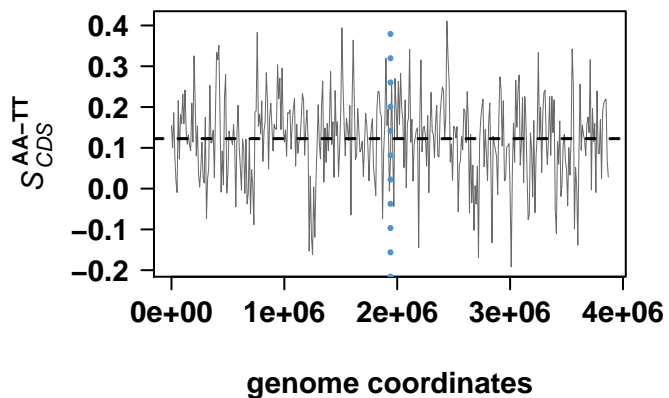
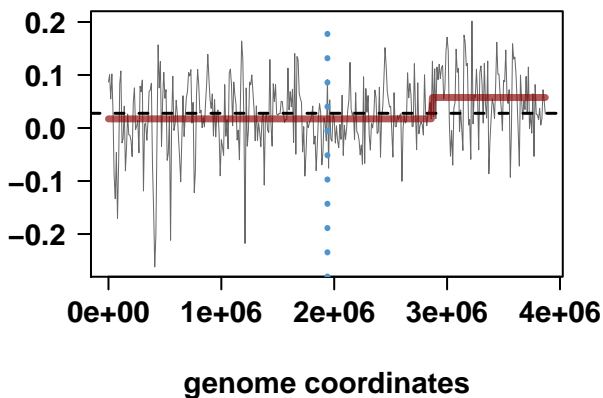
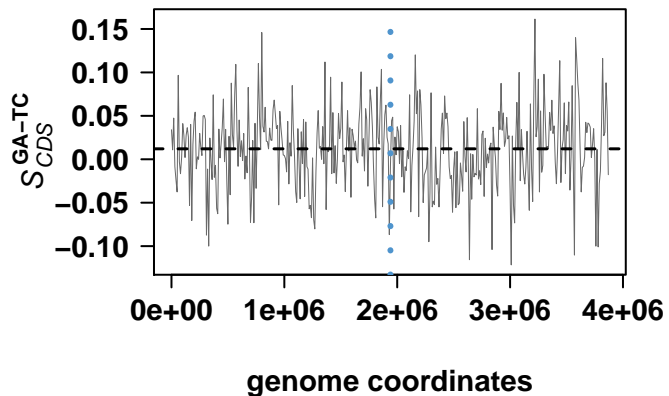
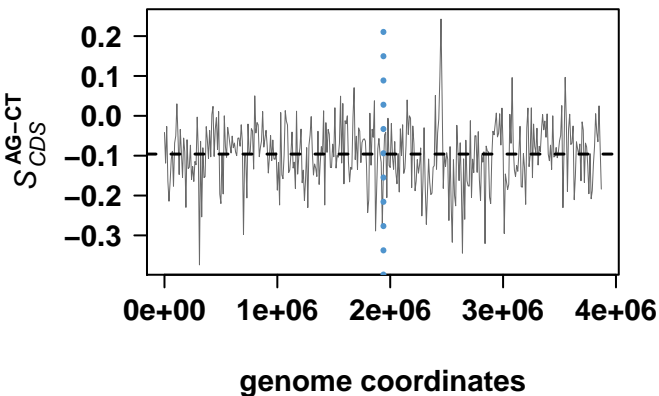


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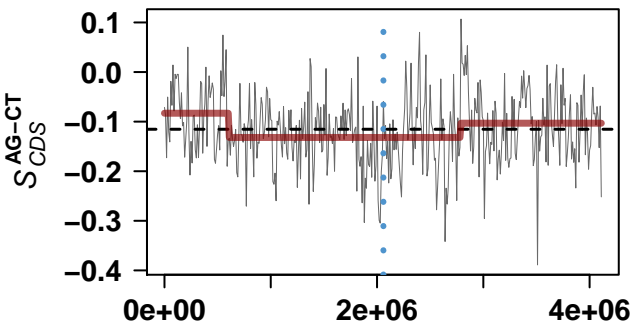


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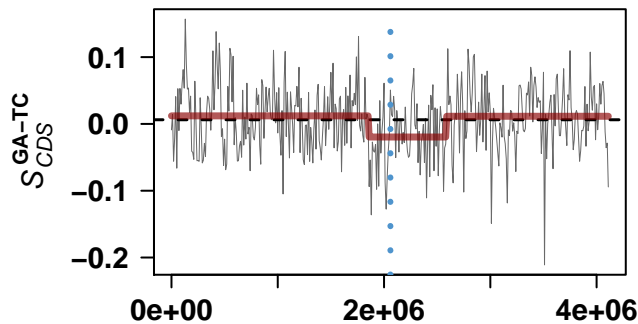
Aromatoleum aromaticum EbN1



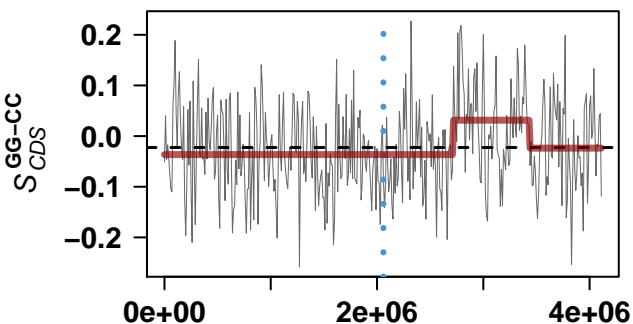
Dechloromonas aromatica RCB



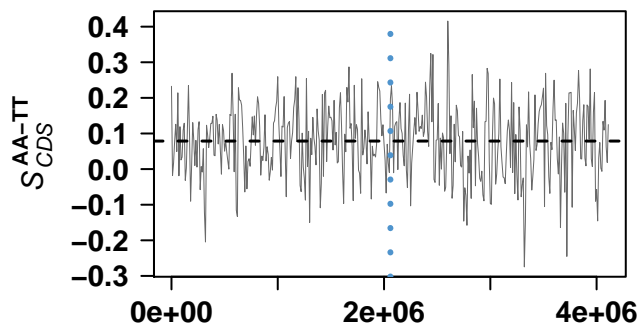
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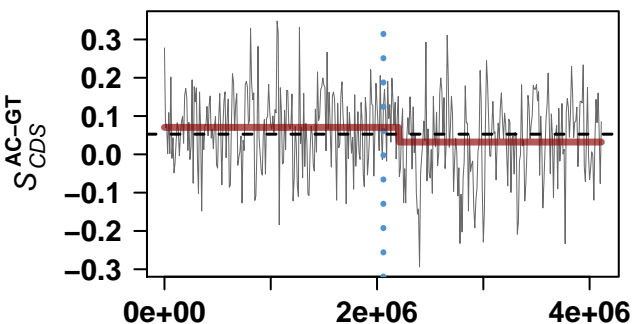
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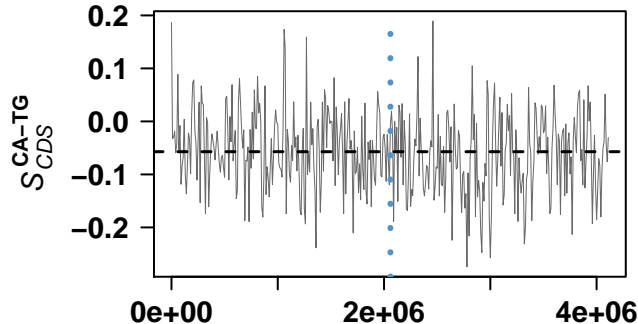
genome coordinates



genome coordinates

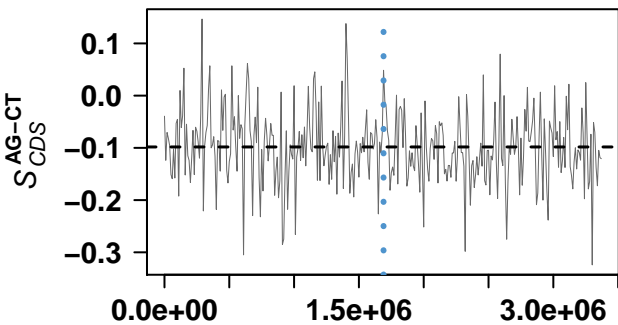


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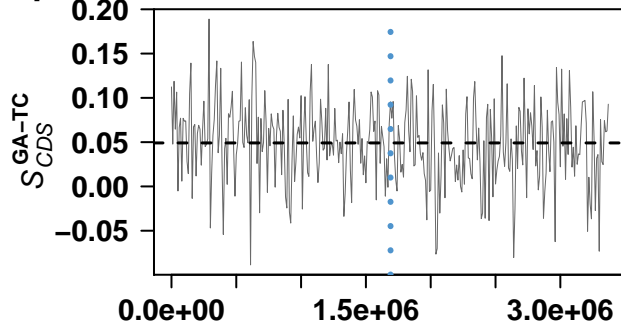


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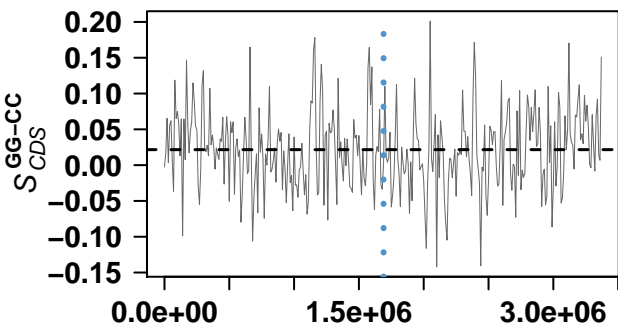
Ralstonia eutropha JMP134



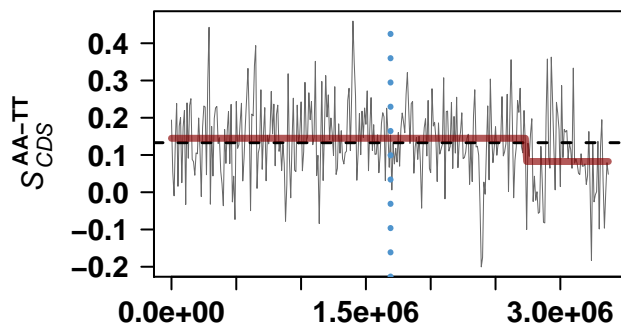
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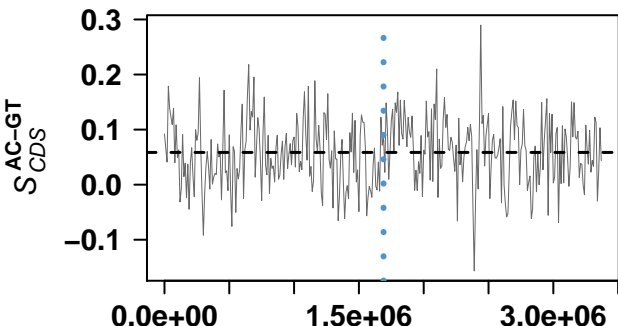
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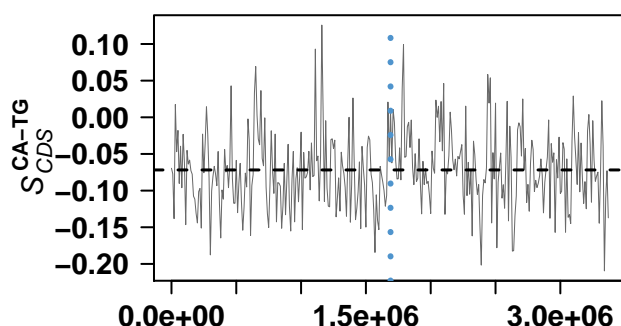
genome coordinates



genome coordinates

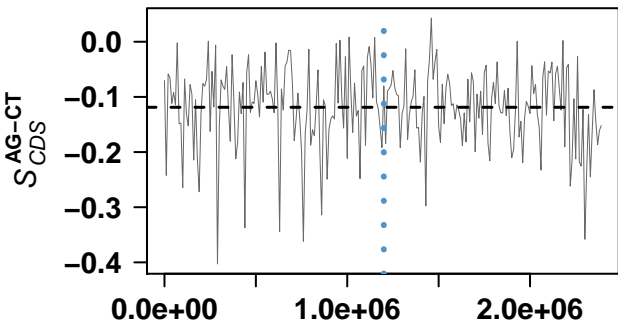


genome coordinates

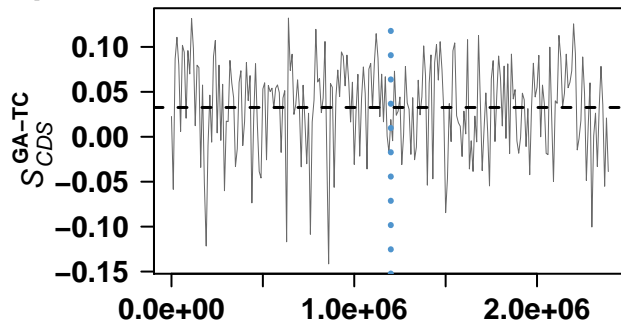


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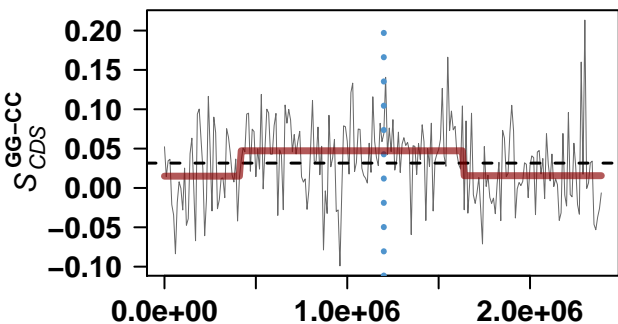
Ralstonia eutropha JMP134



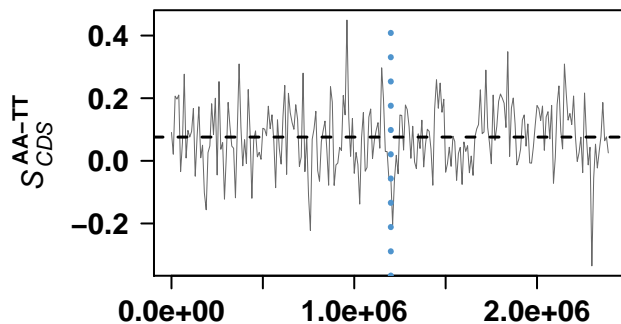
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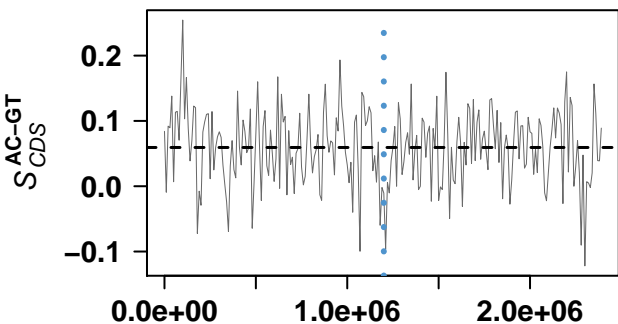
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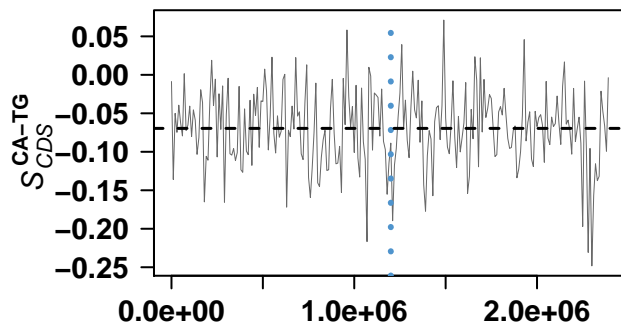
genome coordinates



genome coordinates

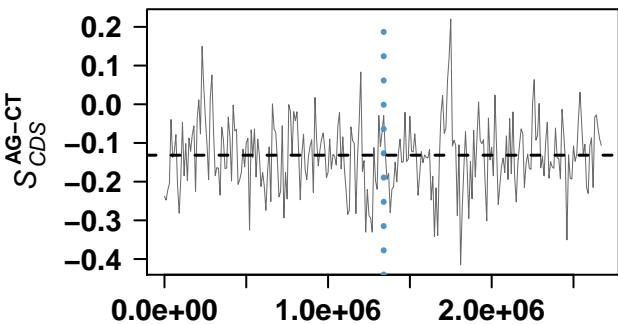


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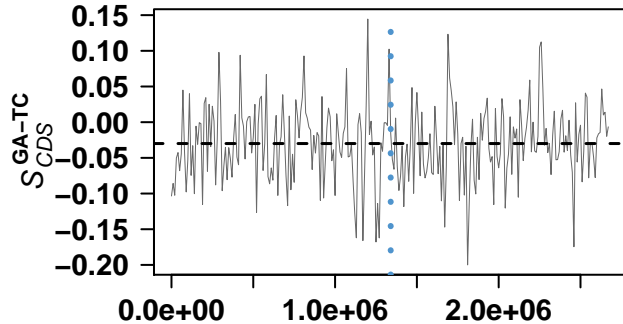


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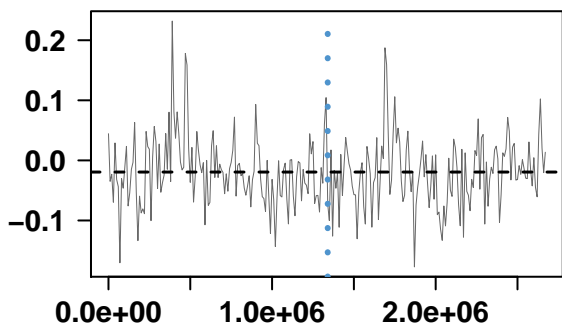
Thiobacillus denitrificans ATCC 25259



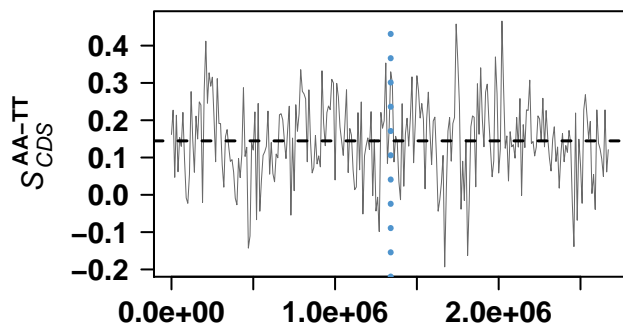
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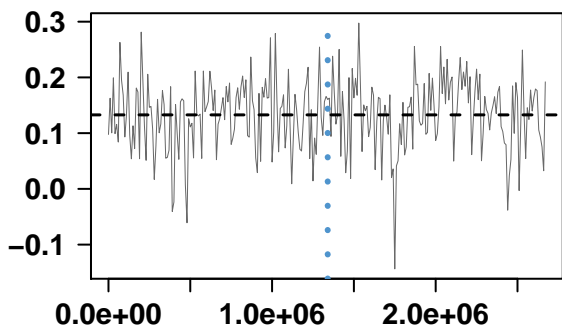
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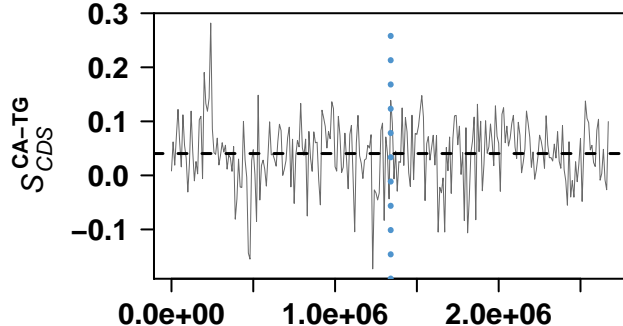
genome coordinates



genome coordinates

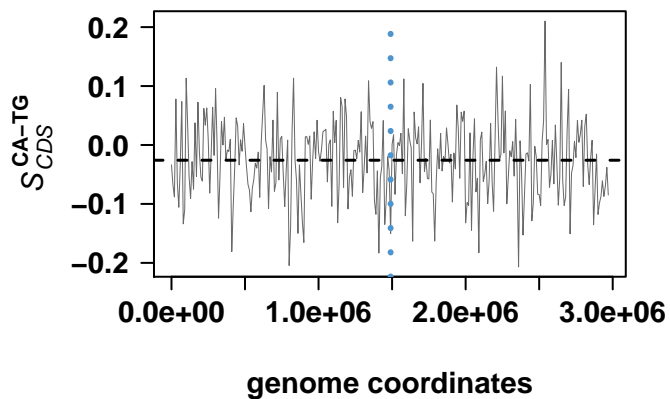
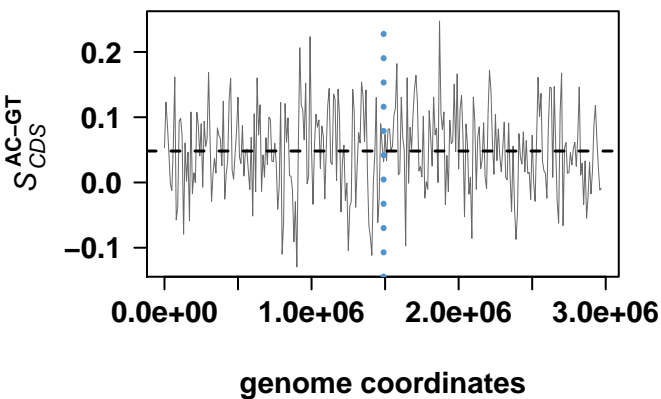
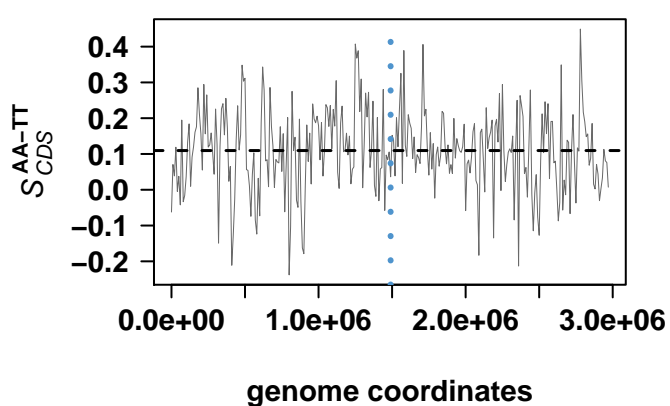
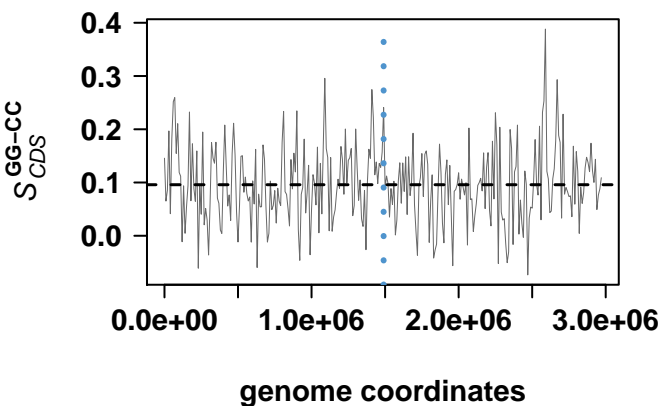
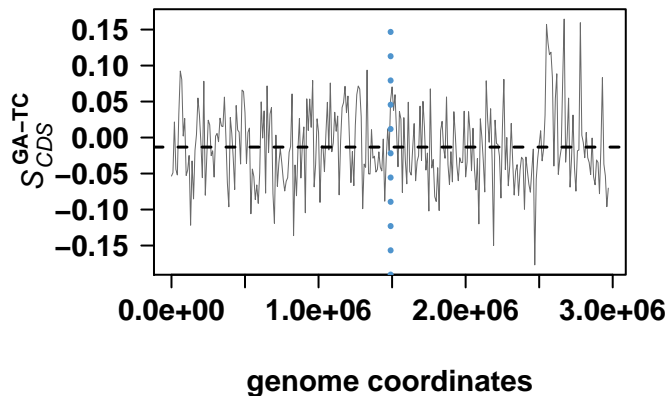
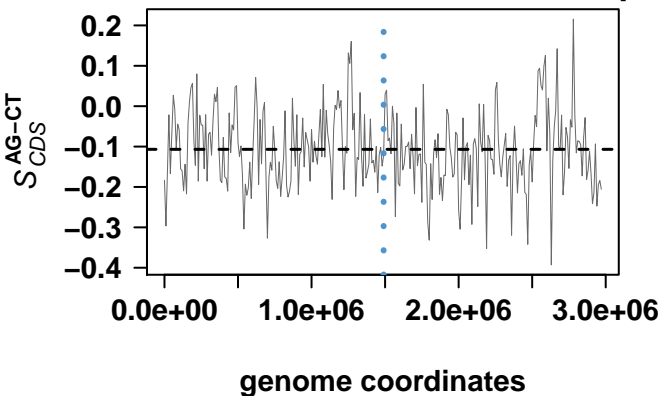


genome coordinates

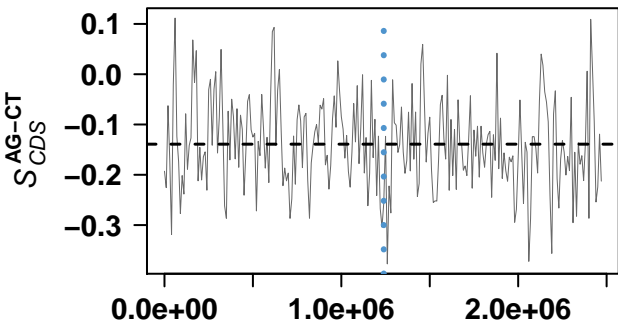


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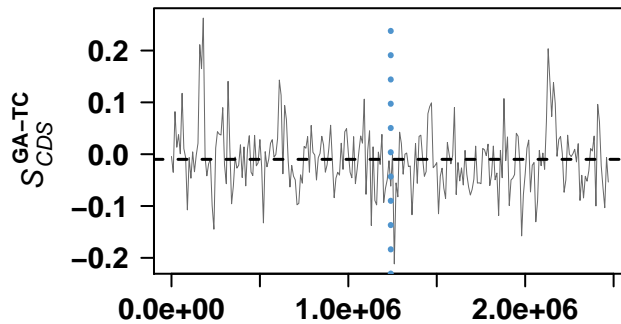
Burkholderia pseudomallei 1710b



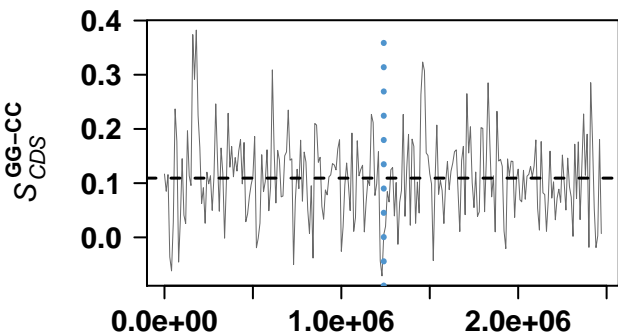
Burkholderia pseudomallei 1710b



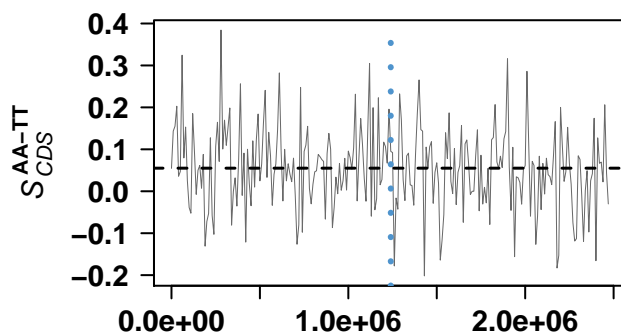
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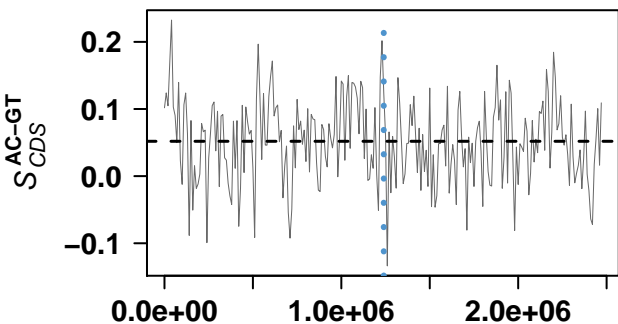
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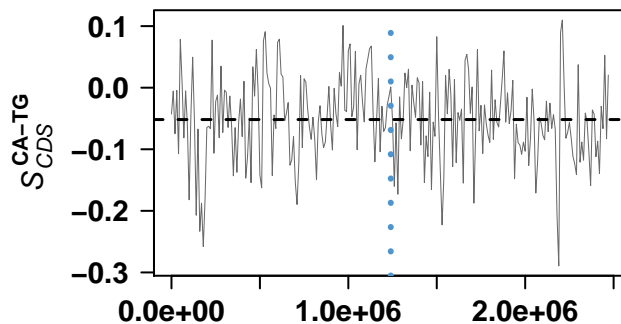
genome coordinates



genome coordinates

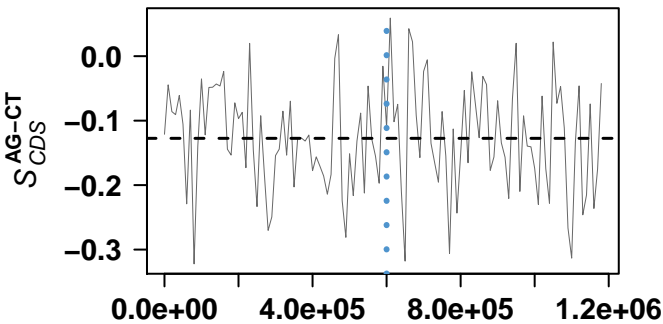


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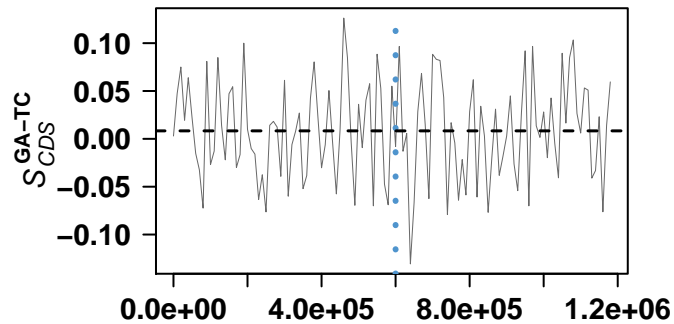


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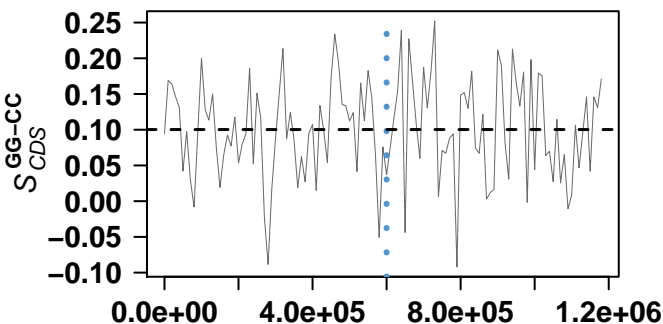
Burkholderia lata



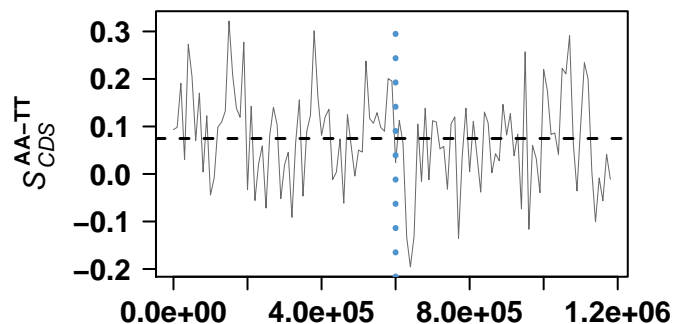
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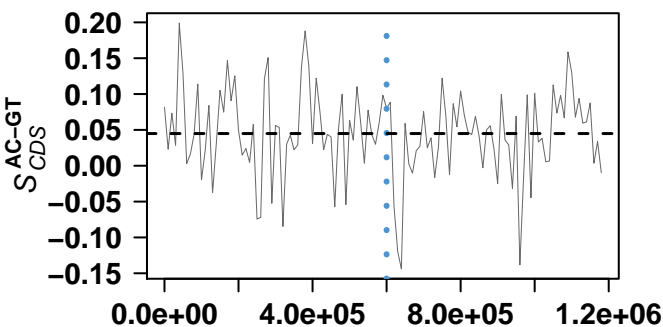
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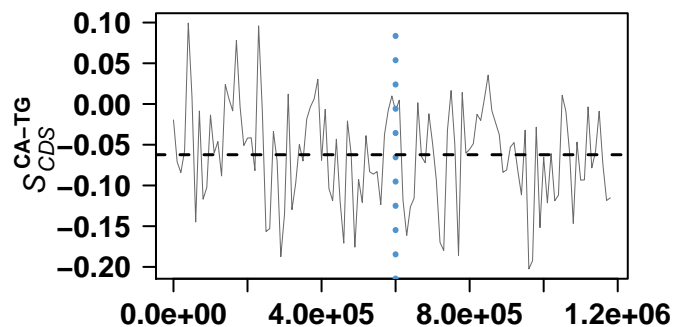
genome coordinates



genome coordinates

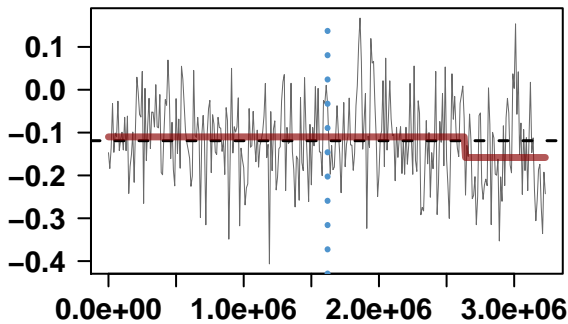


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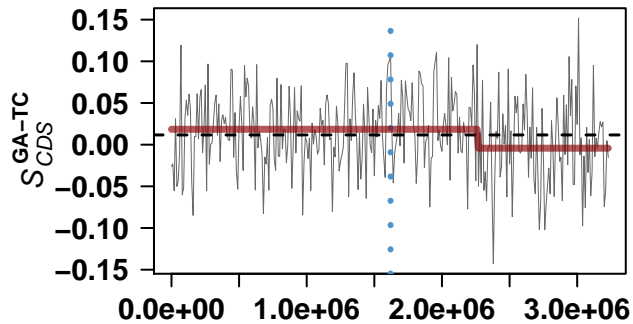


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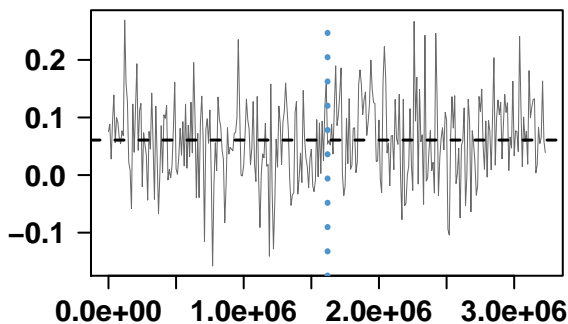
Burkholderia lata



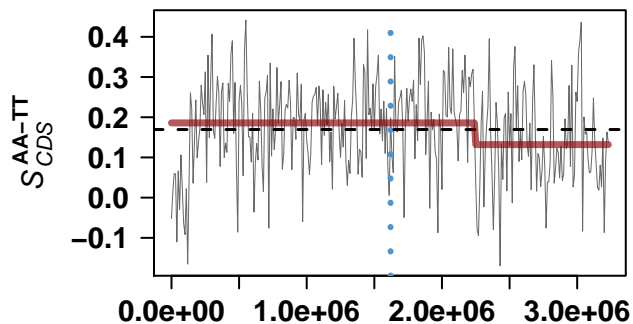
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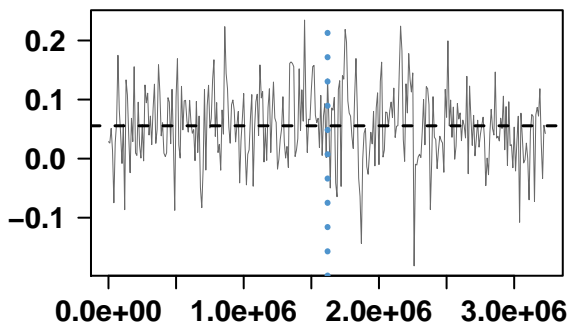
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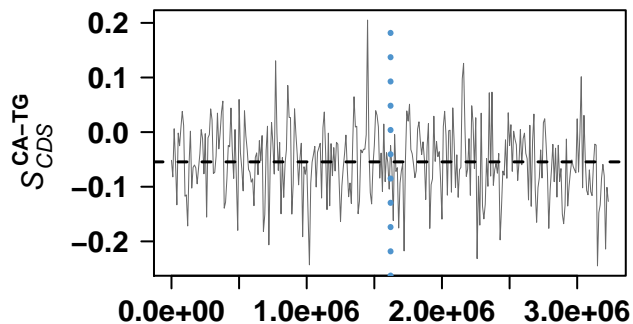
genome coordinates



genome coordinates

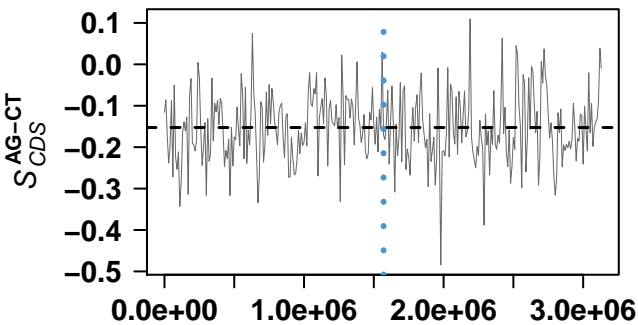


genome coordinates

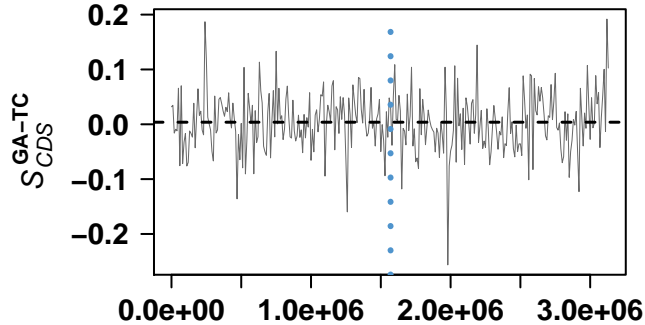


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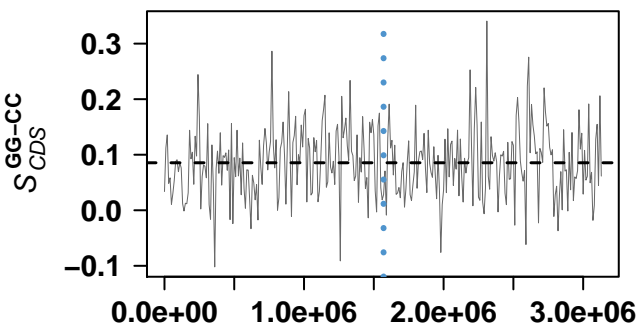
Burkholderia lata



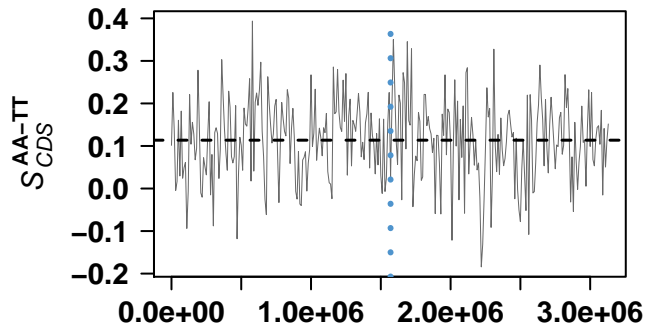
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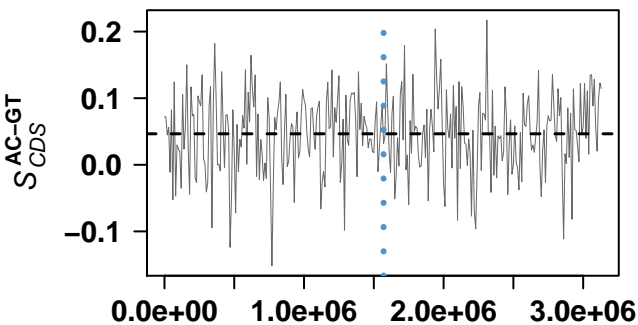
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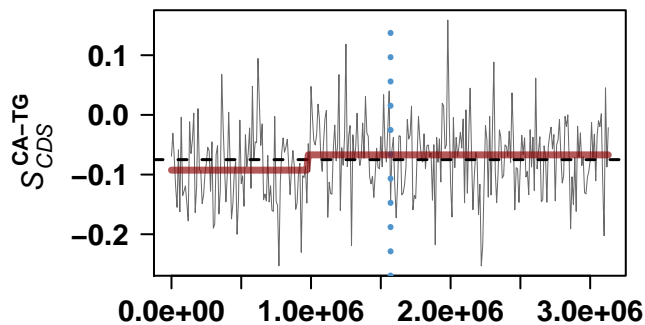
genome coordinates



genome coordinates

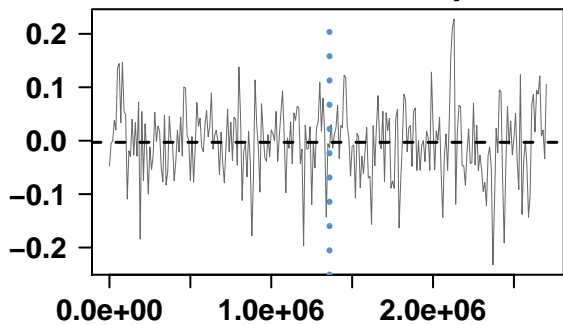


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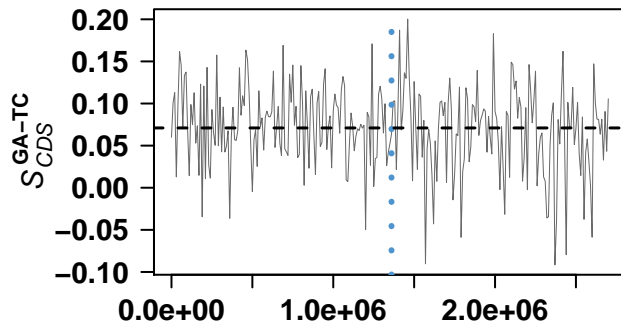


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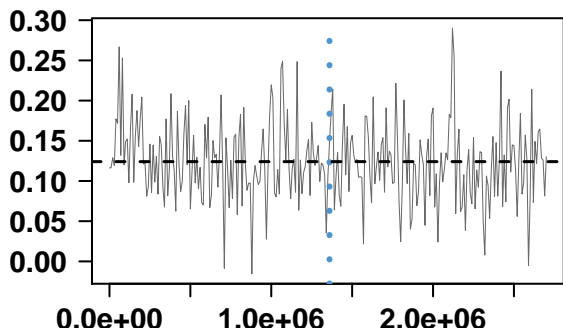
Nitrosospira multiformis ATCC 25196



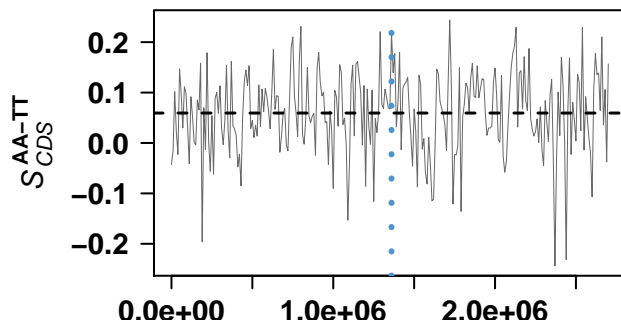
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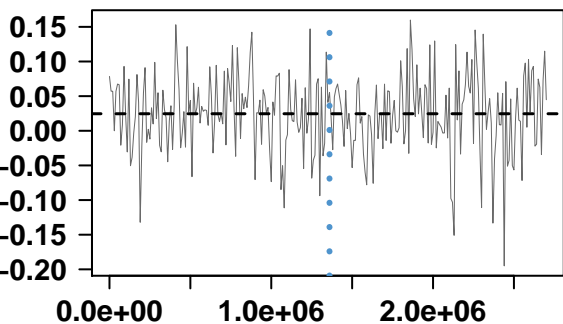
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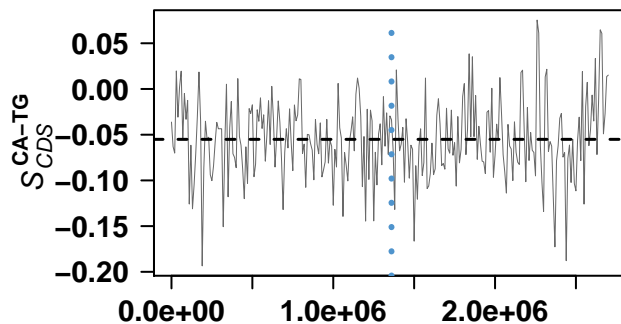
genome coordinates



genome coordinates

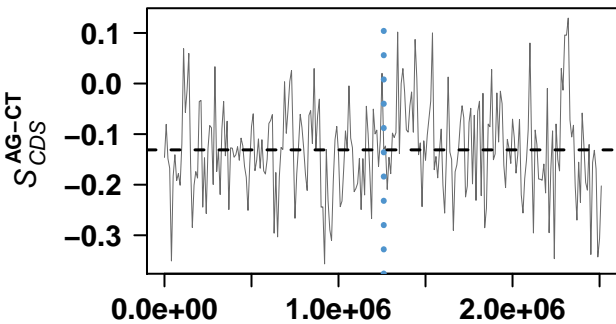


genome coordinates

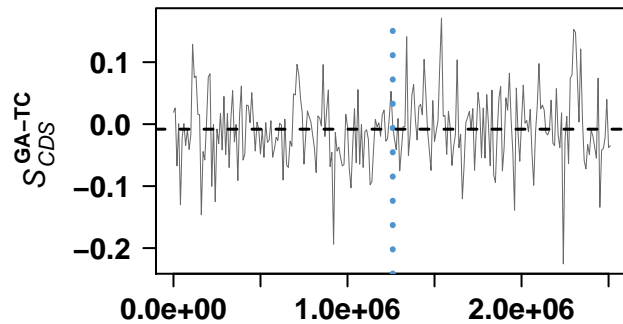


genome coordinates

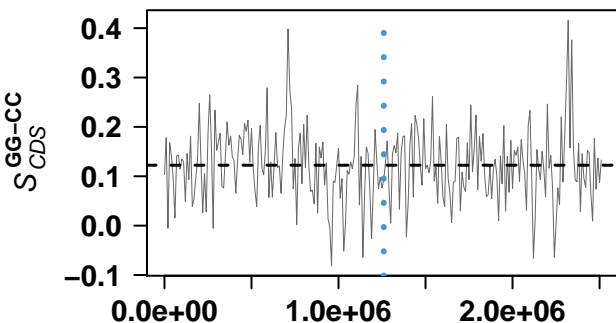
Burkholderia thailandensis E264



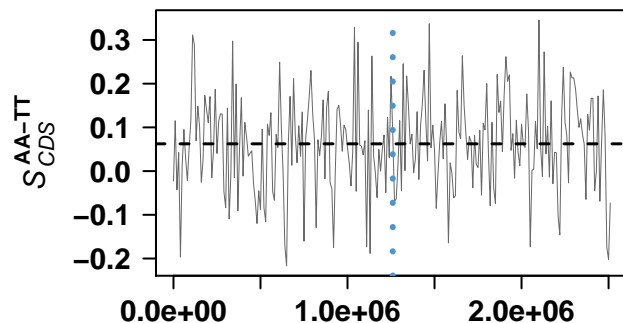
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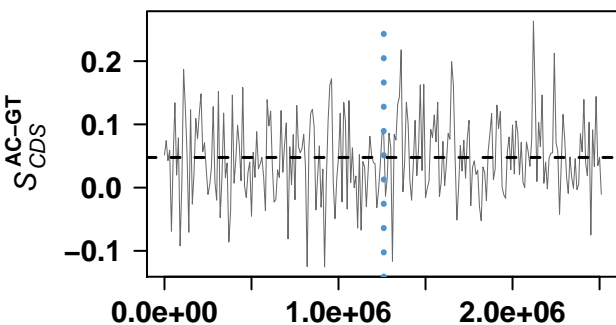
genome coordinates



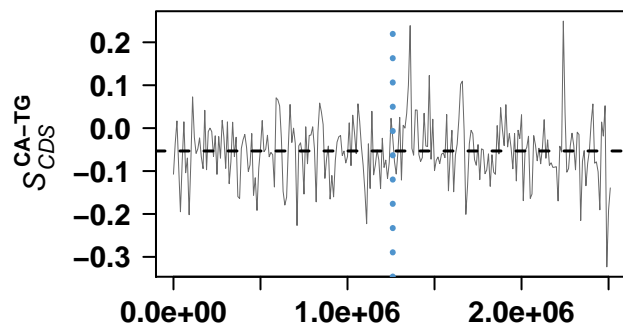
genome coordinates



genome coordinates

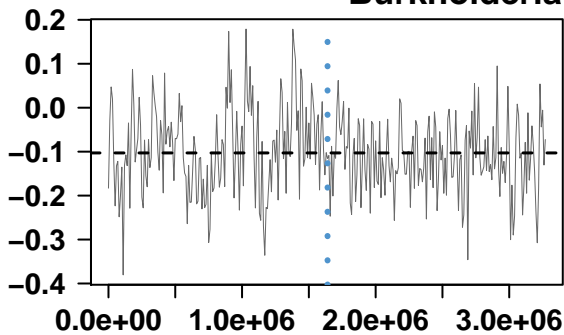


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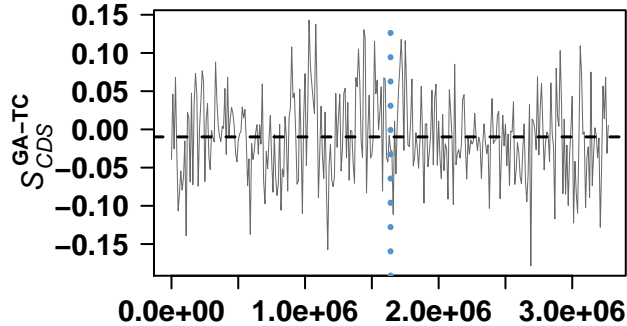


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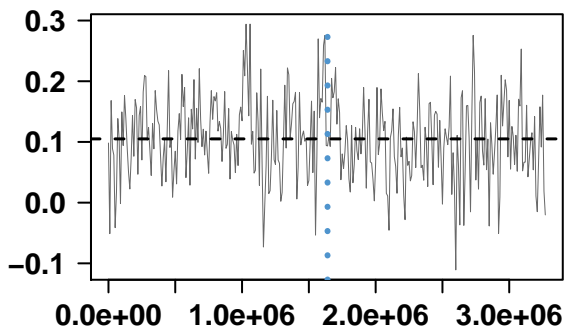
Burkholderia thailandensis E264



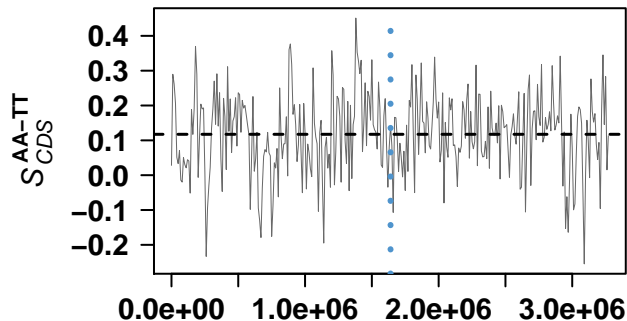
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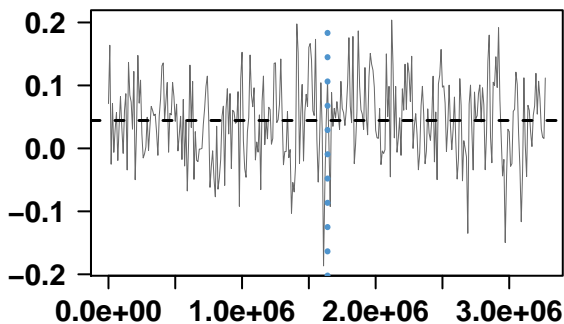
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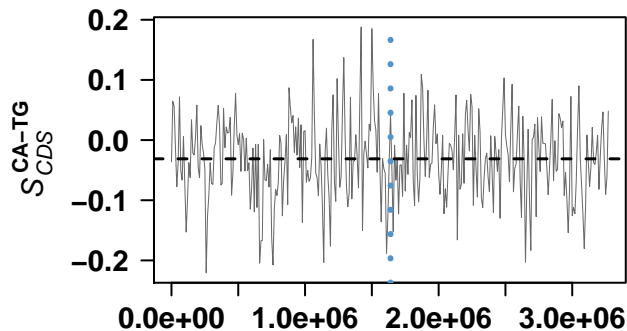
genome coordinates



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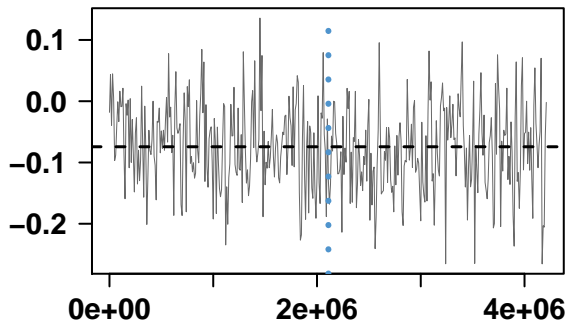


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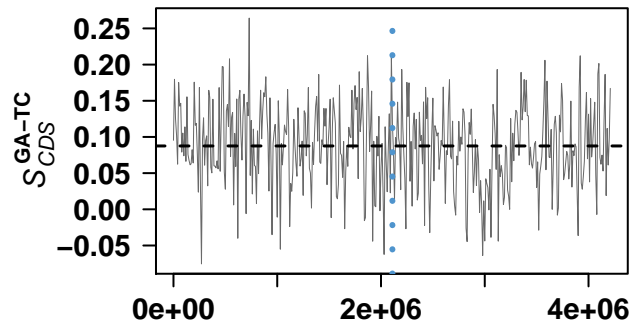


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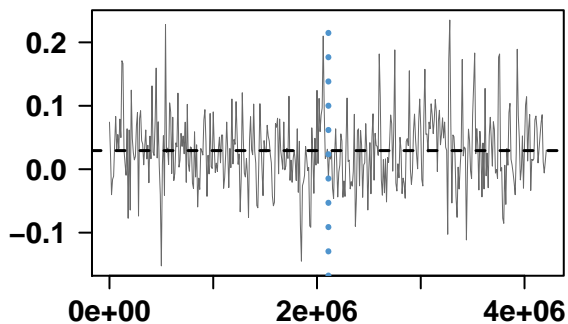
Albidiferax ferrireducens T118



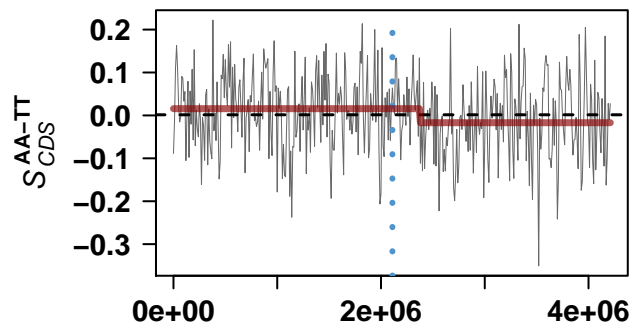
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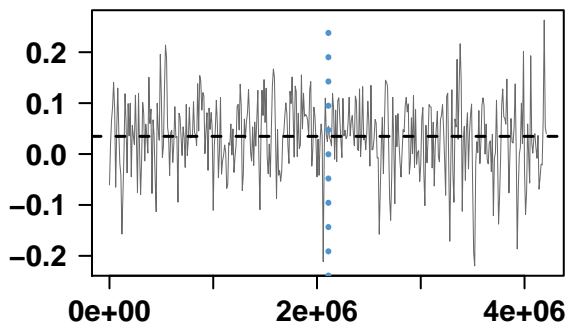
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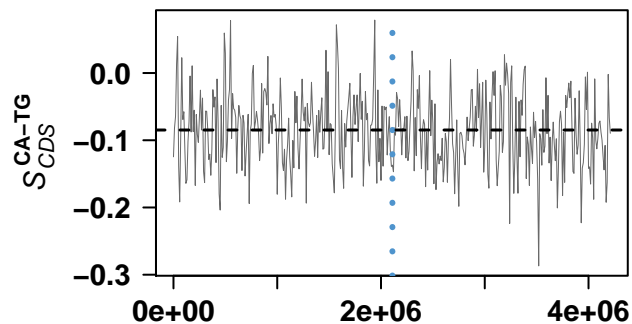
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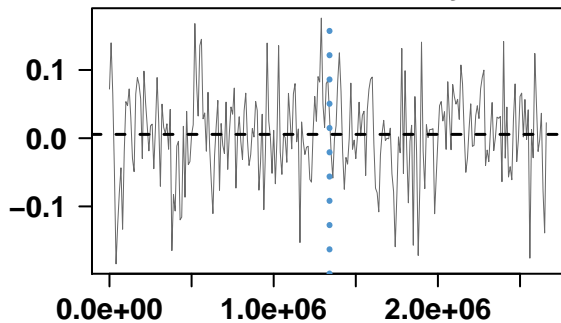


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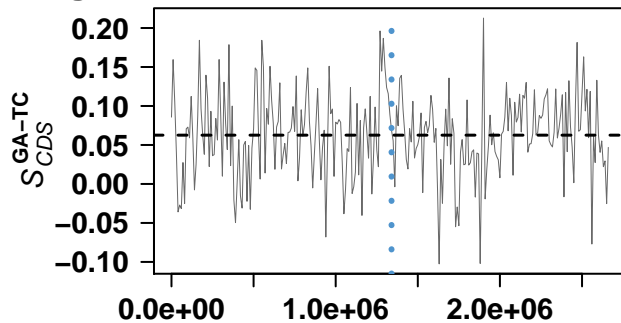


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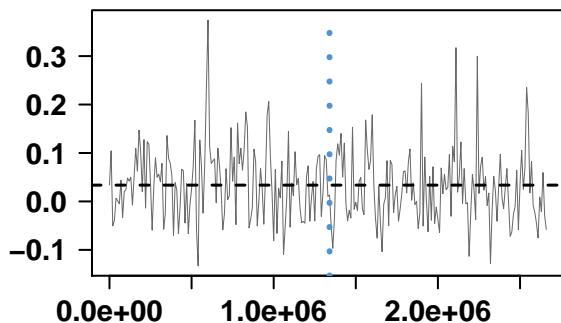
Methylobacillus flagellatus KT



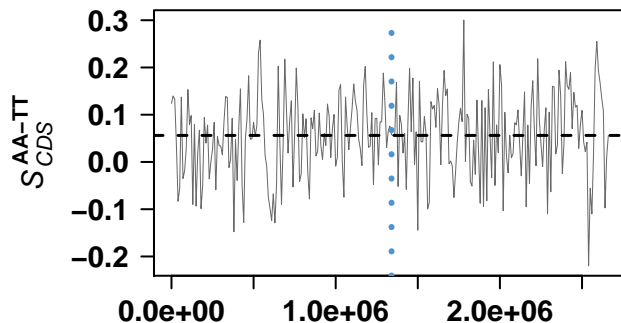
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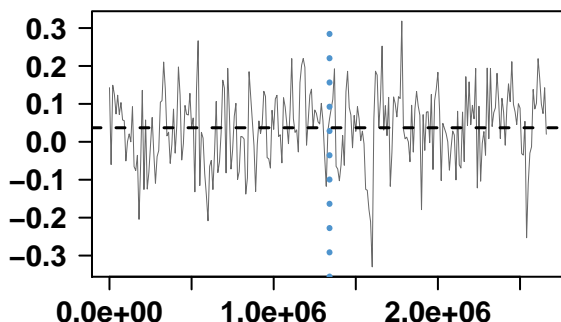
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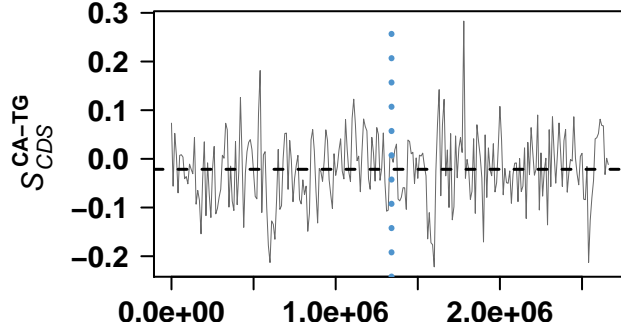
genome coordinates



genome coordinates

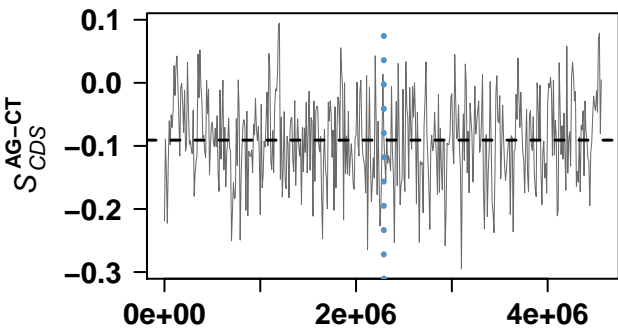


genome coordinates

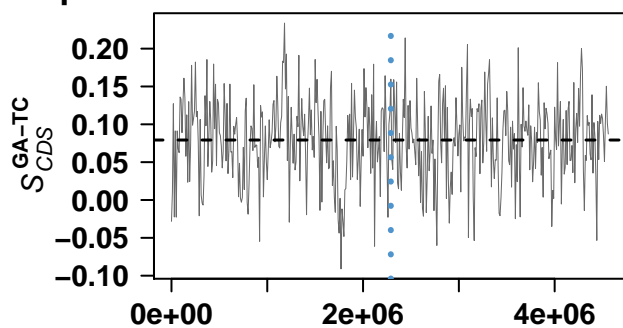


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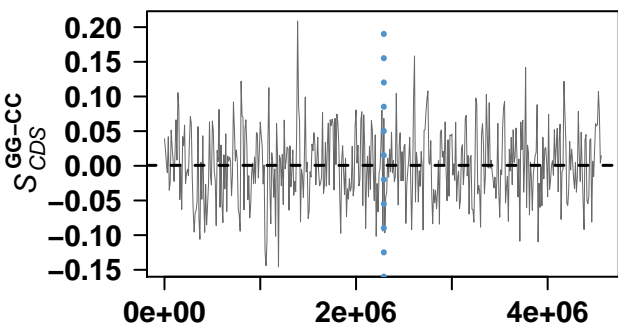
Polaromonas sp. JS666



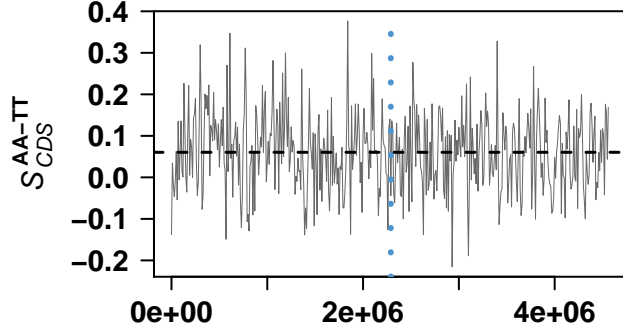
genome coordinates



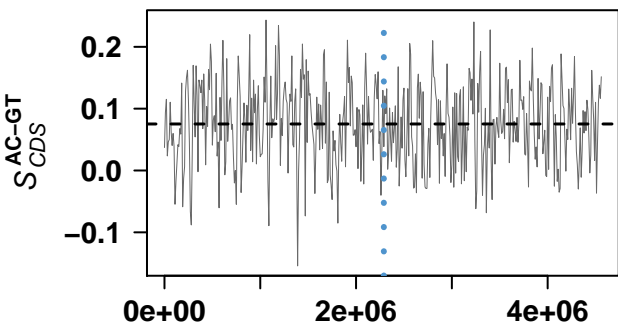
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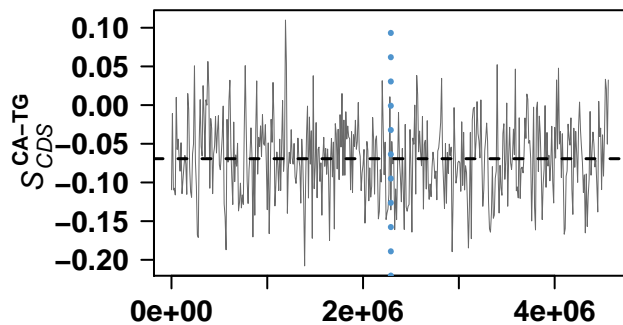
genome coordinates



genome coordinates

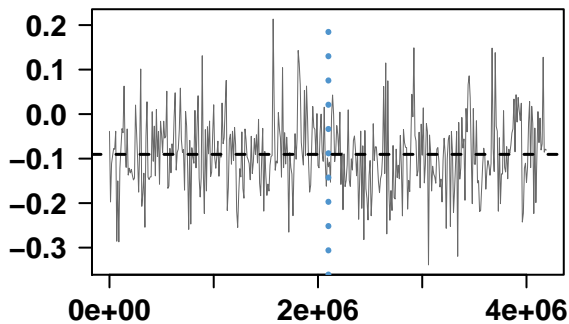


genome coordinates

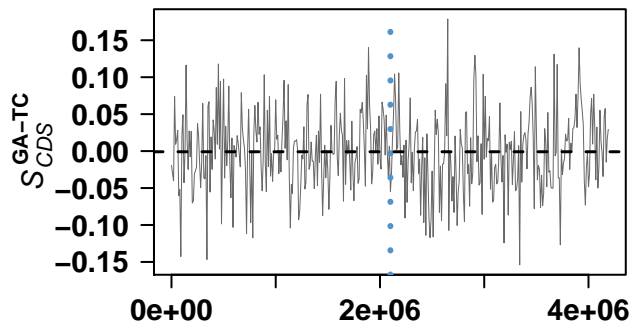


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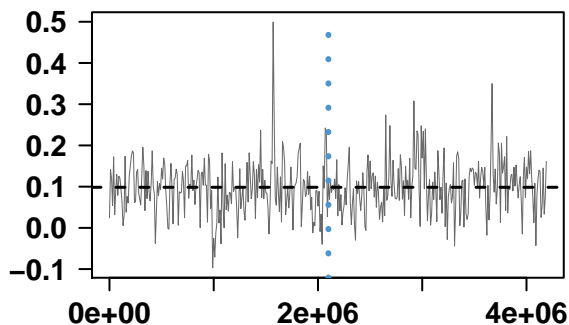
Burkholderia xenovorans LB400



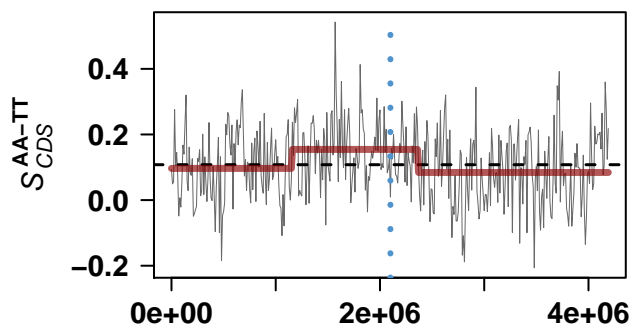
genome coordinates



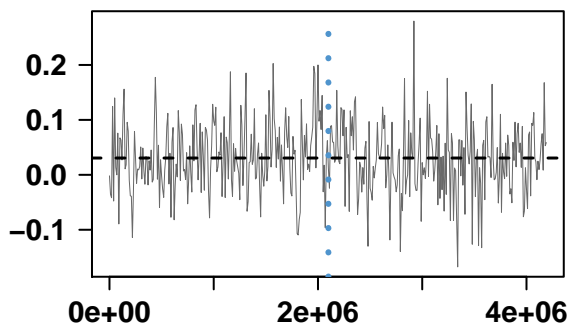
genome coordinates



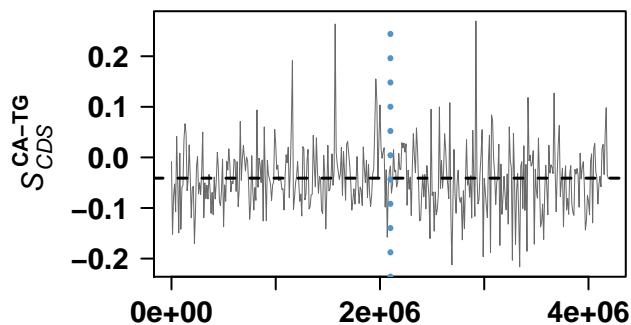
genome coordinates



genome coordinates

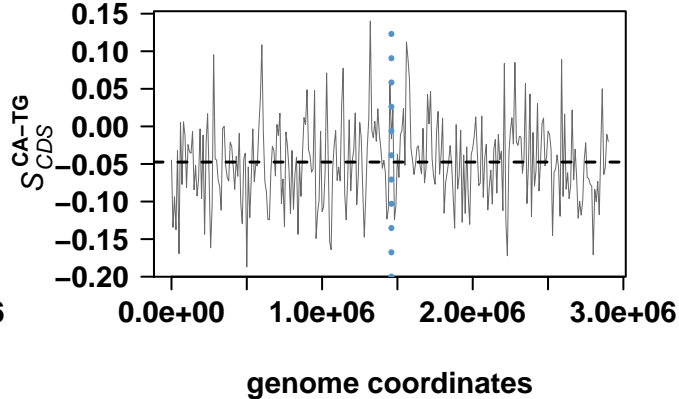
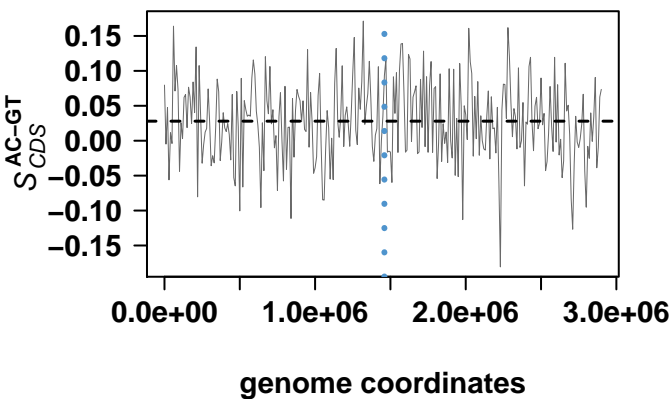
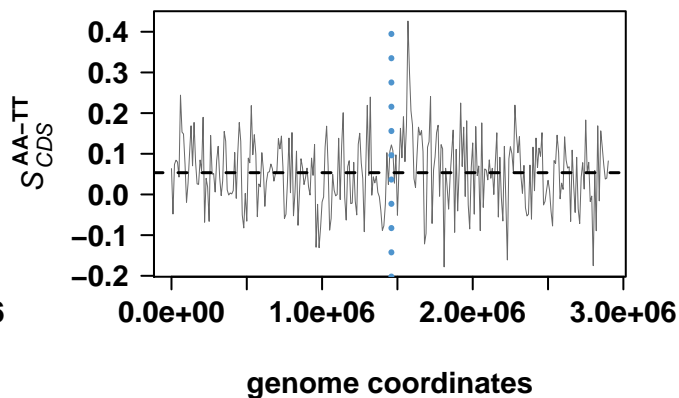
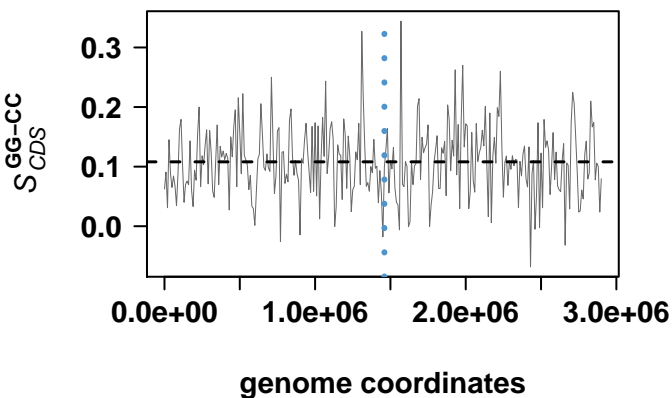
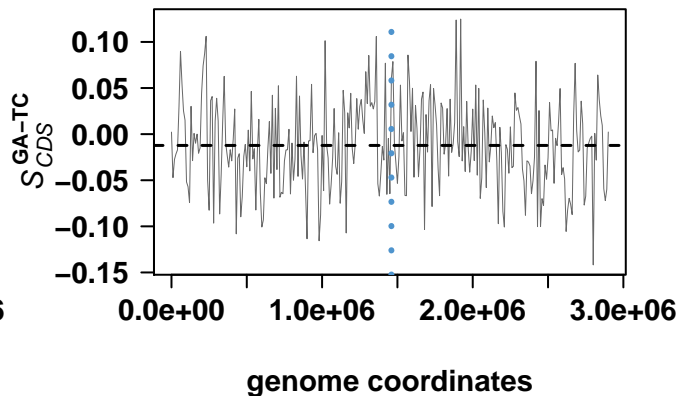
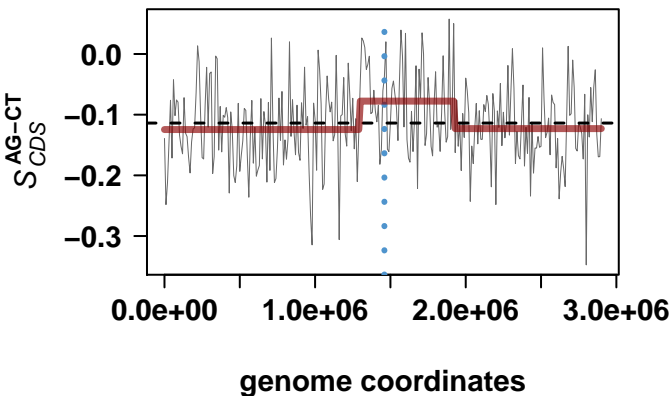


genome coordinates

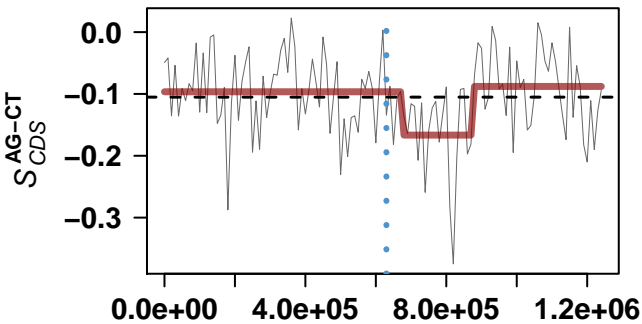


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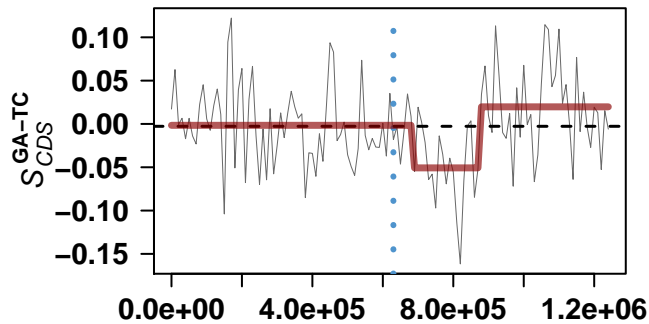
Burkholderia xenovorans LB400



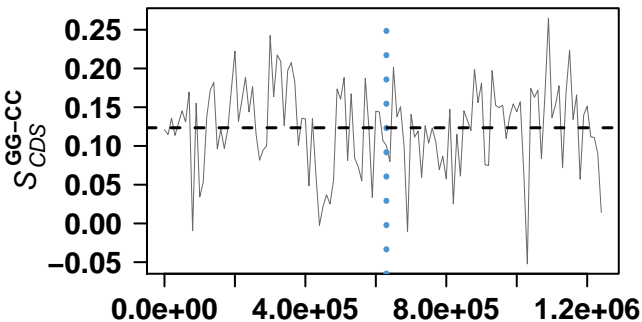
Burkholderia xenovorans LB400



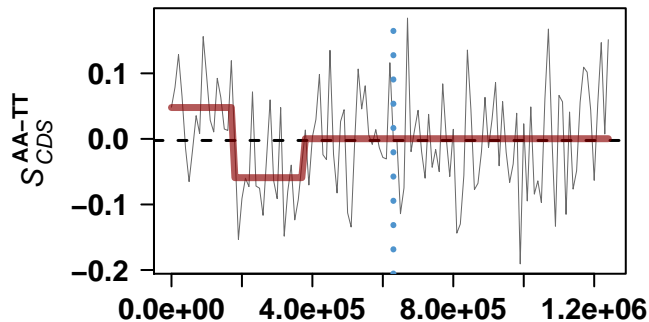
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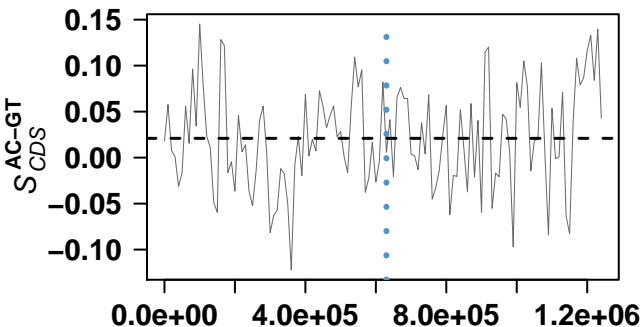
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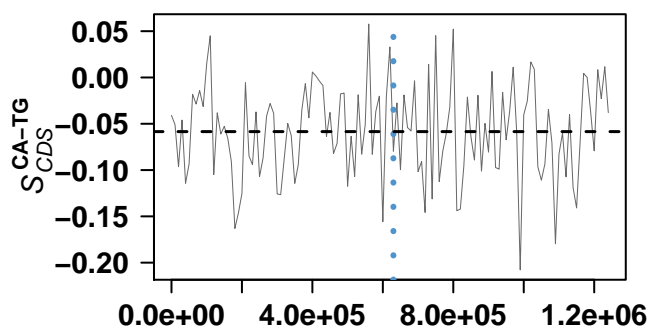
genome coordinates



genome coordinates

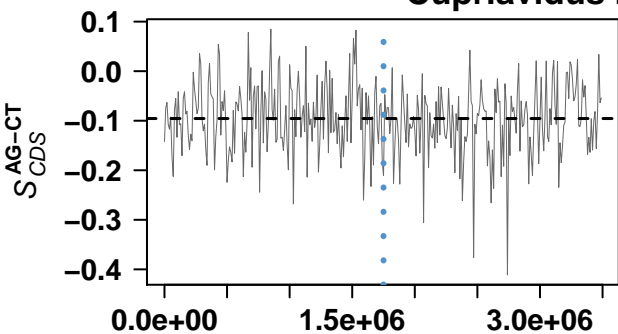


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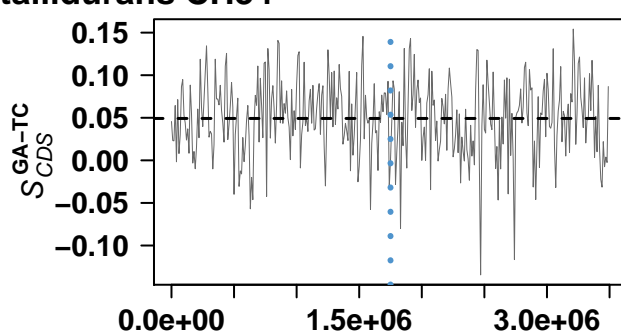


genome coordinates

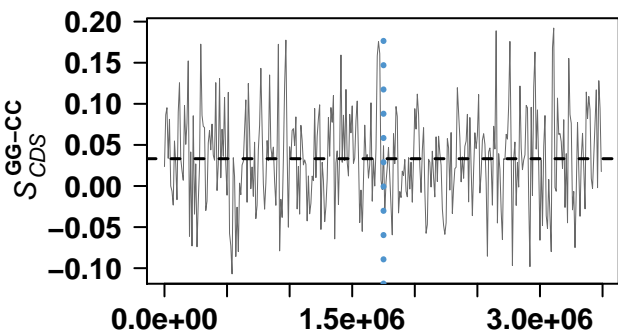
Cupriavidus metallidurans CH34



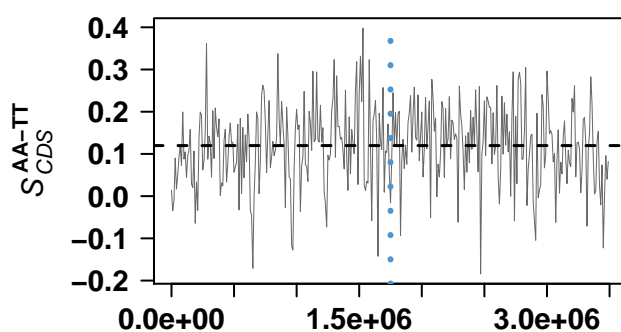
genome coordinates



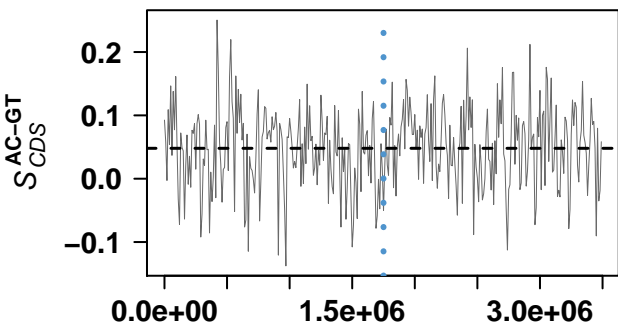
genome coordinates



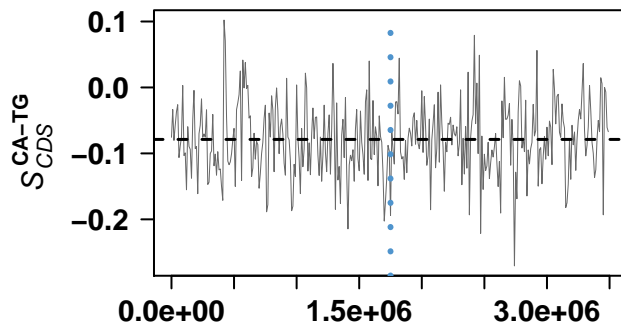
genome coordinates



genome coordinates

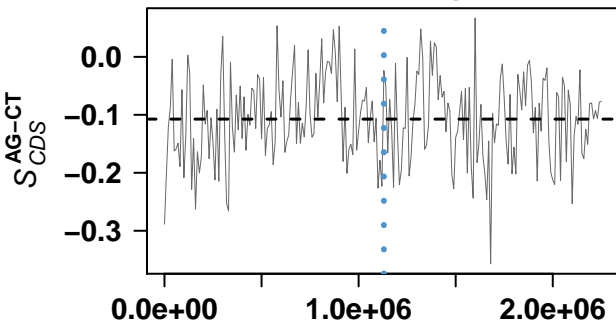


genome coordinates

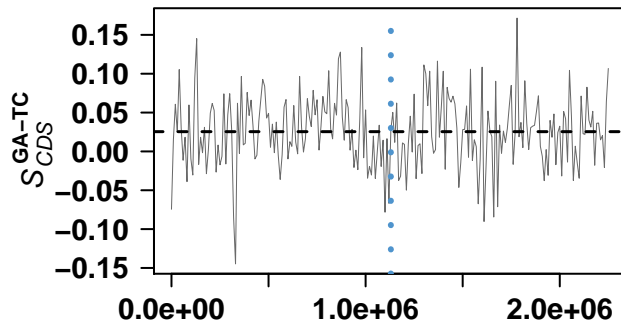


genome coordinates

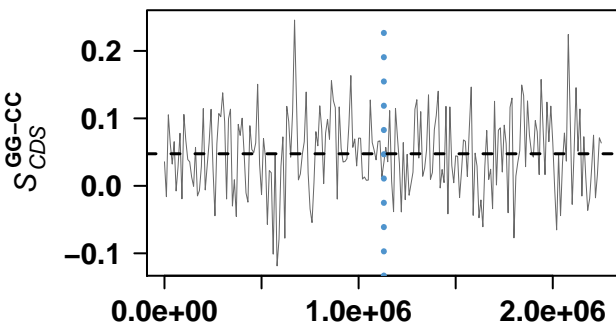
Cupriavidus metallidurans CH34



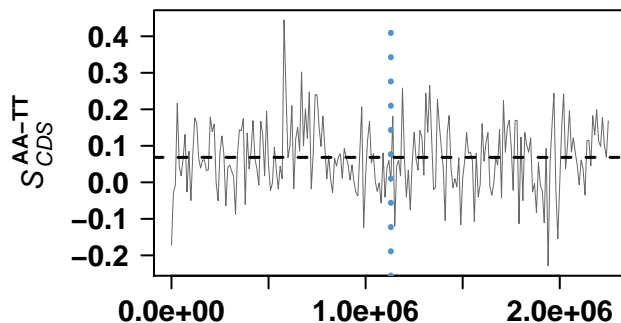
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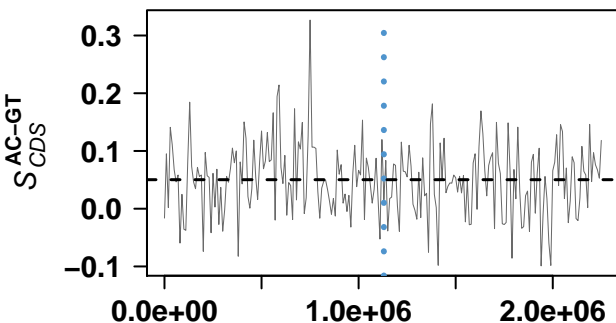
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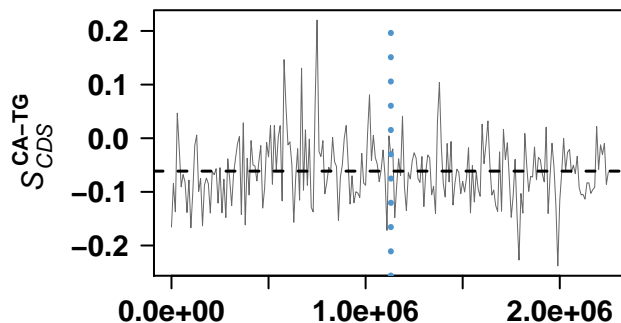
genome coordinates



genome coordinates

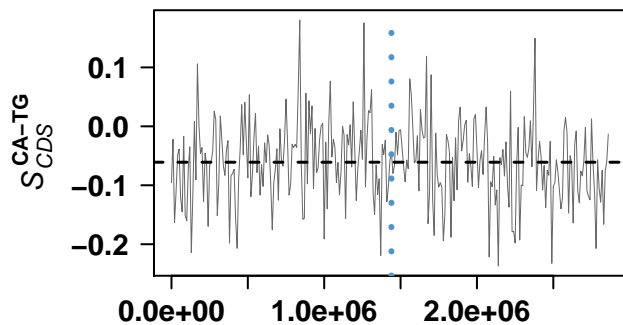
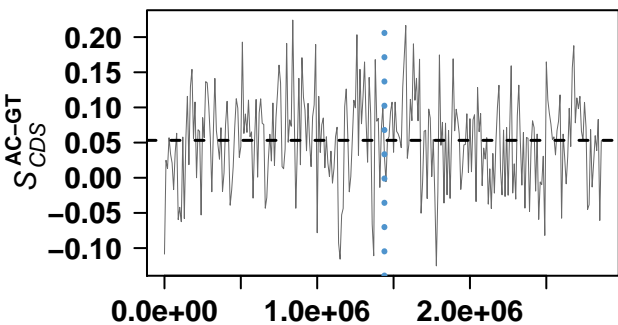
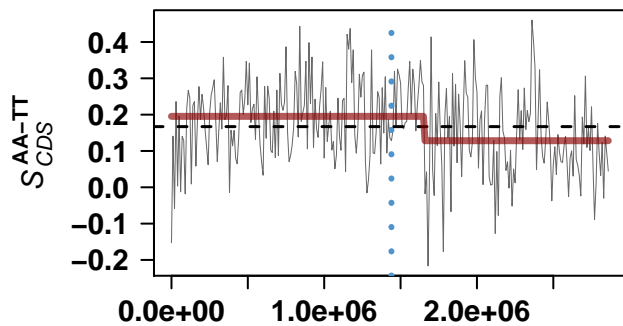
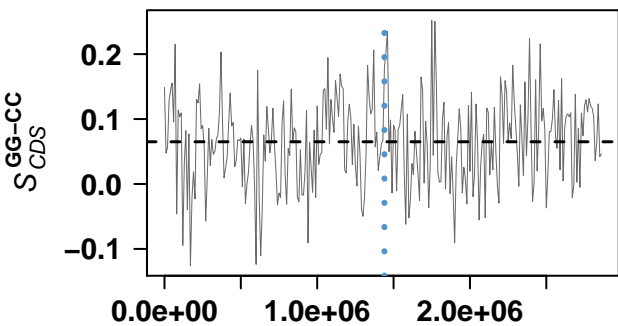
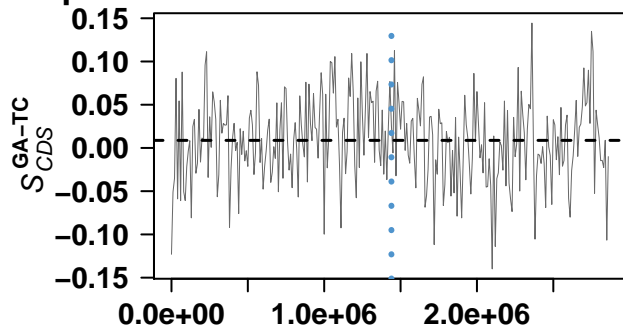
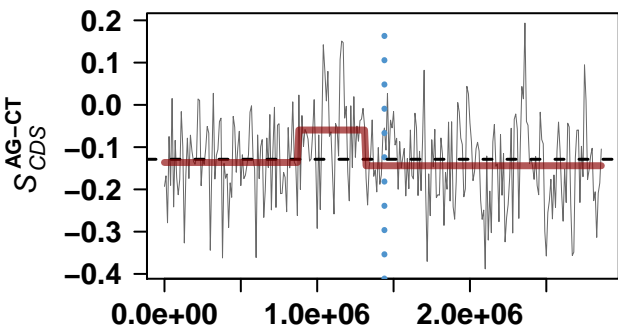


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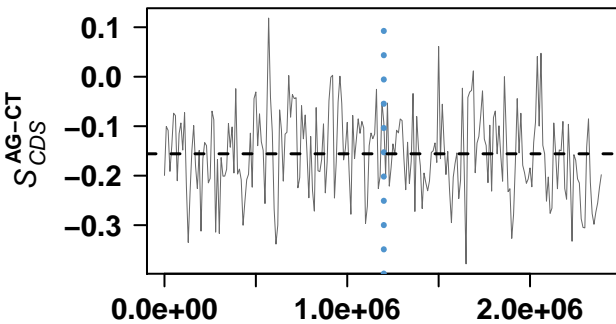


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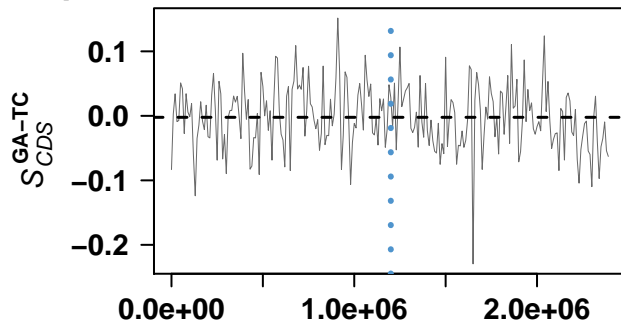
Burkholderia cenocepacia AU 1054



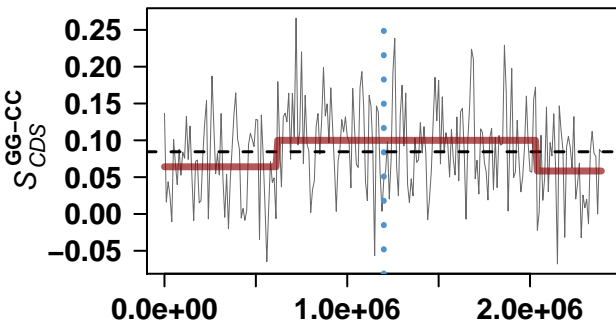
Burkholderia cenocepacia AU 1054



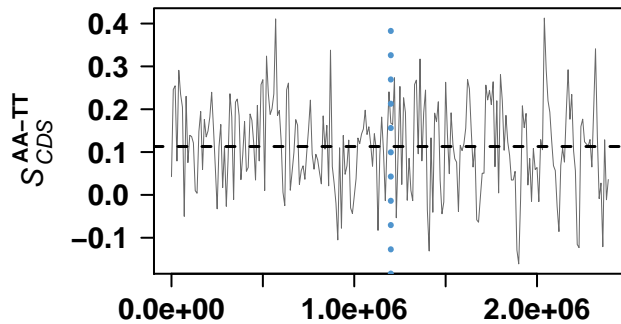
genome coordinates



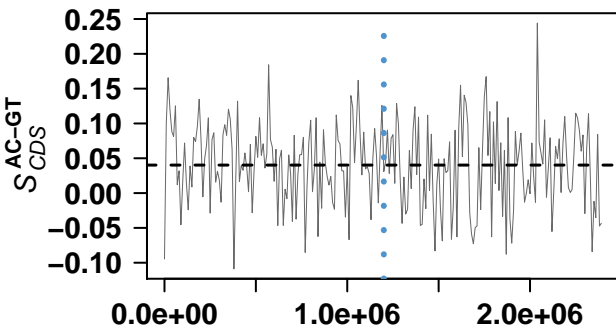
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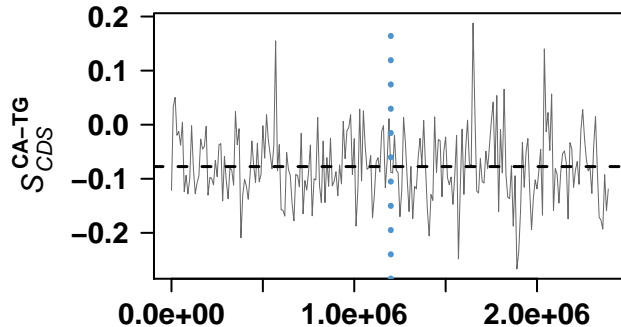
genome coordinates



genome coordinates

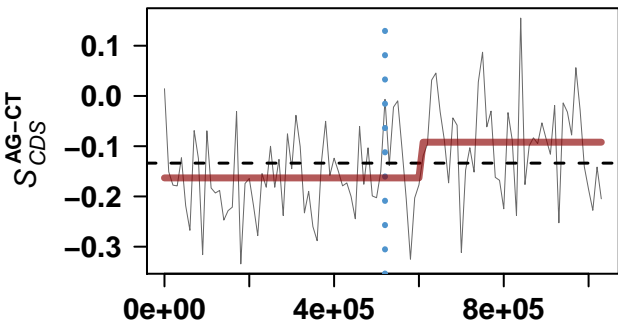


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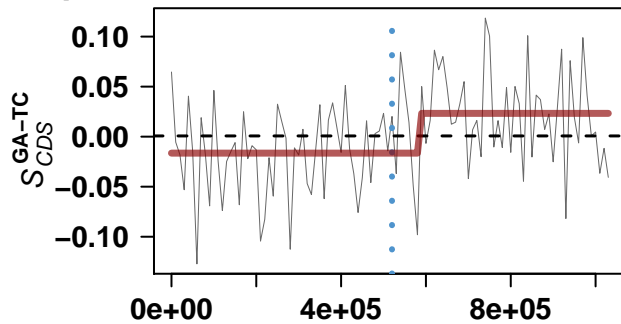


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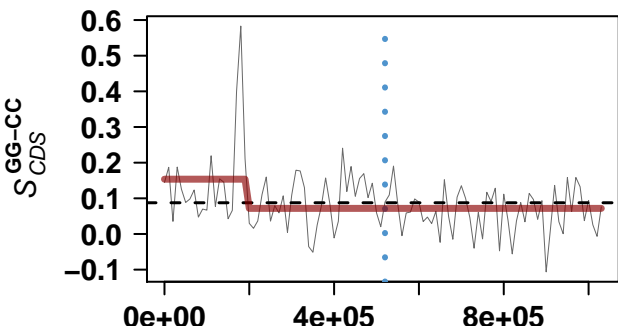
Burkholderia cenocepacia AU 1054



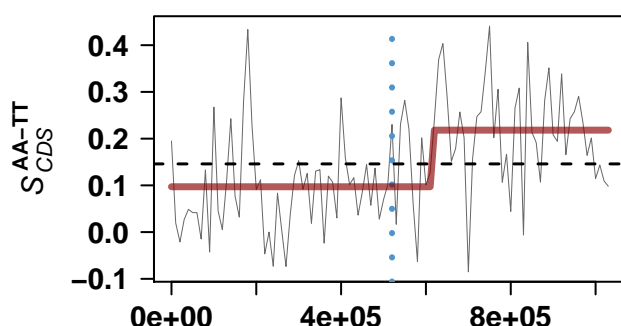
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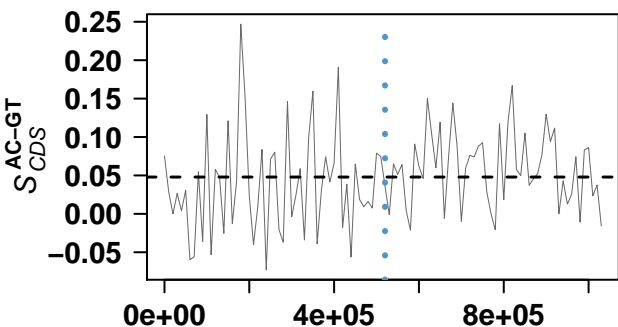
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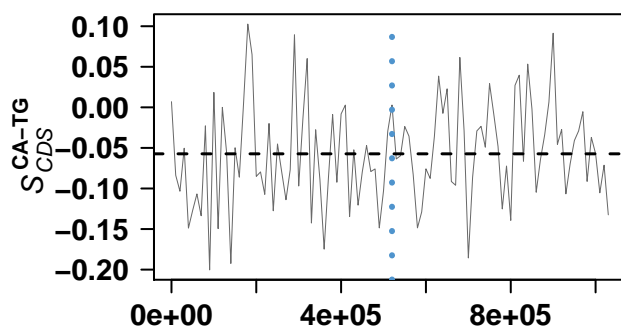
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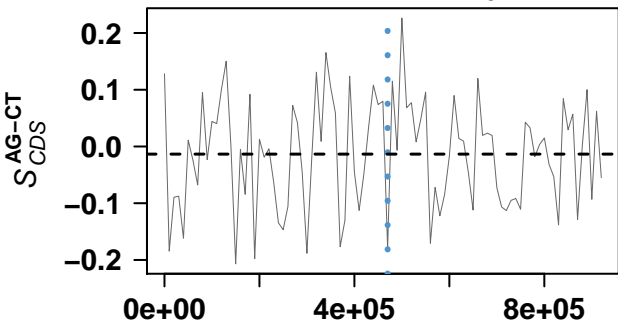


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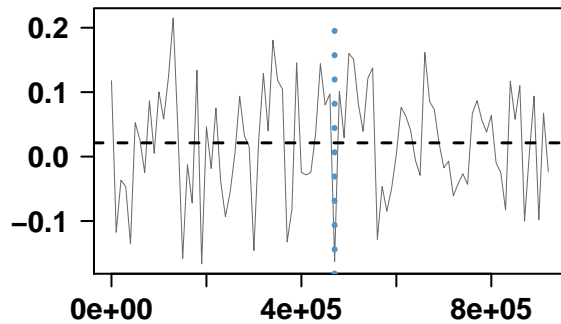


genome coordinates

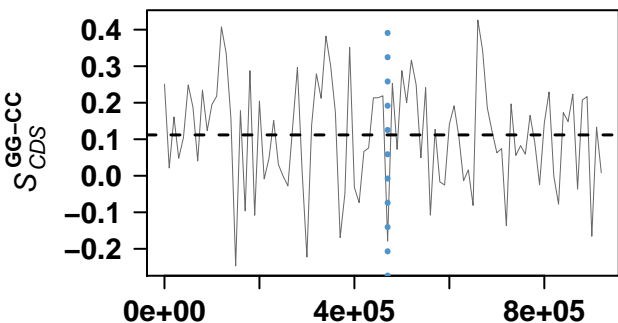
Chlamydia trachomatis D/UW-3/CX



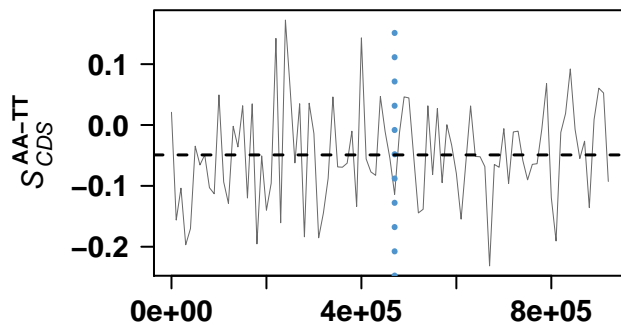
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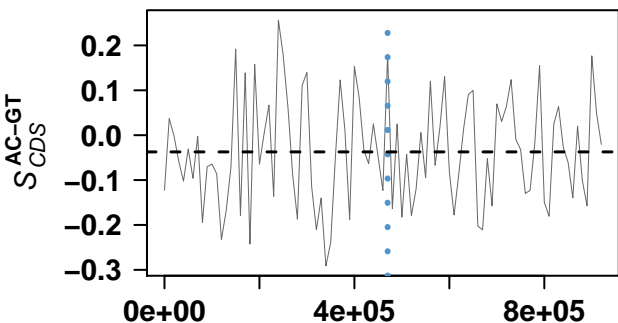
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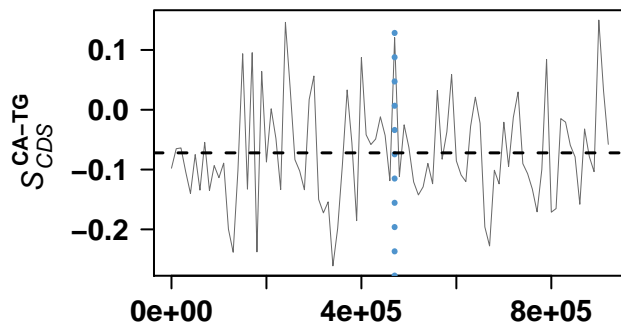
genome coordinates



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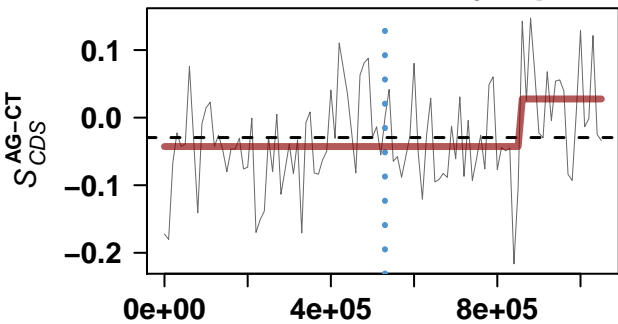


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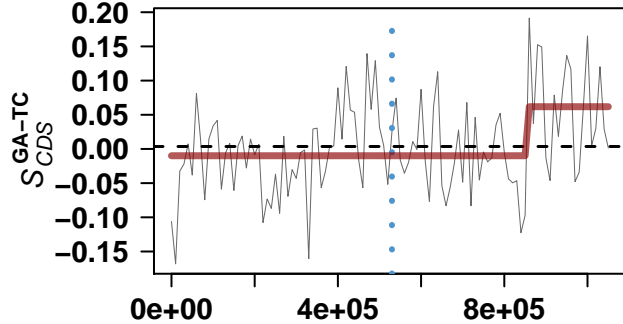


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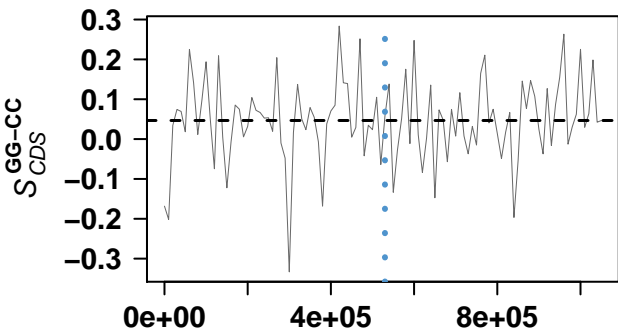
Chlamydophila pneumoniae CWL029



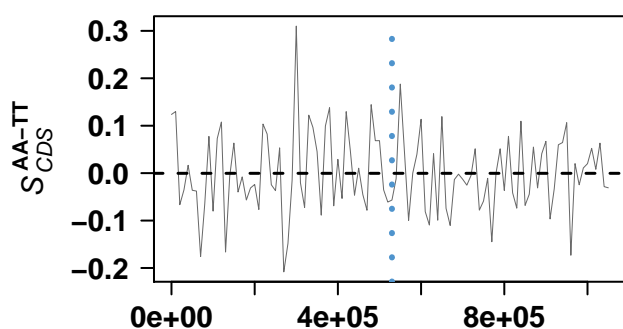
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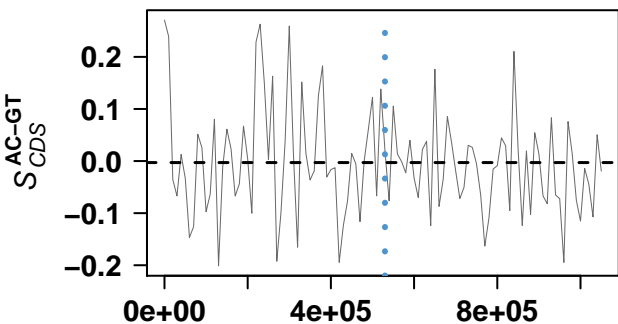
genome coordinates



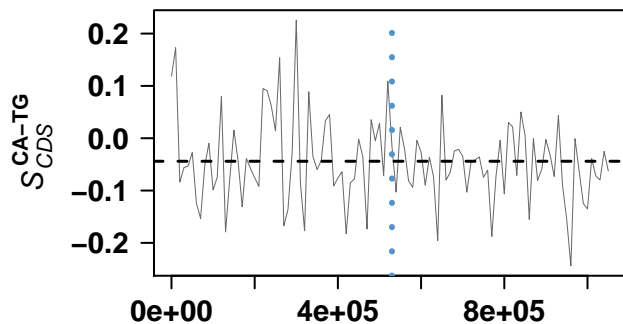
genome coordinates



genome coordinates

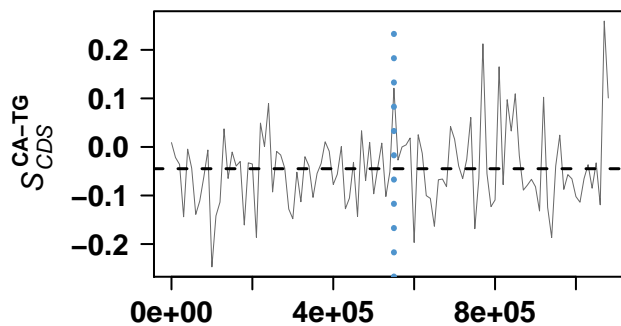
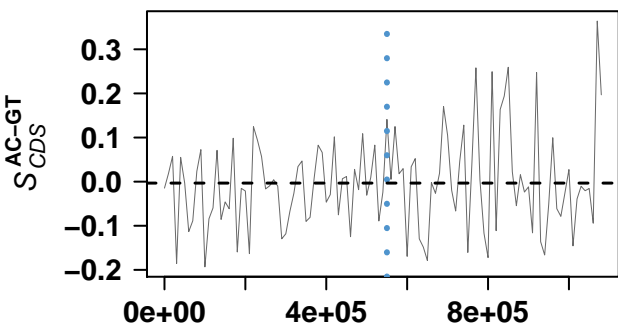
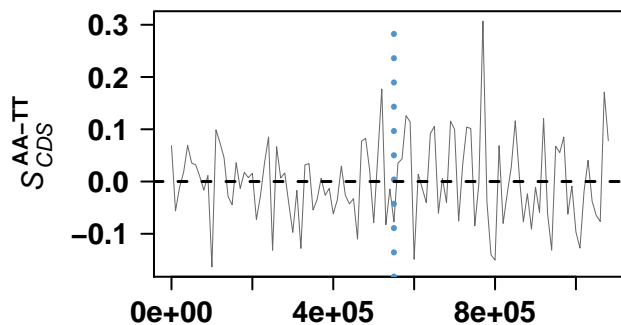
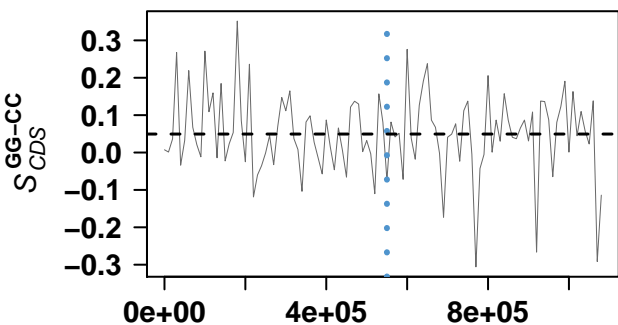
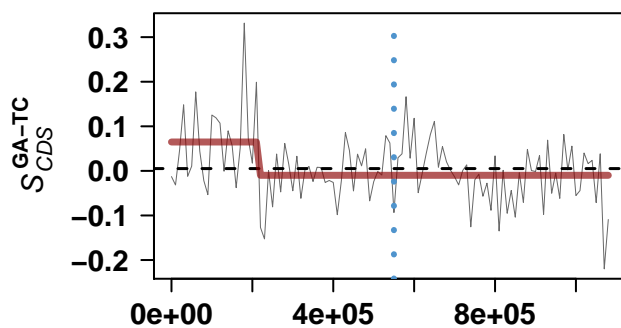
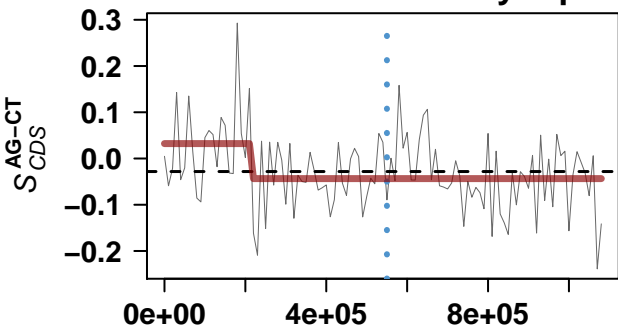


genome coordinates

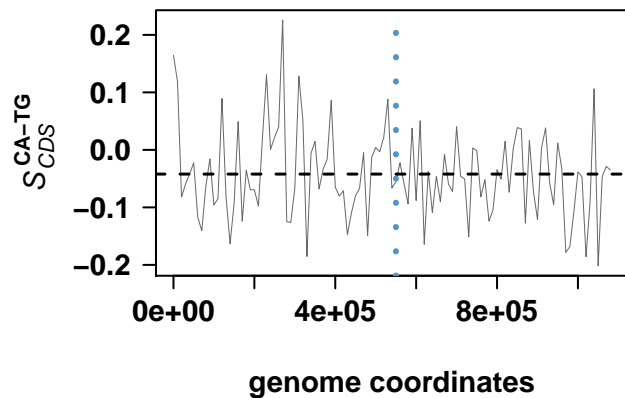
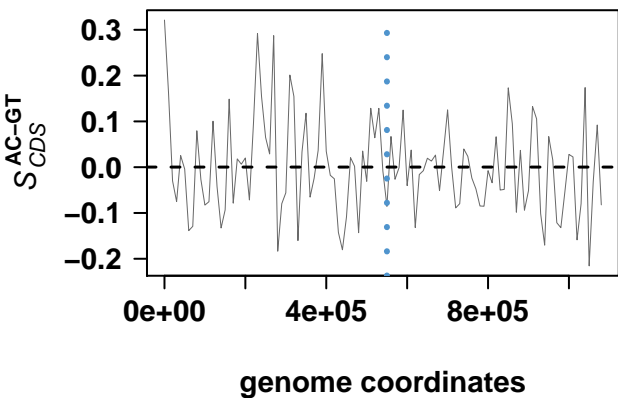
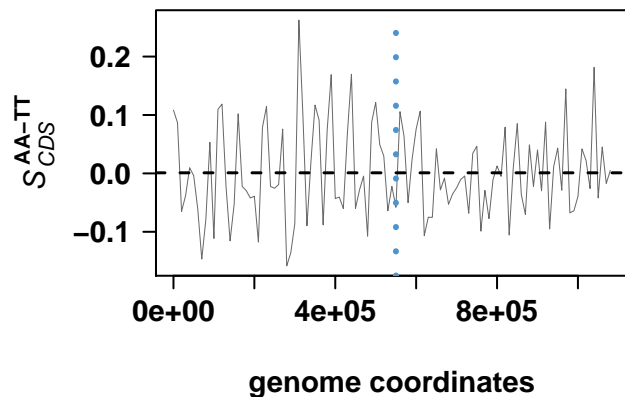
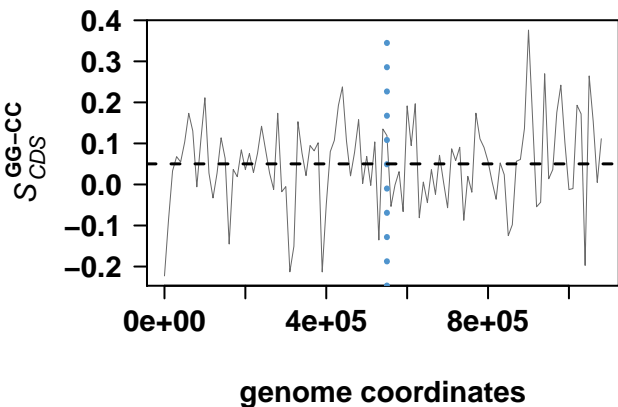
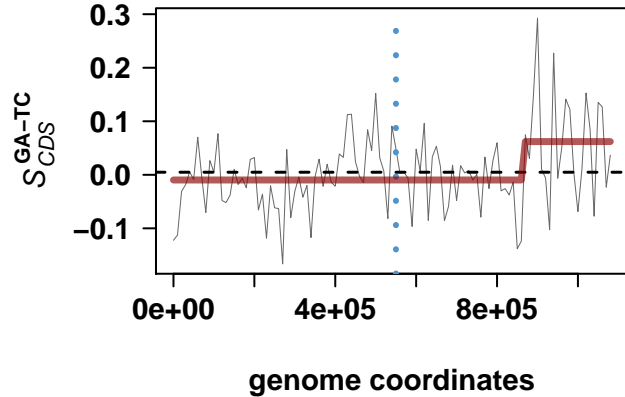
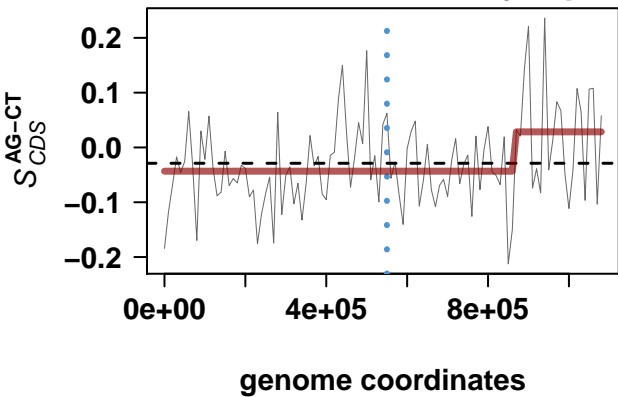


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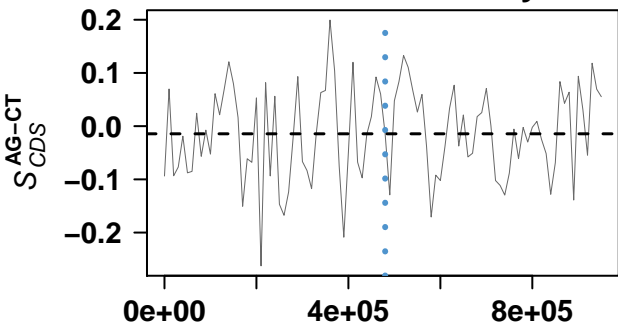
Chlamydomophila pneumoniae AR39



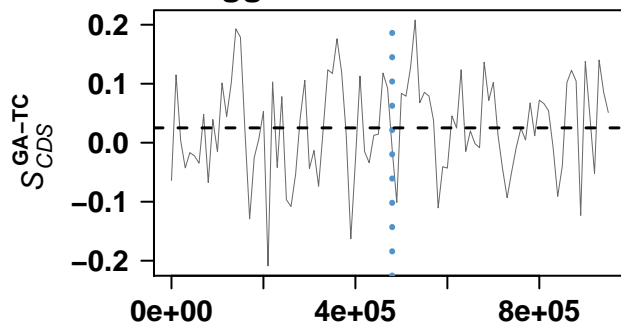
Chlamydomophila pneumoniae J138



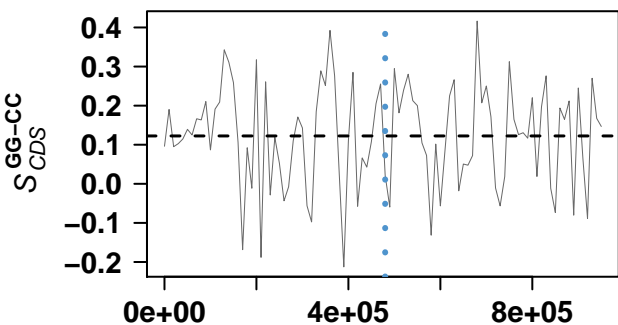
Chlamydia muridarum str. Nigg



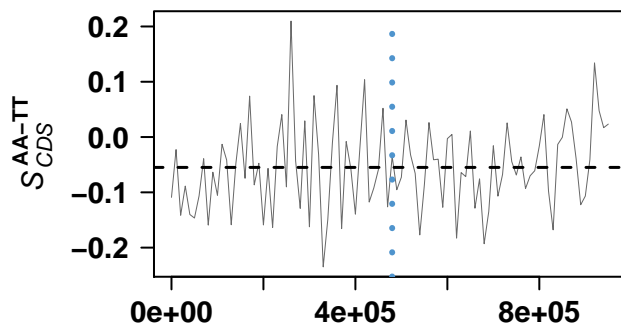
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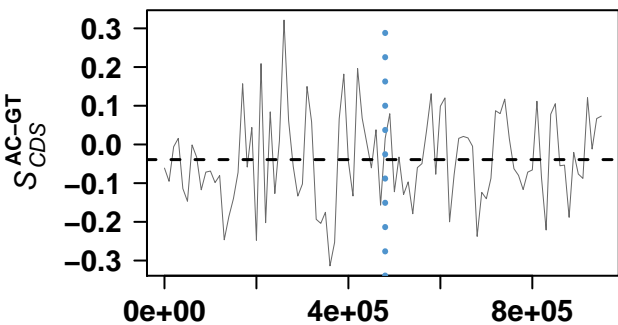
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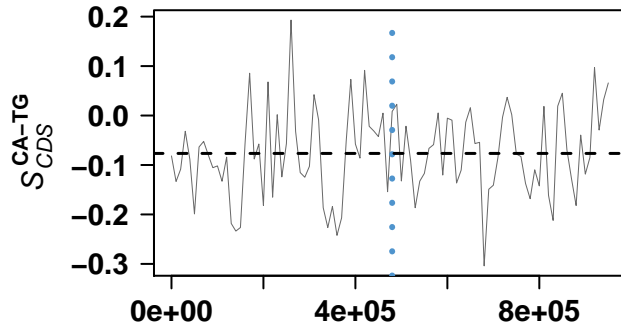
genome coordinates



genome coordinates

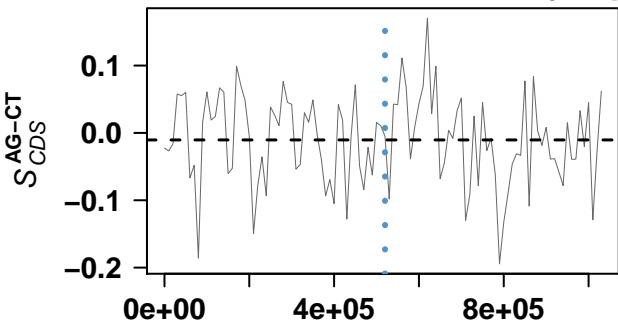


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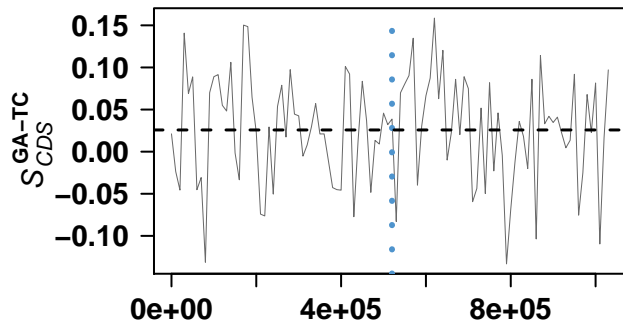


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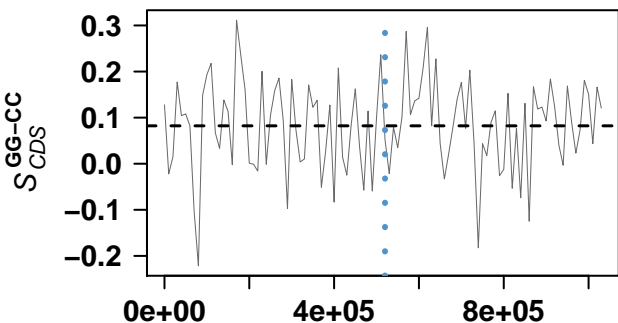
Chlamydomonas reinhardtii GPIC



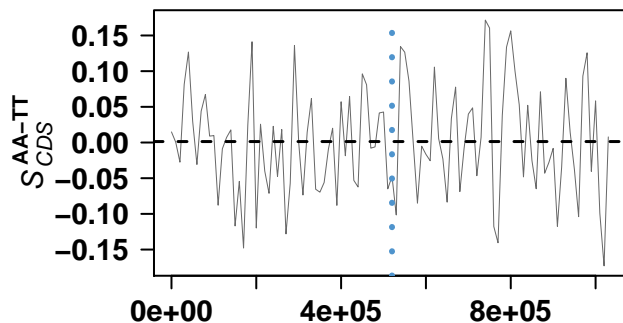
genome coordinates



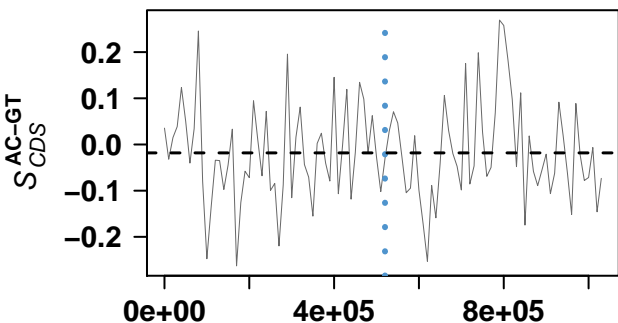
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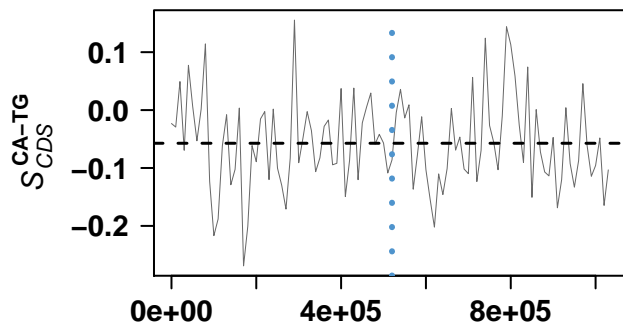
genome coordinates



genome coordinates

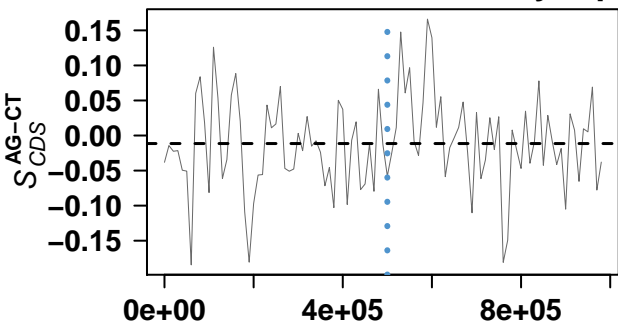


genome coordinates

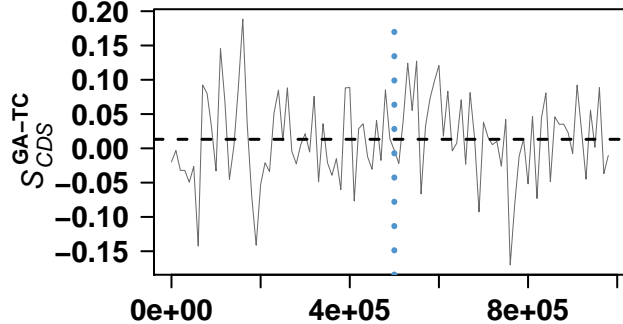


genome coordinates

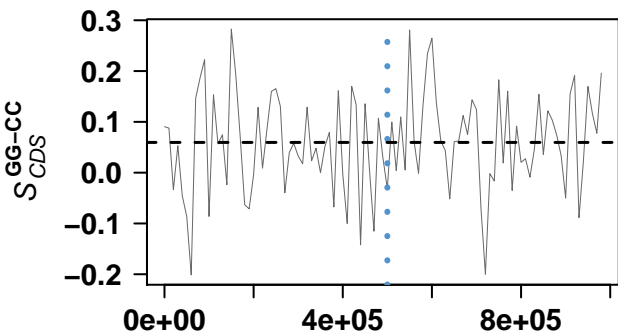
Chlamydomonas abortus S26/3



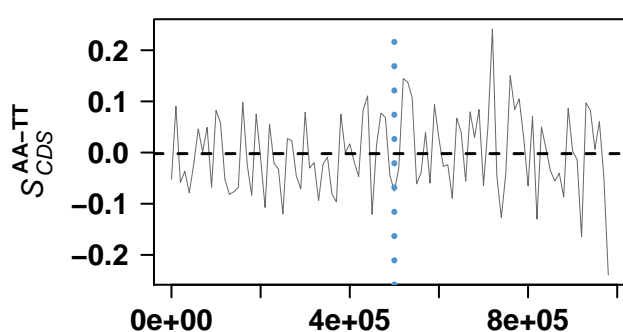
genome coordinates



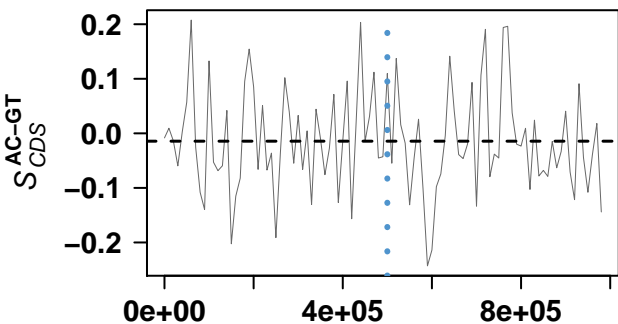
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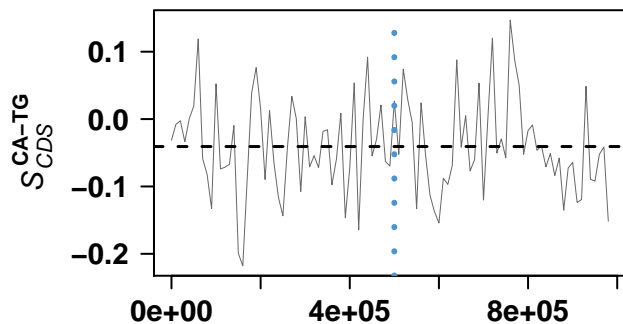
genome coordinates



genome coordinates

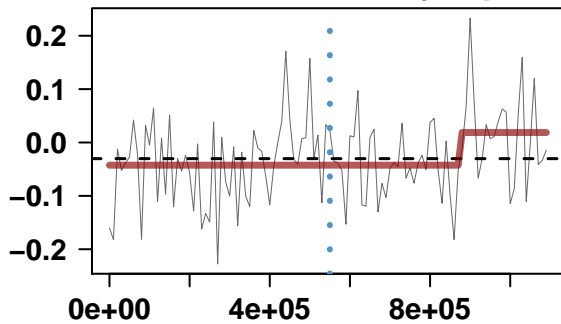


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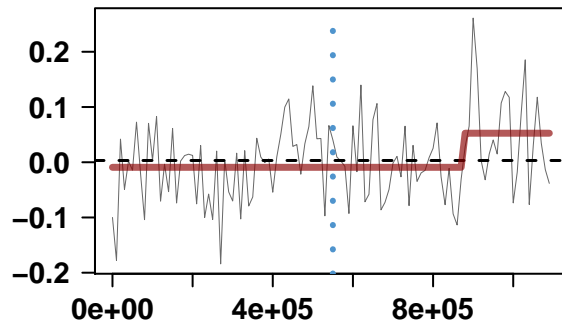


genome coordinates

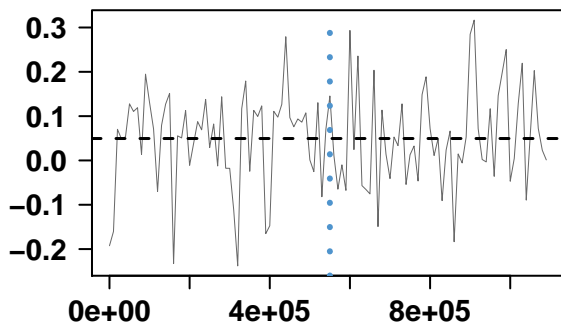
Chlamydophila pneumoniae TW-183



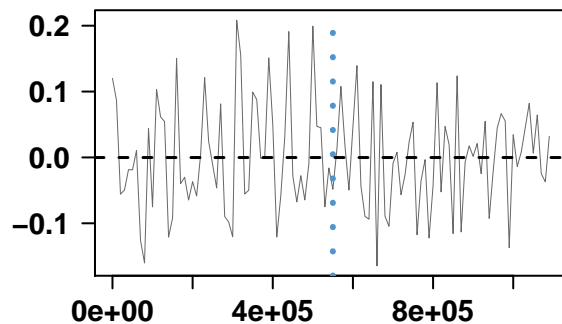
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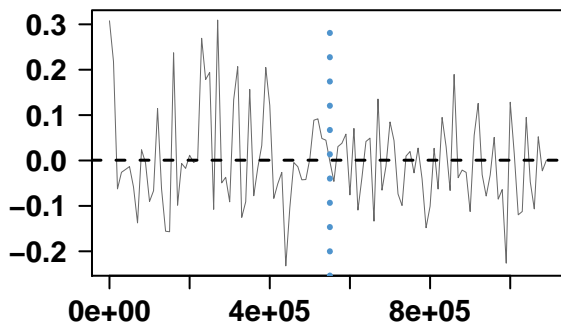
genome coordinates



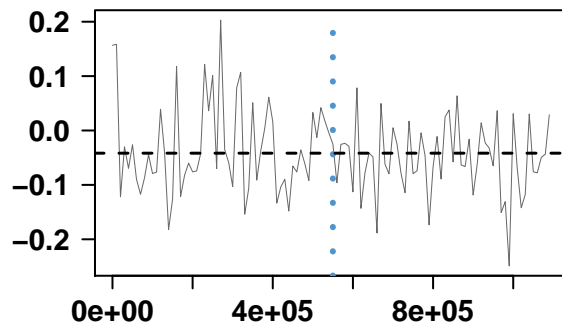
genome coordinates



genome coordinates

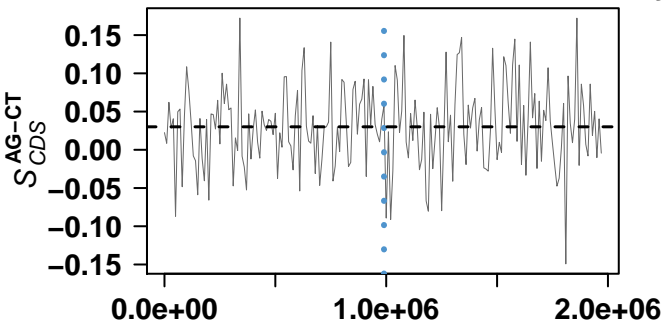


genome coordinates

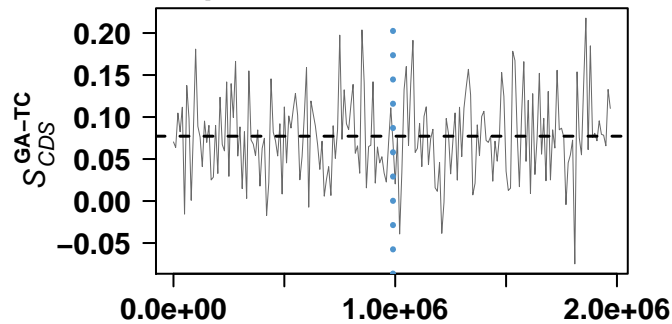


genome coordinates

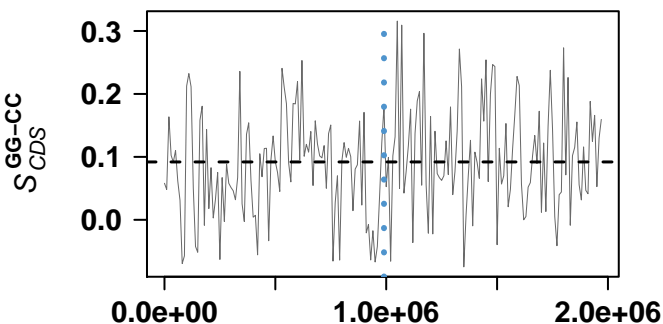
Candidatus Protochlamydia amoebophila UWE25



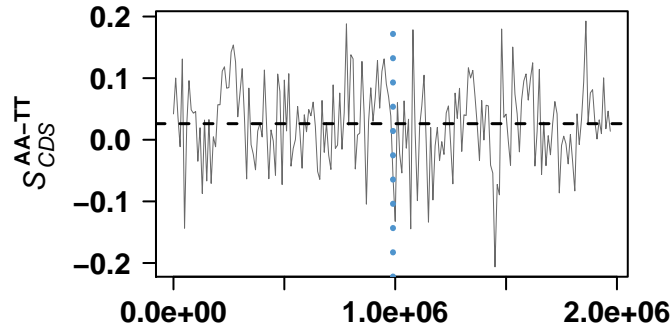
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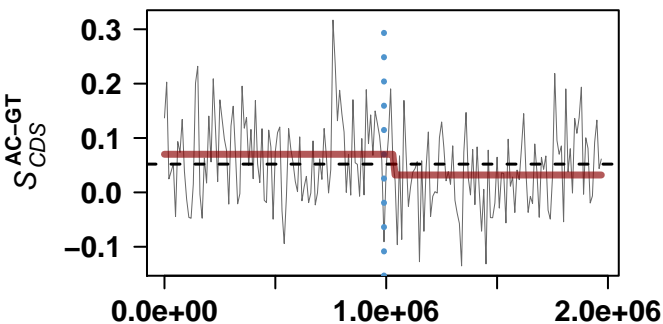
genome coordinates



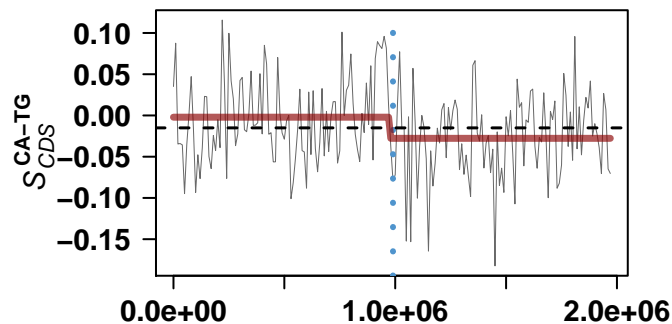
genome coordinates



genome coordinates

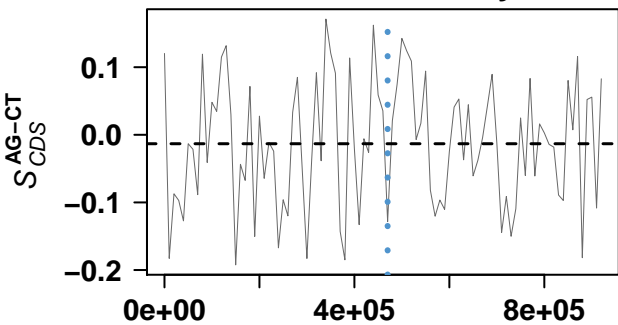


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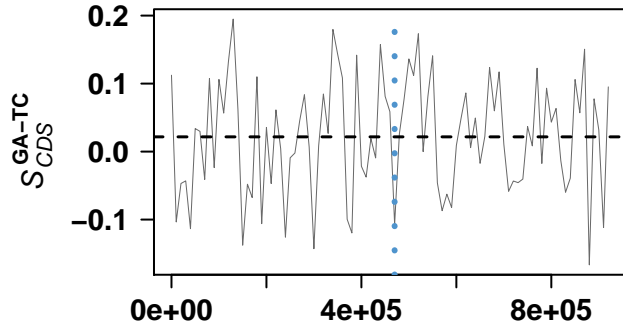


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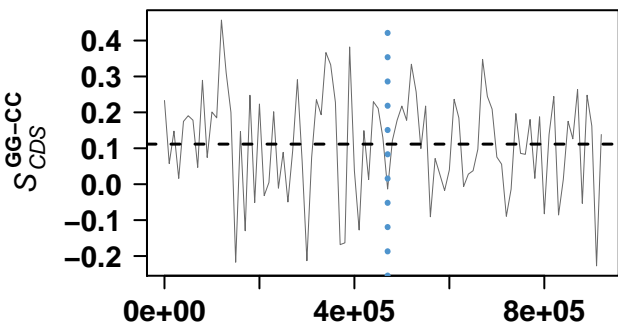
Chlamydia trachomatis A/HAR-13



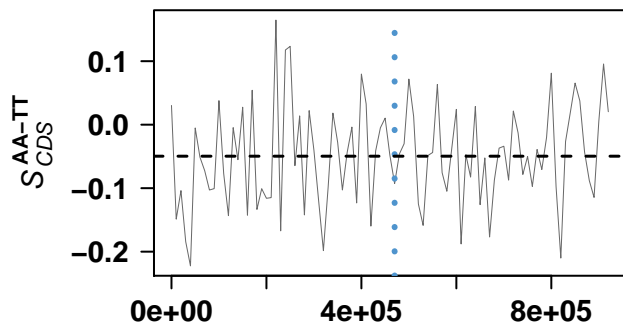
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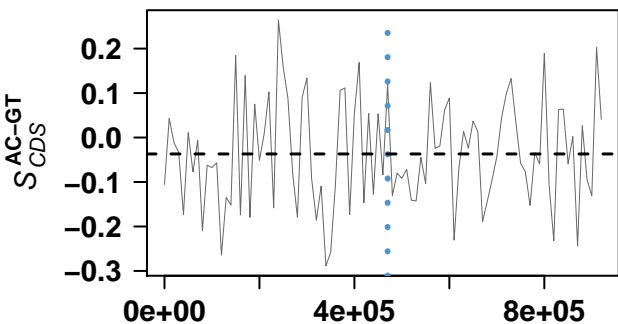
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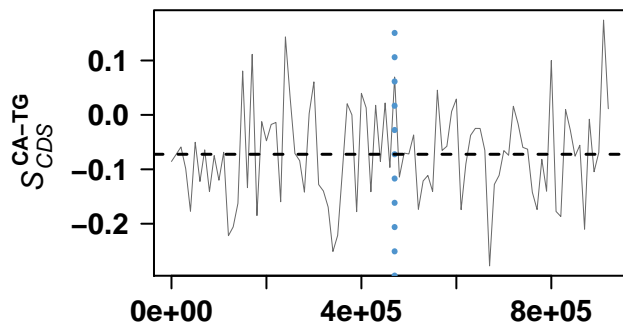
genome coordinates



genome coordinates

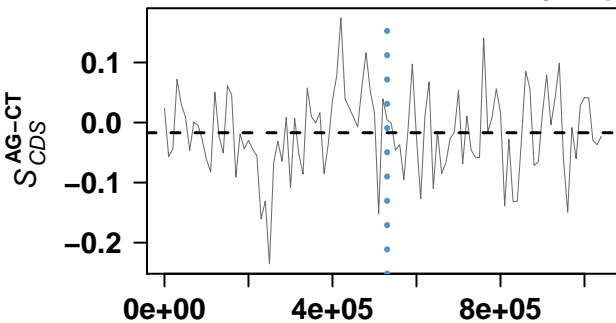


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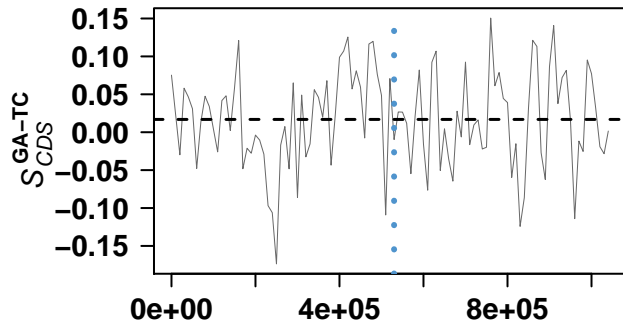


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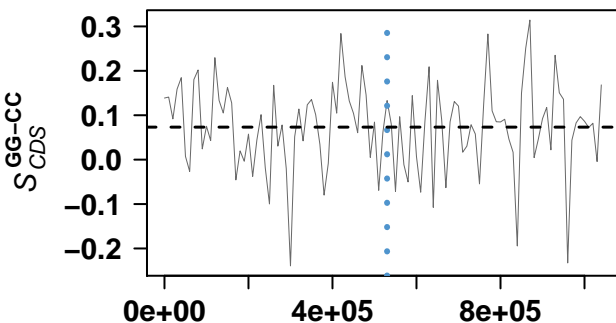
Chlamydophila felis Fe/C-56



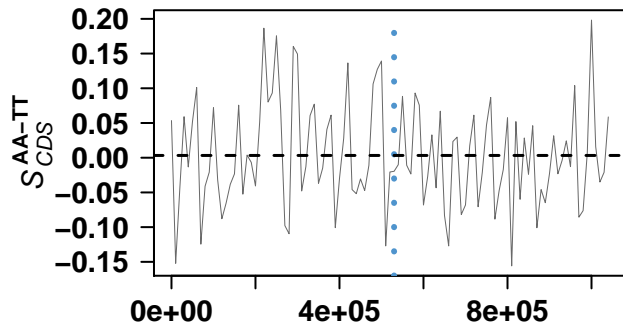
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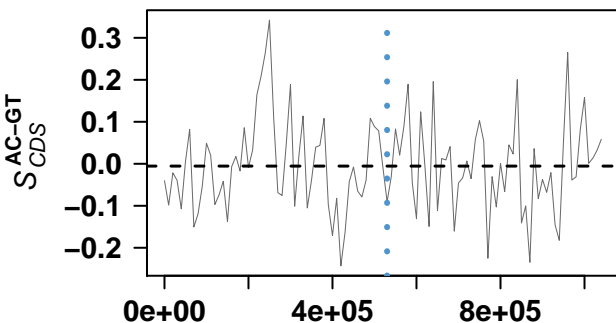
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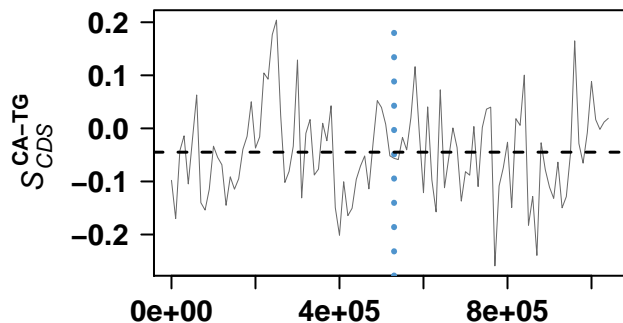
genome coordinates



genome coordinates

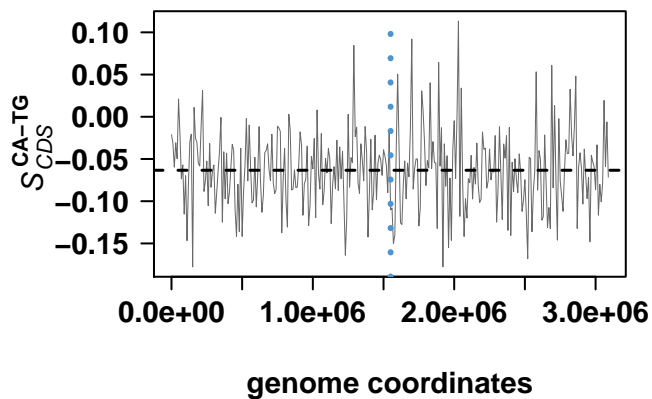
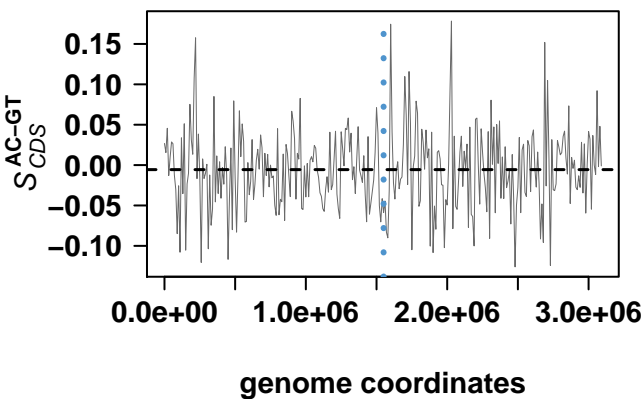
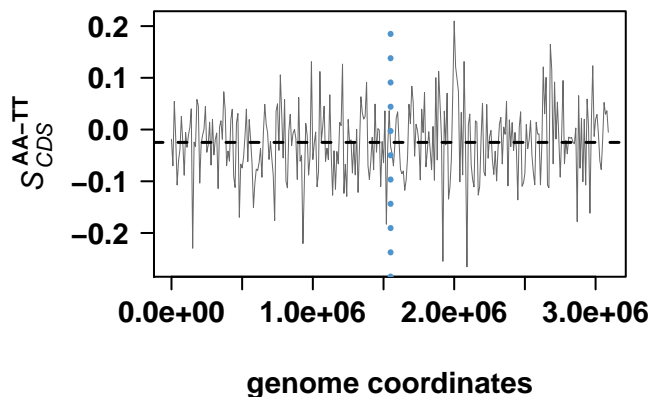
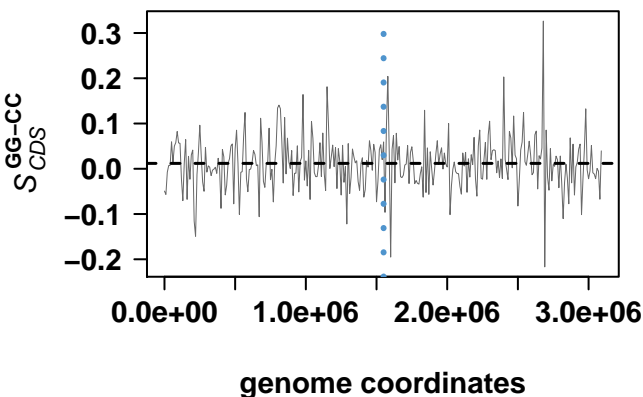
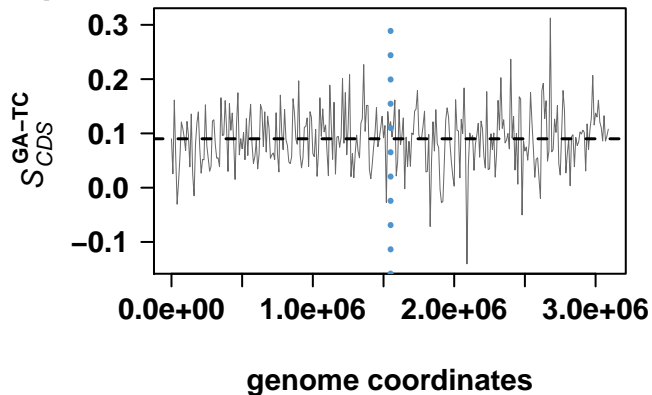
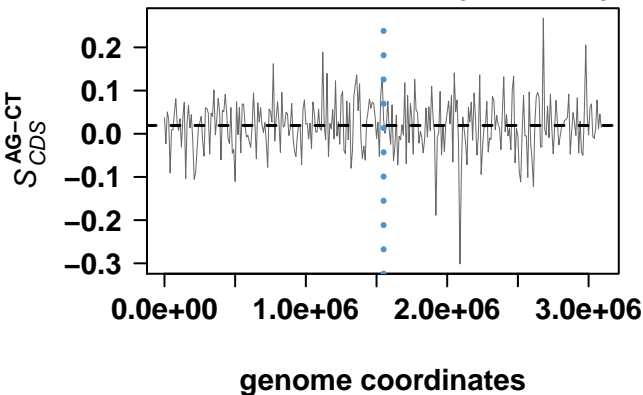


genome coordinates

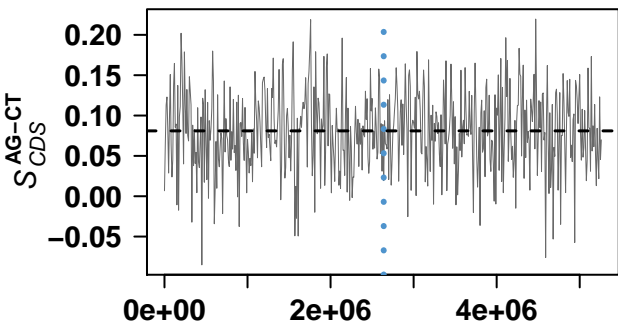


genome coordinates

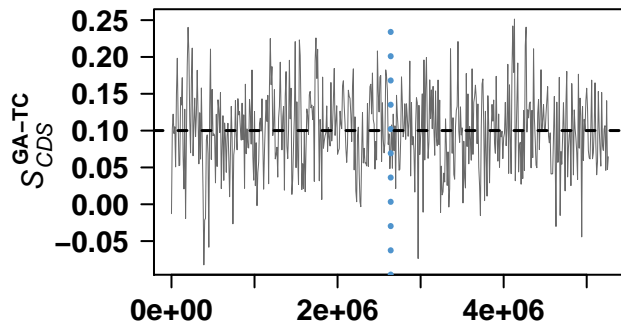
Synechocystis sp. PCC 6803



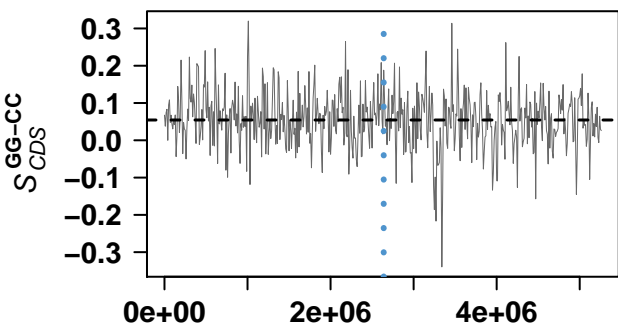
Nostoc sp. PCC 7120



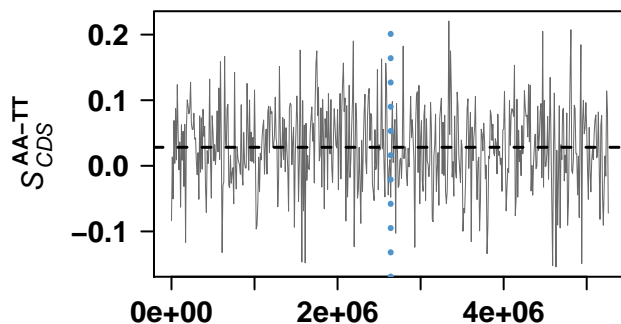
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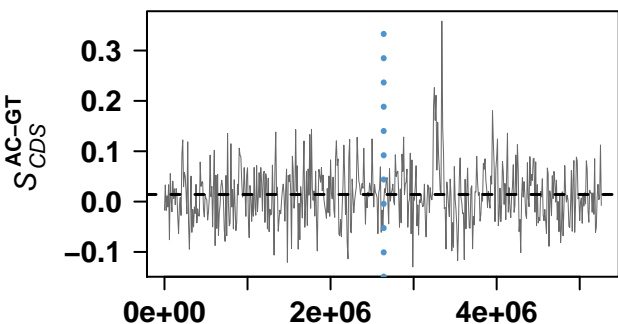
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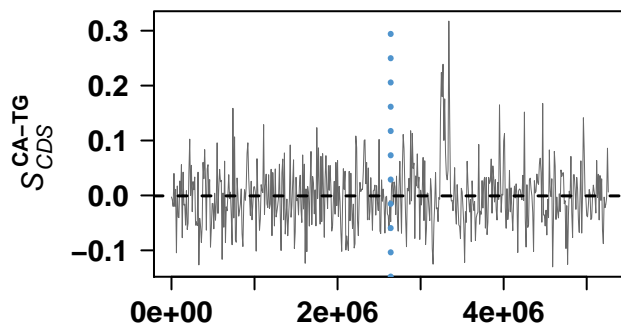
genome coordinates



genome coordinates

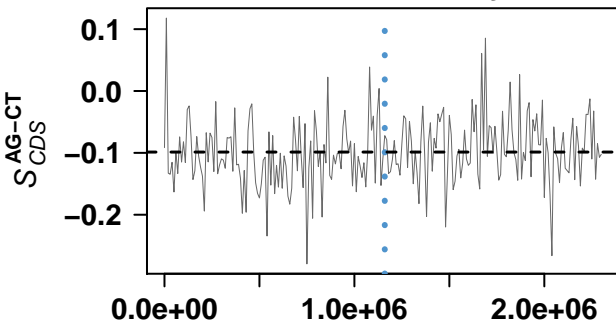


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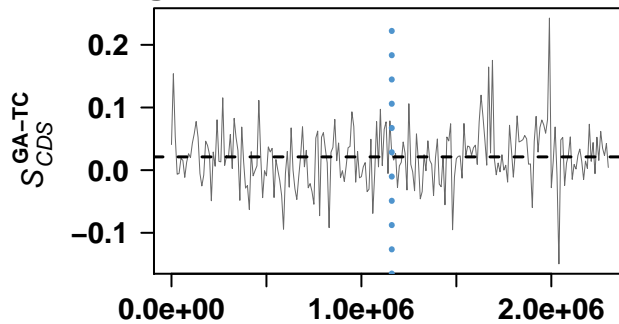


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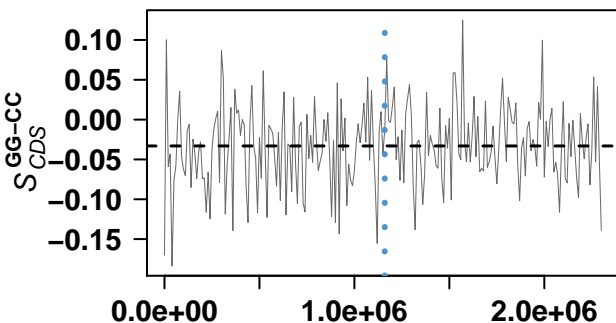
Thermosynechococcus elongatus BP-1



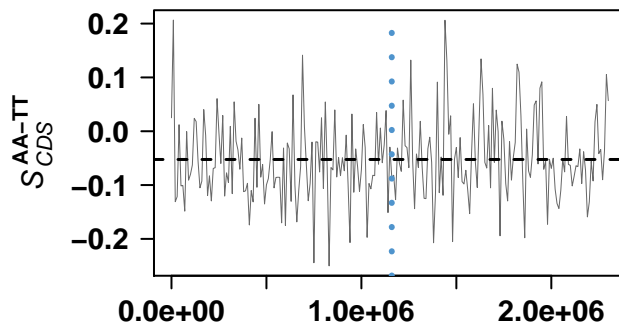
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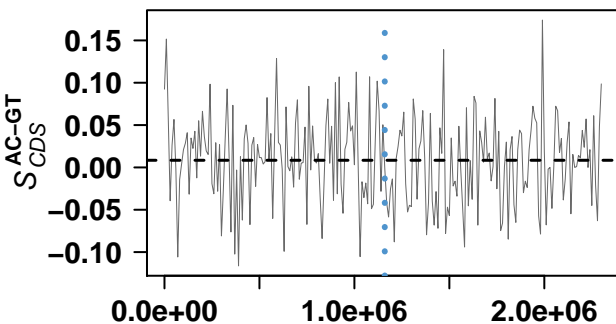
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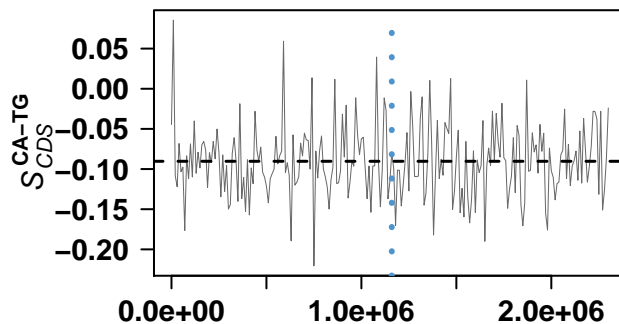
genome coordinates



genome coordinates

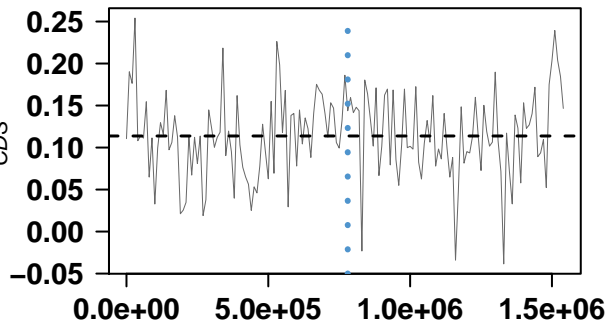


genome coordinates

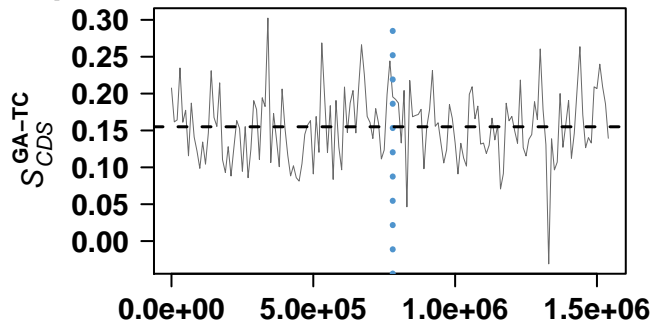


genome coordinates

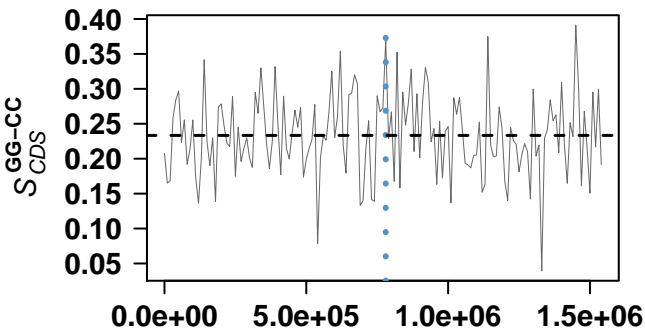
Prochlorococcus marinus subsp. marinus str. CCMP1375



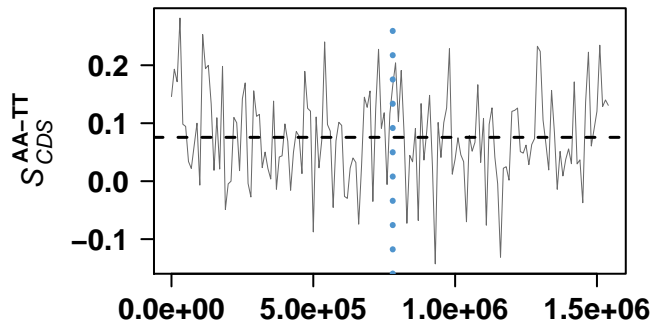
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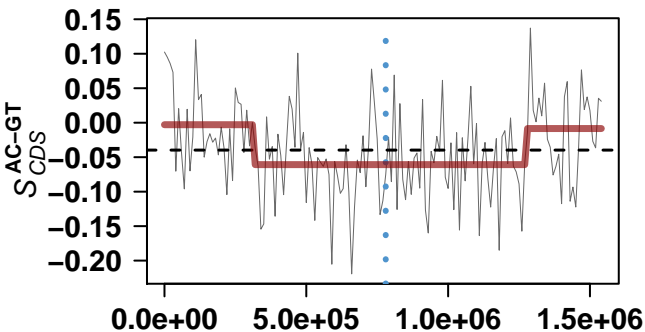
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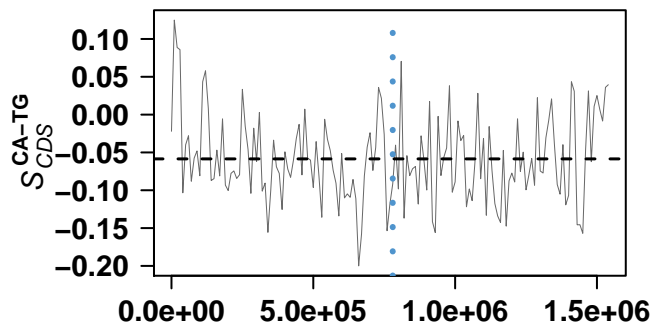
genome coordinates



genome coordinates

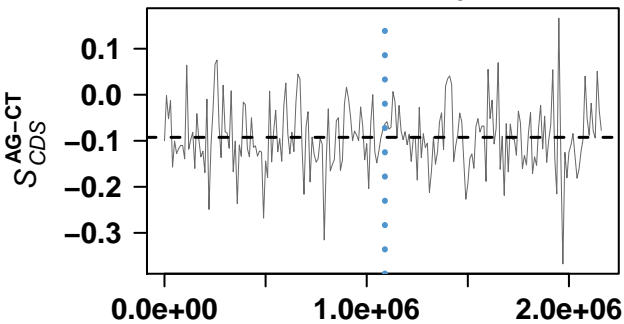


genome coordinates

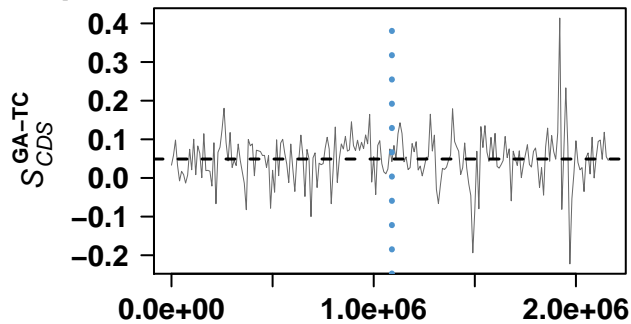


genome coordinates

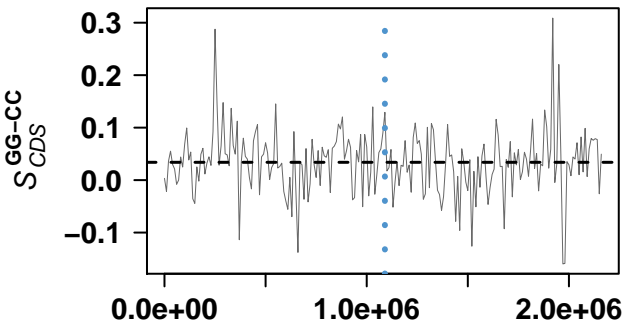
Synechococcus sp. WH 8102



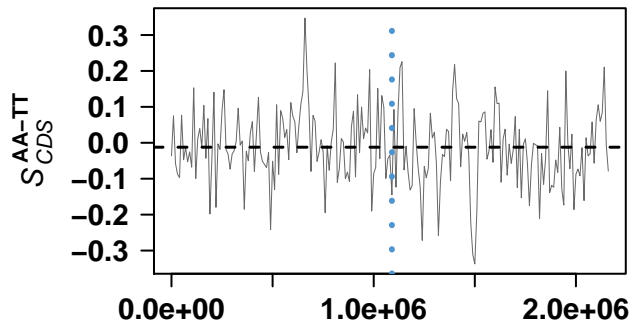
genome coordinates



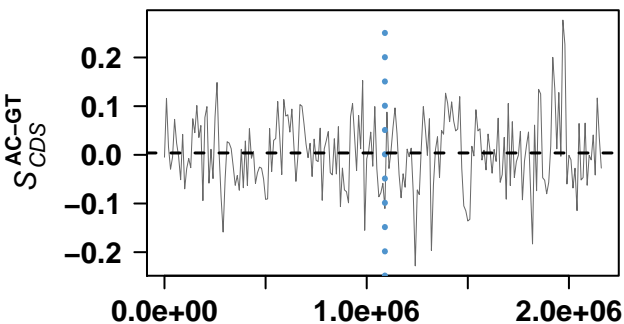
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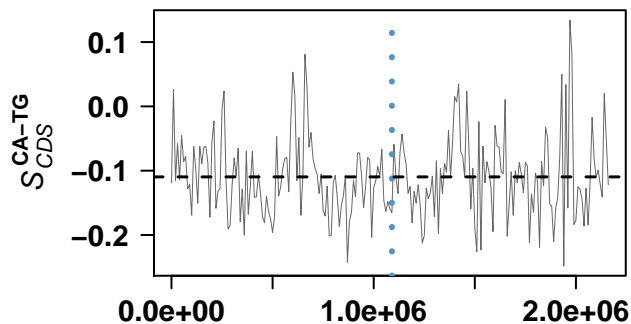
genome coordinates



genome coordinates

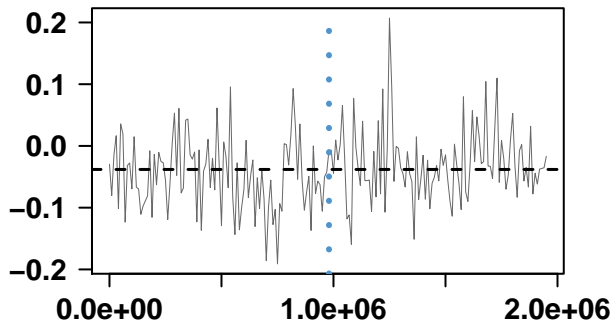


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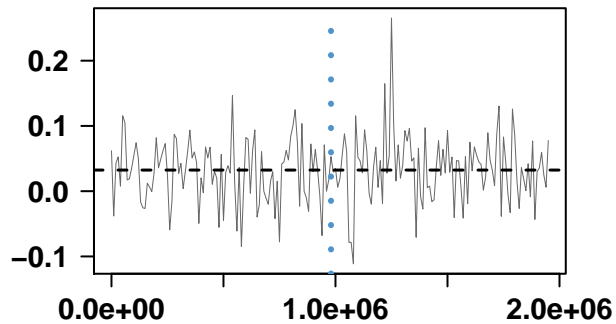


genome coordinates

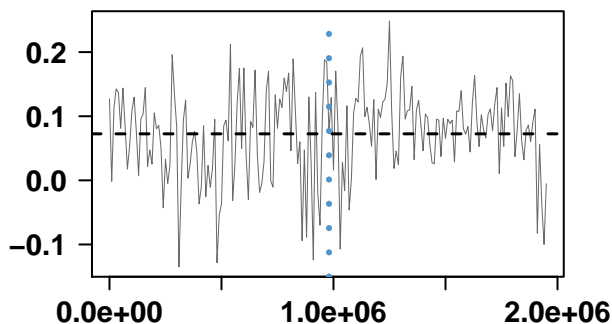
Prochlorococcus marinus str. MIT 9313



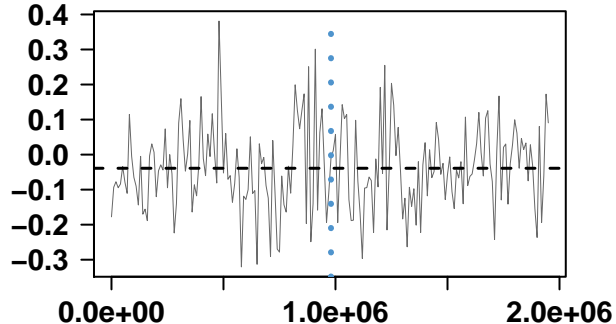
genome coordinates



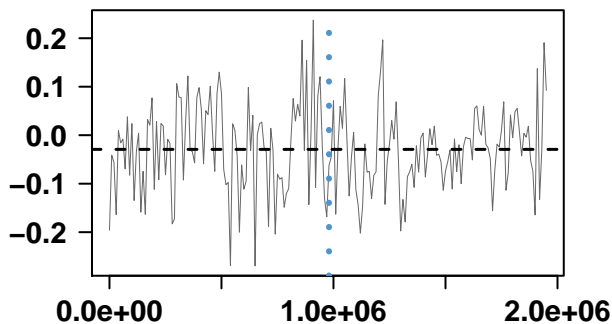
genome coordinates



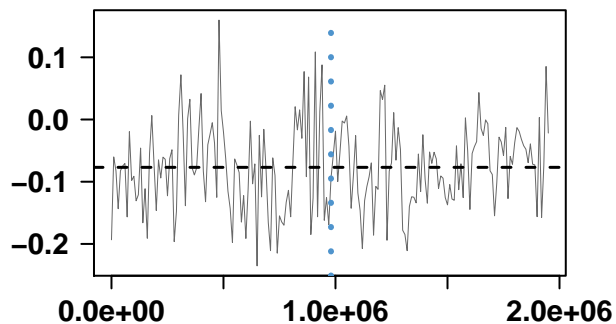
genome coordinates



genome coordinates

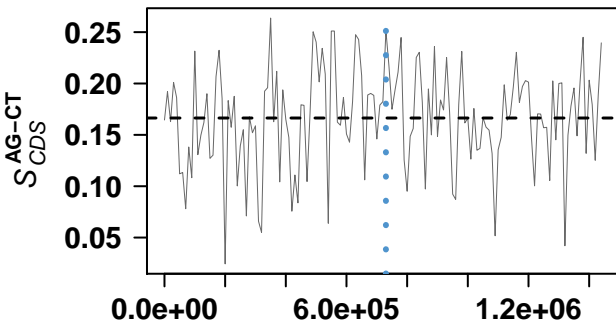


genome coordinates

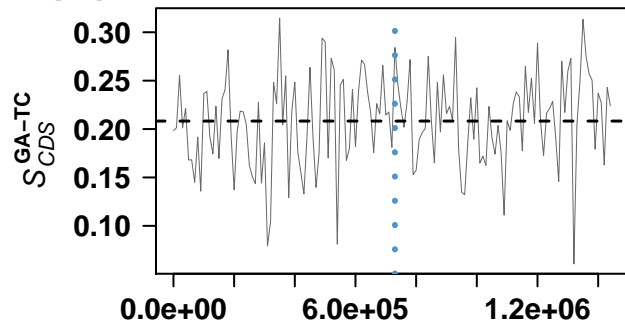


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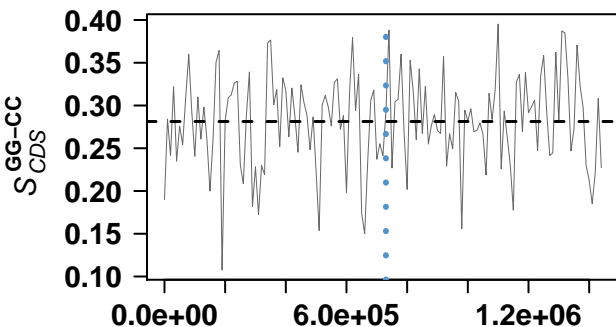
Prochlorococcus marinus subsp. pastoris str. CCMP1986



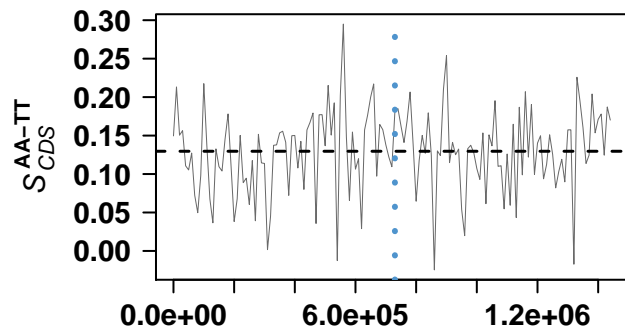
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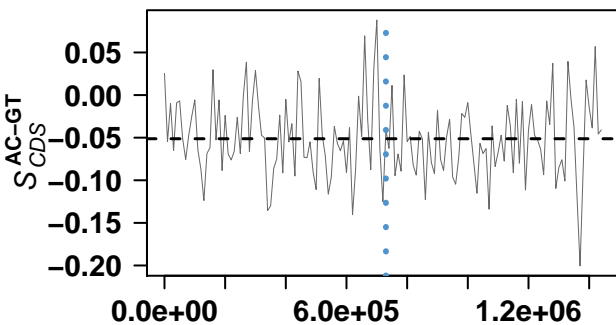
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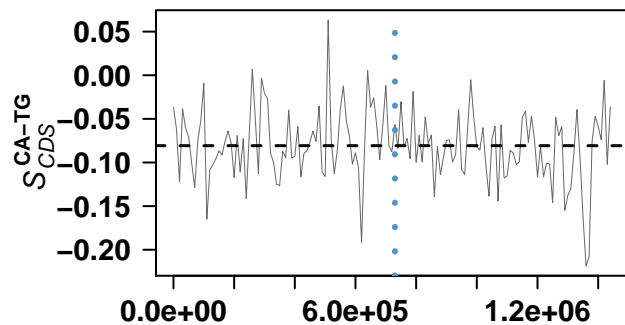
genome coordinates



genome coordinates

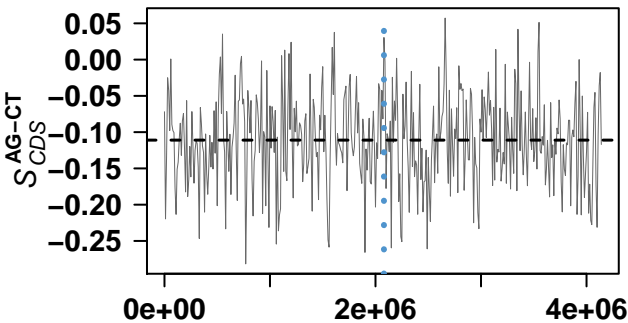


genome coordinates

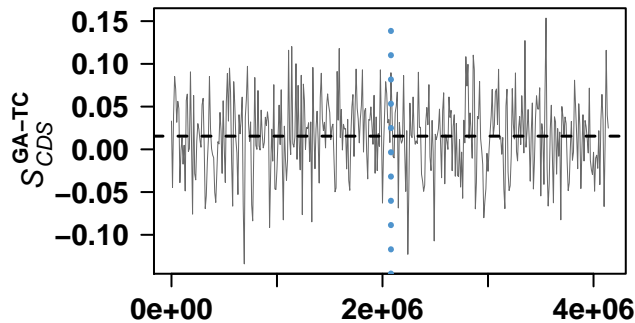


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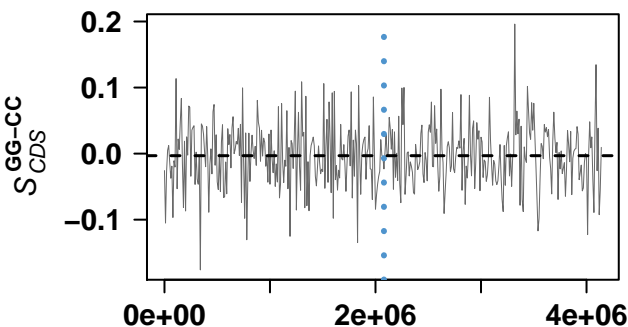
Gloeobacter violaceus PCC 7421



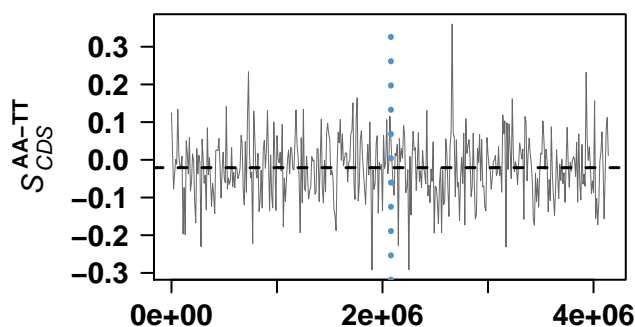
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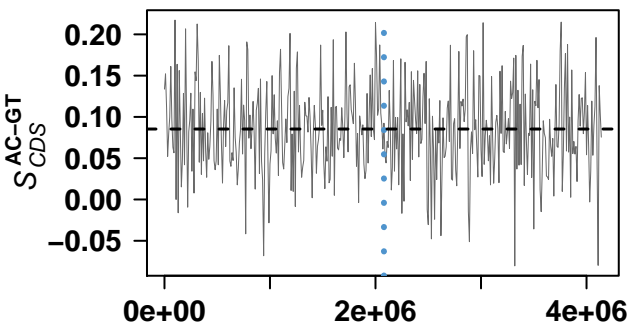
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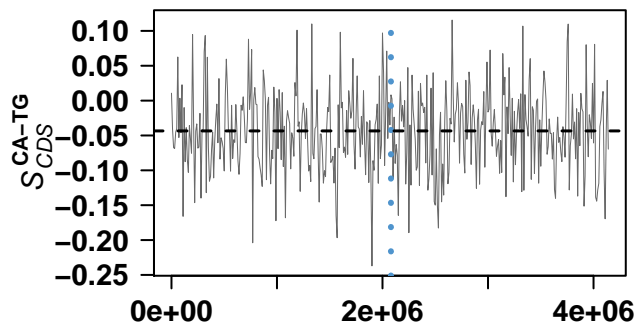
genome coordinates



genome coordinates

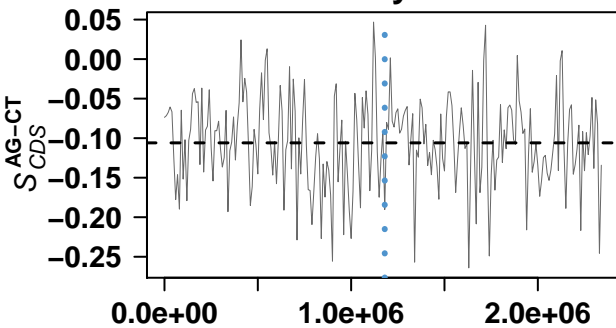


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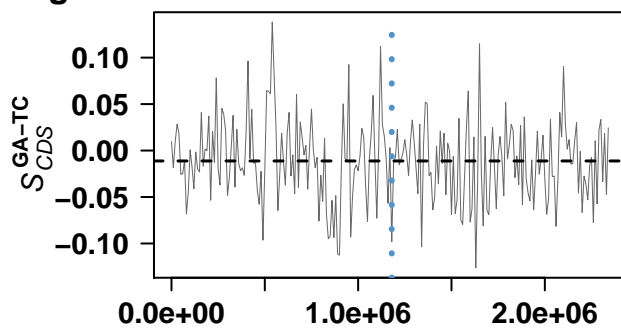


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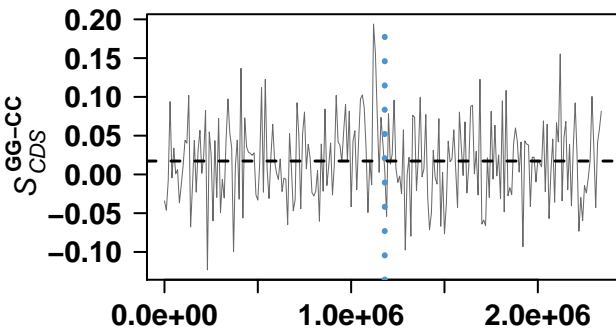
Synechococcus elongatus PCC 6301



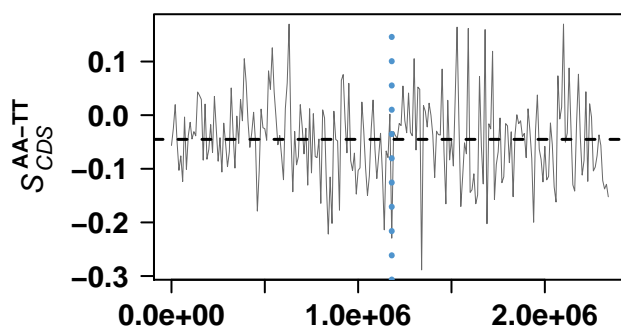
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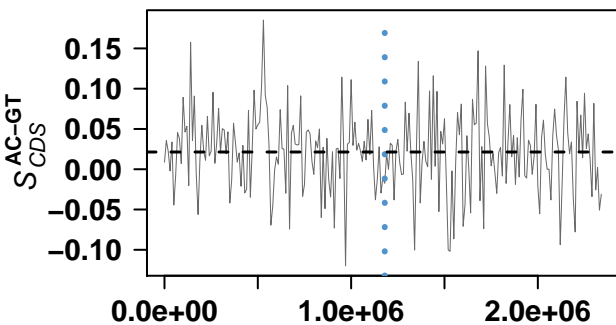
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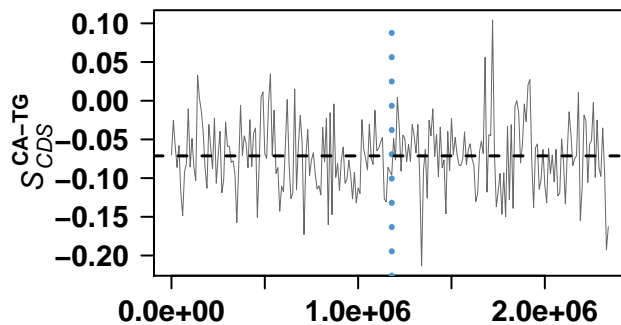
genome coordinates



genome coordinates

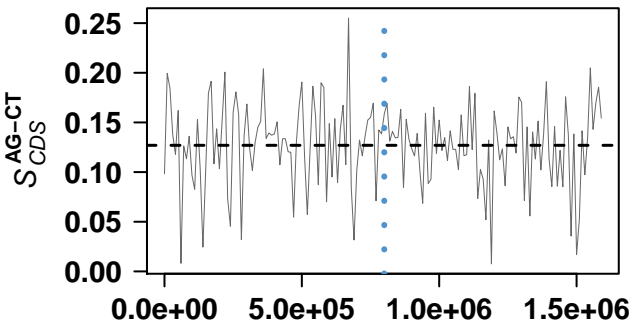


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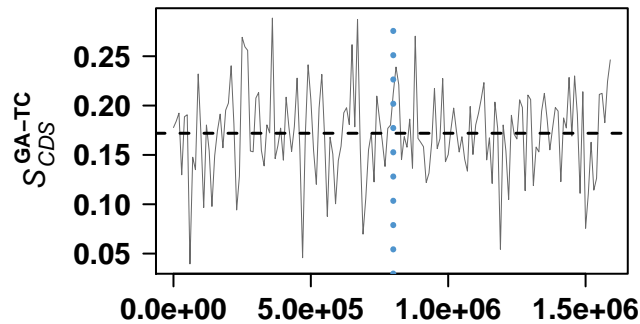


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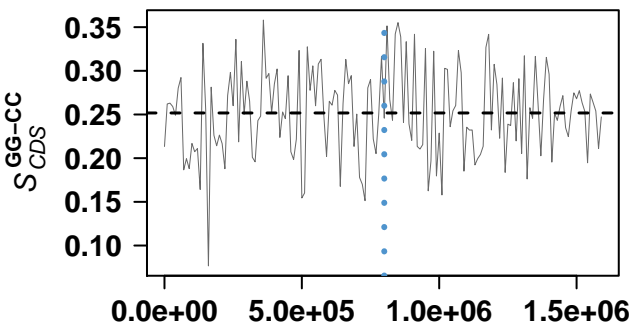
Prochlorococcus marinus str. NATL2A



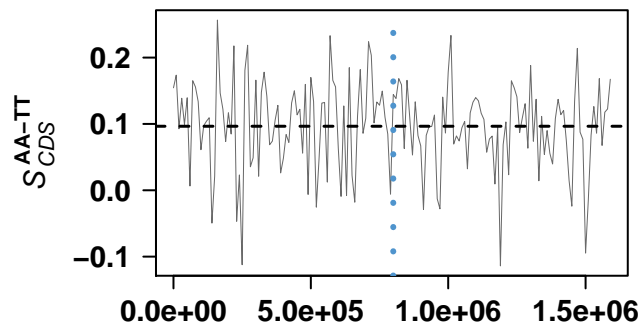
genome coordinates



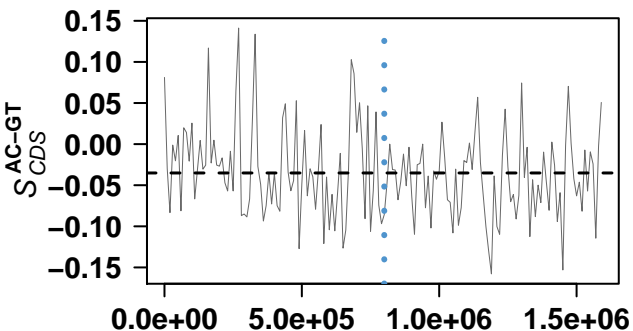
genome coordinates



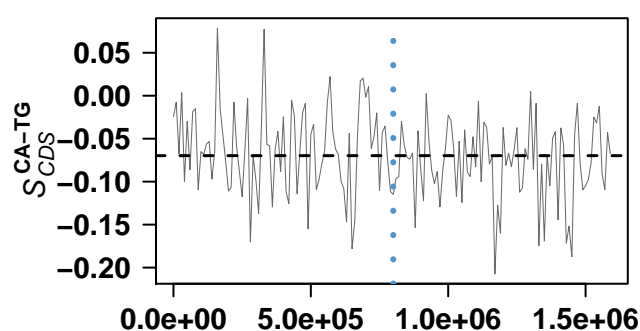
genome coordinates



genome coordinates

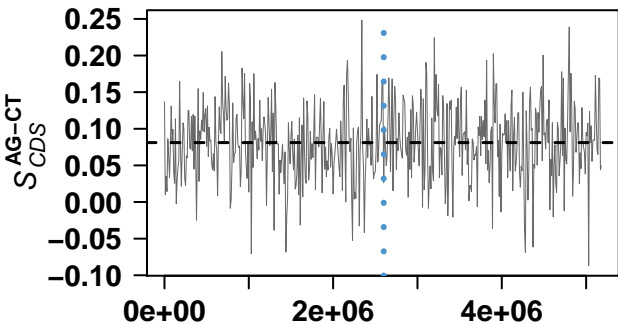


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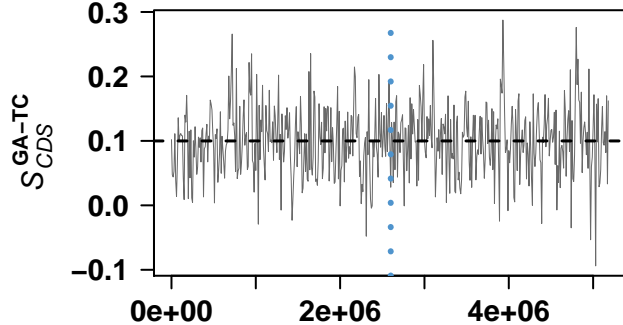


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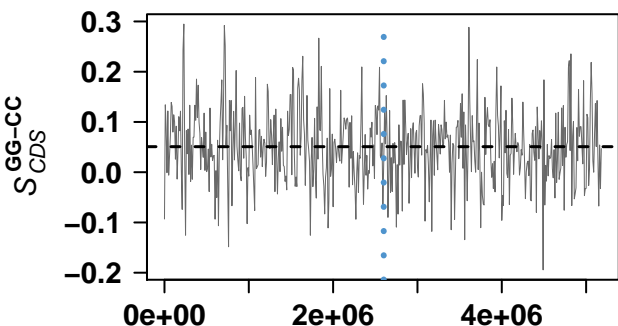
Anabaena variabilis ATCC 29413



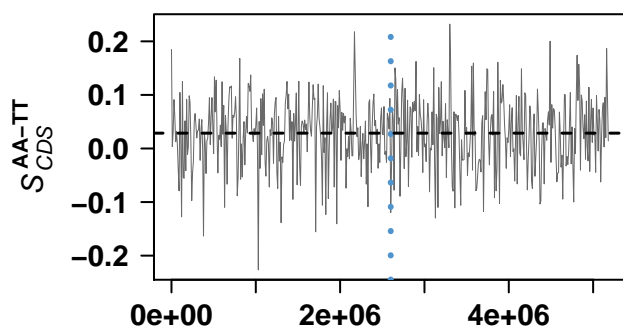
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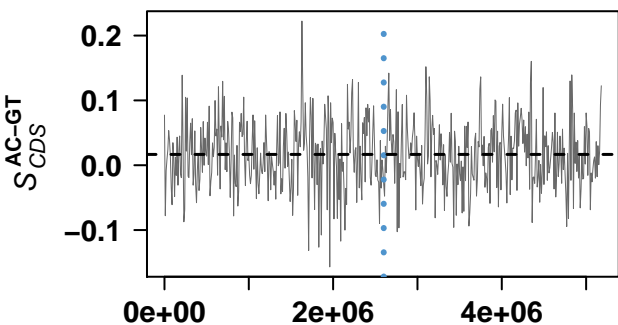
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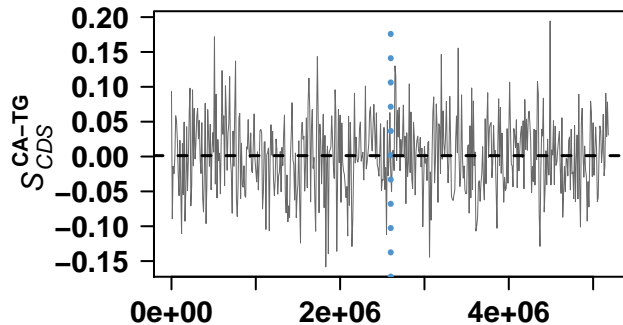
genome coordinates



genome coordinates

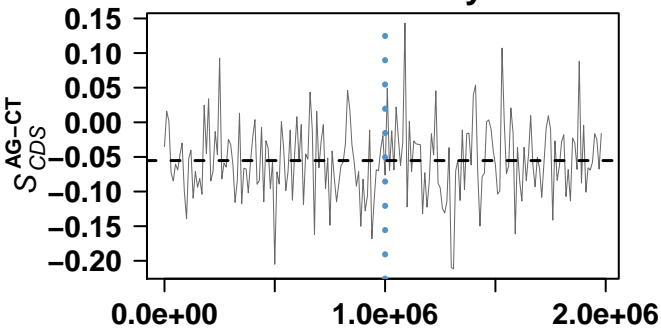


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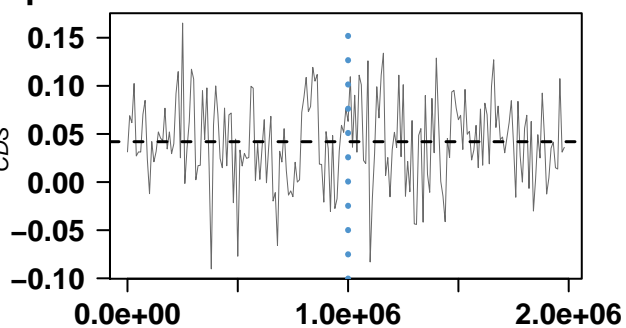


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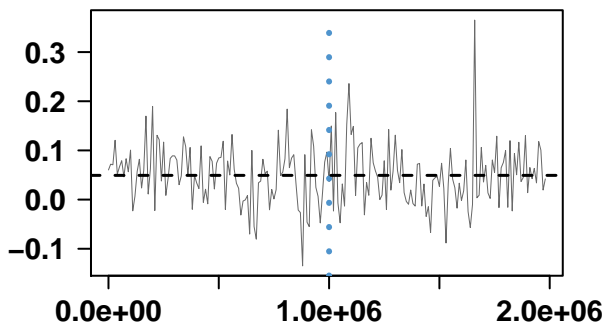
Synechococcus sp. CC9902



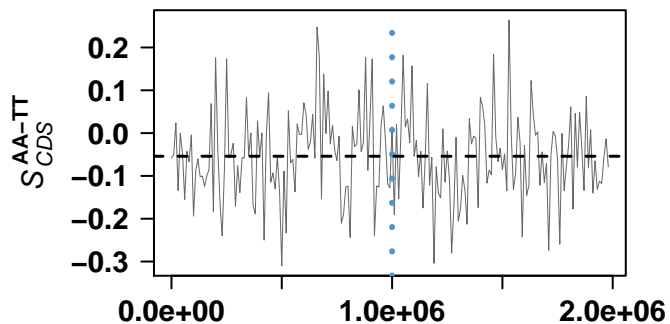
genome coordinates



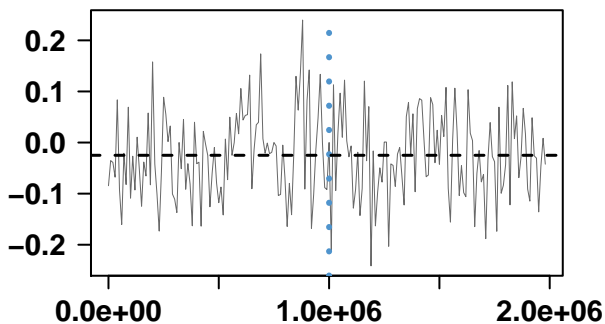
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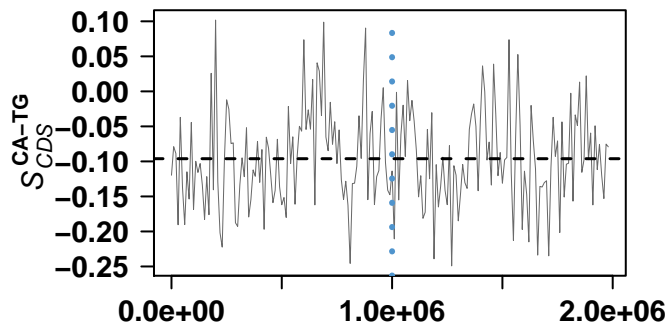
genome coordinates



genome coordinates

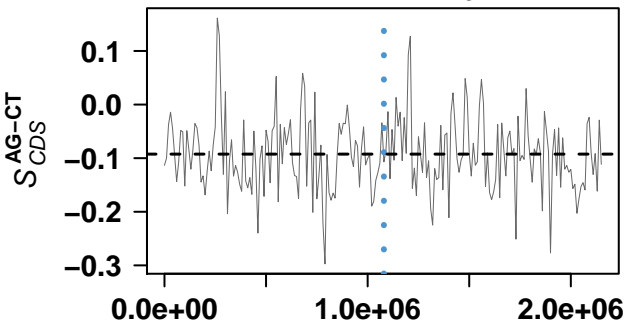


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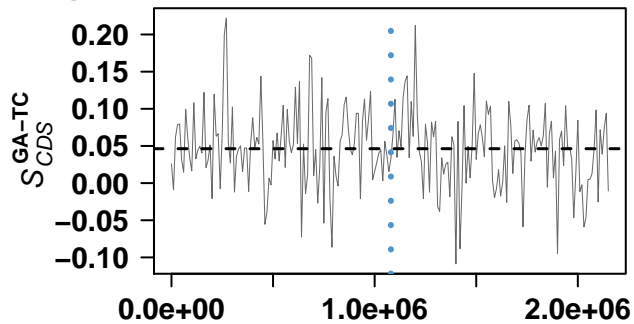


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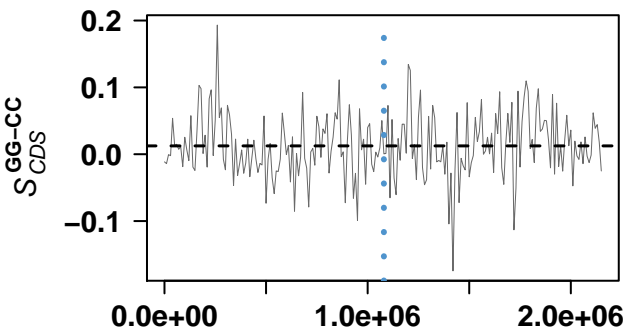
Synechococcus sp. CC9605



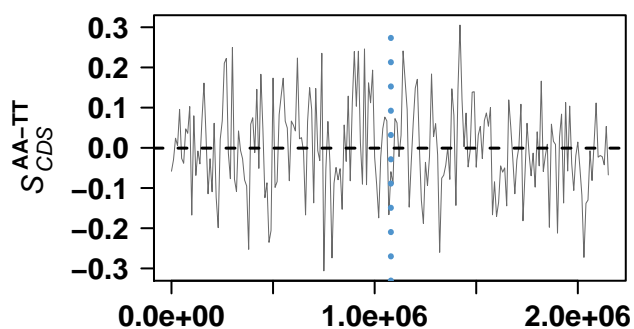
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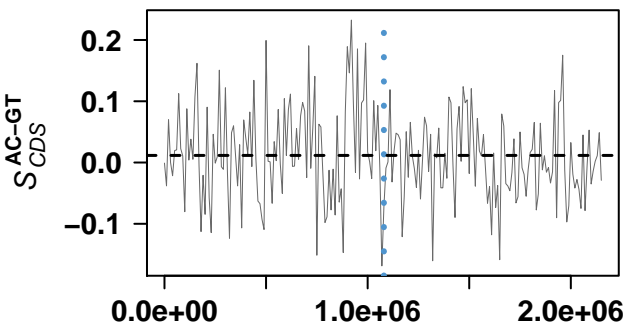
genome coordinates



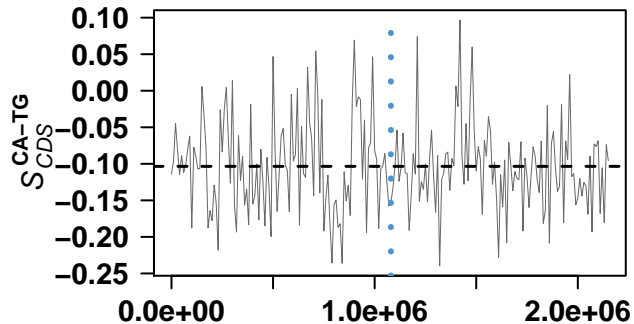
genome coordinates



genome coordinates

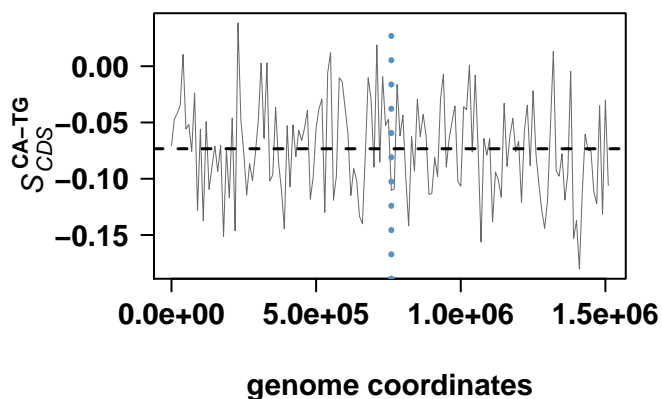
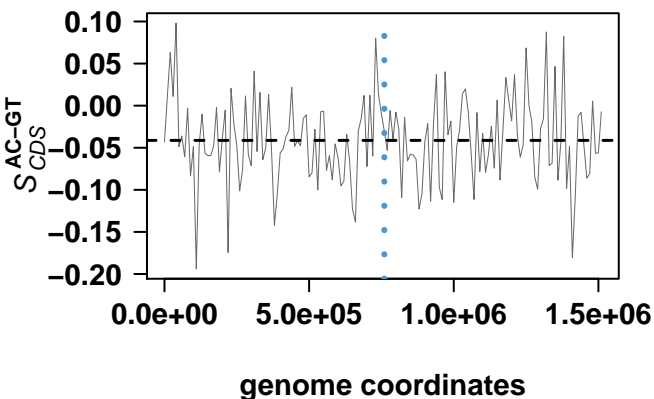
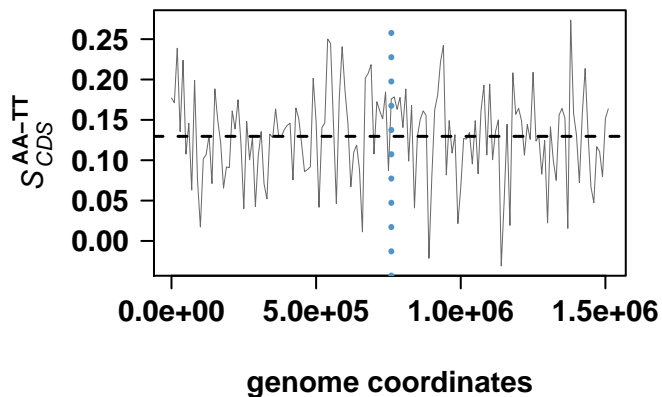
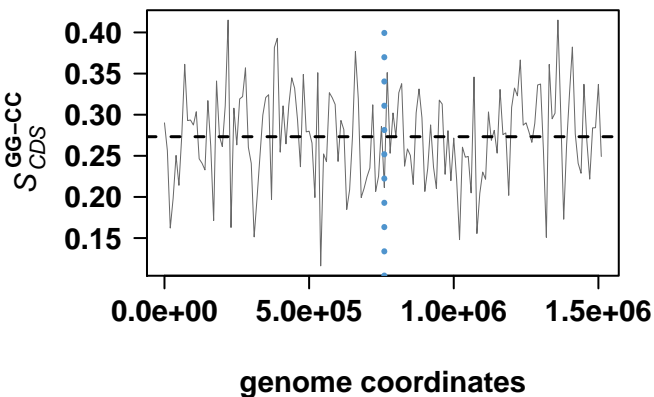
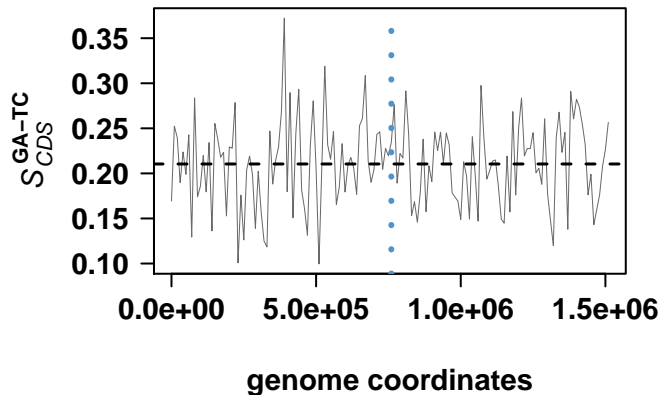
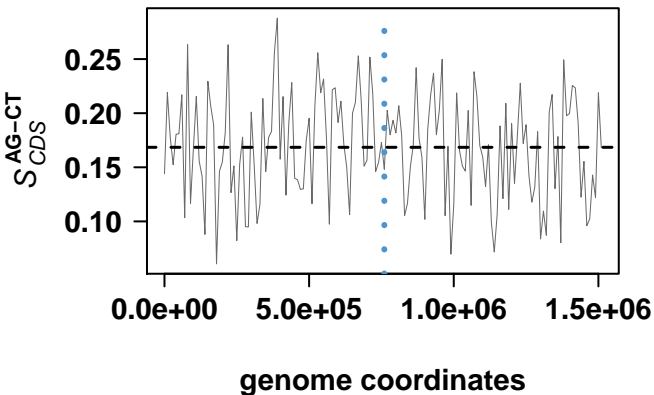


genome coordinates

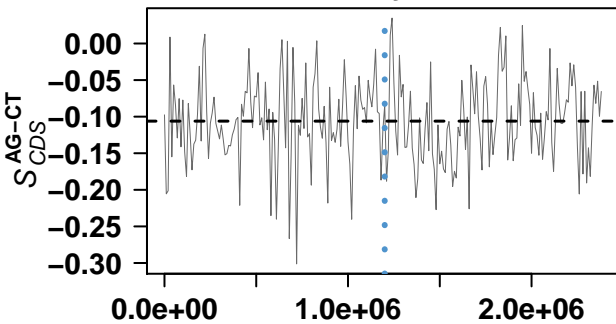


genome coordinates

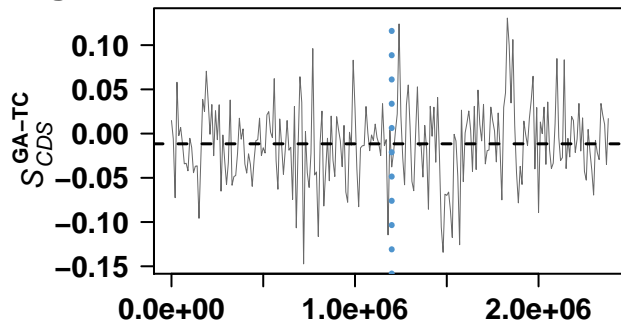
Prochlorococcus marinus str. MIT 9312



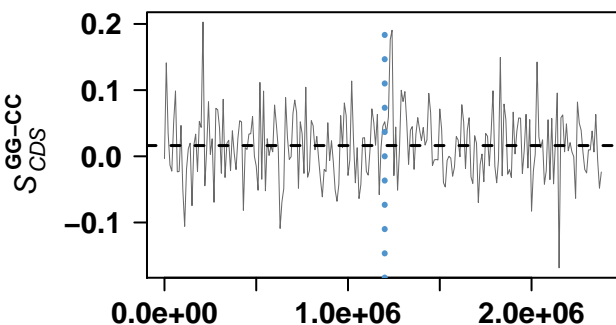
Synechococcus elongatus PCC 7942



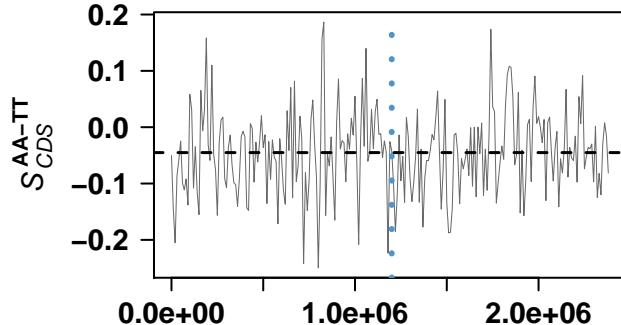
genome coordinates



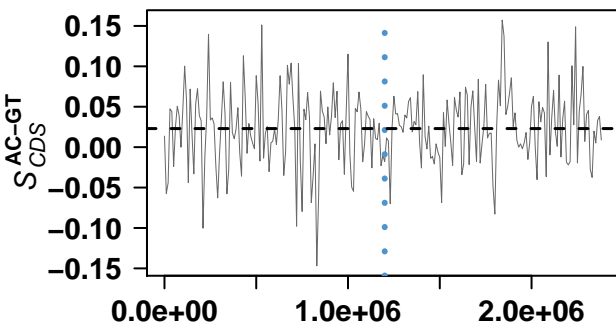
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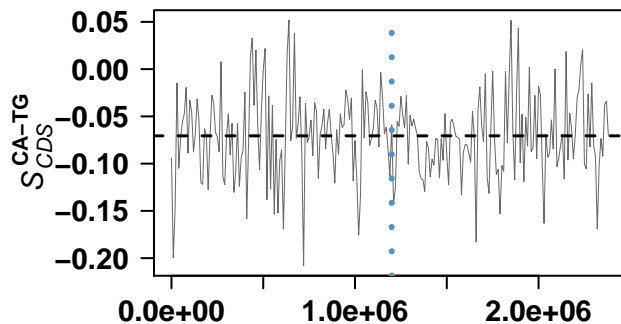
genome coordinates



genome coordinates

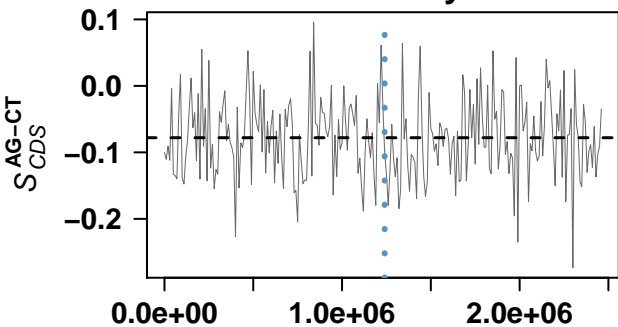


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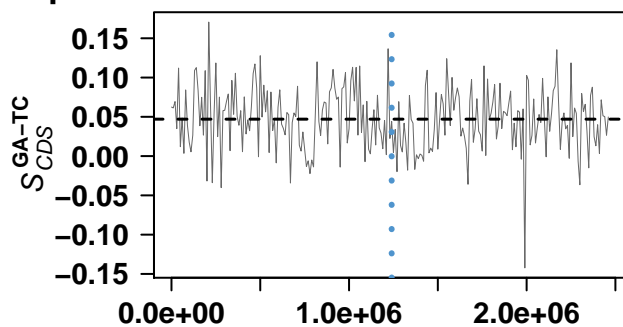


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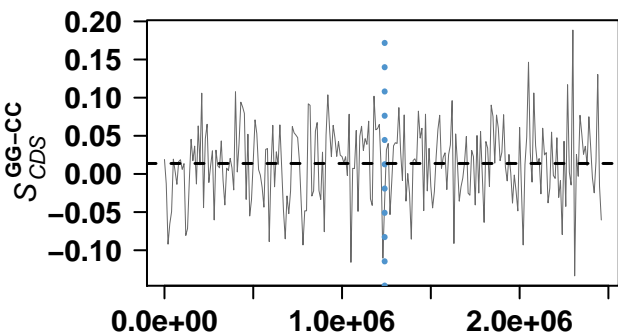
Synechococcus sp. JA-3-3Ab



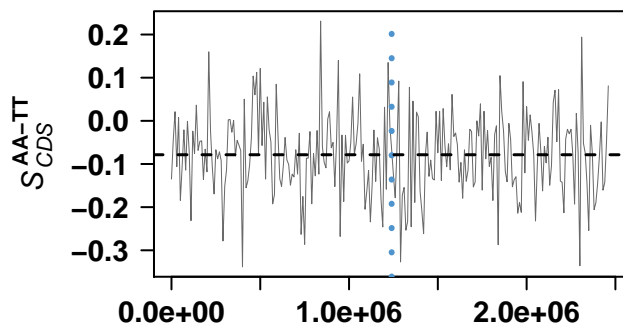
genome coordinates



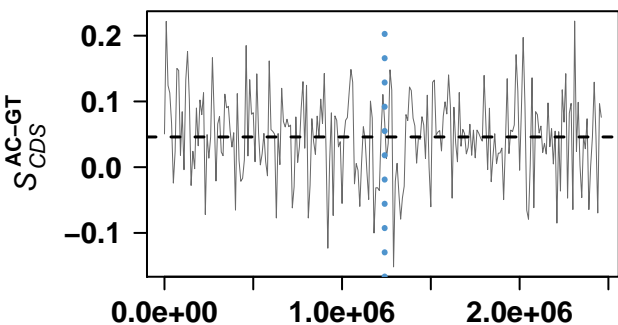
genome coordinates



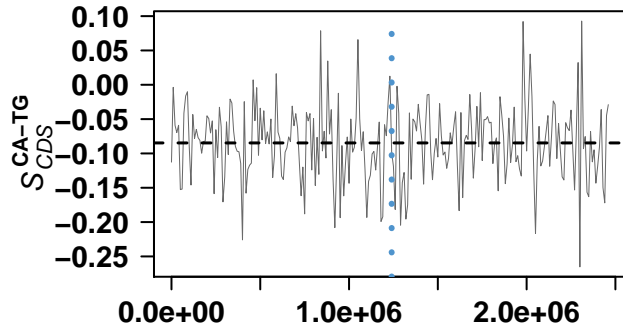
genome coordinates



genome coordinates

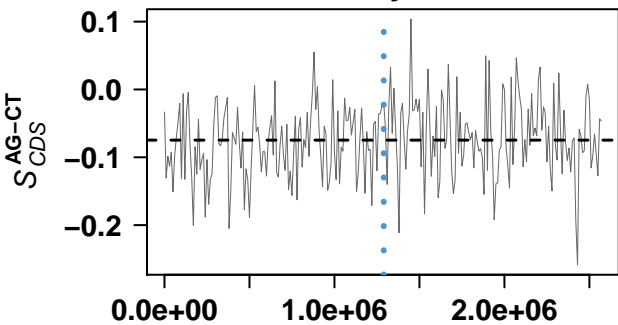


genome coordinates

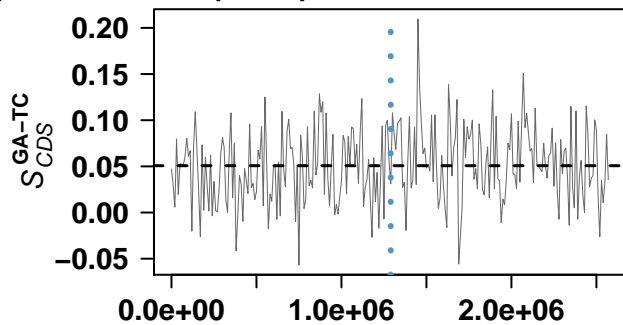


genome coordinates

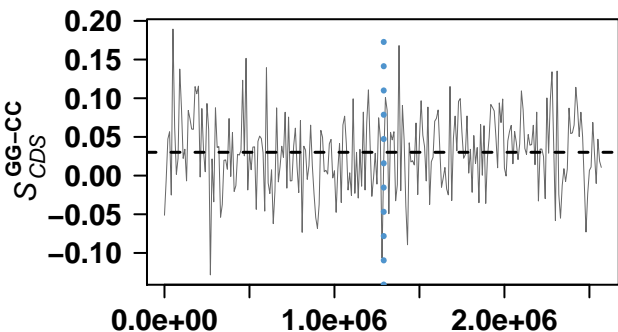
Synechococcus sp. JA-2-3B'a(2-13)



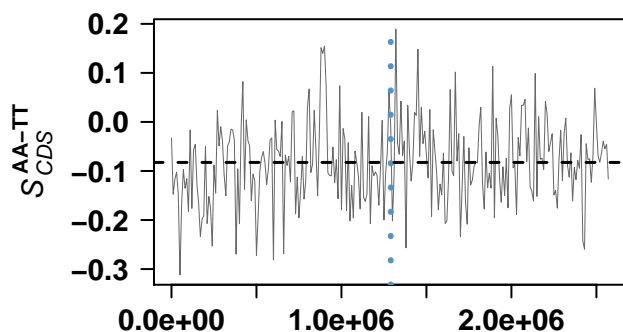
genome coordinates



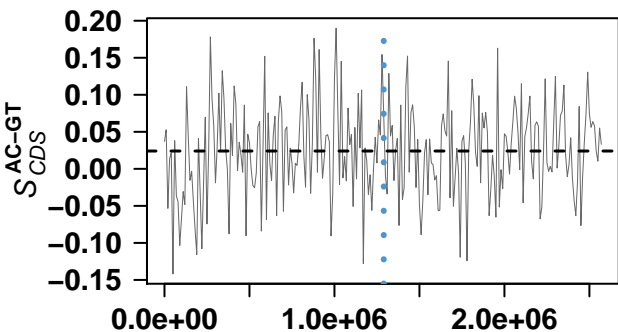
genome coordinates



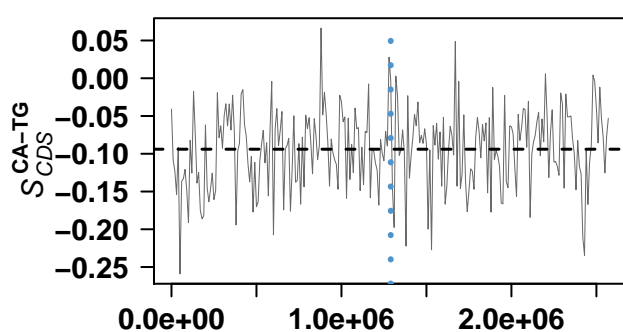
genome coordinates



genome coordinates

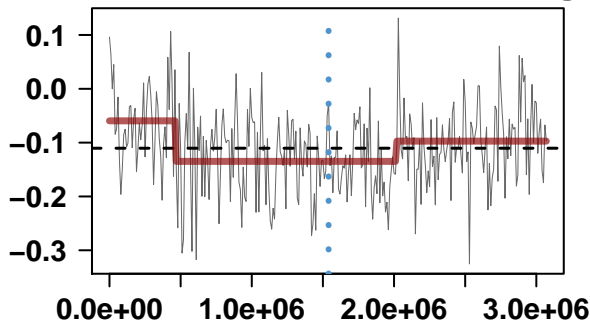


genome coordinates

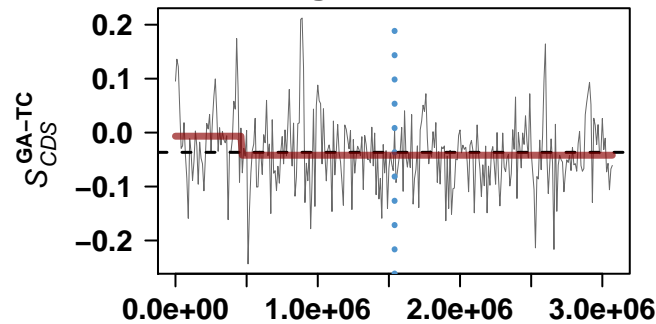


genome coordinates

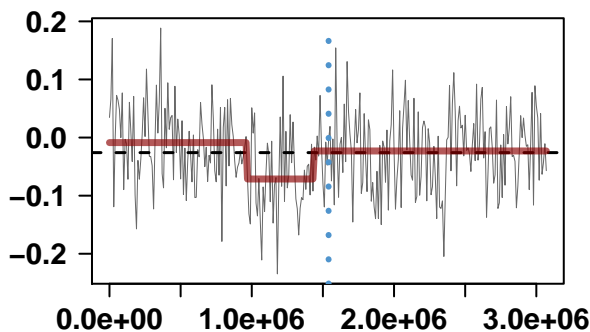
Desulfovibrio vulgaris str. Hildenborough



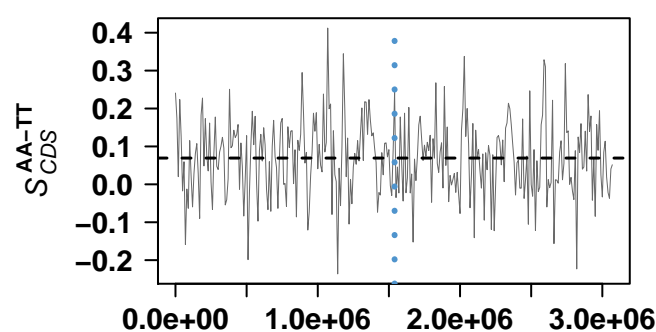
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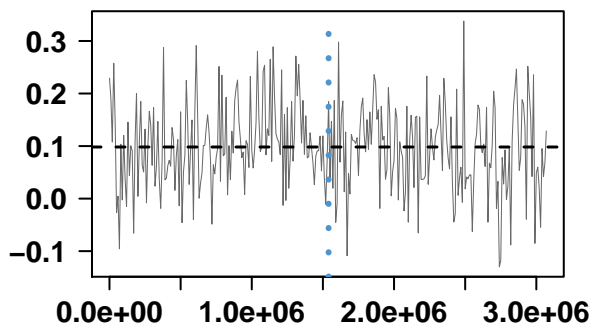
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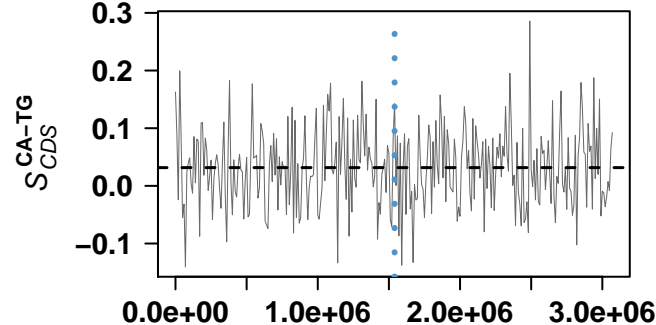
genome coordinates



genome coordinates

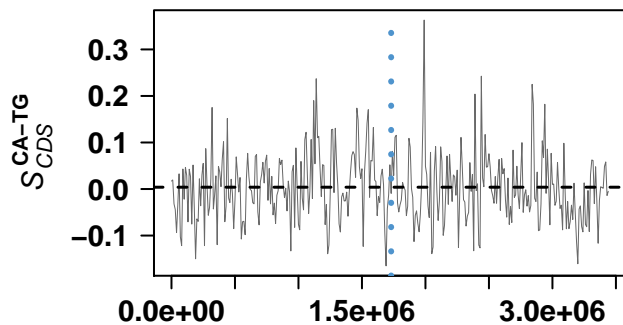
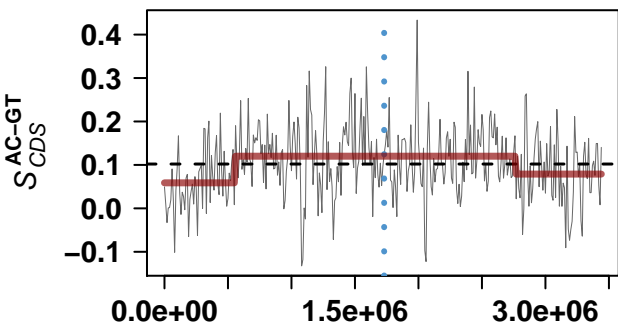
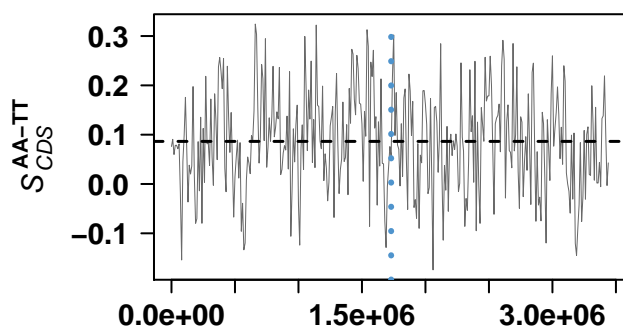
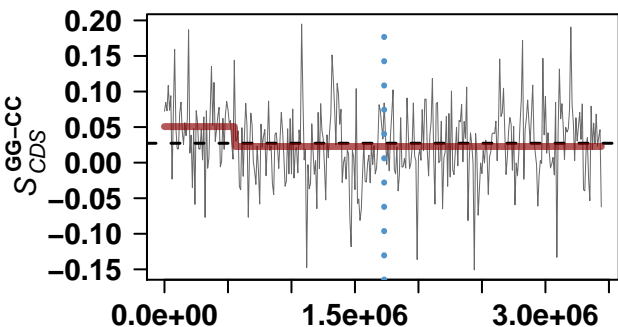
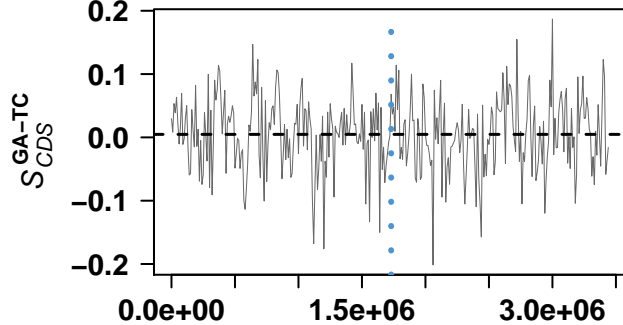
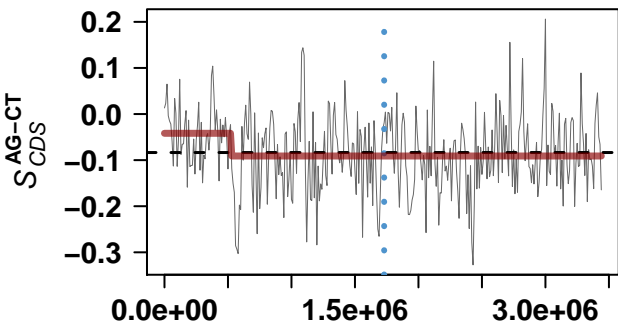


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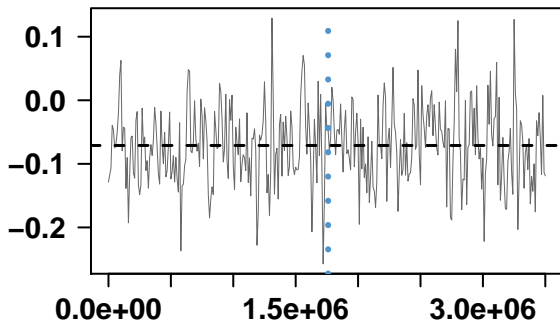


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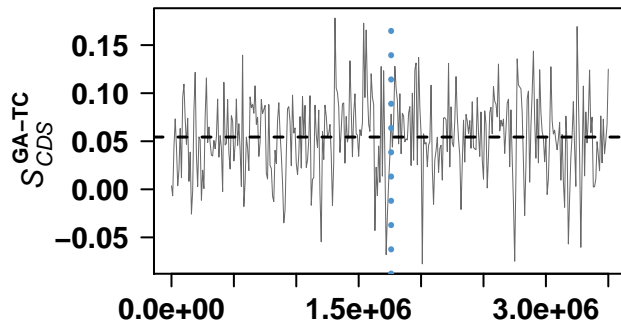
Geobacter sulfurreducens PCA



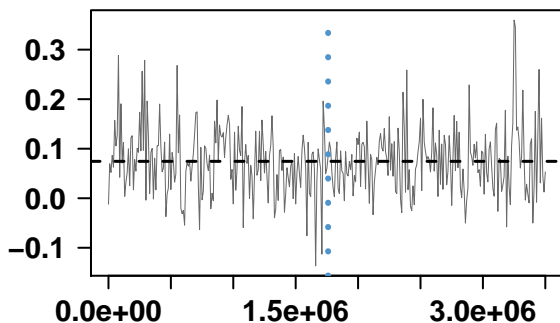
Bdellovibrio bacteriovorus HD100



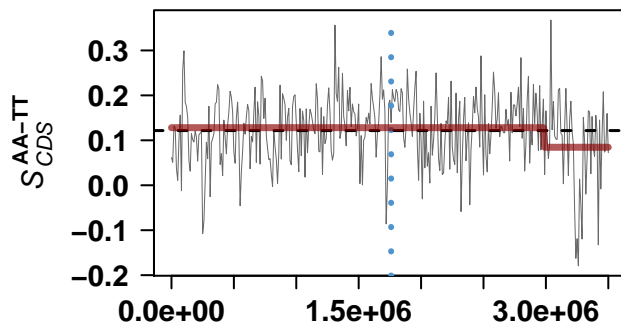
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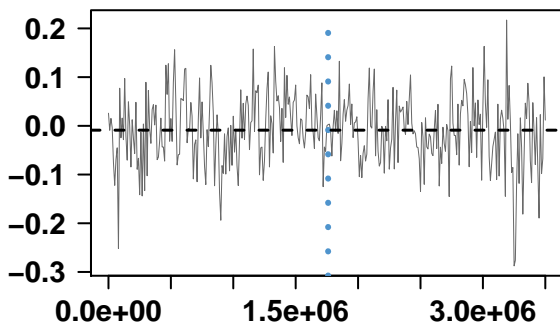
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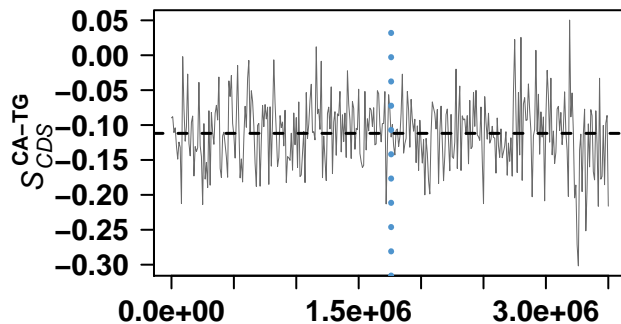
genome coordinates



genome coordinates

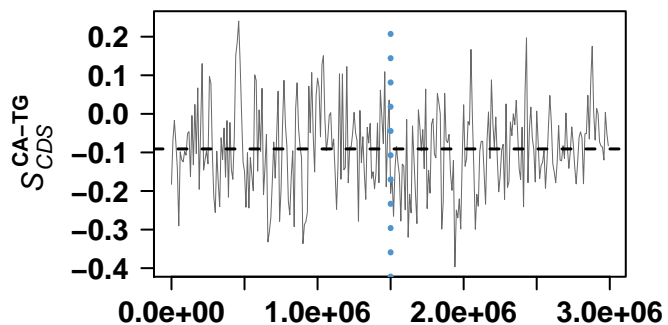
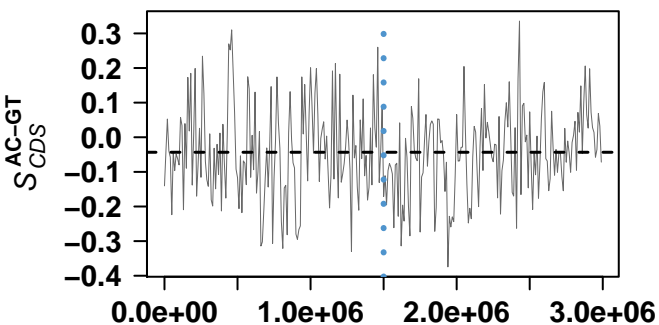
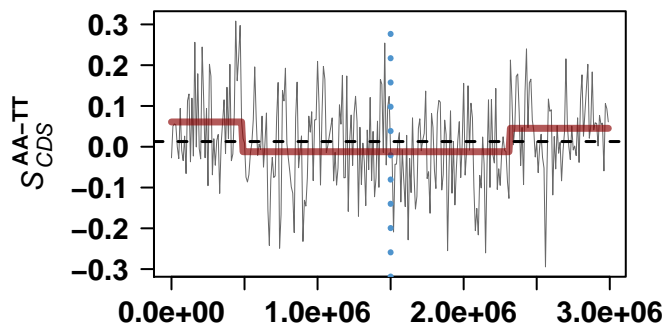
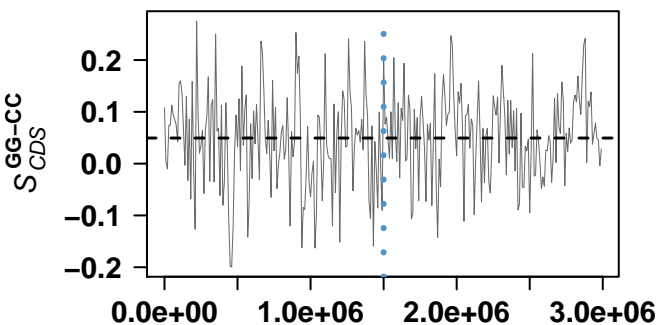
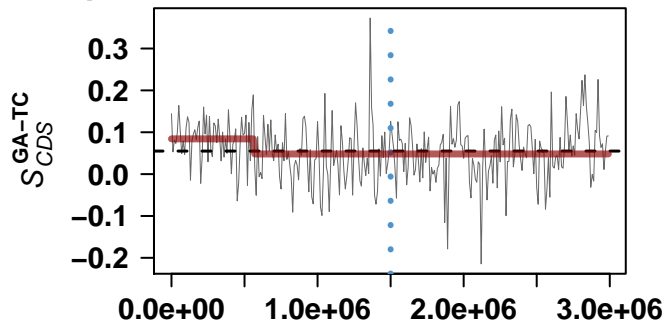
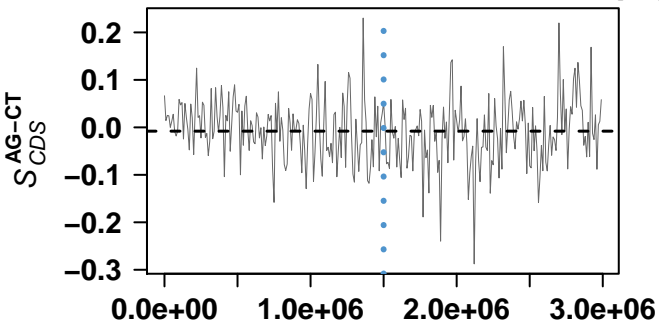


genome coordinates

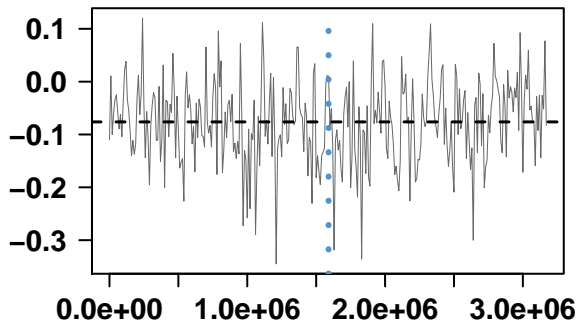


genome coordinates

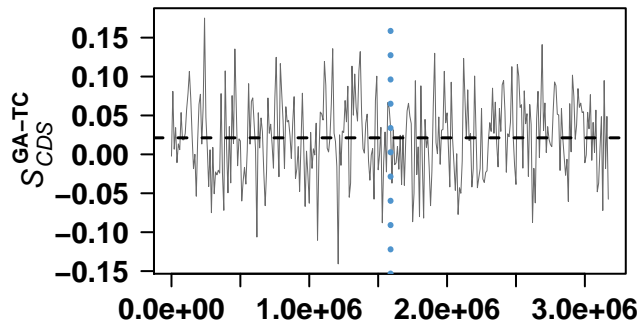
Desulfotalea psychrophila LSv54



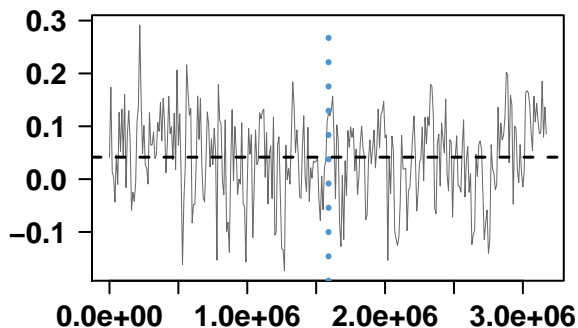
Pelobacter carbinolicus DSM 2380



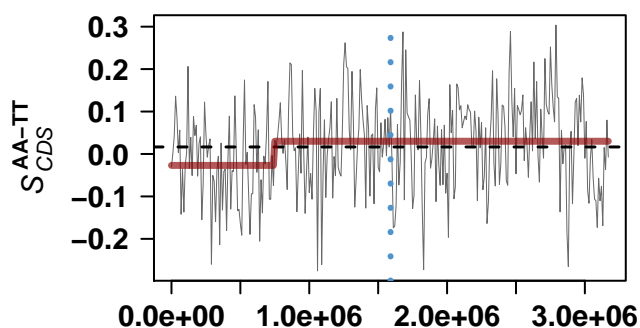
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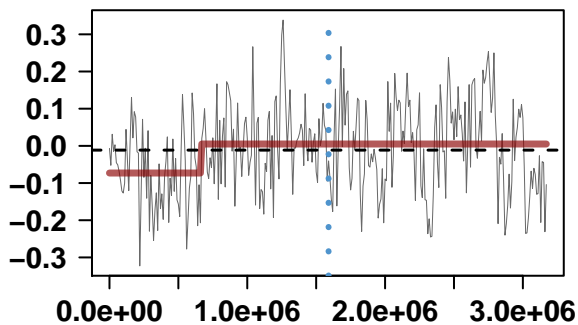
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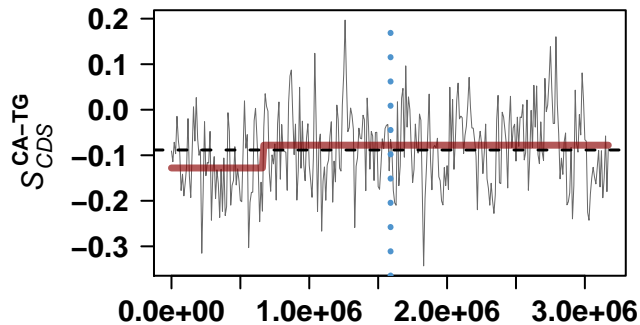
genome coordinates



genome coordinates

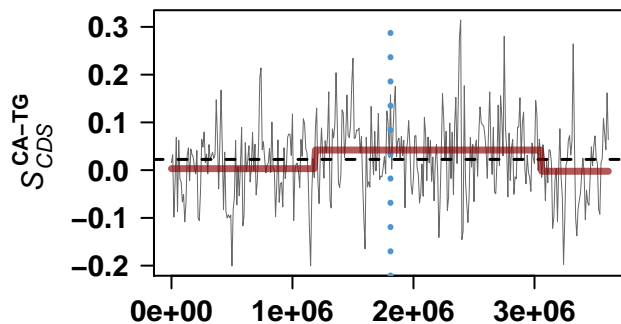
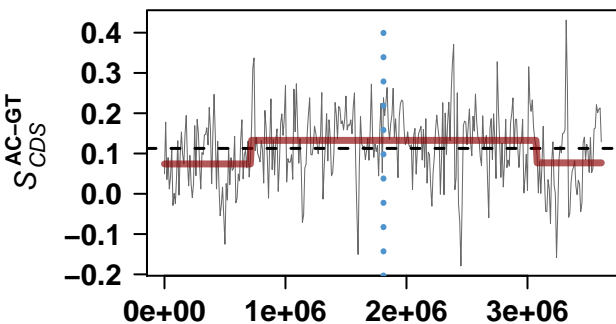
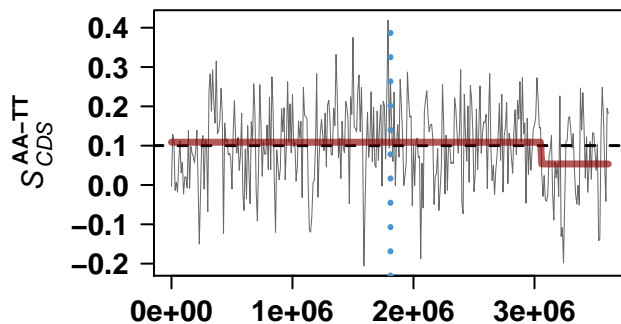
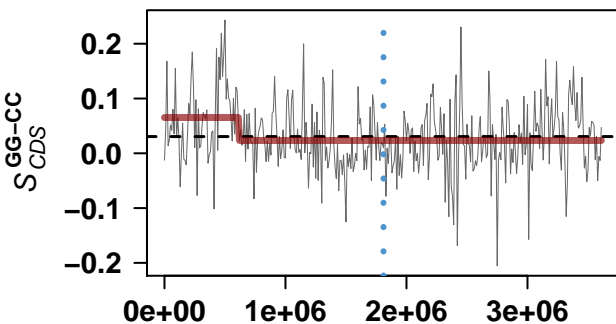
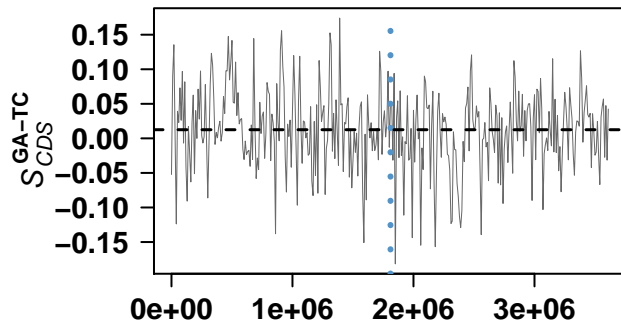
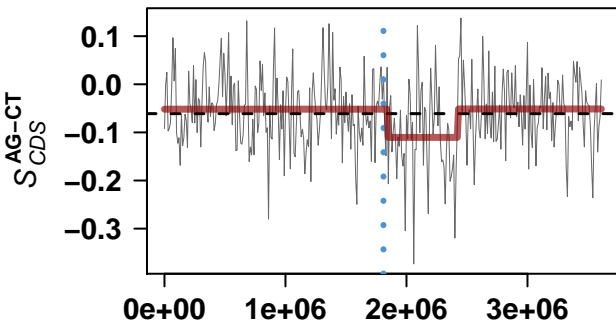


genome coordinates

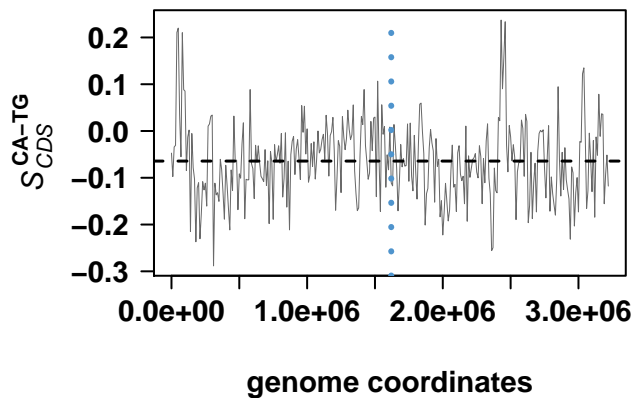
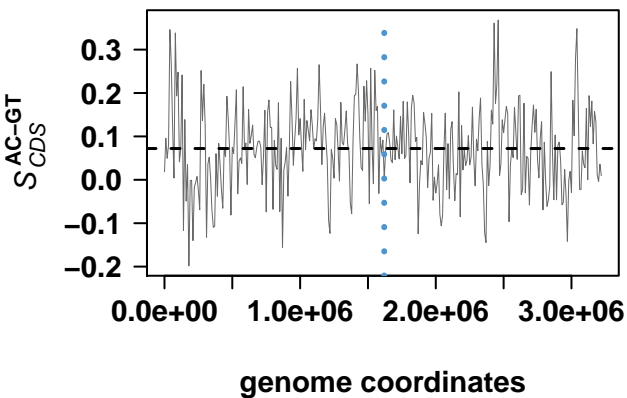
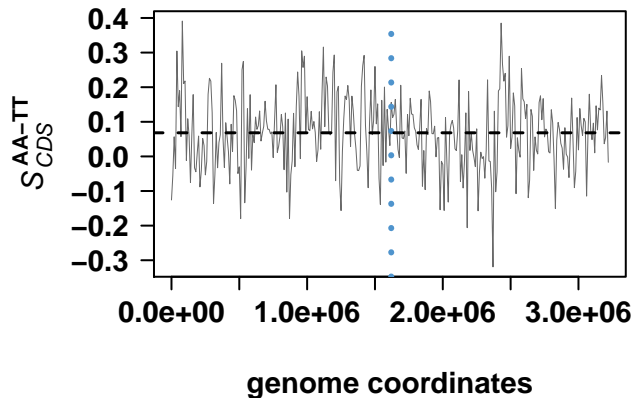
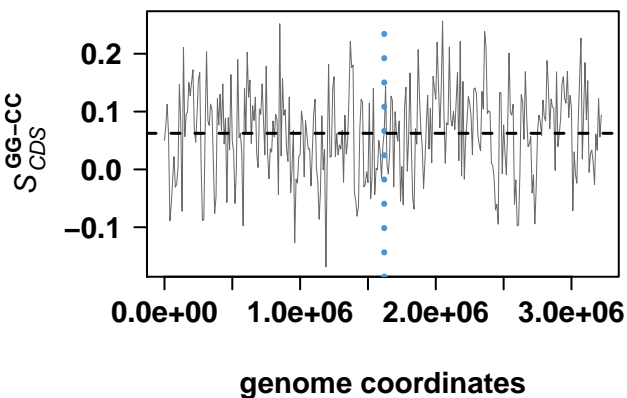
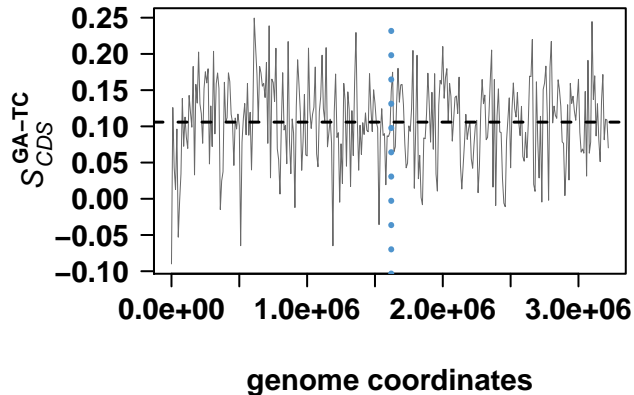
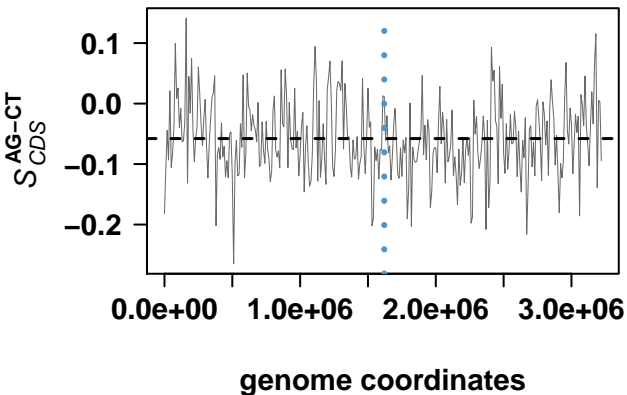


genome coordinates

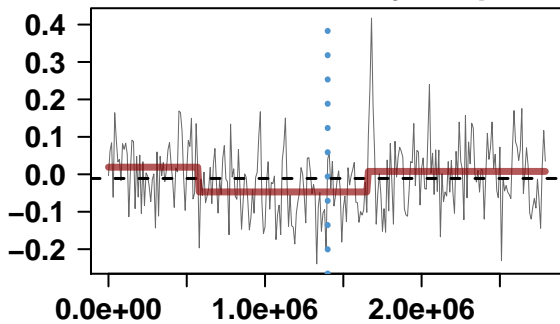
Geobacter metallireducens GS-15



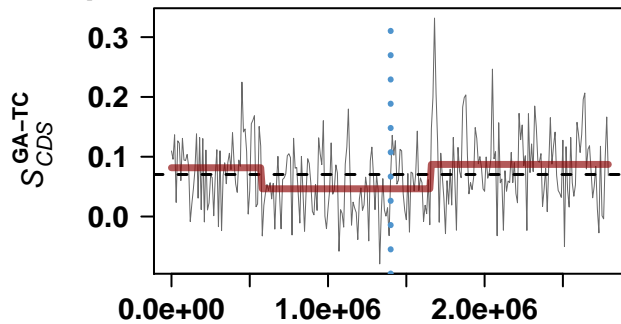
Desulfovibrio alaskensis G20



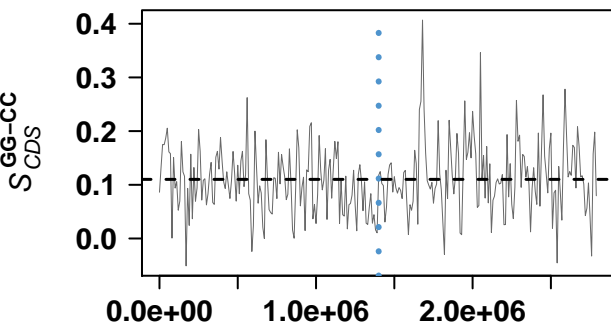
Syntrophus aciditrophicus SB



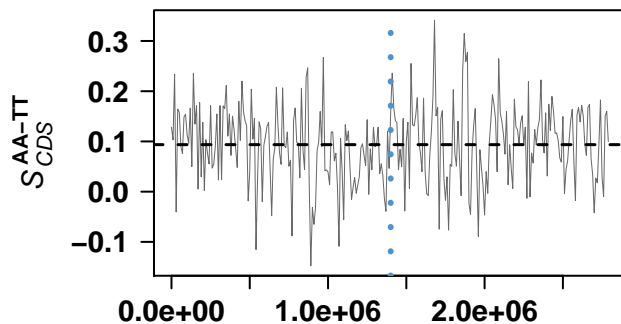
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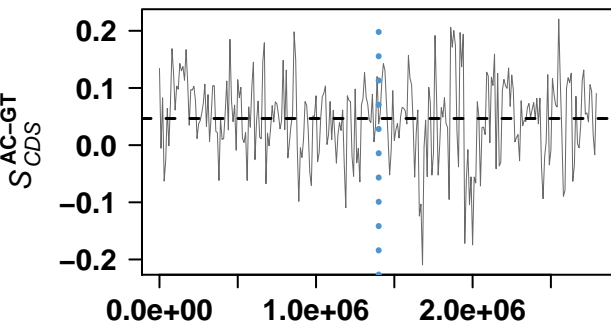
genome coordinates



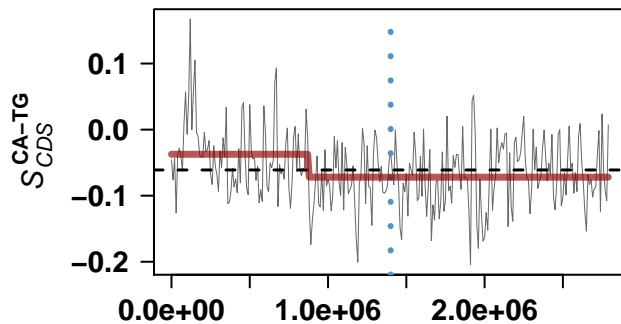
genome coordinates



genome coordinates

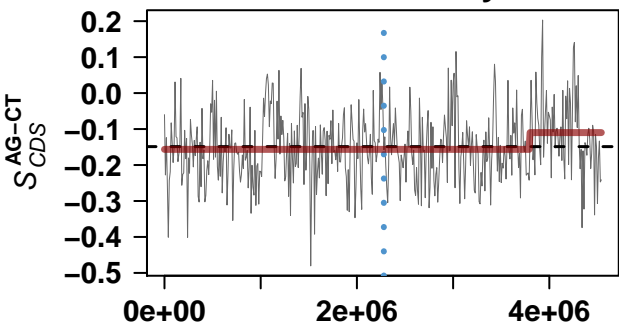


genome coordinates

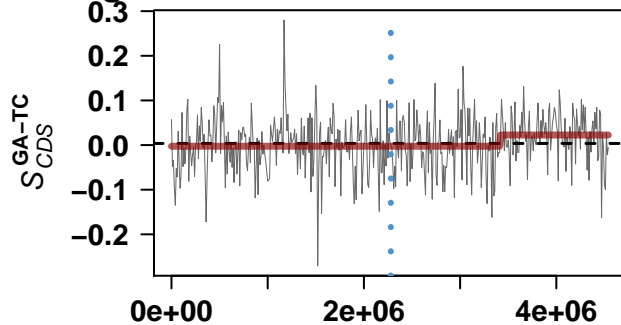


genome coordinates

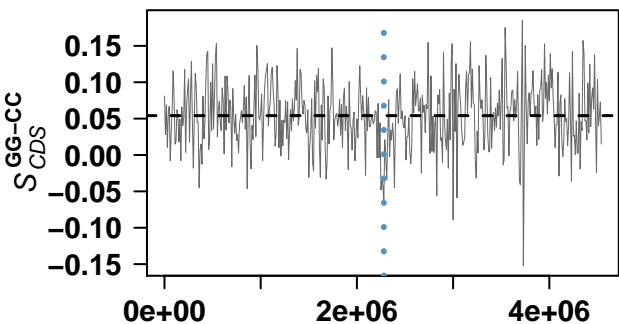
Anaeromyxobacter dehalogenans 2CP-C



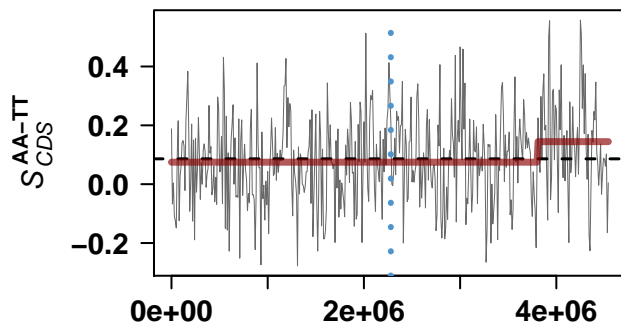
genome coordinates



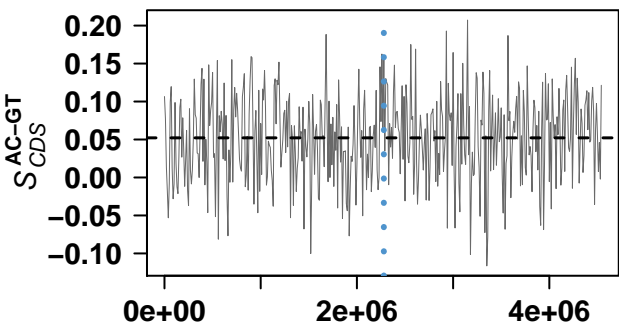
genome coordinates



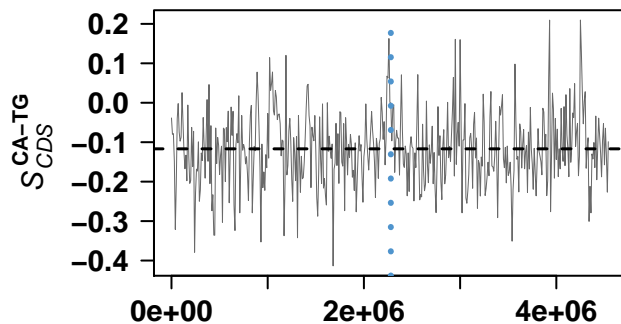
genome coordinates



genome coordinates

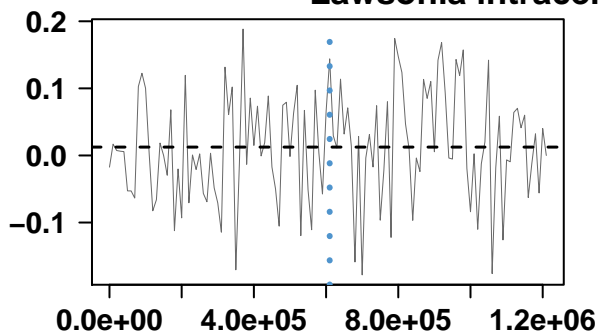


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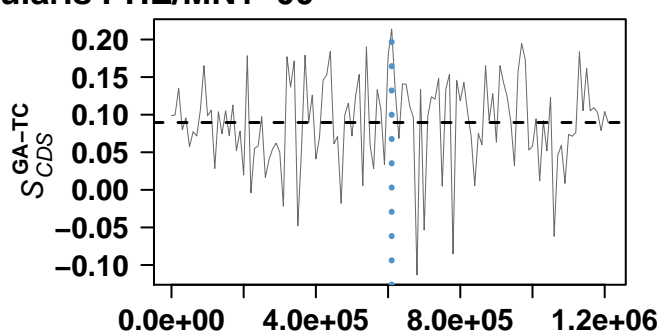


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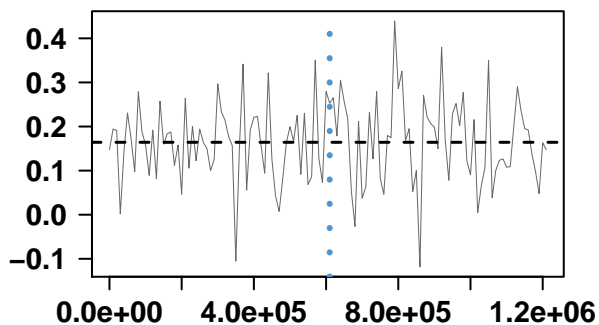
Lawsonia intracellularis PHE/MN1-00



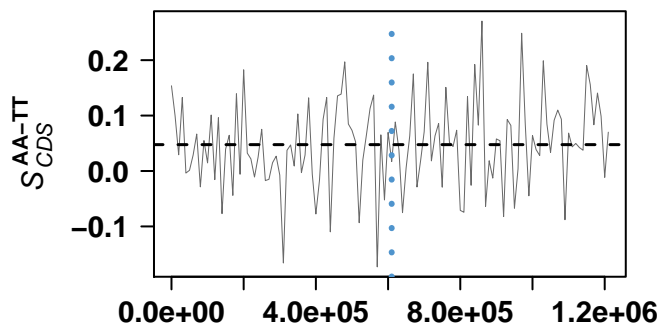
genome coordinates



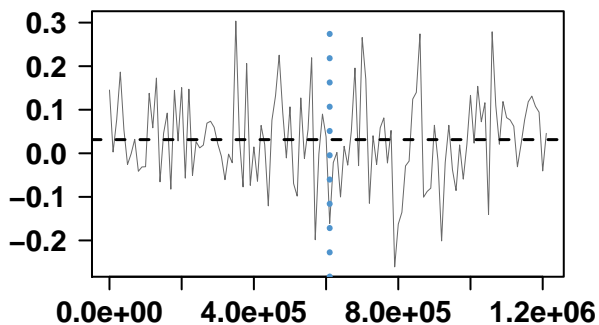
genome coordinates



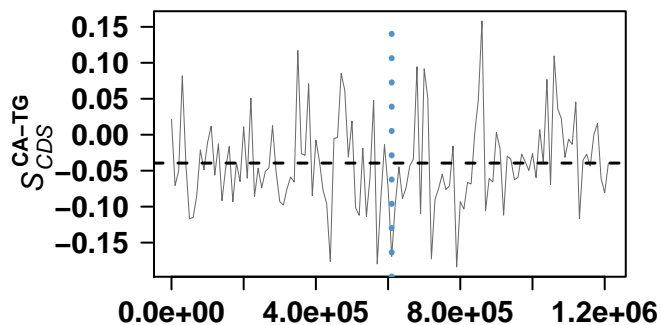
genome coordinates



genome coordinates

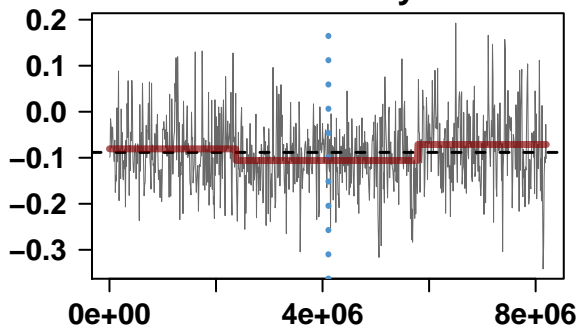


genome coordinates

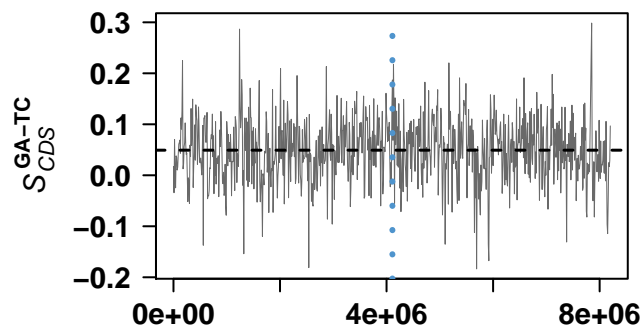


genome coordinates

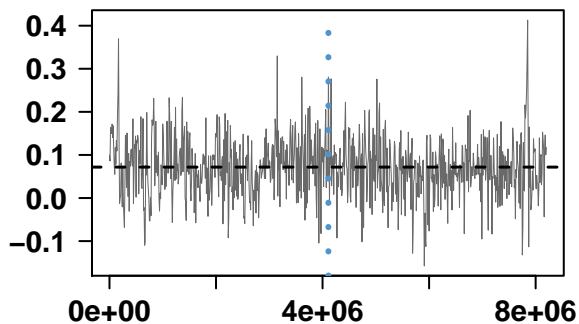
Myxococcus xanthus DK 1622



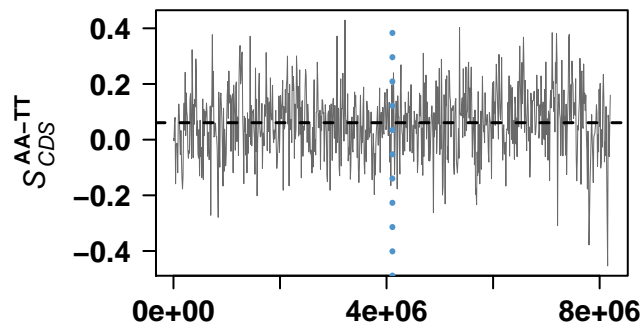
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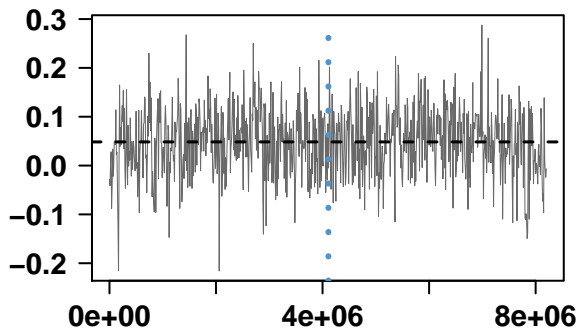
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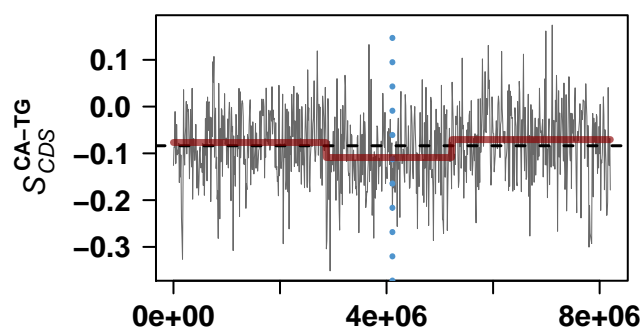
genome coordinates



genome coordinates

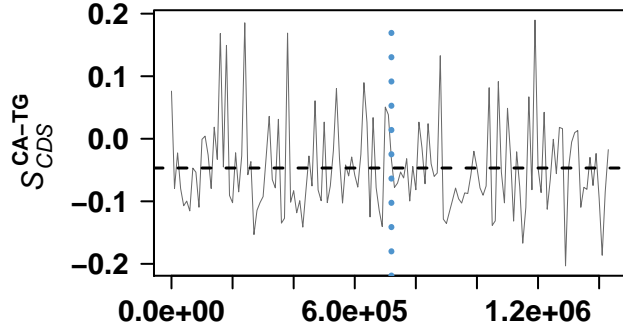
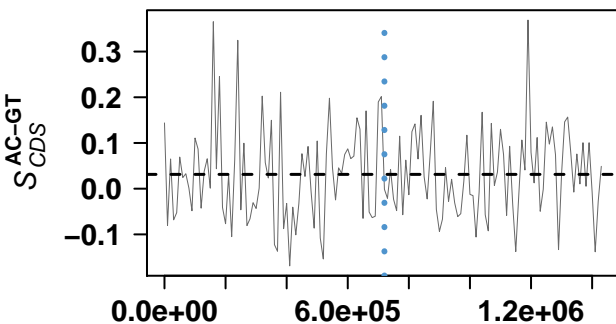
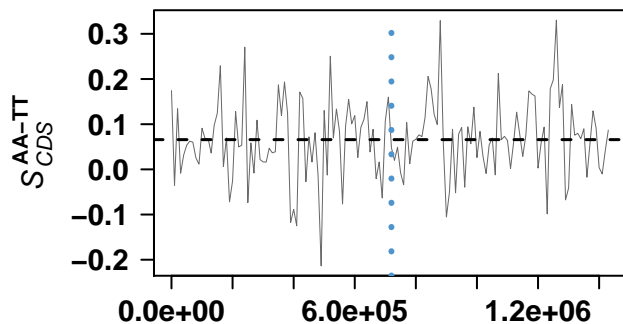
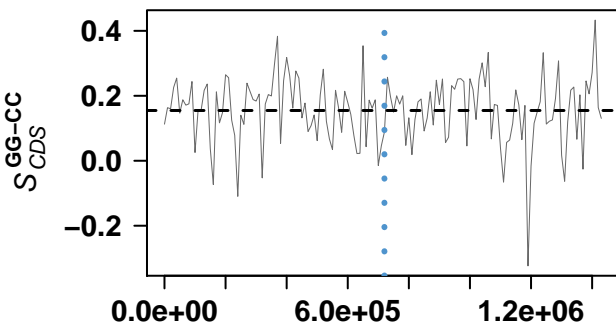
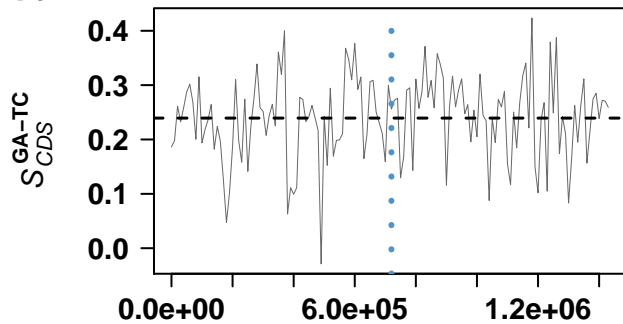
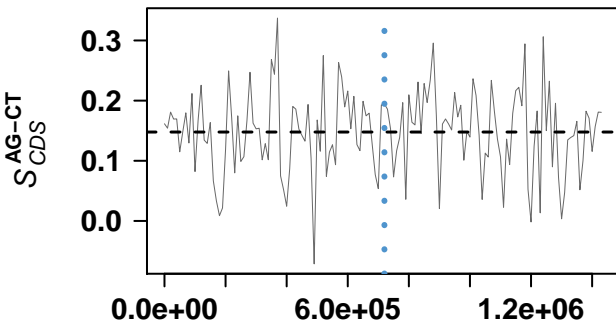


genome coordinates

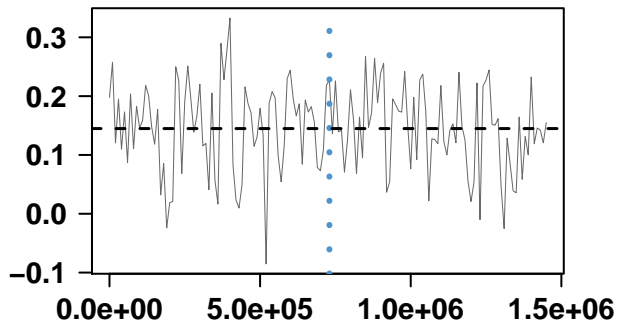


genome coordinates

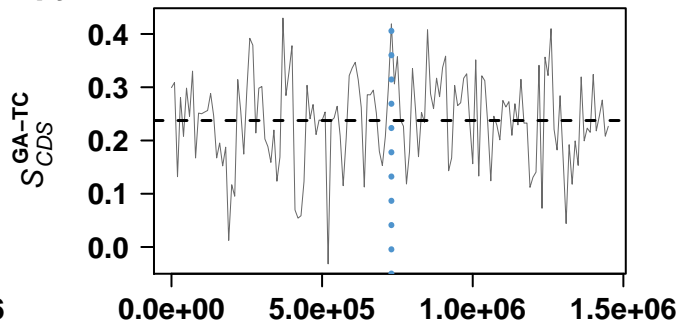
Helicobacter pylori 26695



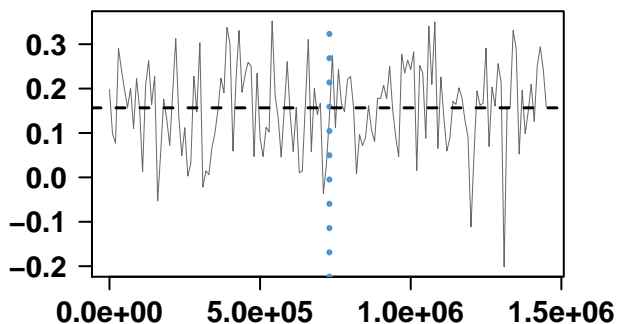
Helicobacter pylori J99



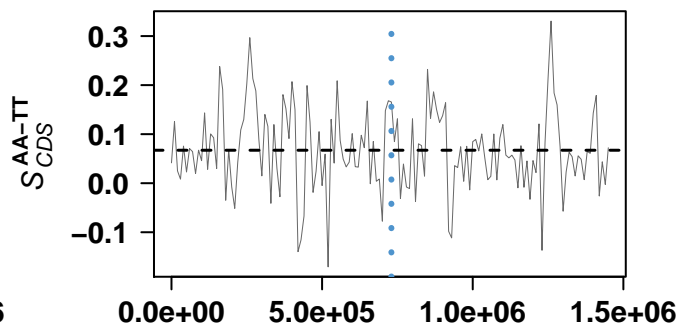
genome coordinates



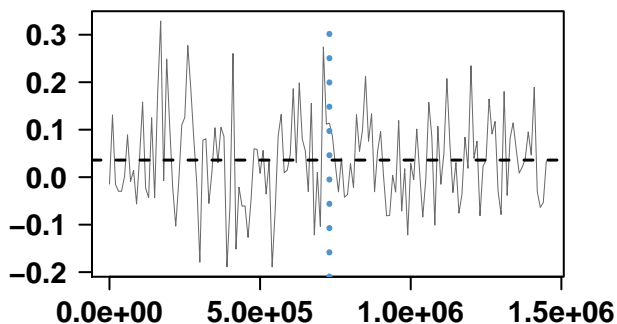
genome coordinates



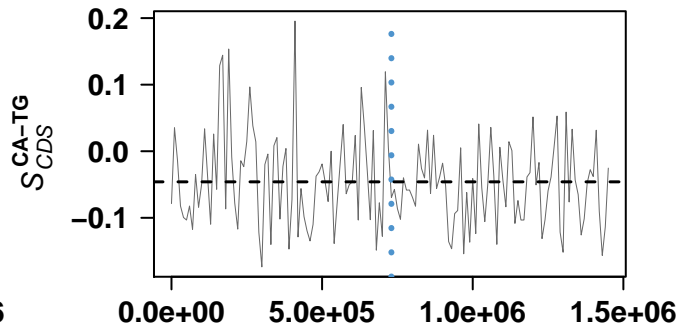
genome coordinates



genome coordinates

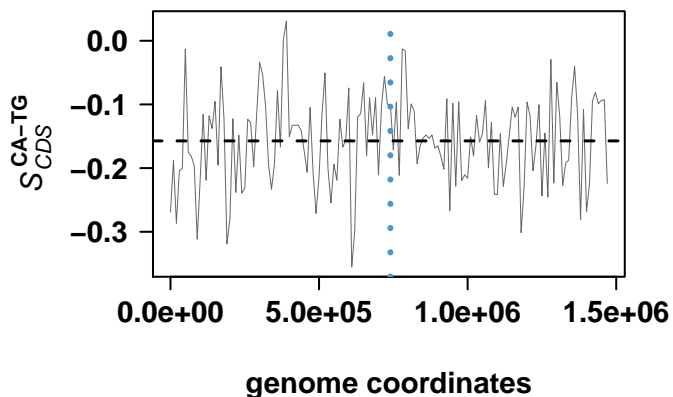
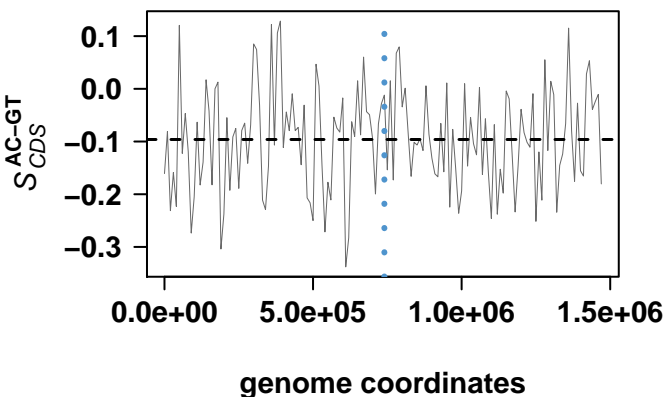
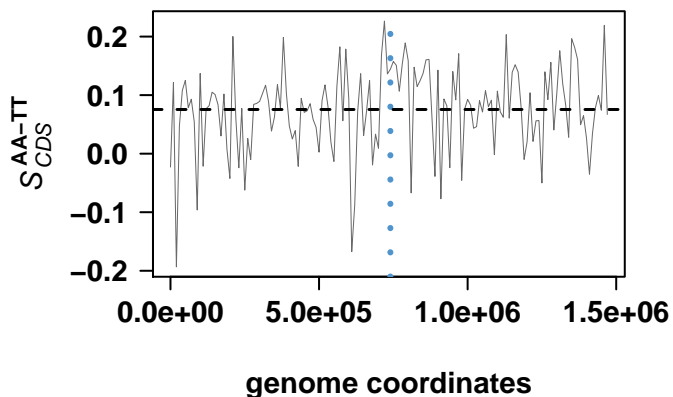
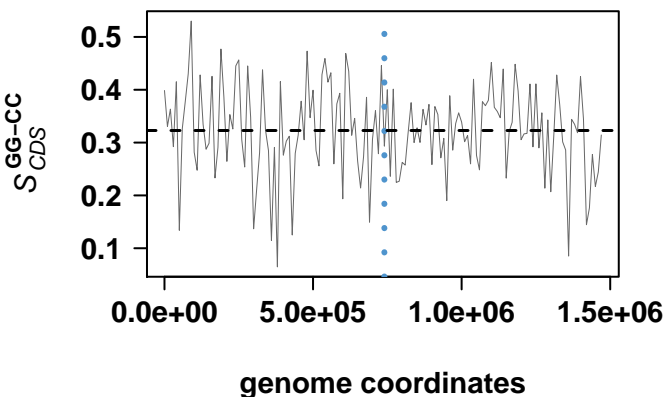
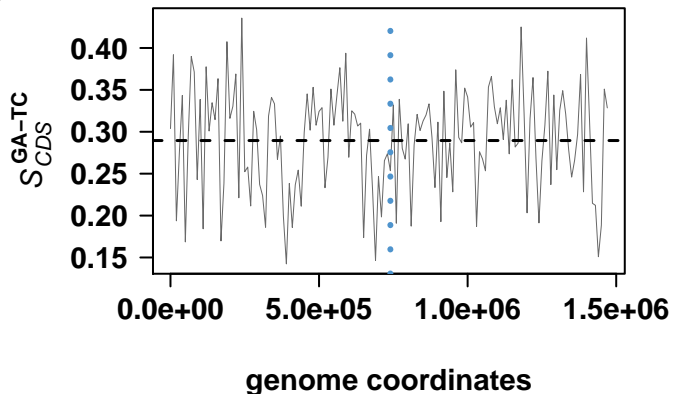
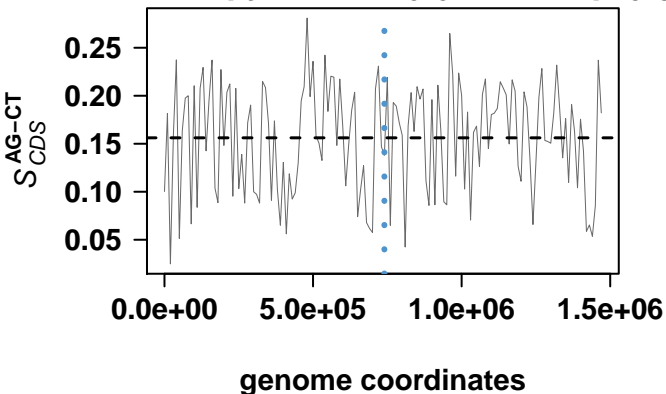


genome coordinates

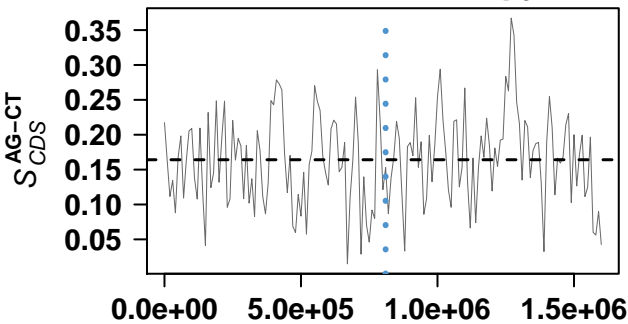


genome coordinates

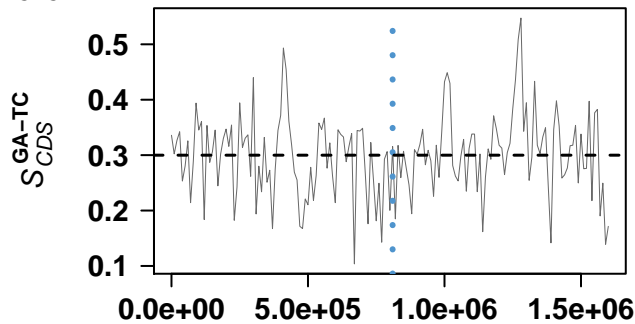
Campylobacter jejuni subsp. jejuni NCTC 11168 = ATCC 700819



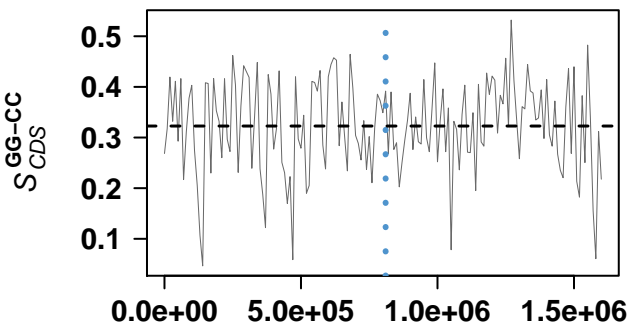
Campylobacter jejuni RM1221



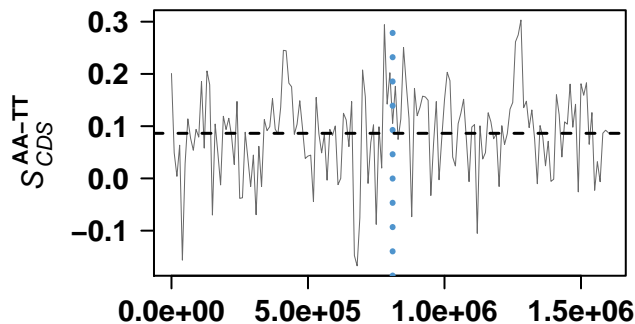
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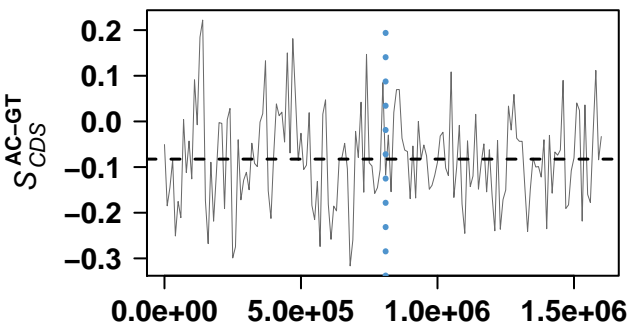
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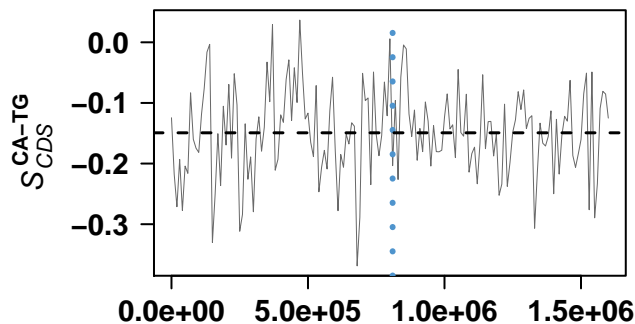
genome coordinates



genome coordinates

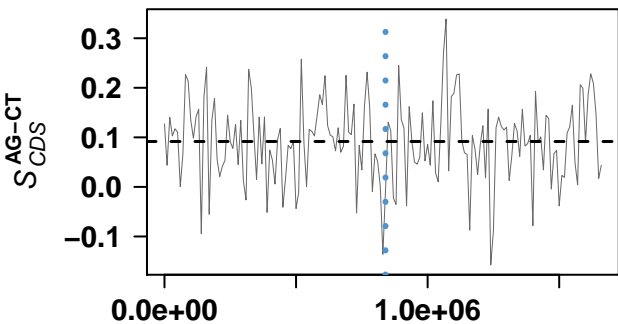


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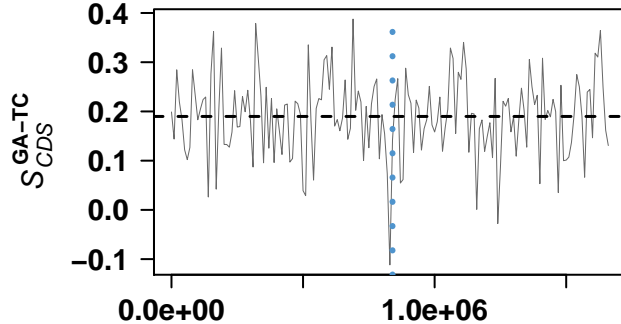


genome coordinates

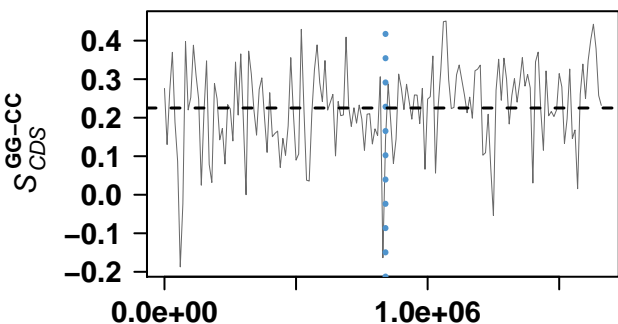
Helicobacter hepaticus ATCC 51449



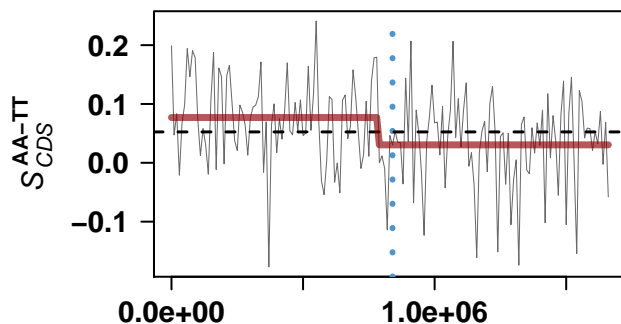
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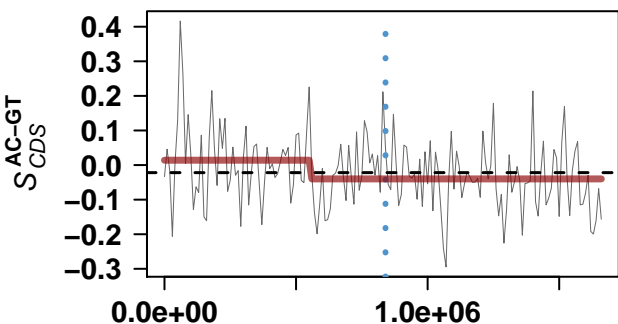
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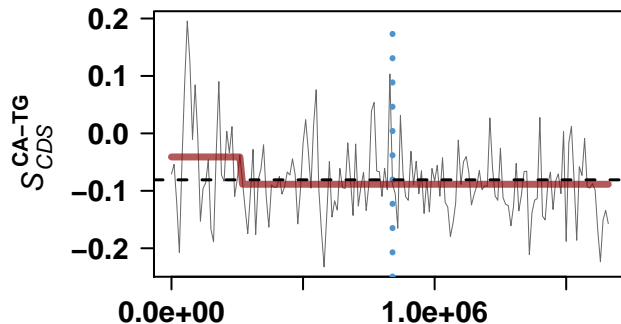
genome coordinates



genome coordinates

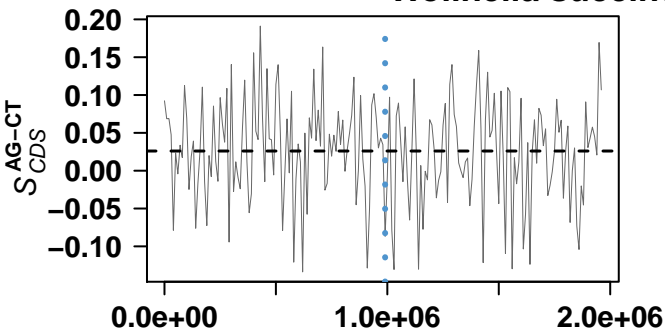


genome coordinates

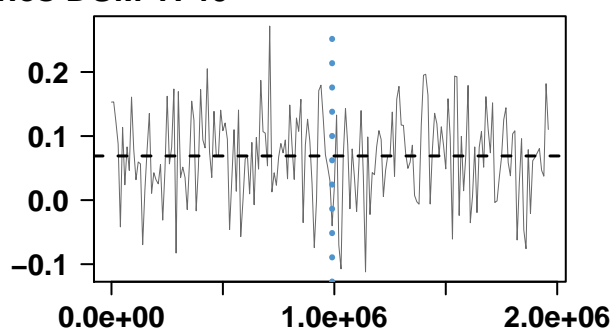


genome coordinates

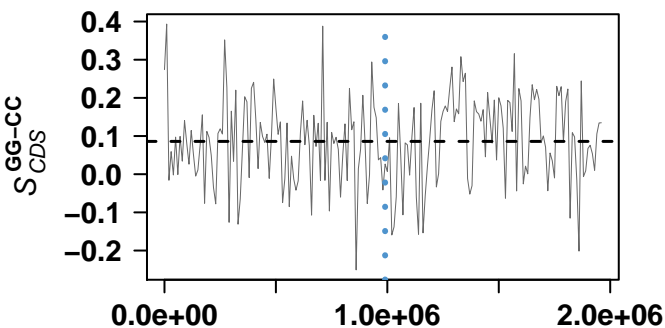
Wolinella succinogenes DSM 1740



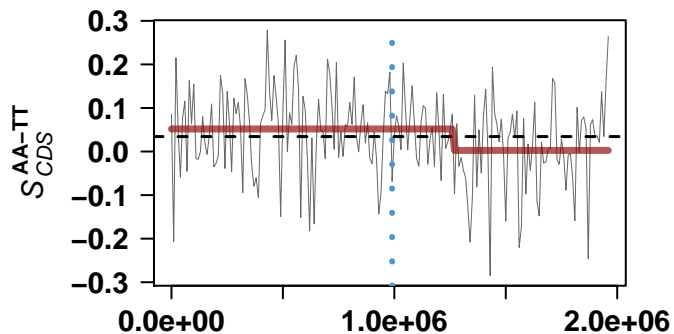
genome coordinates



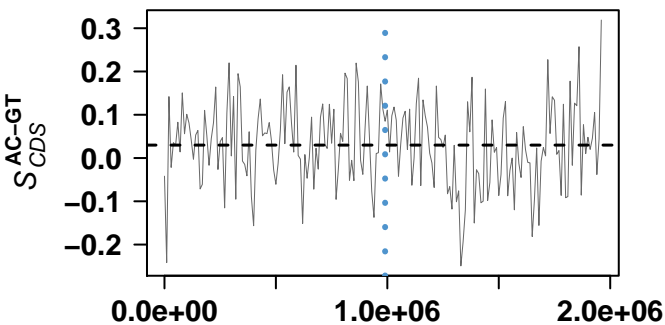
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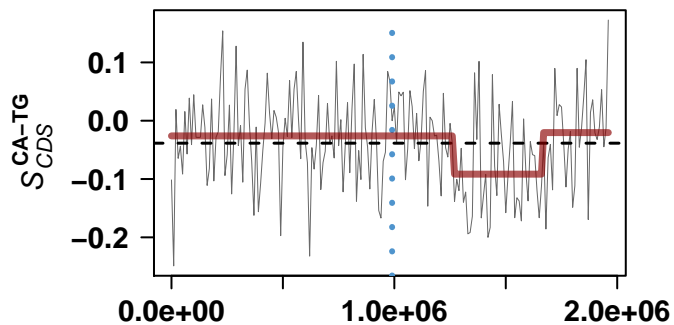
genome coordinates



genome coordinates

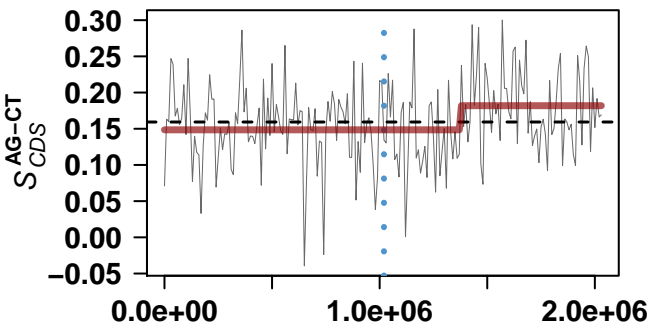


genome coordinates

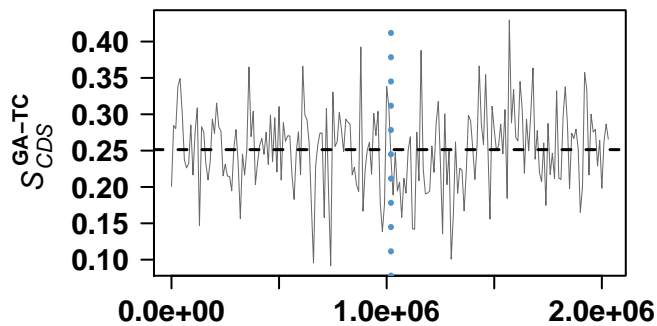


genome coordinates

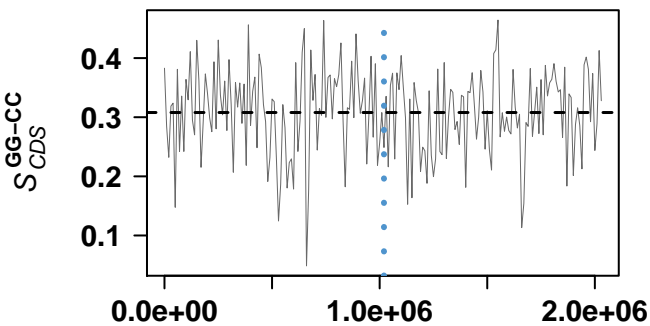
Sulfurimonas denitrificans DSM 1251



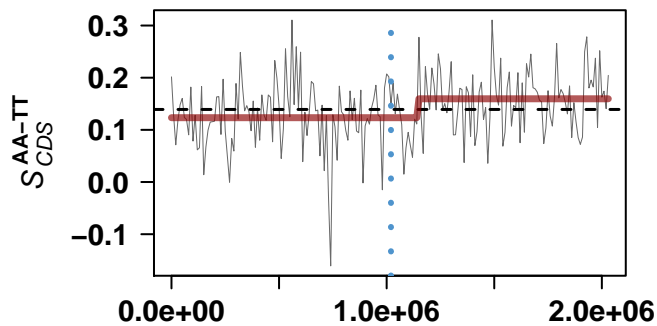
genome coordinates



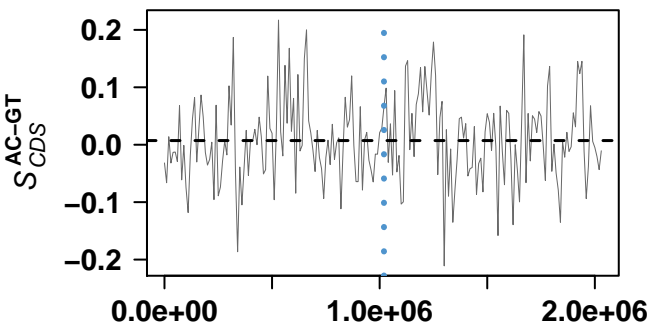
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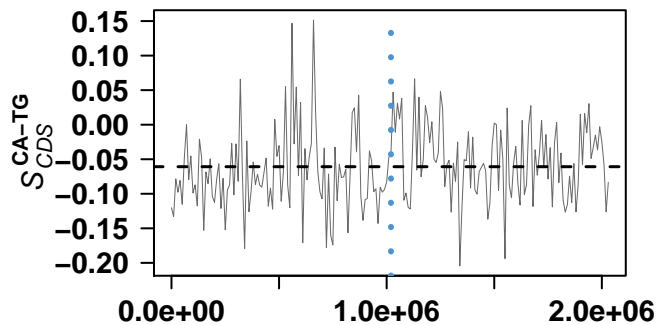
genome coordinates



genome coordinates

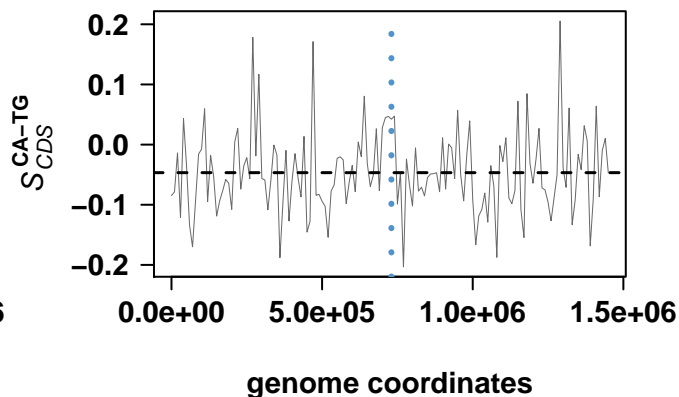
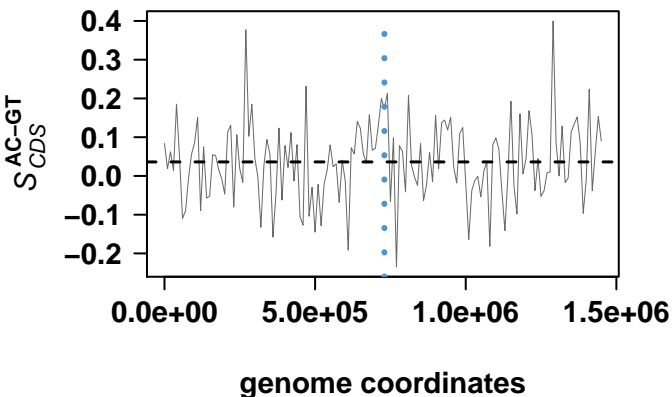
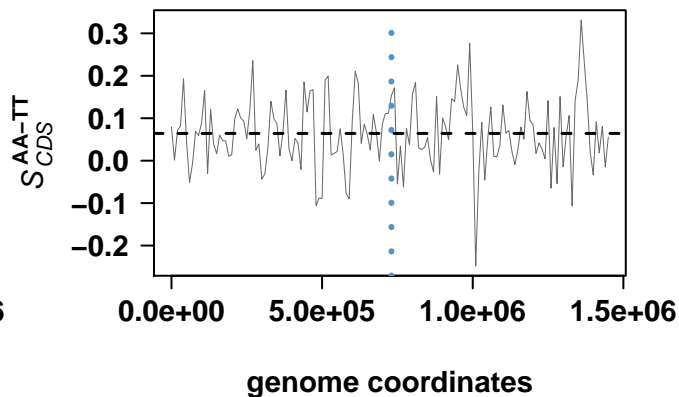
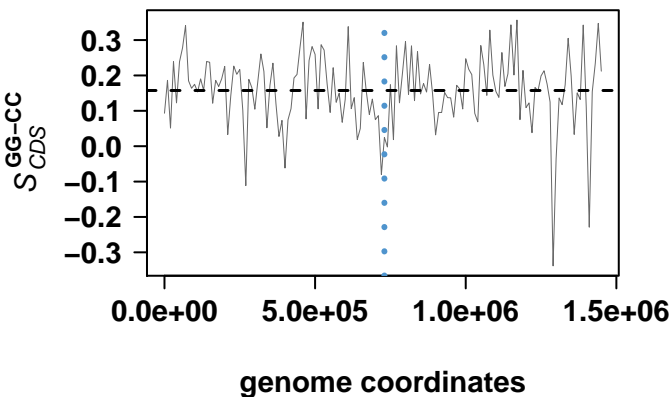
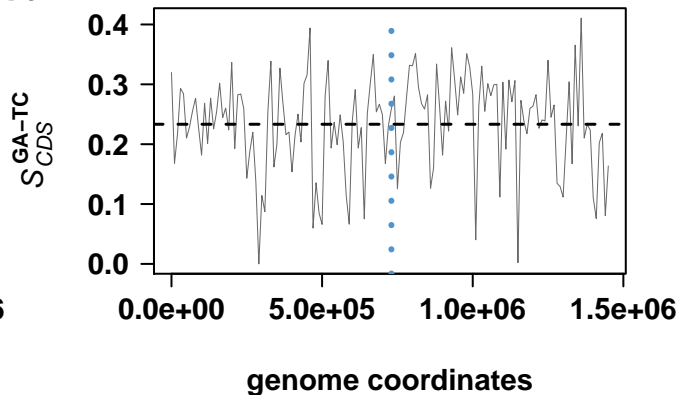
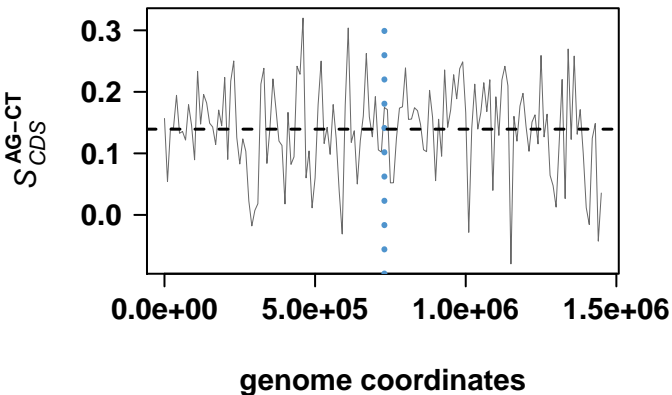


genome coordinates

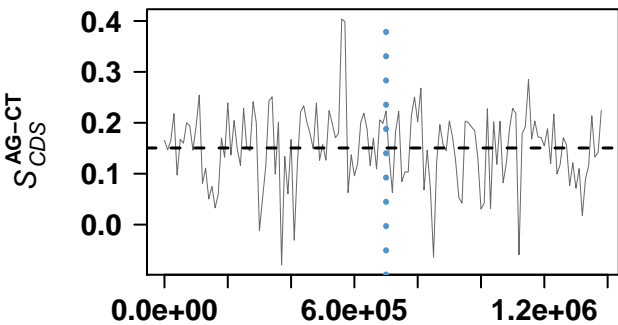


genome coordinates

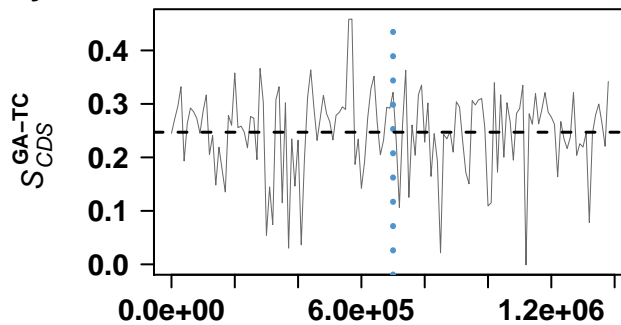
Helicobacter pylori HPAG1



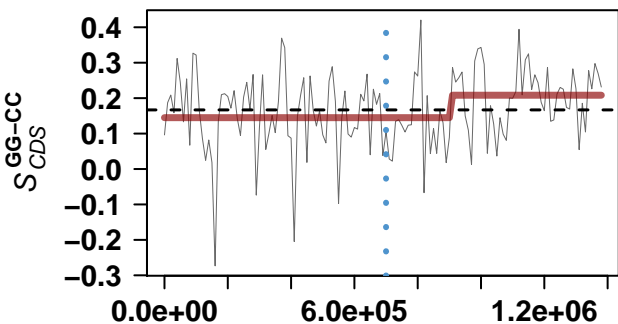
Helicobacter acinonychis str. Sheeba



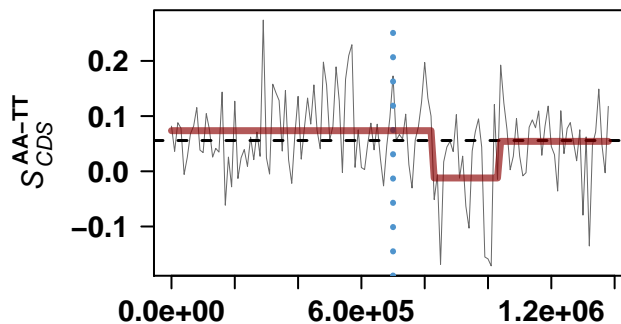
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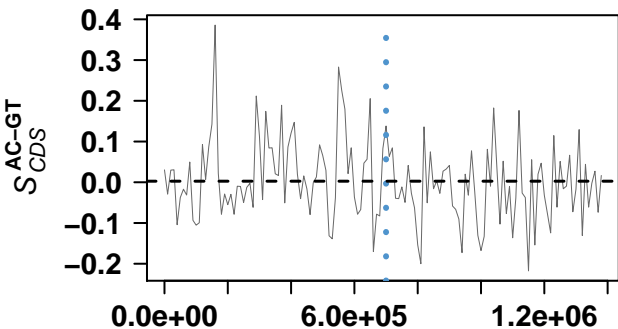
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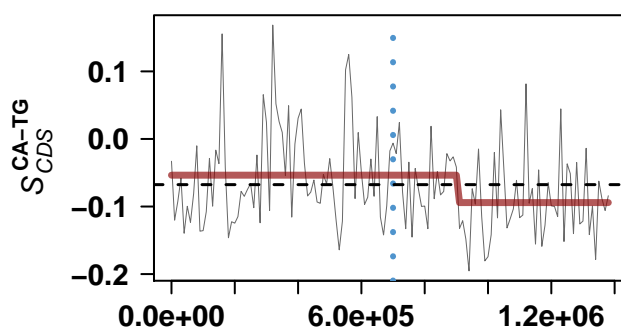
genome coordinates



genome coordinates

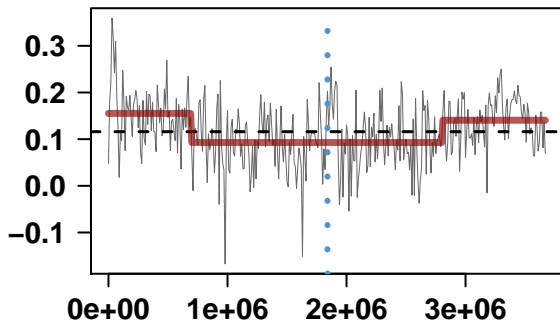


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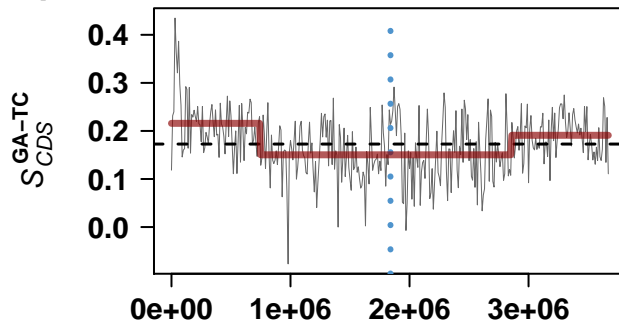


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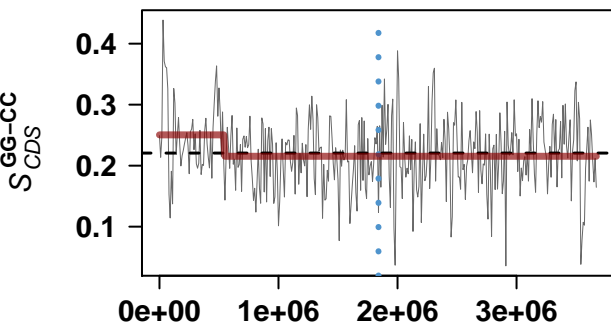
Bacillus subtilis subsp. subtilis str. 168



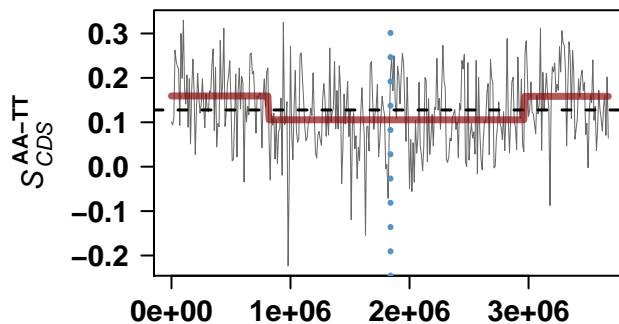
genome coordinates



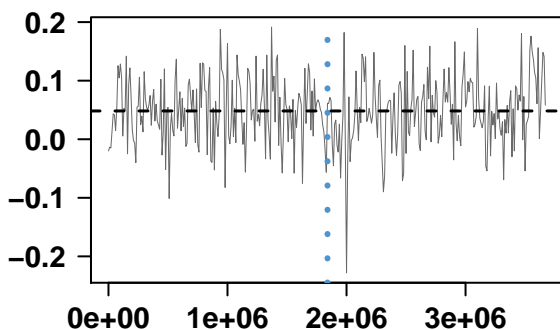
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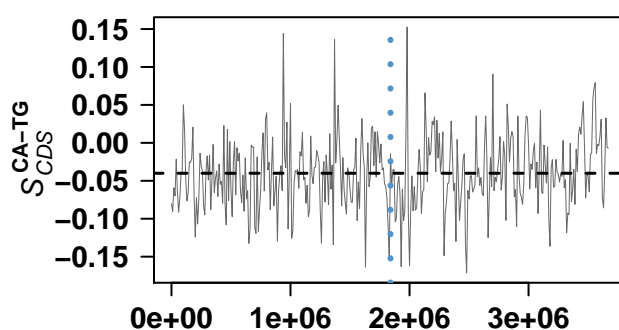
genome coordinates



genome coordinates

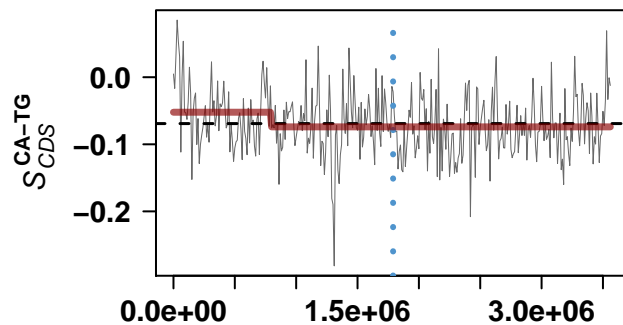
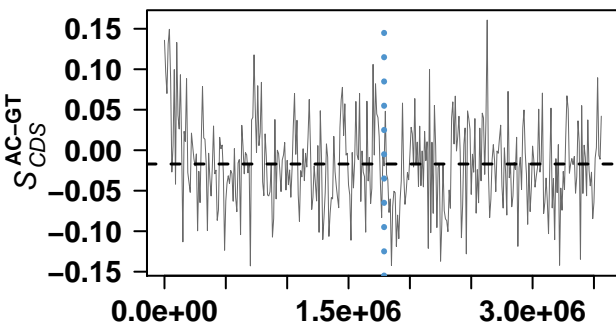
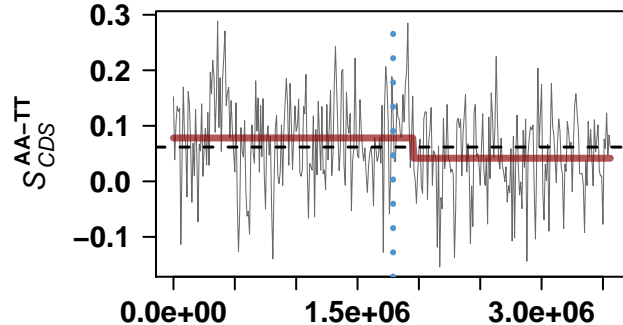
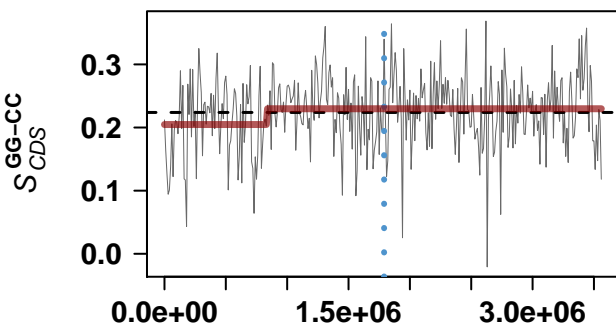
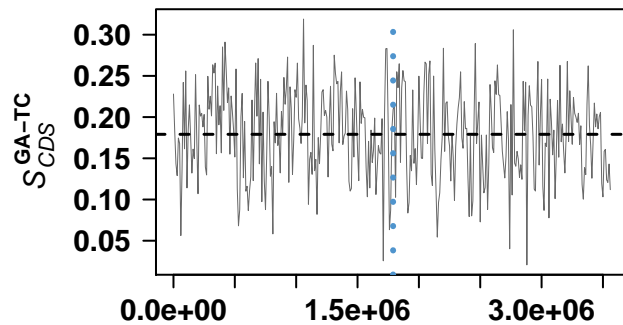
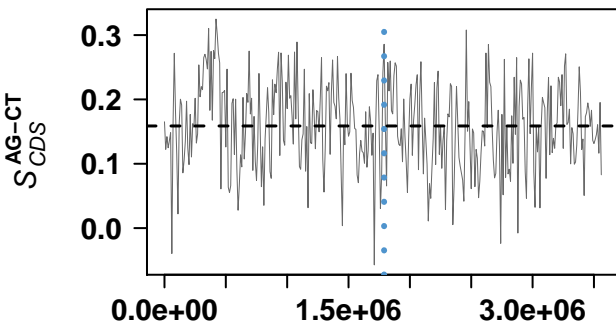


genome coordinates

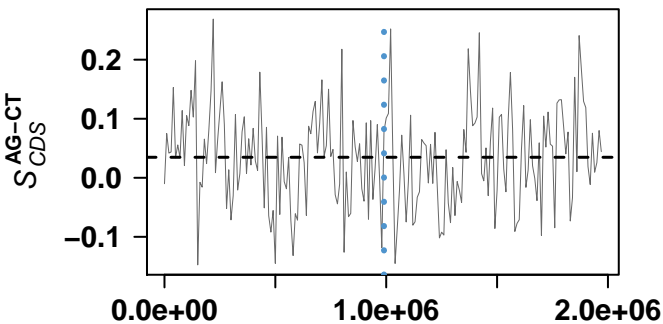


genome coordinates

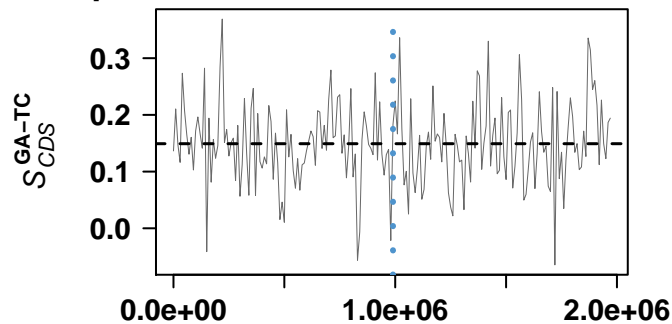
Bacillus halodurans C-125



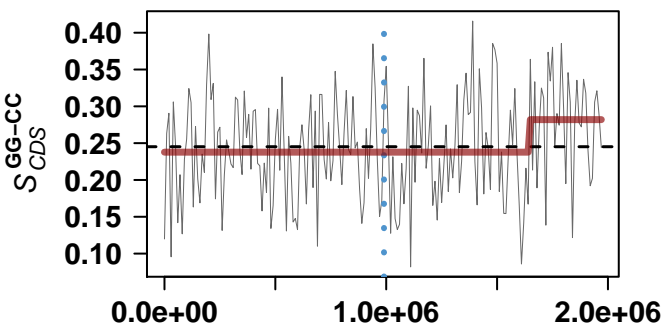
Lactococcus lactis subsp. lactis II1403



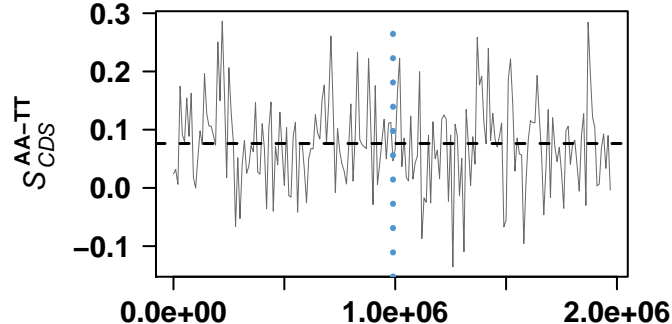
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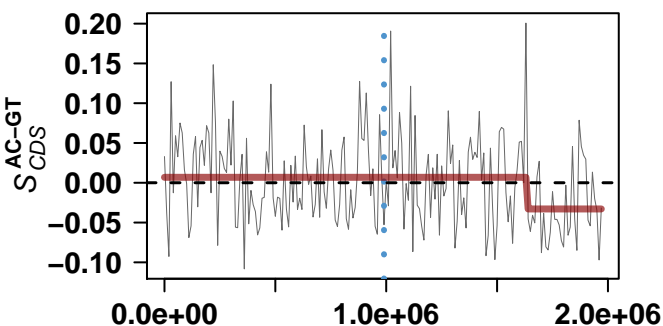
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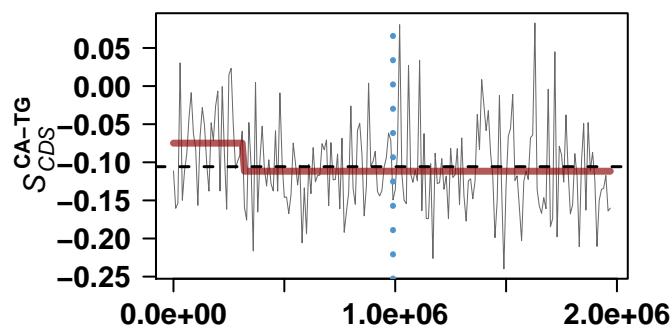
genome coordinates



genome coordinates

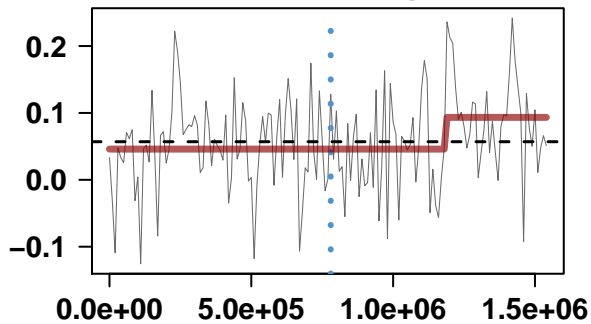


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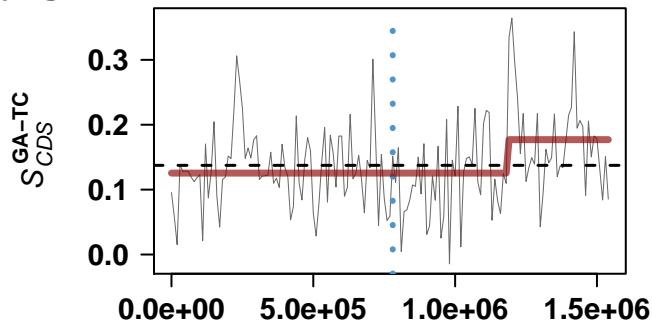


genome coordinates

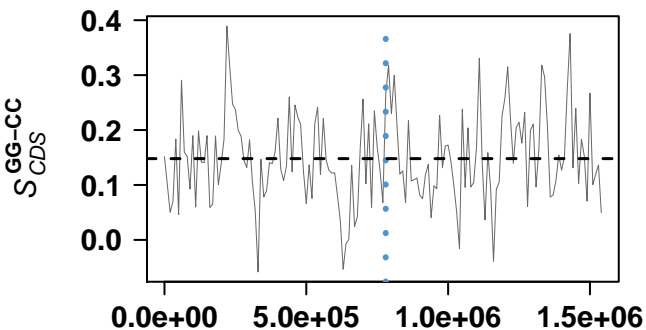
Streptococcus pyogenes M1 GAS



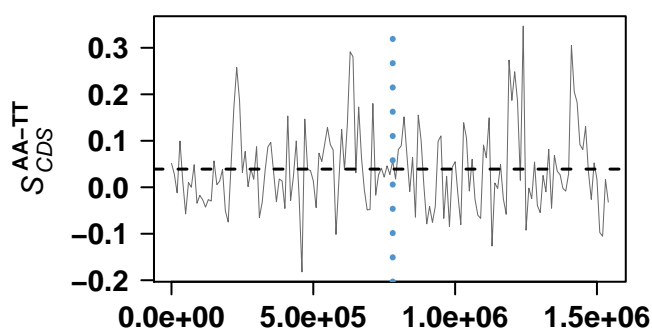
genome coordinates



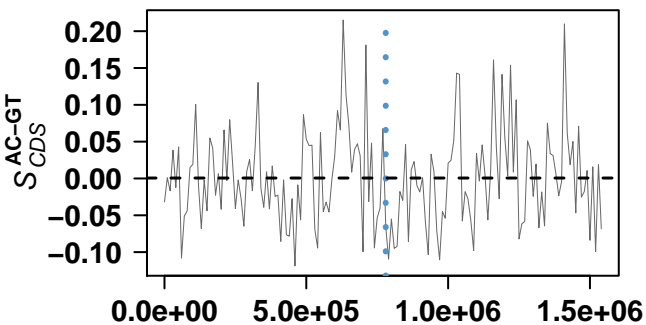
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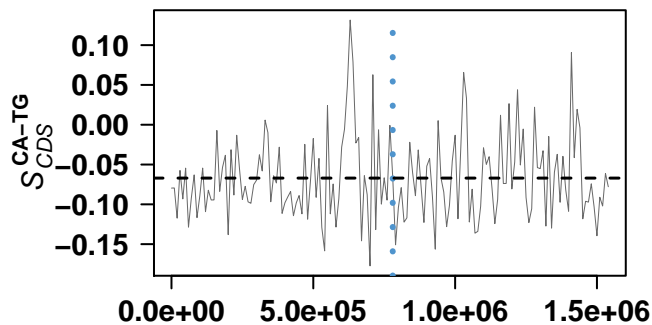
genome coordinates



genome coordinates

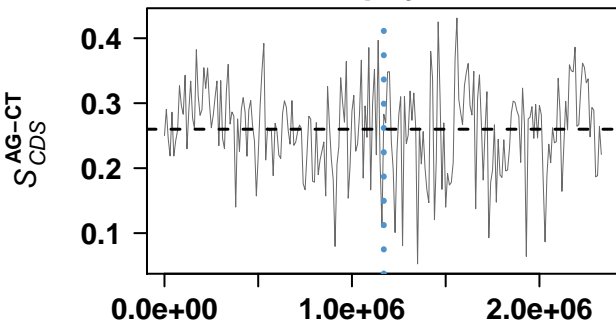


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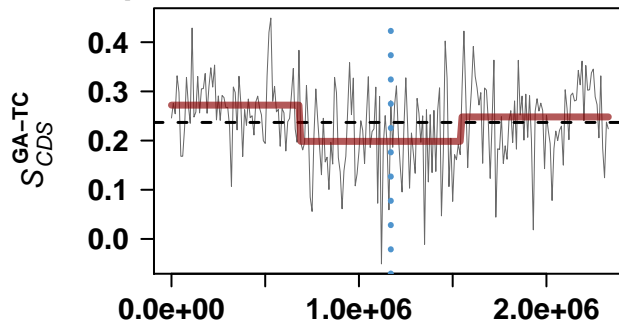


genome coordinates

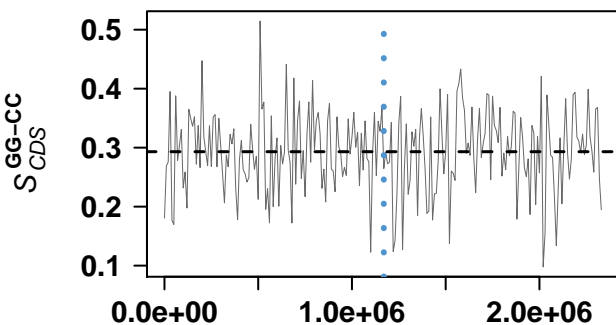
Staphylococcus aureus subsp. aureus N315



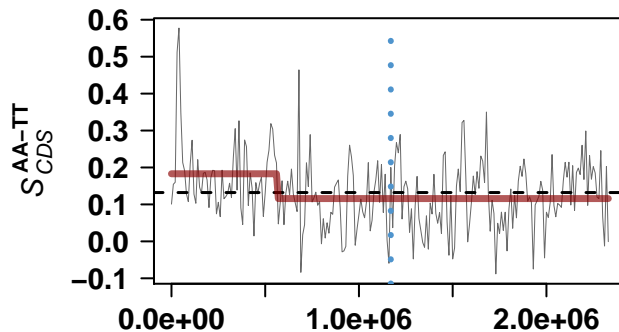
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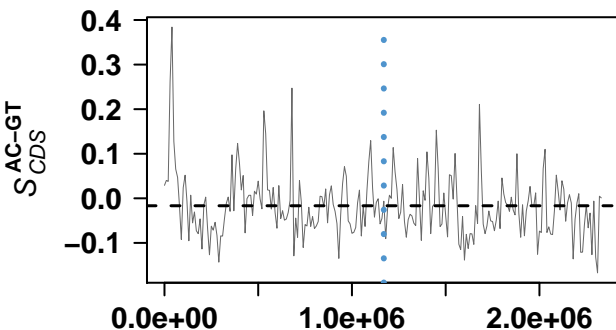
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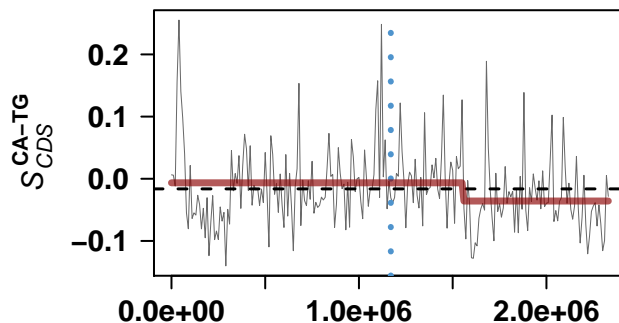
genome coordinates



genome coordinates

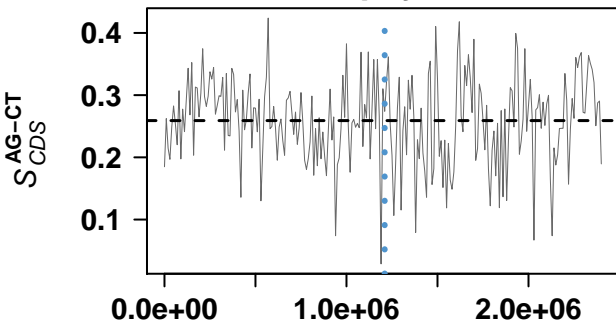


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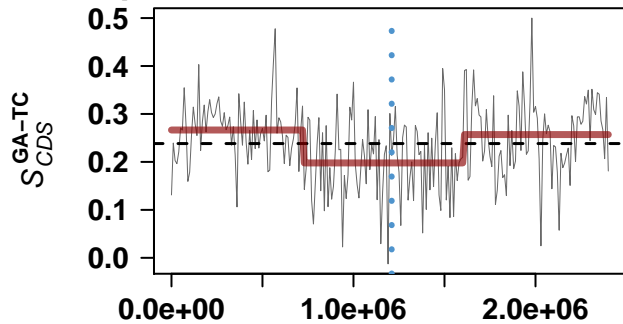


genome coordinates

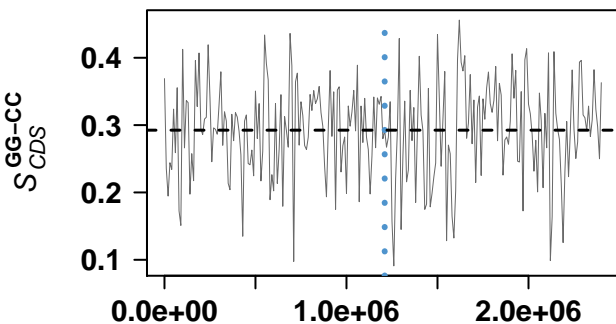
Staphylococcus aureus subsp. aureus Mu50



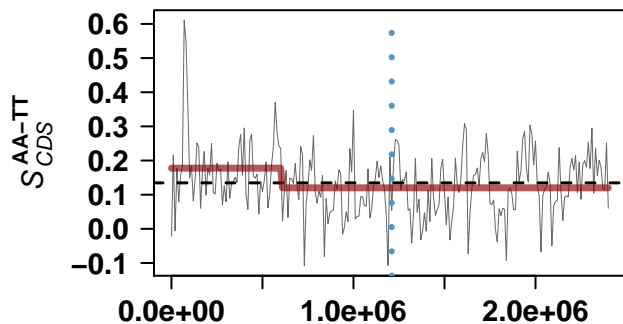
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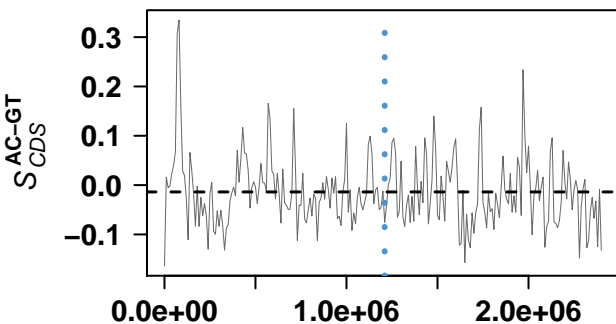
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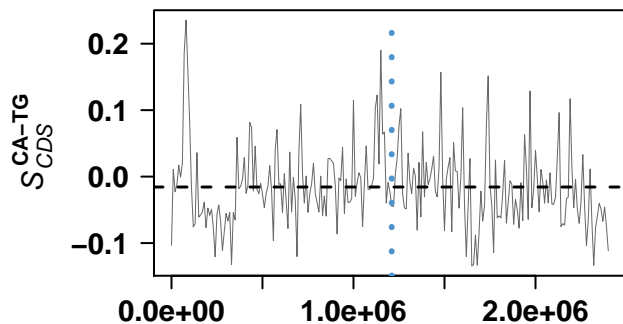
genome coordinates



genome coordinates

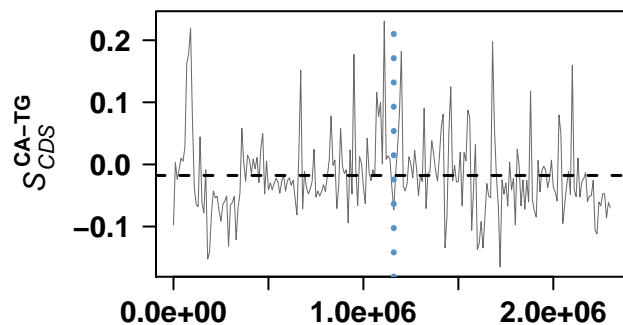
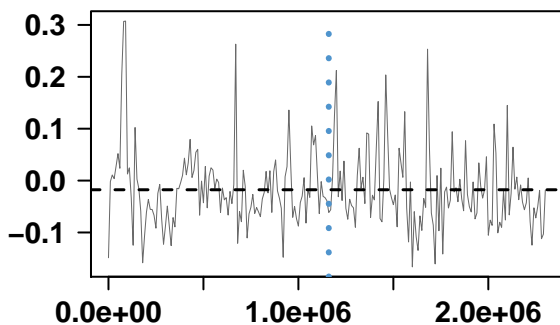
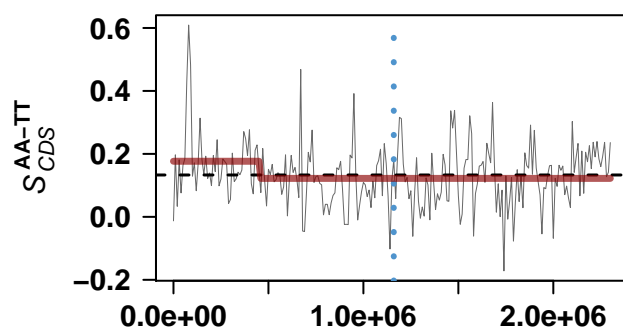
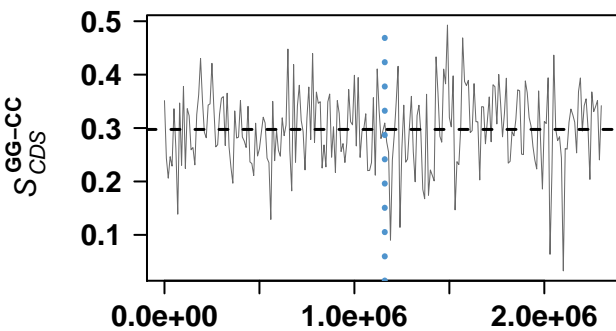
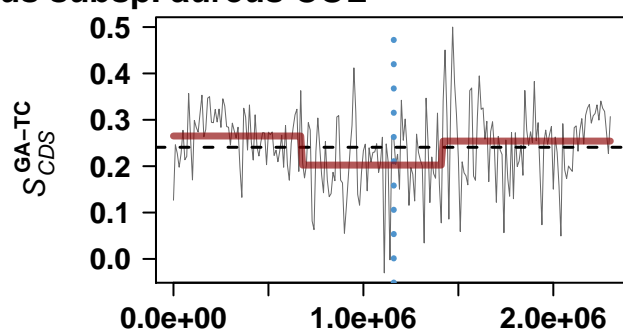
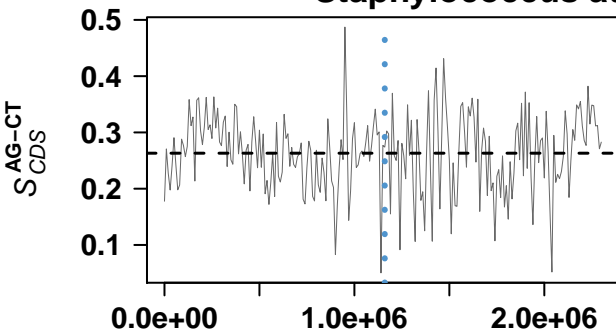


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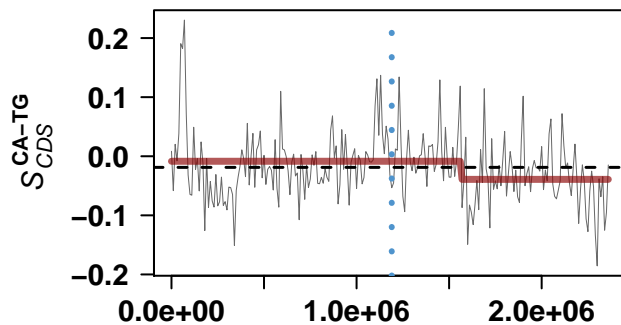
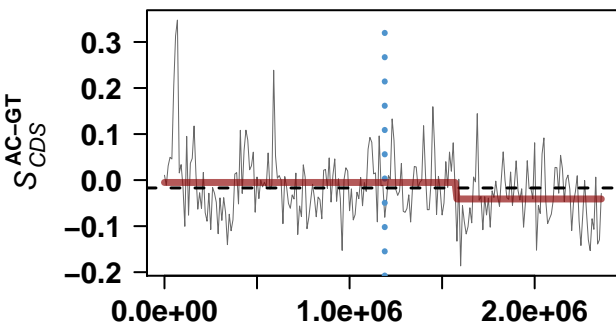
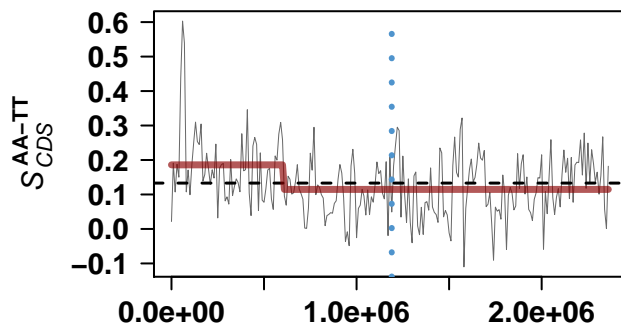
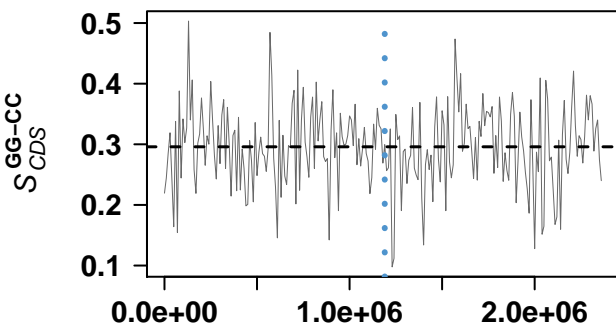
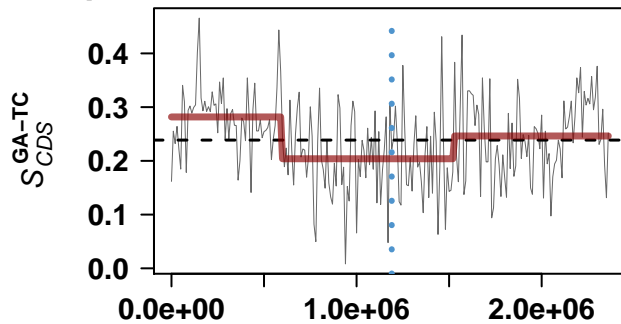
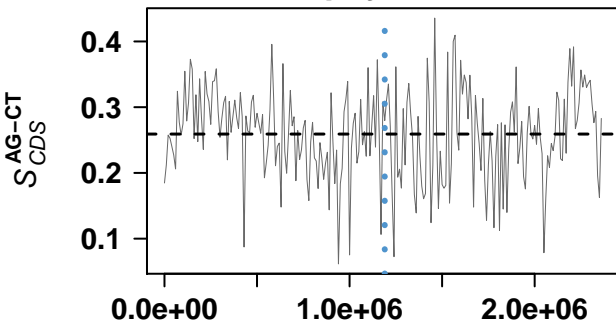


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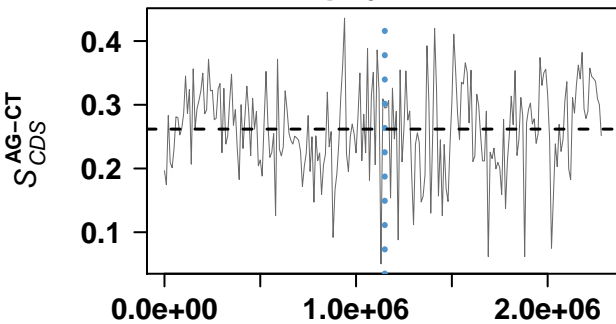
Staphylococcus aureus subsp. aureus COL



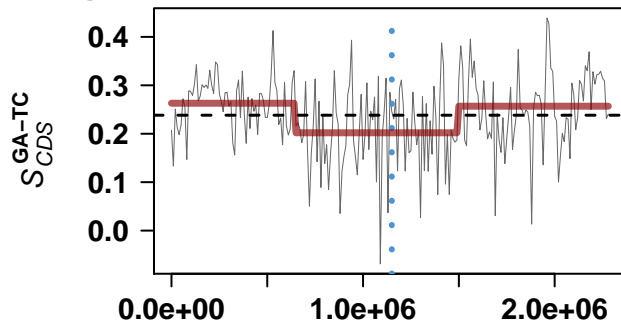
Staphylococcus aureus subsp. aureus MRSA252



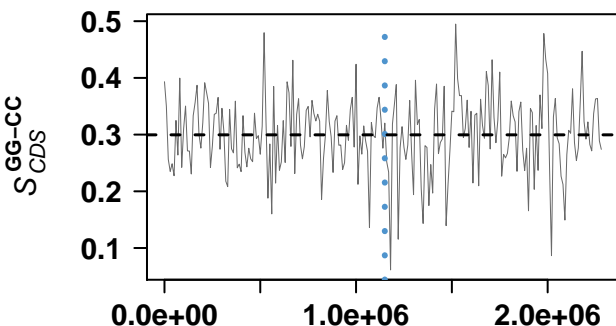
Staphylococcus aureus subsp. aureus MSSA476



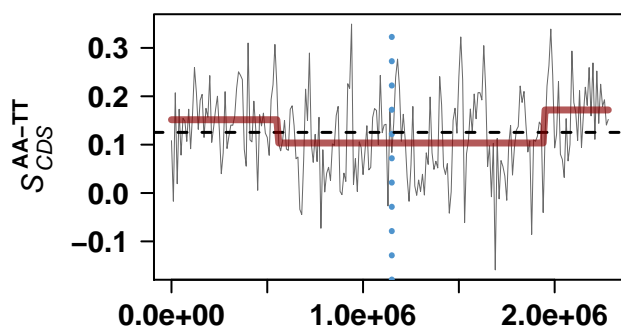
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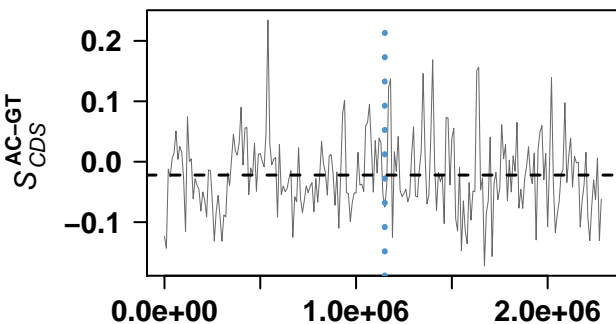
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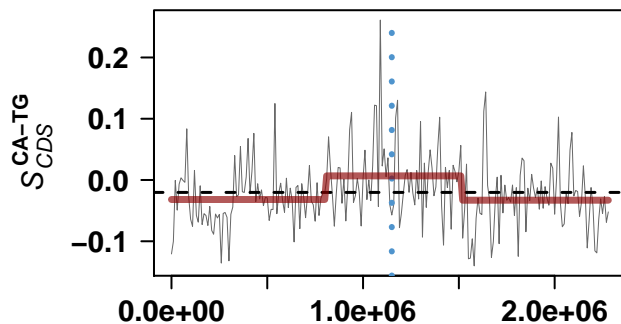
genome coordinates



genome coordinates

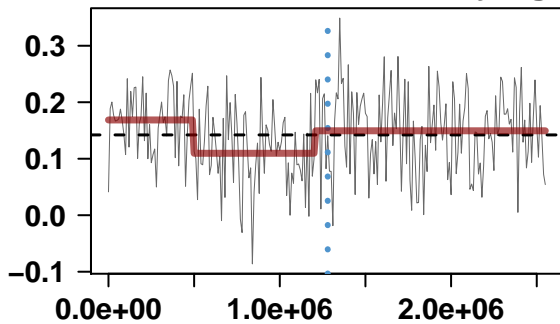


genome coordinates

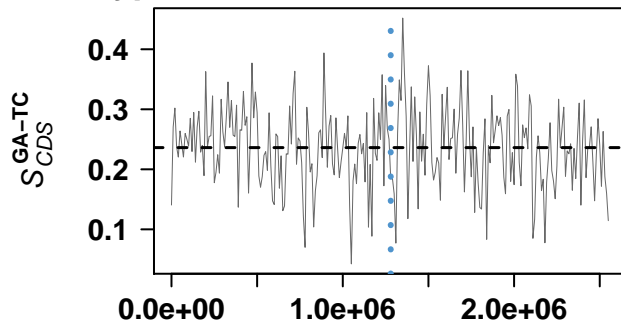


genome coordinates

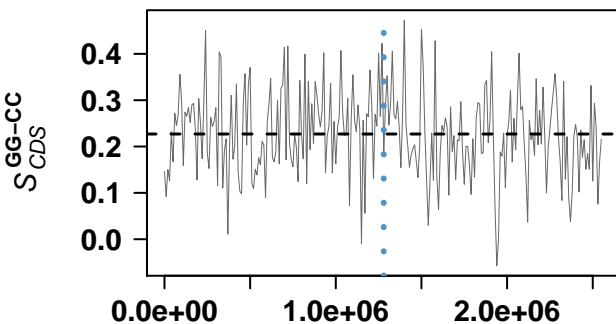
Listeria monocytogenes serotype 4b str. F2365



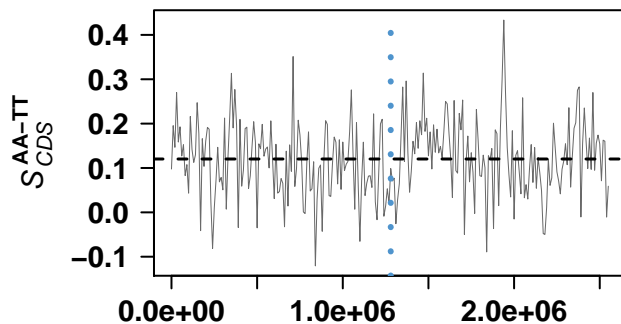
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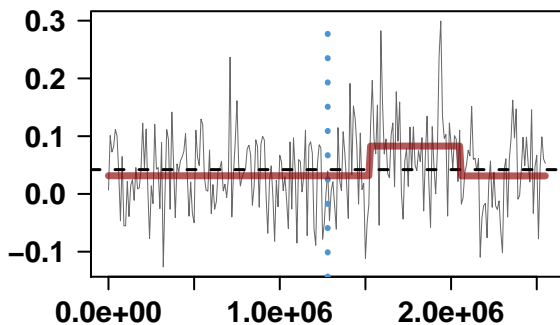
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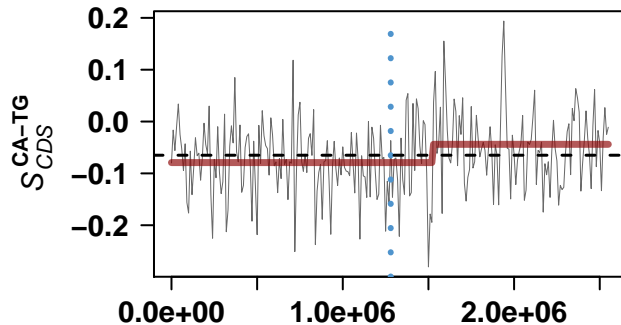
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genome coordinates

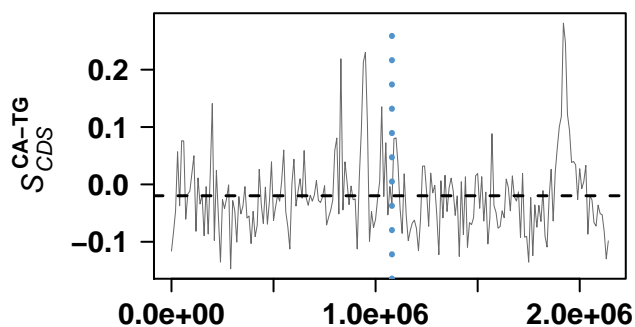
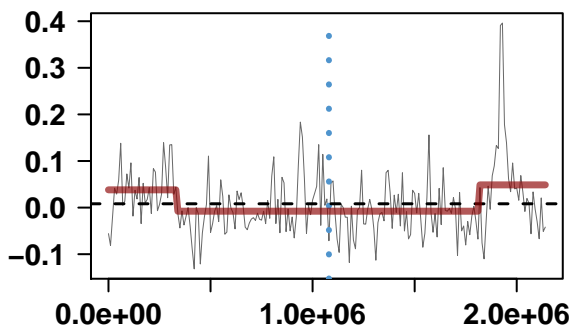
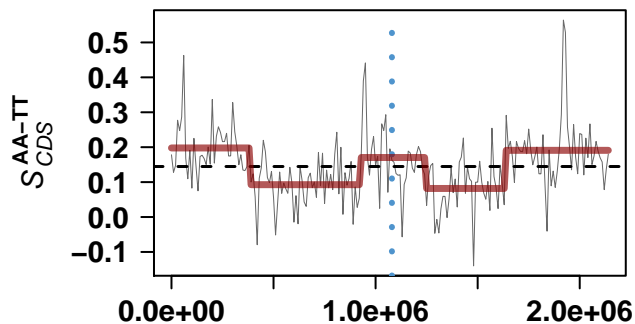
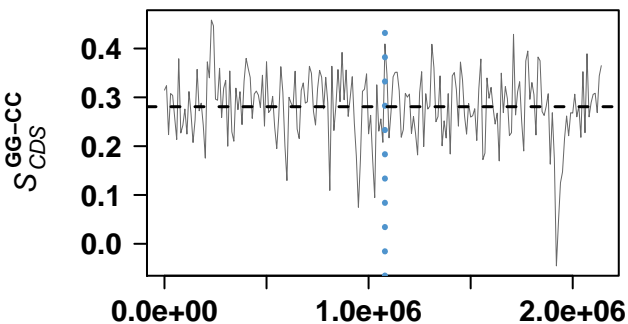
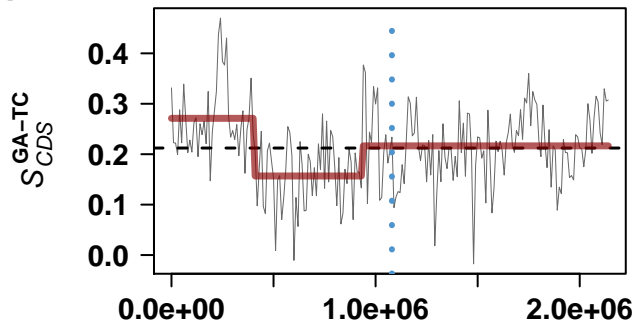
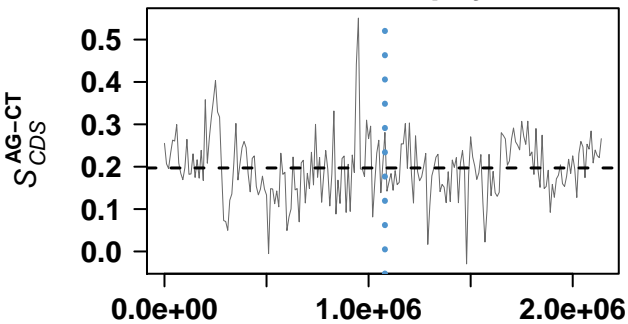


genome coordinates

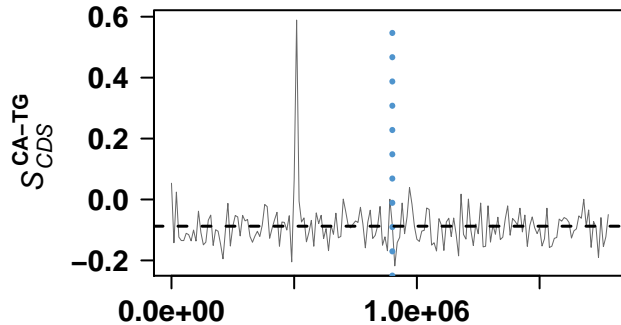
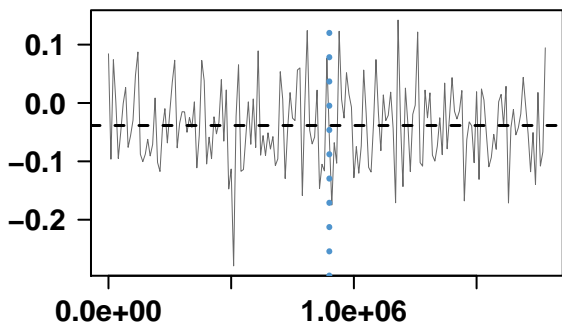
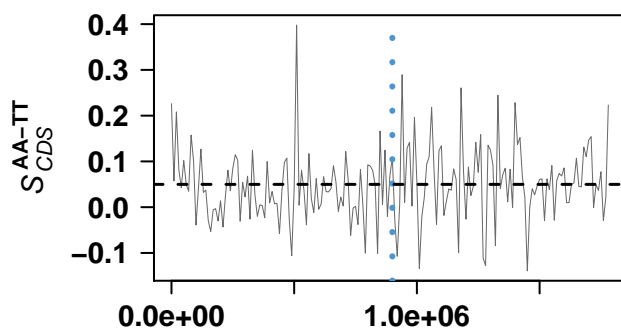
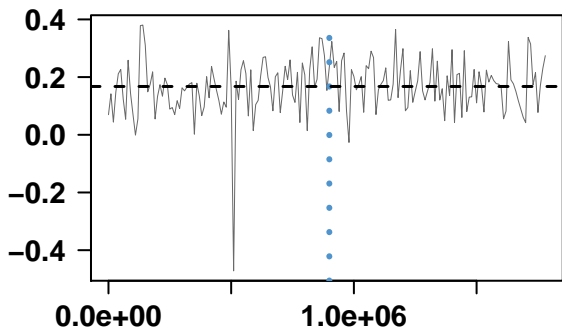
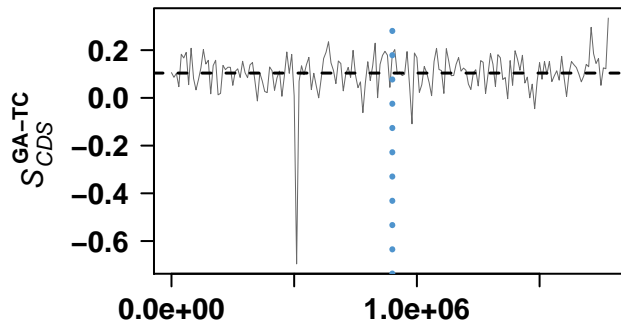
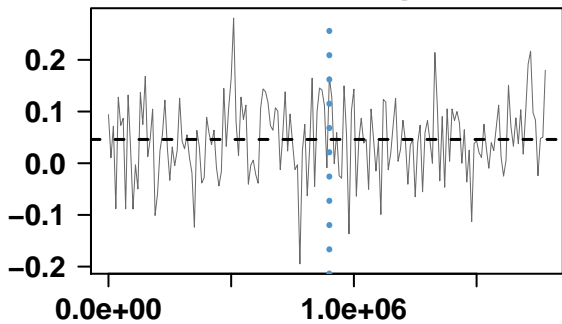


genome coordinates

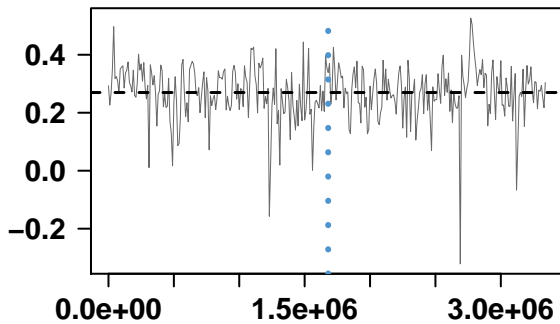
Staphylococcus epidermidis RP62A



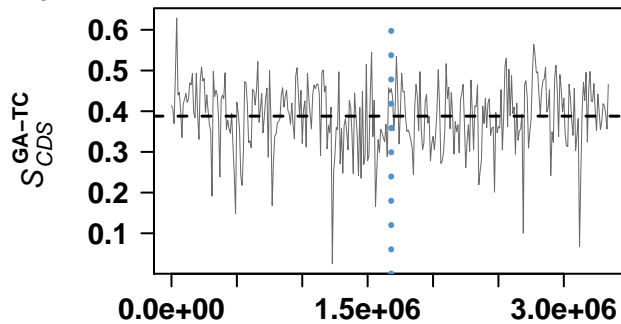
Streptococcus pneumoniae TIGR4



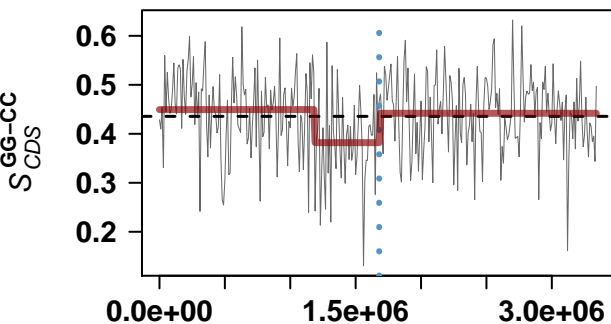
Clostridium acetobutylicum ATCC 824



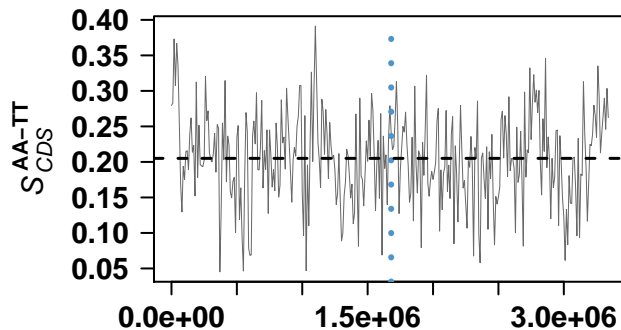
genome coordinates



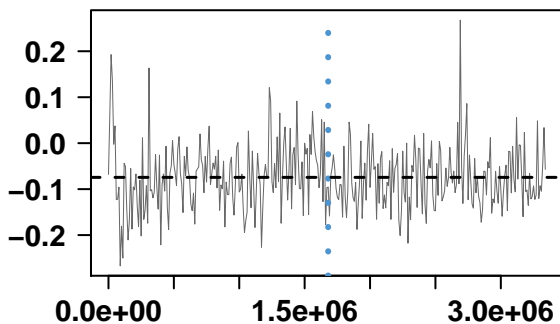
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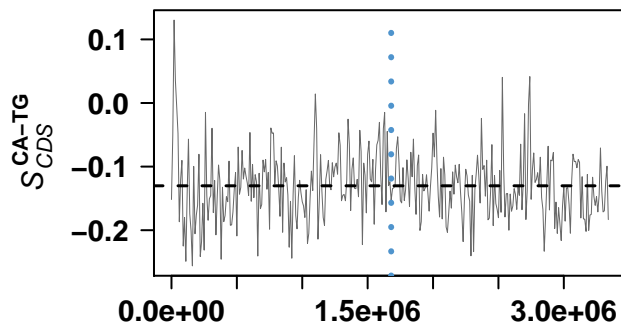
genome coordinates



genome coordinates

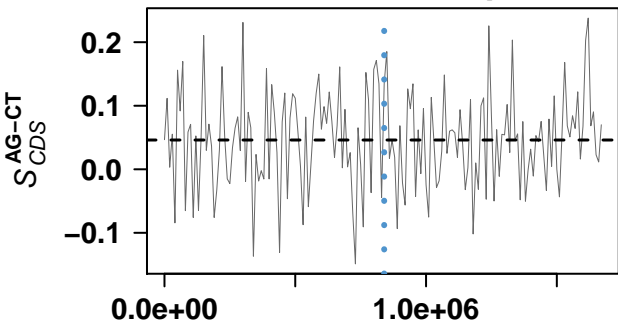


genome coordinates

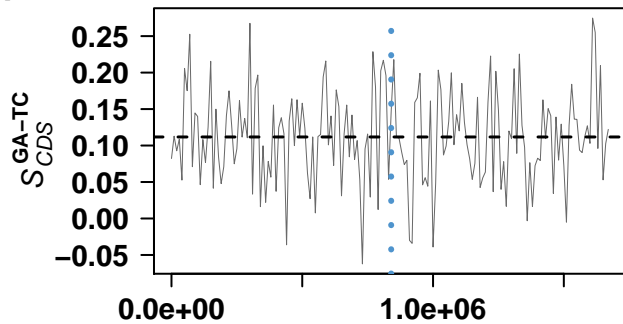


genome coordinates

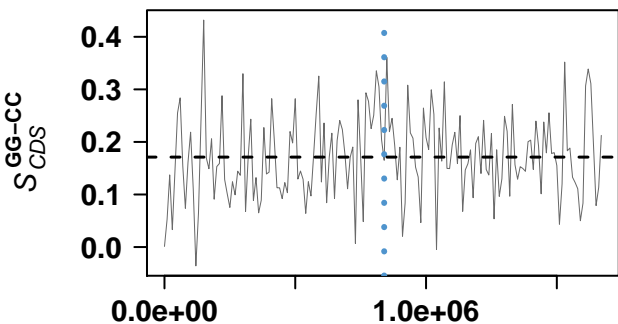
Streptococcus pneumoniae R6



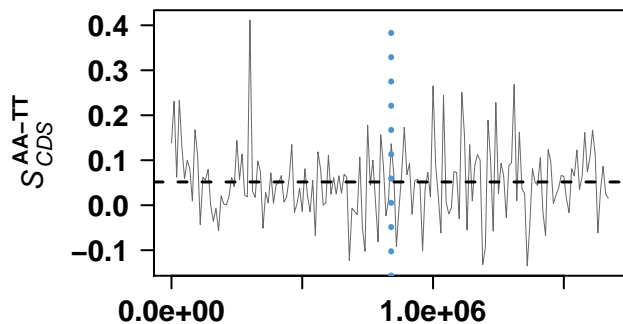
genome coordinates



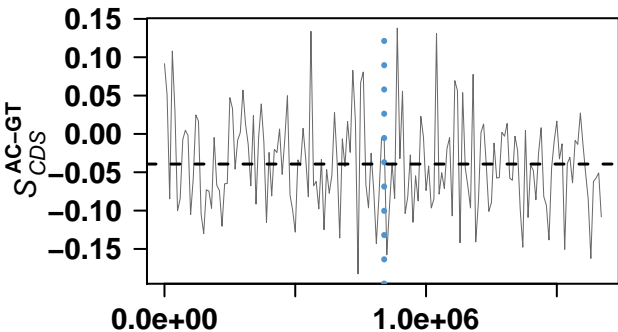
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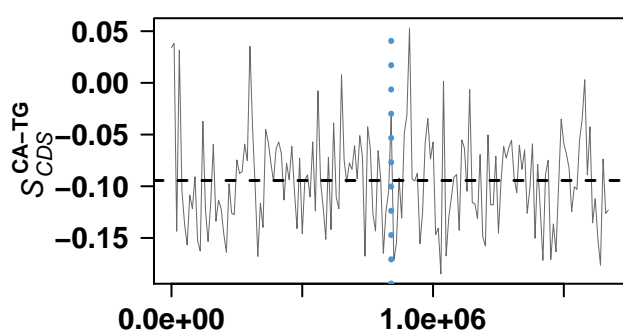
genome coordinates



genome coordinates

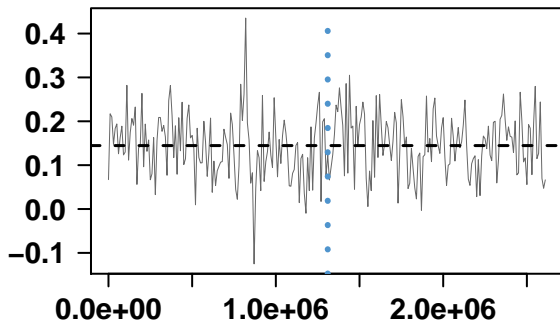


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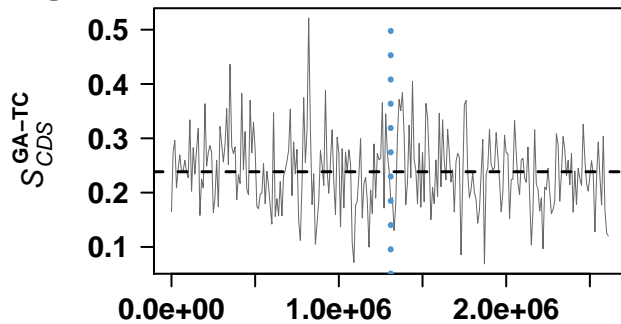


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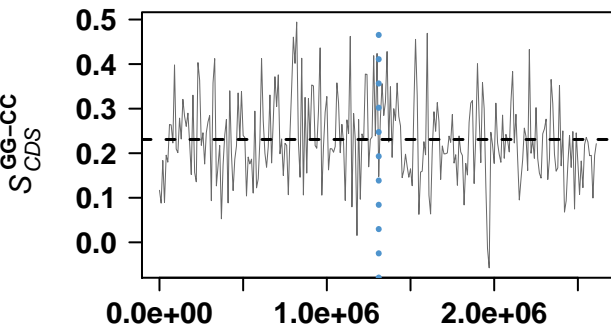
Listeria monocytogenes EGD-e



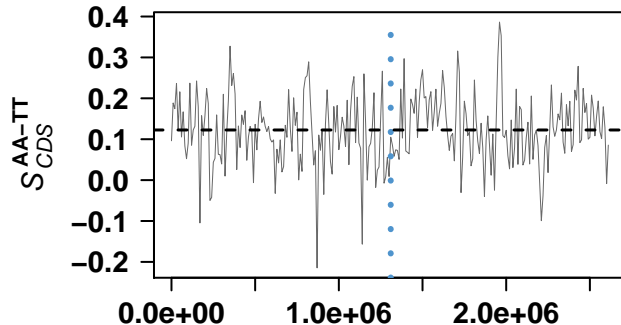
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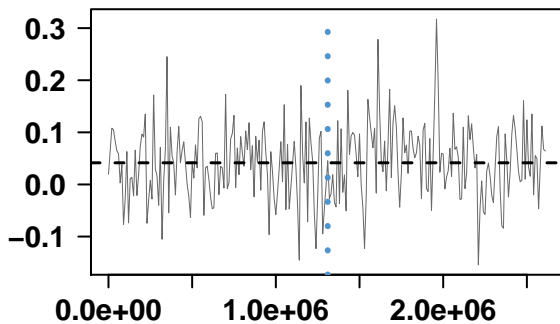
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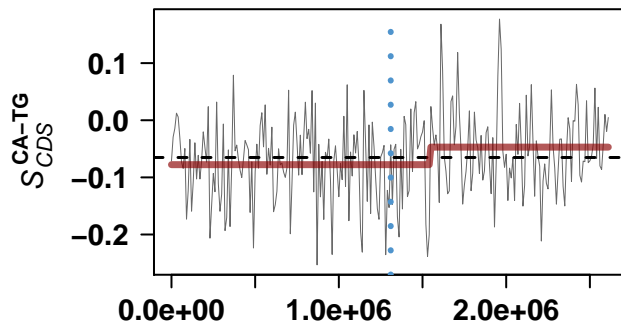
genome coordinates



genome coordinates

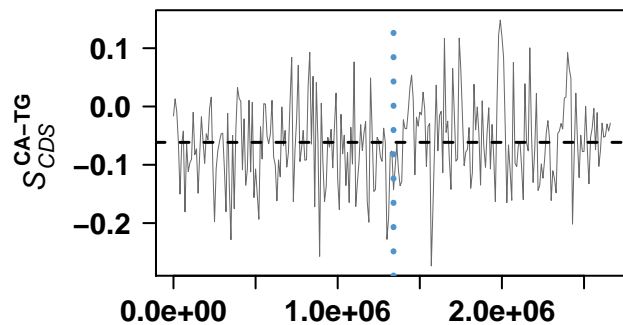
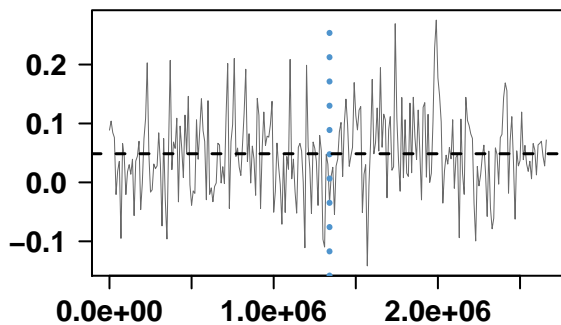
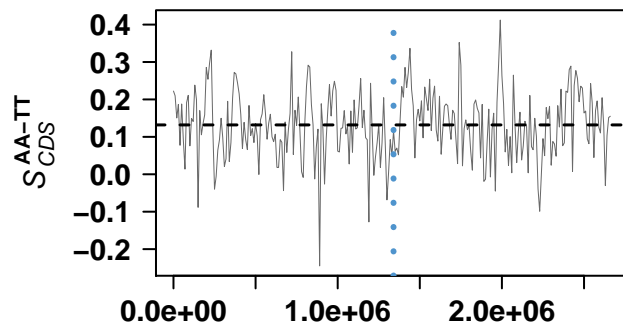
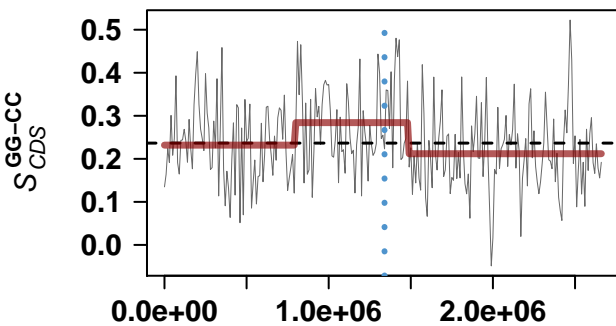
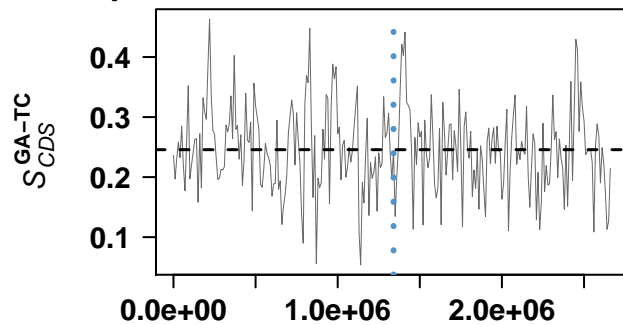
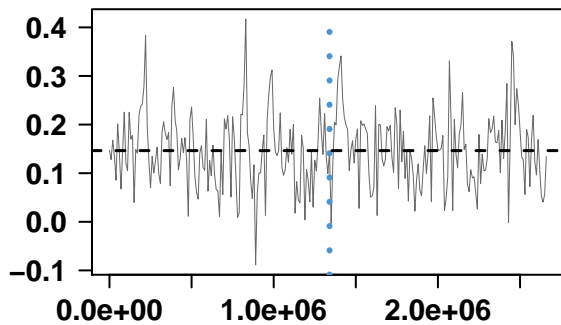


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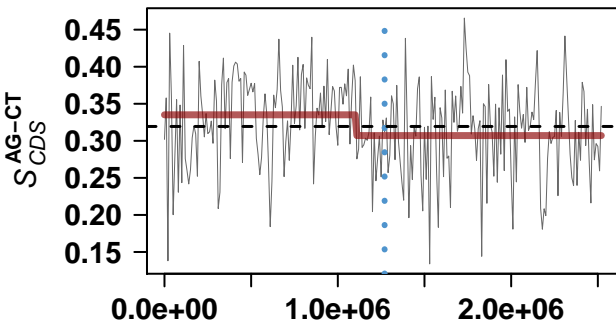


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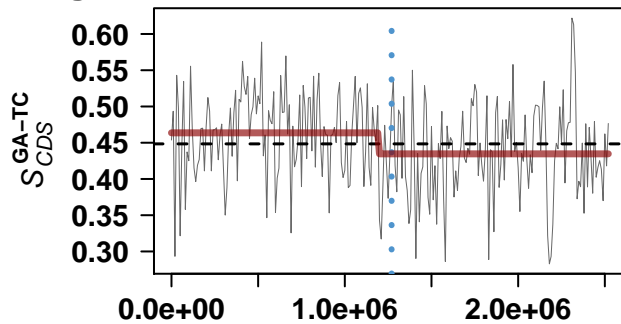
Listeria innocua Clip11262



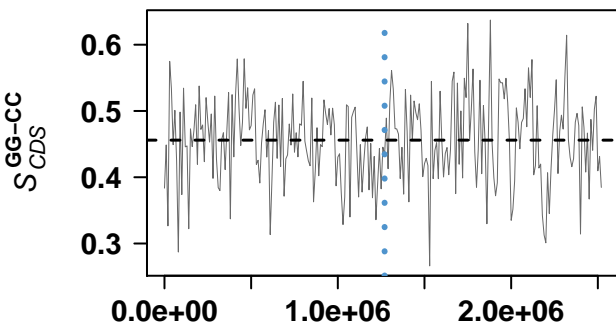
Clostridium perfringens str. 13



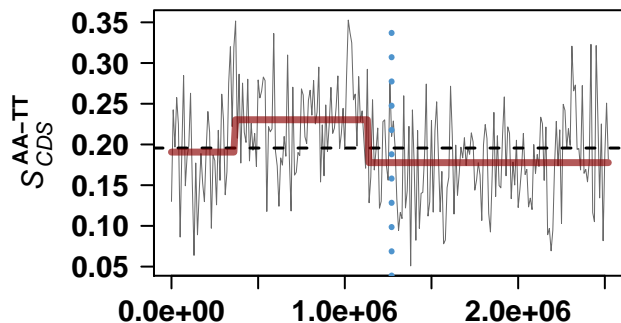
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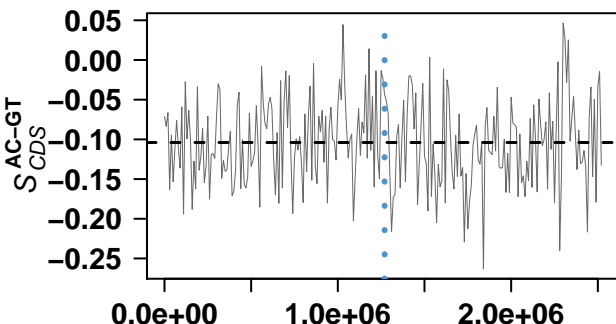
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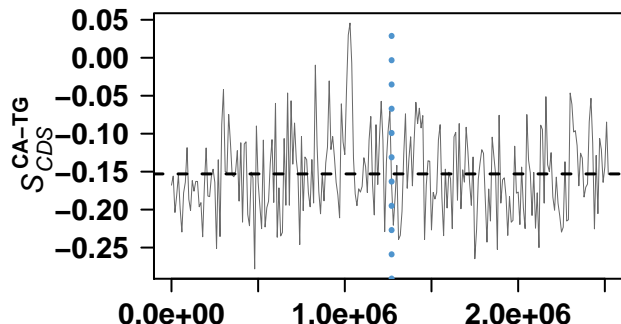
genome coordinates



genome coordinates

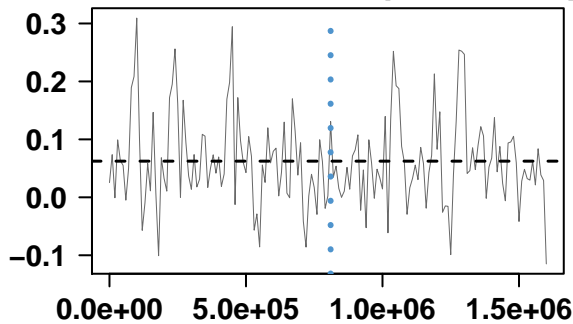


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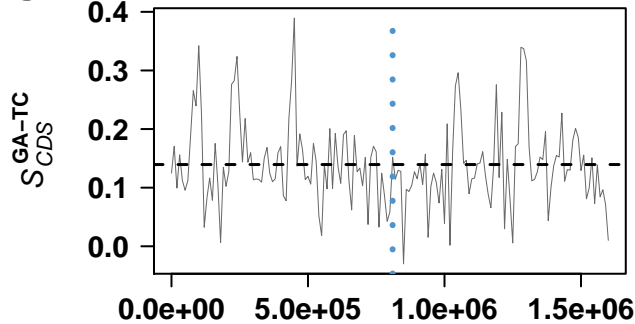


genome coordinates

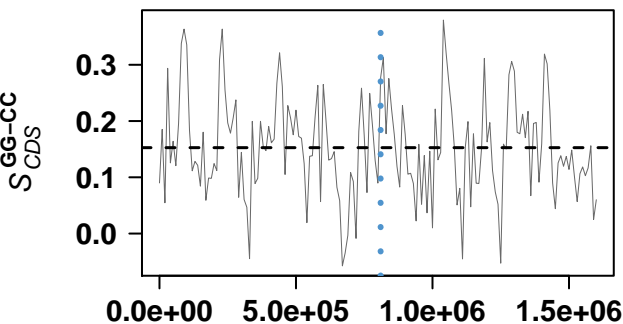
Streptococcus pyogenes MGAS8232



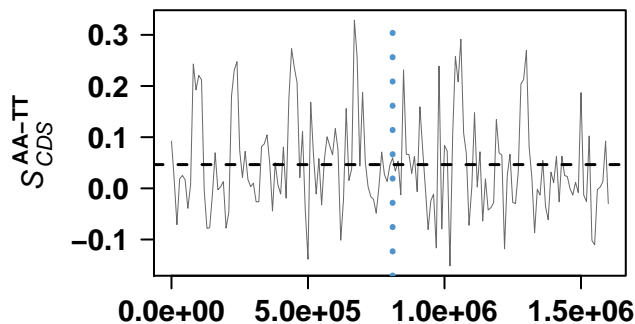
genome coordinates



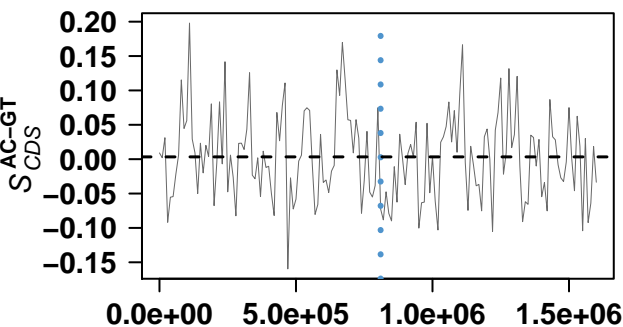
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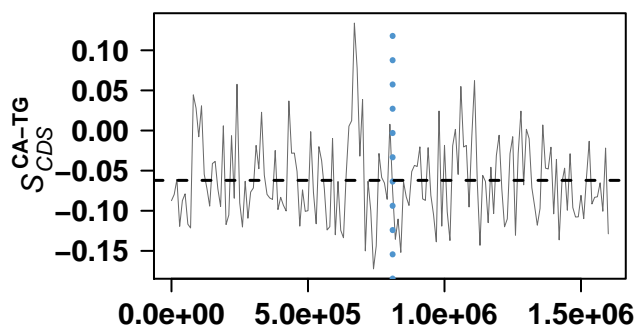
genome coordinates



genome coordinates

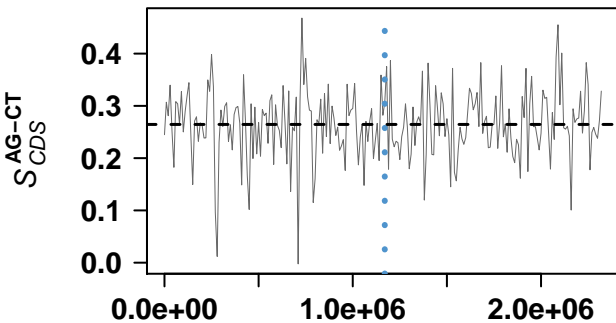


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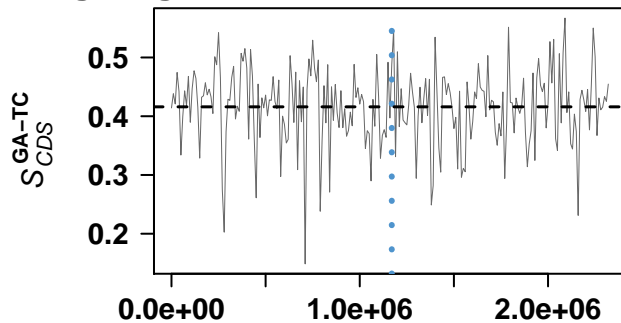


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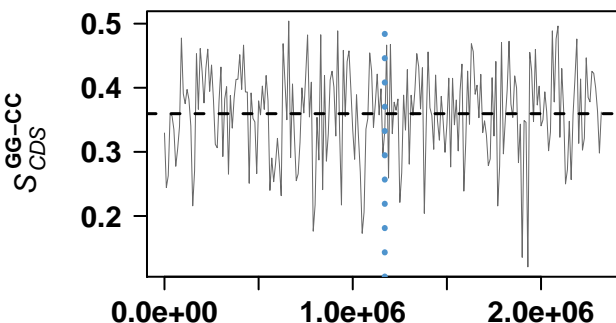
Thermoanaerobacter tengcongensis MB4



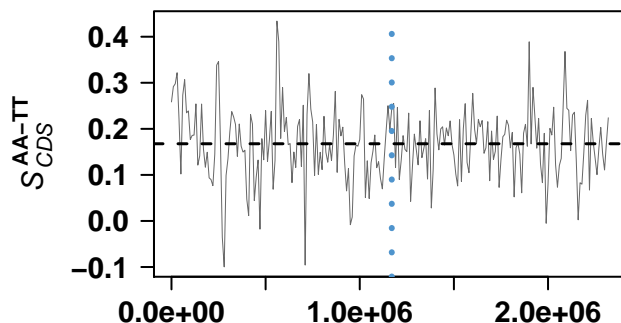
genome coordinates



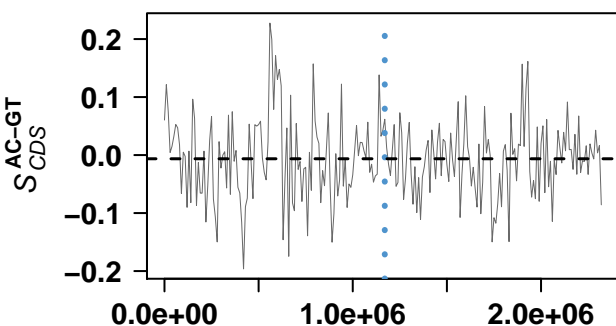
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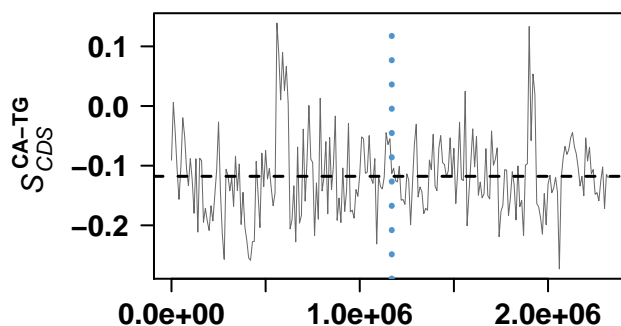
genome coordinates



genome coordinates

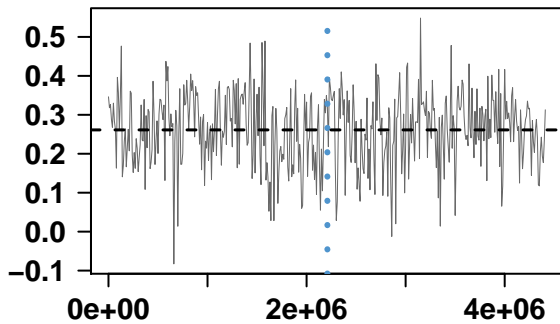


genome coordinates

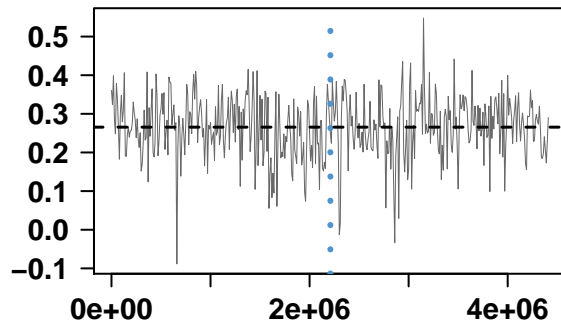


genome coordinates

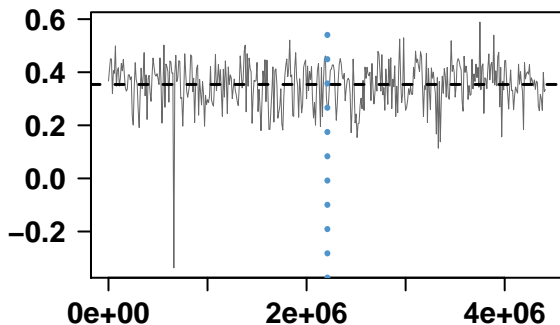
Bacillus cereus ATCC 10987



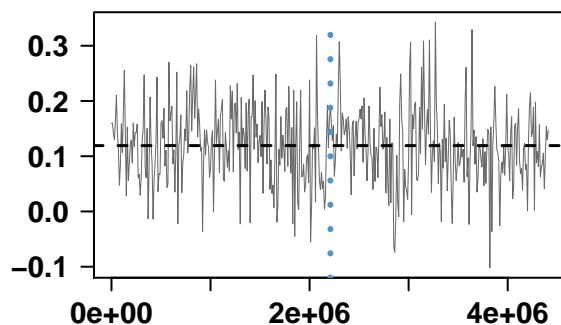
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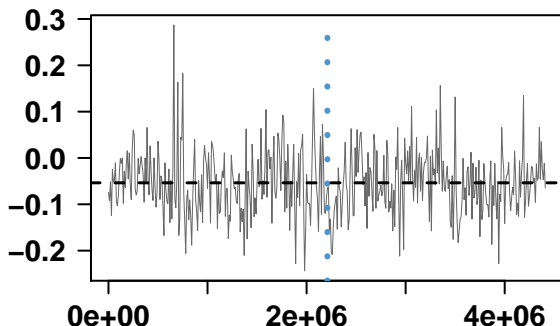
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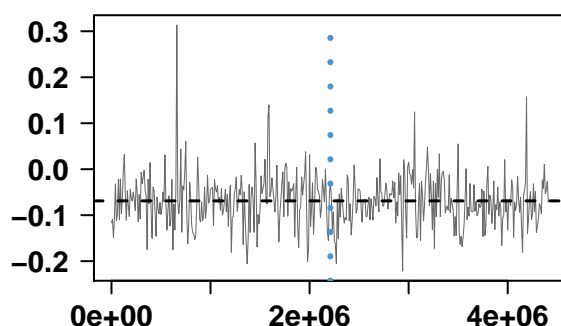
genome coordinates



genome coordinates

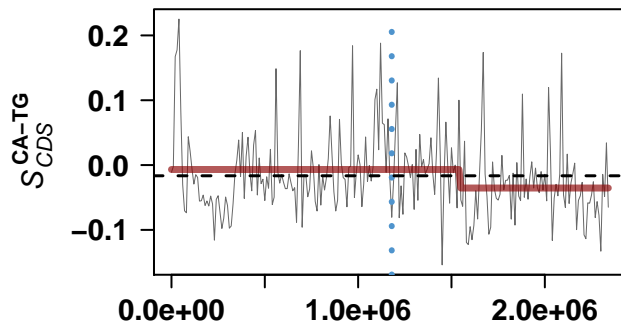
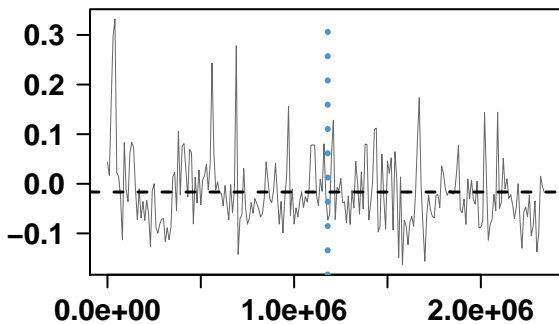
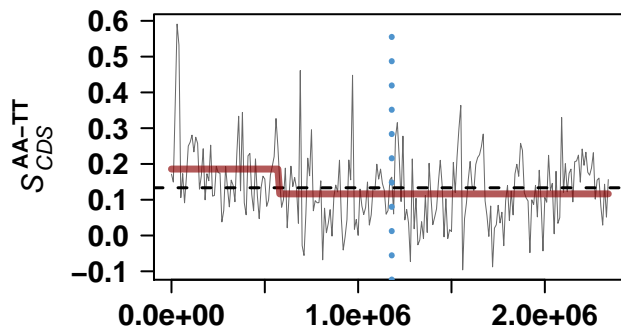
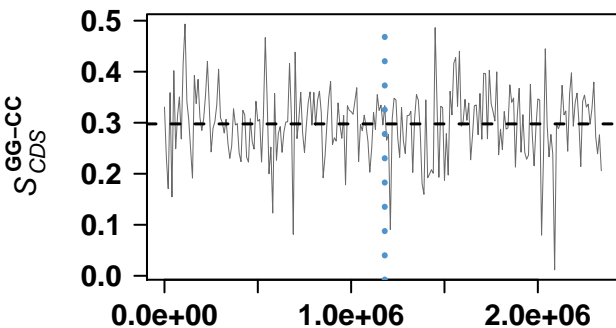
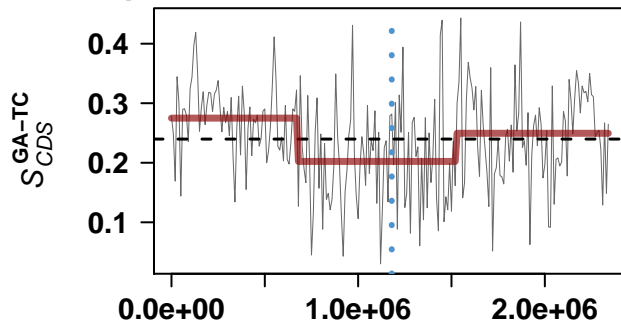
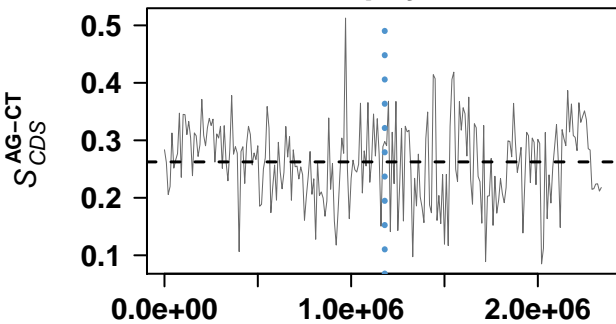


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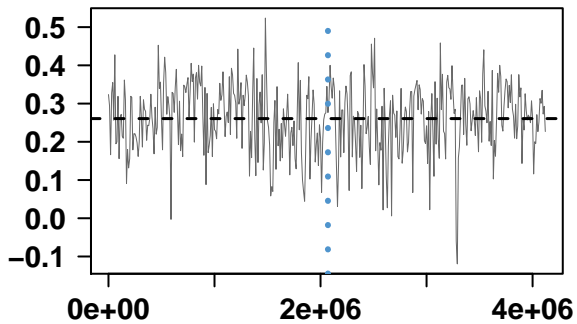


genome coordinates

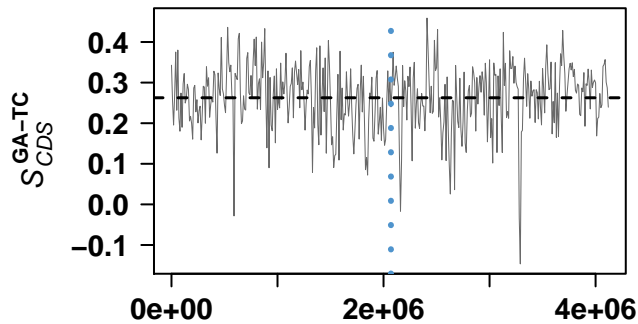
Staphylococcus aureus subsp. aureus MW2



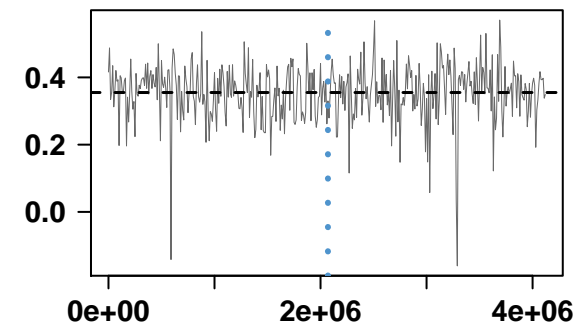
Bacillus anthracis str. Ames



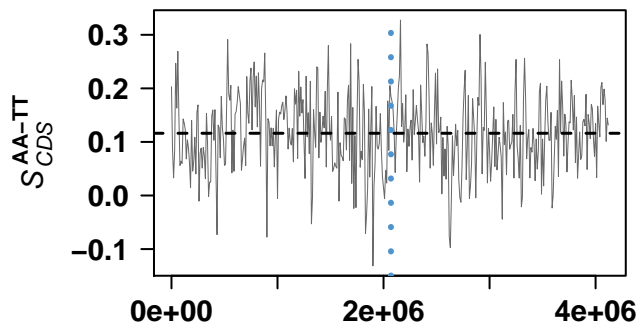
genome coordinates



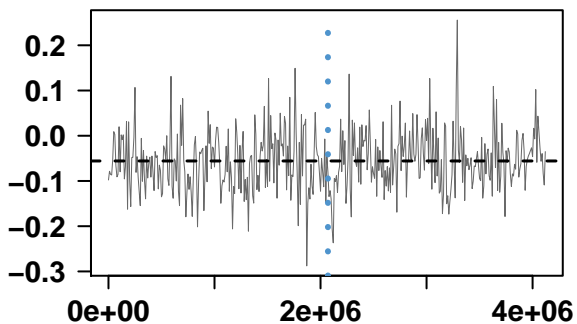
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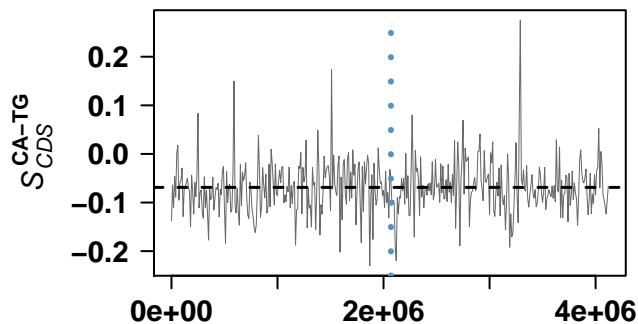
genome coordinates



genome coordinates

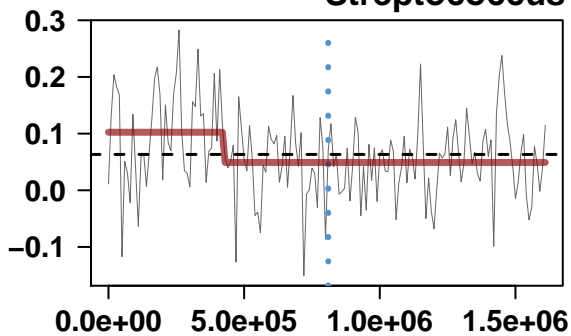


genome coordinates

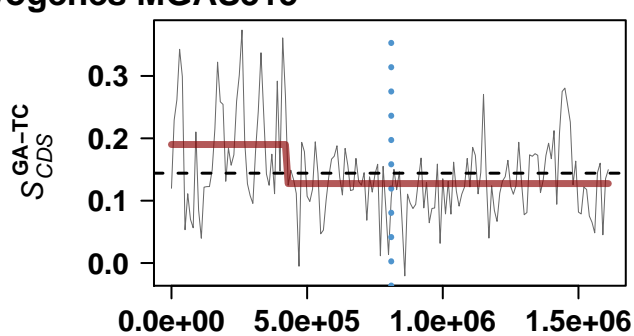


genome coordinates

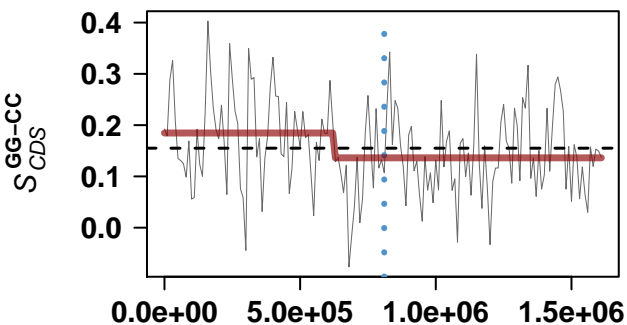
Streptococcus pyogenes MGAS315



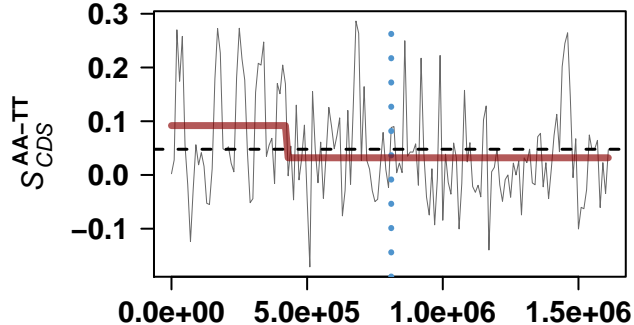
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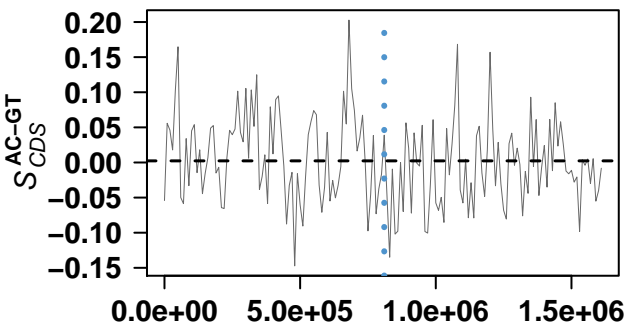
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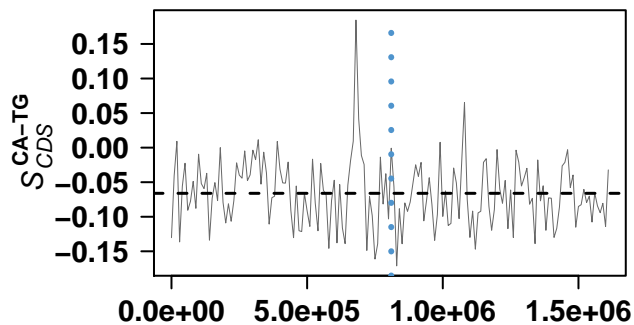
genome coordinates



genome coordinates

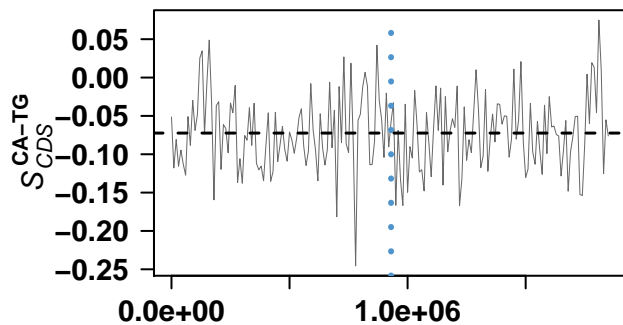
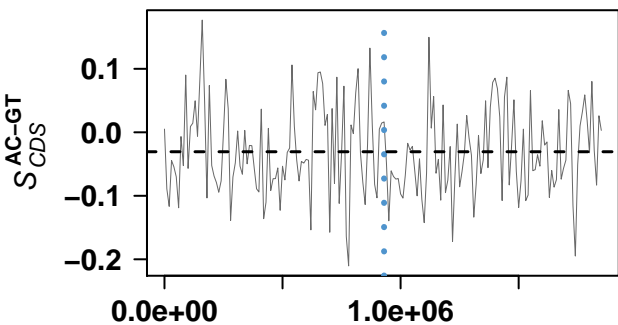
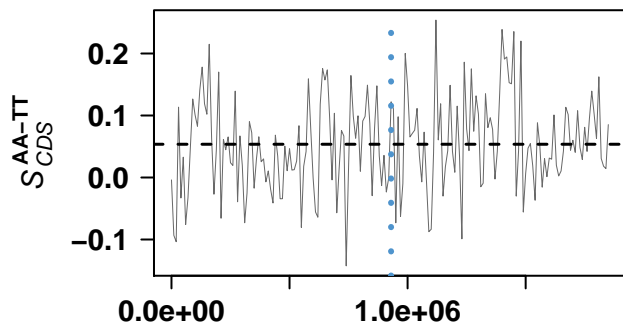
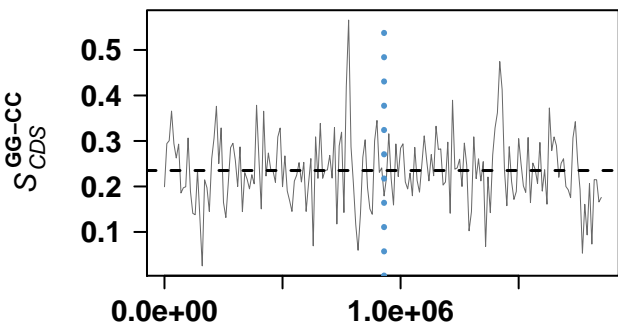
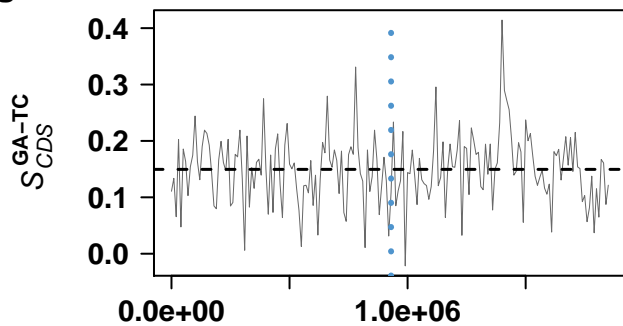
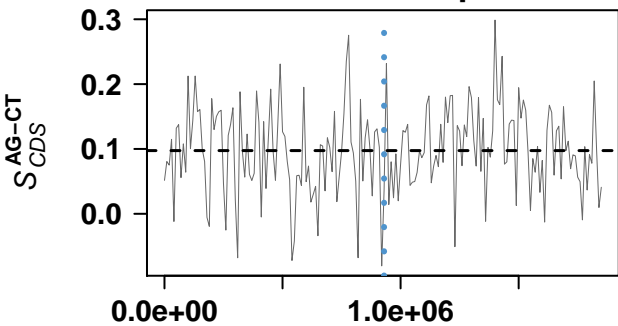


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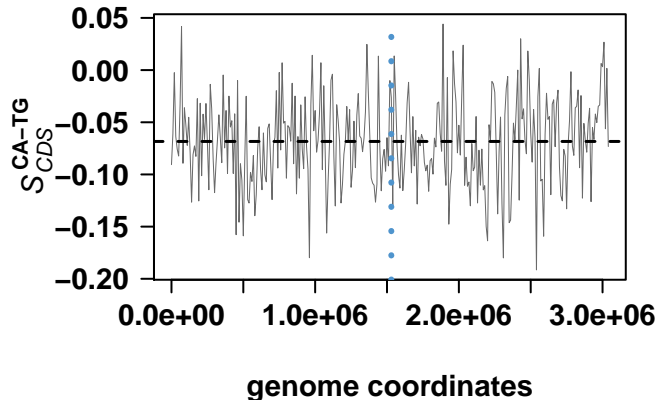
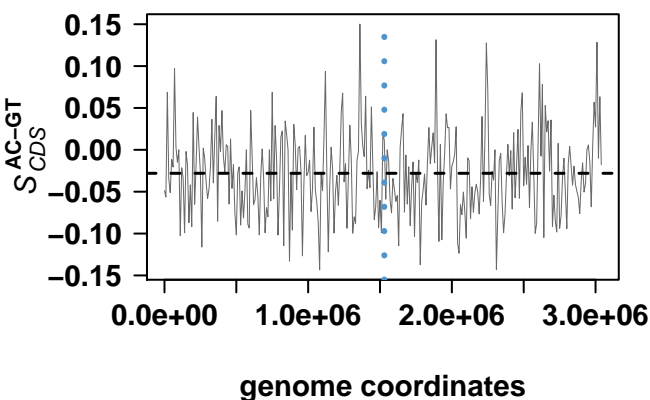
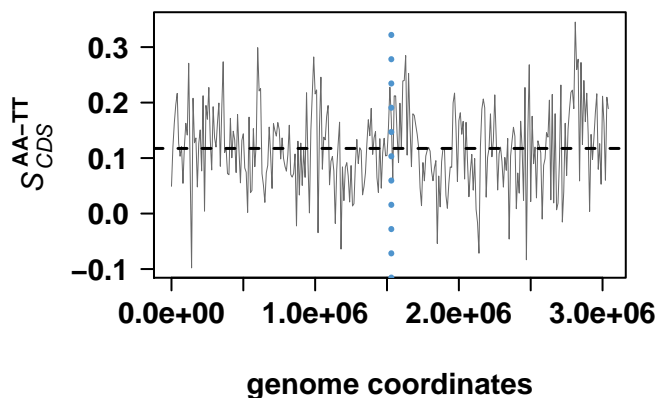
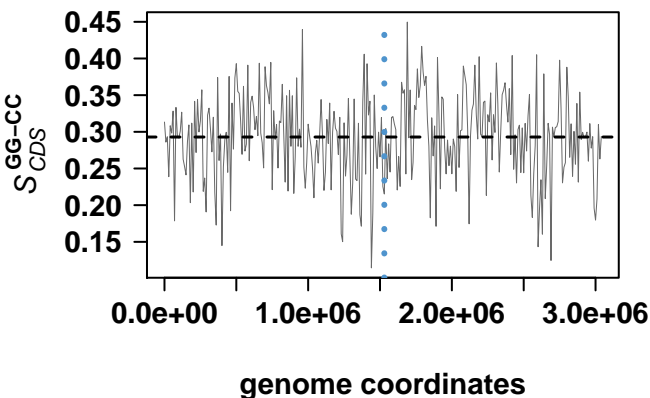
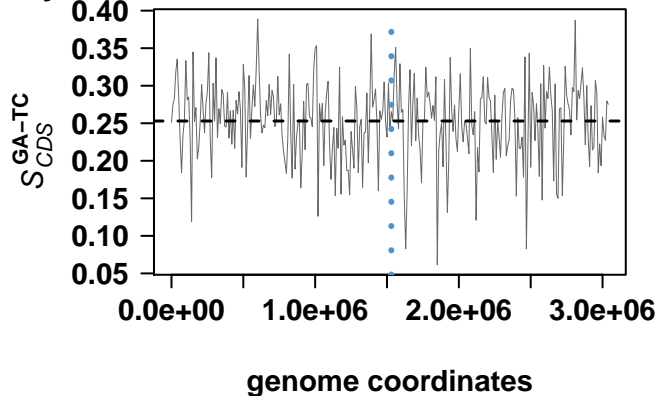
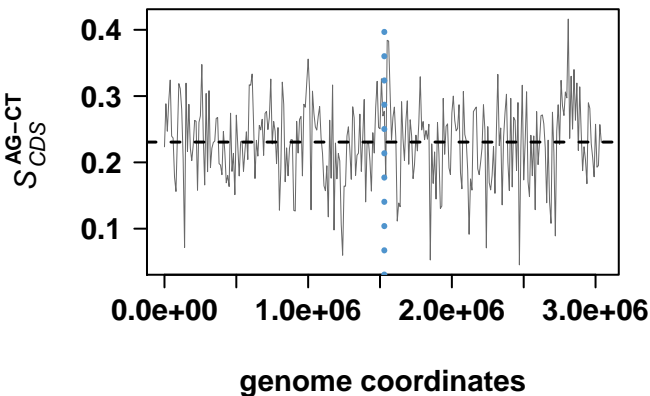


genome coordinates

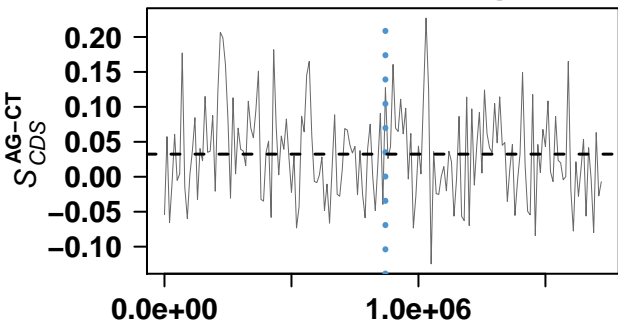
Streptococcus agalactiae 2603V/R



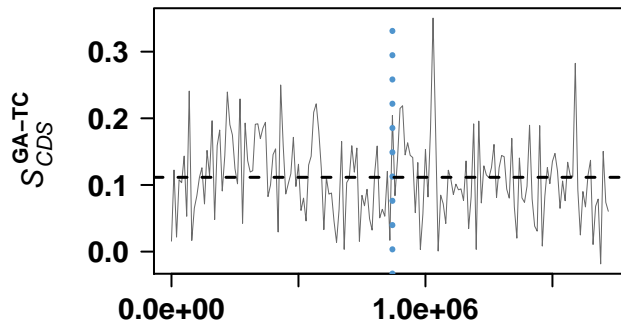
Oceanobacillus iheyensis HTE831



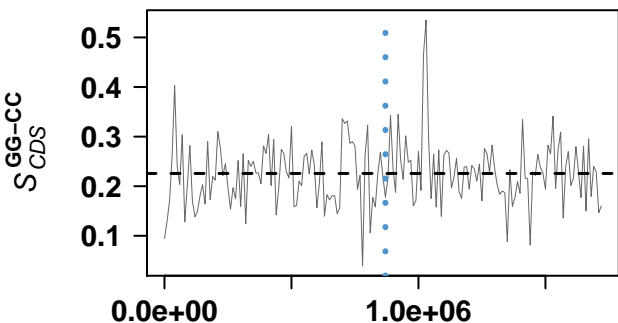
Streptococcus mutans UA159



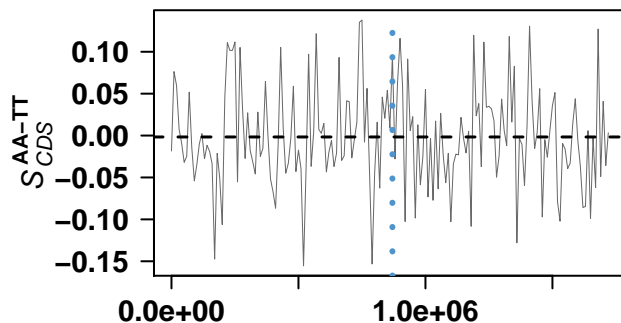
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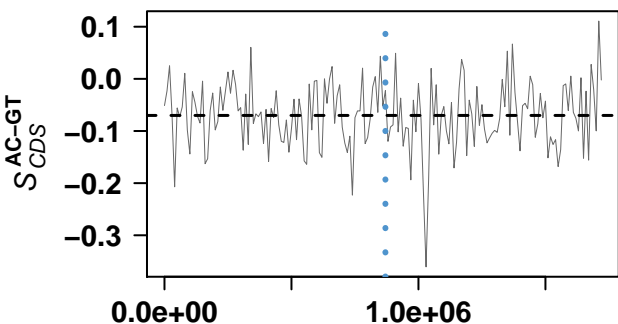
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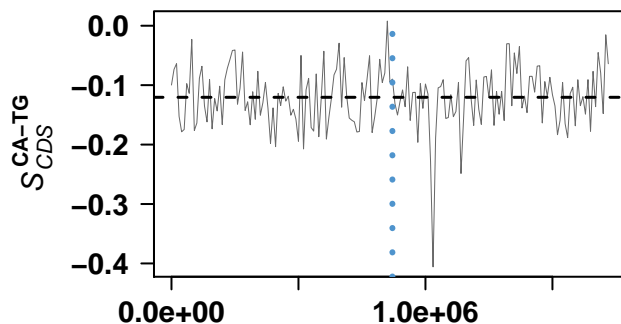
genome coordinates



genome coordinates

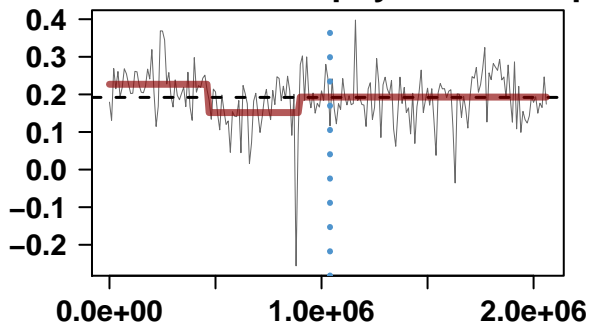


genome coordinates

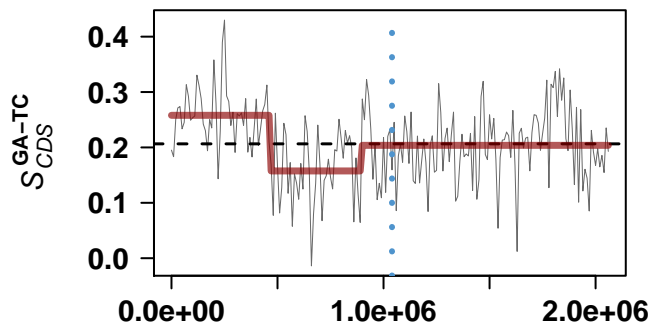


genome coordinates

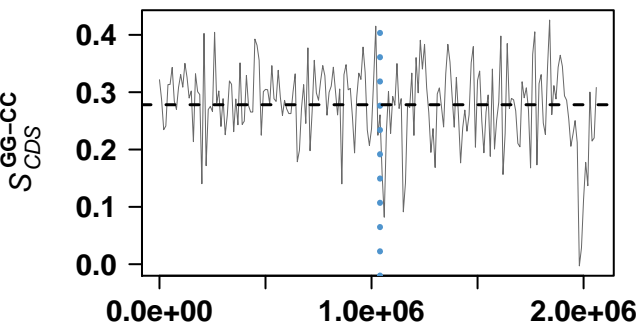
Staphylococcus epidermidis ATCC 12228



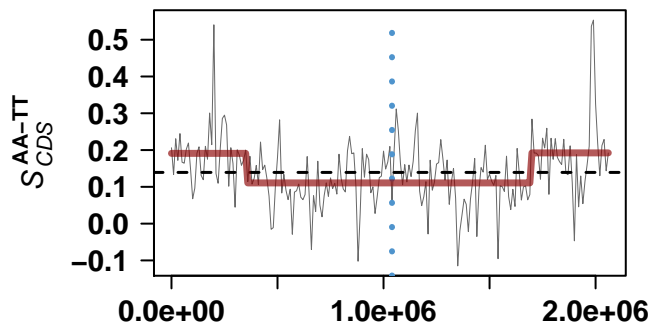
genome coordinates



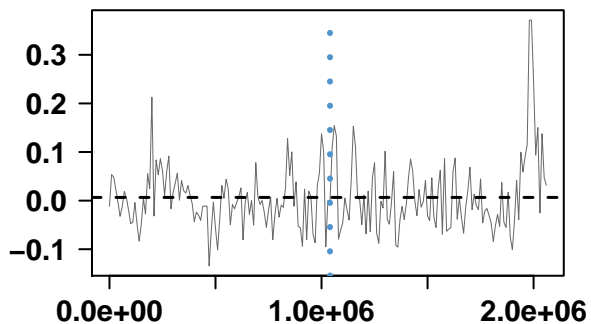
genome coordinates



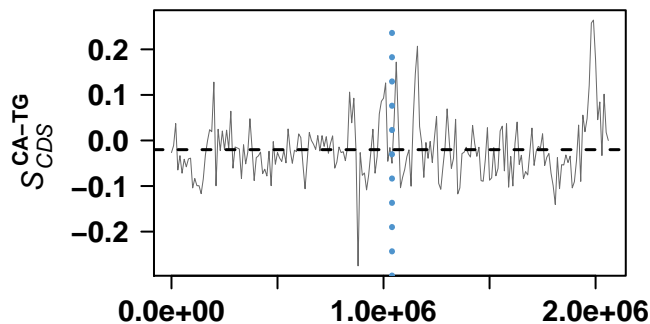
genome coordinates



genome coordinates

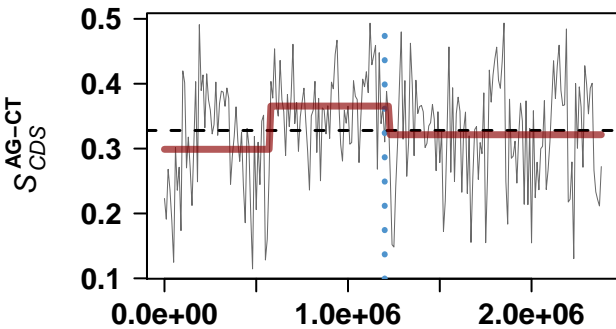


genome coordinates

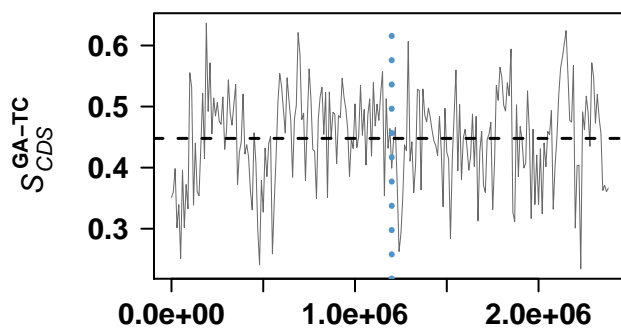


genome coordinates

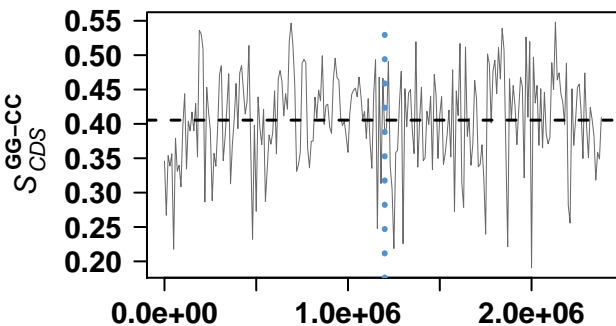
Clostridium tetani E88



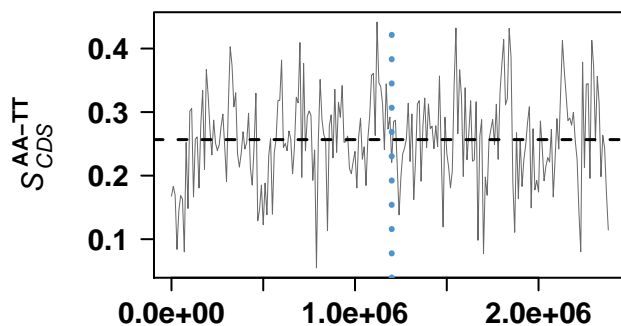
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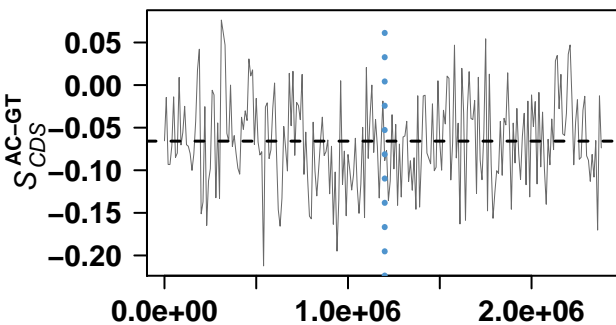
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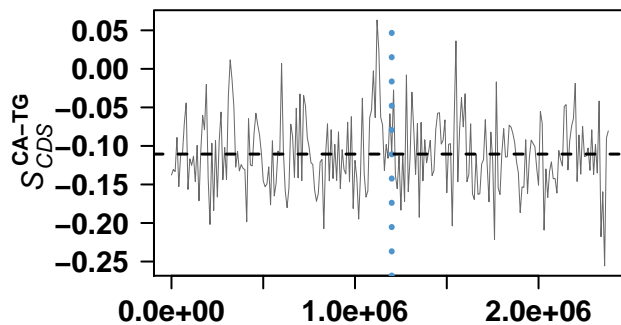
genome coordinates



genome coordinates

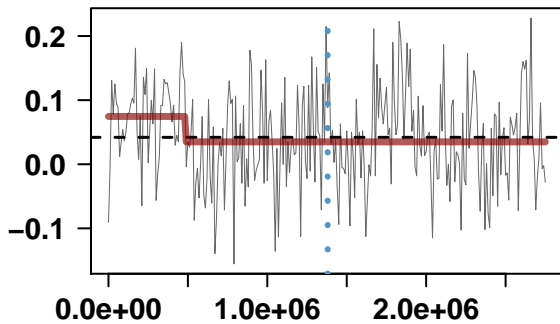


genome coordinates

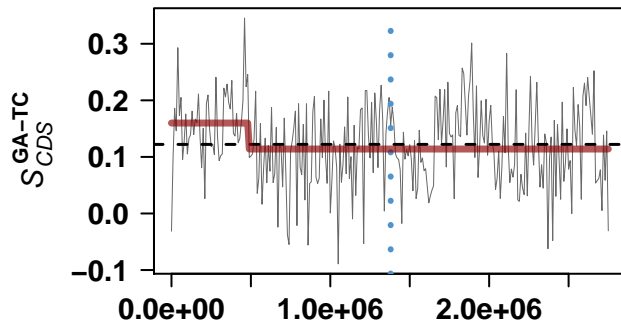


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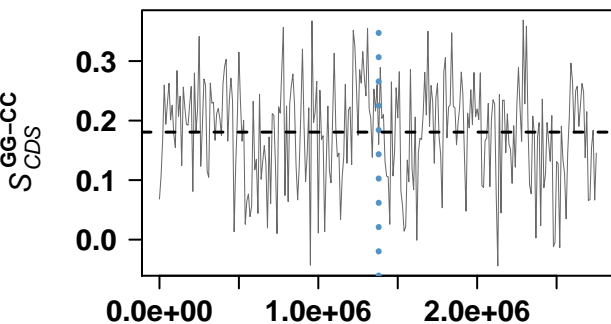
Lactobacillus plantarum WCFS1



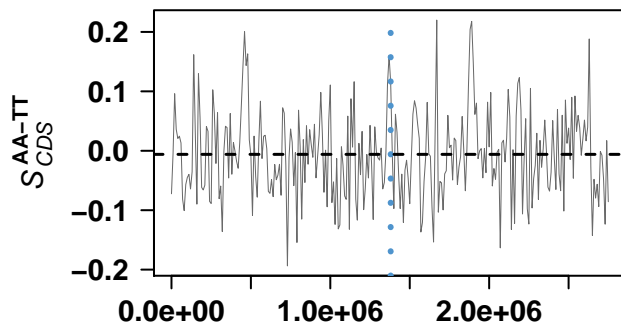
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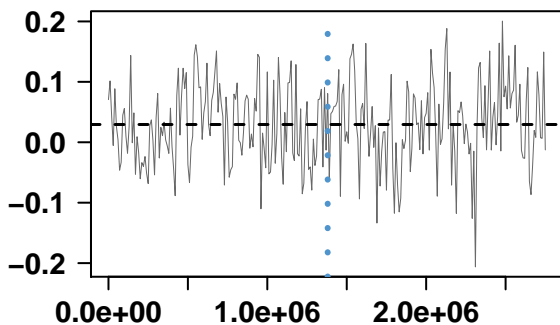
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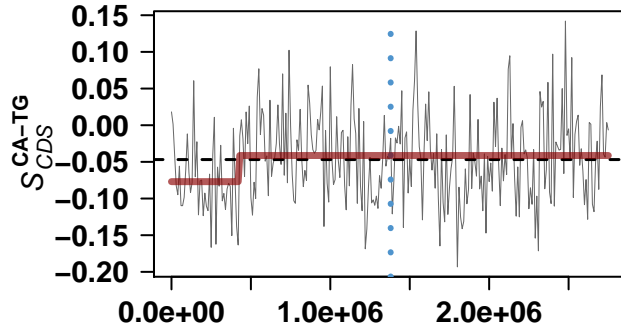
genome coordinates



genome coordinates

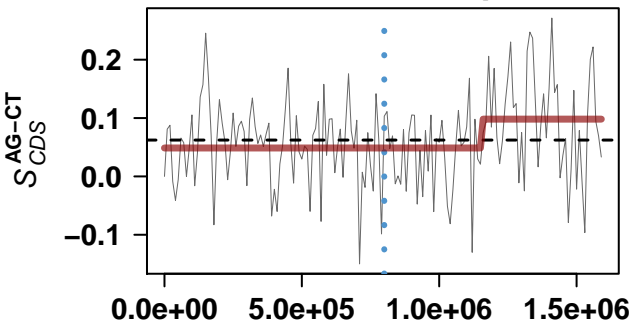


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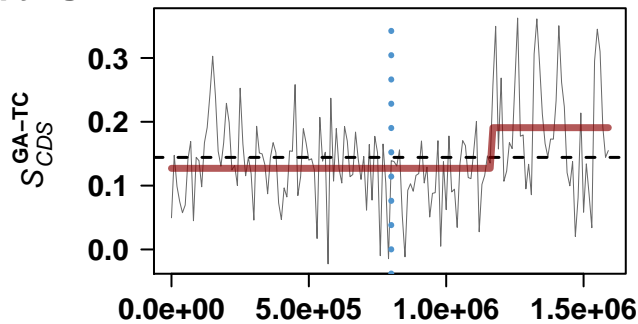


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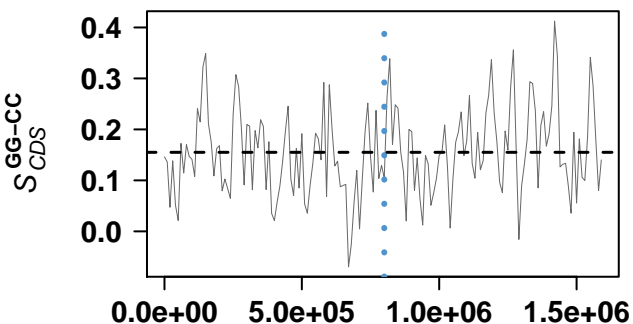
Streptococcus pyogenes SSI-1



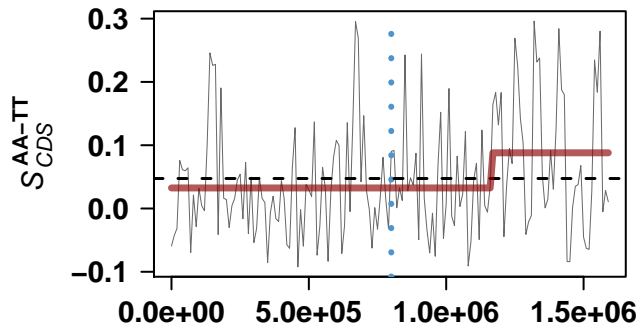
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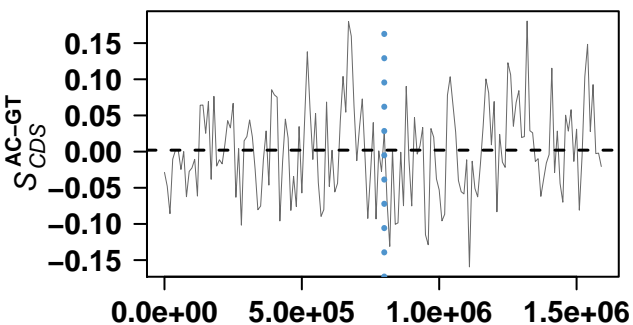
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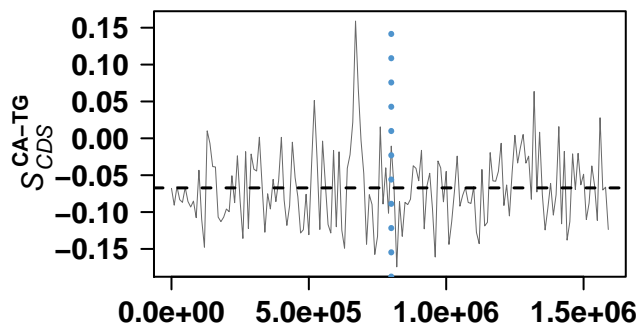
genome coordinates



genome coordinates

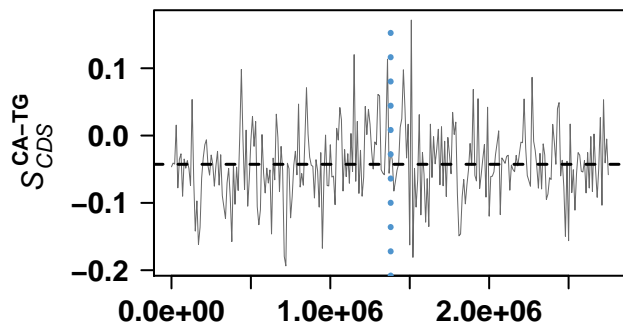
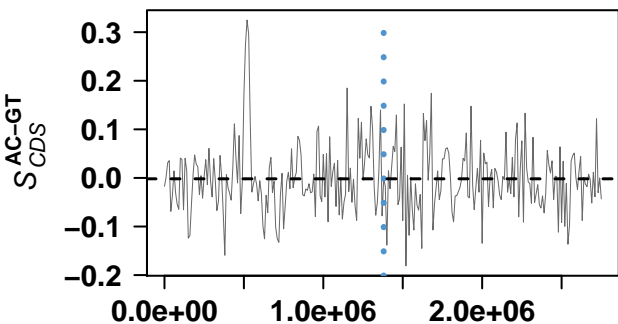
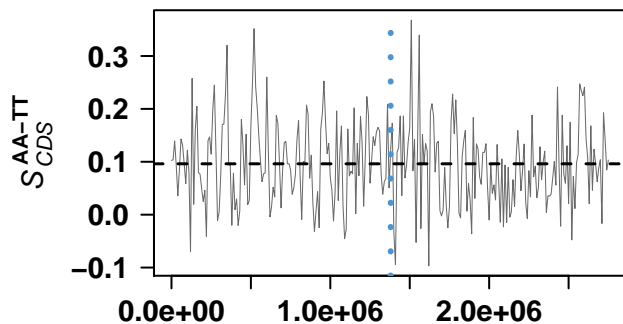
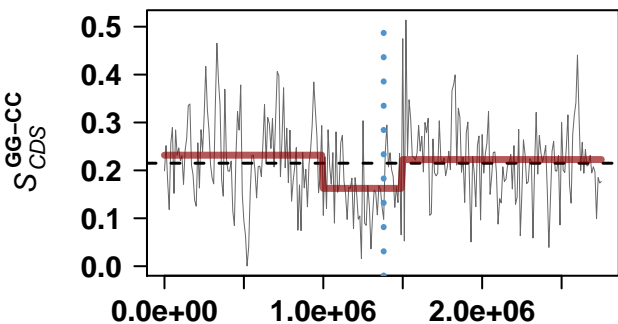
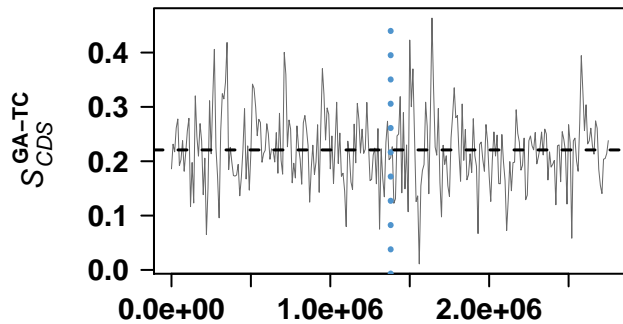
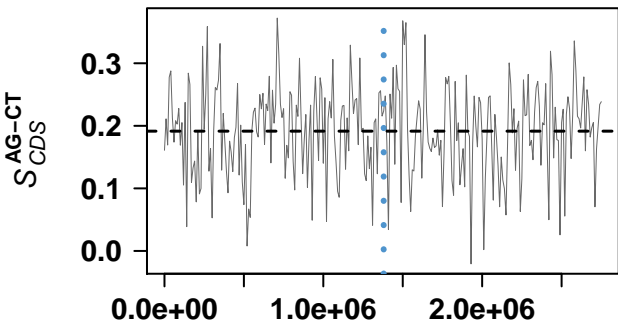


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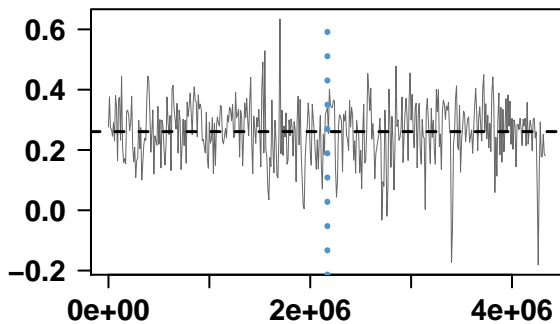


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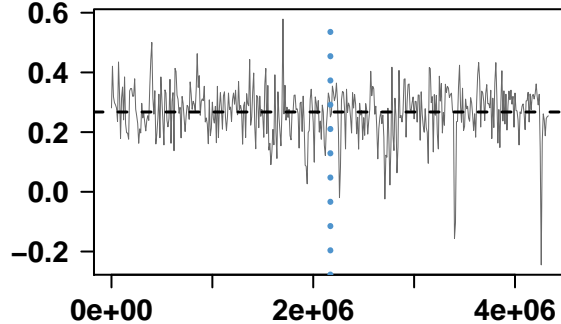
Enterococcus faecalis V583



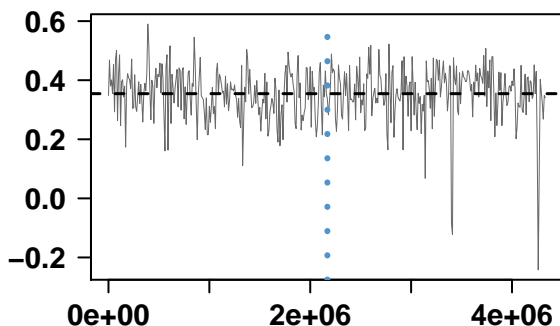
Bacillus cereus ATCC 14579



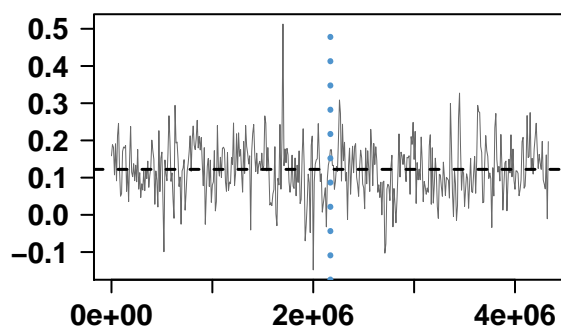
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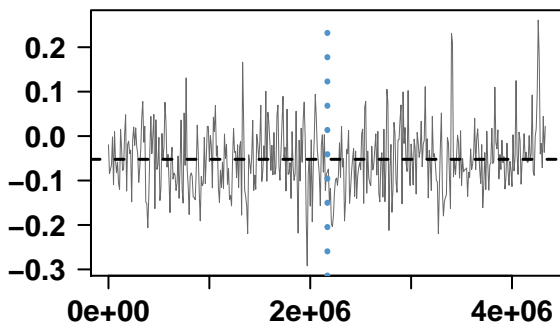
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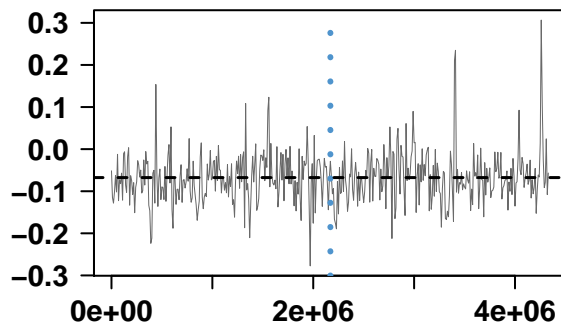
genome coordinates



genome coordinates

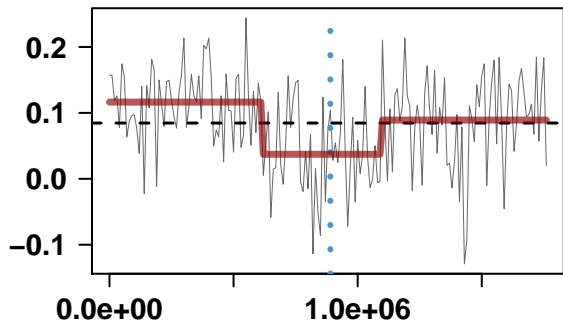


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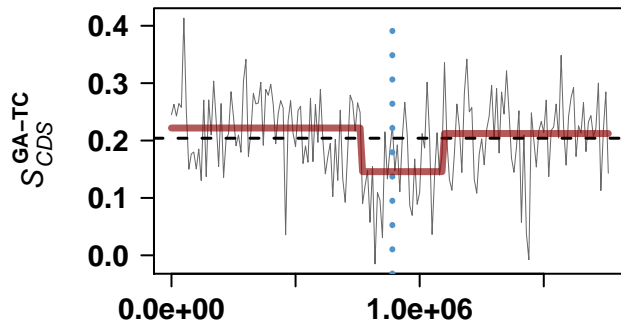


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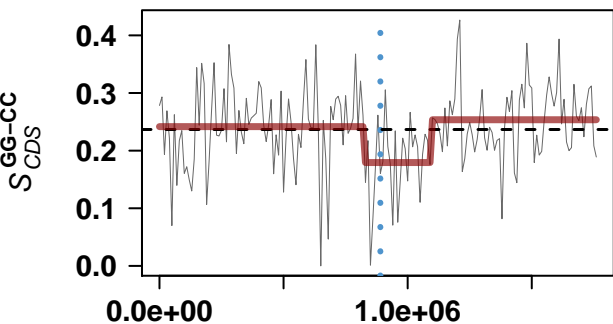
Lactobacillus johnsonii NCC 533



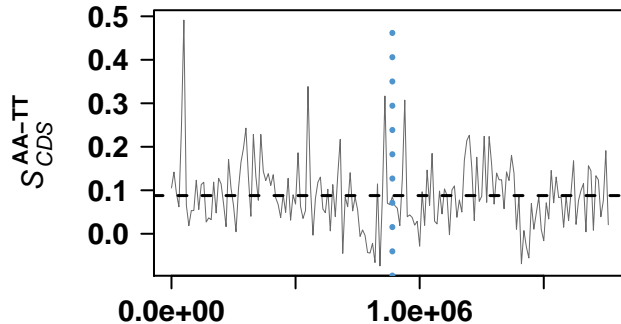
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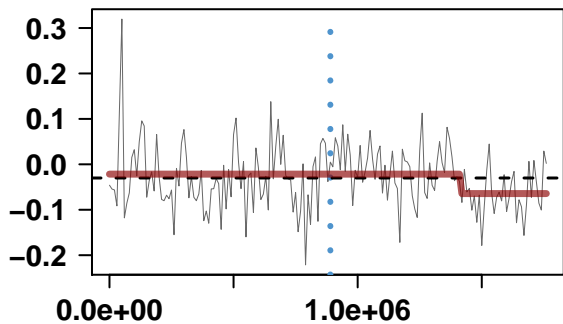
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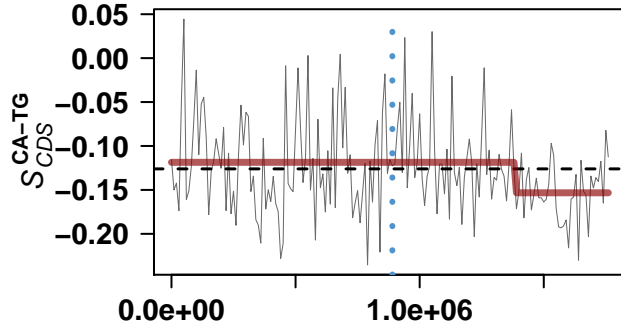
genome coordinates



genome coordinates

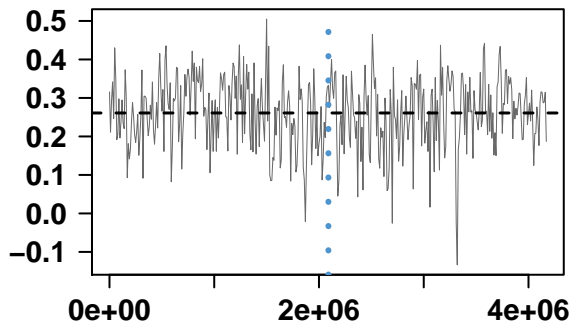


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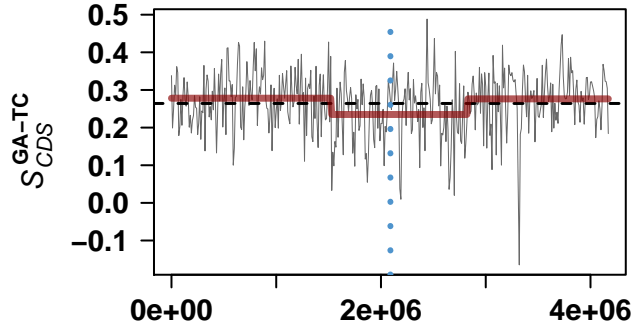


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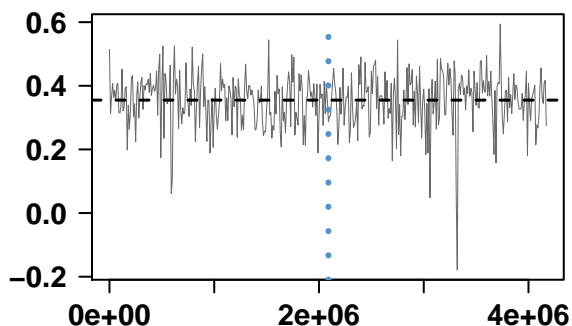
Bacillus anthracis str. Sterne



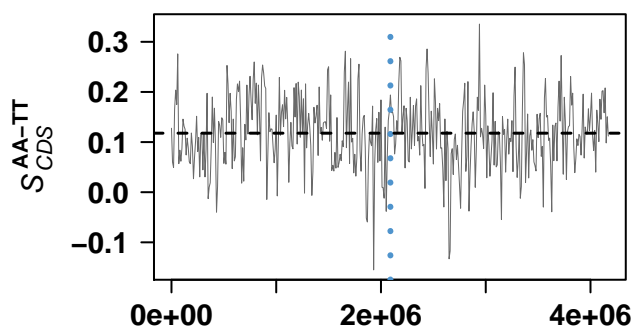
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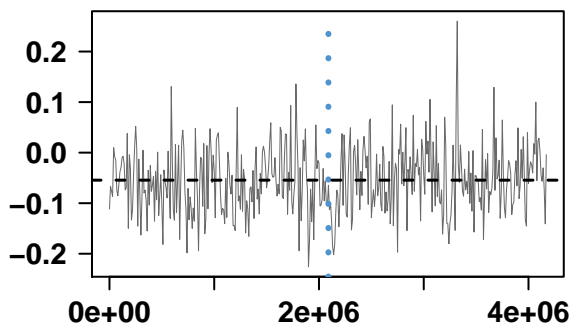
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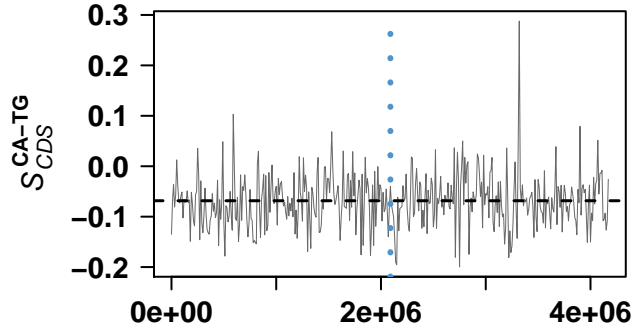
genome coordinates



genome coordinates

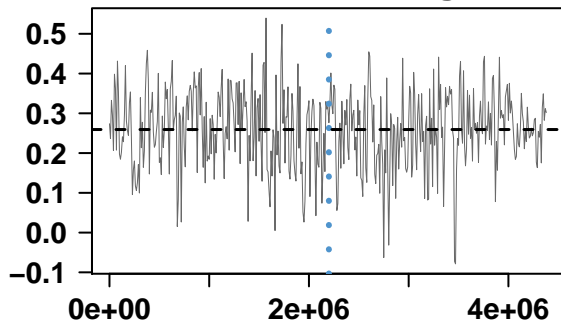


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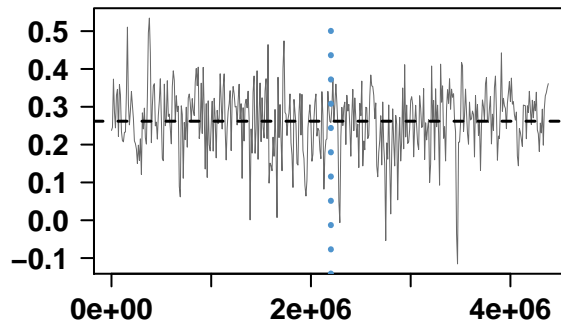


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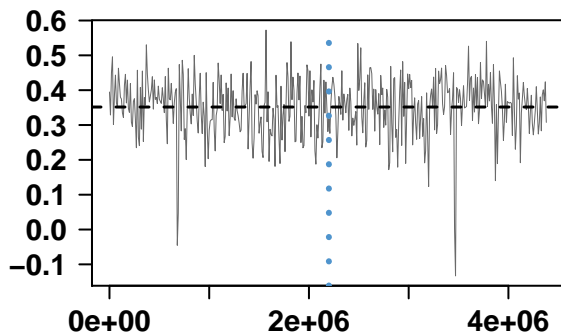
Bacillus thuringiensis serovar konkukian str. 97-27



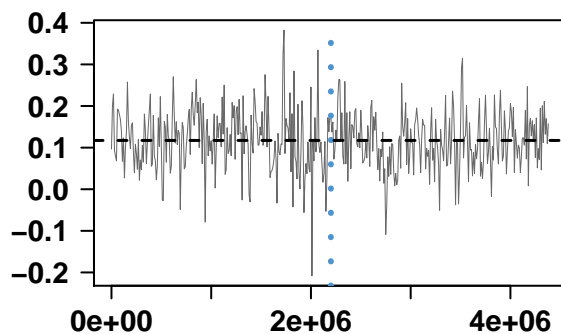
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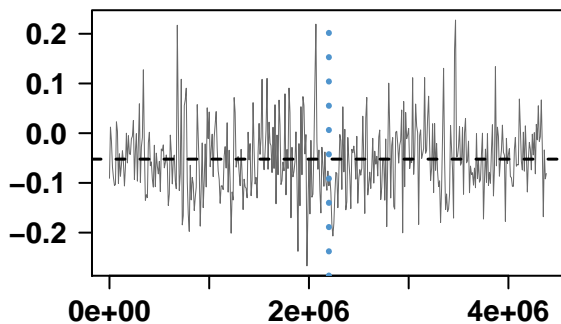
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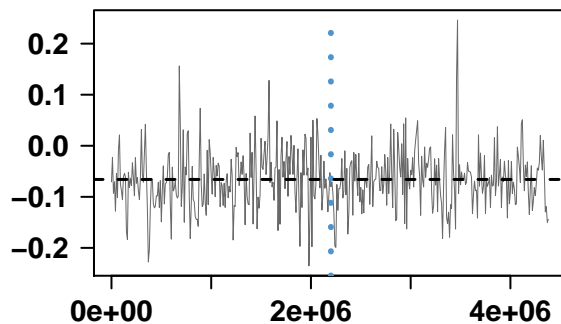
genome coordinates



genome coordinates

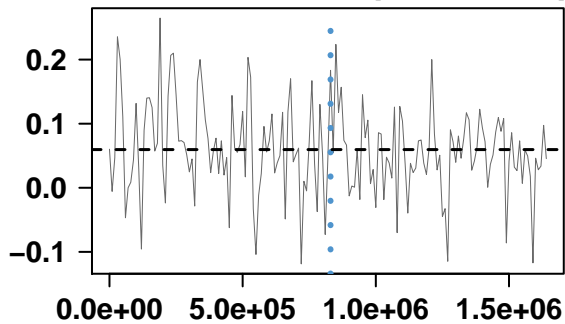


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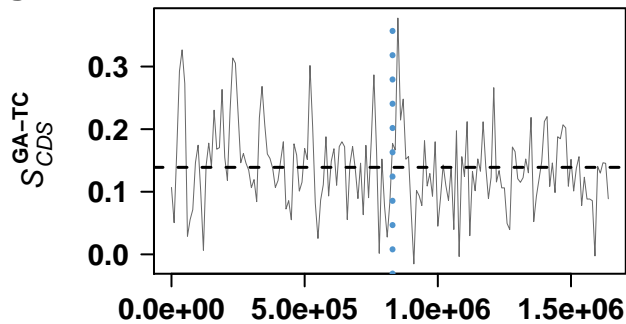


genome coordinates

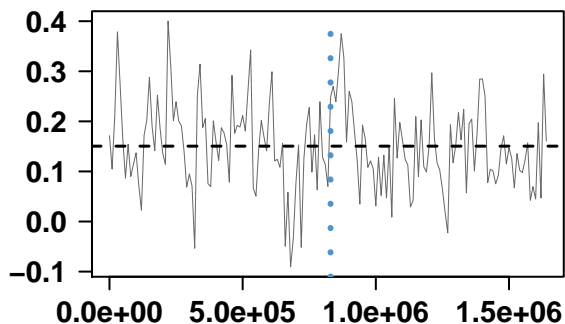
Streptococcus pyogenes MGAS10394



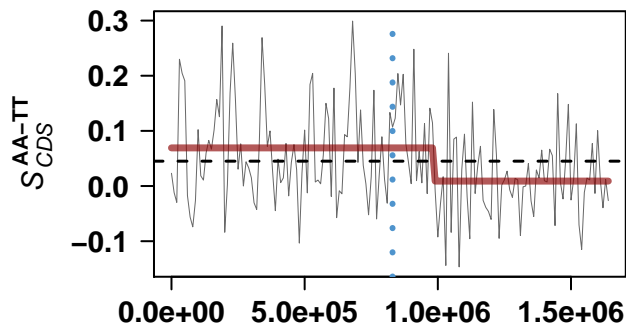
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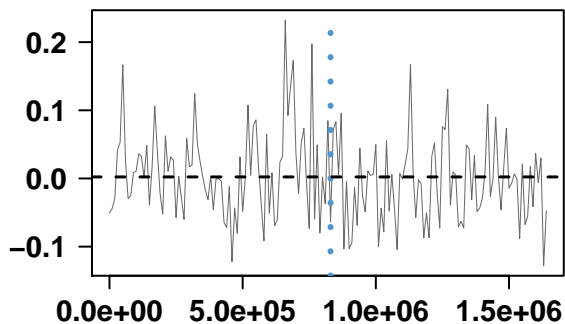
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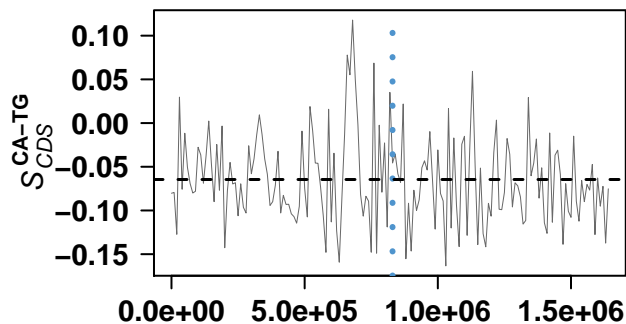
genome coordinates



genome coordinates

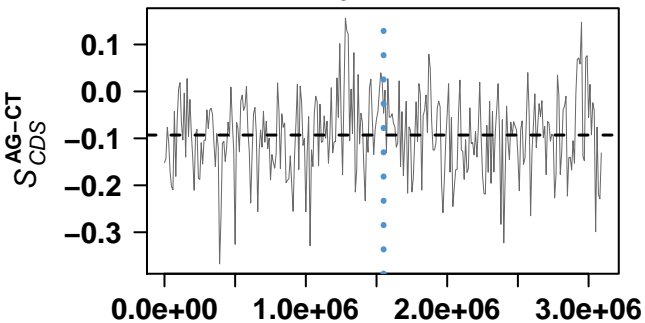


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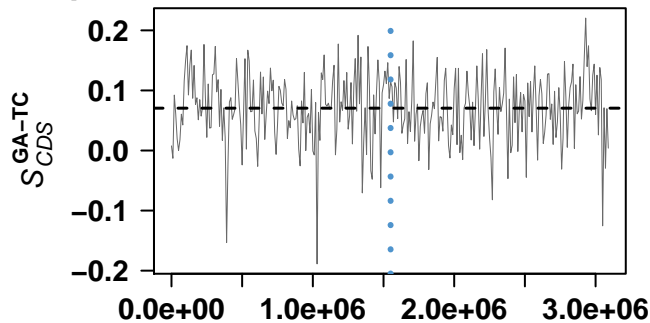


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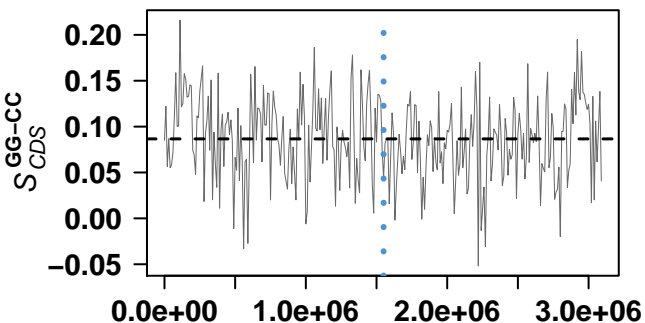
Symbiobacterium thermophilum IAM 14863



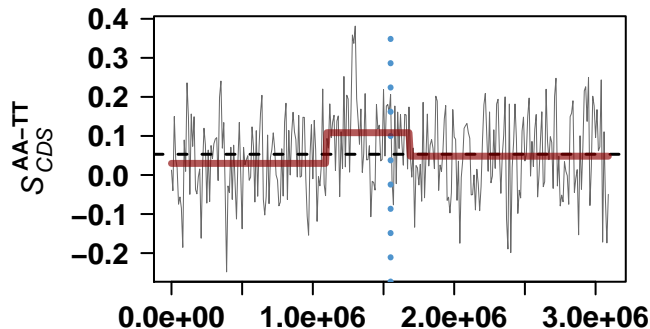
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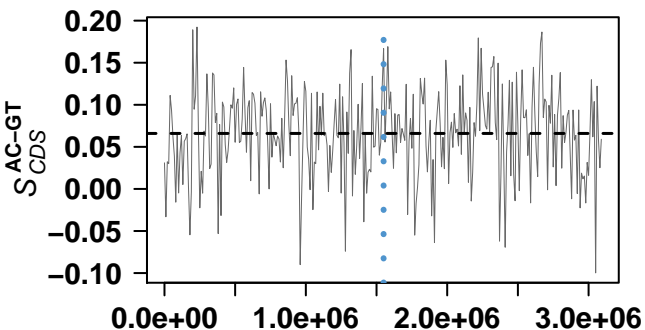
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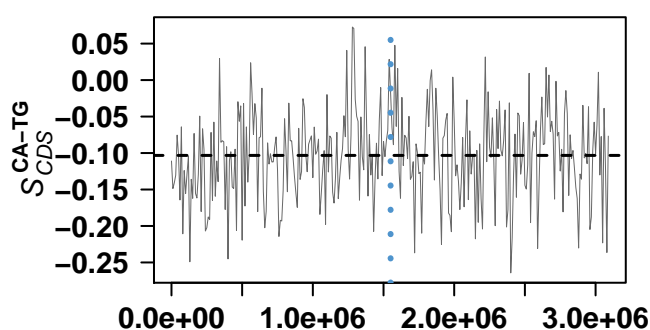
genome coordinates



genome coordinates

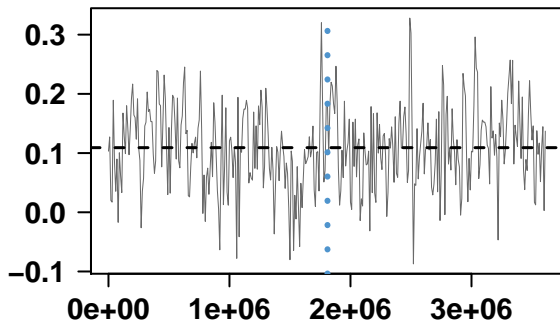


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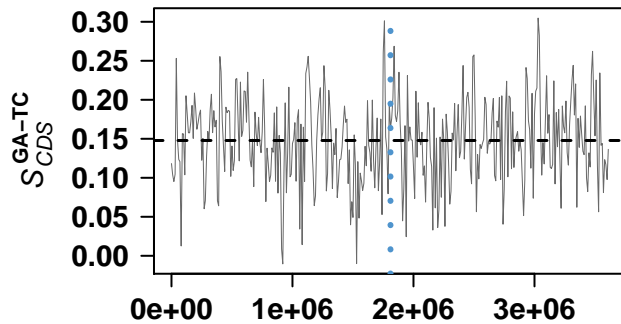


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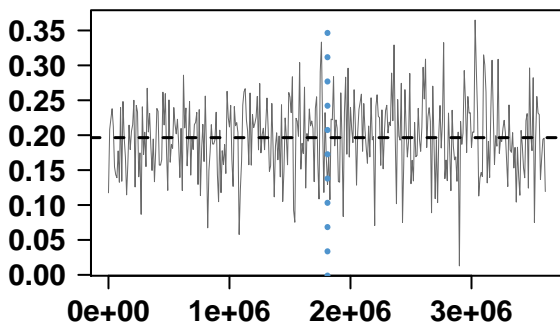
Bacillus licheniformis DSM 13 = ATCC 14580



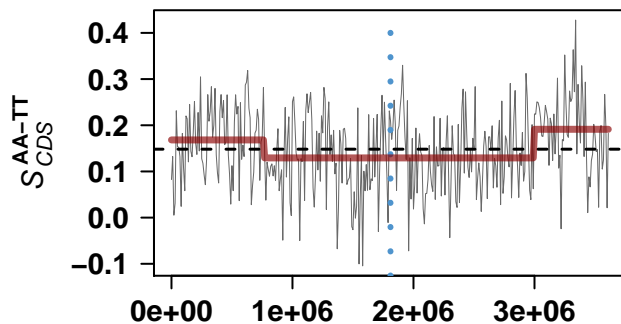
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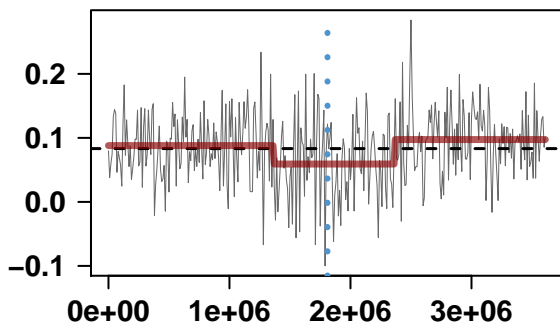
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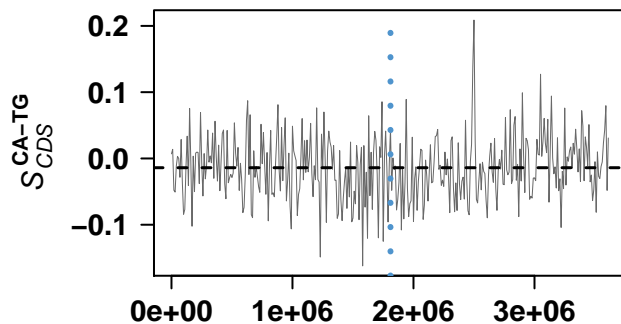
genome coordinates



genome coordinates

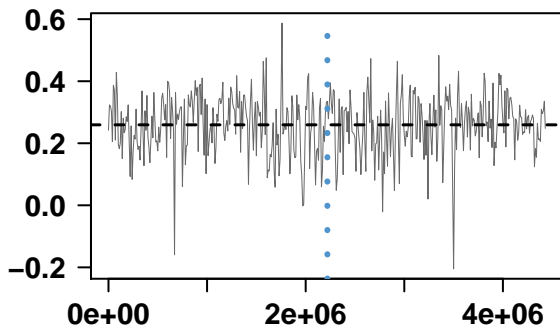


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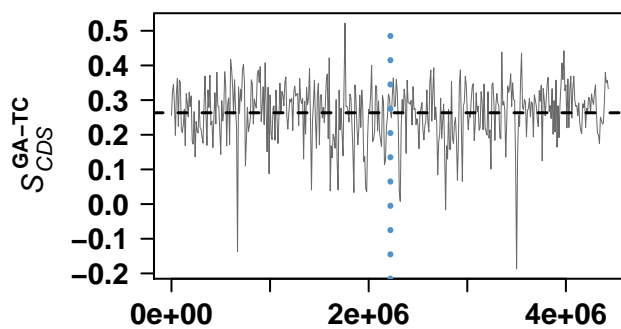


genome coordinates

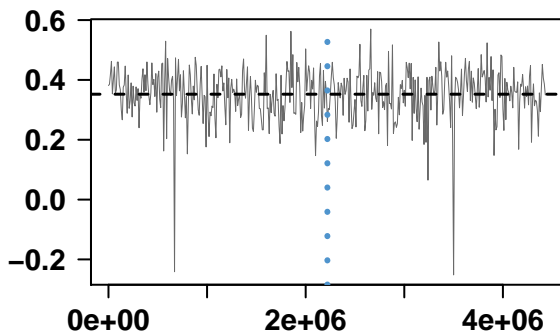
Bacillus cereus E33L



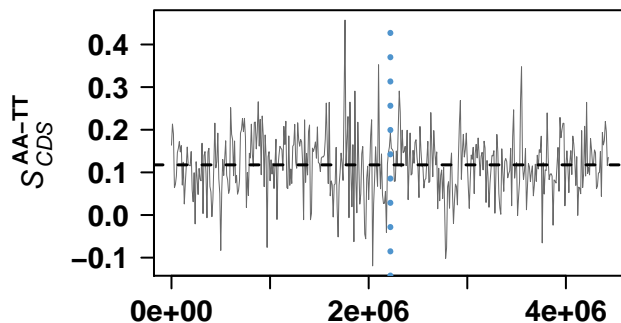
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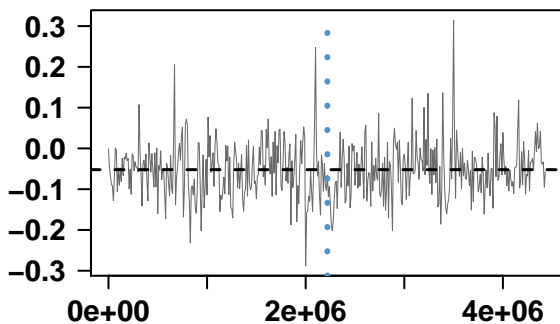
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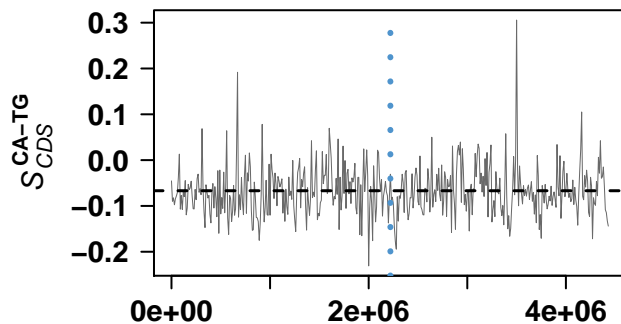
genome coordinates



genome coordinates

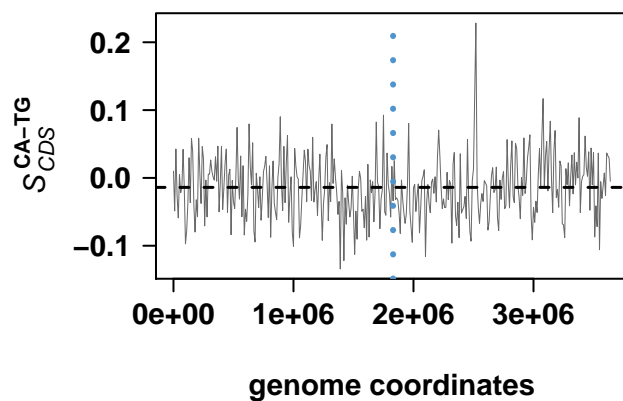
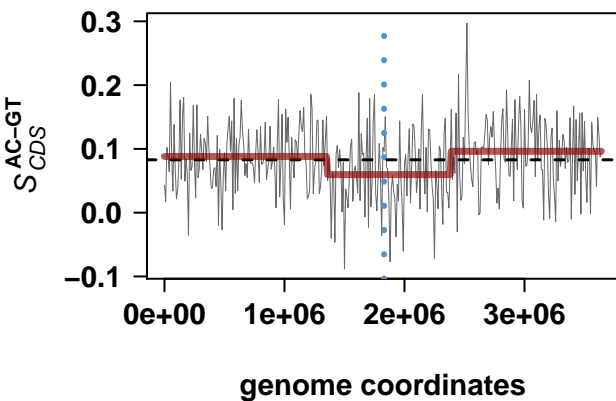
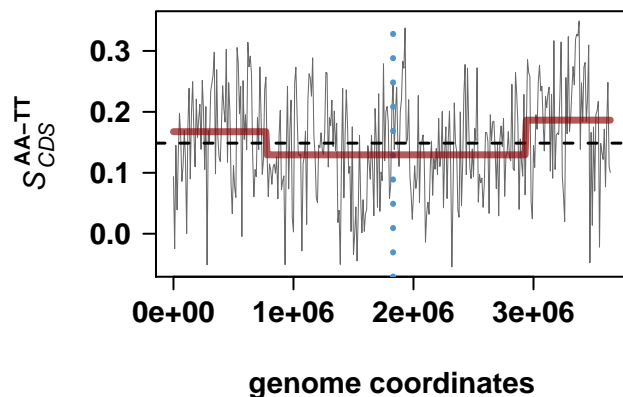
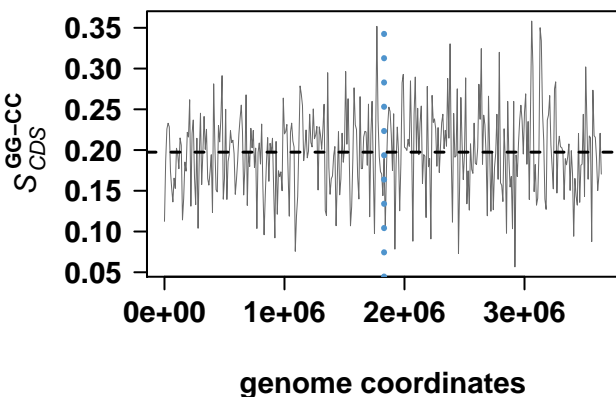
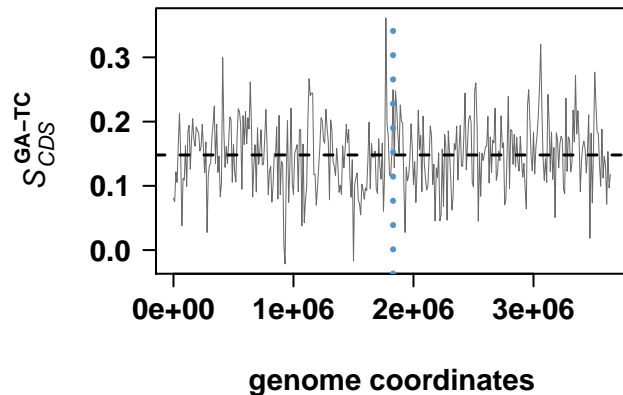
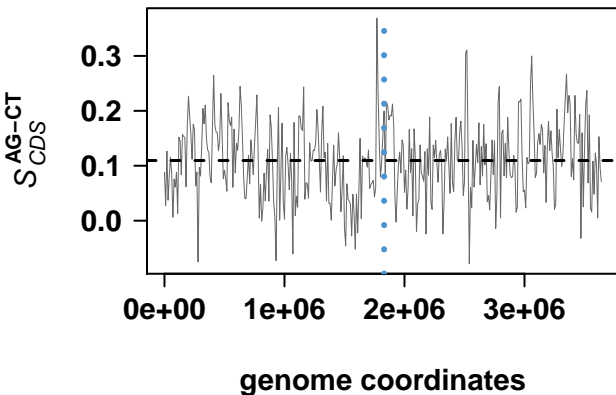


genome coordinates

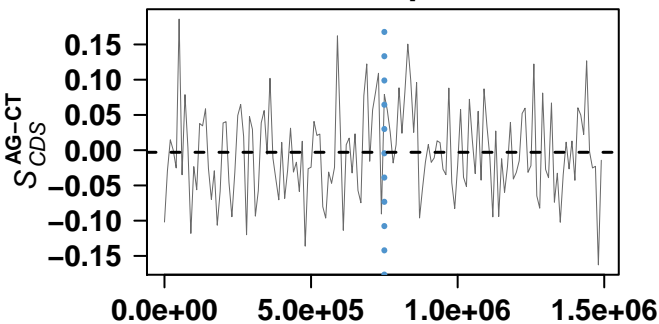


genome coordinates

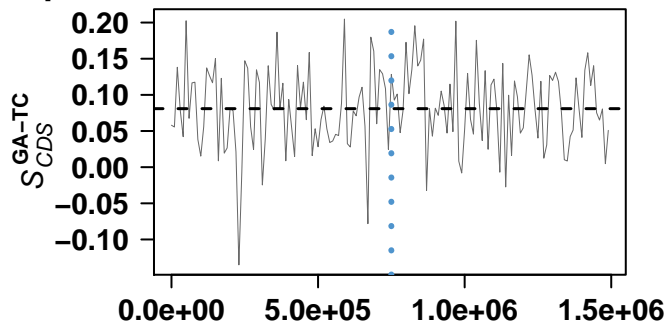
Bacillus licheniformis DSM 13 = ATCC 14580



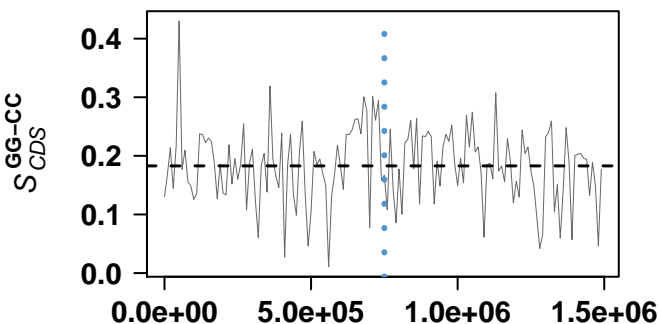
Streptococcus thermophilus LMG 18311



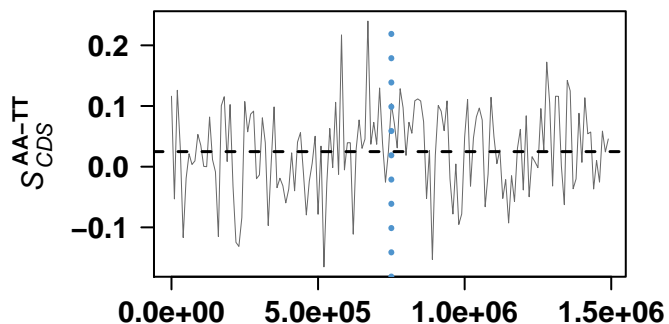
genome coordinates



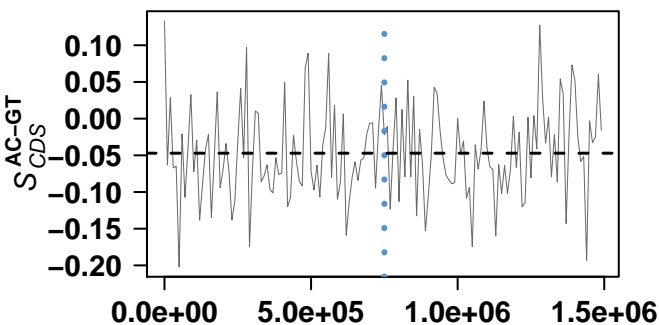
genome coordinates



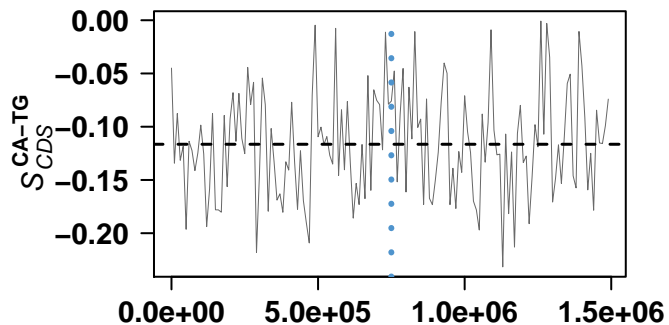
genome coordinates



genome coordinates

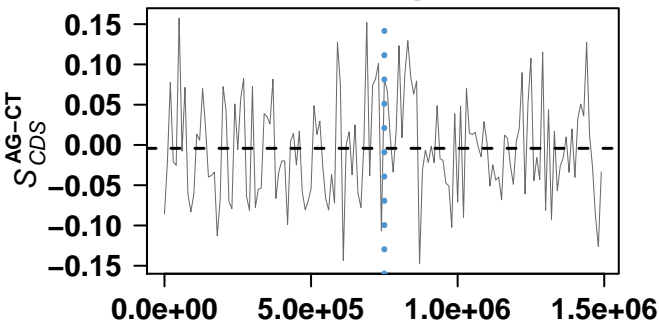


genome coordinates

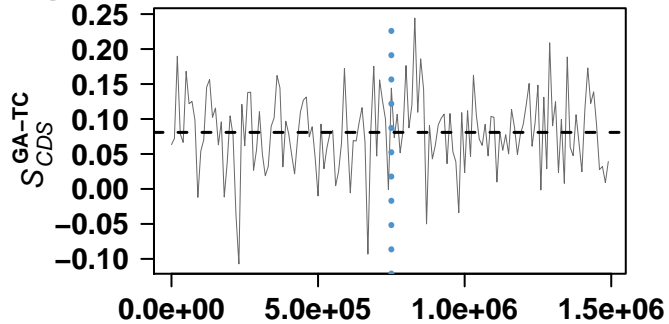


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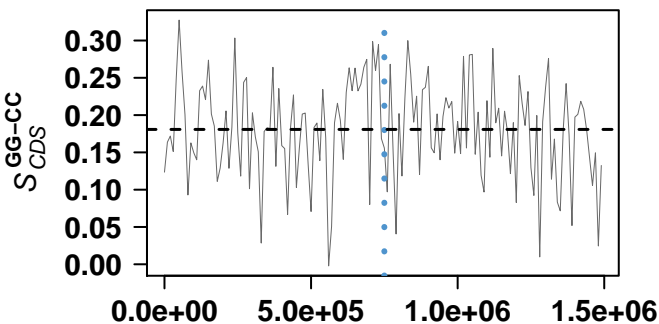
Streptococcus thermophilus CNRZ1066



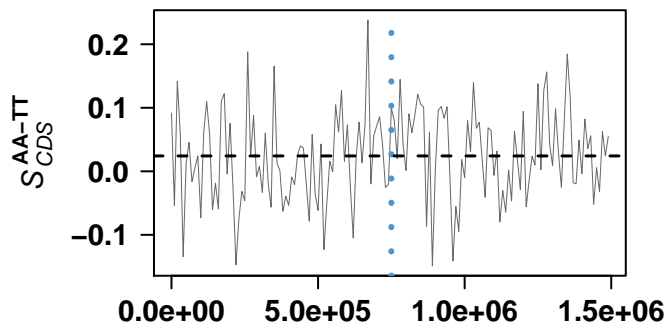
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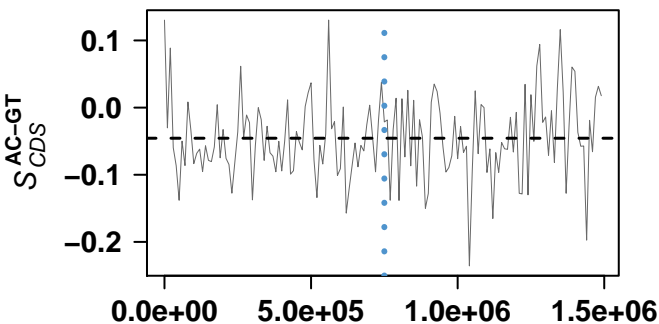
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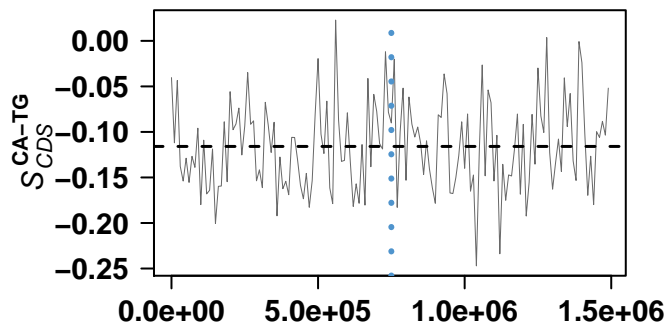
genome coordinates



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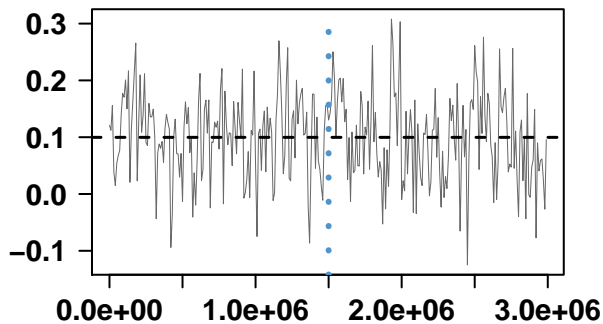


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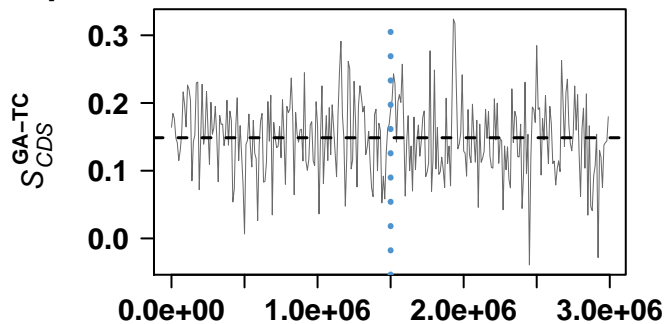


genome coordinates

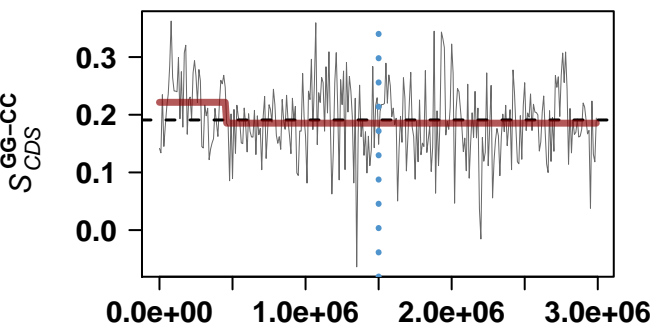
Geobacillus kaustophilus HTA426



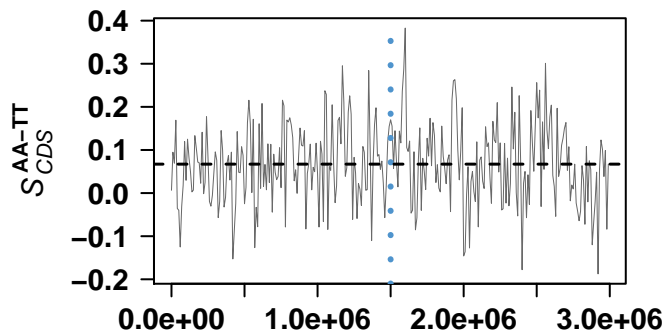
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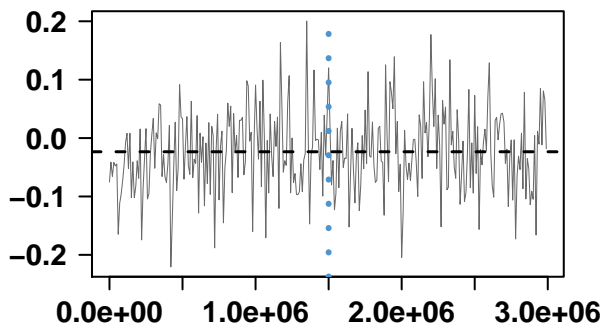
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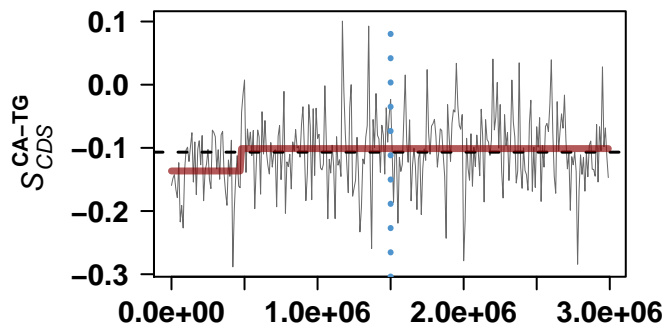
genome coordinates



genome coordinates

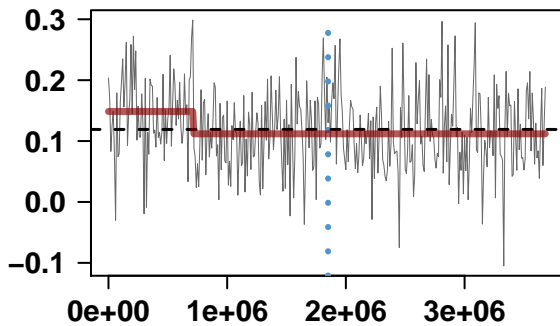


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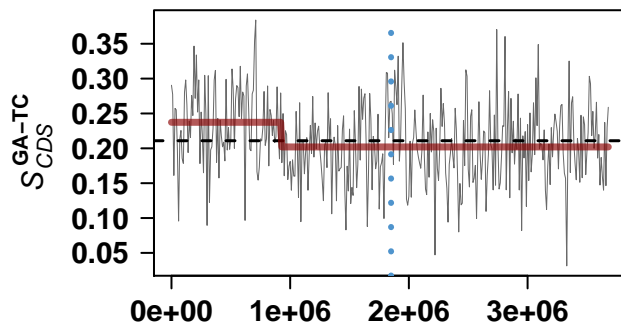


genome coordinates

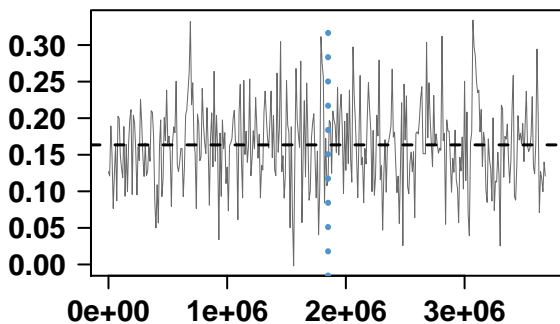
Bacillus clausii KSM-K16



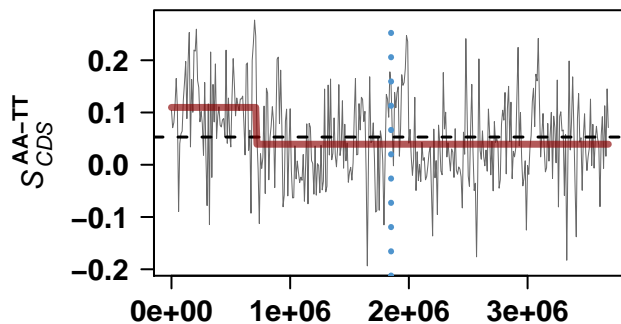
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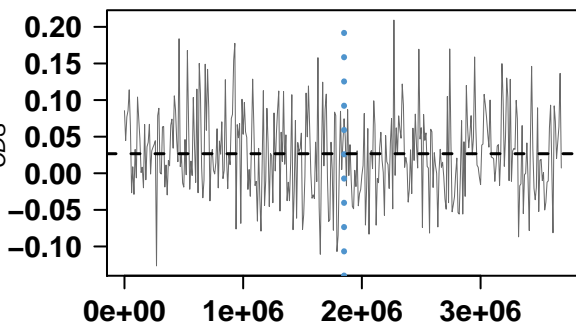
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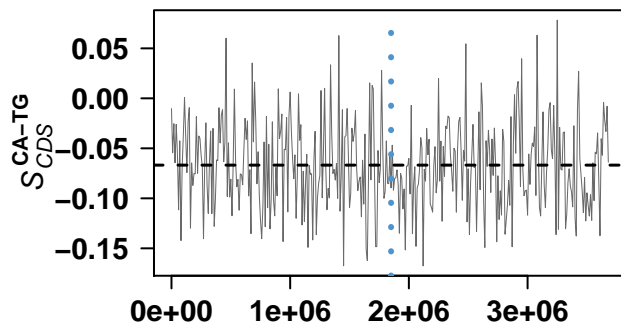
genome coordinates



genome coordinates

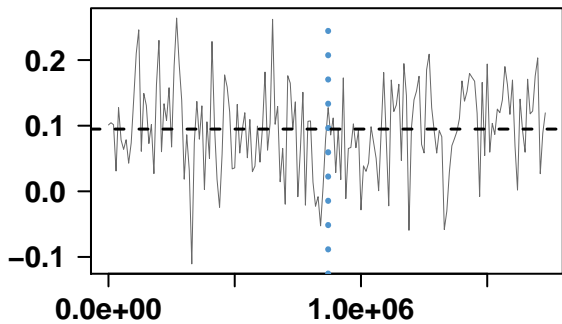


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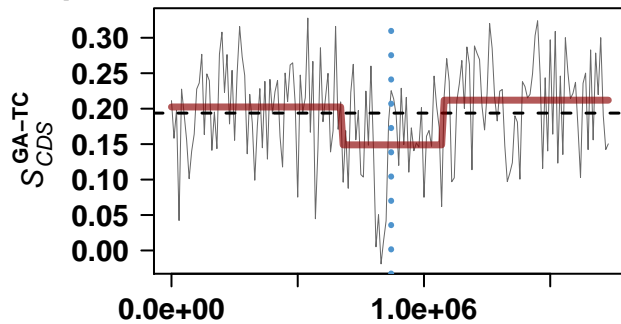


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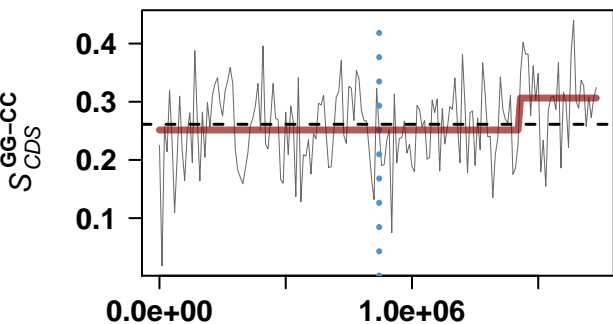
Lactobacillus acidophilus NCFM



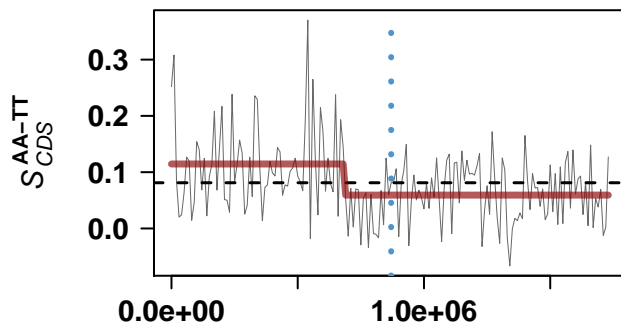
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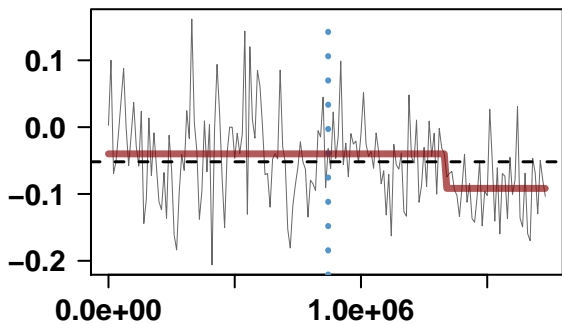
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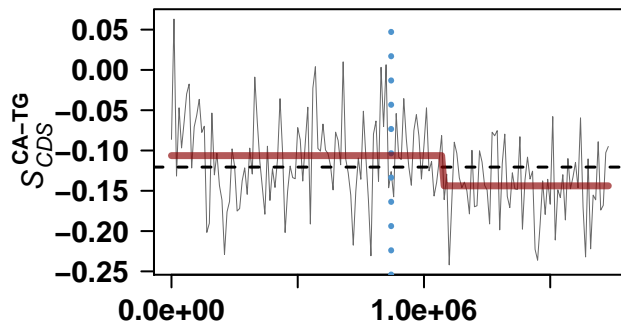
genome coordinates



genome coordinates

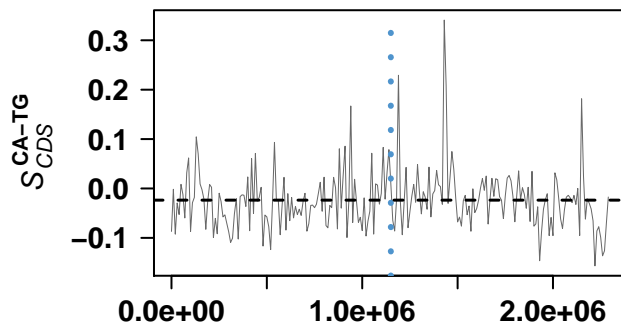
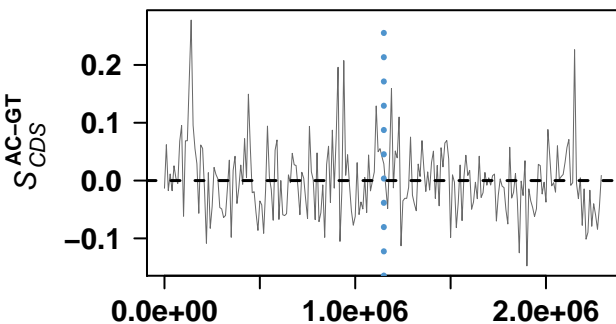
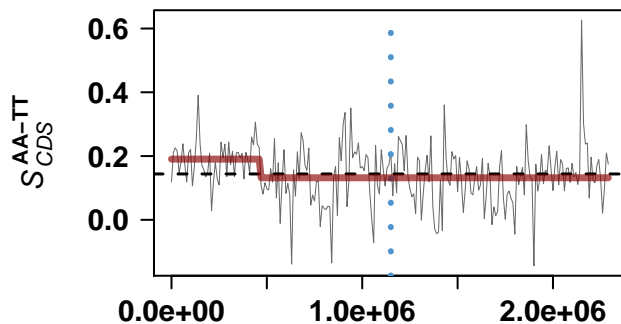
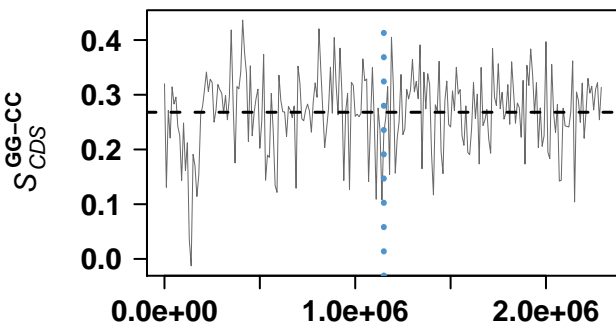
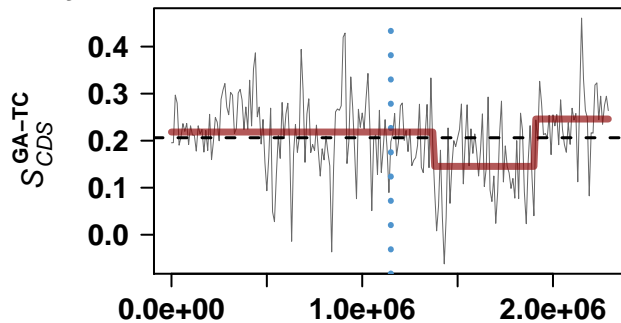
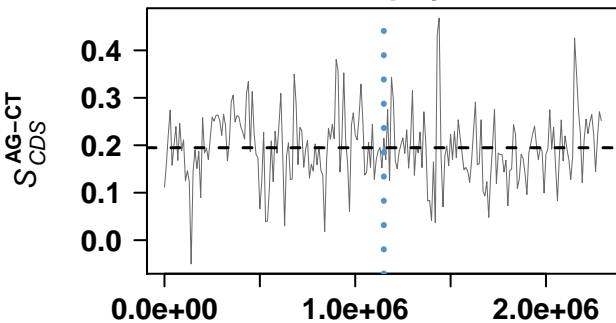


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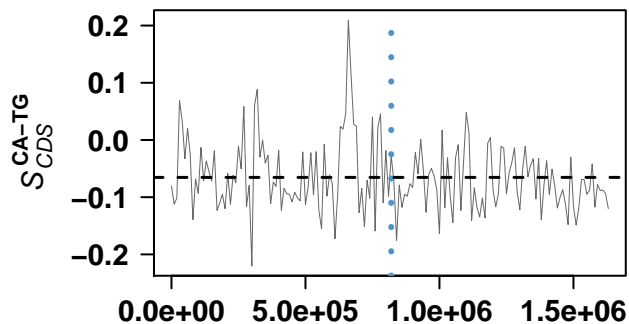
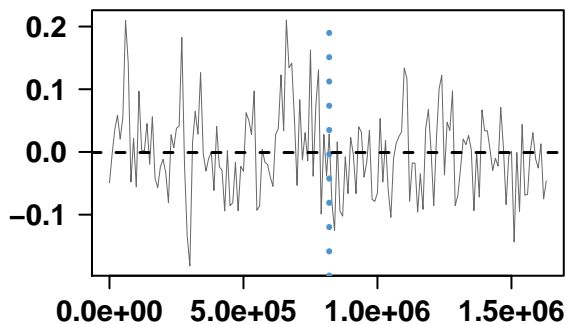
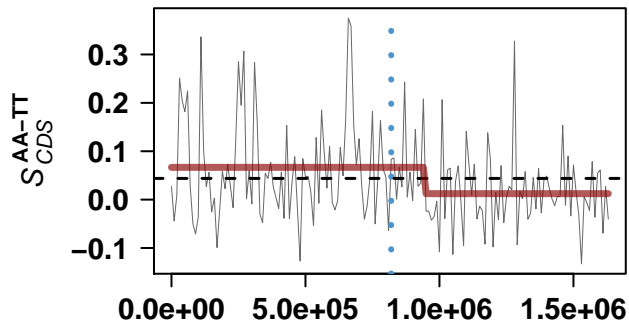
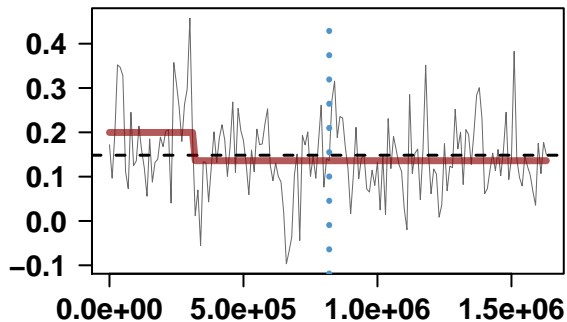
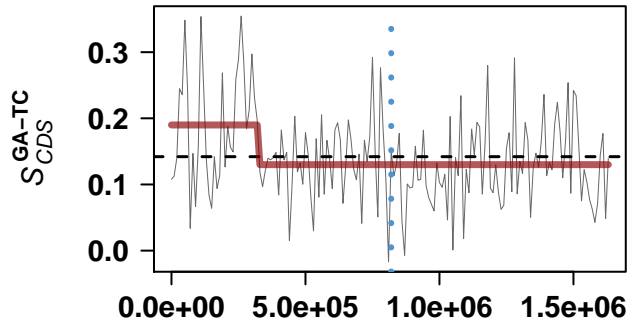
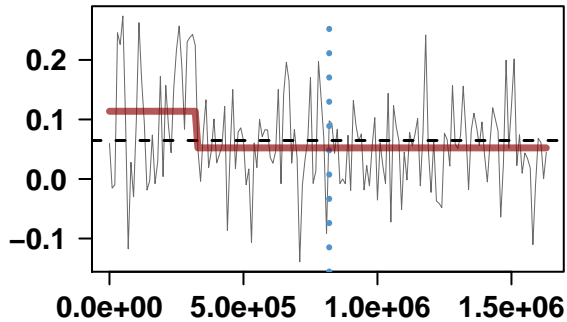


genome coordinates

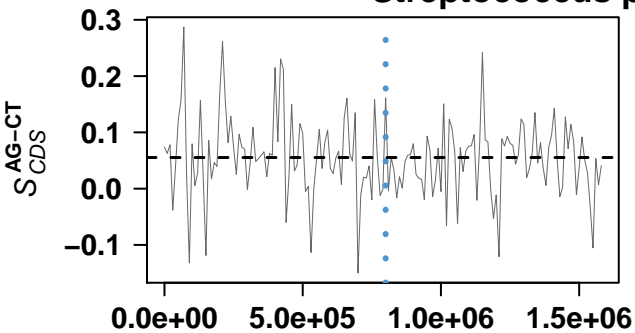
Staphylococcus haemolyticus JCSC1435



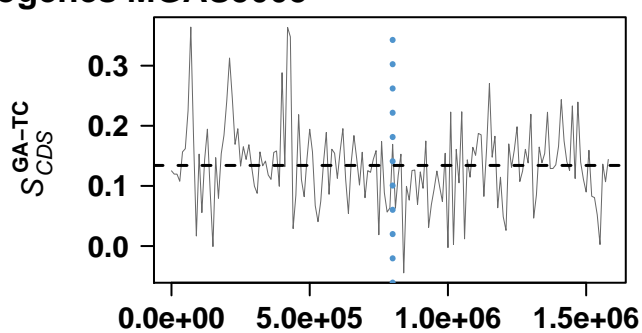
Streptococcus pyogenes MGAS6180



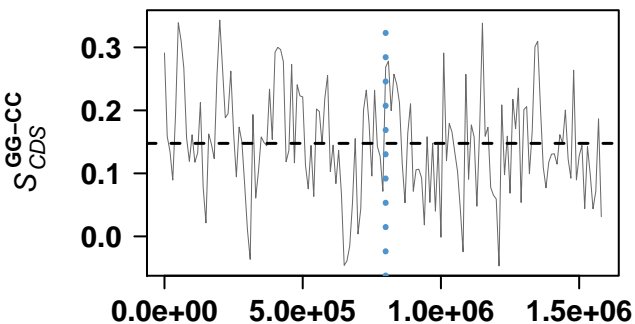
Streptococcus pyogenes MGAS5005



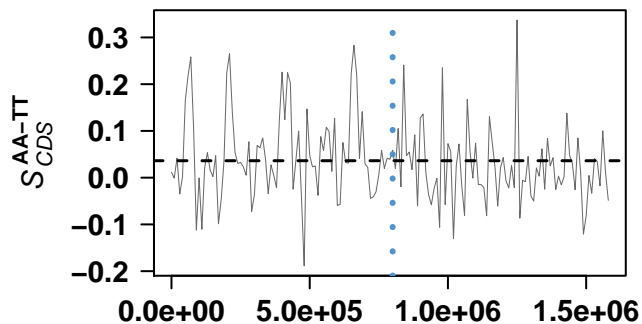
genome coordinates



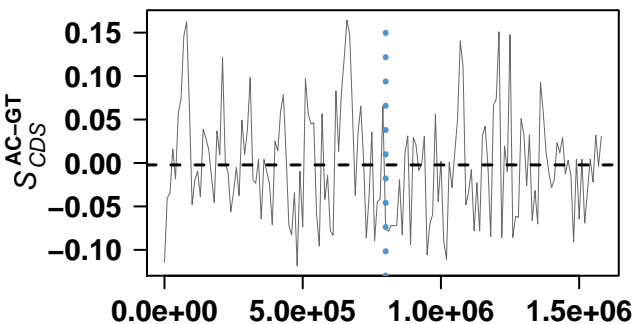
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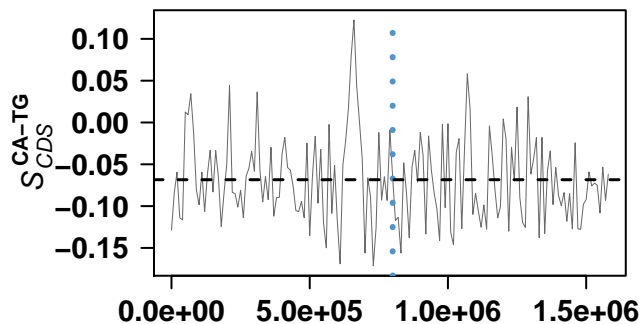
genome coordinates



genome coordinates

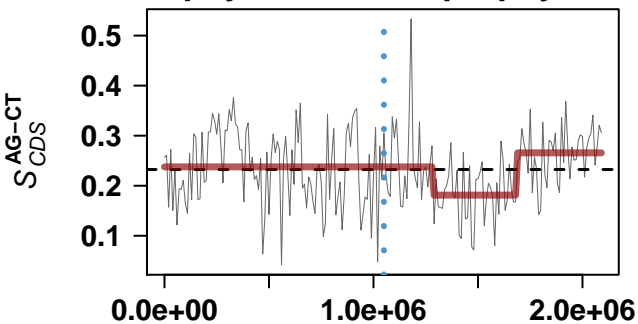


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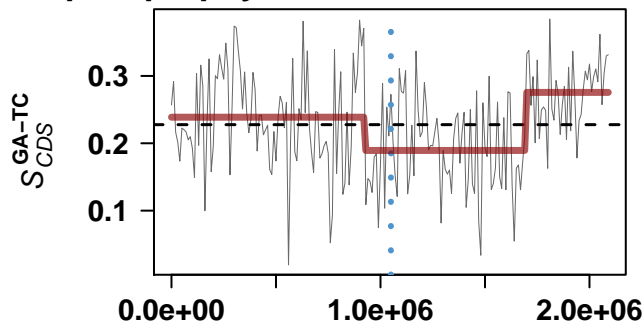


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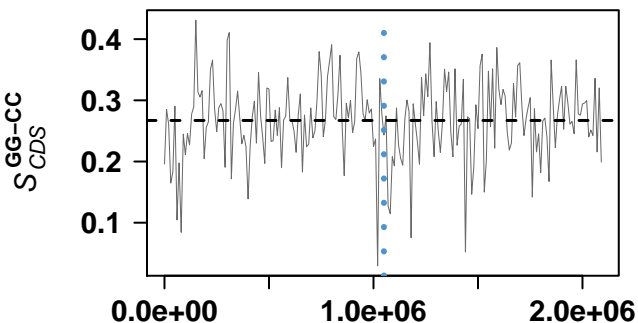
Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305



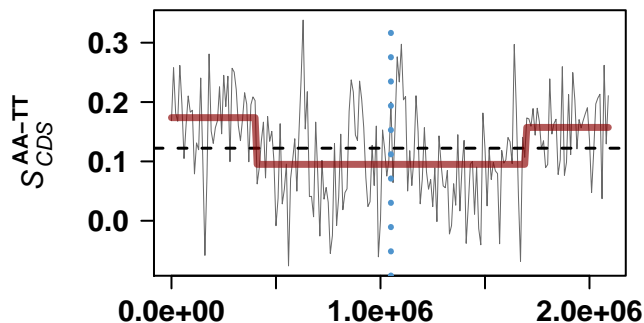
genome coordinates



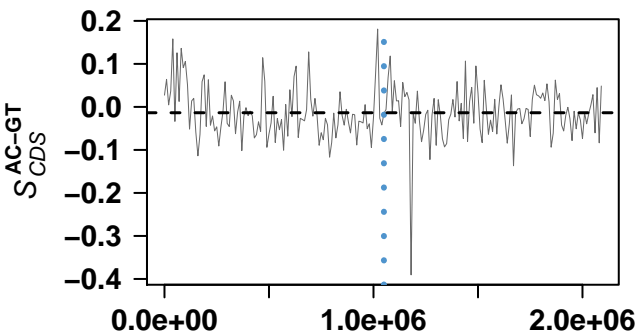
genome coordinates



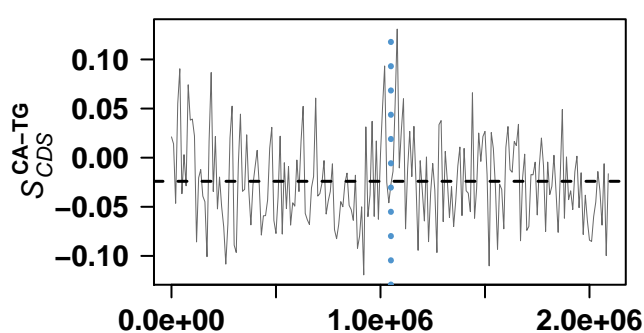
genome coordinates



genome coordinates

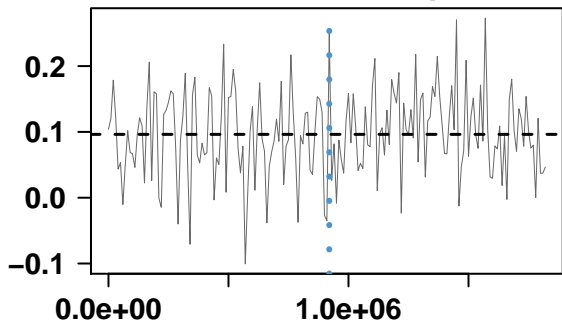


genome coordinates

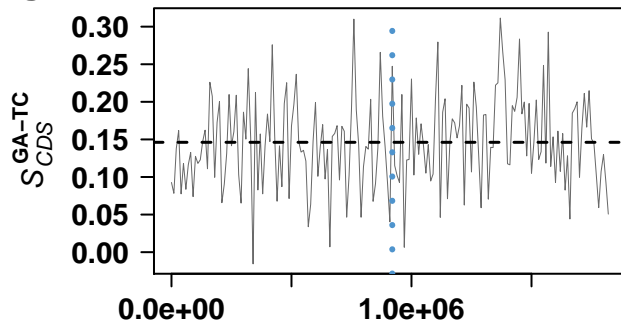


genome coordinates

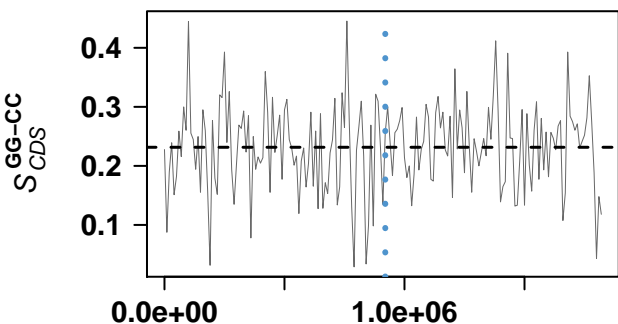
Streptococcus agalactiae A909



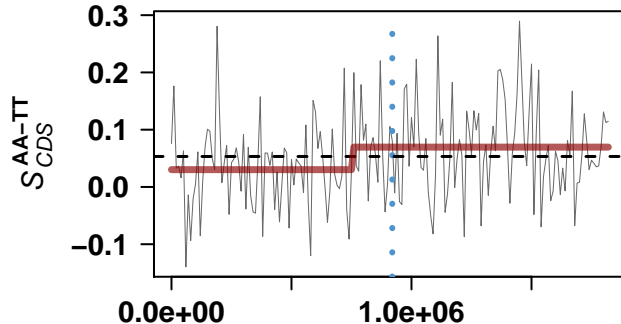
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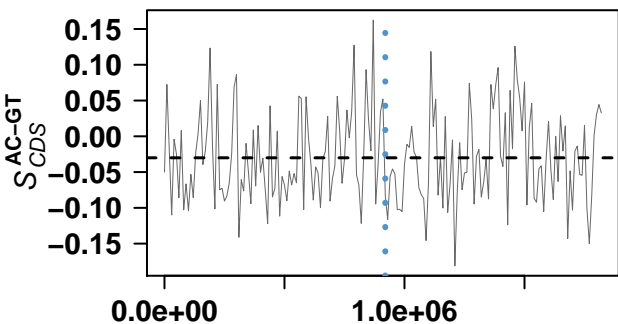
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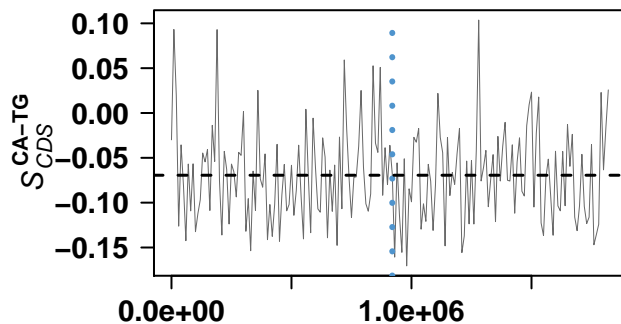
genome coordinates



genome coordinates

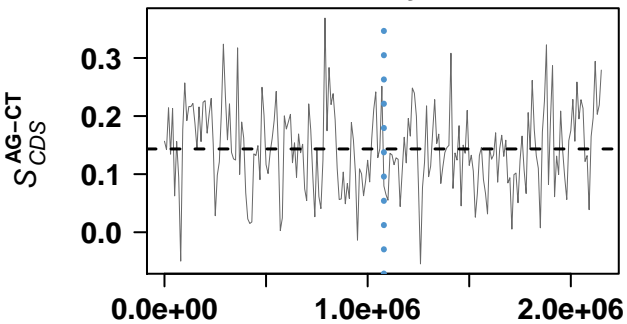


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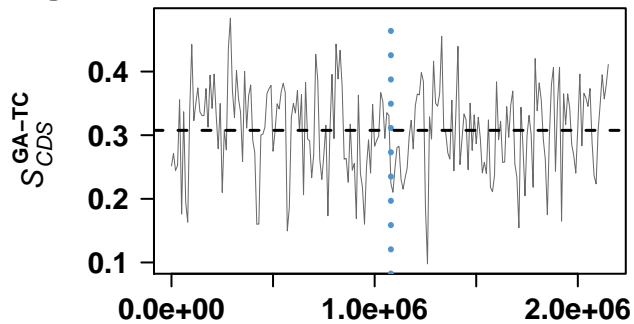


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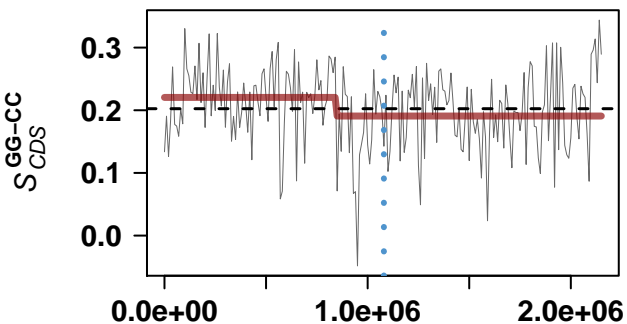
Carboxydothemus hydrogenoformans Z-2901



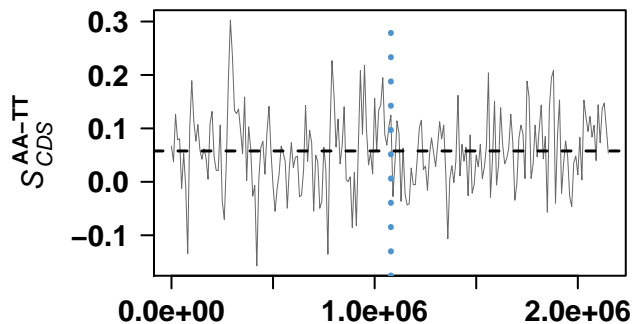
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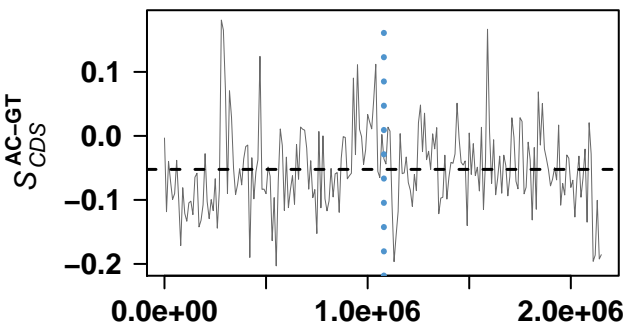
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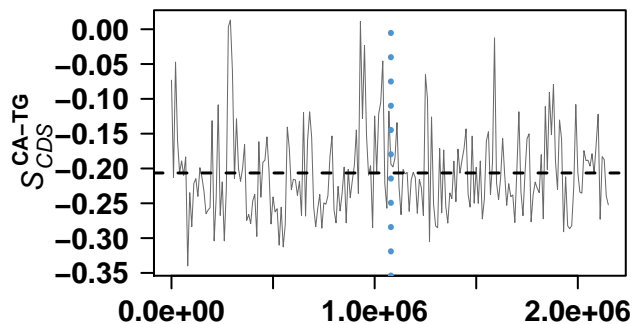
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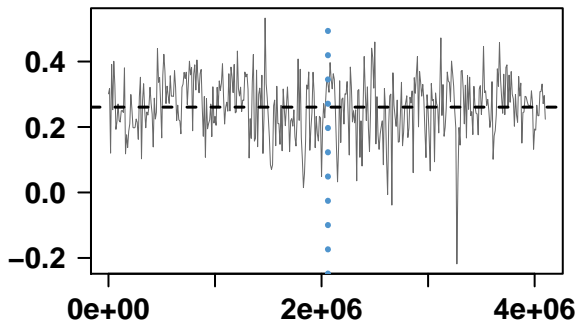


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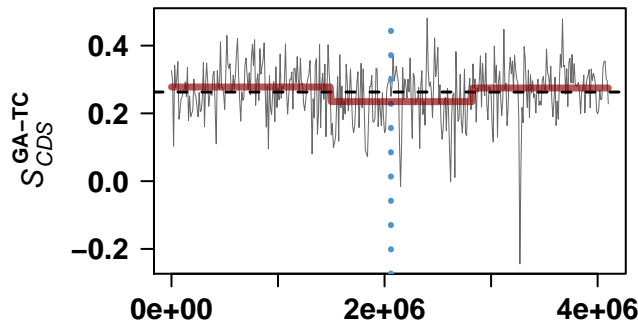


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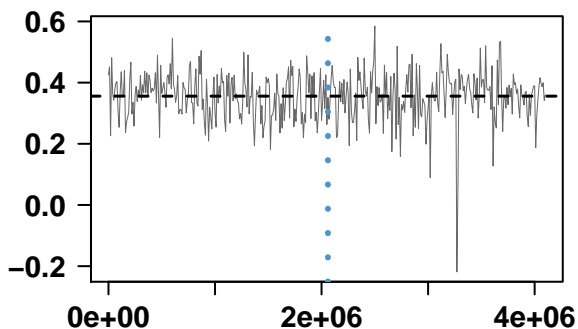
Bacillus anthracis str. 'Ames Ancestor'



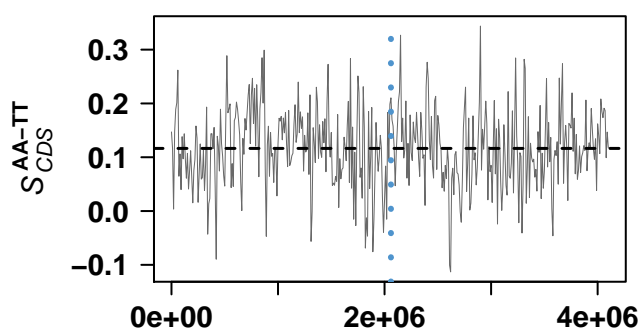
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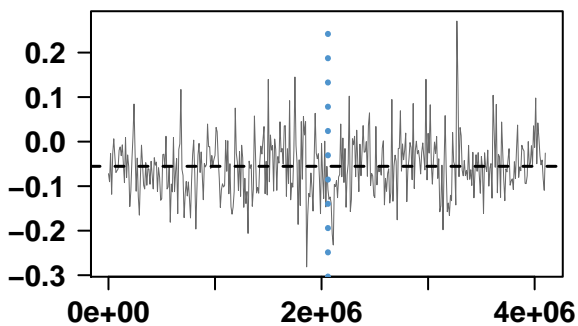
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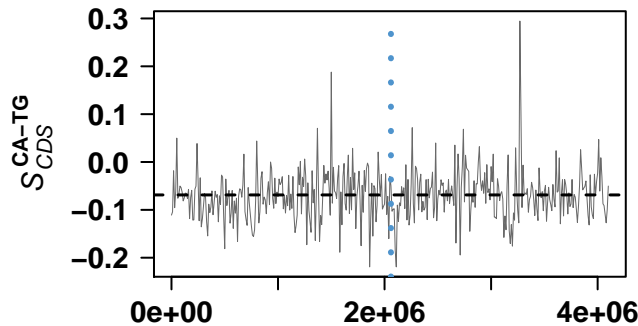
genome coordinates



genome coordinates

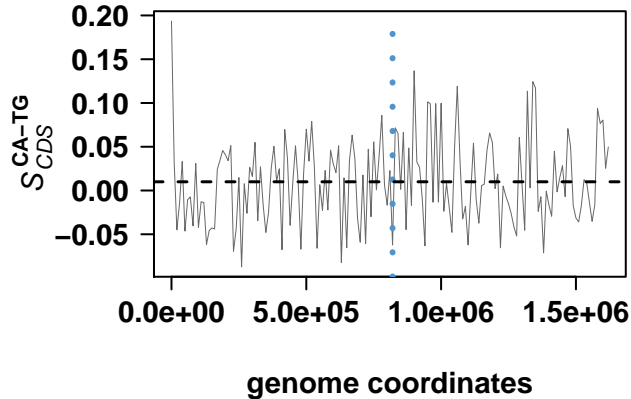
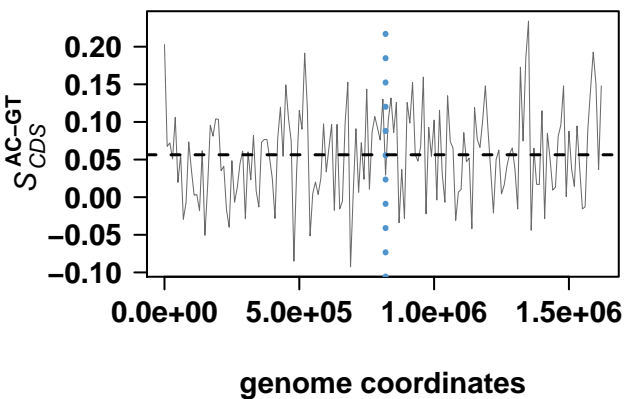
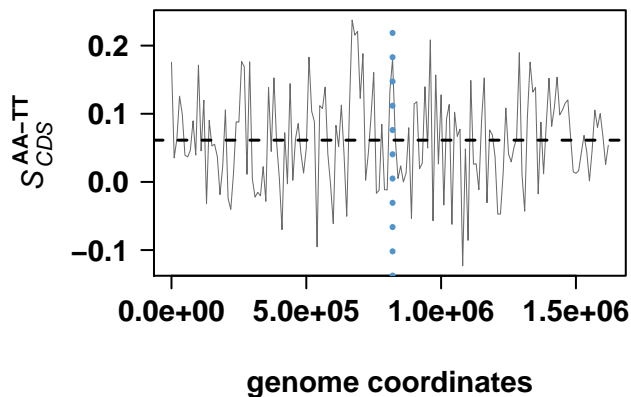
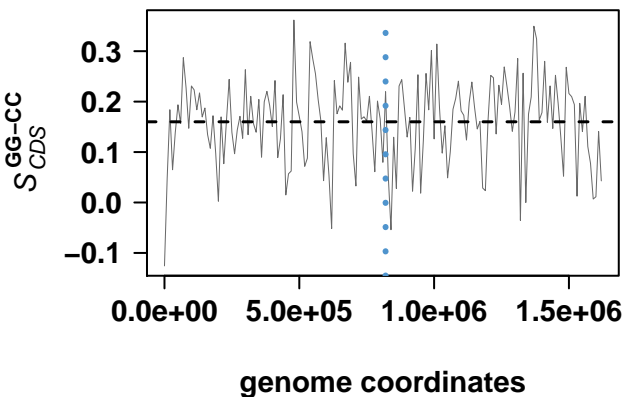
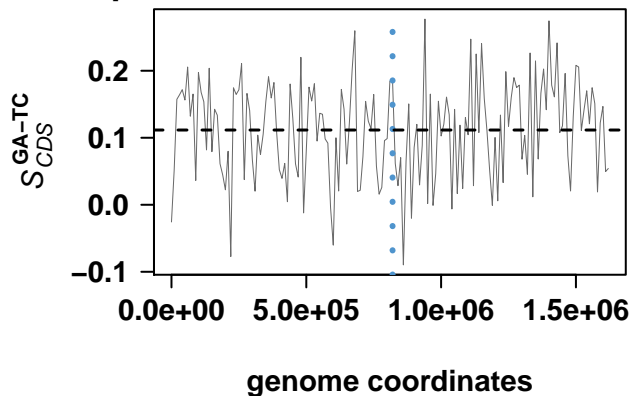
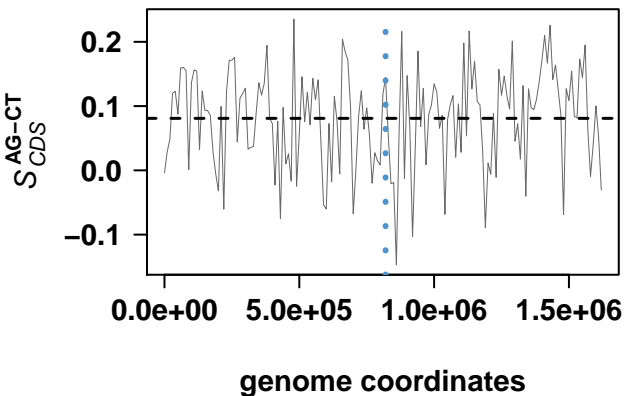


genome coordinates

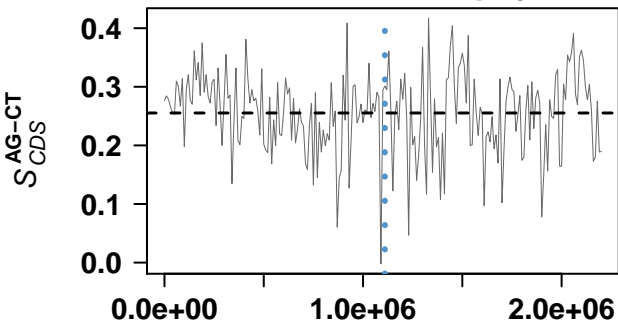


genome coordinates

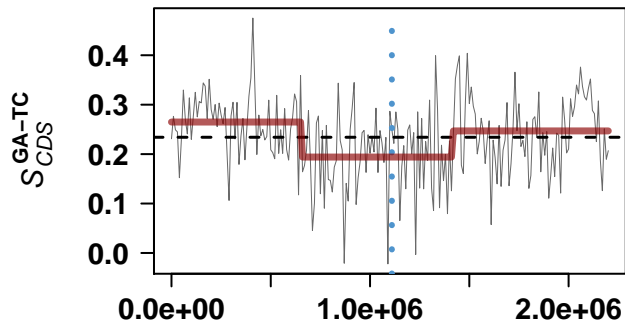
Lactobacillus sakei subsp. sakei 23K



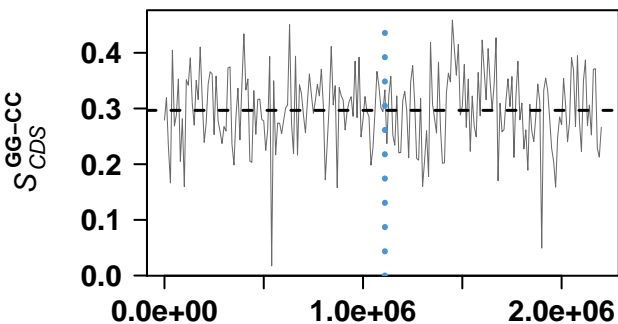
Staphylococcus aureus RF122



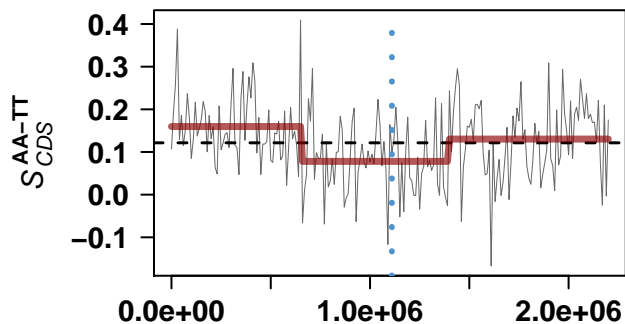
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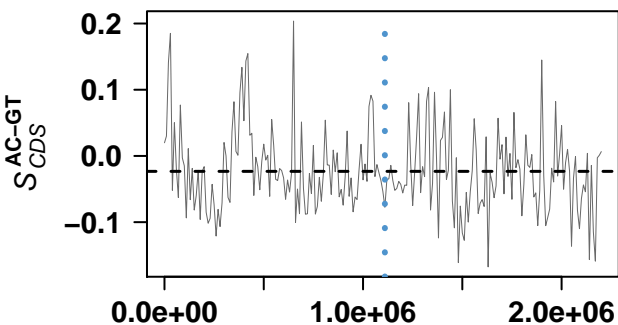
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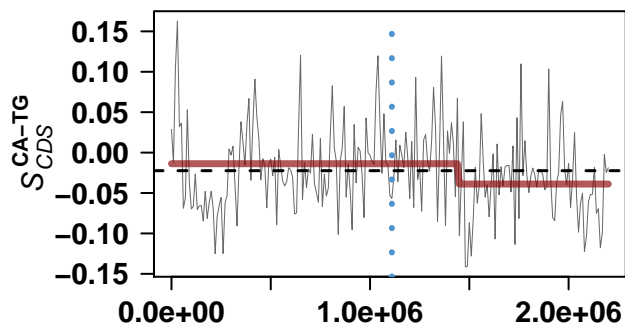
genome coordinates



genome coordinates

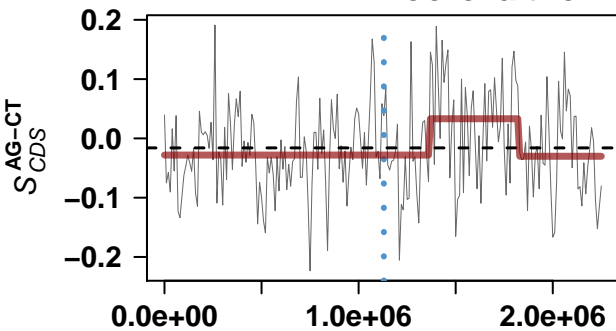


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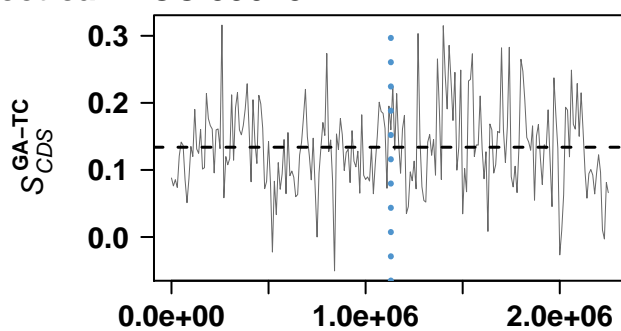


genome coordinates

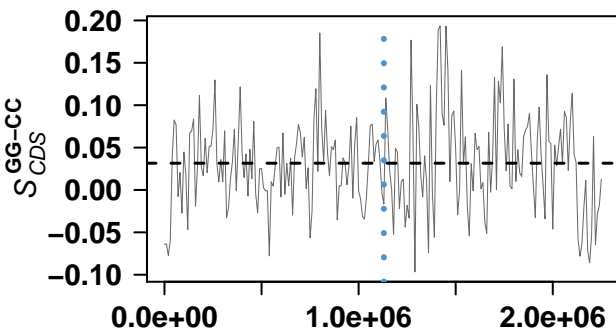
Moorella thermoacetica ATCC 39073



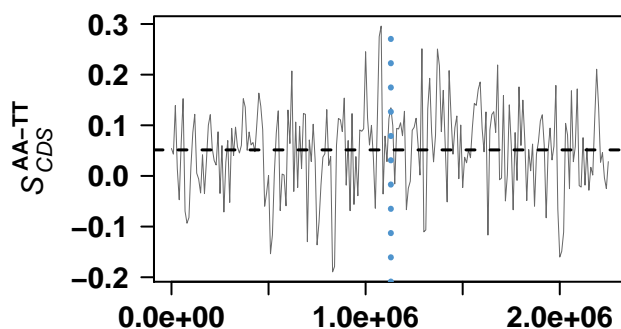
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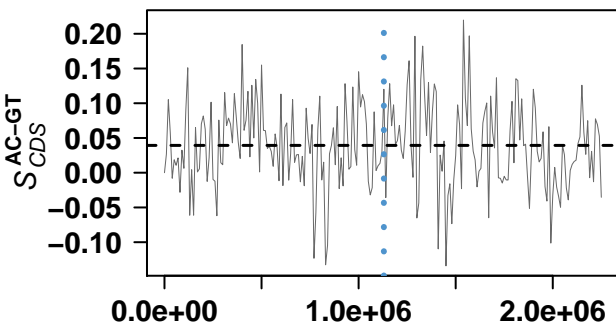
genome coordinates



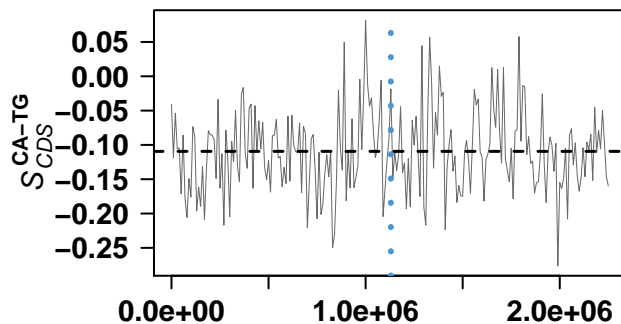
genome coordinates



genome coordinates

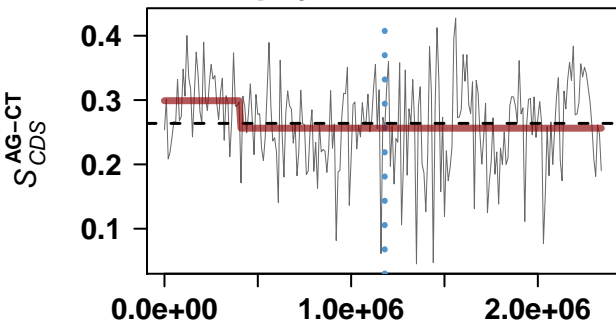


genome coordinates

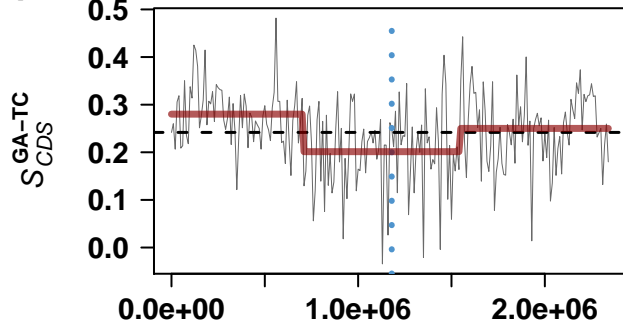


genome coordinates

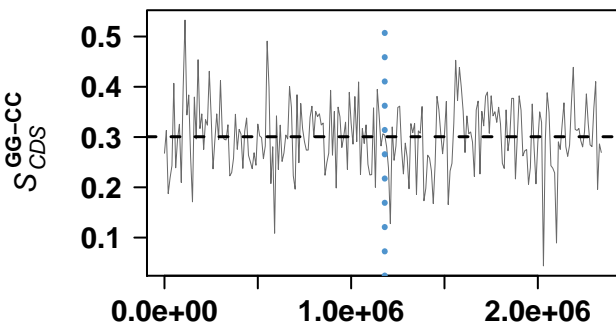
Staphylococcus aureus subsp. aureus USA300_FPR3757



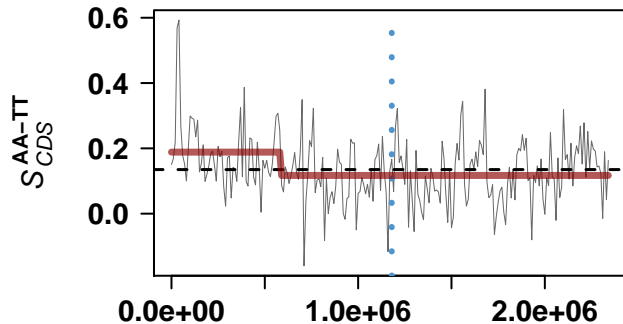
genome coordinates



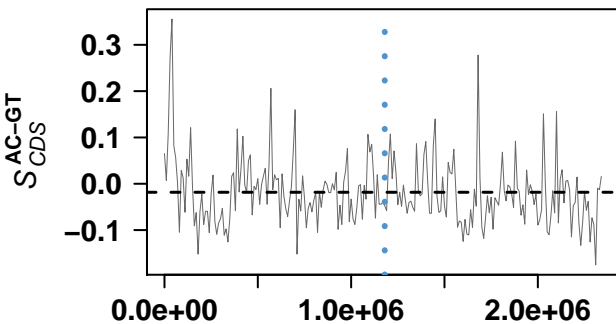
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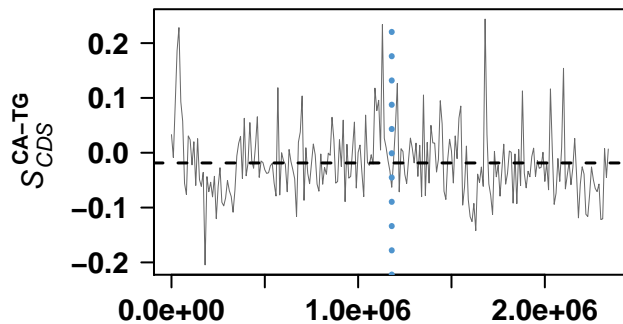
genome coordinates



genome coordinates

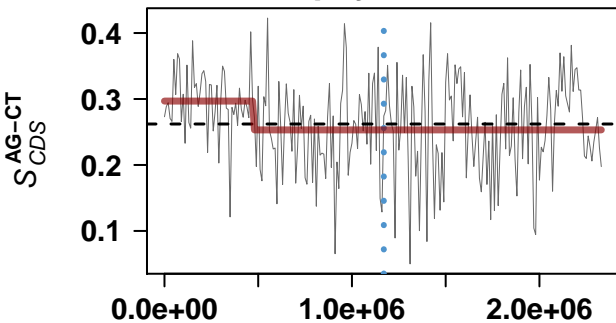


genome coordinates

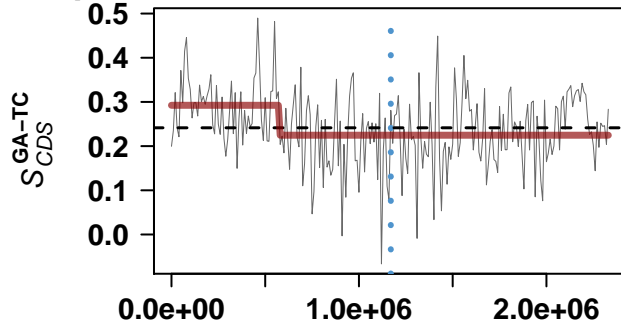


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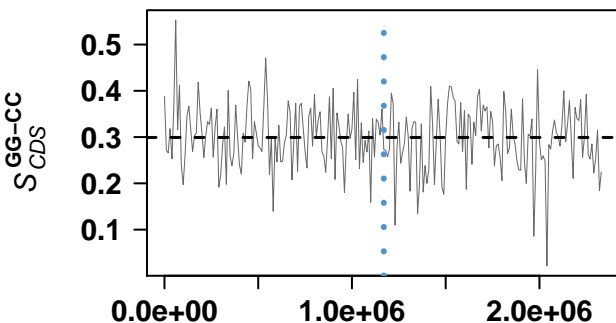
Staphylococcus aureus subsp. aureus NCTC 8325



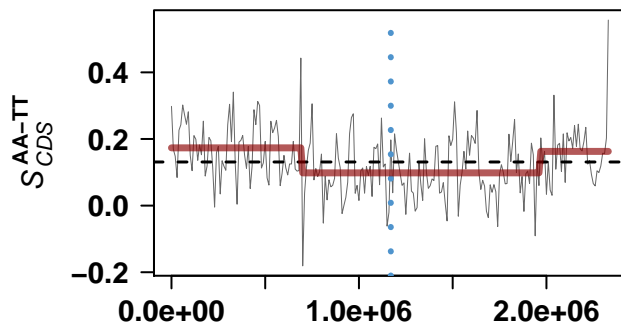
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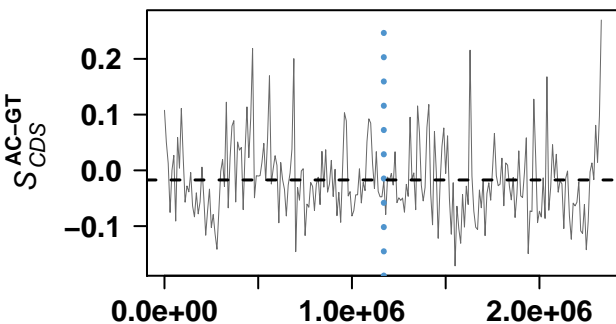
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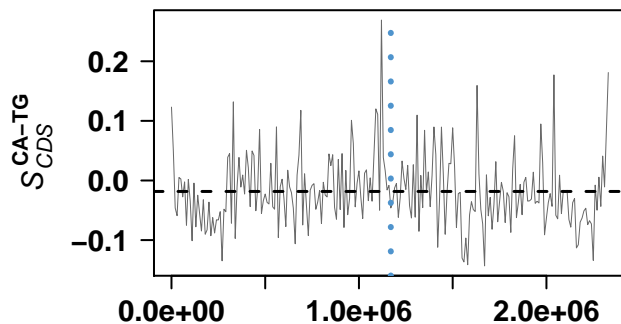
genome coordinates



genome coordinates

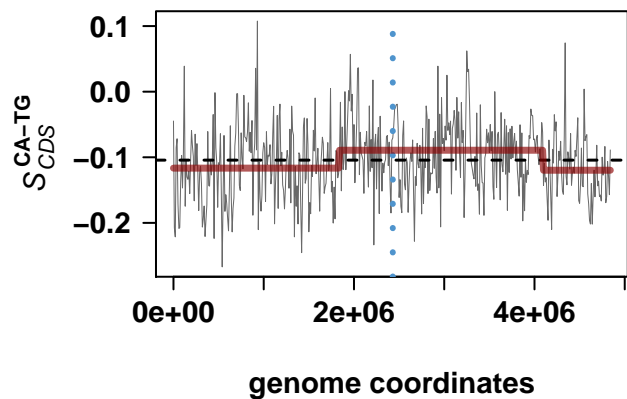
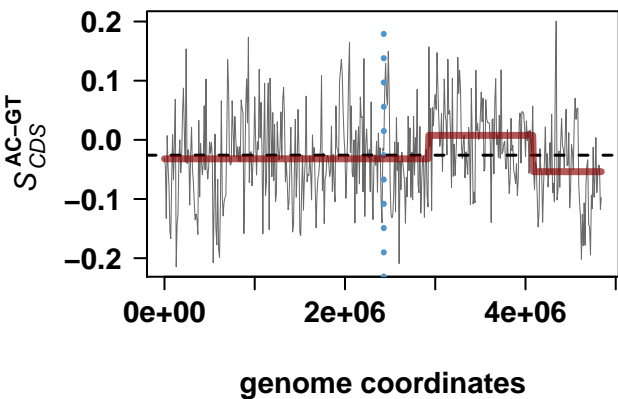
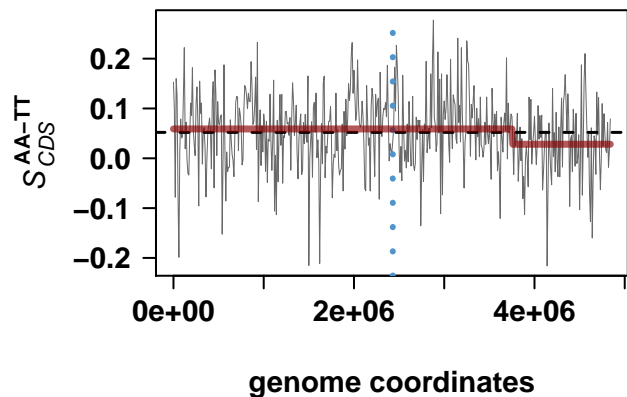
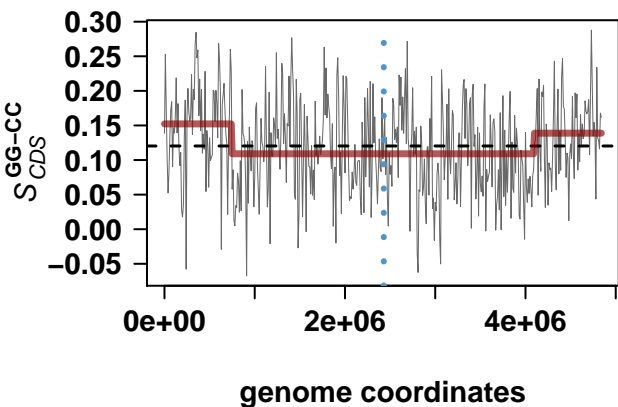
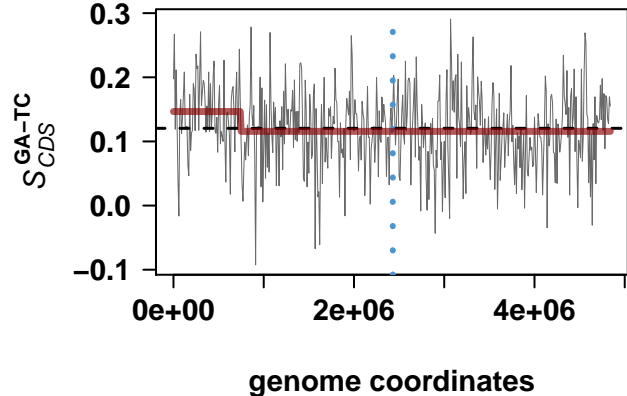
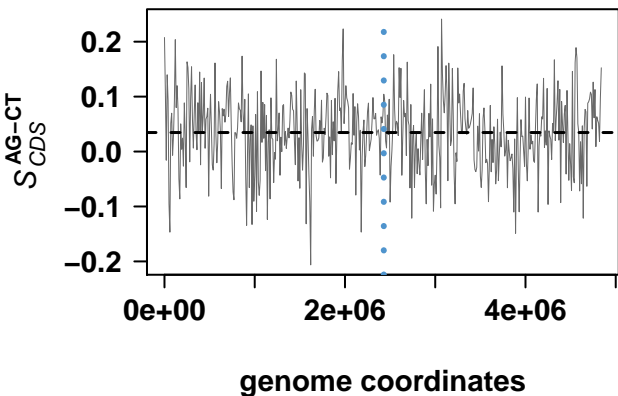


genome coordinates

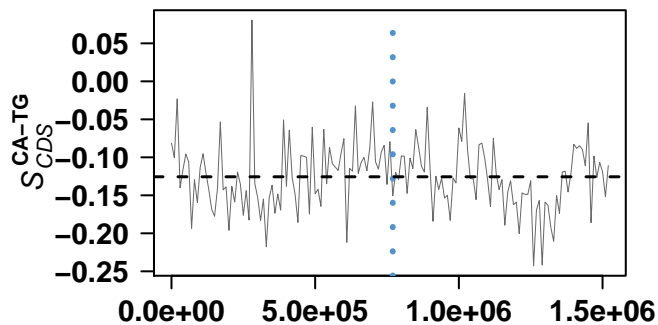
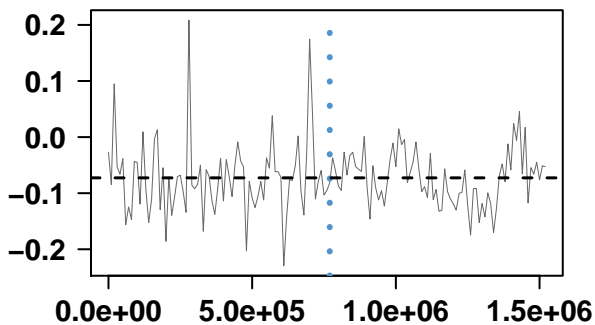
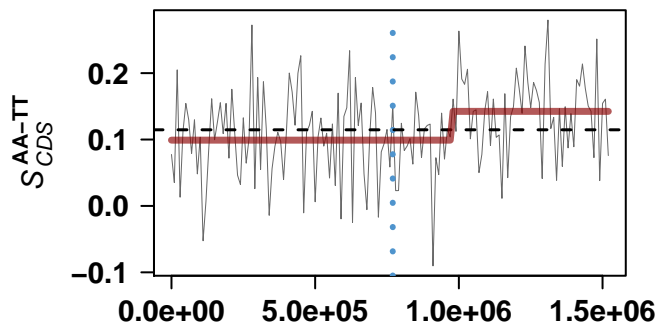
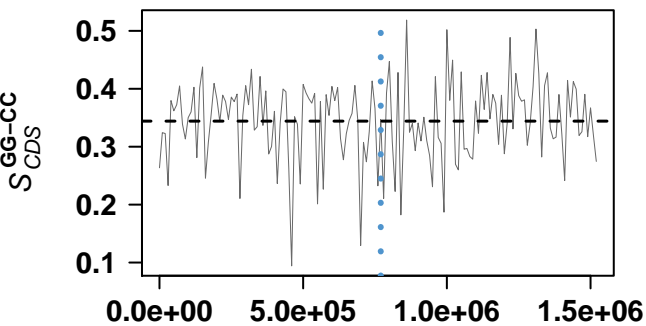
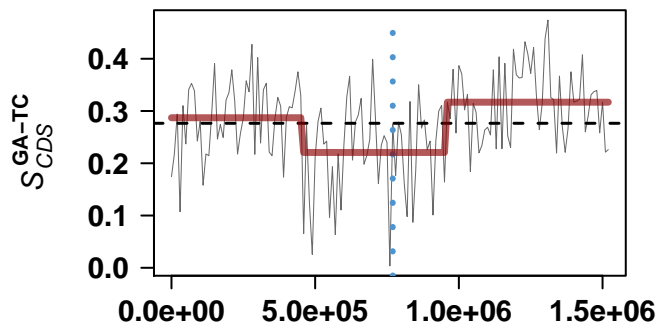
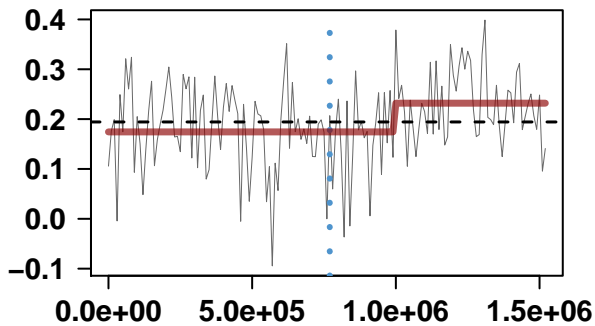


genome coordinates

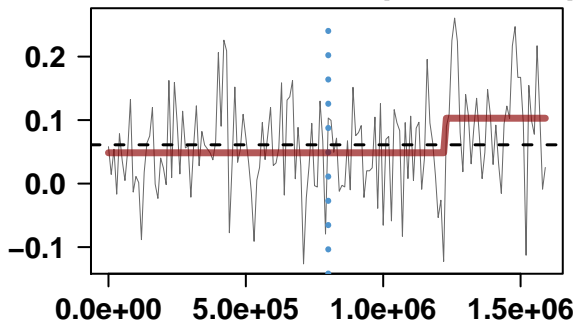
Desulfitobacterium hafniense Y51



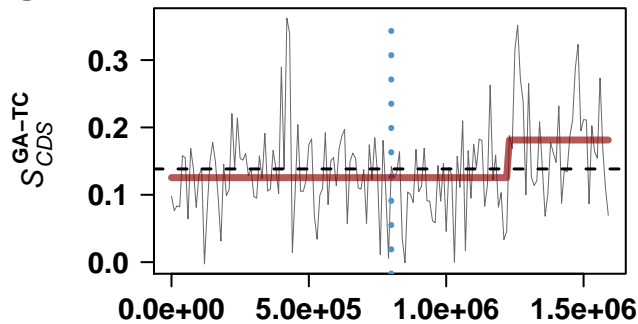
Lactobacillus salivarius UCC118



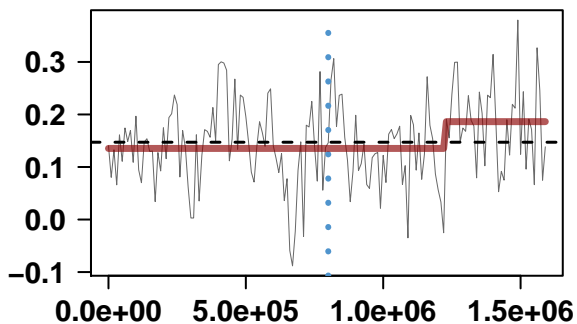
Streptococcus pyogenes MGAS9429



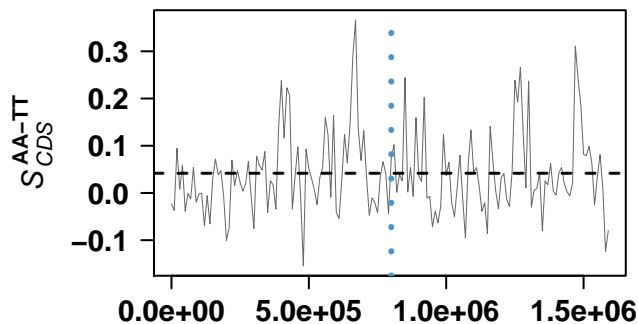
genome coordinates



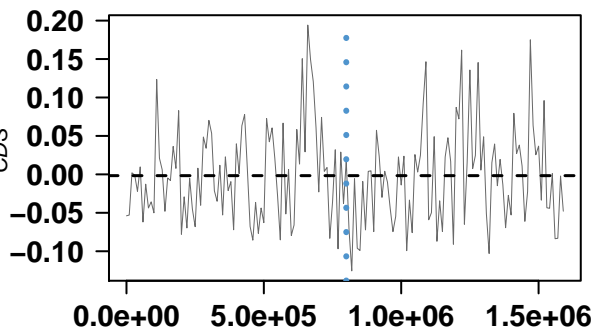
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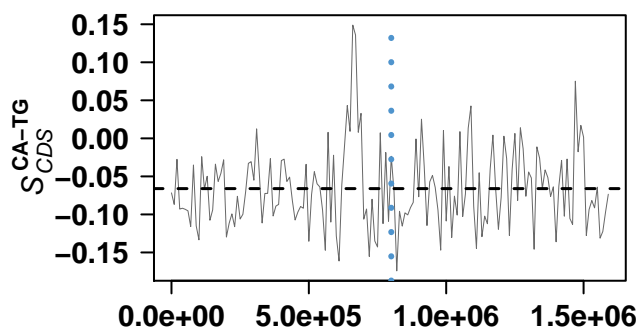
genome coordinates



genome coordinates

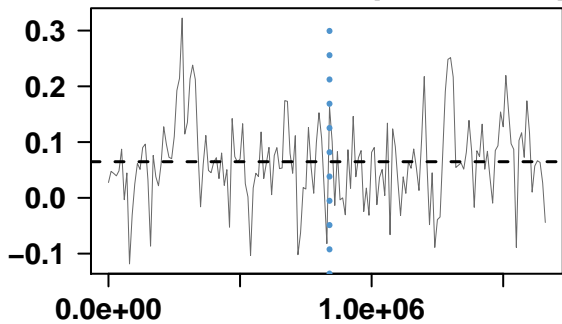


genome coordinates

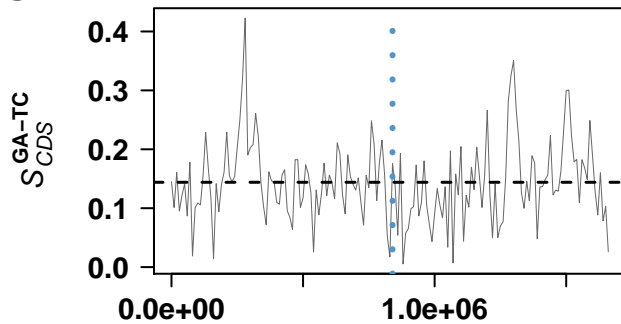


genome coordinates

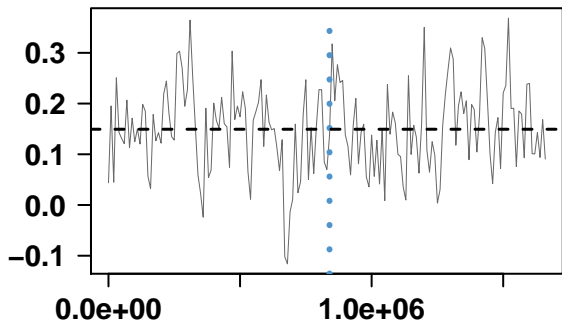
Streptococcus pyogenes MGAS10270



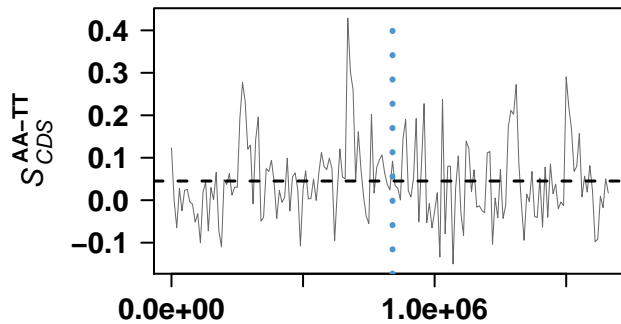
genome coordinates



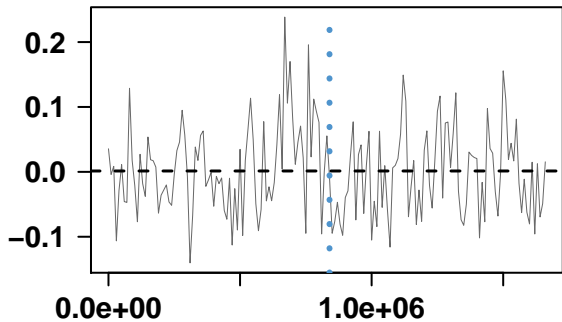
genome coordinates



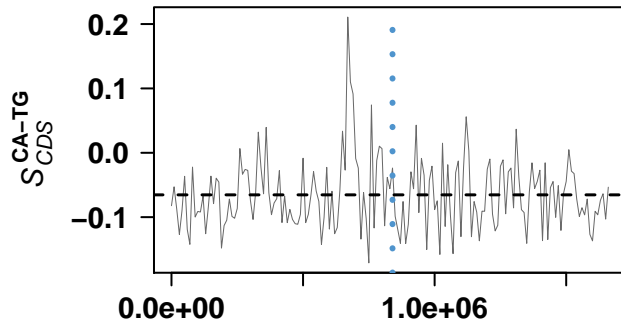
genome coordinates



genome coordinates

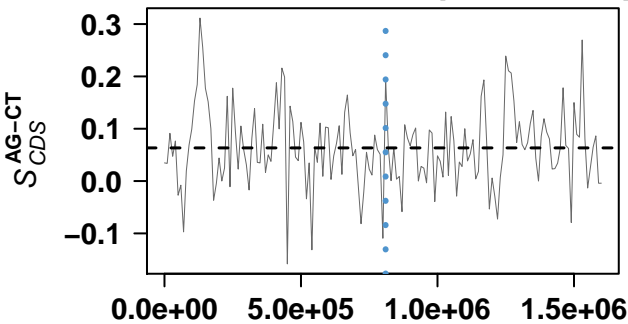


genome coordinates

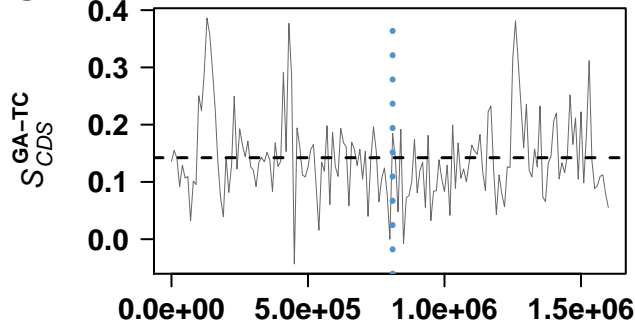


genome coordinates

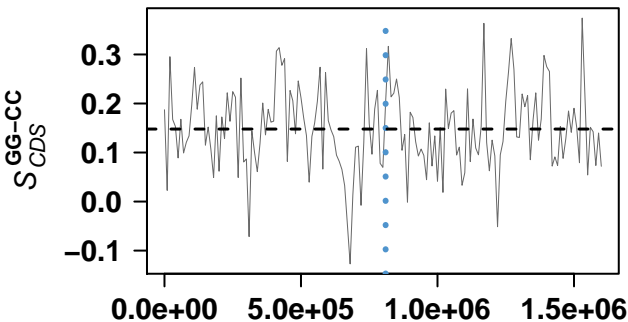
Streptococcus pyogenes MGAS2096



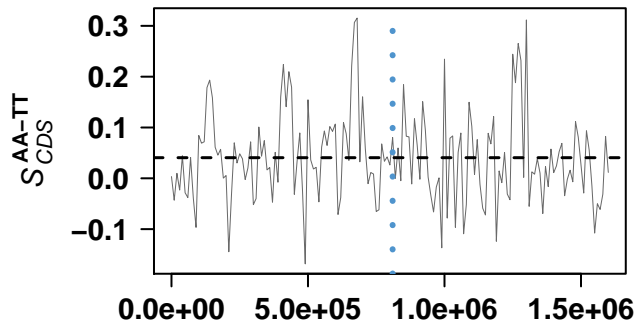
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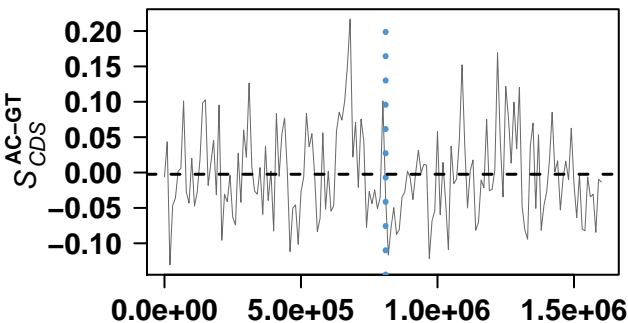
genome coordinates



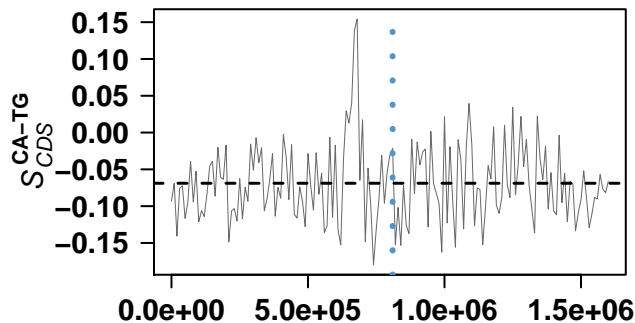
genome coordinates



genome coordinates

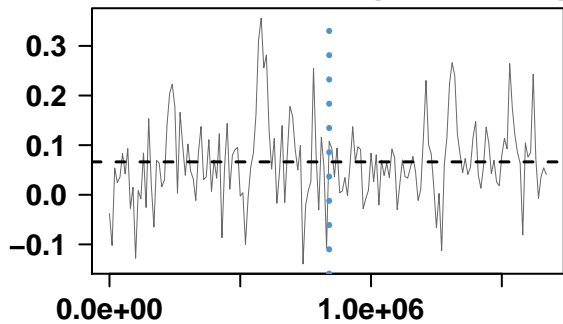


genome coordinates

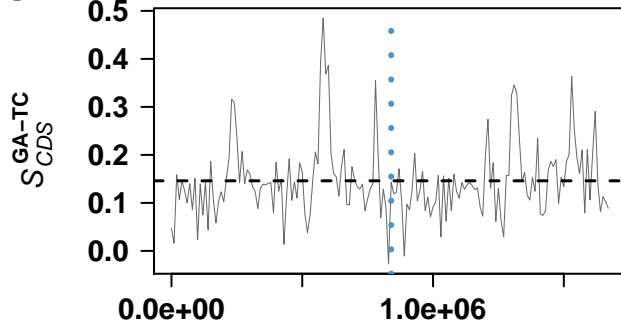


genome coordinates

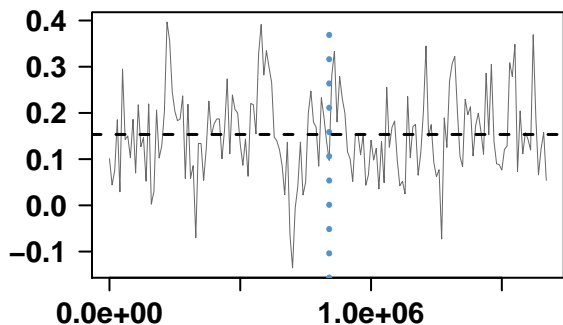
Streptococcus pyogenes MGAS10750



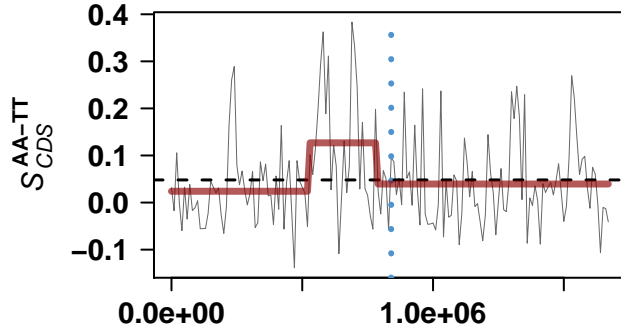
genome coordinates



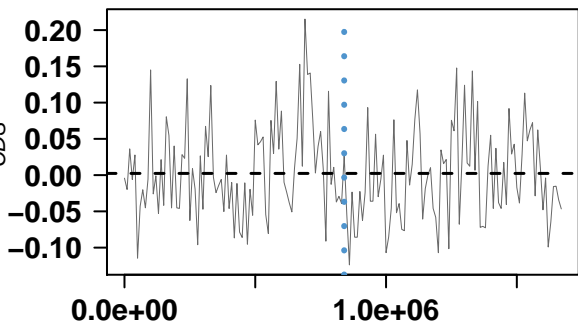
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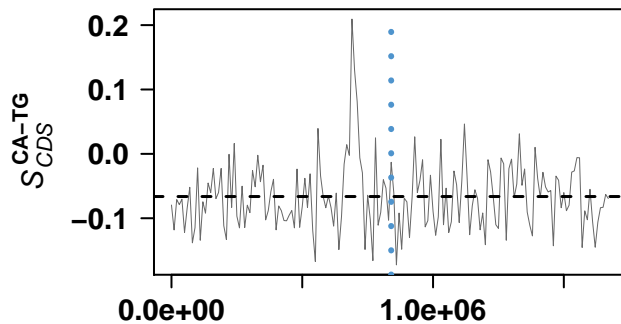
genome coordinates



genome coordinates

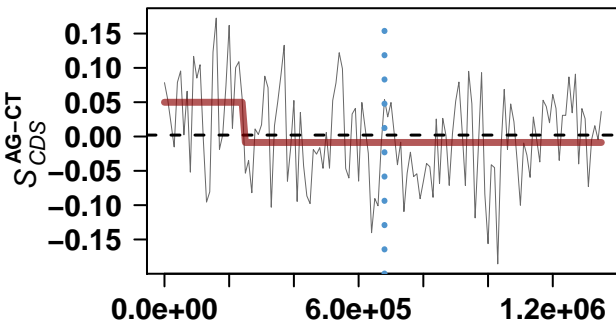


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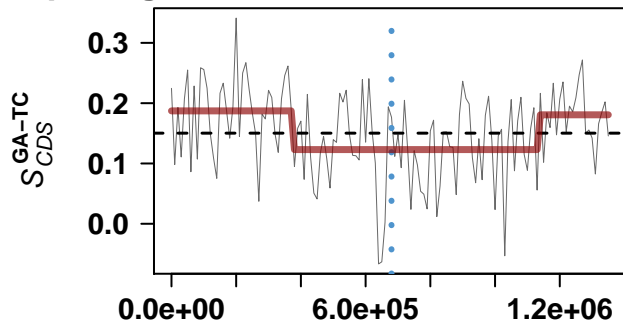


genome coordinates

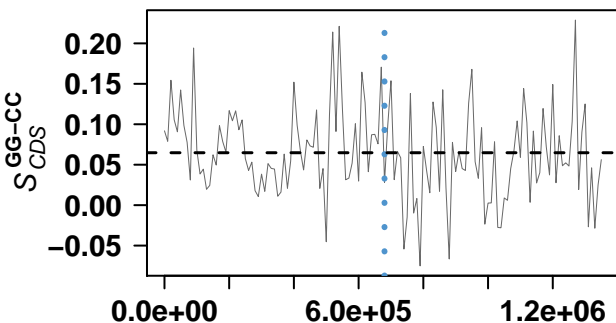
Lactobacillus delbrueckii subsp. bulgaricus ATCC 11842



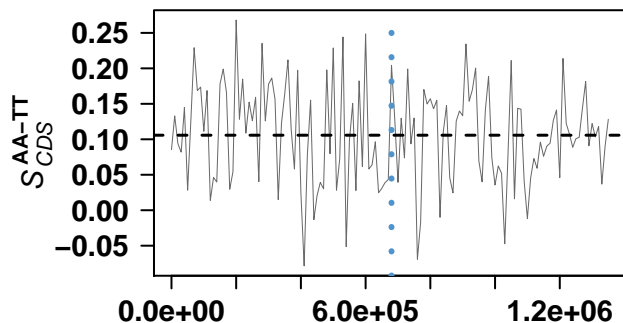
genome coordinates



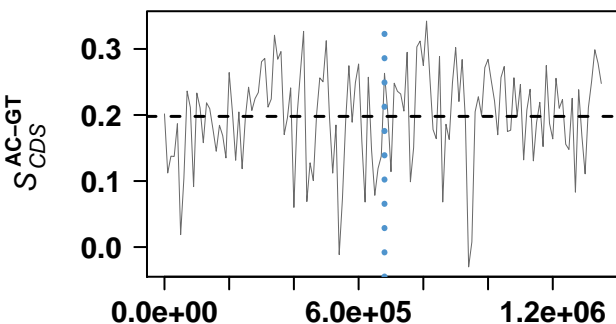
genome coordinates



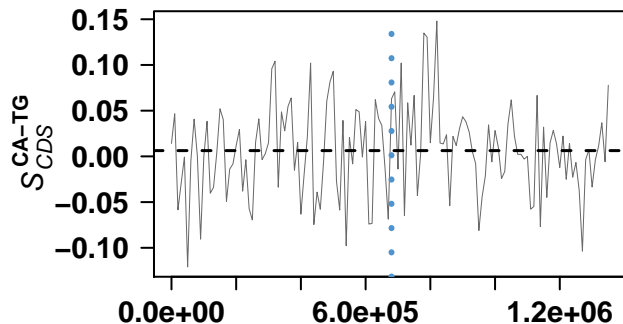
genome coordinates



genome coordinates

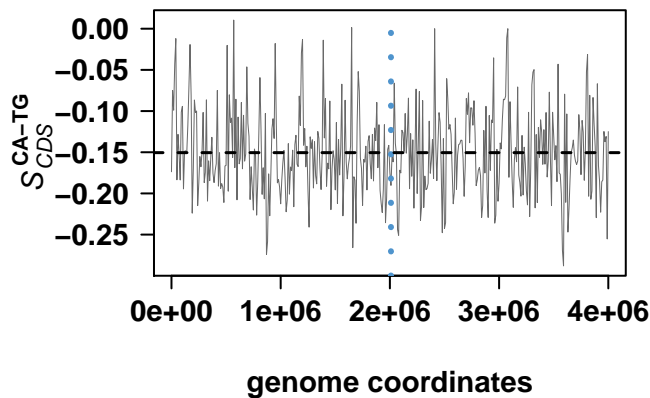
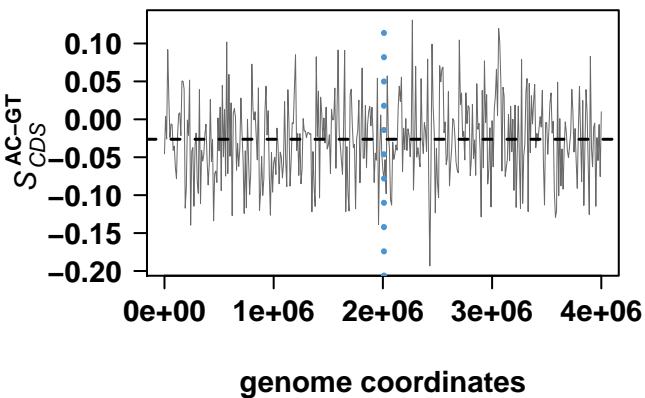
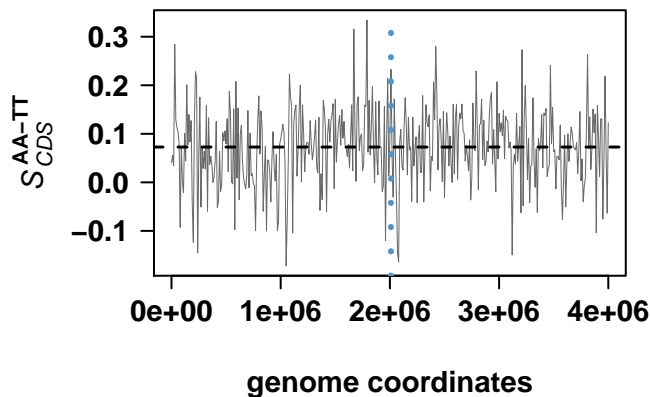
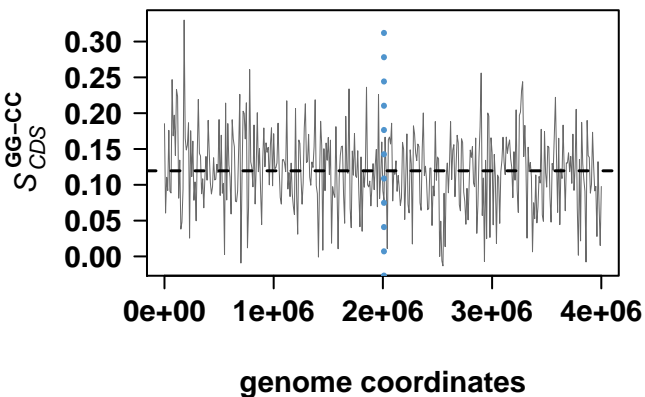
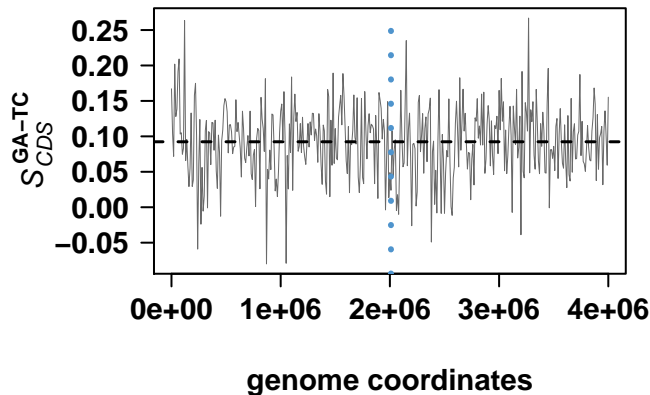
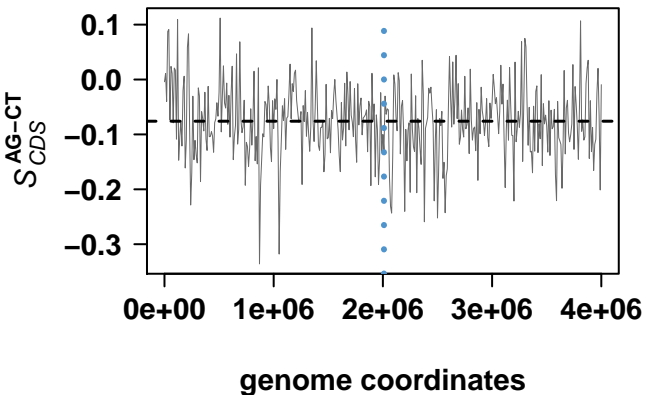


genome coordinates

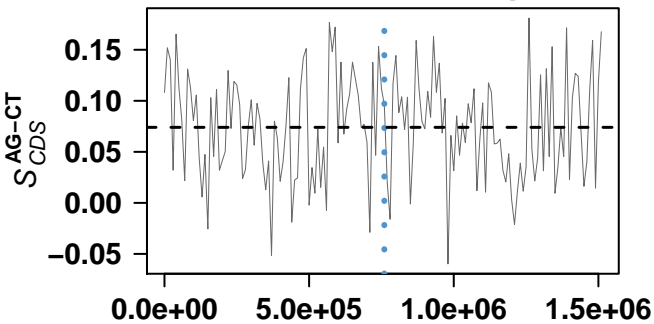


genome coordinates

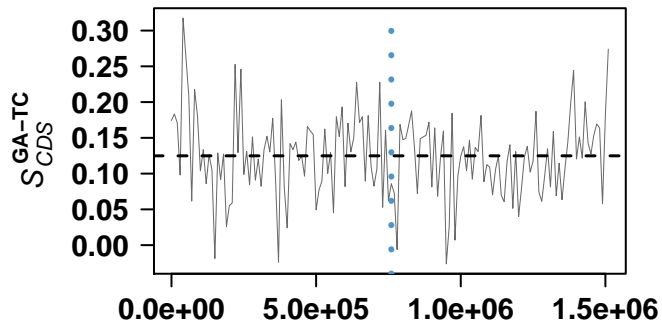
Escherichia coli str. K-12 substr. W3110



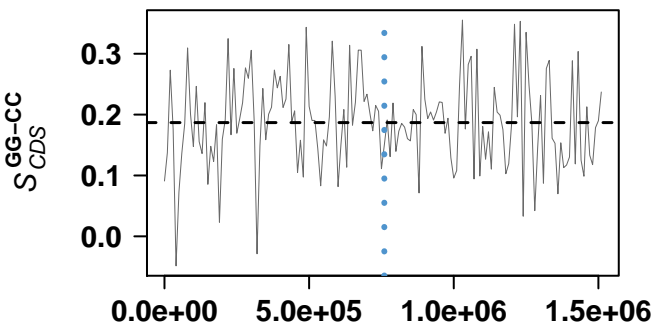
Haemophilus influenzae Rd KW20



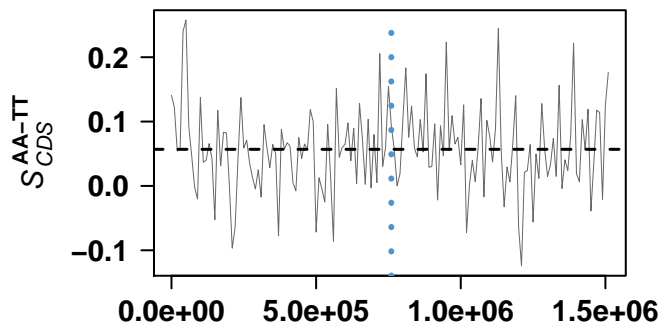
genome coordinates



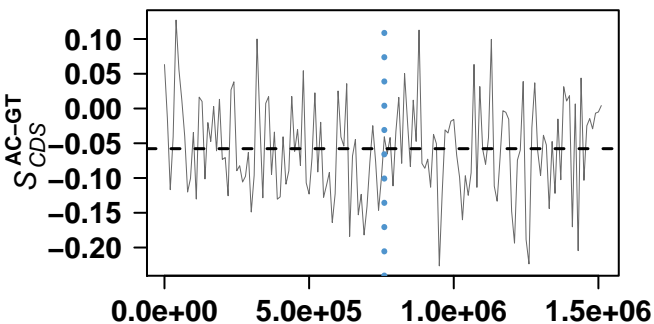
genome coordinates



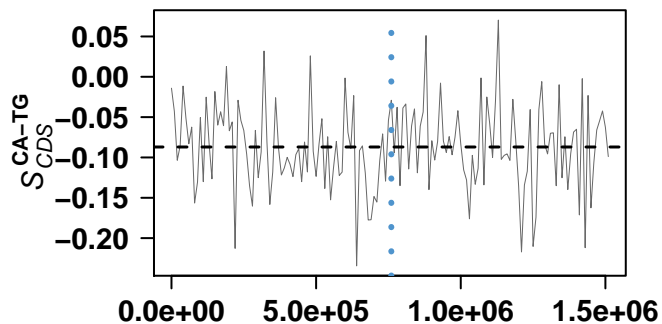
genome coordinates



genome coordinates

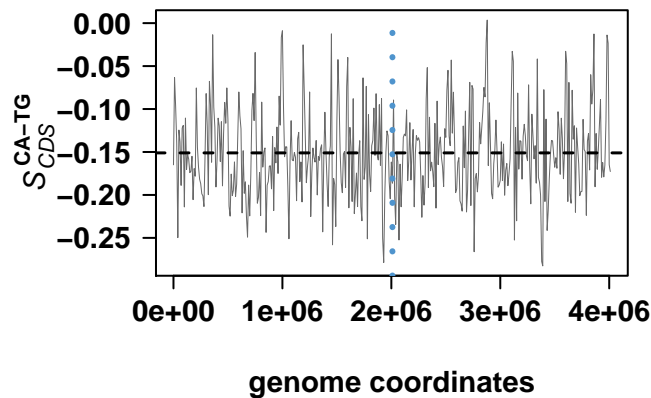
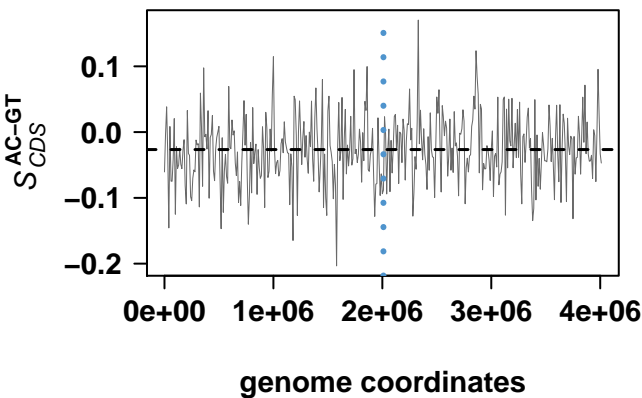
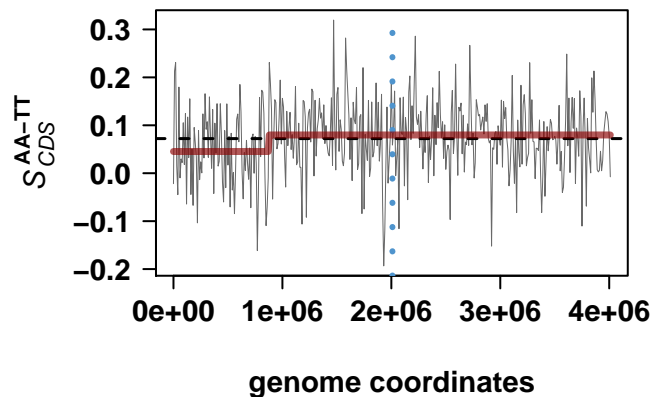
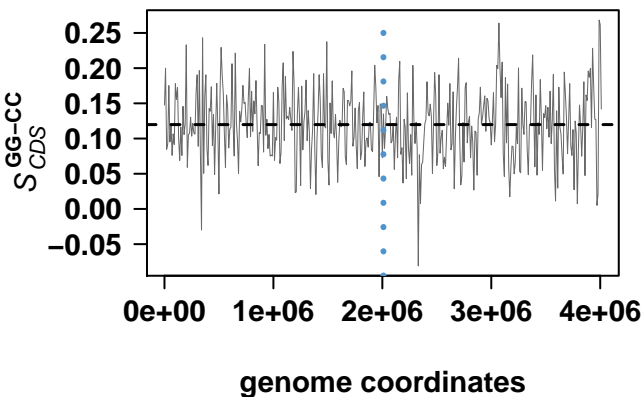
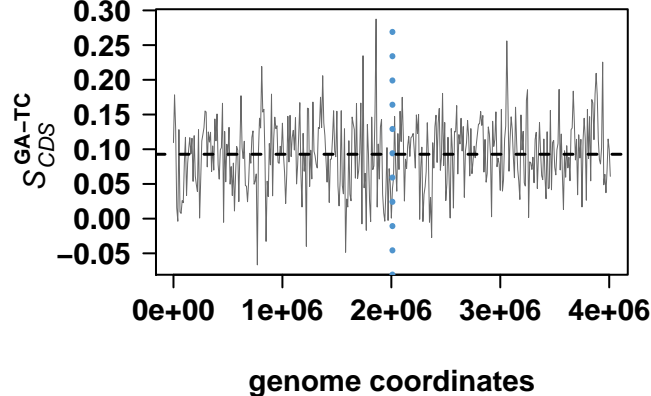
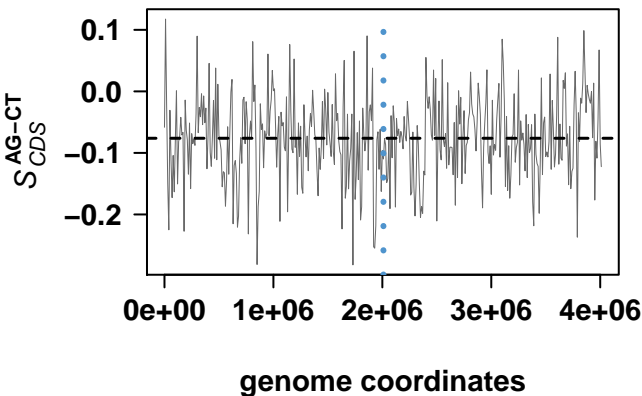


genome coordinates

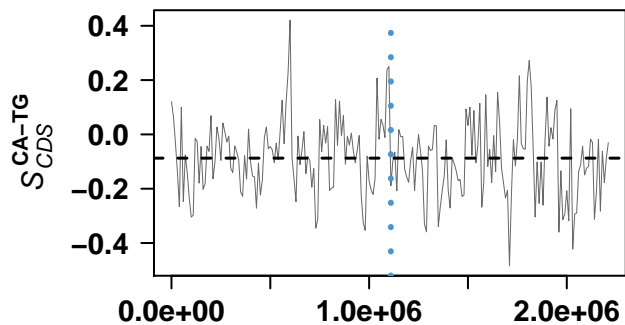
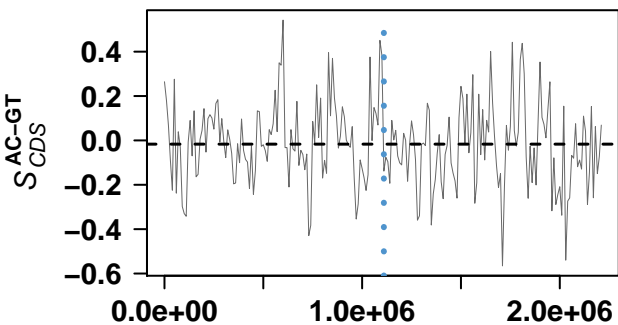
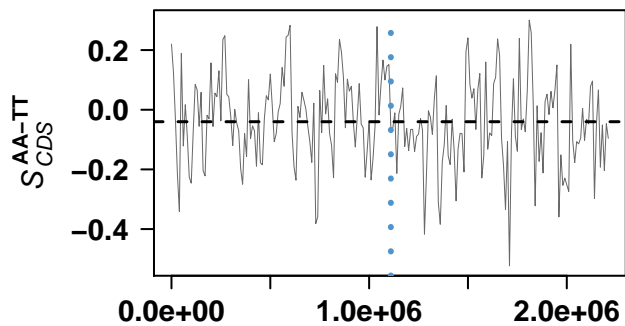
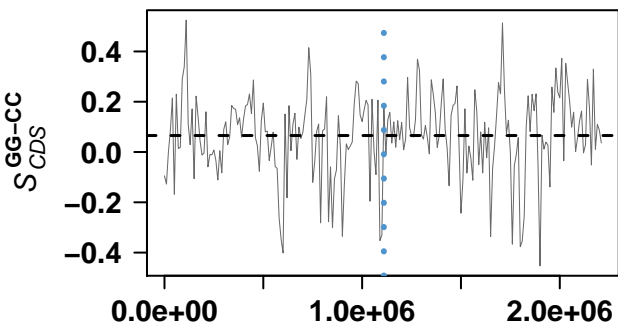
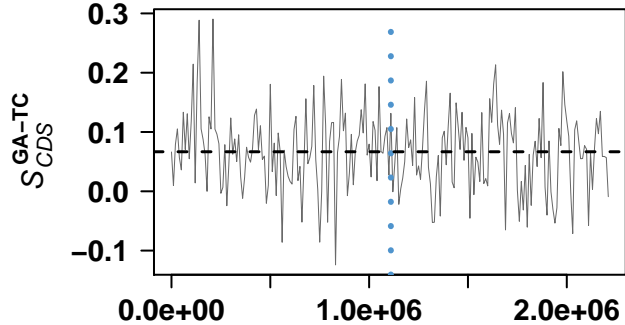
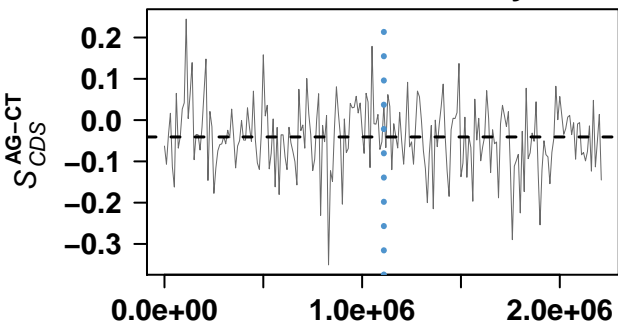


genome coordinates

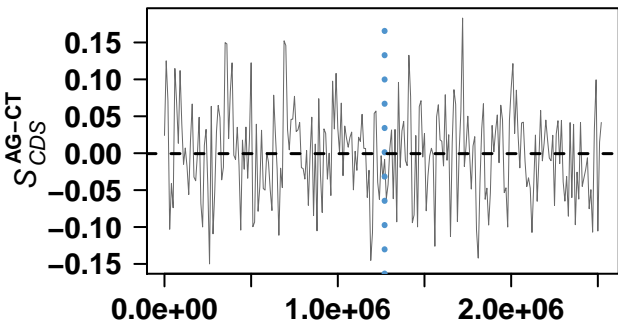
Escherichia coli str. K-12 substr. MG1655



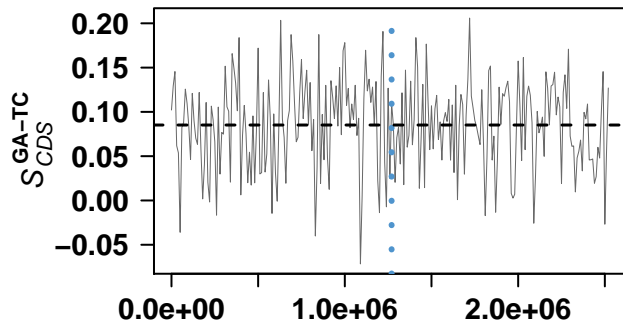
Xylella fastidiosa 9a5c



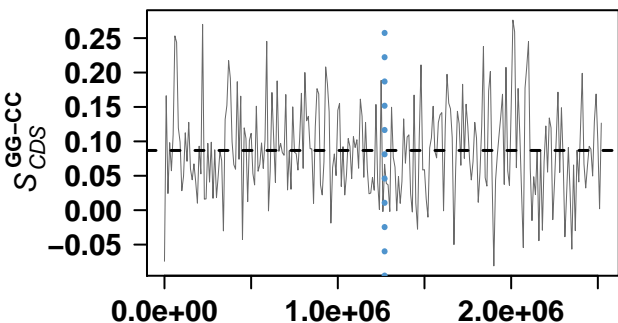
Vibrio cholerae O1 biovar El Tor str. N16961



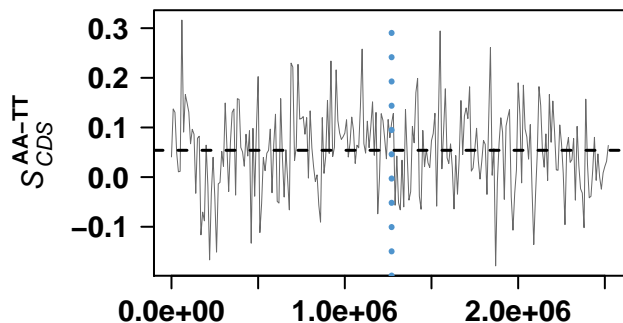
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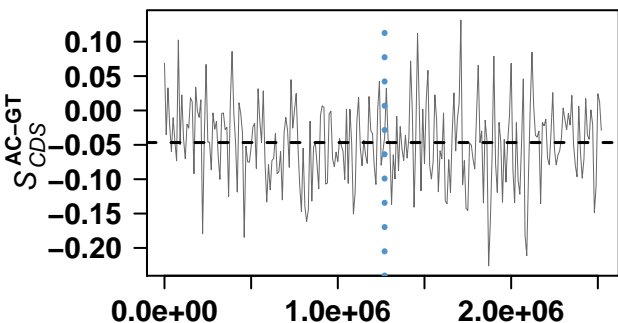
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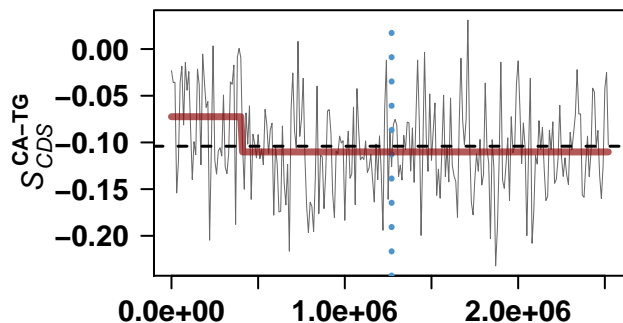
genome coordinates



genome coordinates

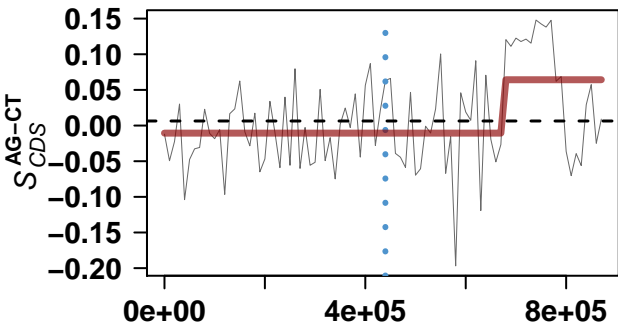


genome coordinates

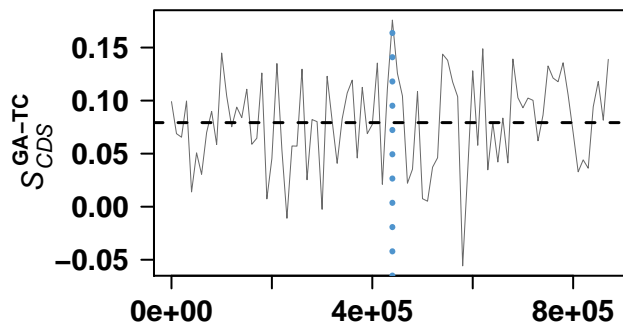


genome coordinates

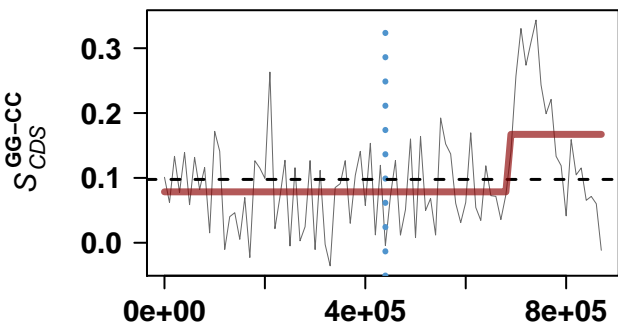
Vibrio cholerae O1 biovar El Tor str. N16961



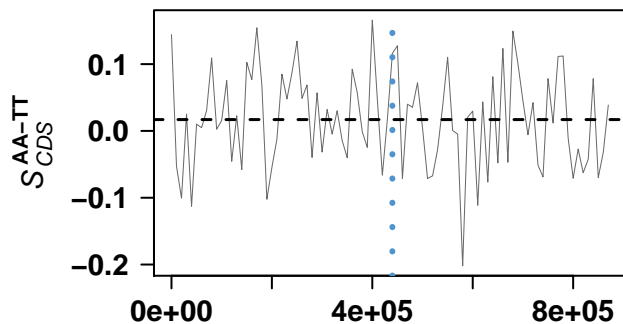
genome coordinates



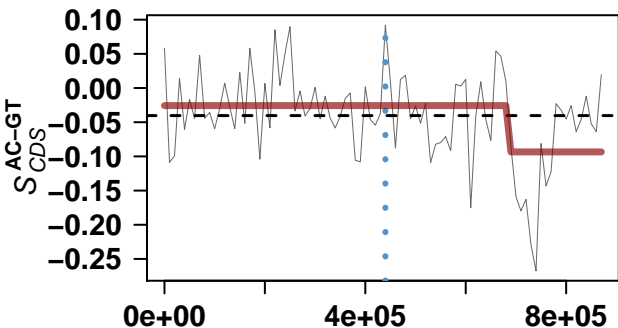
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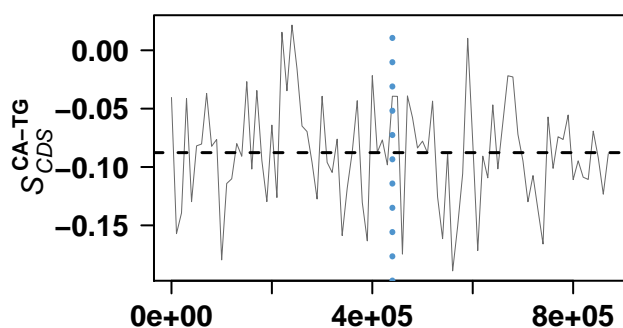
genome coordinates



genome coordinates

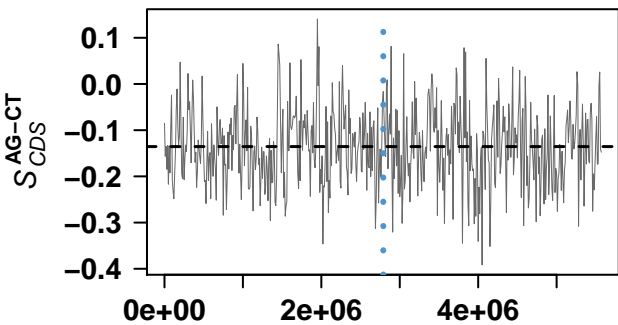


genome coordinates

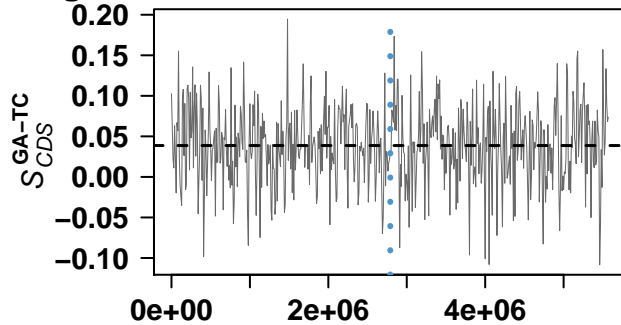


genome coordinates

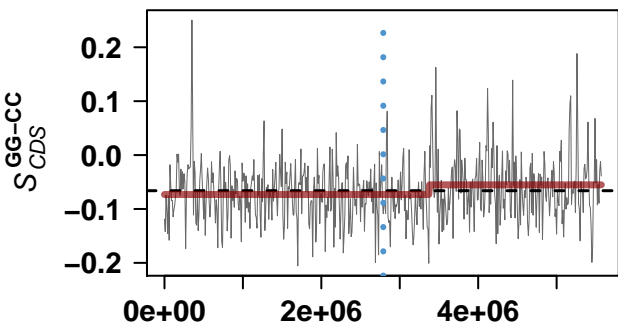
Pseudomonas aeruginosa PAO1



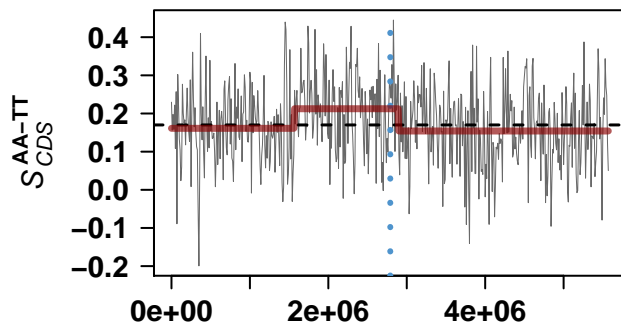
genome coordinates



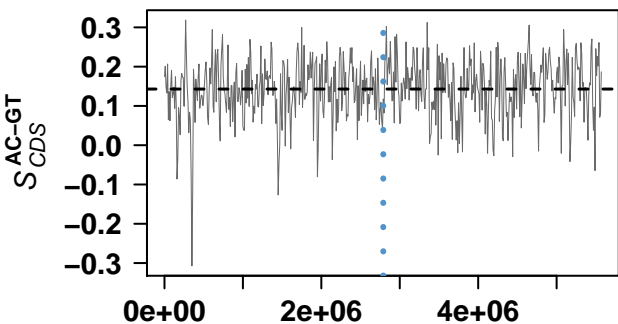
genome coordinates



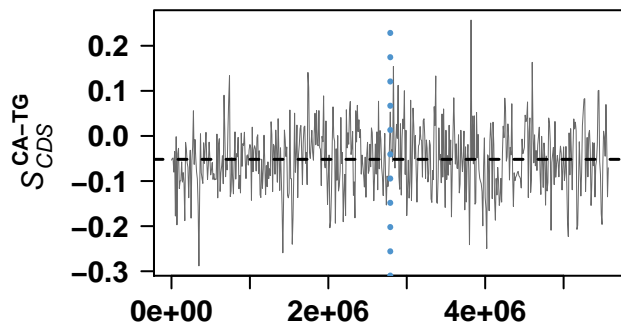
genome coordinates



genome coordinates

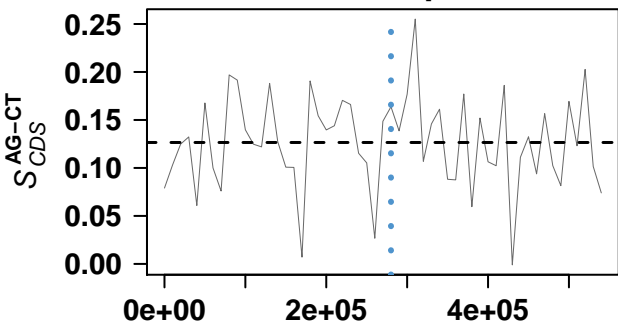


genome coordinates

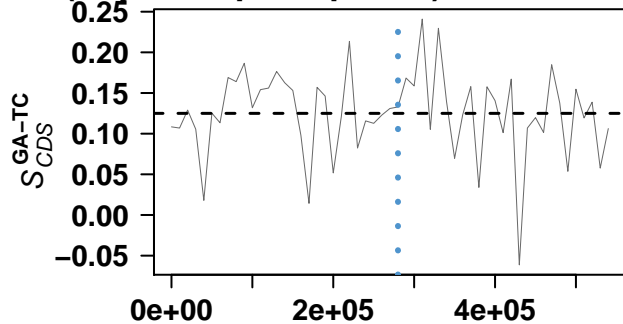


genome coordinates

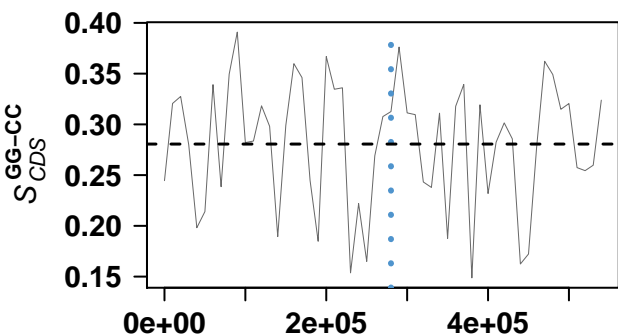
Buchnera aphidicola str. APS (Acyrtosiphon pisum)



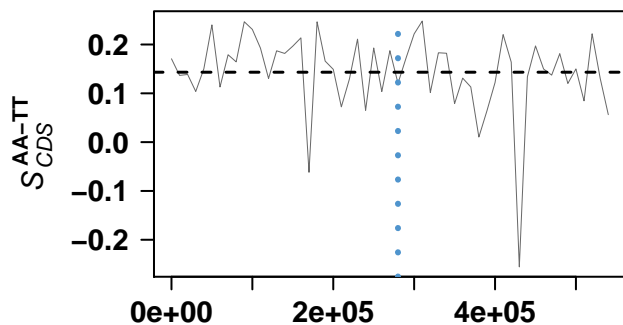
genome coordinates



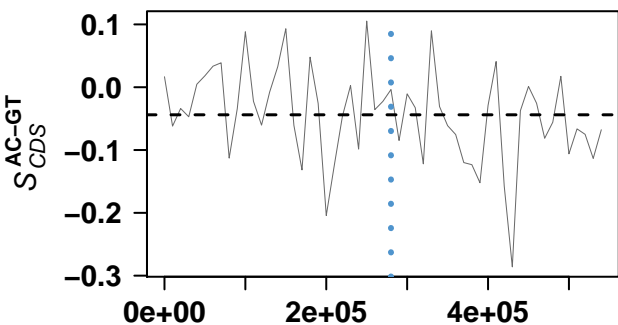
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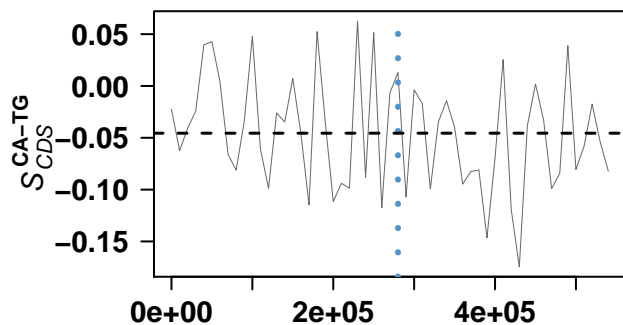
genome coordinates



genome coordinates

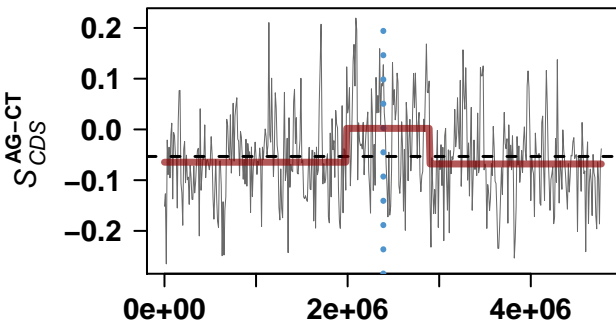


genome coordinates

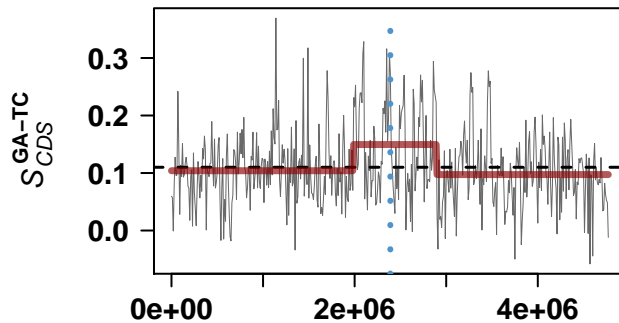


genome coordinates

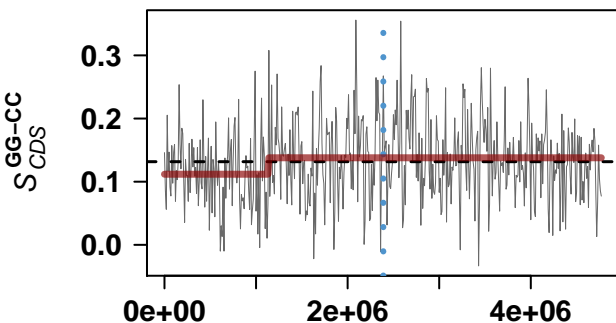
Escherichia coli O157:H7 str. EDL933



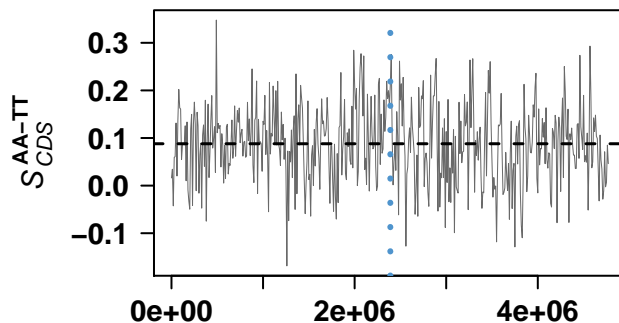
genome coordinates



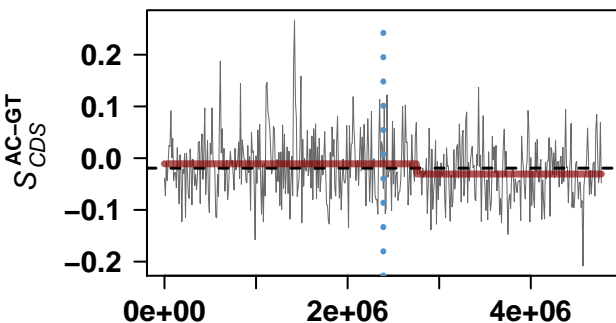
genome coordinates



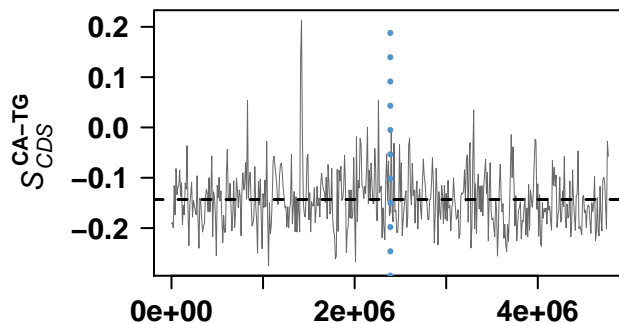
genome coordinates



genome coordinates

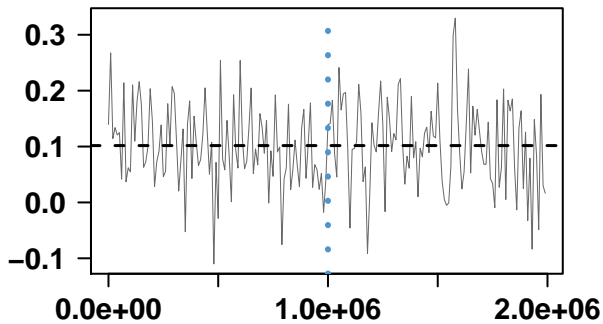


genome coordinates

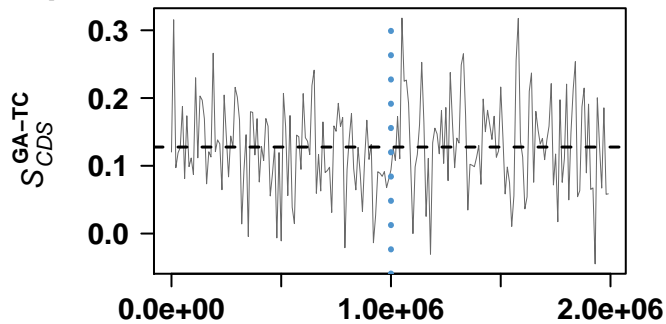


genome coordinates

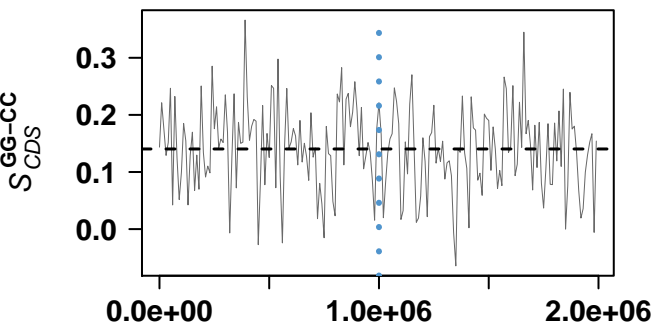
Pasteurella multocida subsp. multocida str. Pm70



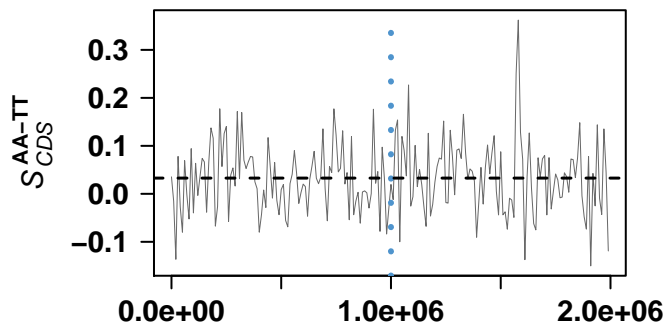
genome coordinates



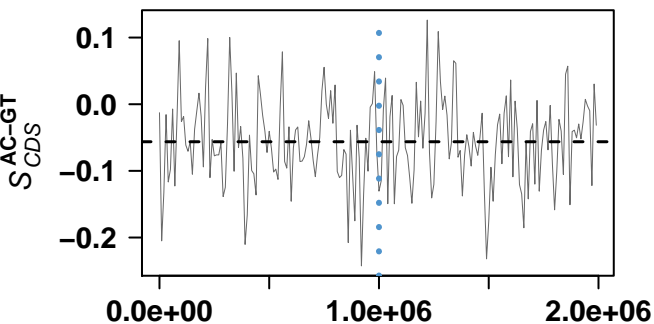
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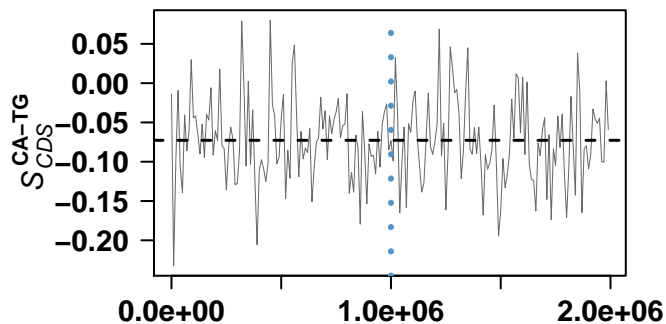
genome coordinates



genome coordinates

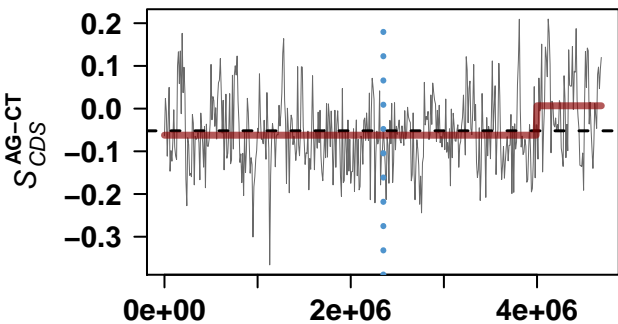


genome coordinates

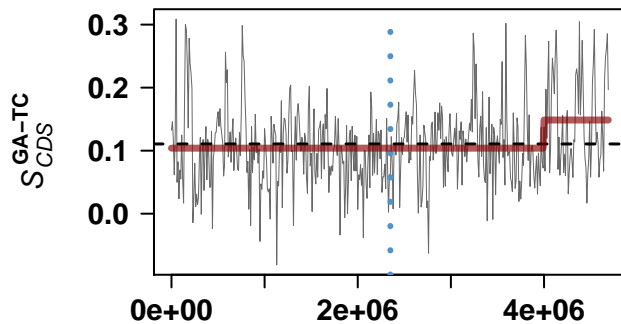


genome coordinates

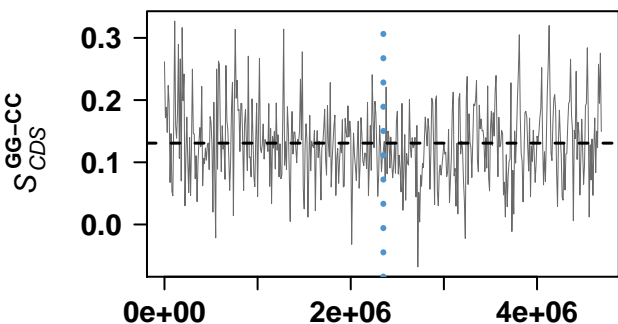
Escherichia coli O157:H7 str. Sakai



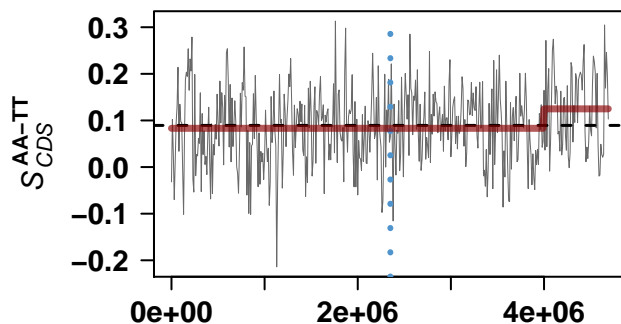
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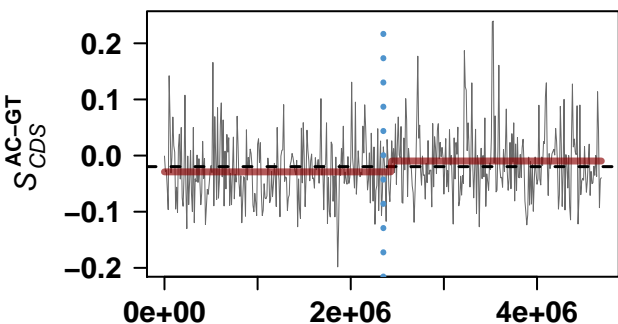
genome coordinates



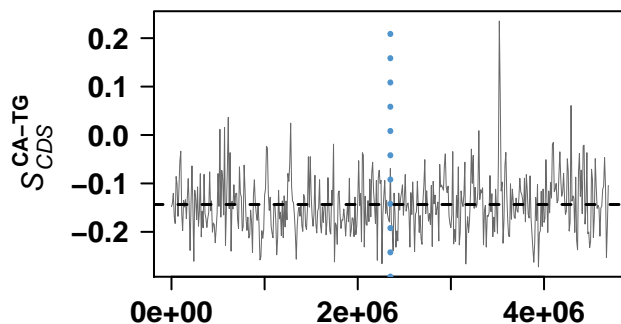
genome coordinates



genome coordinates

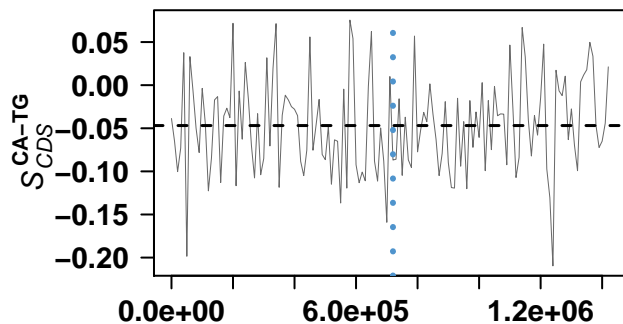
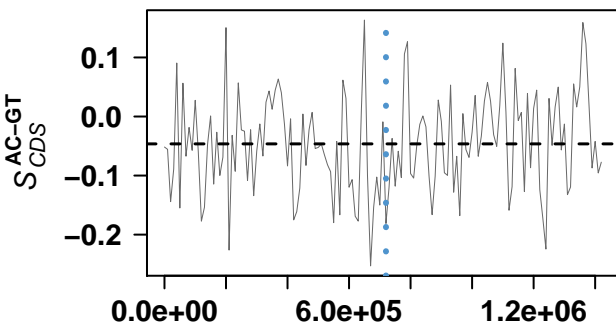
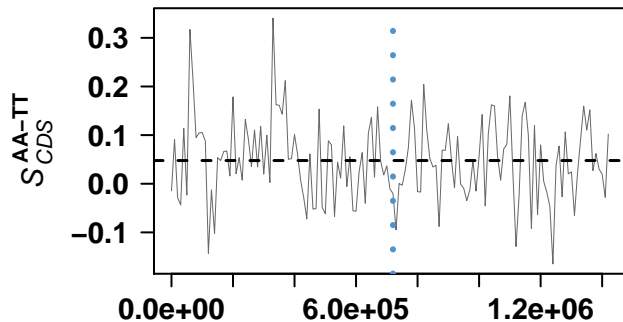
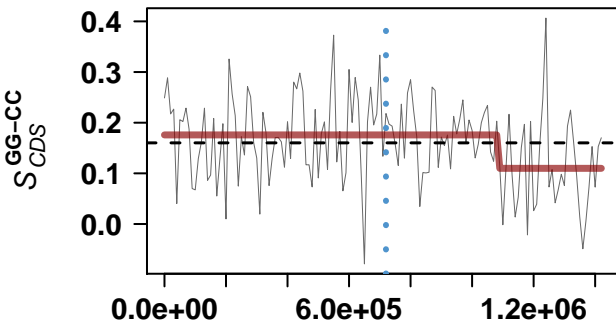
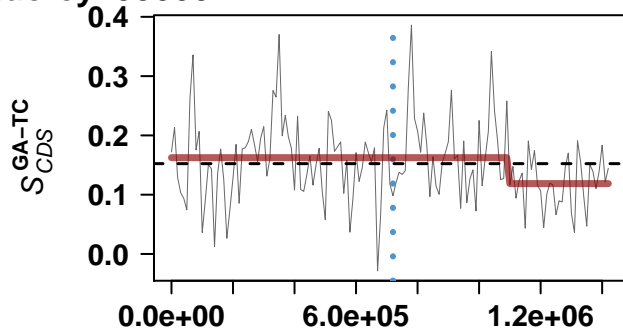
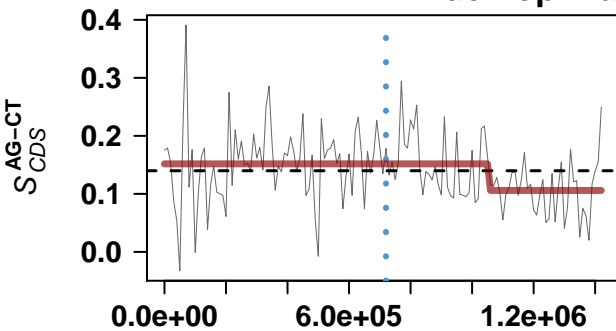


genome coordinates

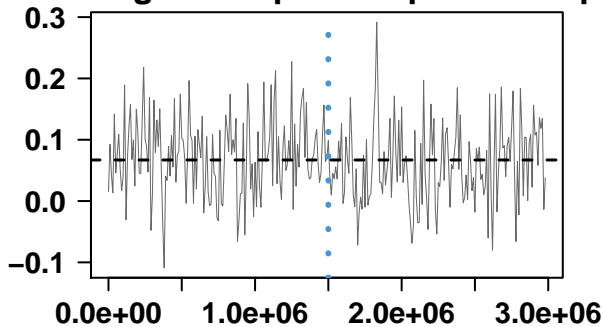


genome coordinates

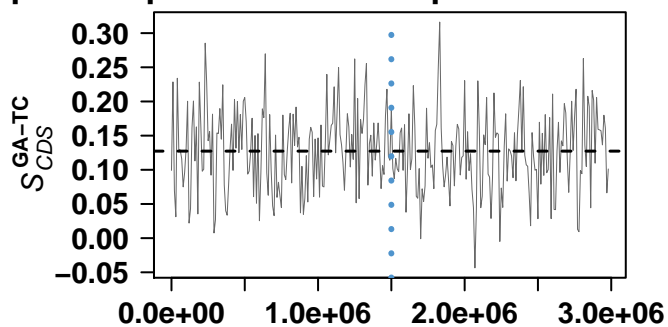
Haemophilus ducreyi 35000HP



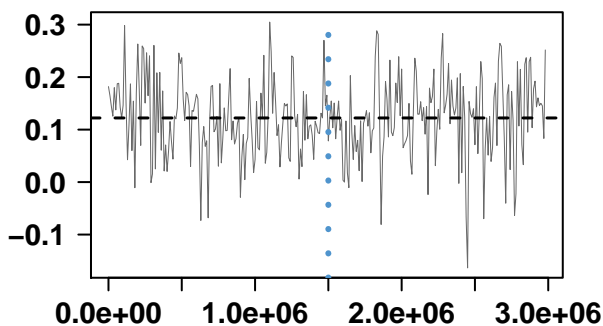
Legionella pneumophila subsp. pneumophila str. Philadelphia 1



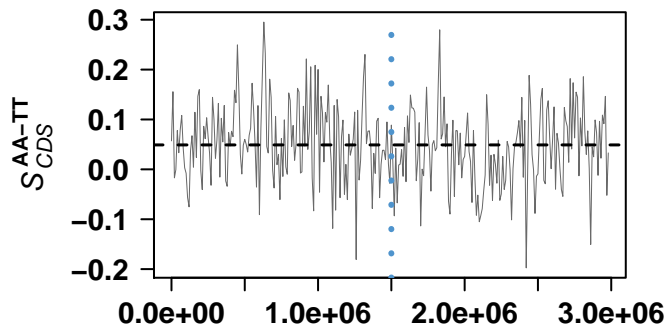
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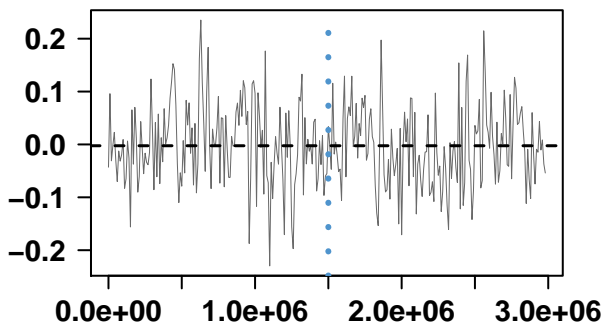
genome coordinates



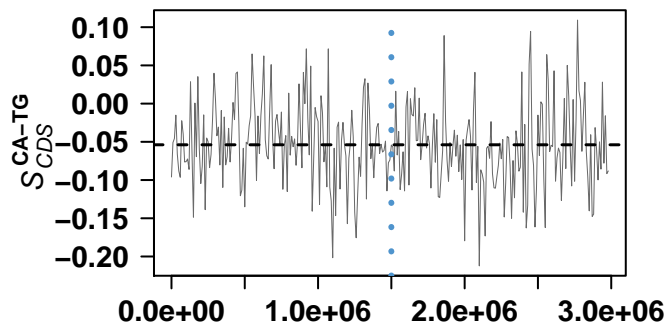
genome coordinates



genome coordinates

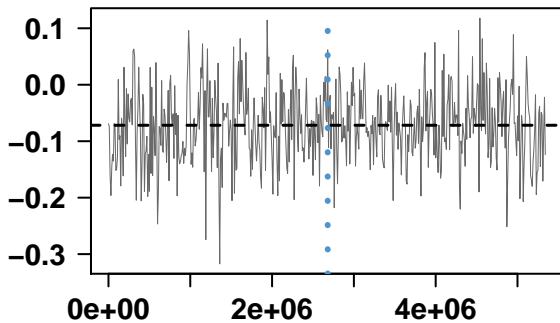


genome coordinates

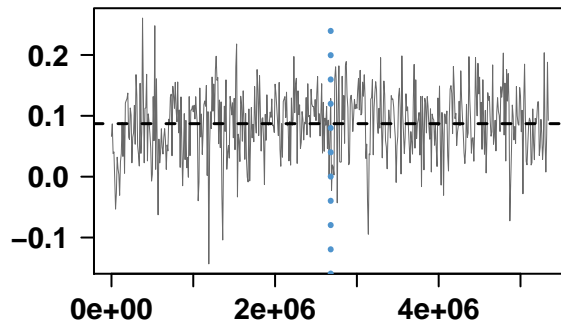


genome coordinates

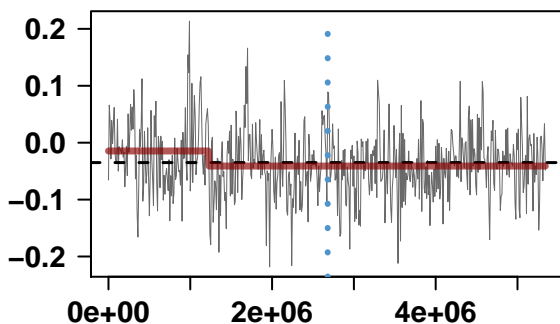
Pseudomonas putida KT2440



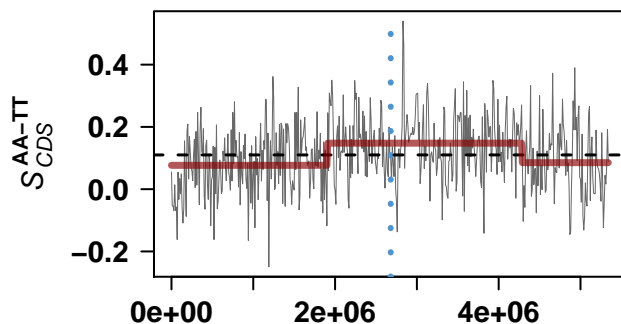
genome coordinates



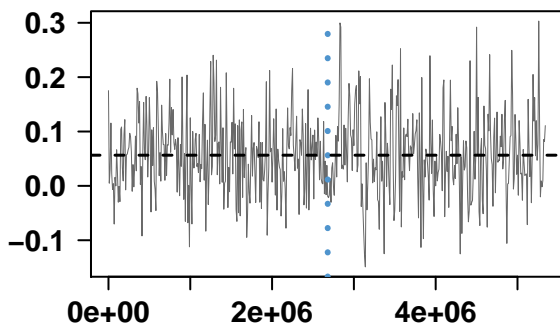
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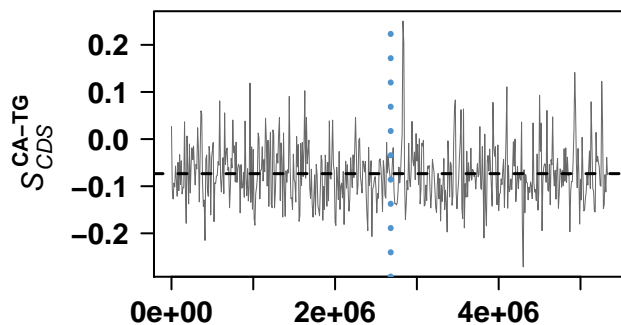
genome coordinates



genome coordinates

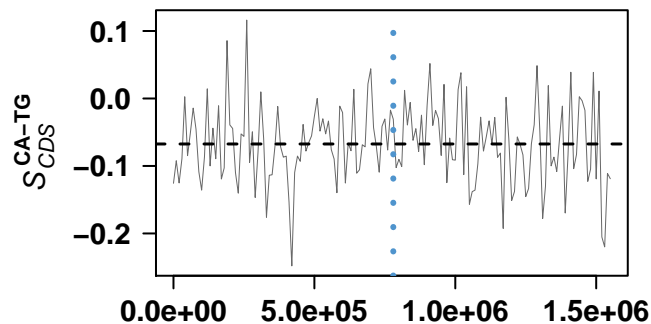
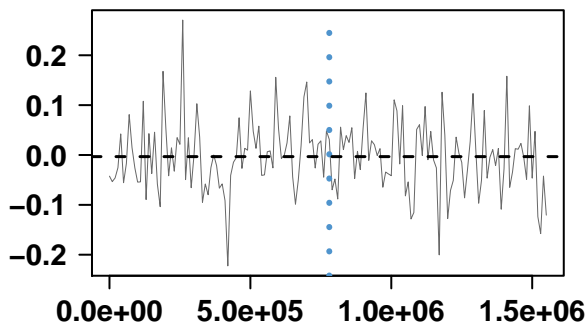
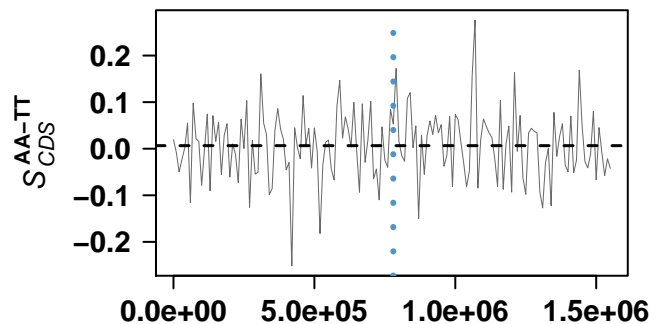
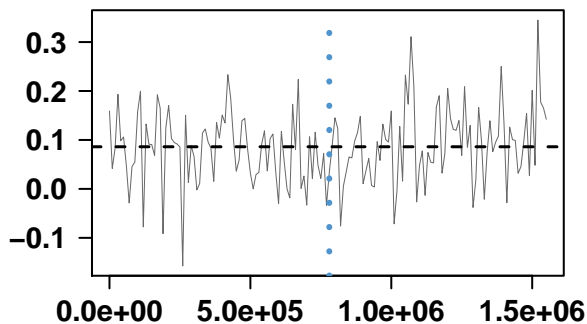
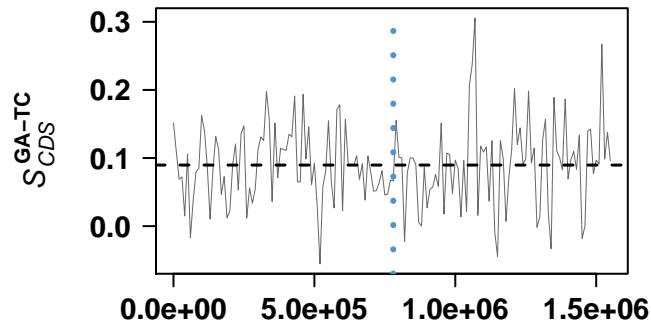
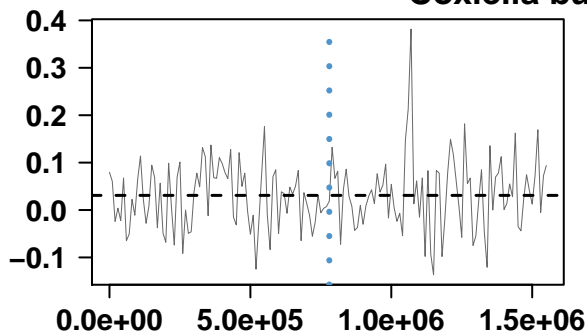


genome coordinates

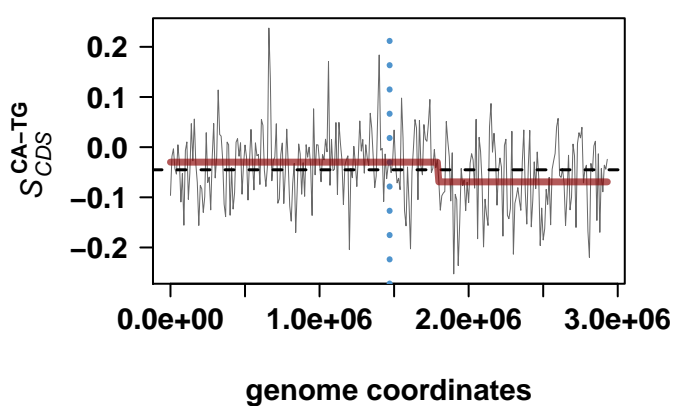
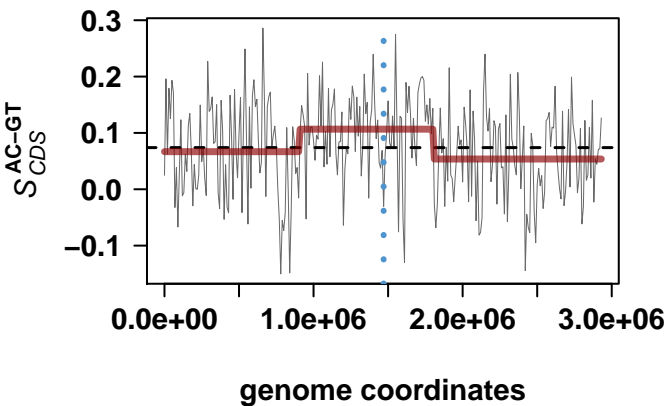
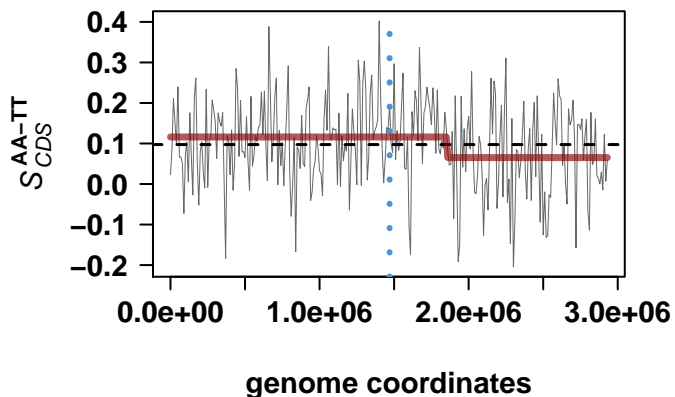
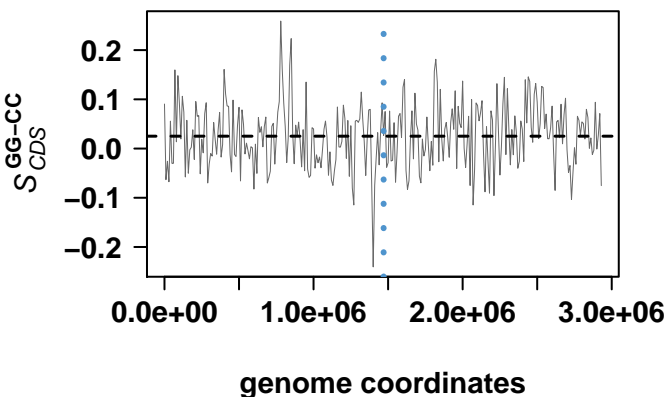
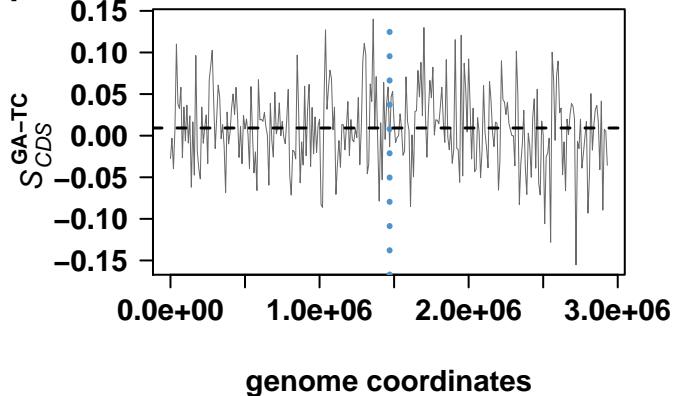
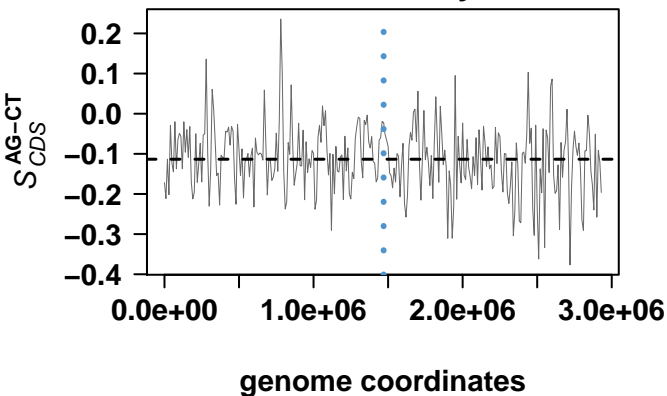


genome coordinates

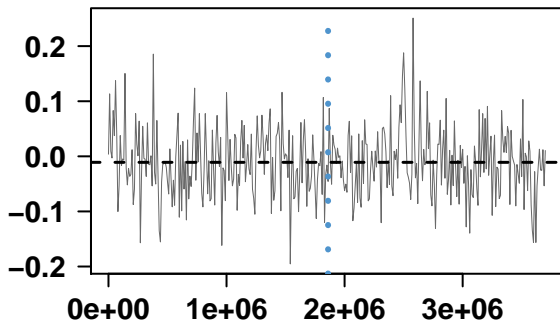
Coxiella burnetii RSA 493



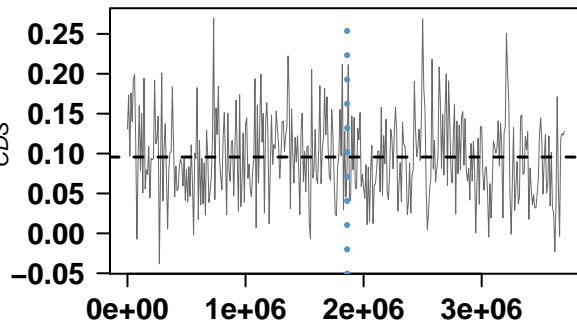
Methylococcus capsulatus str. Bath



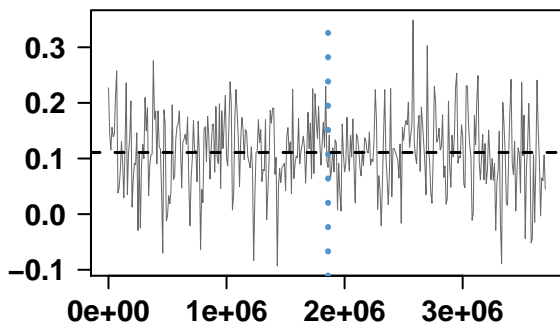
Yersinia pestis CO92



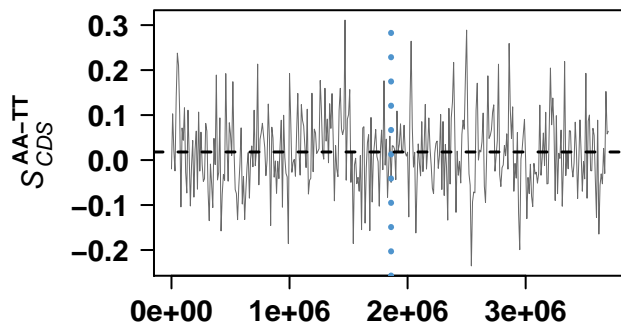
genome coordinates



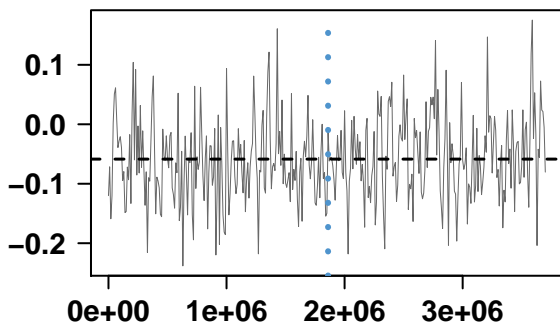
genome coordinates



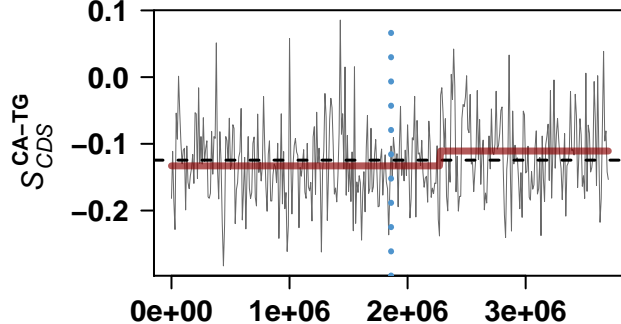
genome coordinates



genome coordinates

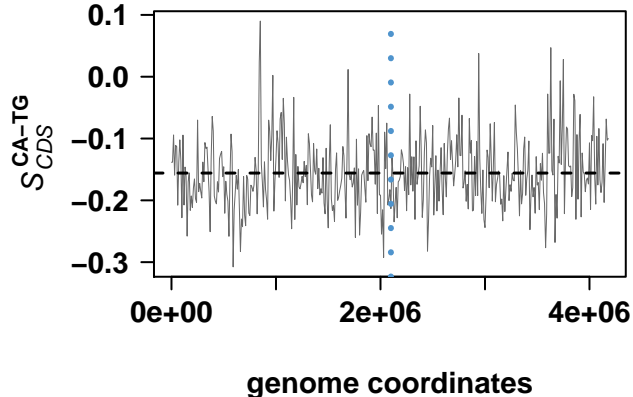
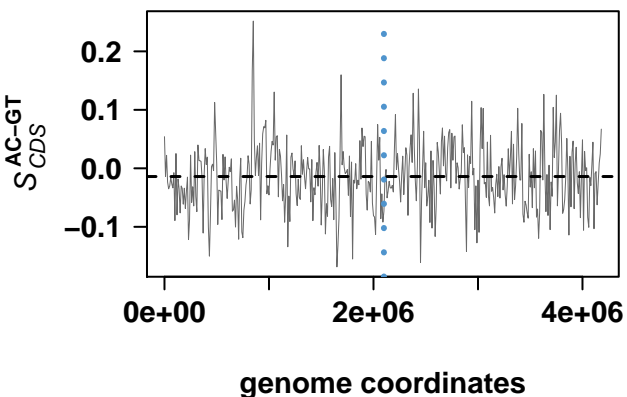
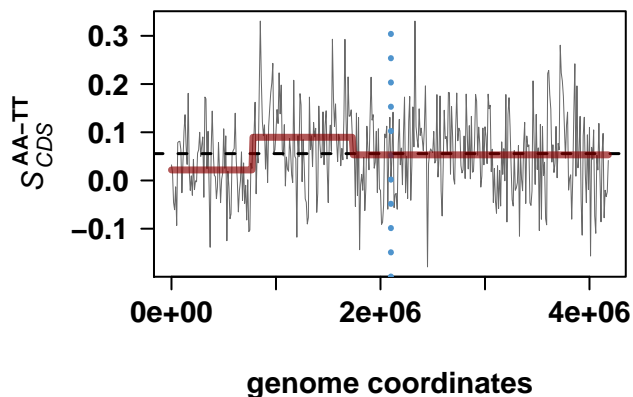
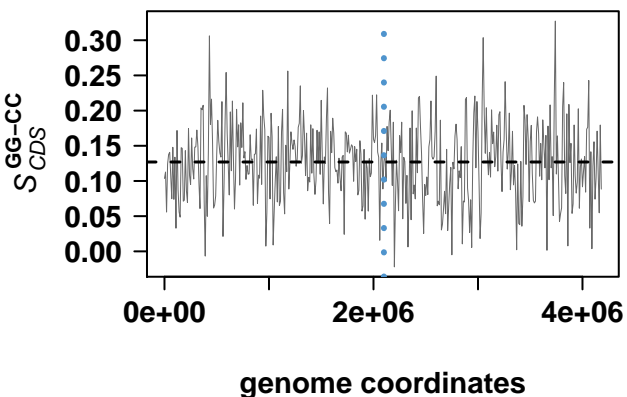
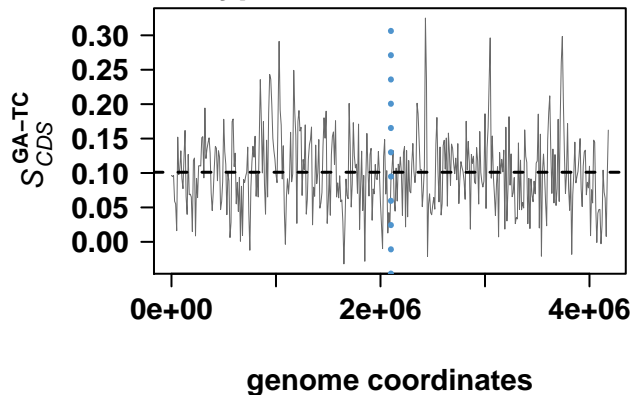
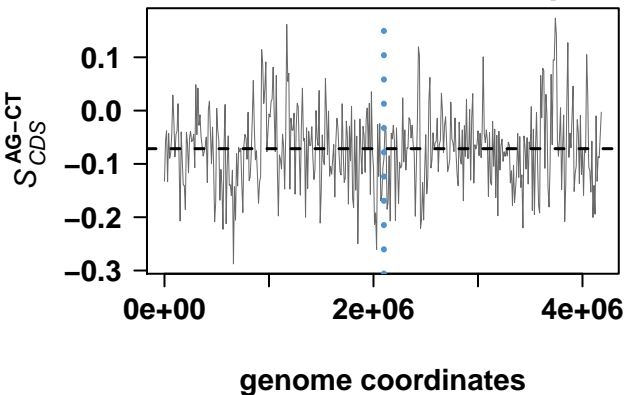


genome coordinates

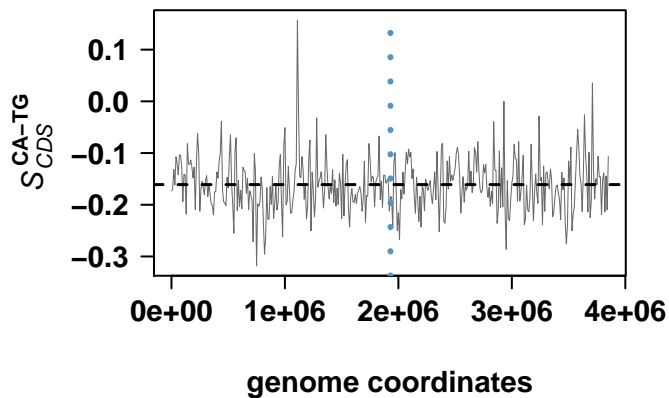
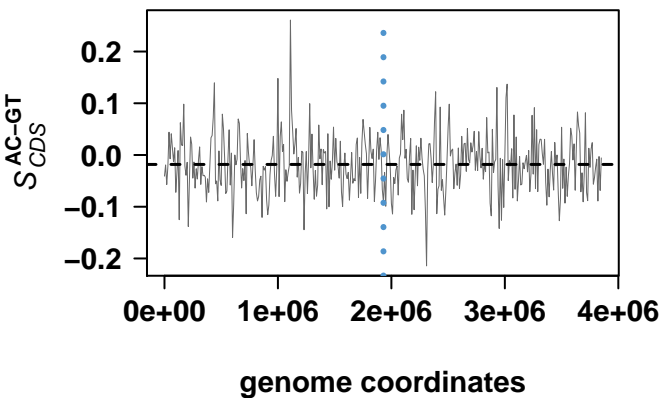
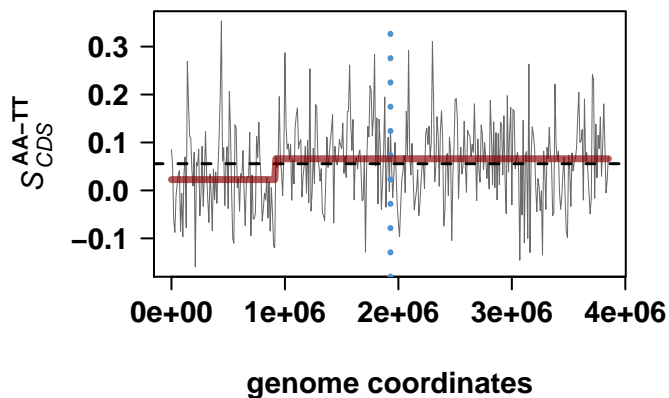
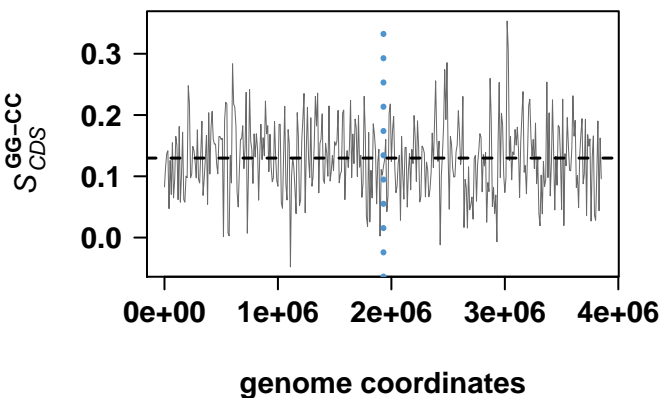
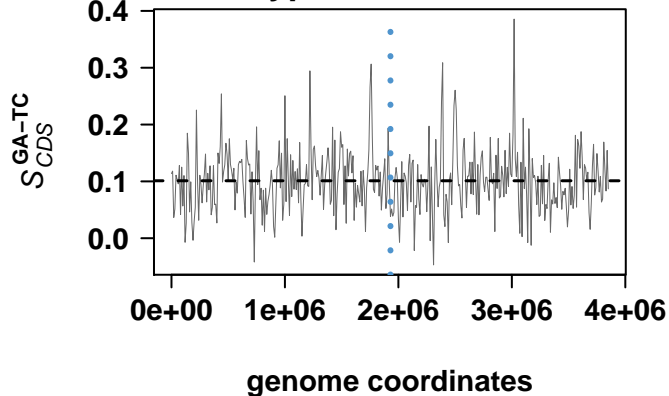
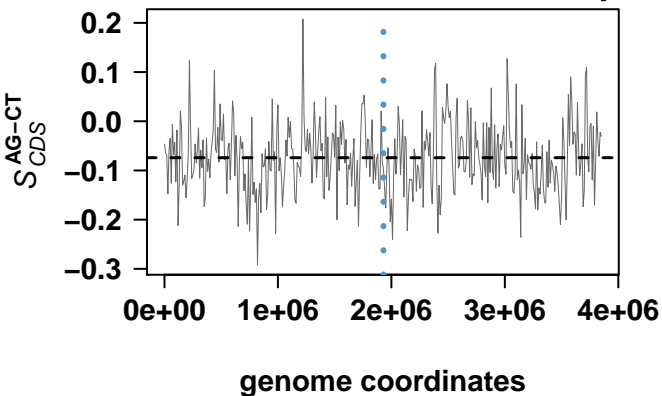


genome coordinates

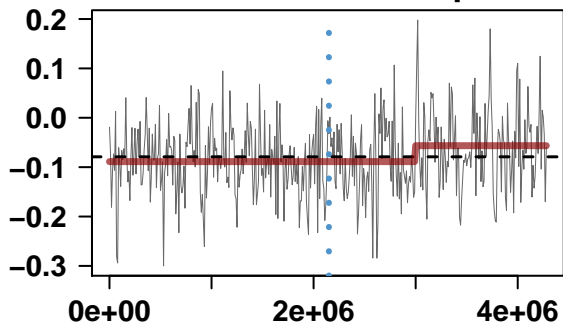
Salmonella enterica subsp. enterica serovar Typhimurium str. LT2



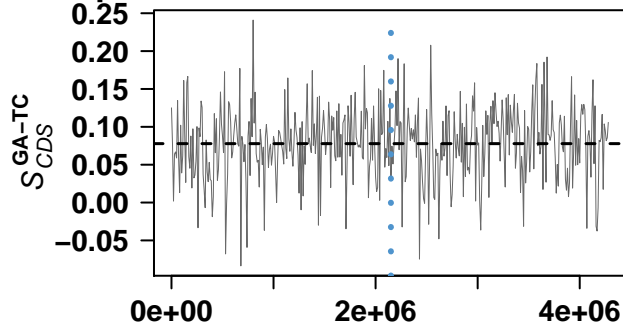
Salmonella enterica subsp. enterica serovar Typhi str. CT18



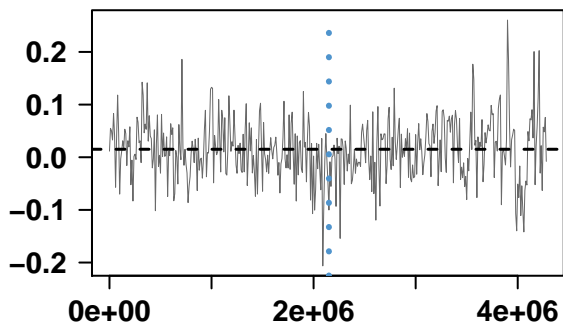
Xanthomonas campestris pv. *campestris* str. ATCC 33913



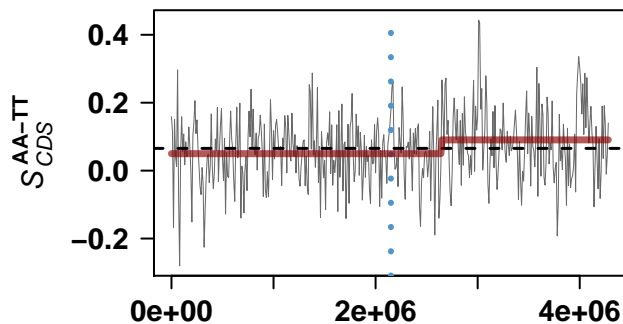
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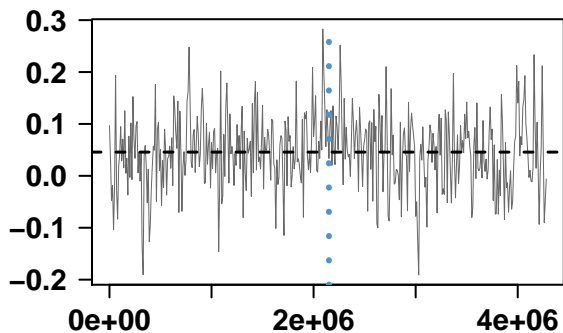
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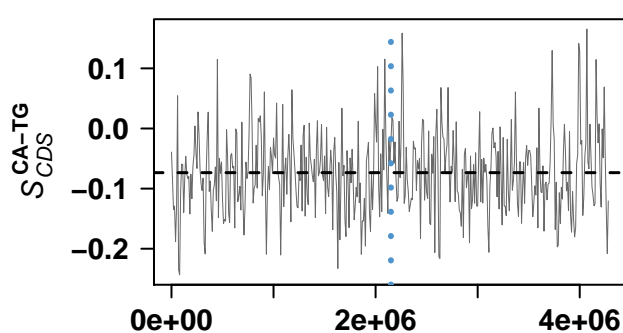
genome coordinates



genome coordinates

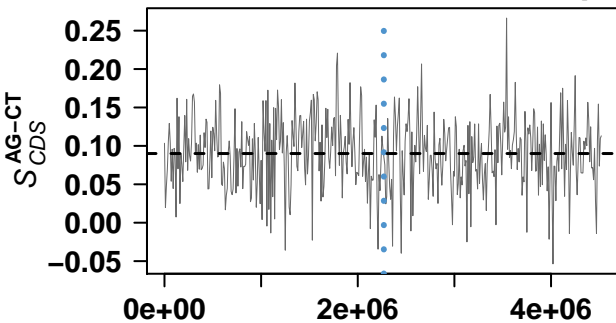


genome coordinates

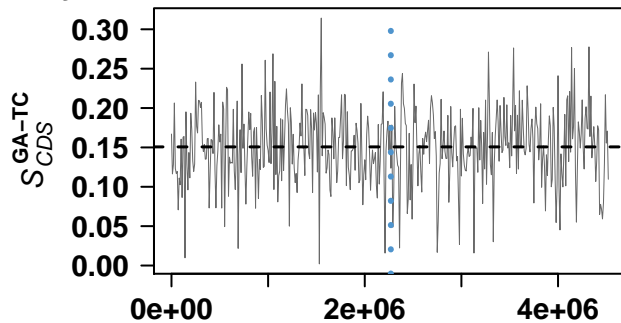


genome coordinates

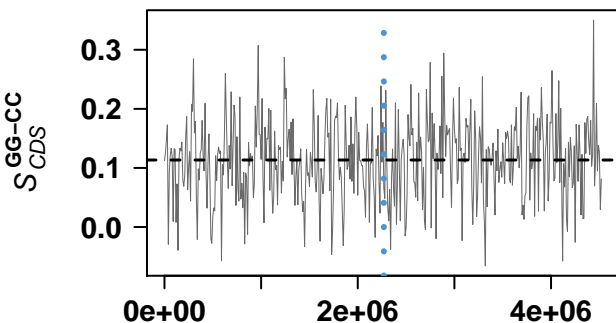
Colwellia psychrerythraea 34H



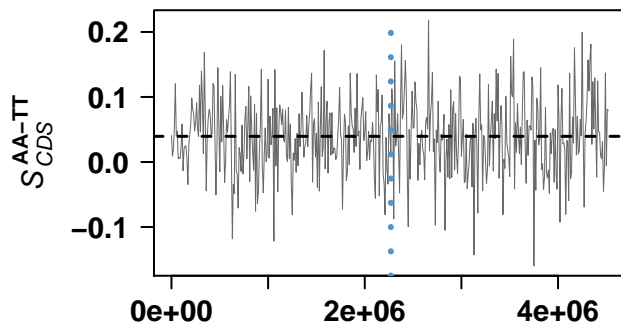
genome coordinates



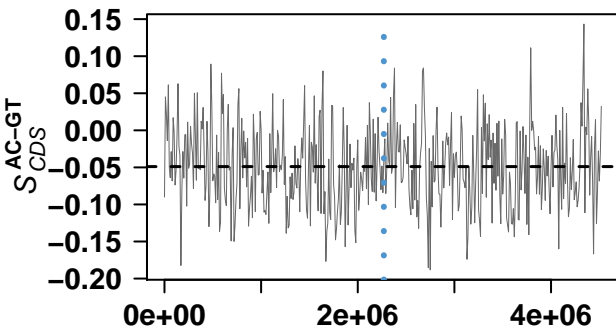
genome coordinates



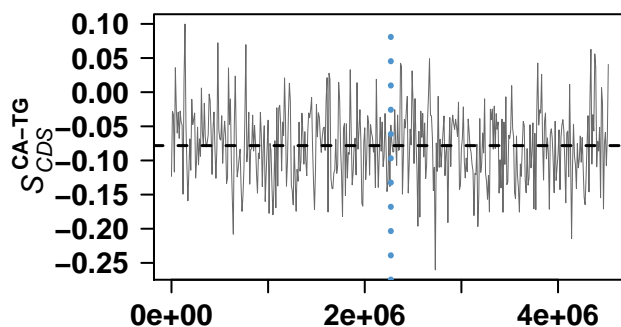
genome coordinates



genome coordinates

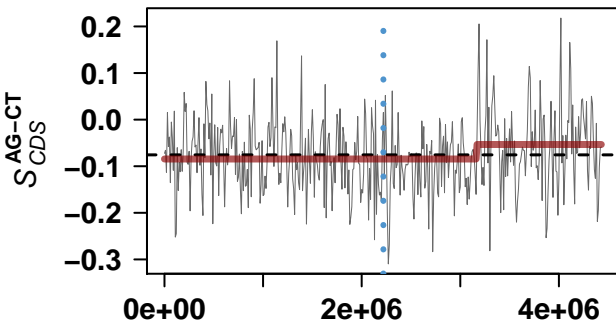


genome coordinates

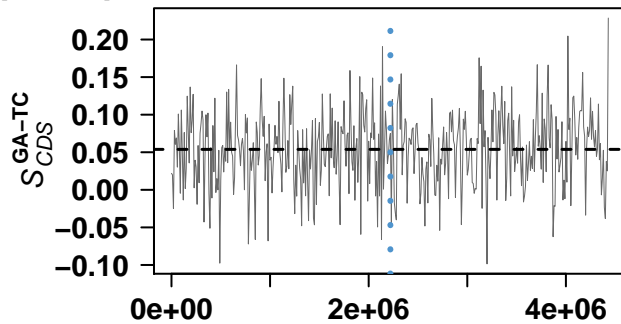


genome coordinates

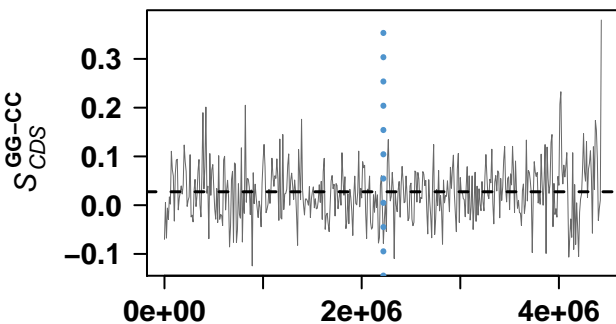
Xanthomonas axonopodis pv. citri str. 306



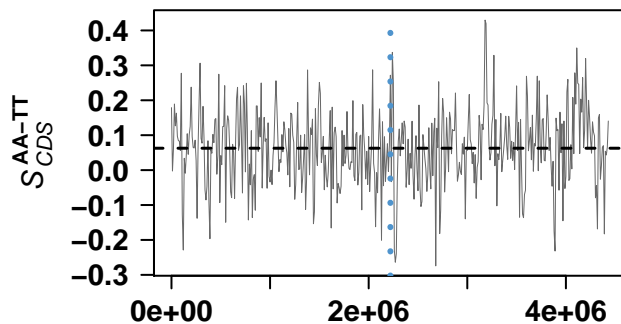
genome coordinates



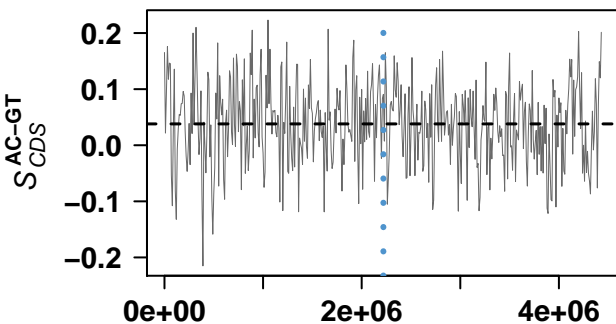
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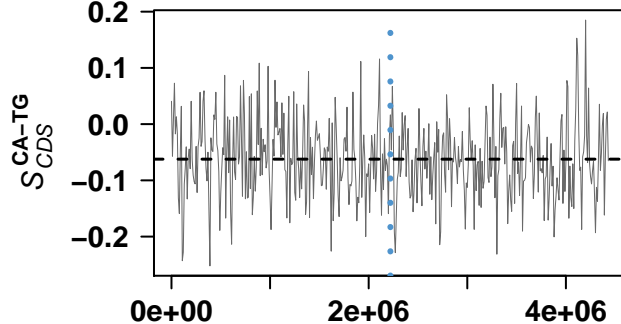
genome coordinates



genome coordinates

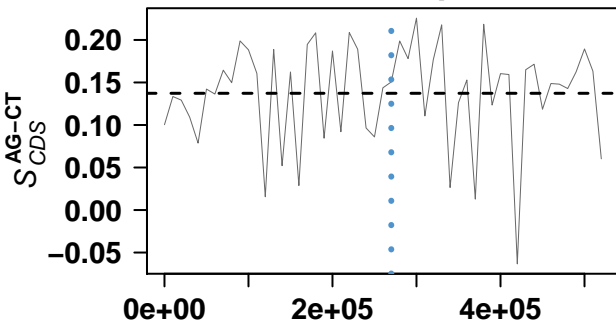


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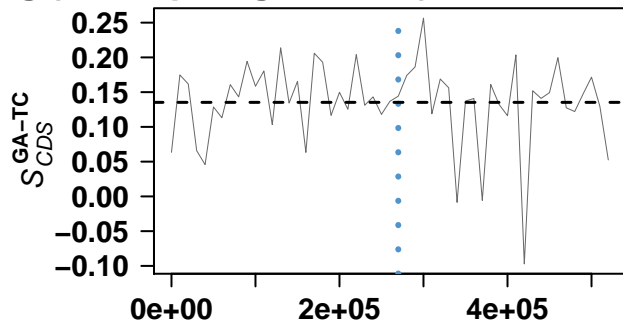


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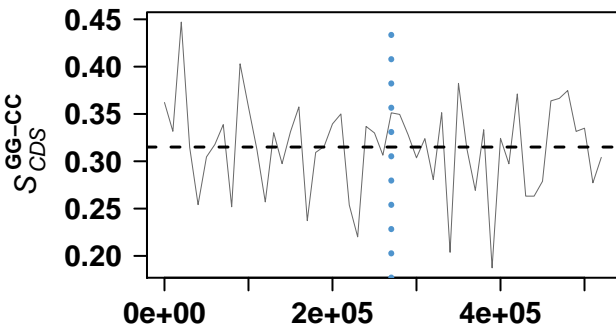
Buchnera aphidicola str. Sg (Schizaphis graminum)



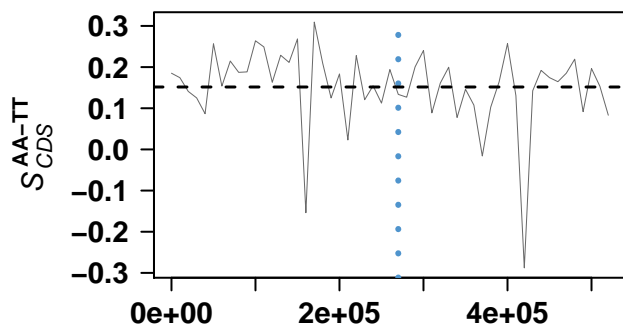
genome coordinates



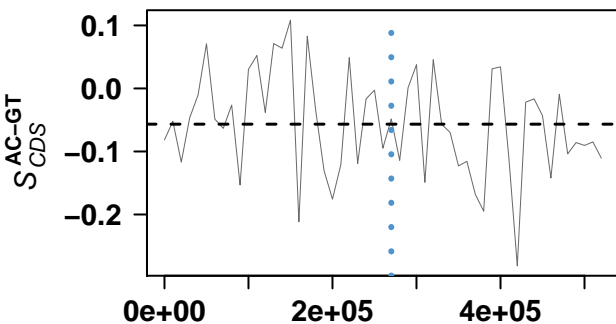
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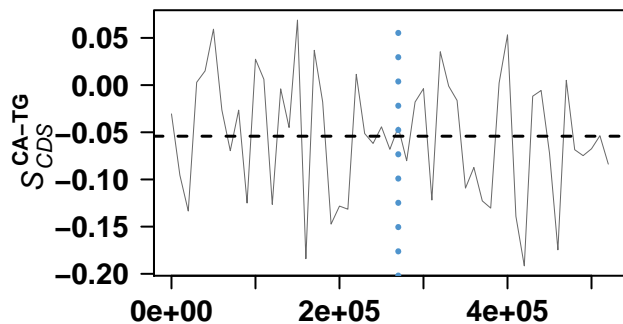
genome coordinates



genome coordinates

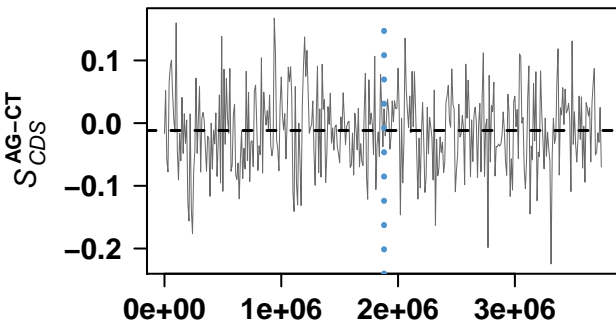


genome coordinates

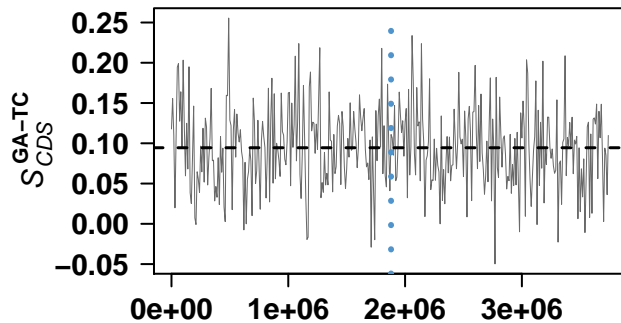


genome coordinates

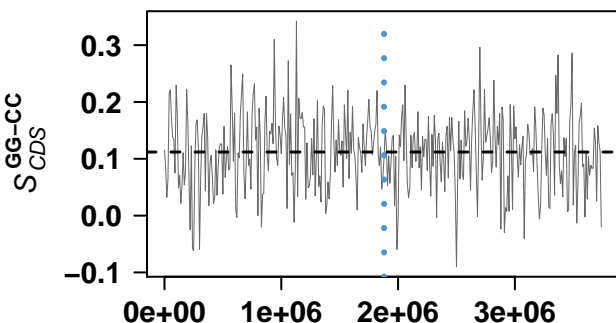
Yersinia pestis KIM10+



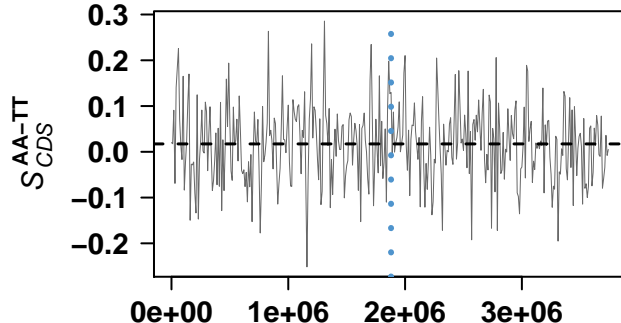
genome coordinates



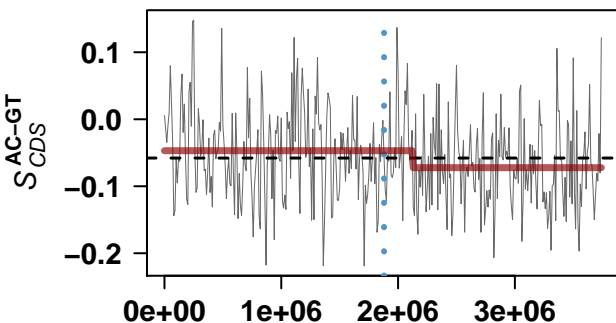
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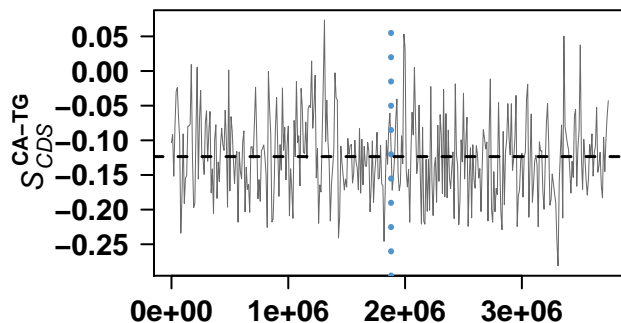
genome coordinates



genome coordinates

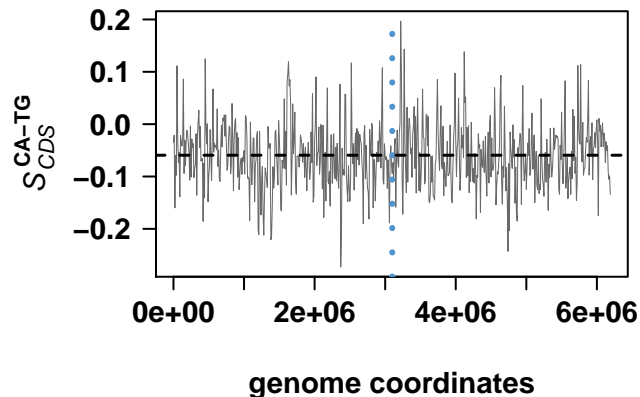
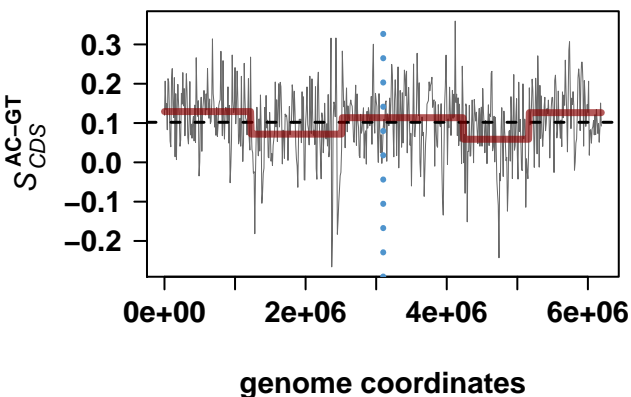
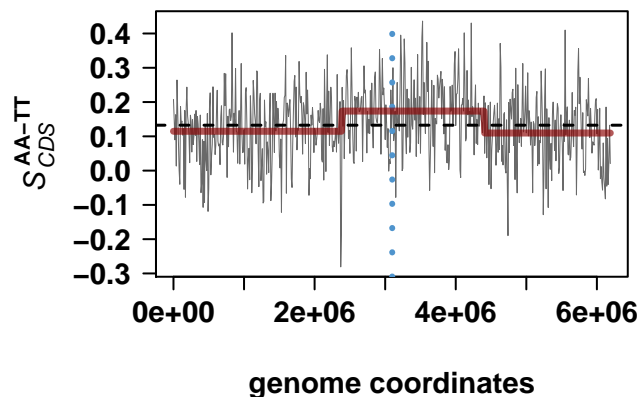
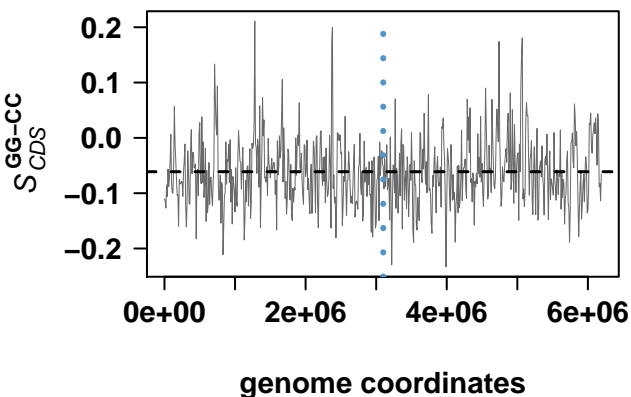
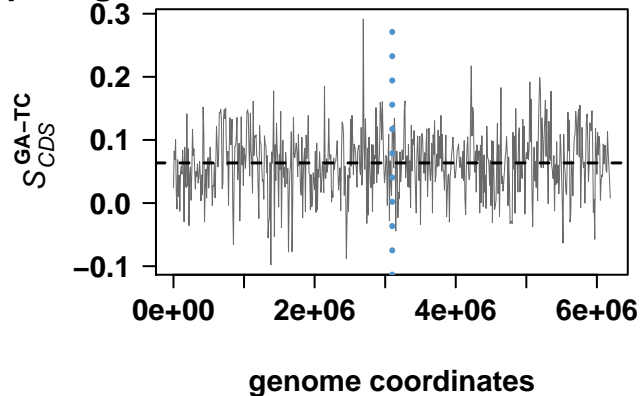
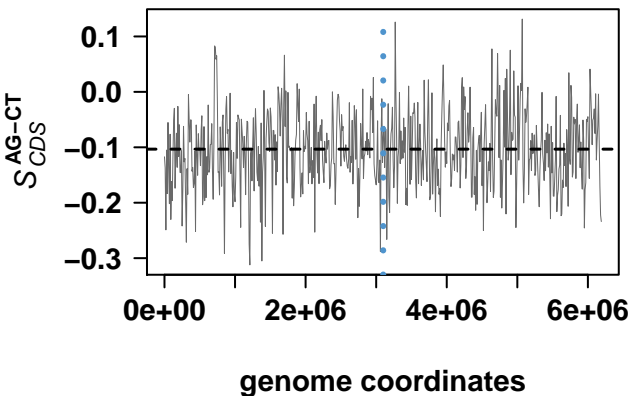


genome coordinates

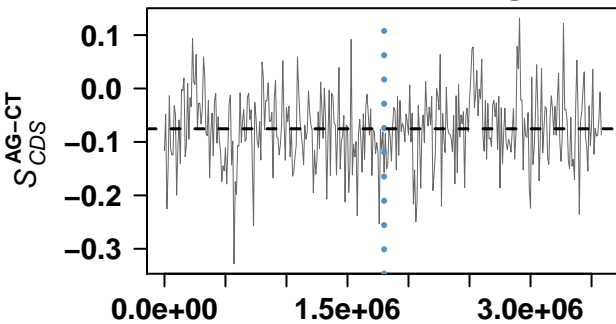


genome coordinates

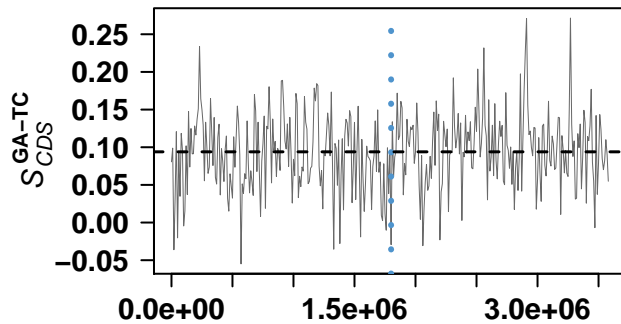
Pseudomonas protegens Pf-5



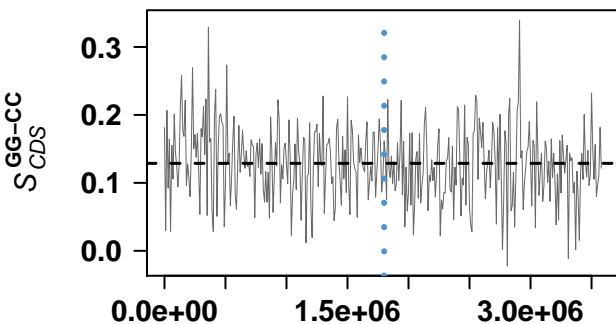
Shigella flexneri 2a str. 301



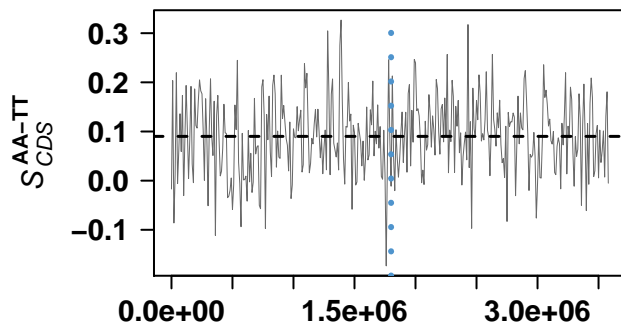
genome coordinates



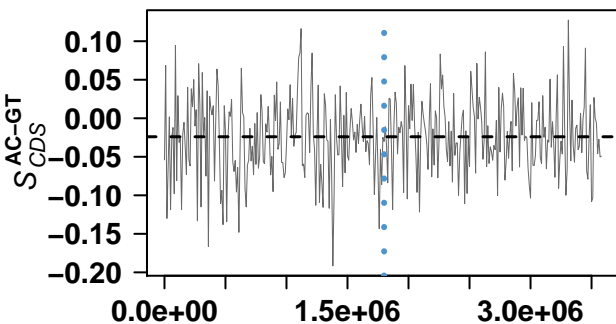
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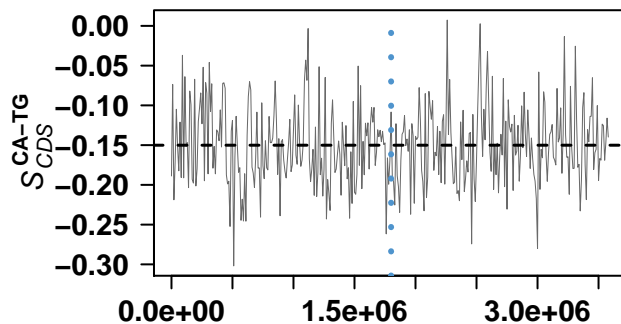
genome coordinates



genome coordinates

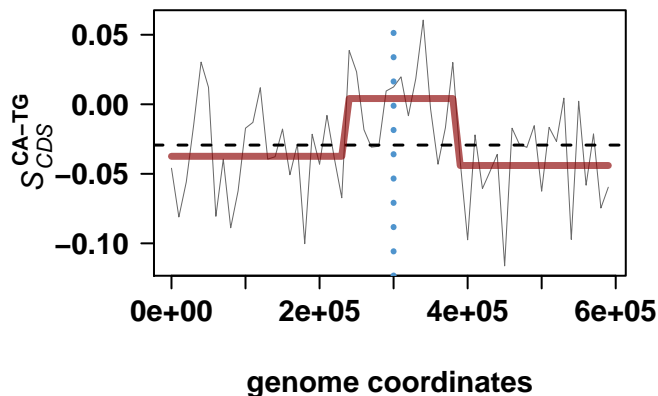
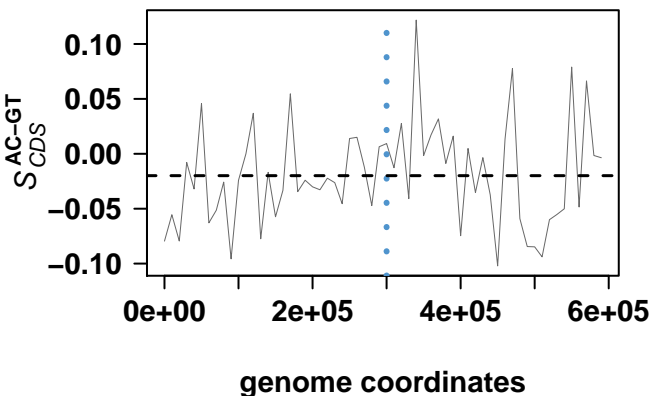
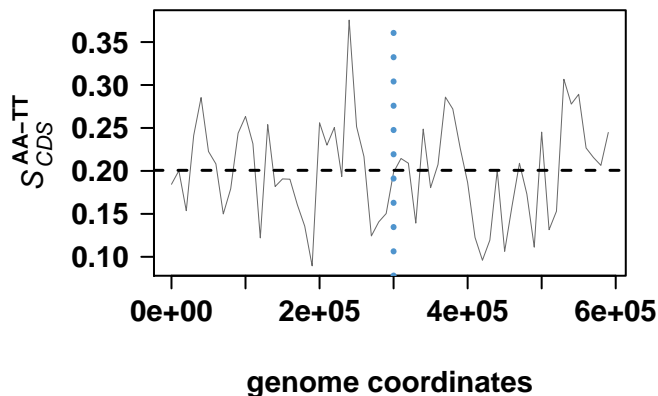
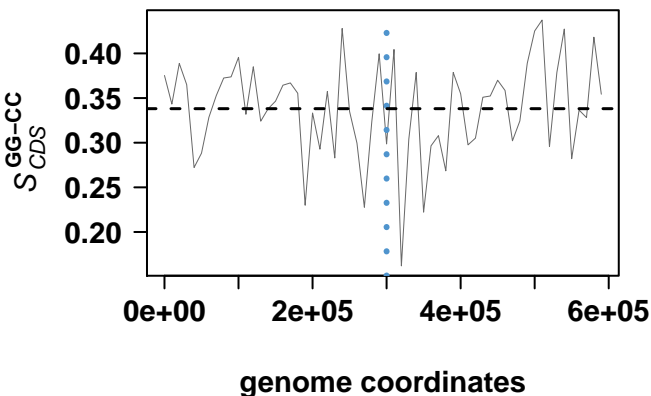
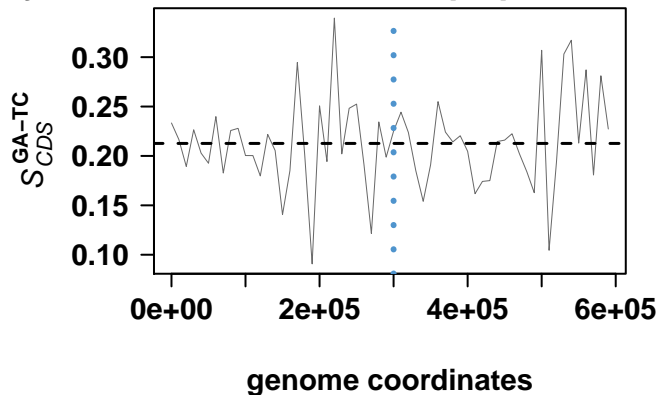
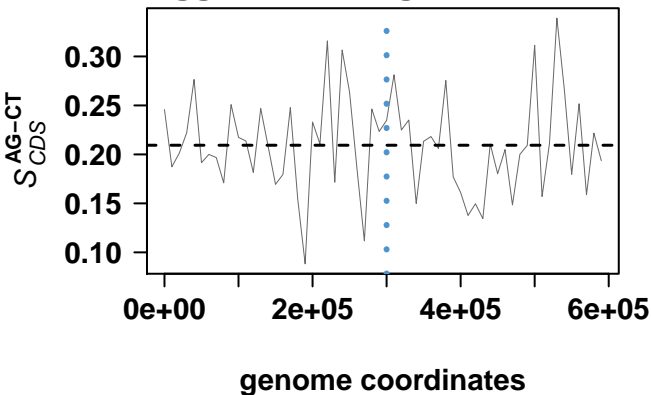


genome coordinates

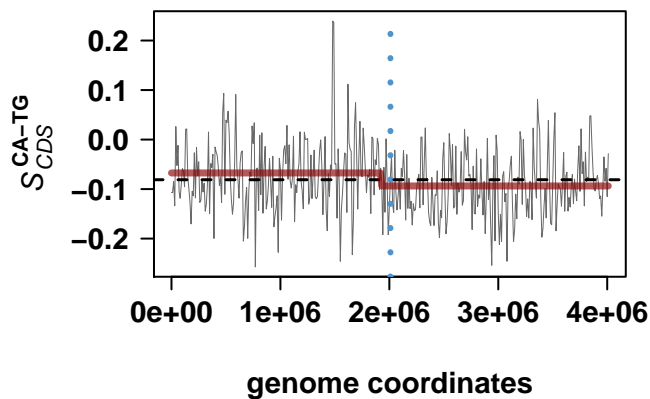
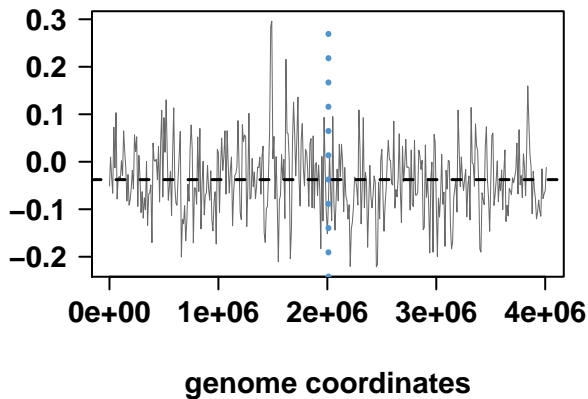
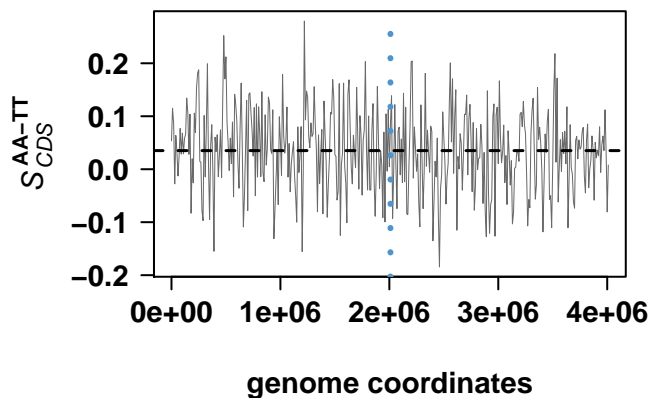
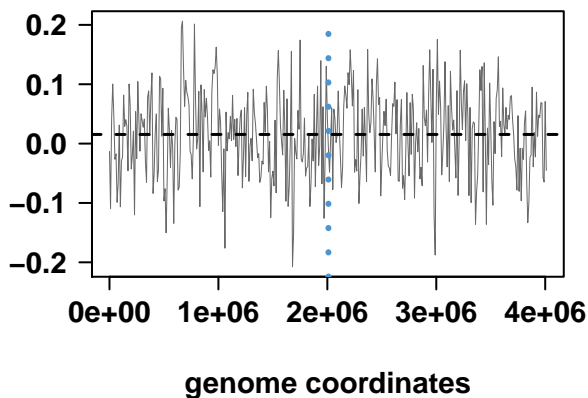
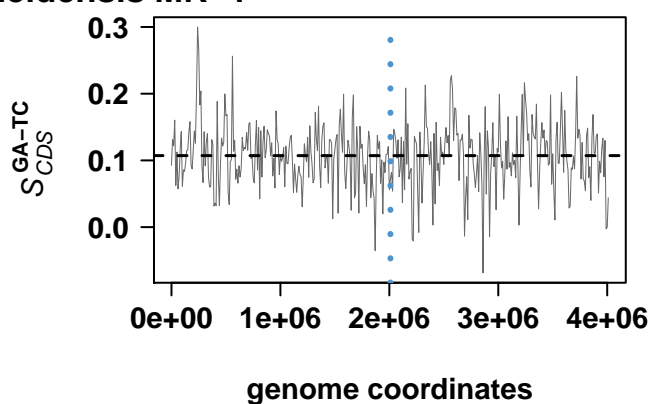
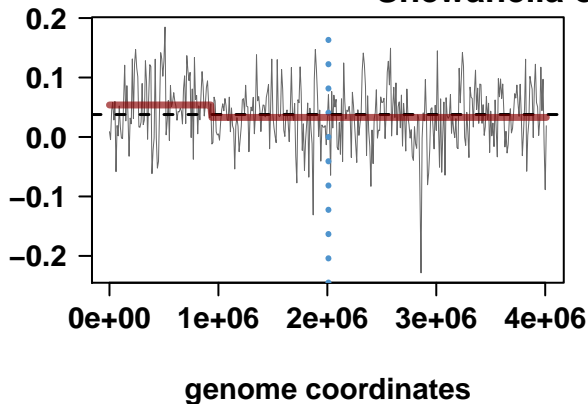


genome coordinates

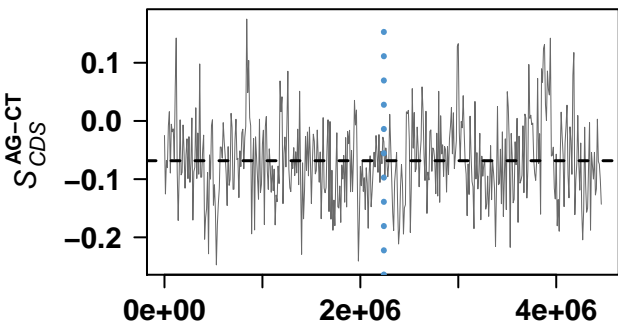
Wigglesworthia glossinidia endosymbiont of Glossina brevipalpis



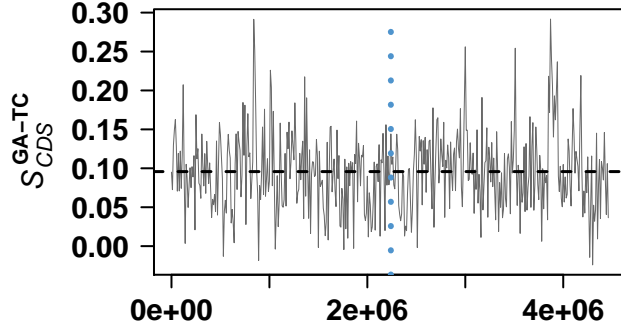
Shewanella oneidensis MR-1



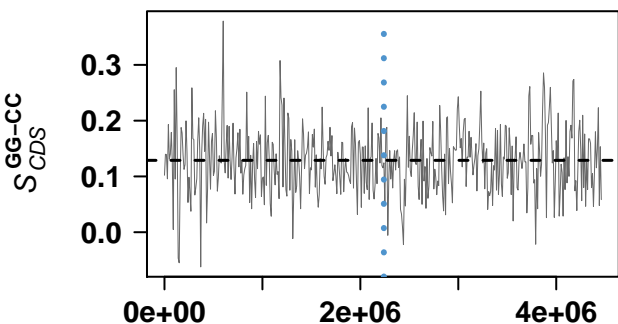
Escherichia coli CFT073



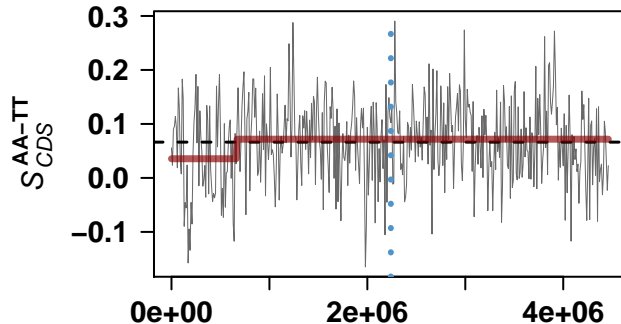
genome coordinates



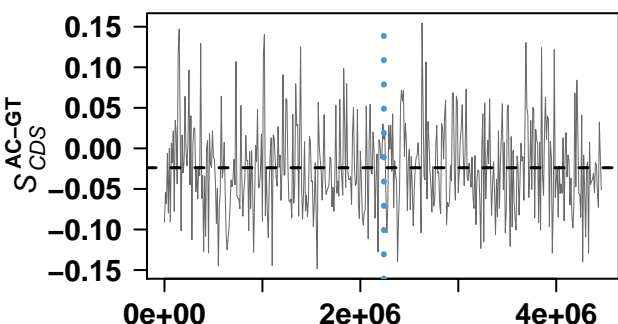
genome coordinates



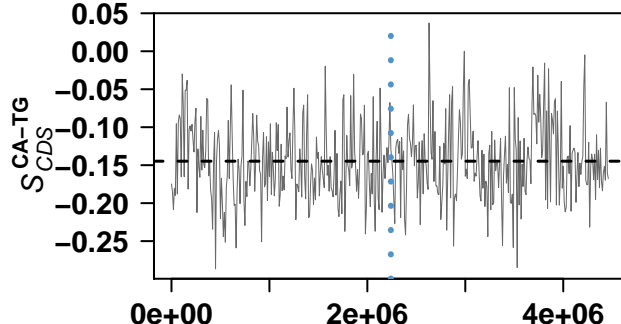
genome coordinates



genome coordinates

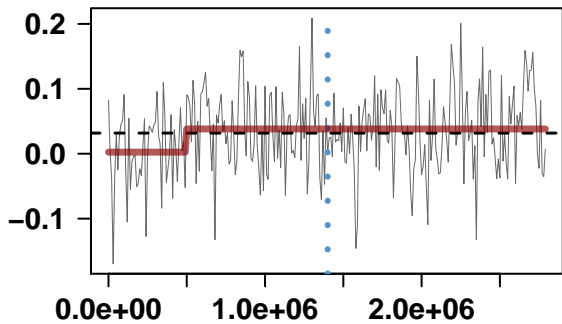


genome coordinates

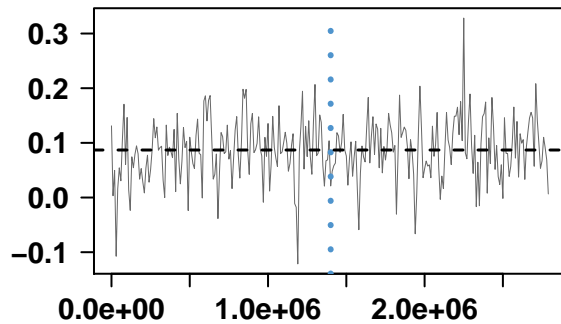


genome coordinates

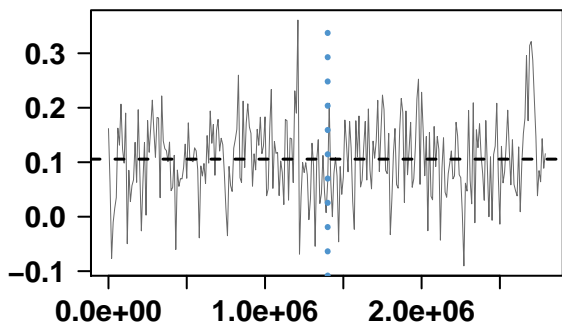
Vibrio vulnificus CMCP6



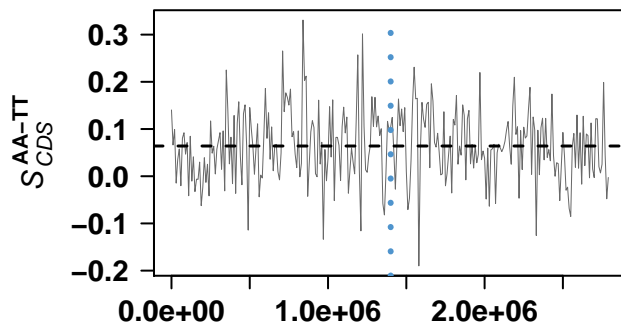
genome coordinates



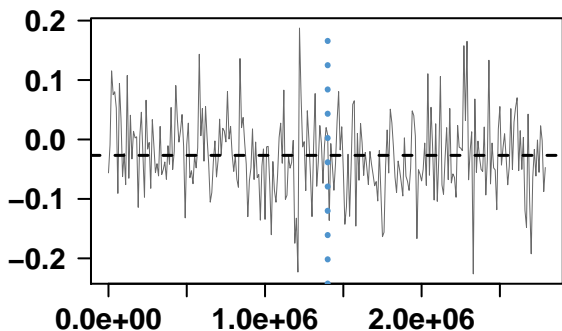
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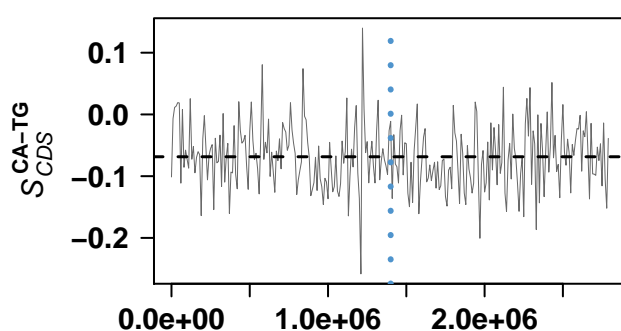
genome coordinates



genome coordinates

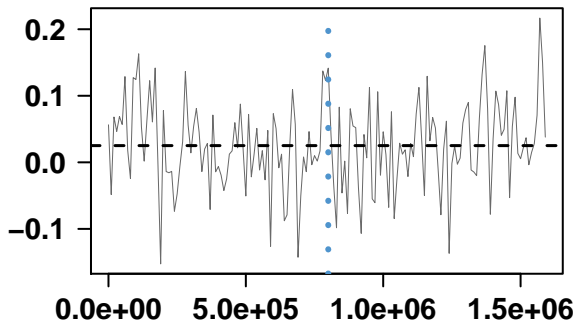


genome coordinates

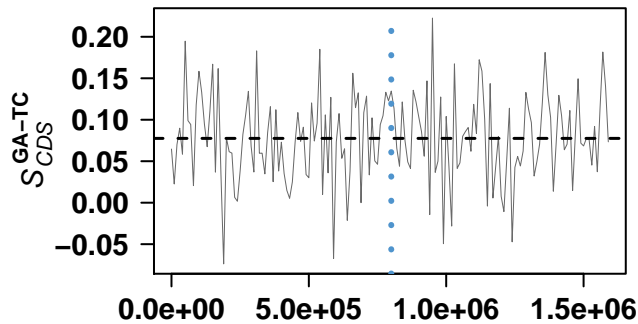


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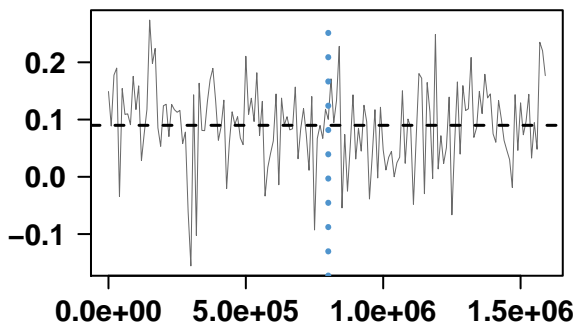
Vibrio vulnificus CMCP6



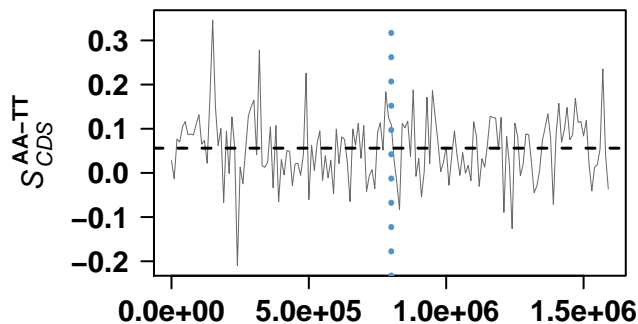
genome coordinates



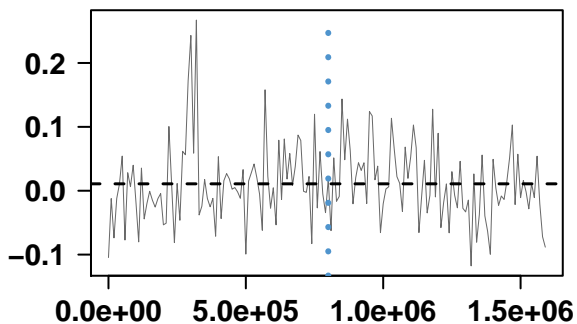
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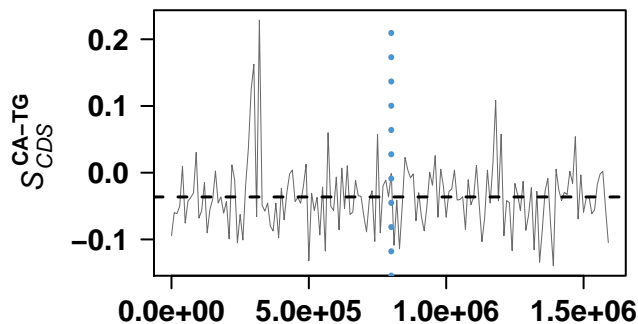
genome coordinates



genome coordinates

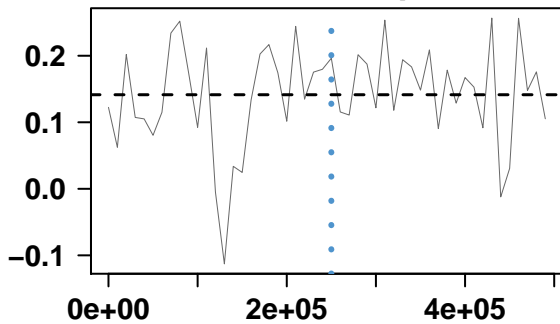


genome coordinates

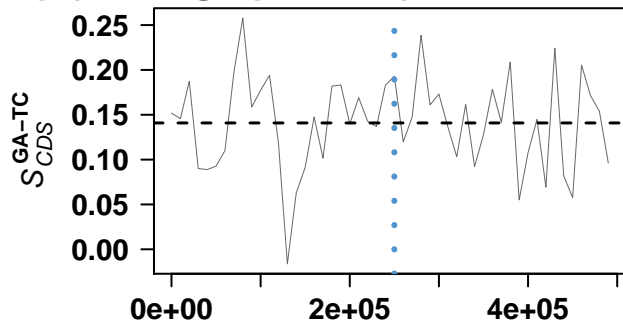


genome coordinates

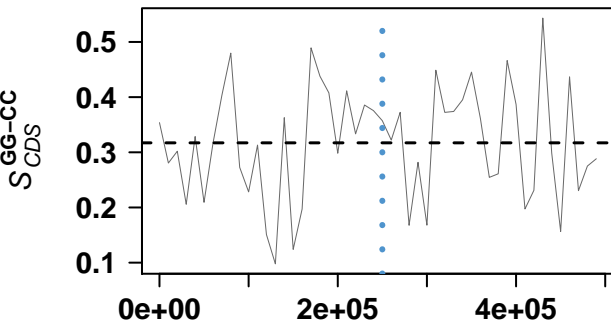
Buchnera aphidicola str. Bp (Baizongia pistaciae)



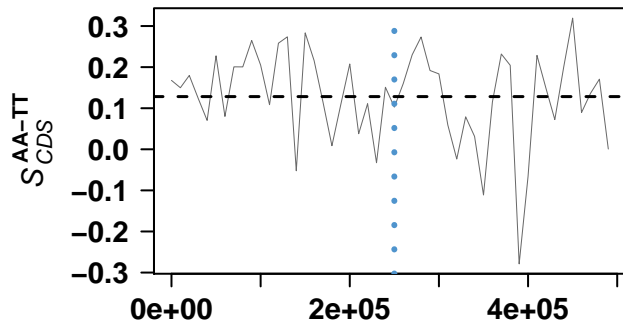
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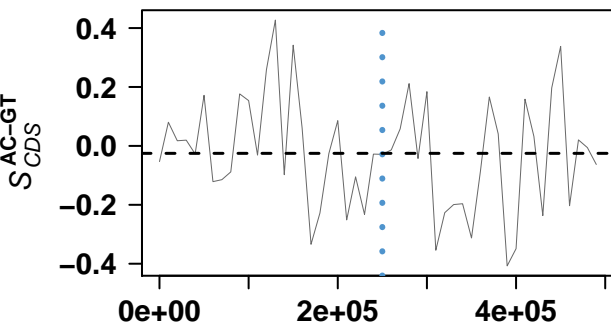
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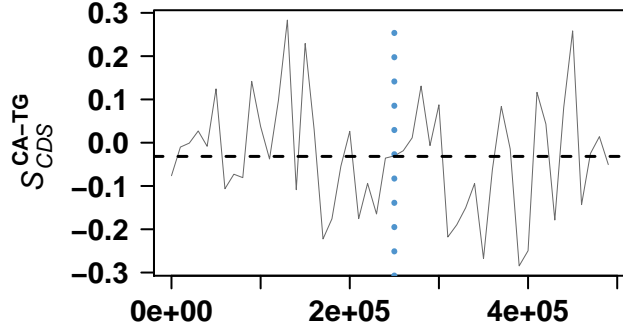
genome coordinates



genome coordinates

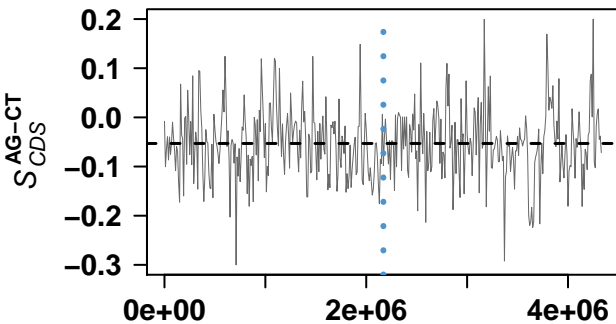


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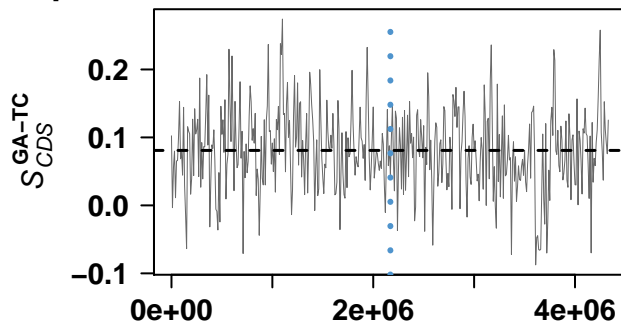


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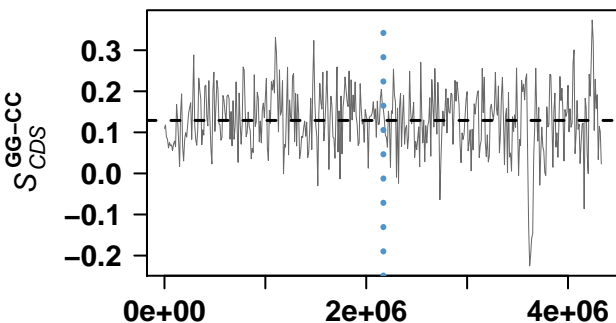
Pectobacterium atrosepticum SCRI1043



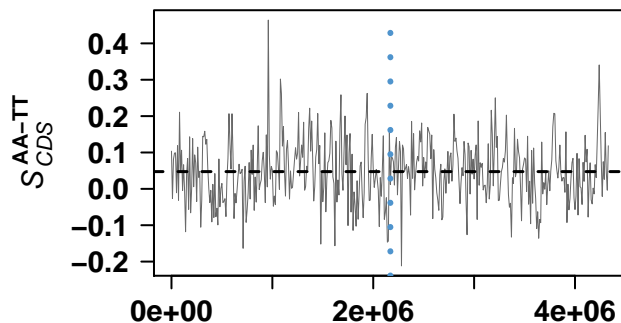
genome coordinates



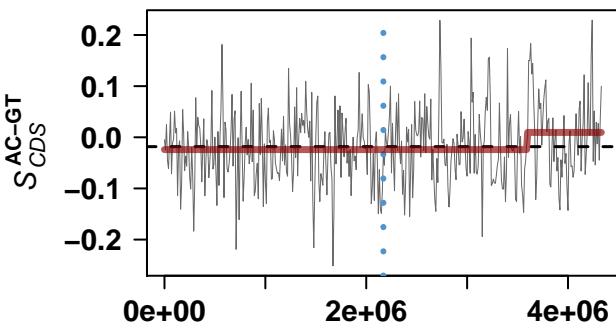
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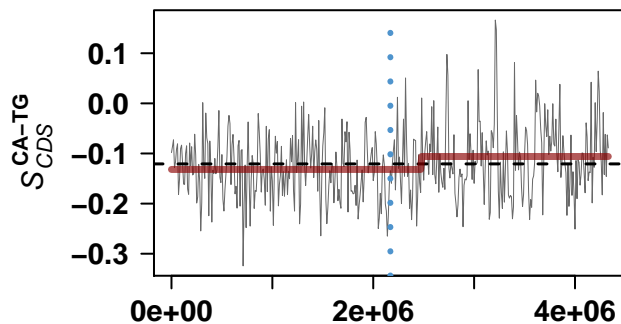
genome coordinates



genome coordinates

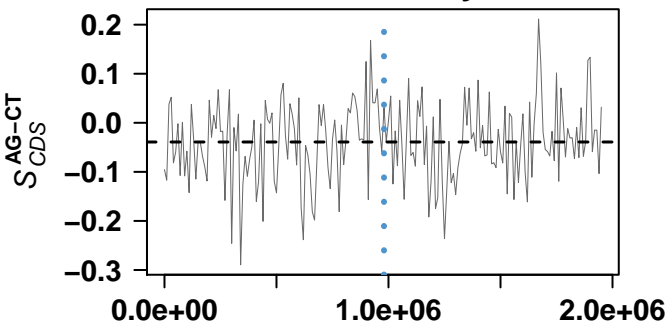


genome coordinates

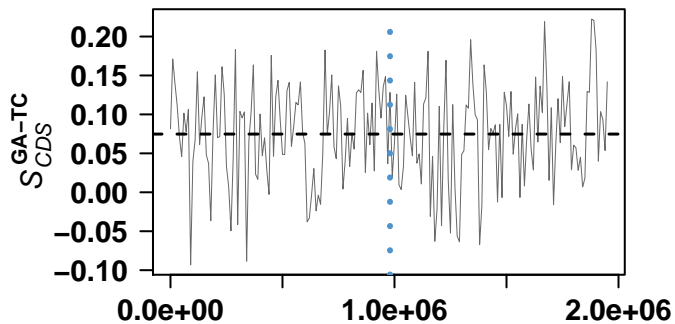


genome coordinates

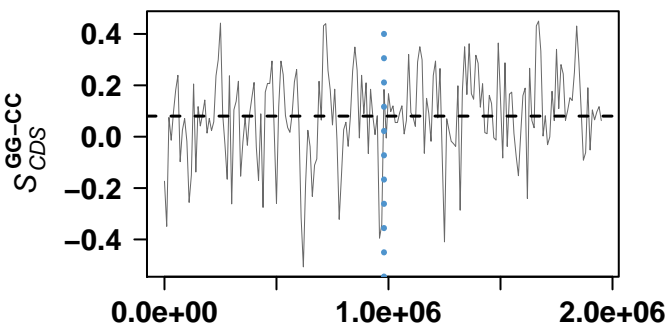
Xylella fastidiosa Temecula1



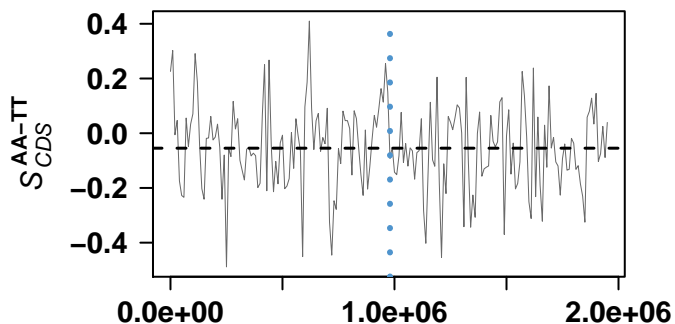
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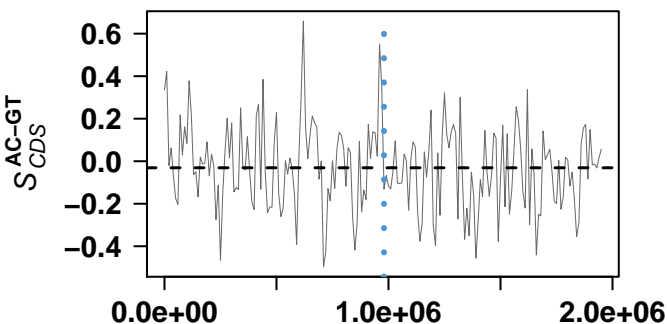
genome coordinates



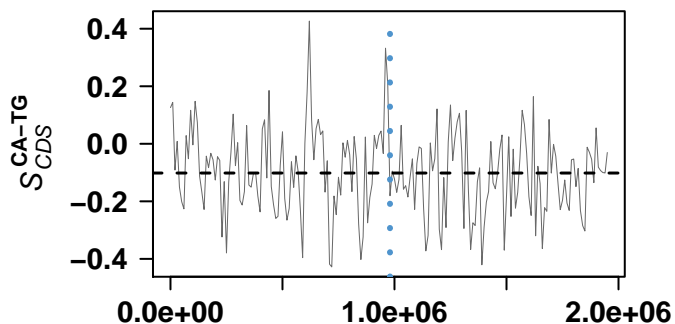
genome coordinates



genome coordinates

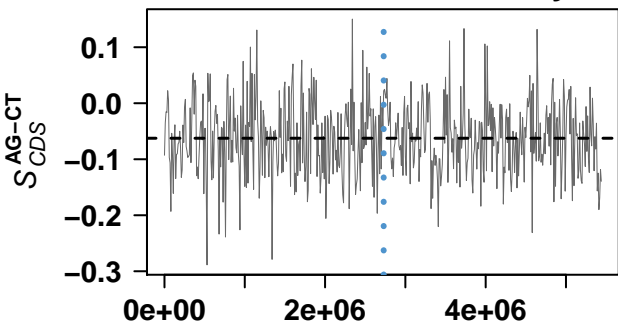


genome coordinates

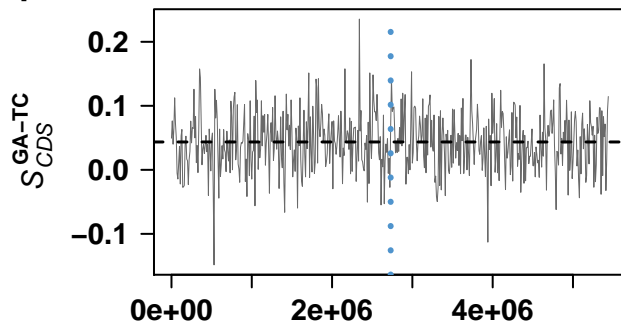


genome coordinates

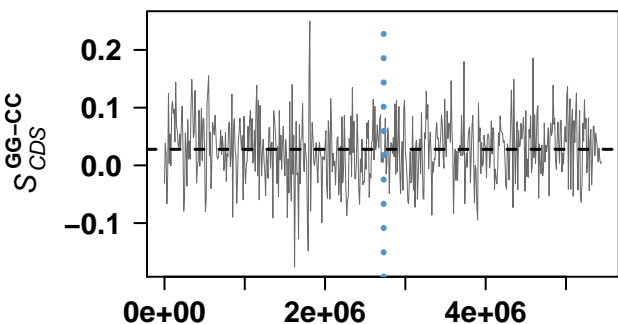
Pseudomonas syringae pv. *tomato* str. DC3000



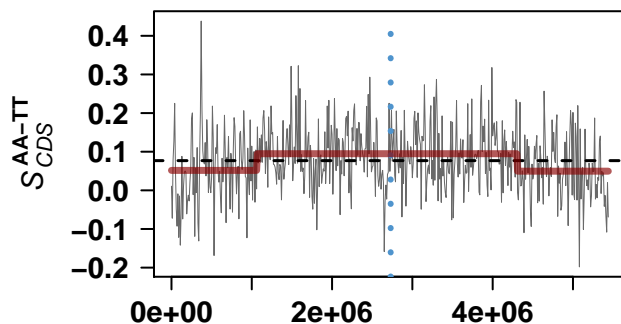
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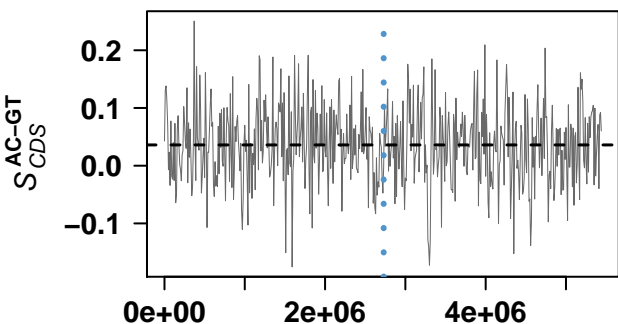
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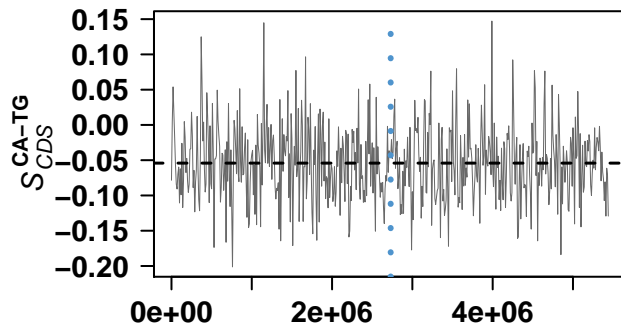
genome coordinates



genome coordinates

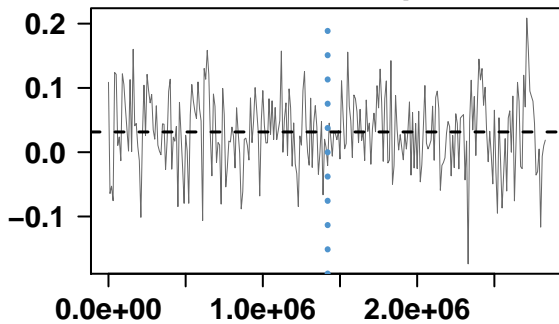


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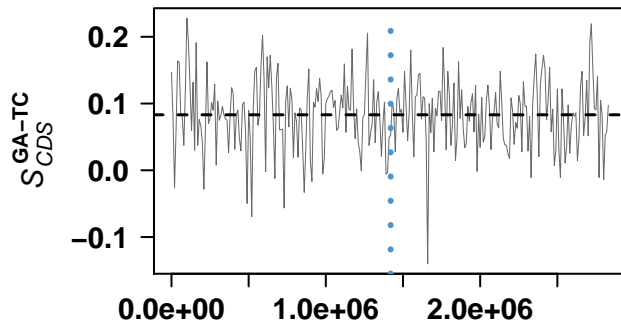


genome coordinates

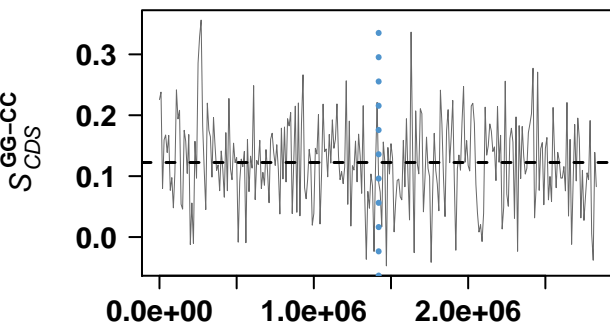
Vibrio parahaemolyticus RIMD 2210633



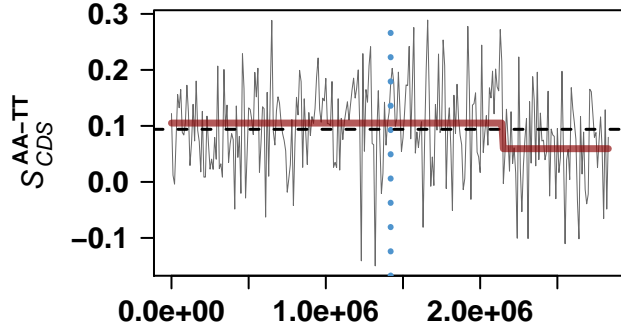
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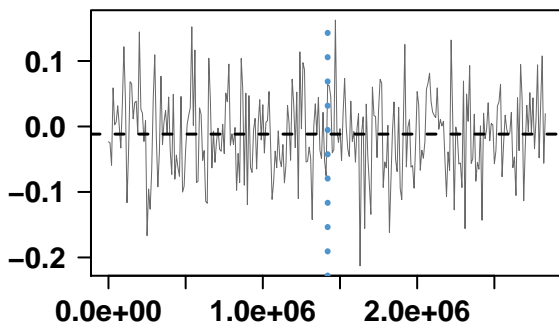
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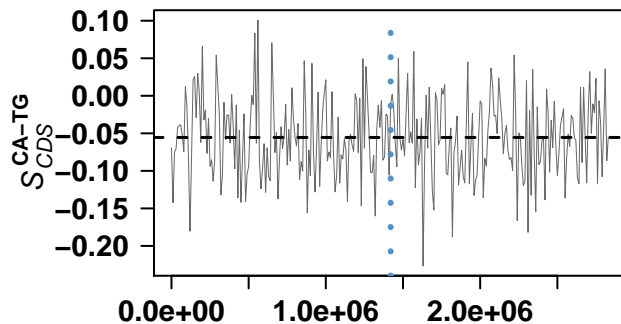
genome coordinates



genome coordinates

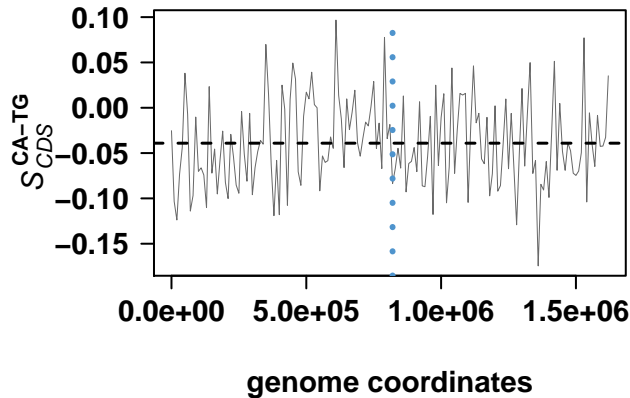
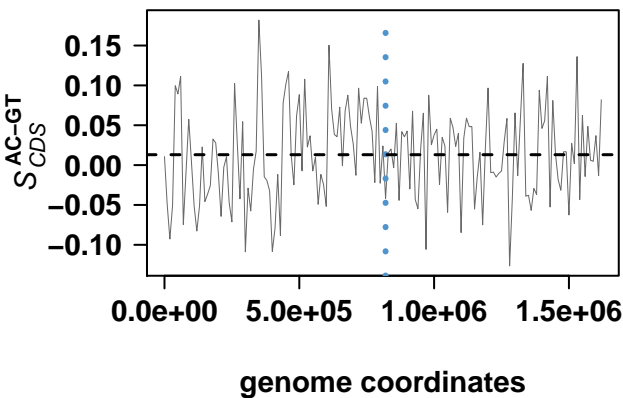
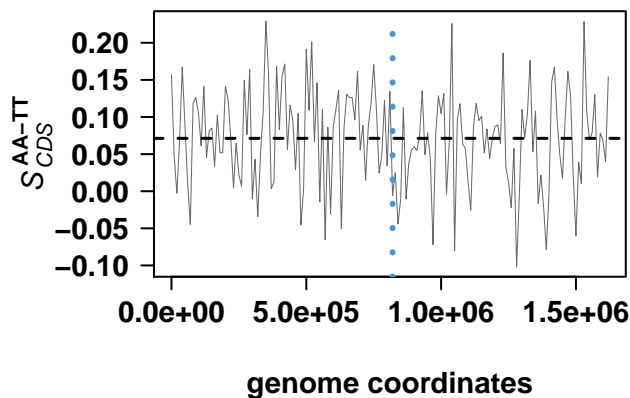
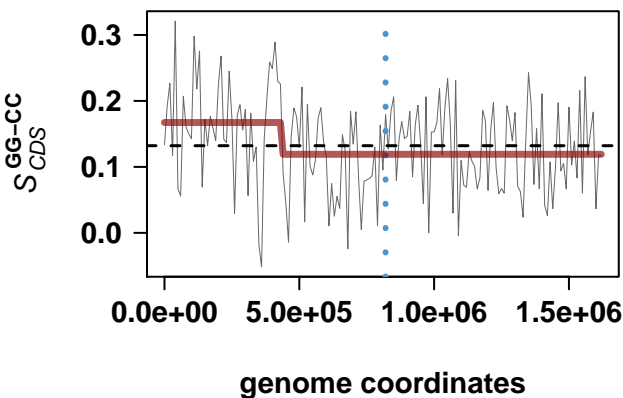
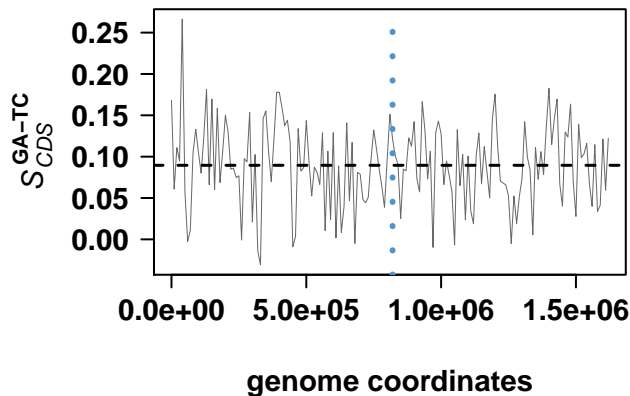
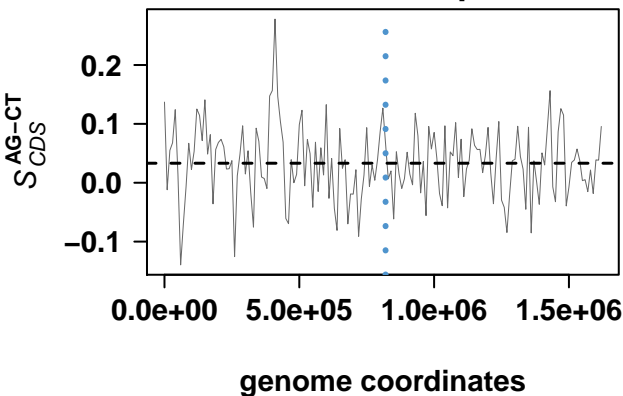


genome coordinates

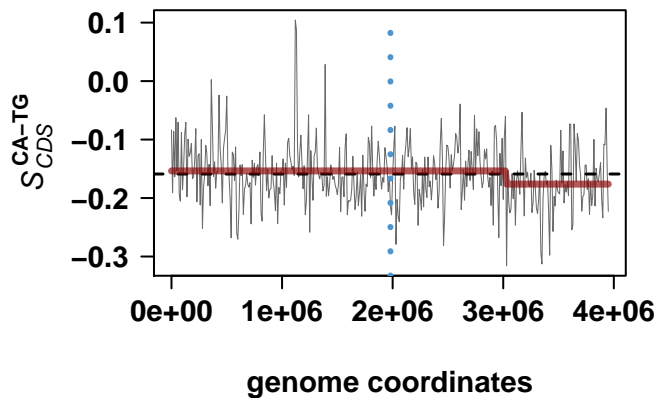
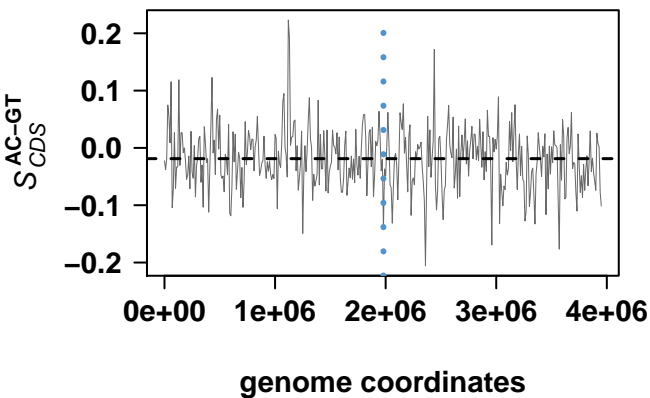
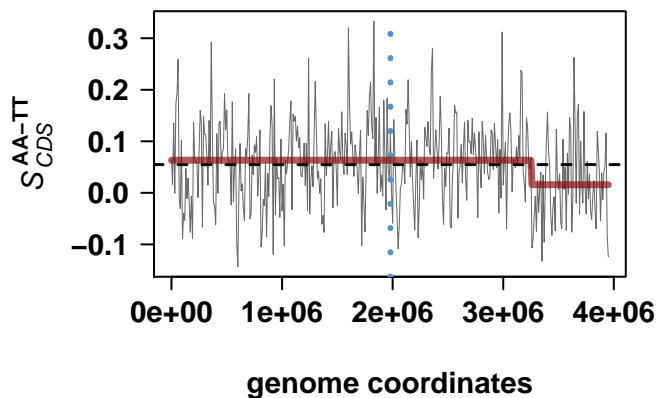
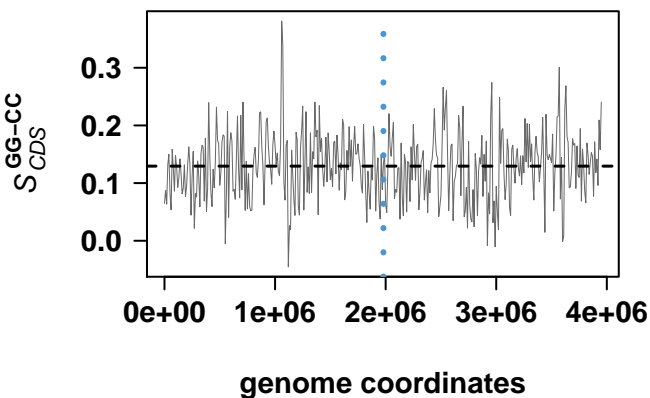
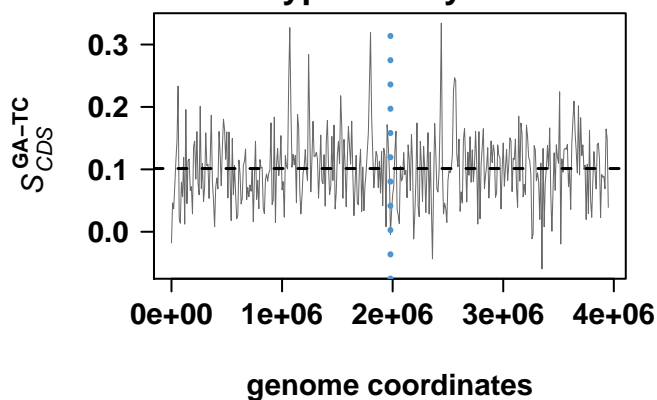
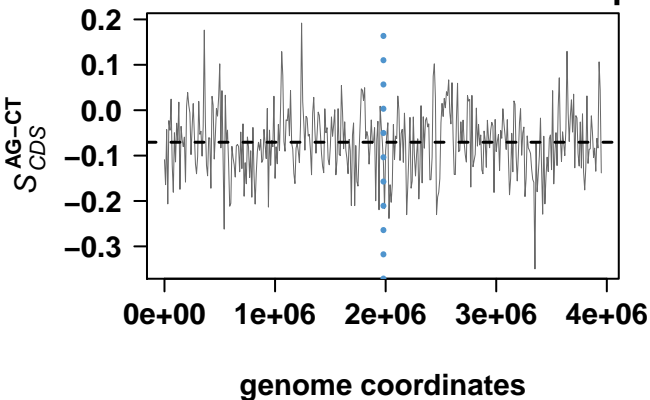


genome coordinates

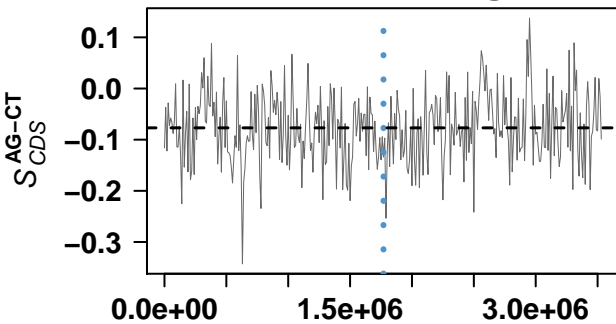
Vibrio parahaemolyticus RIMD 2210633



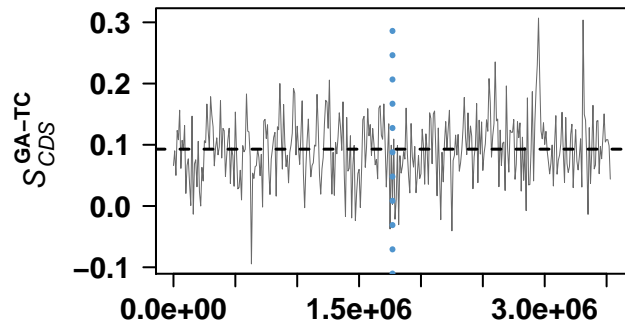
Salmonella enterica subsp. enterica serovar Typhi str. Ty2



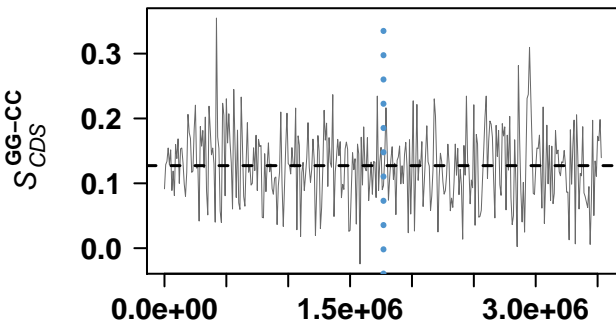
Shigella flexneri 2a str. 2457T



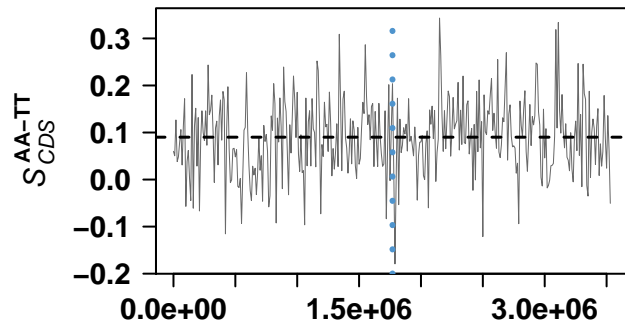
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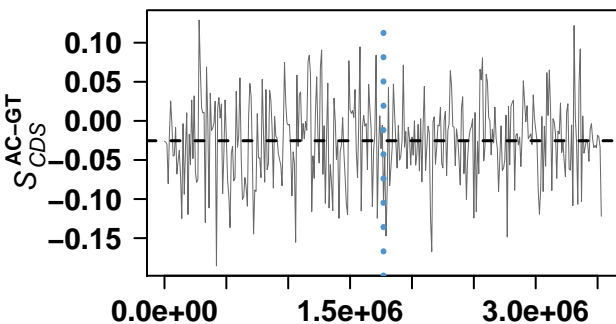
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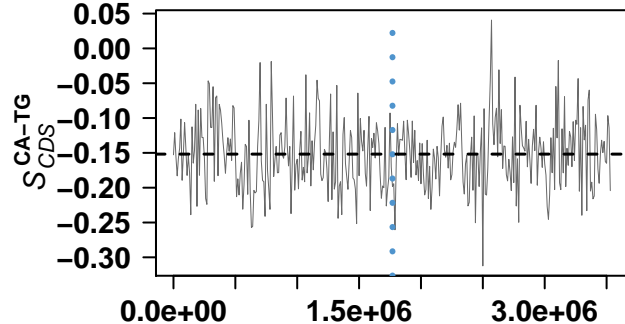
genome coordinates



genome coordinates

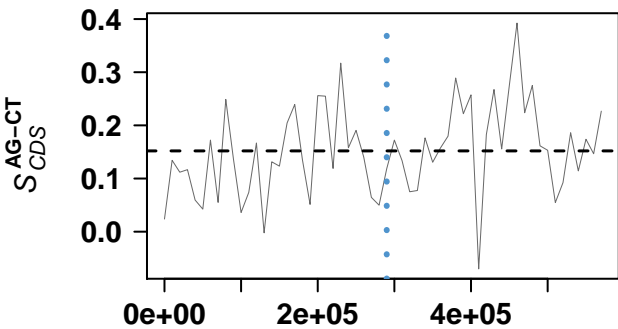


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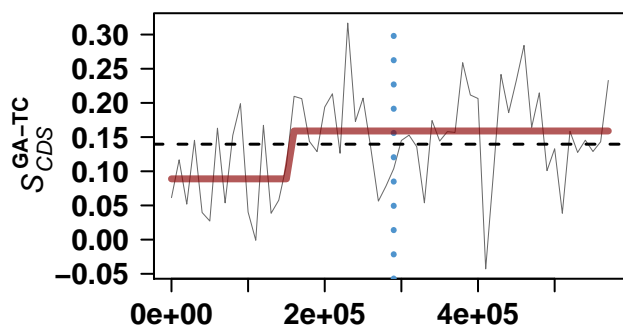


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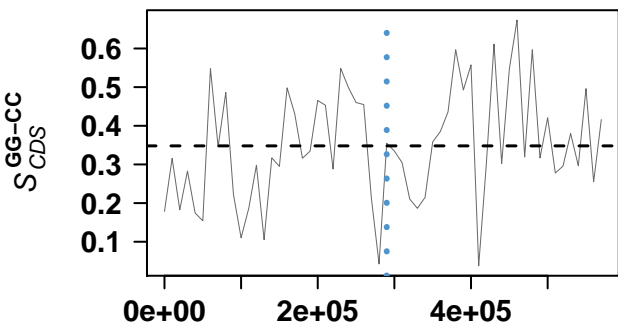
Candidatus Blochmannia floridanus



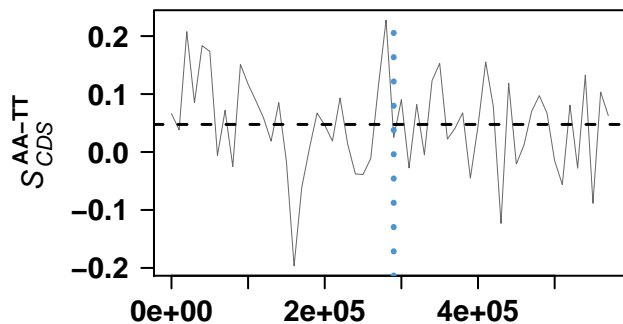
genome coordinates



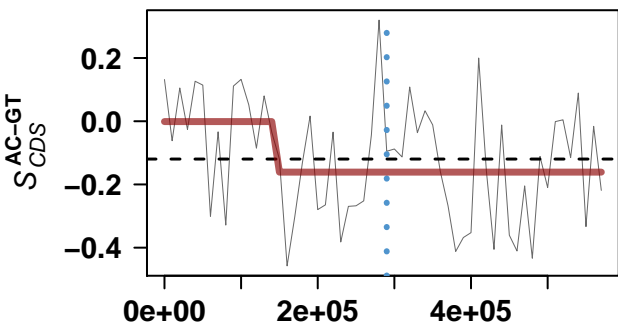
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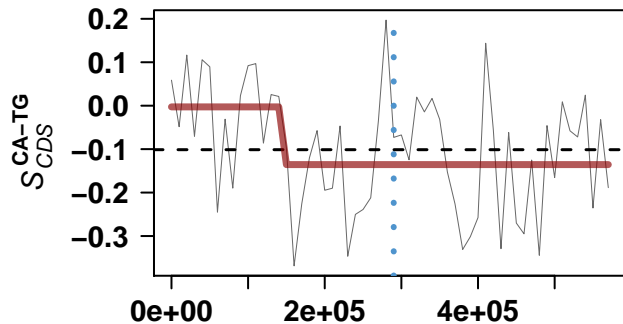
genome coordinates



genome coordinates

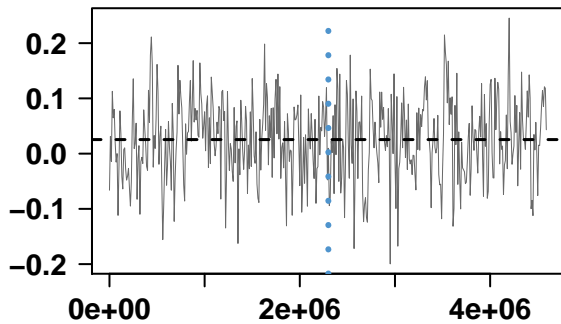


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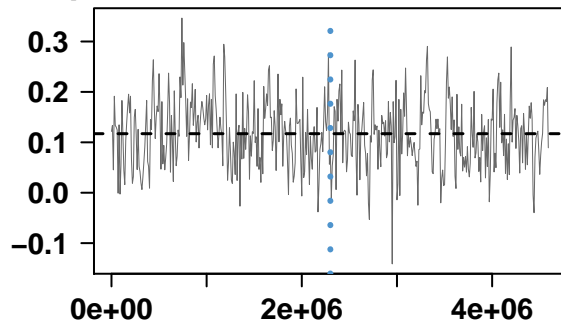


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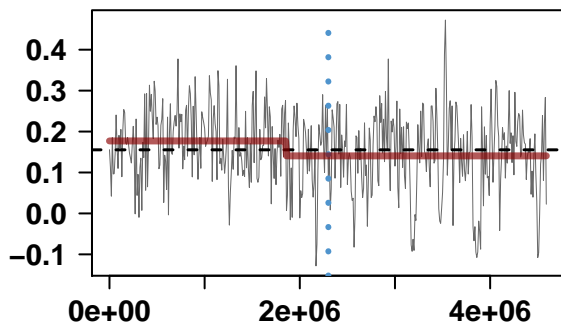
Photorhabdus luminescens subsp. laumondii TTO1



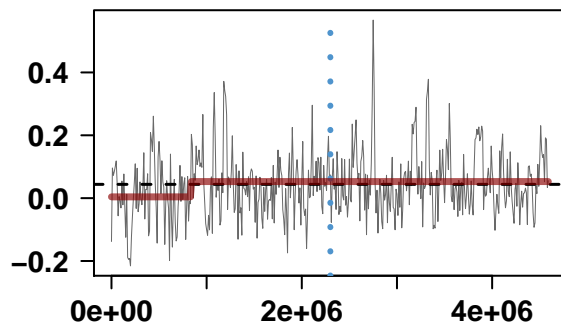
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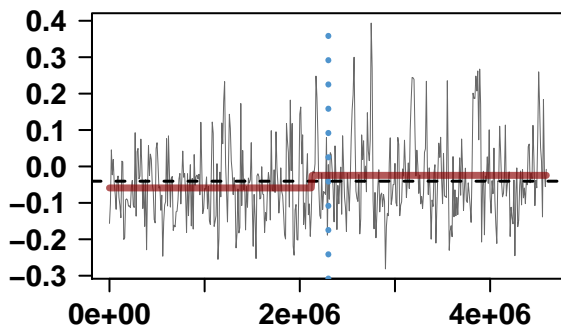
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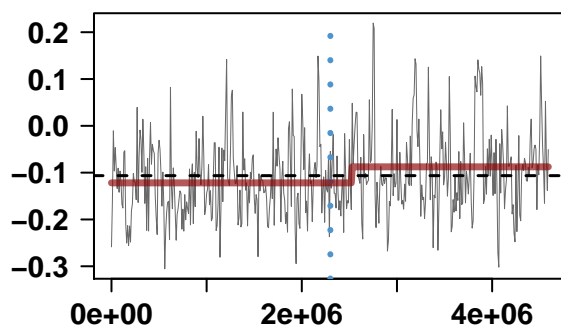
genome coordinates



genome coordinates

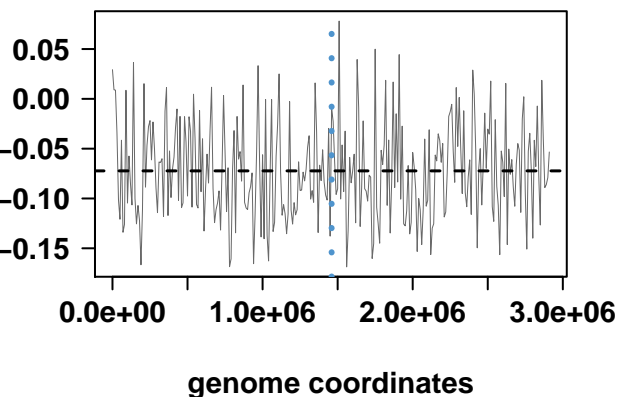
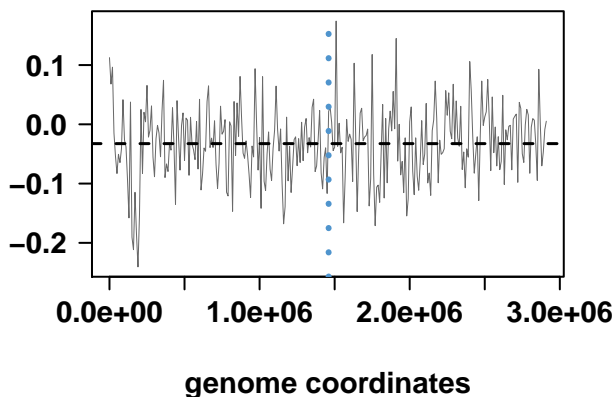
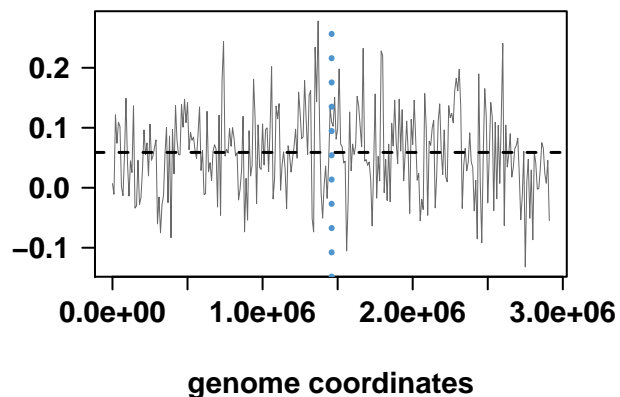
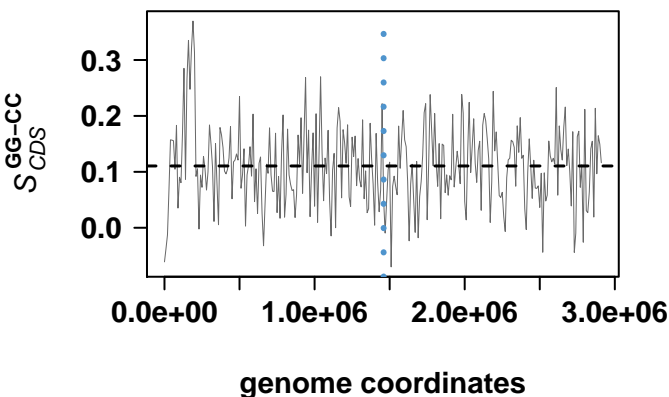
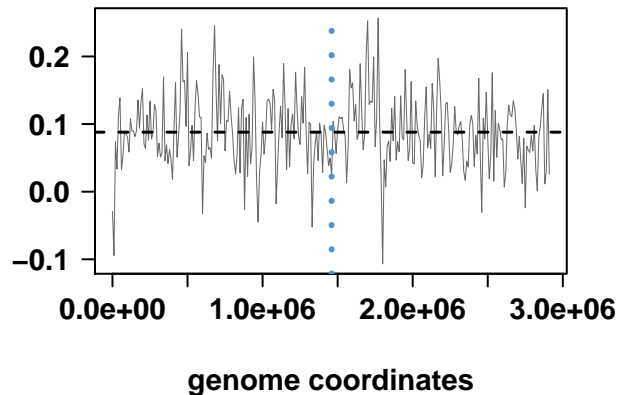
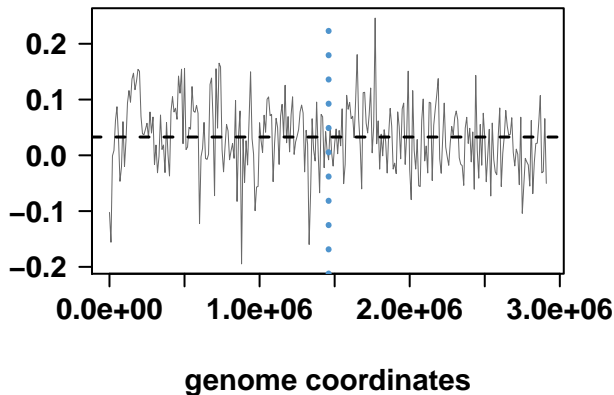


genome coordinates

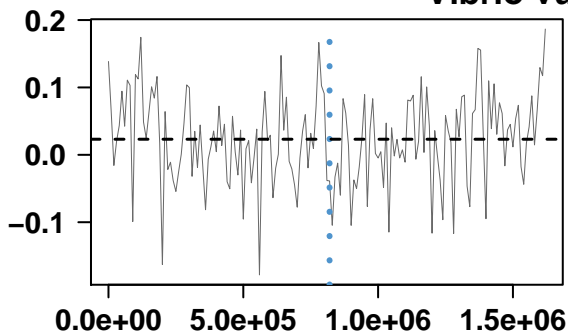


genome coordinates

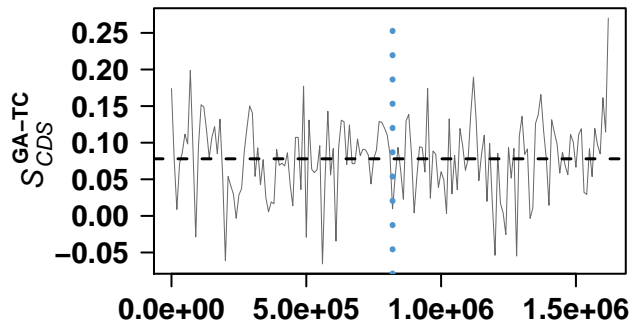
Vibrio vulnificus YJ016



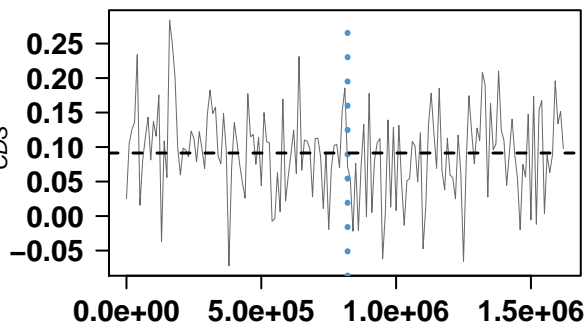
Vibrio vulnificus YJ016



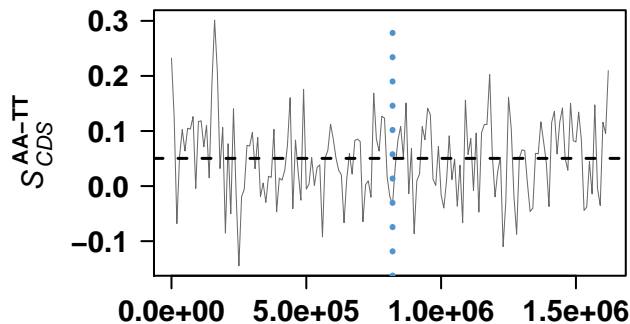
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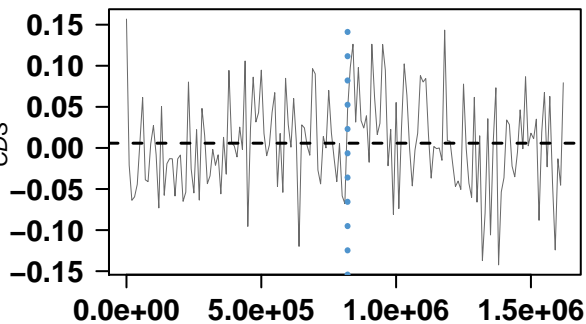
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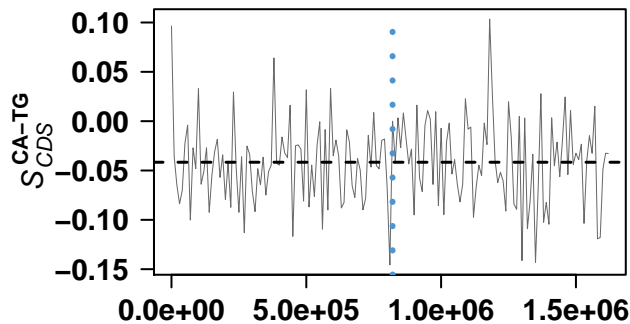
genome coordinates



genome coordinates

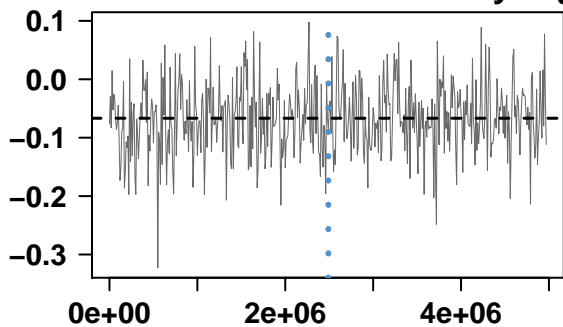


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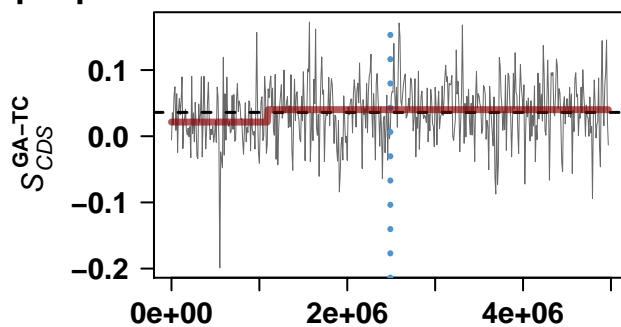


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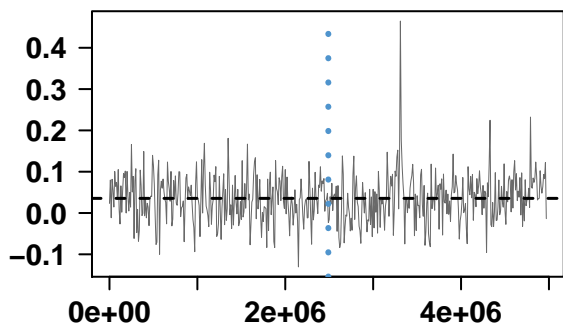
Pseudomonas syringae pv. *phaseolicola* 1448A



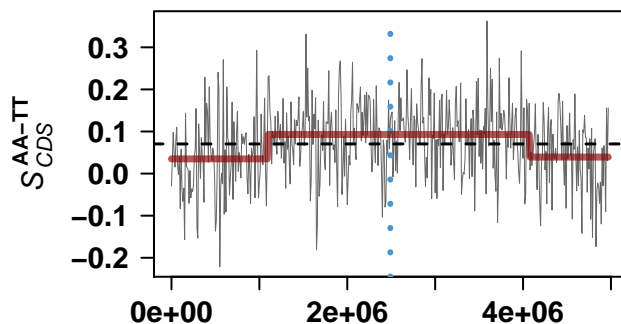
genome coordinates



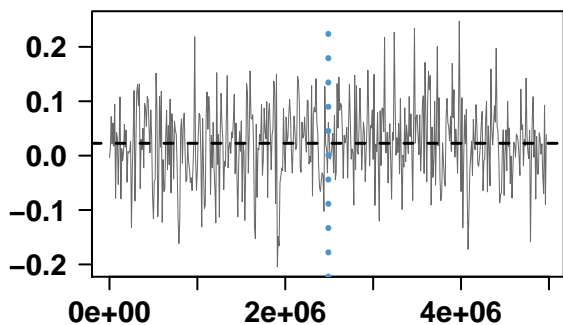
genome coordinates



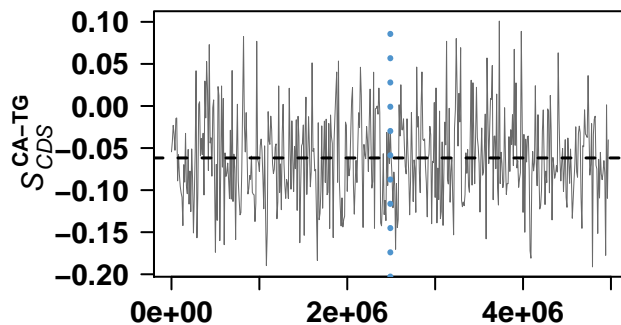
genome coordinates



genome coordinates

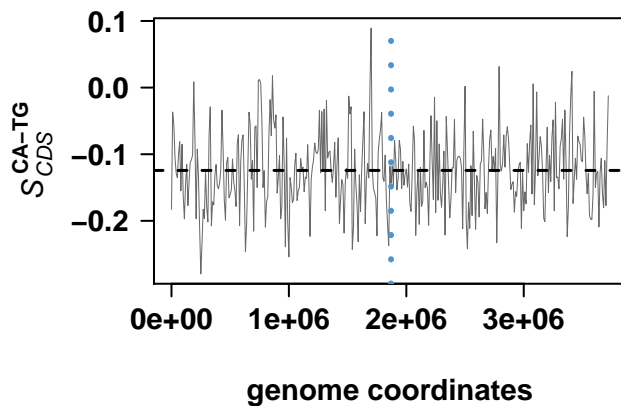
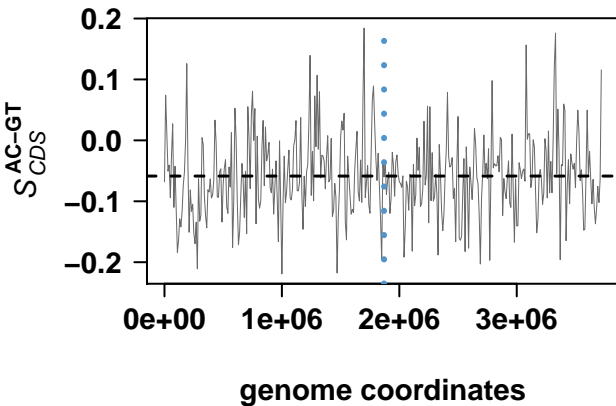
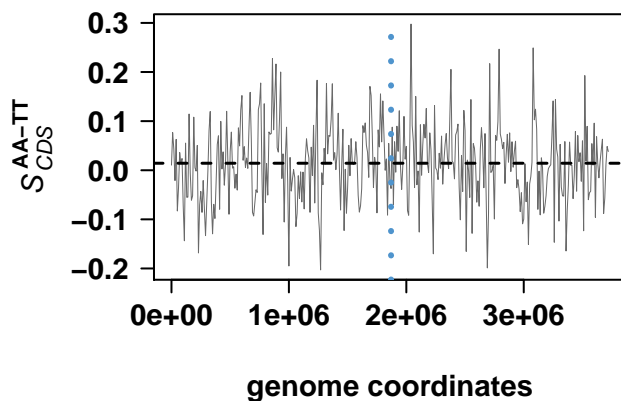
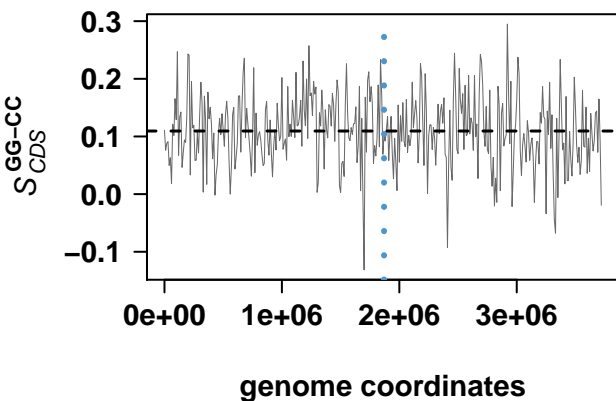
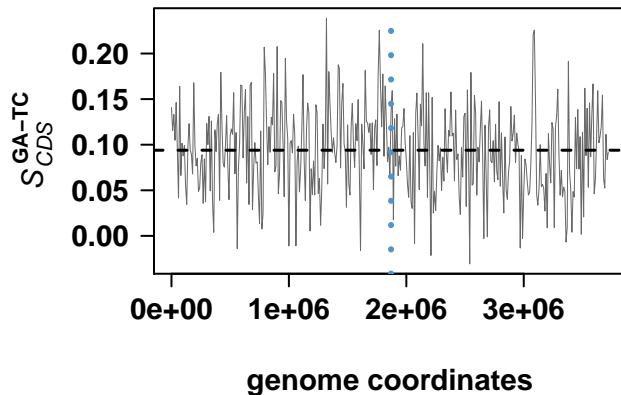
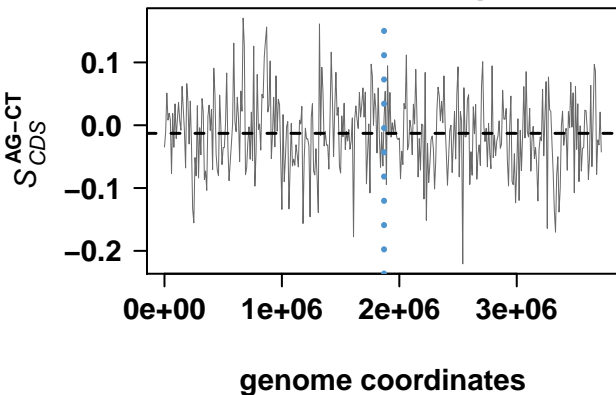


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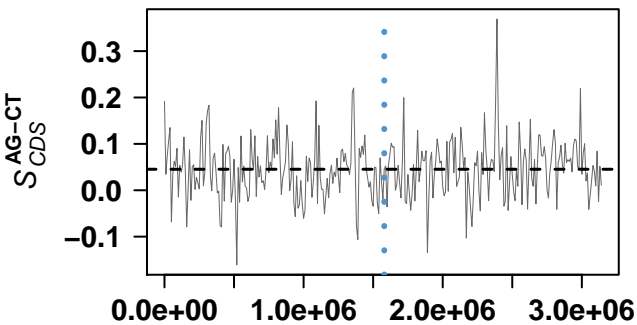


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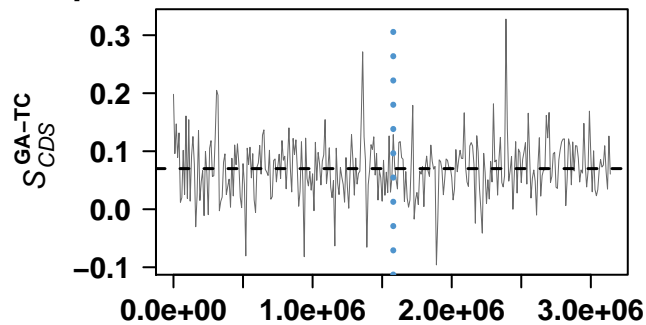
Yersinia pestis biovar *Microtus* str. 91001



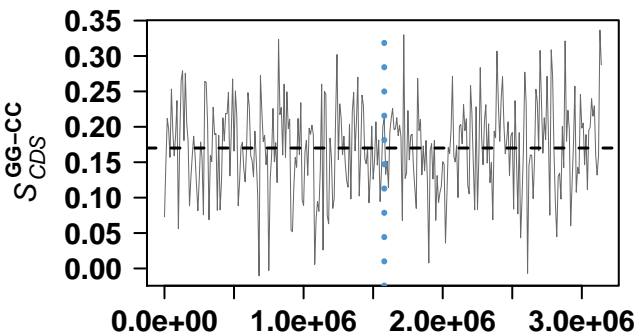
Acinetobacter sp. ADP1



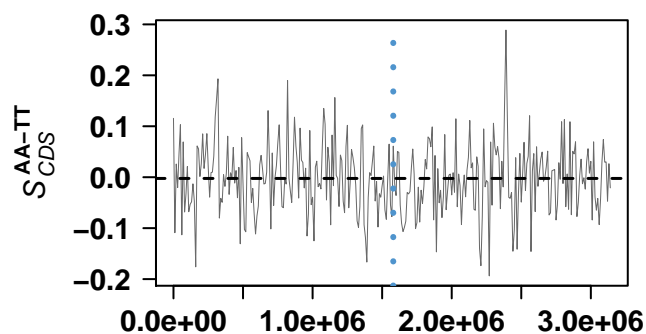
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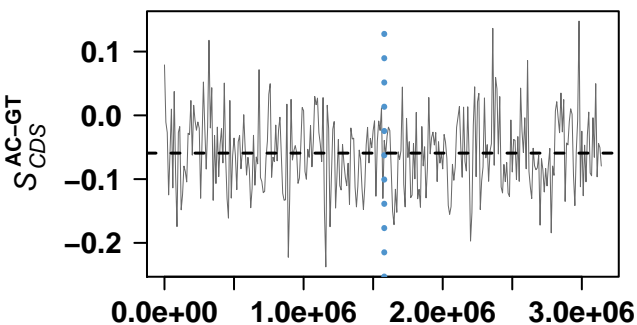
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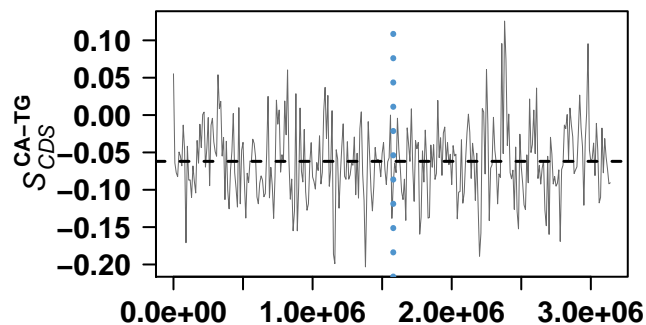
genome coordinates



genome coordinates

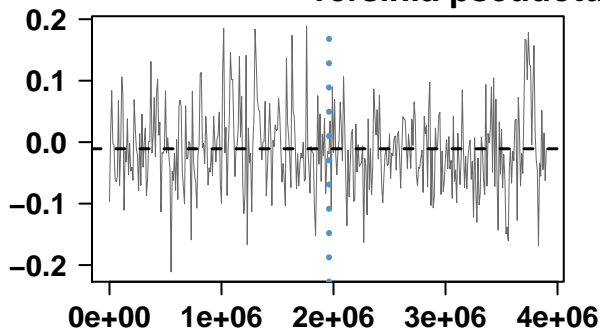


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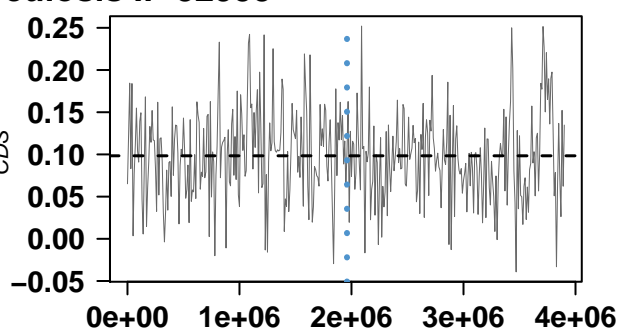


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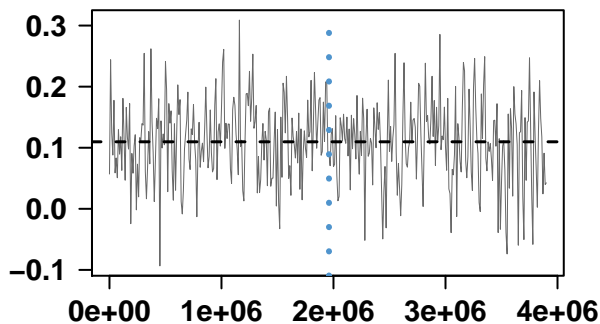
Yersinia pseudotuberculosis IP 32953



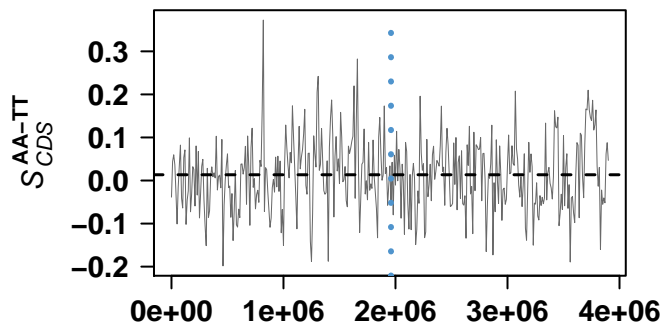
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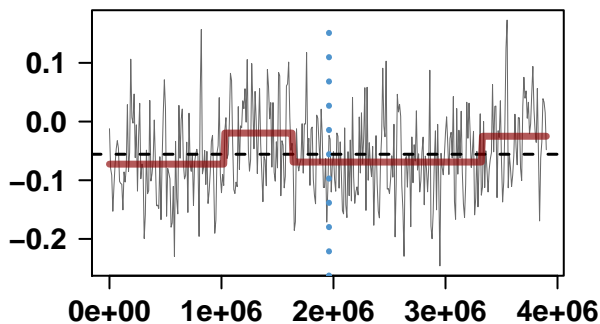
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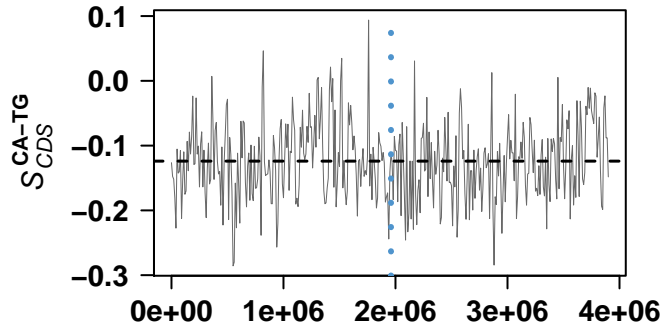
genome coordinates



genome coordinates

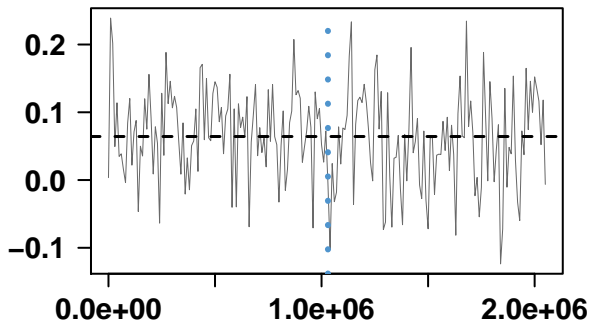


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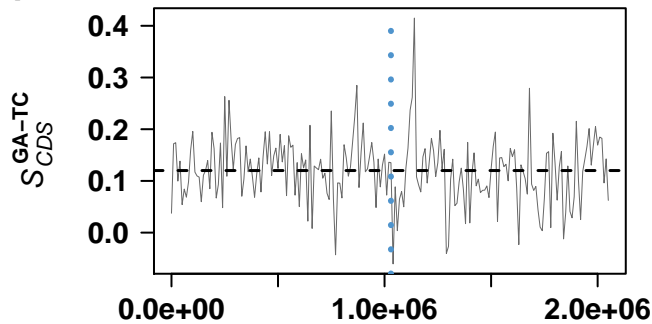


genome coordinates

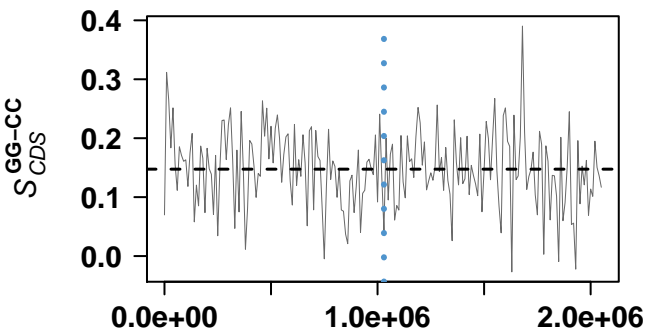
Mannheimia succiniciproducens MBEL55E



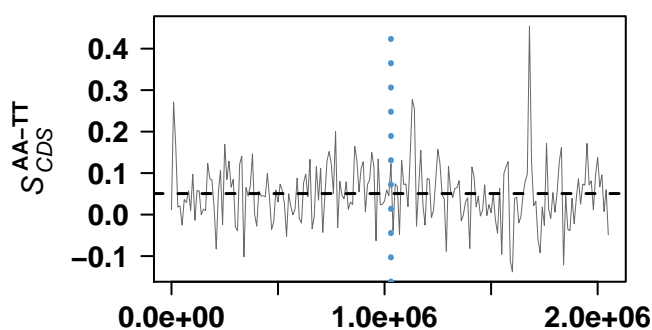
genome coordinates



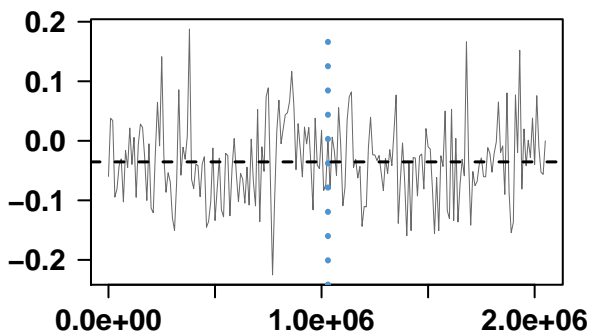
genome coordinates



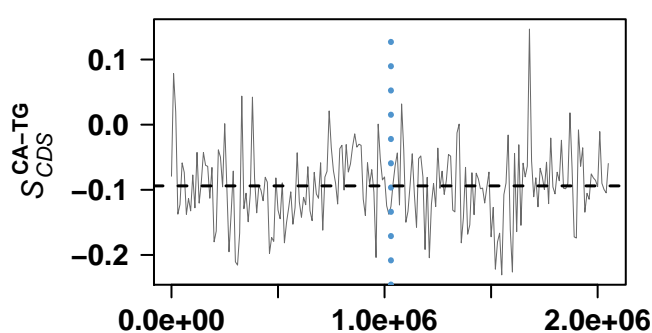
genome coordinates



genome coordinates

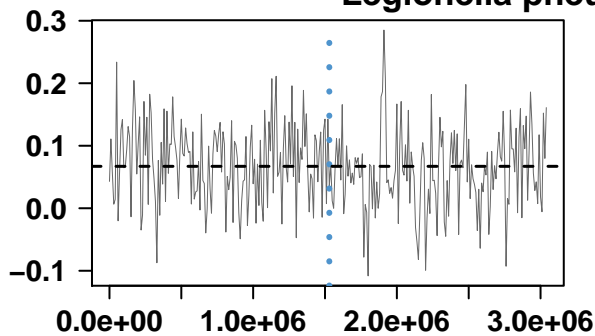


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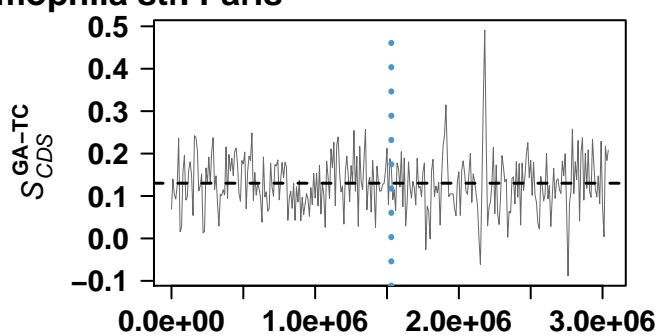


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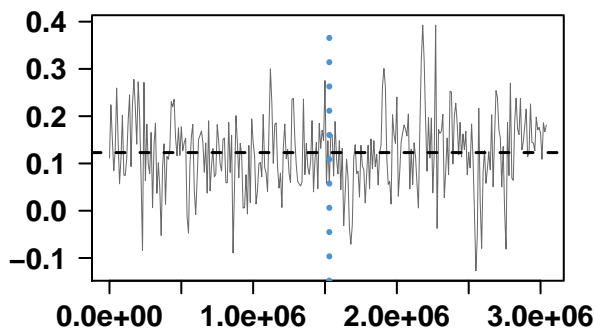
Legionella pneumophila str. Paris



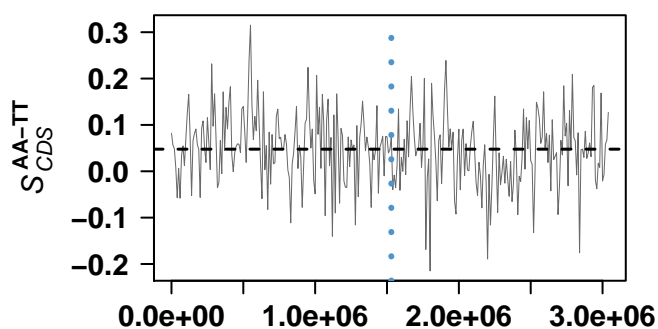
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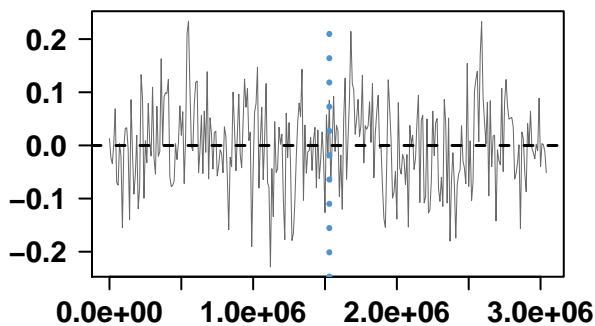
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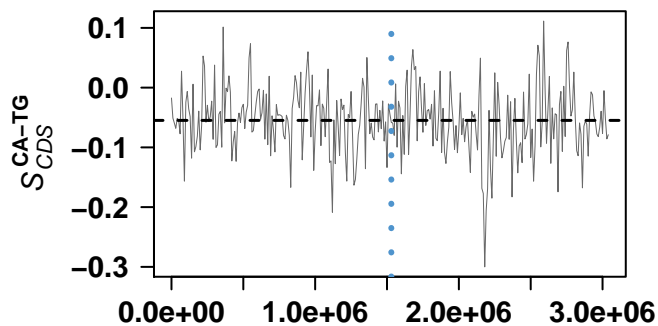
genome coordinates



genome coordinates

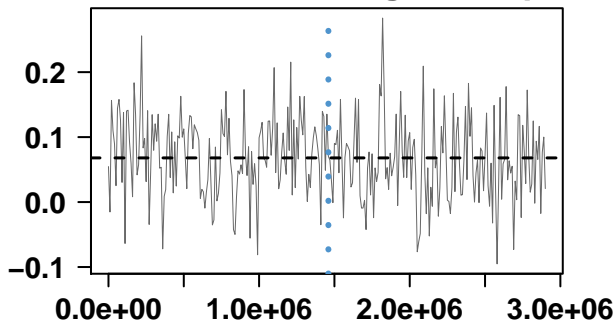


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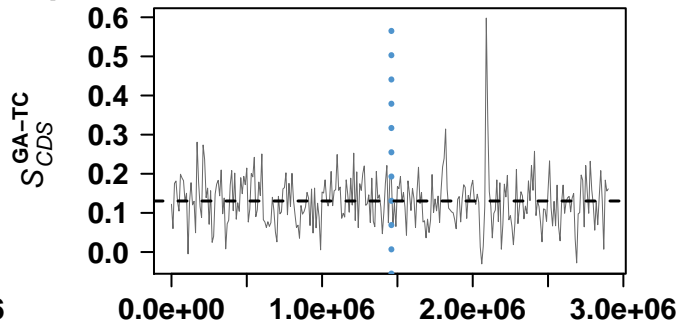


genome coordinates

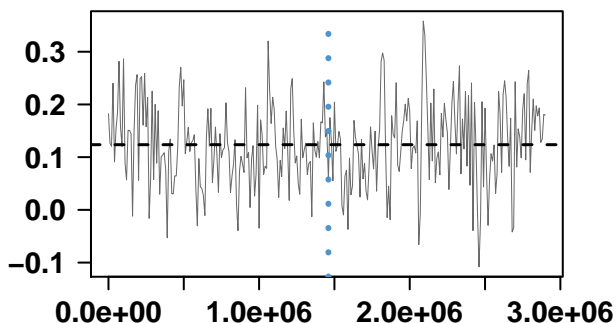
Legionella pneumophila str. Lens



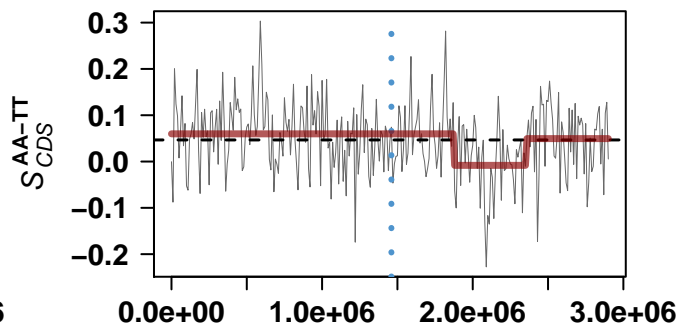
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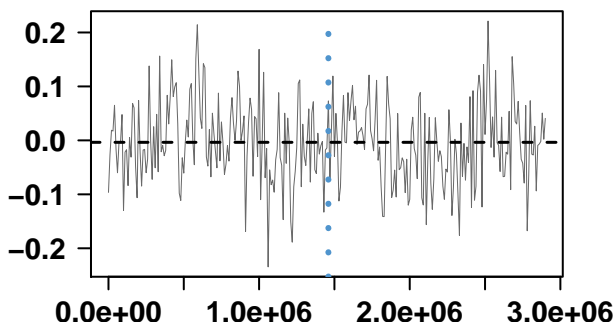
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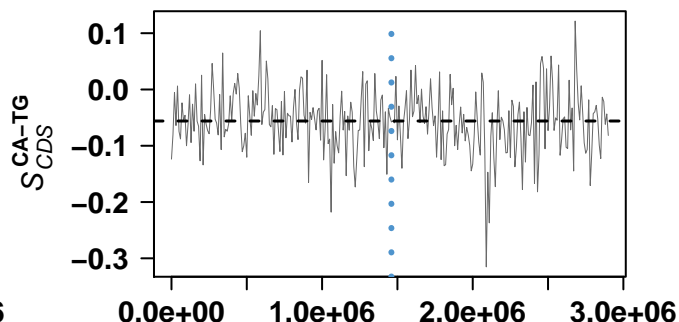
genome coordinates



genome coordinates

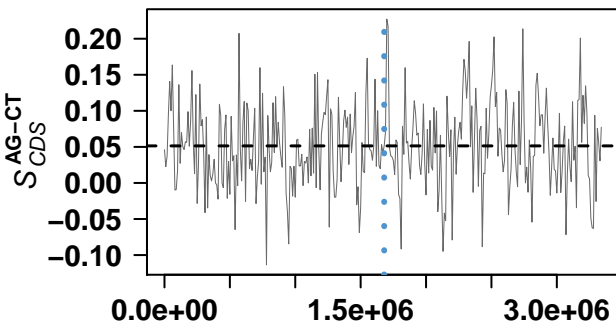


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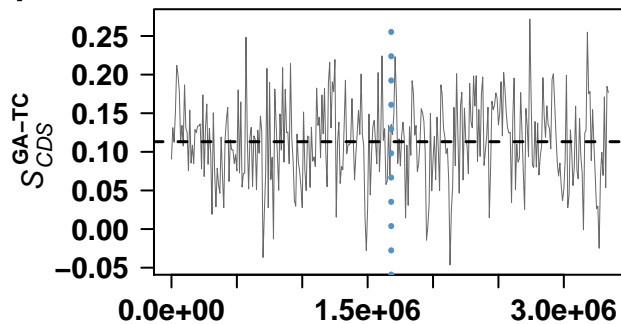


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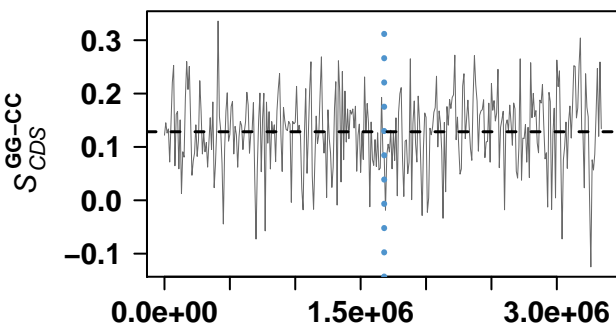
Photobacterium profundum SS9



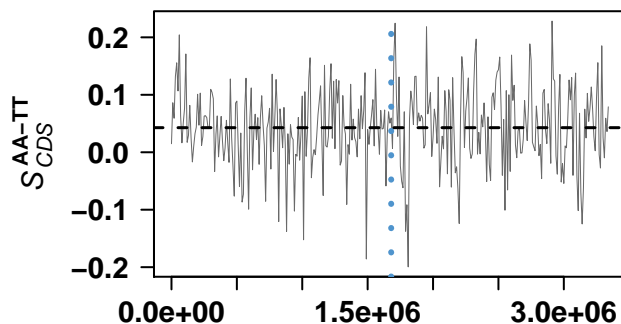
genome coordinates



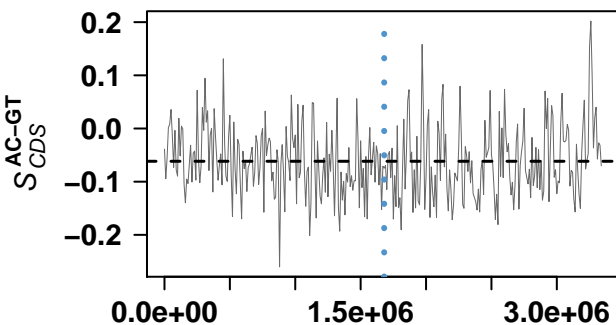
genome coordinates



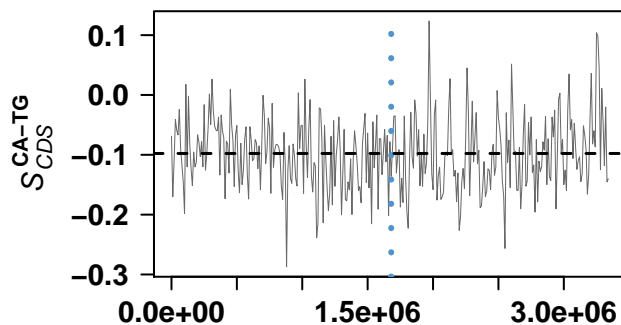
genome coordinates



genome coordinates

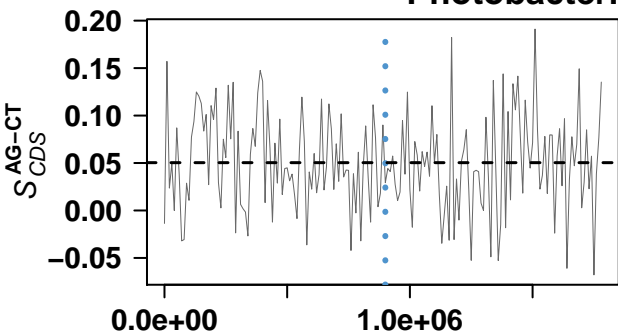


genome coordinates

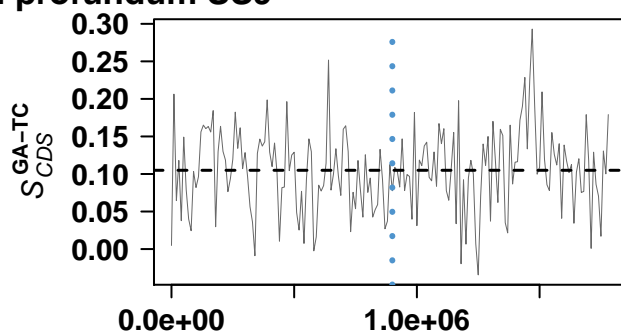


genome coordinates

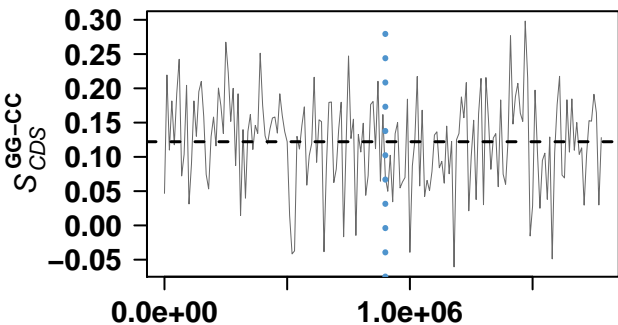
Photobacterium profundum SS9



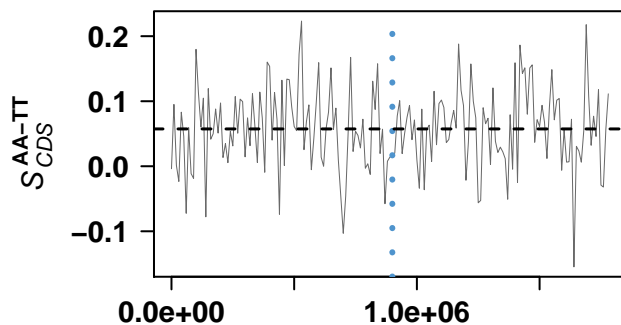
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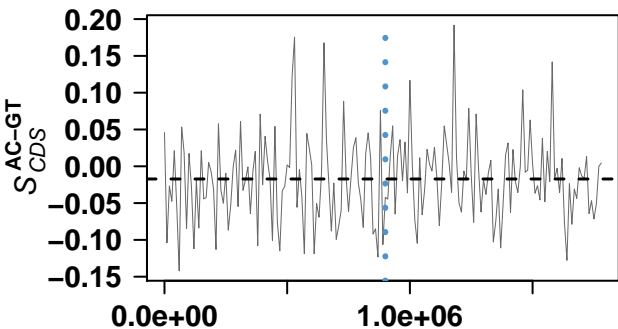
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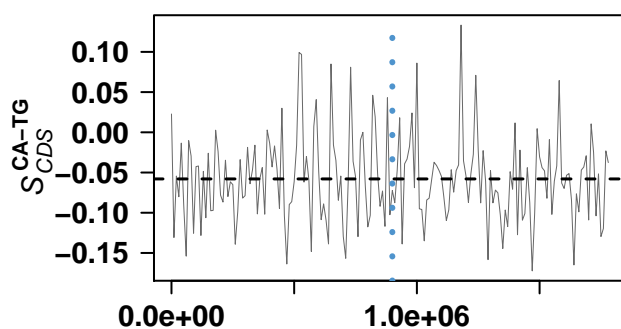
genome coordinates



genome coordinates

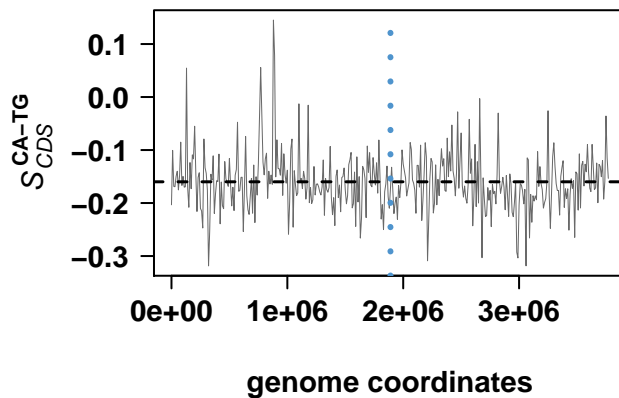
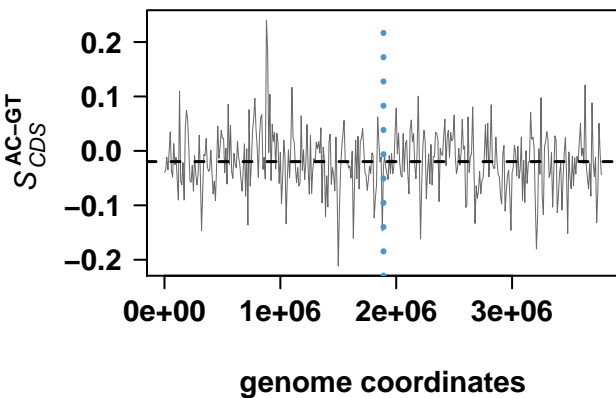
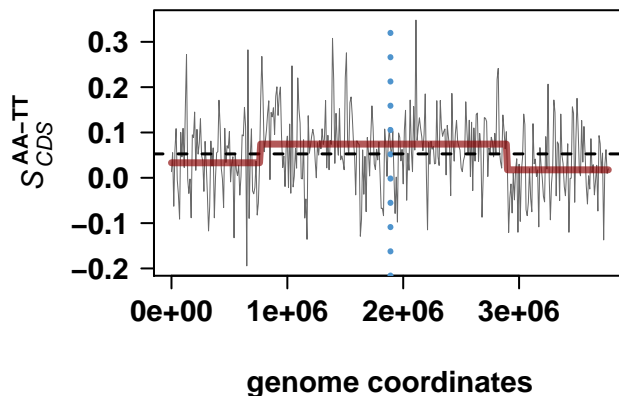
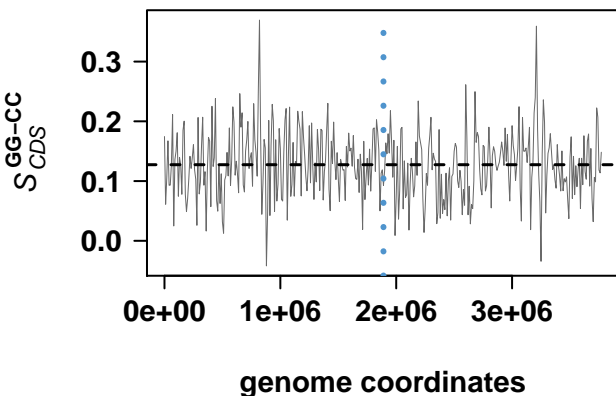
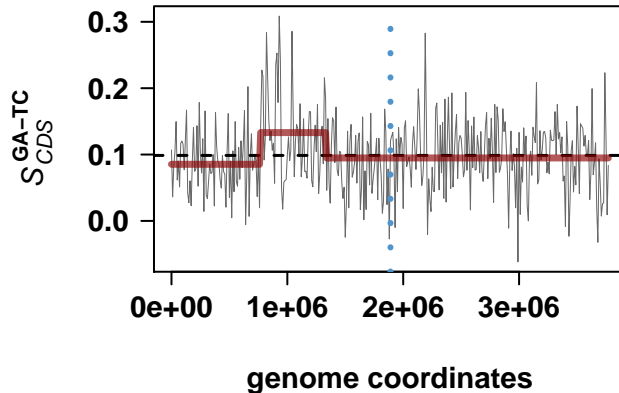
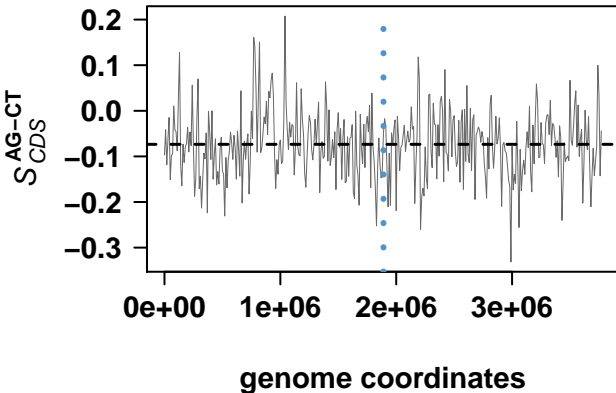


genome coordinates

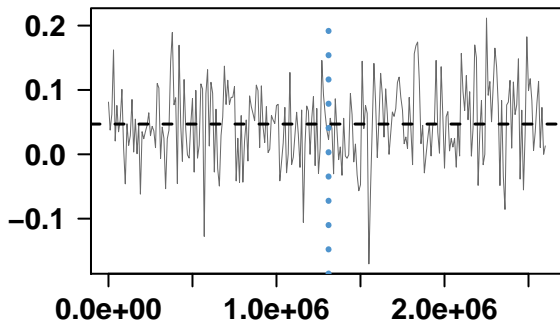


genome coordinates

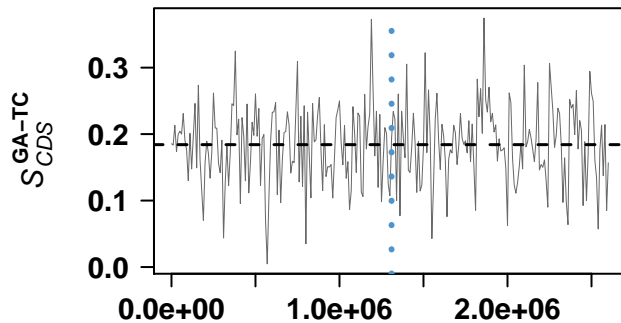
Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150



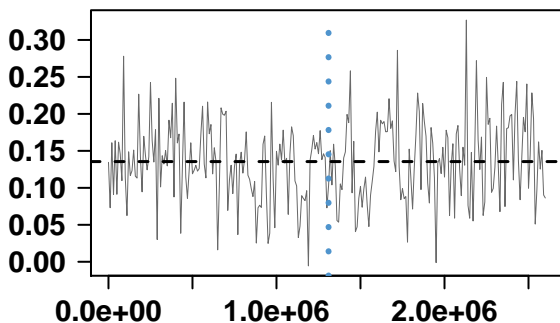
Idiomarina loihiensis L2TR



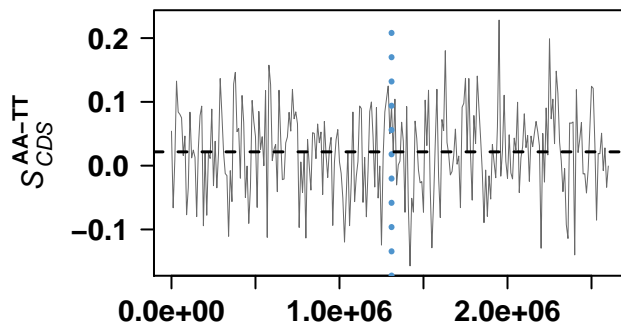
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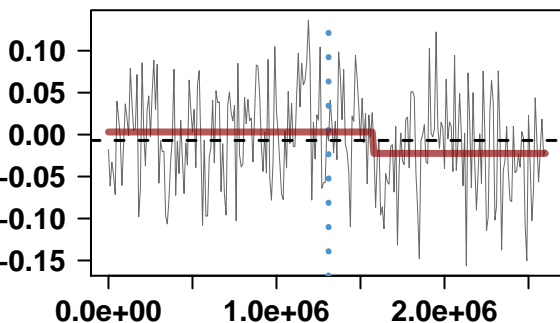
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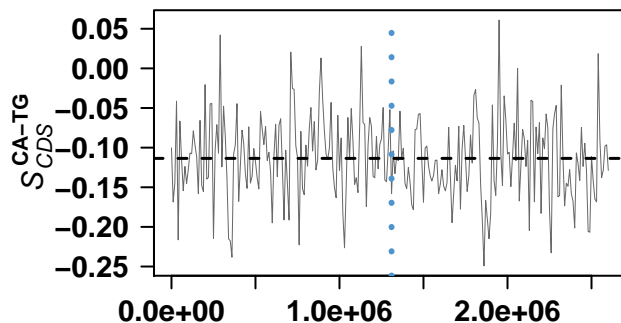
genome coordinates



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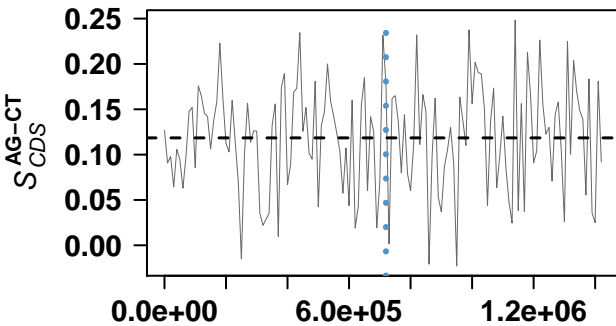


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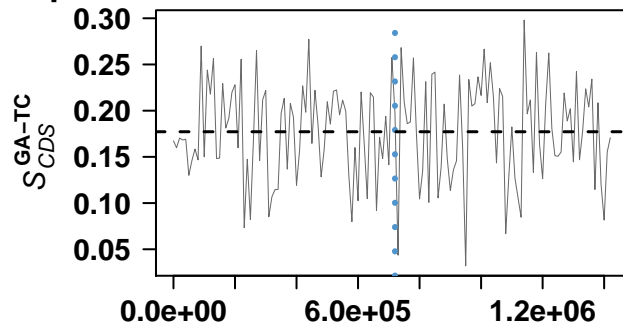


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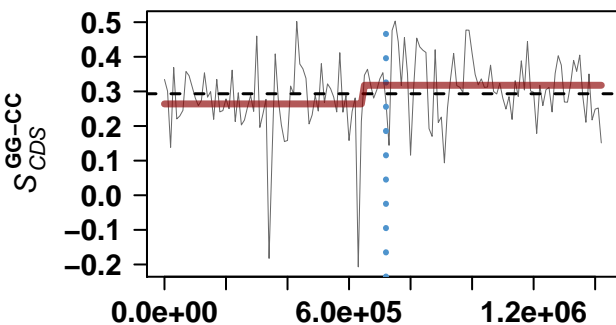
Francisella tularensis subsp. tularensis SCHU S4



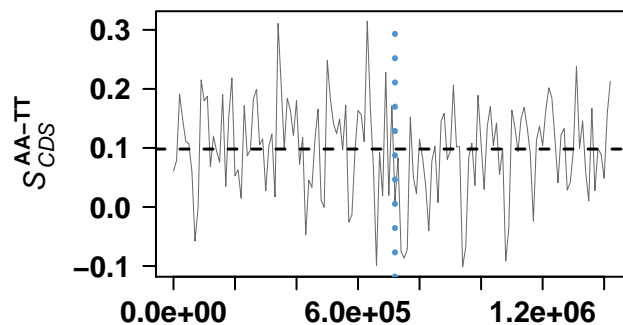
genome coordinates



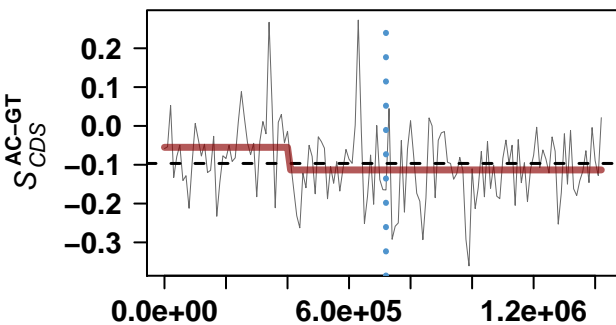
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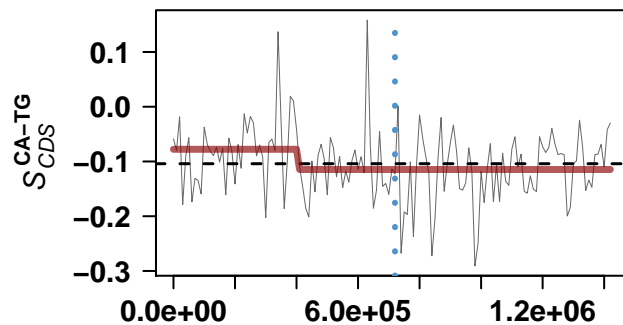
genome coordinates



genome coordinates

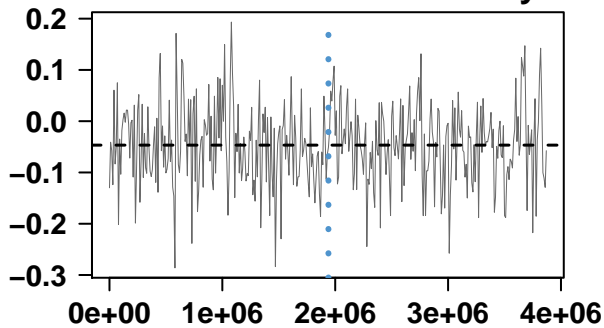


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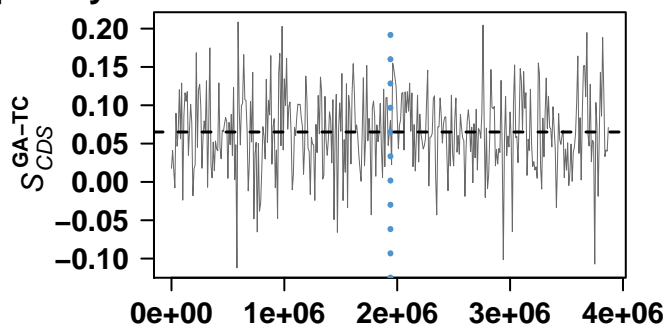


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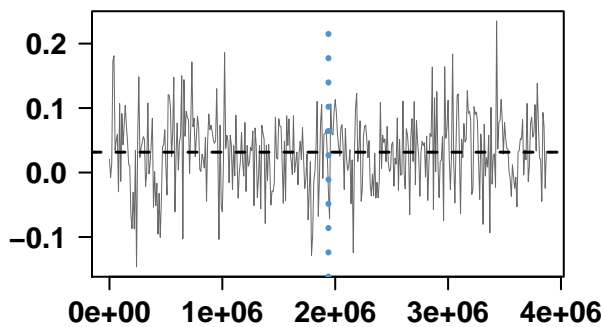
Xanthomonas oryzae pv. oryzae KACC 10331



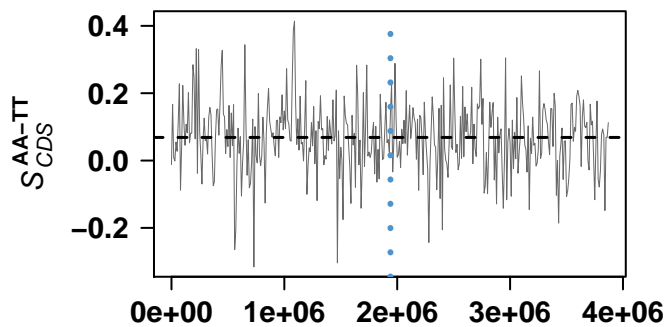
genome coordinates



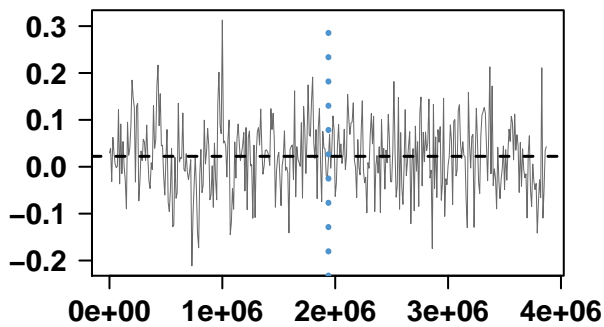
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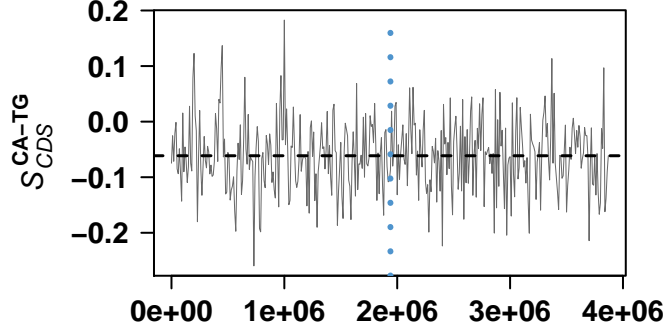
genome coordinates



genome coordinates

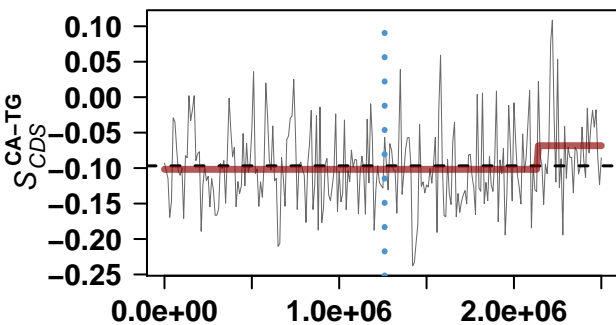
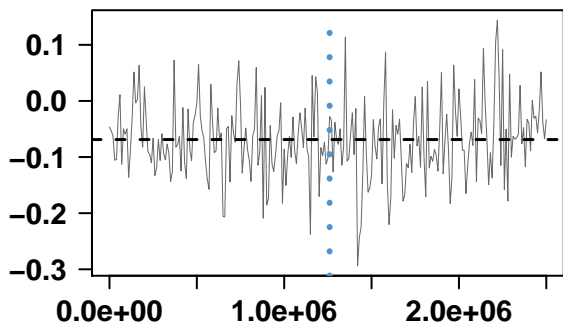
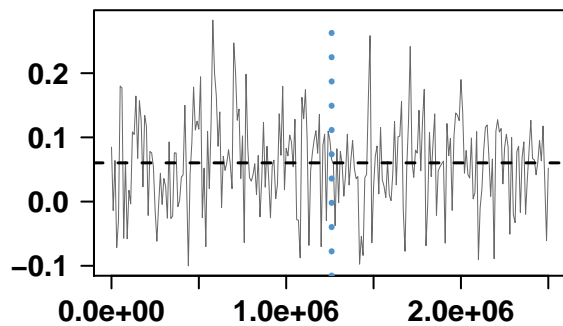
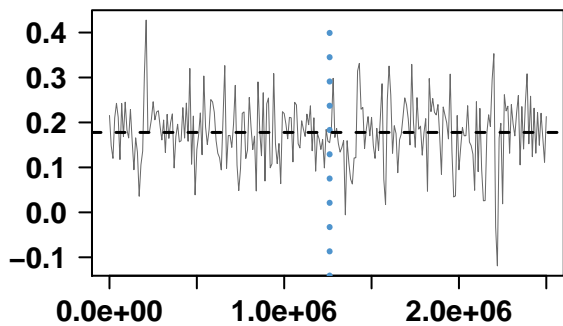
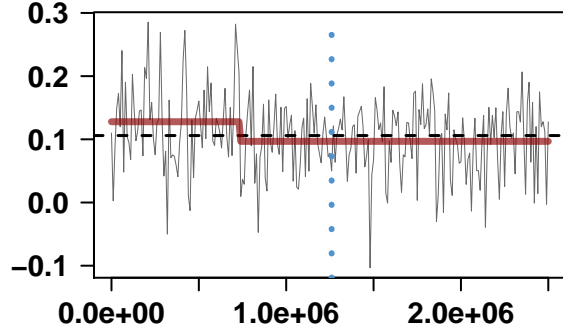
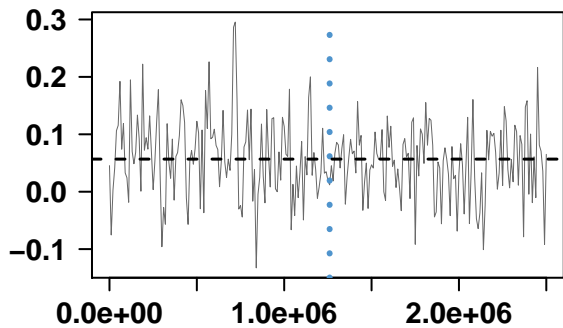


genome coordinates

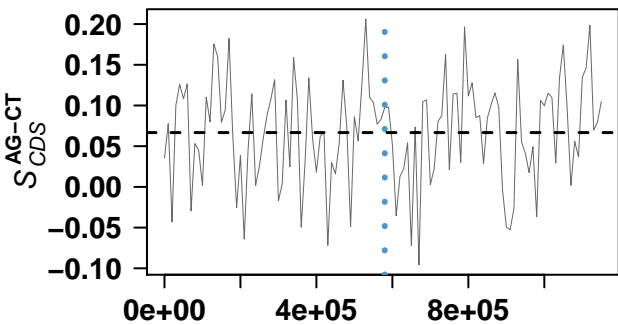


genome coordinates

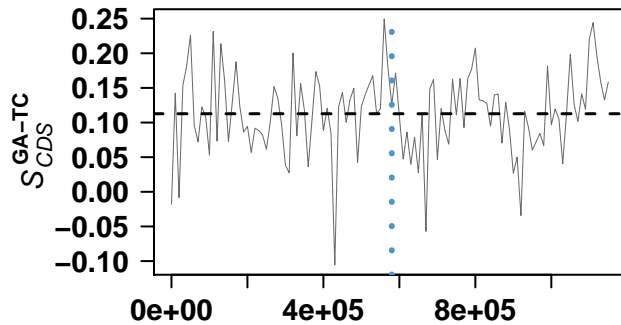
Vibrio fischeri ES114



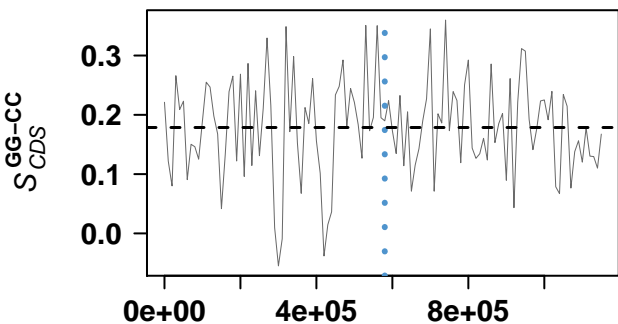
Vibrio fischeri ES114



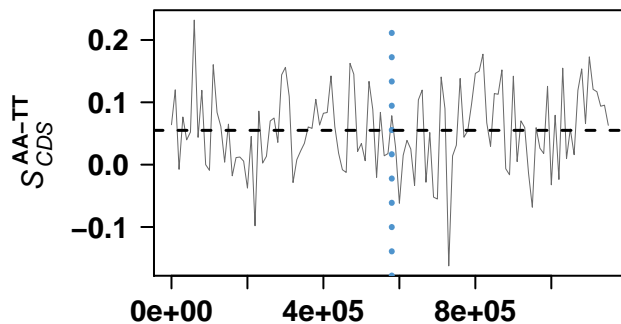
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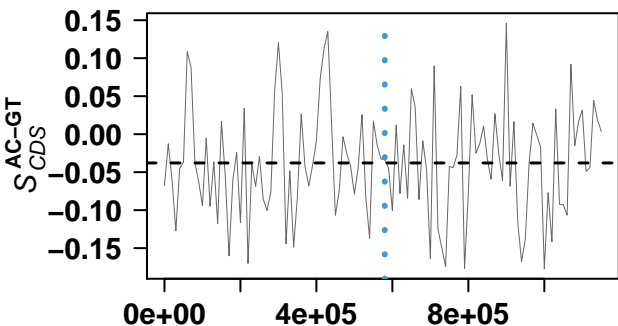
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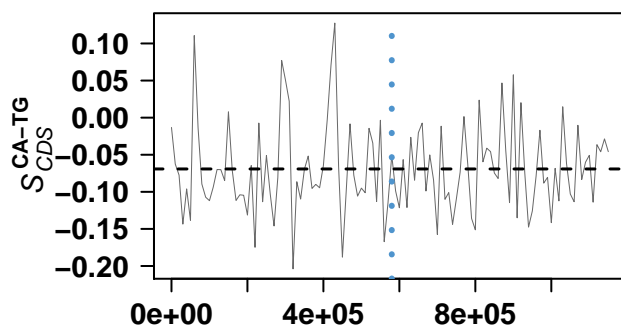
genome coordinates



genome coordinates

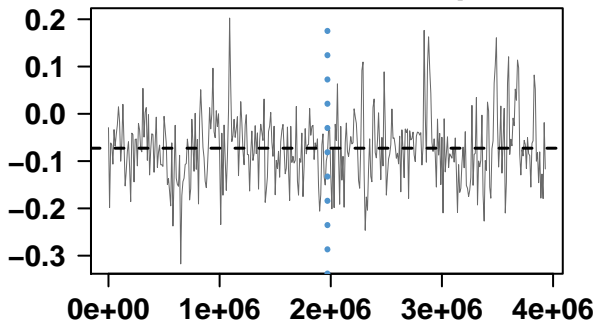


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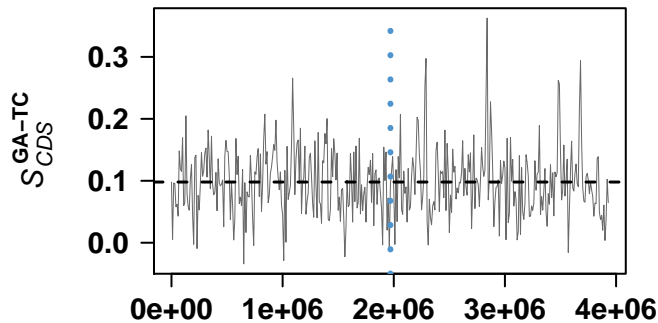


genome coordinates

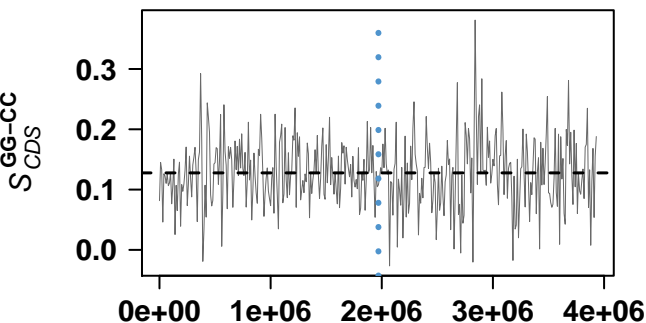
Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67



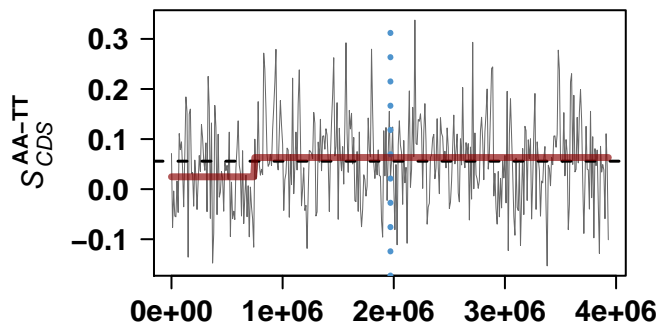
genome coordinates



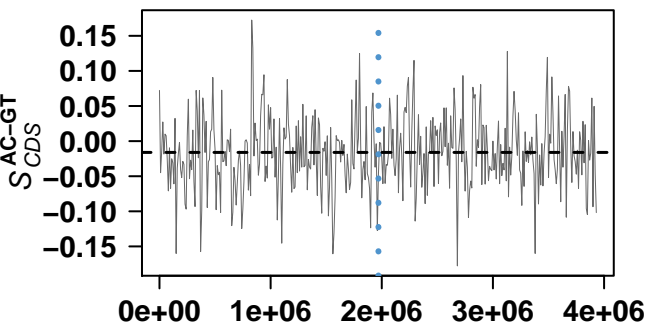
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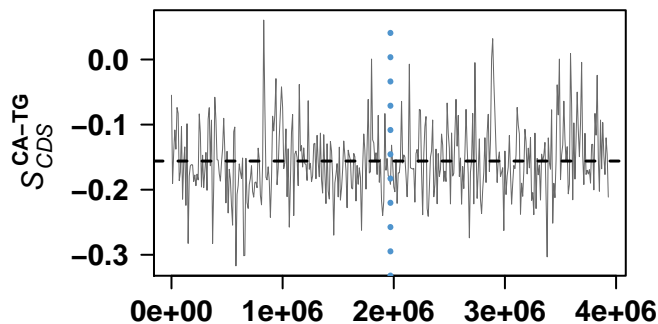
genome coordinates



genome coordinates

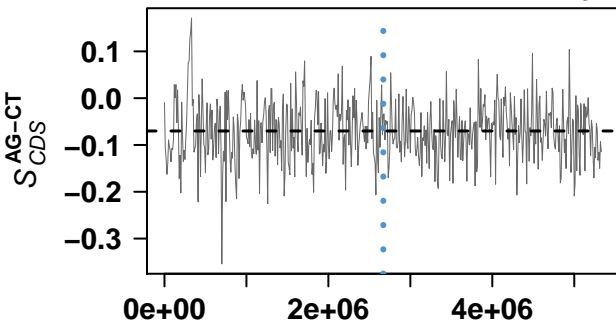


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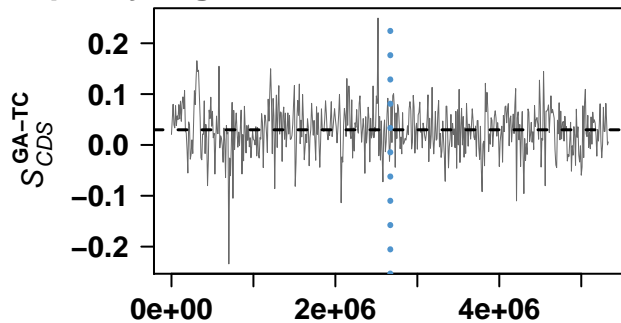


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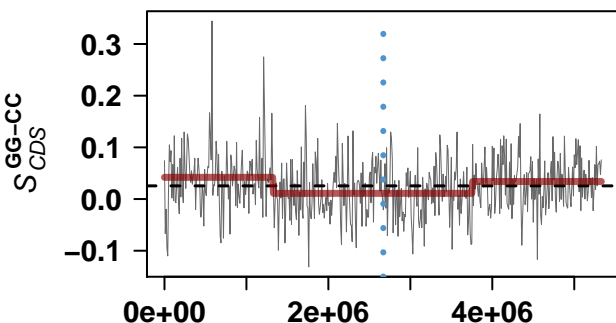
Pseudomonas syringae pv. *syringae* B728a



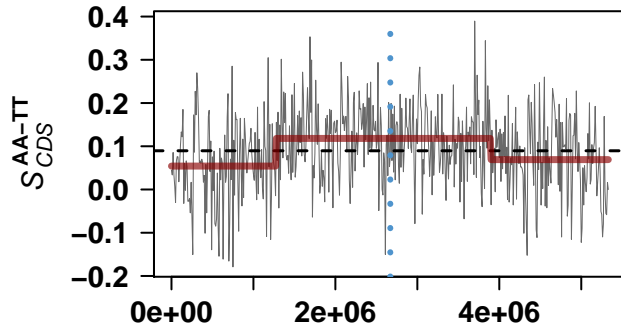
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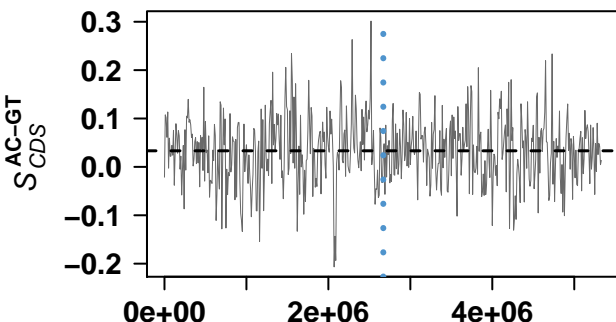
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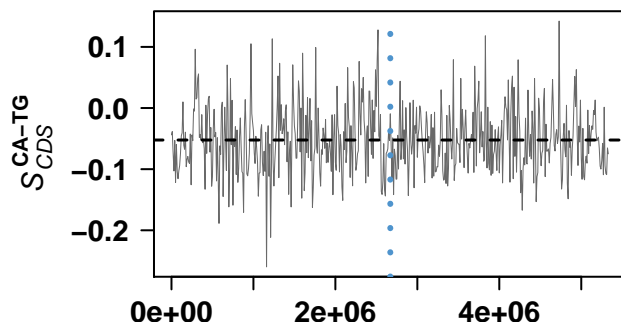
genome coordinates



genome coordinates

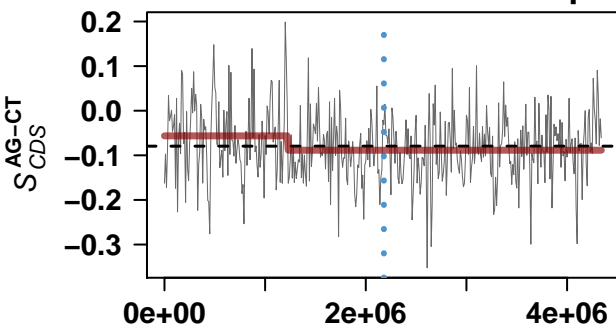


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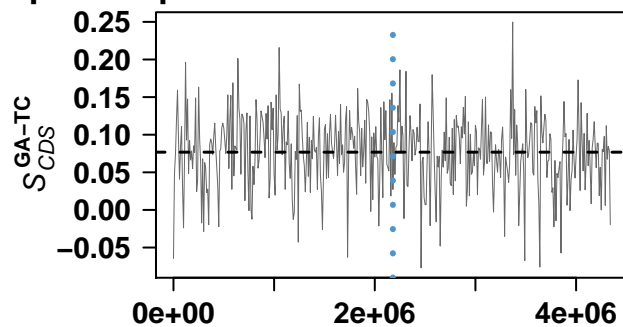


genome coordinates

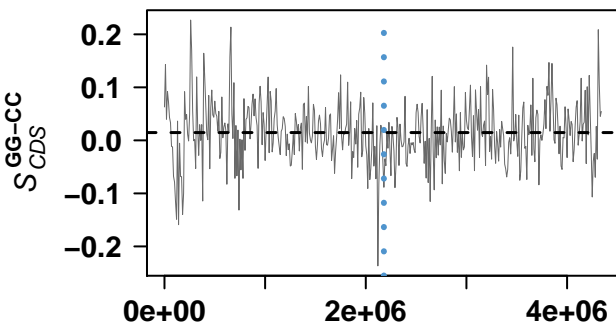
Xanthomonas campestris pv. campestris str. 8004



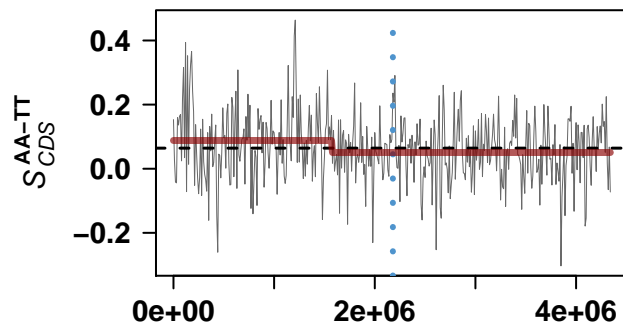
genome coordinates



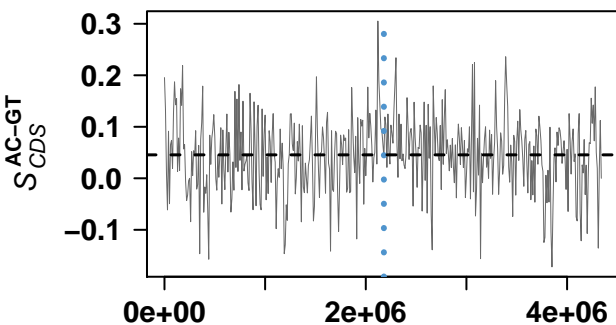
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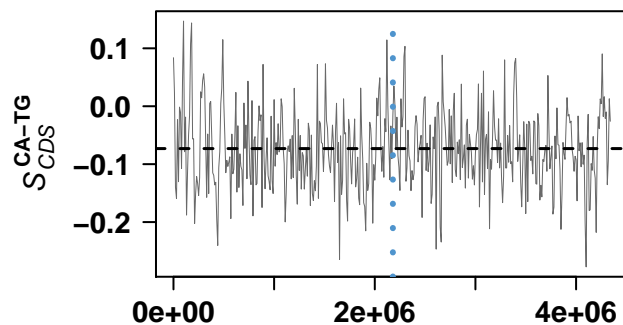
genome coordinates



genome coordinates

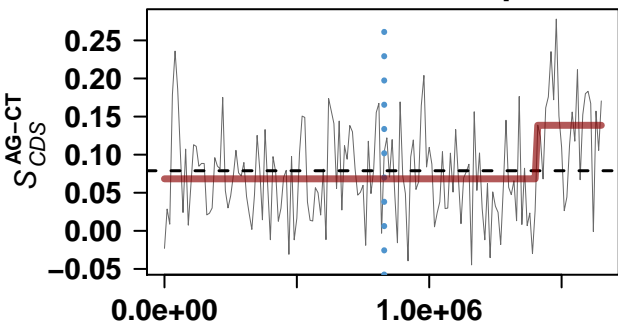


genome coordinates

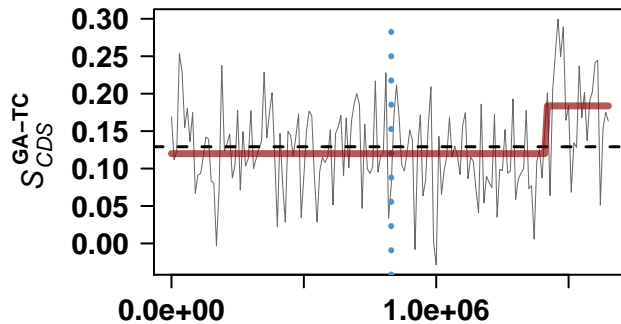


genome coordinates

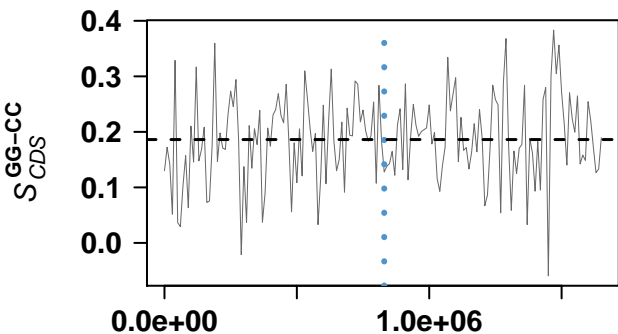
Haemophilus influenzae 86-028NP



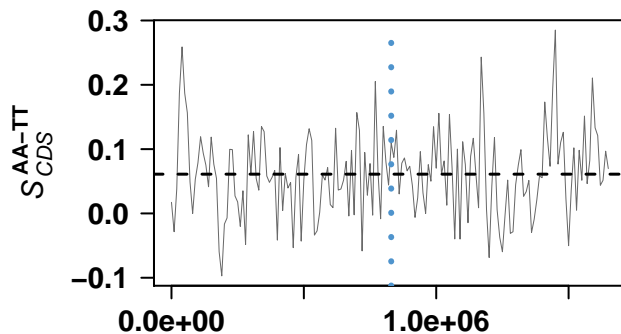
genome coordinates



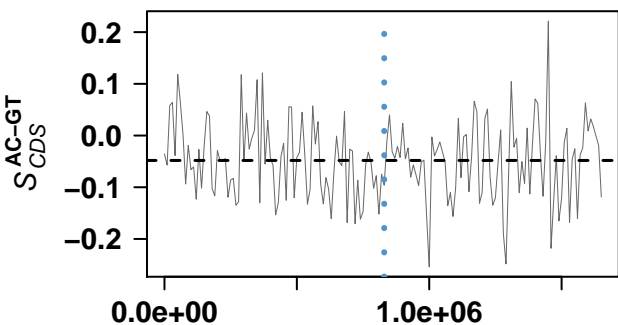
genome coordinates



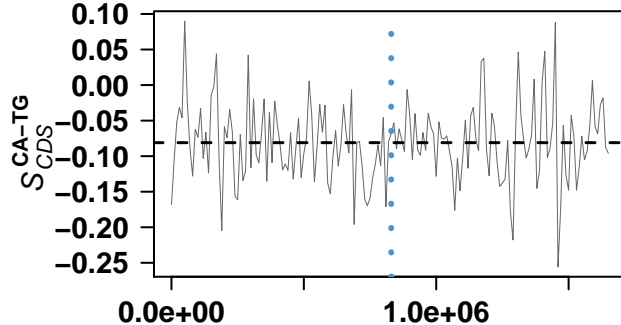
genome coordinates



genome coordinates

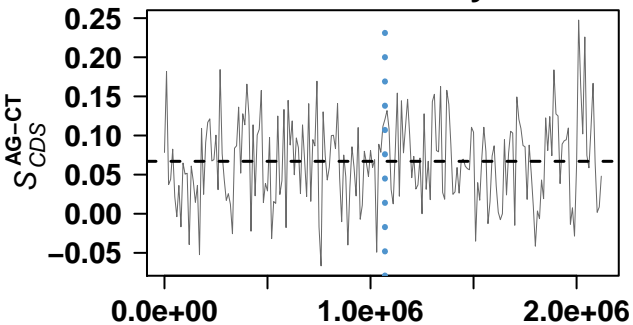


genome coordinates

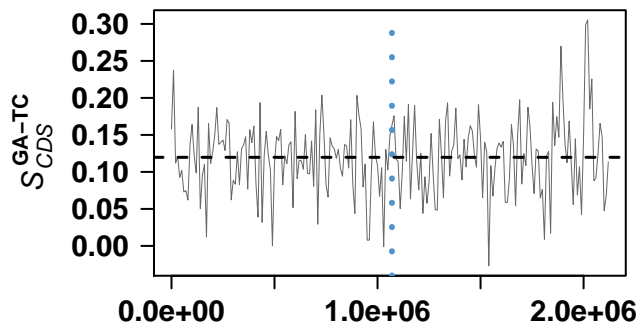


genome coordinates

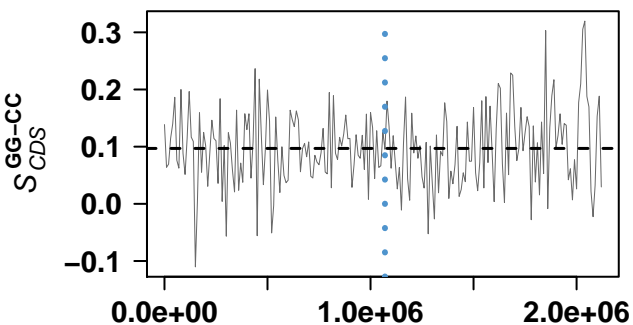
Psychrobacter arcticus 273-4



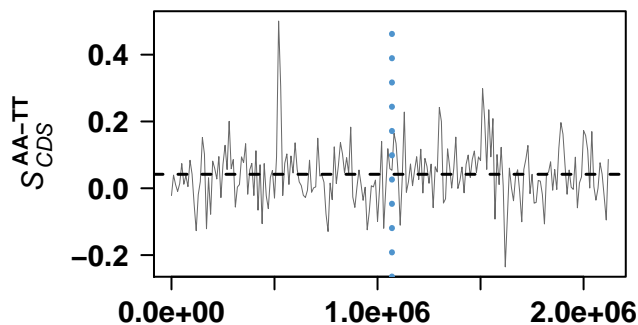
genome coordinates



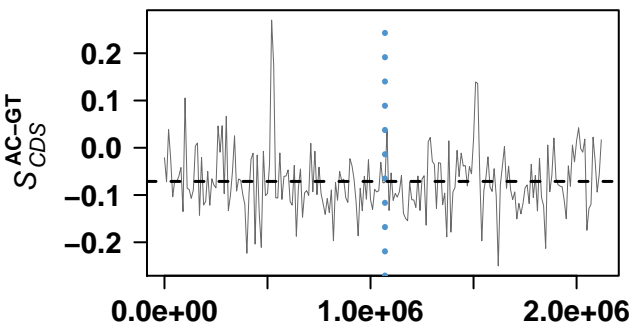
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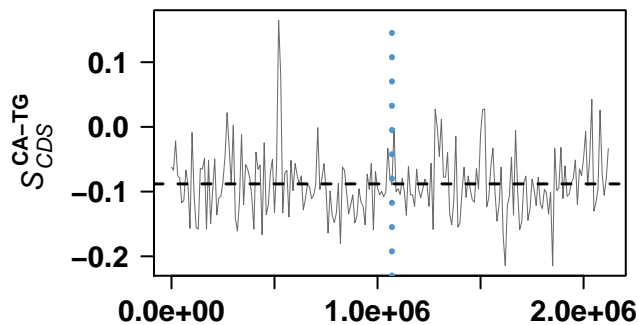
genome coordinates



genome coordinates

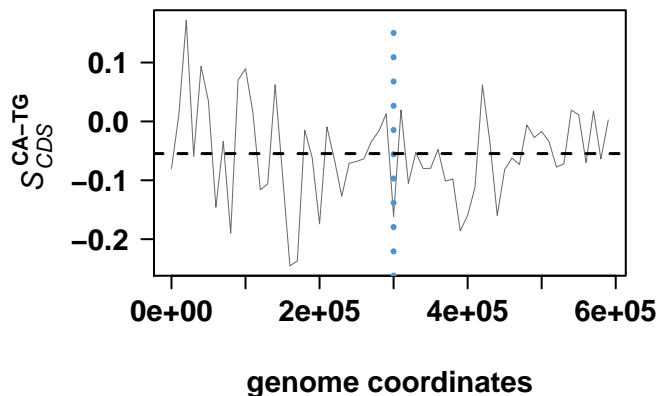
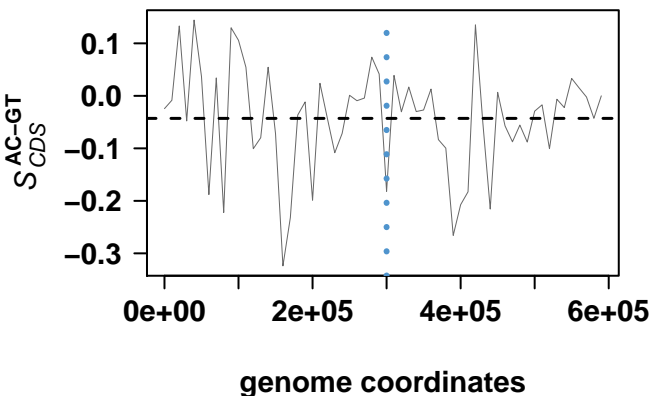
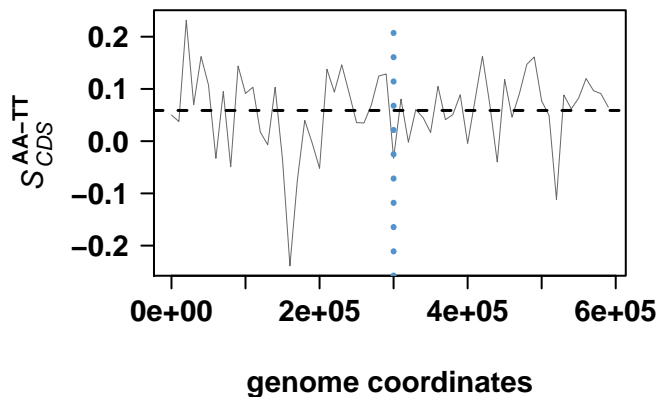
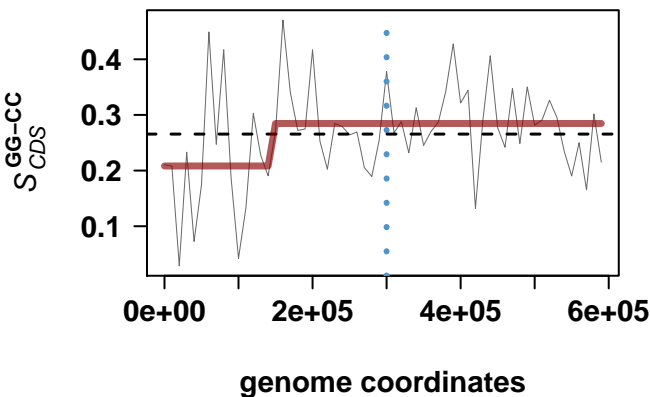
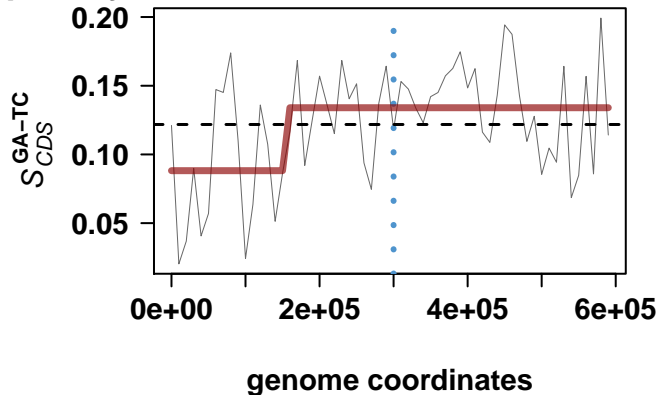
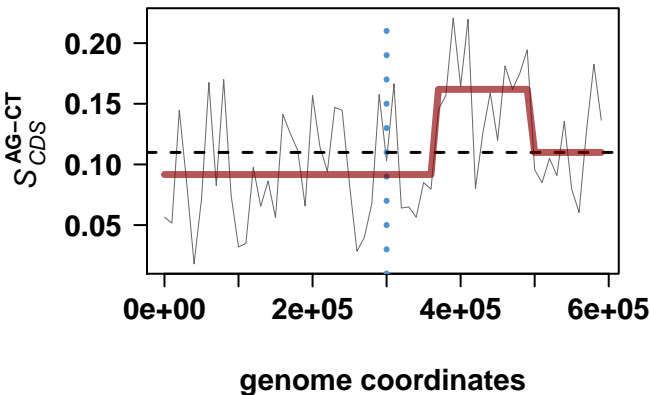


genome coordinates

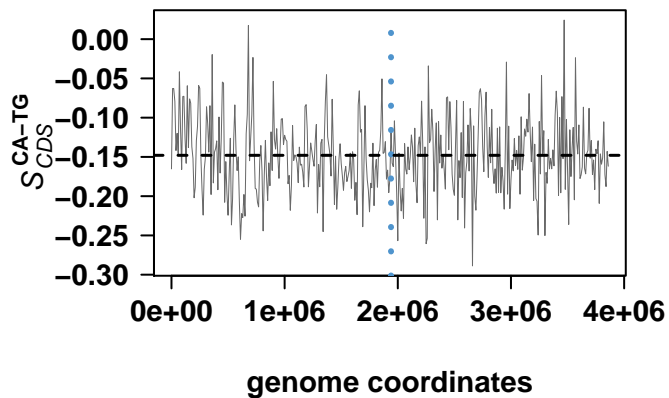
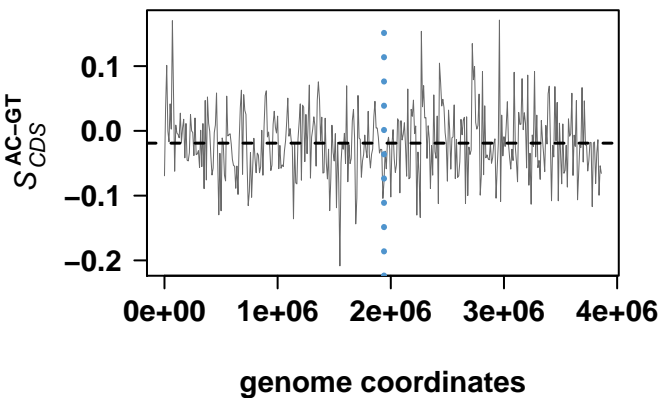
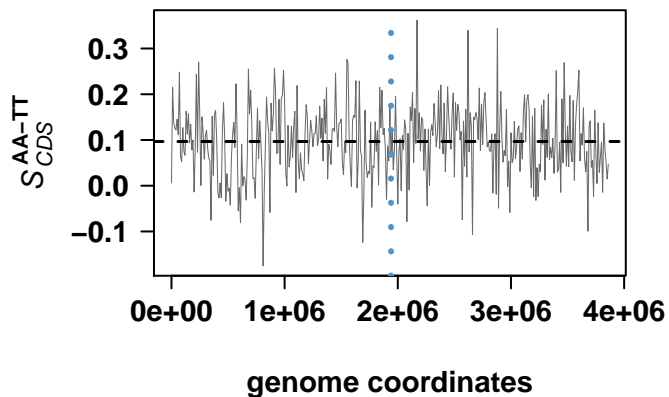
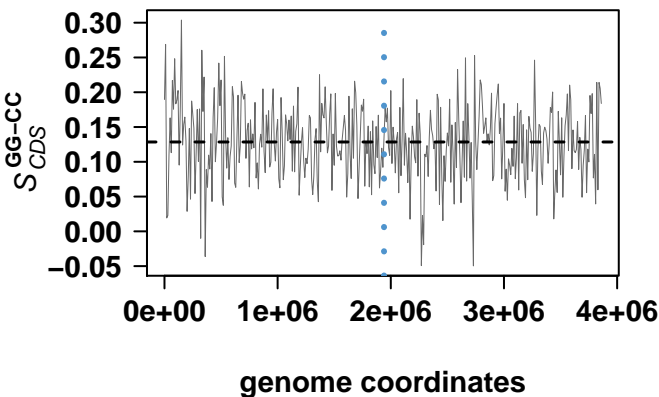
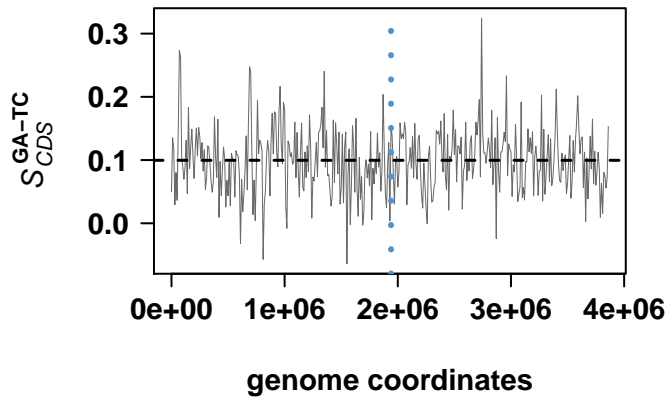
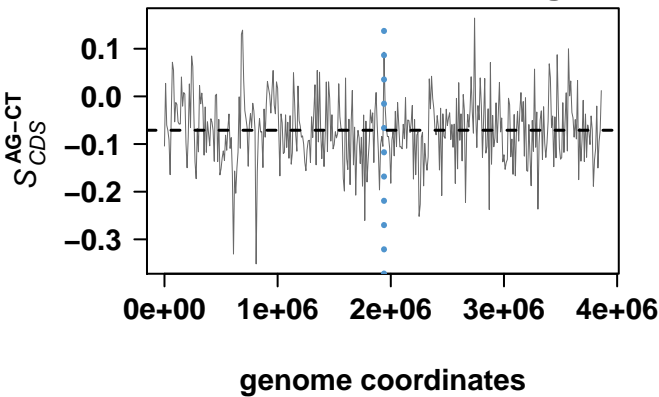


genome coordinates

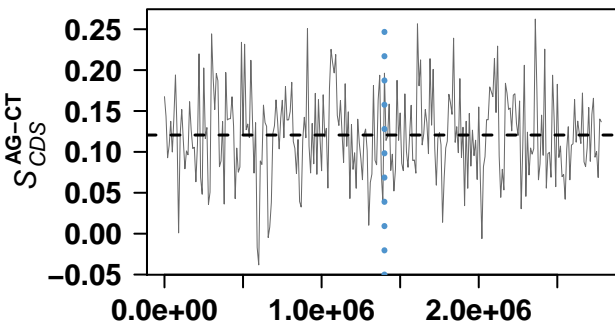
Candidatus Blochmannia pennsylvanicus str. BPEN



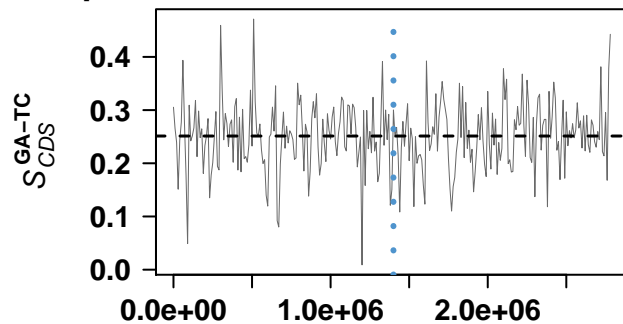
Shigella sonnei Ss046



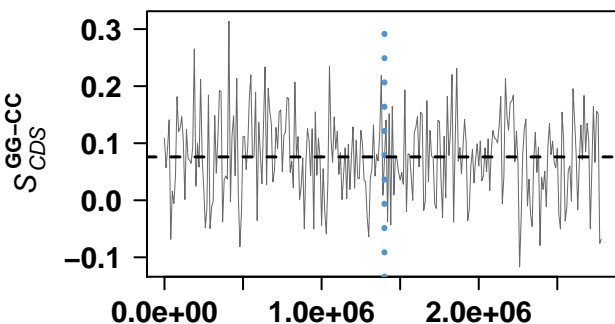
Pseudoalteromonas haloplanktis TAC125



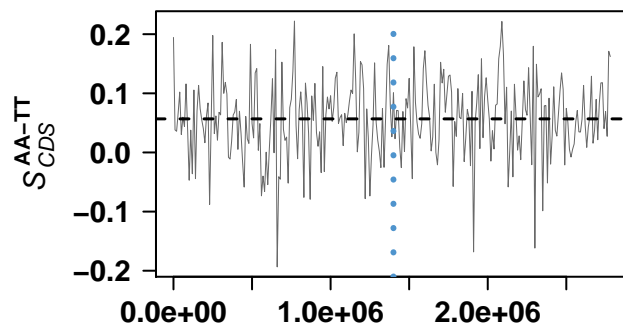
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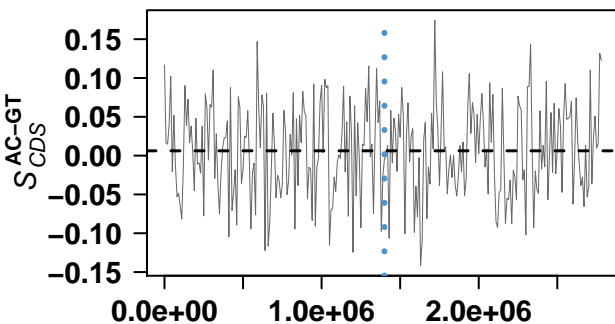
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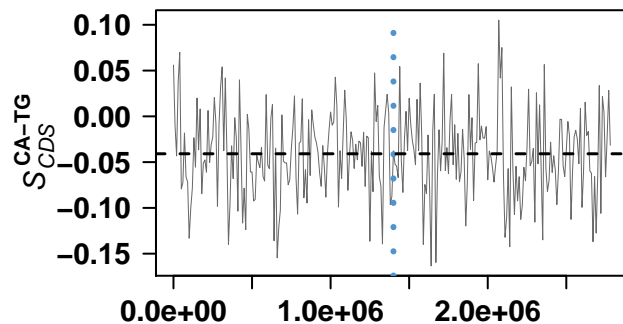
genome coordinates



genome coordinates

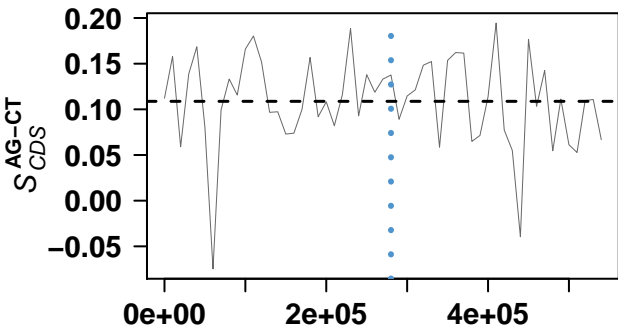


genome coordinates

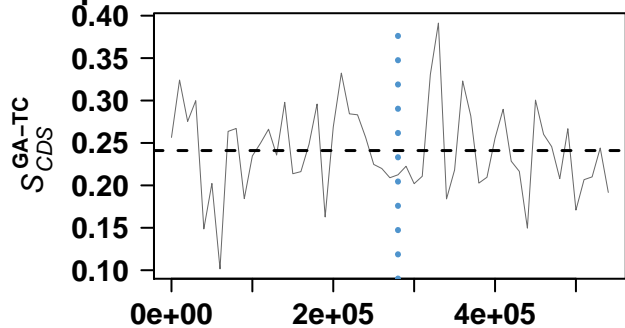


genome coordinates

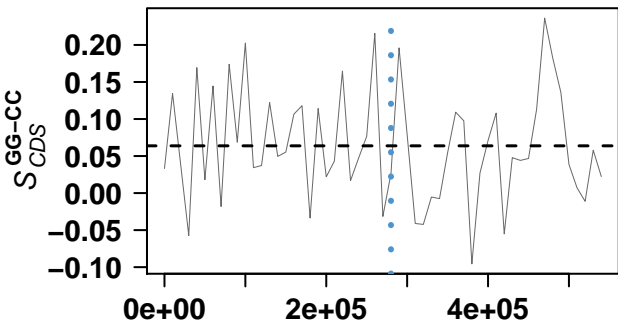
Pseudoalteromonas haloplanktis TAC125



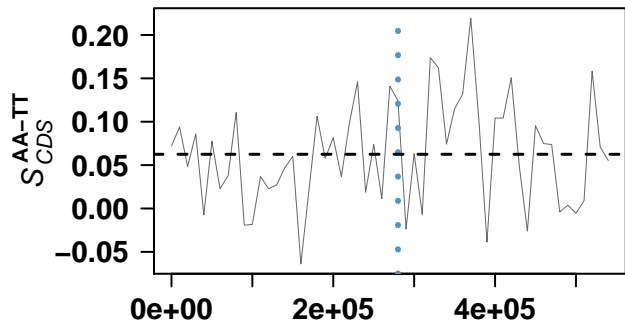
genome coordinates



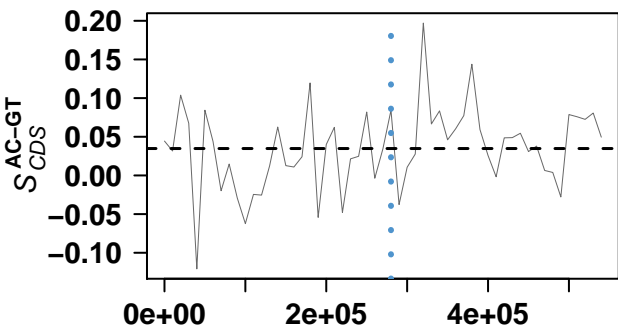
genome coordinates



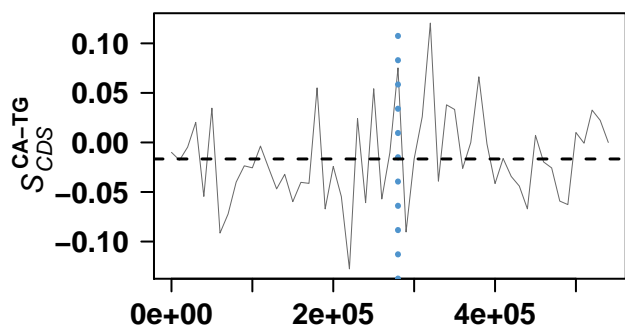
genome coordinates



genome coordinates

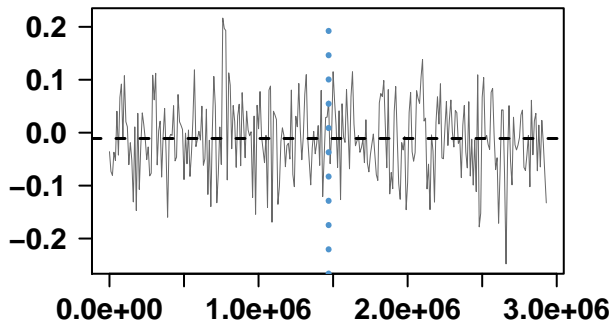


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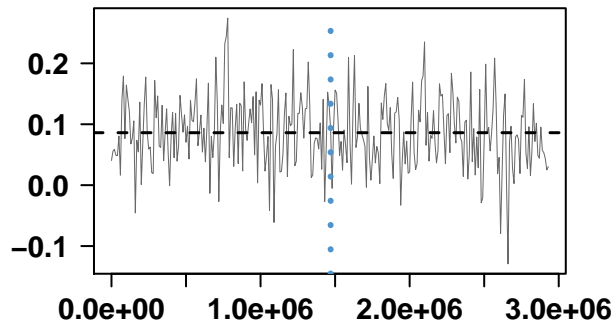


genome coordinates

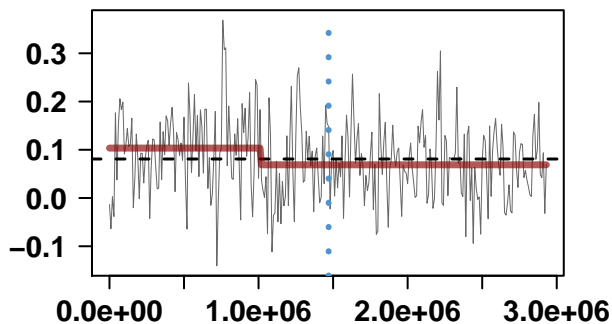
Nitrosococcus oceani ATCC 19707



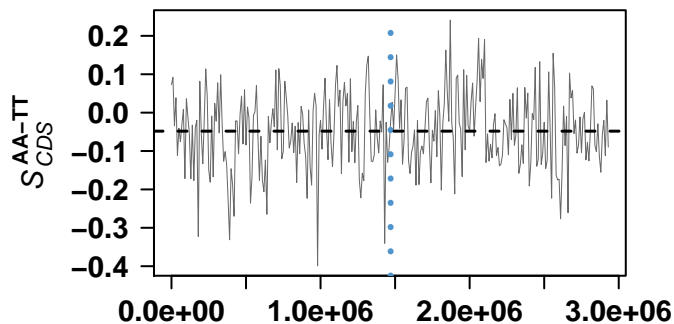
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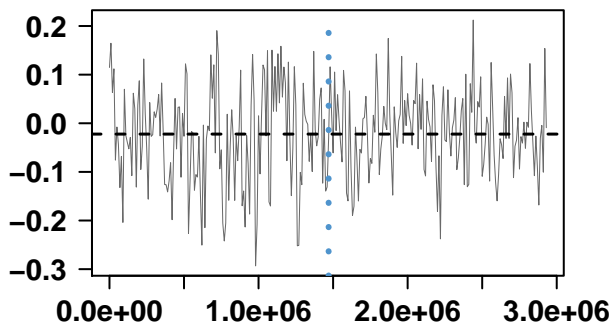
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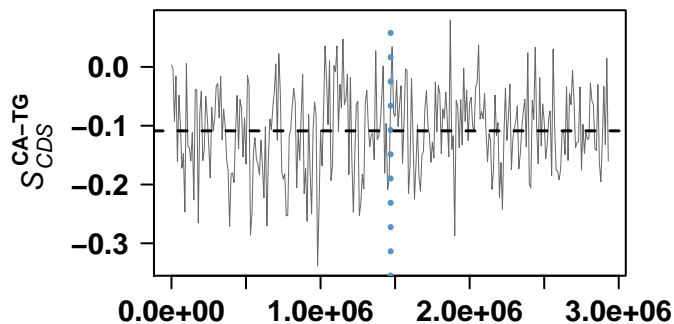
genome coordinates



genome coordinates

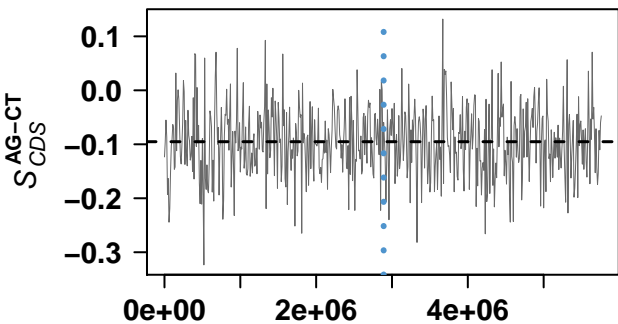


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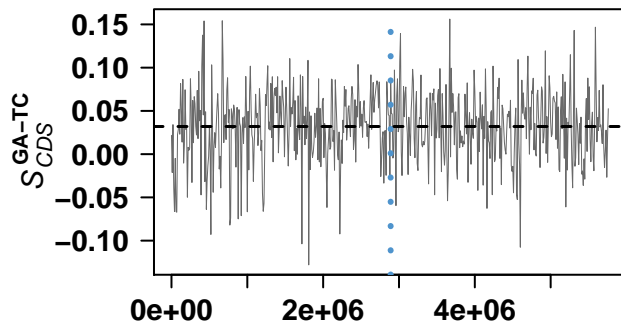


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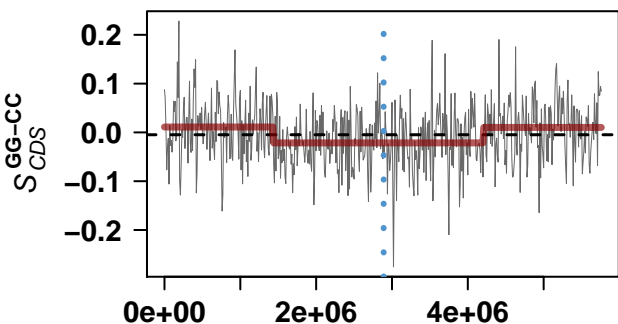
Pseudomonas fluorescens Pf0-1



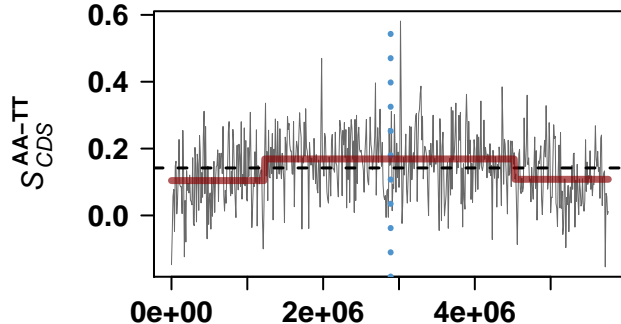
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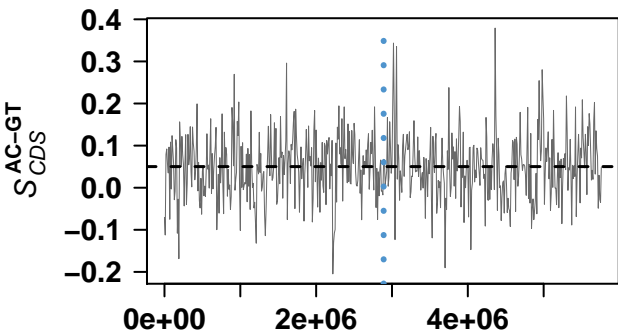
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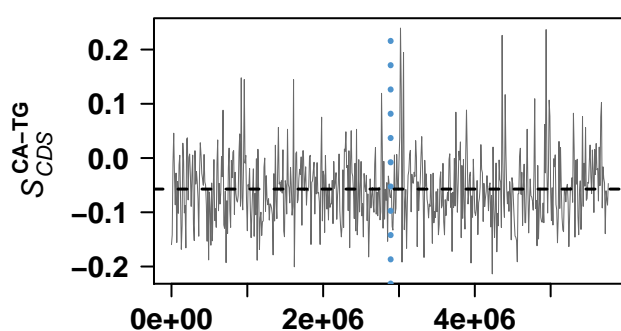
genome coordinates



genome coordinates

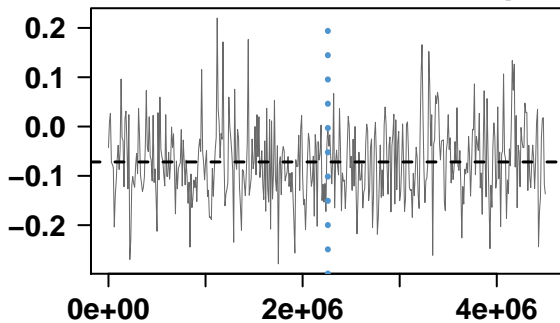


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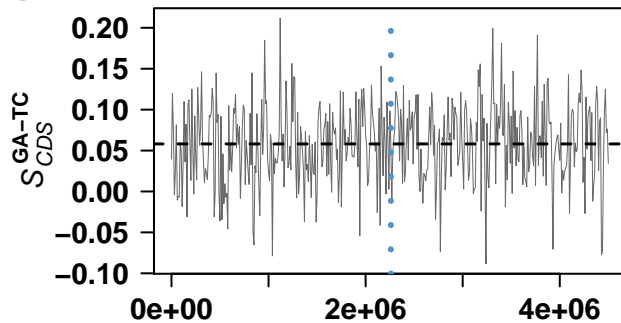


genome coordinates

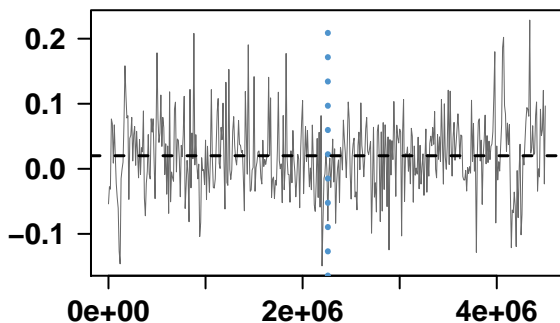
Xanthomonas campestris pv. *vesicatoria* str. 85-10



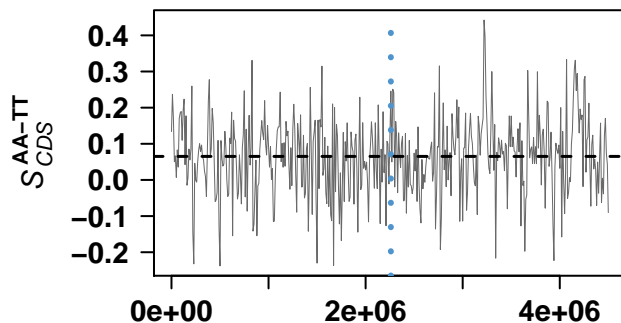
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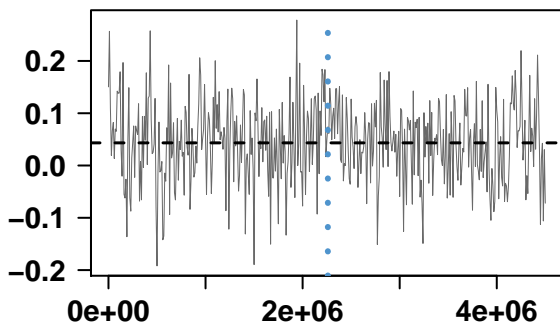
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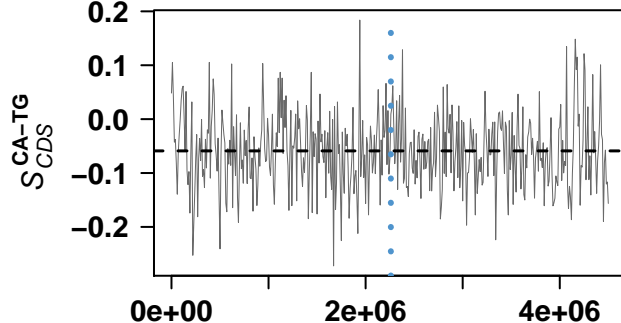
genome coordinates



genome coordinates

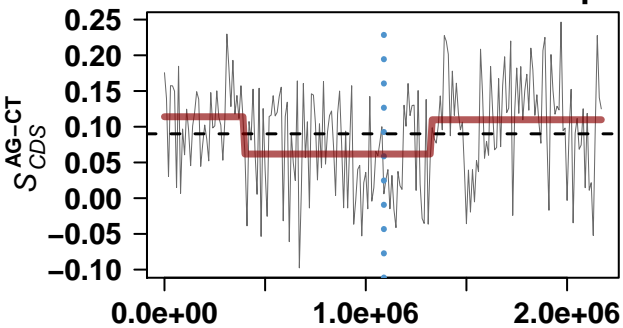


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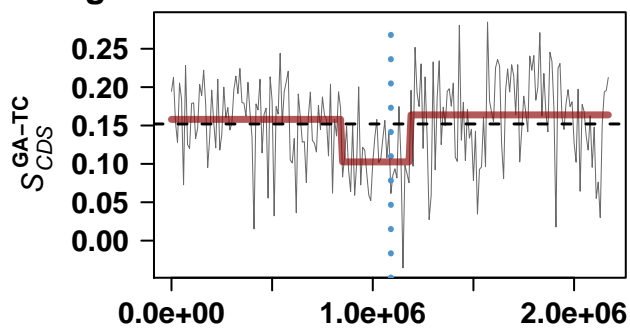


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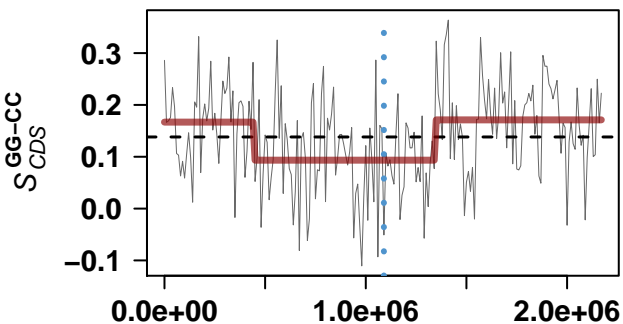
Thiomicrospira crunogena XCL-2



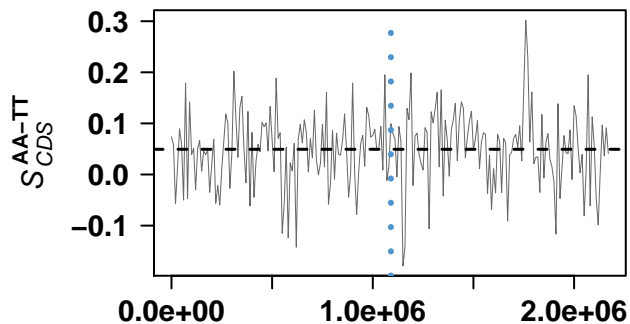
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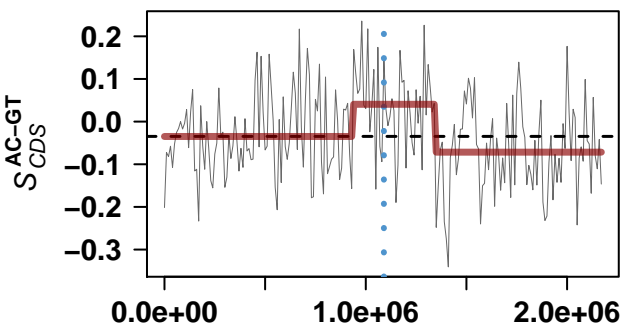
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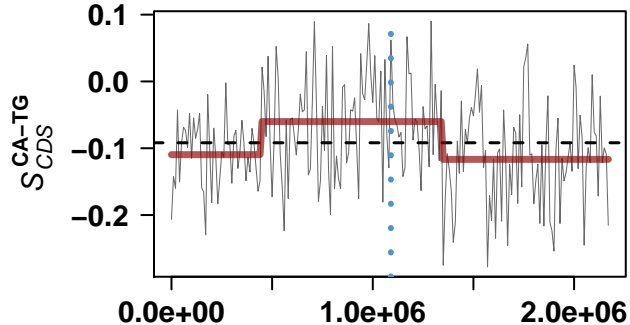
genome coordinates



genome coordinates

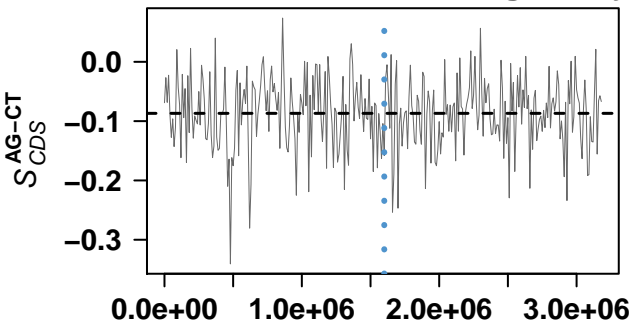


genome coordinates

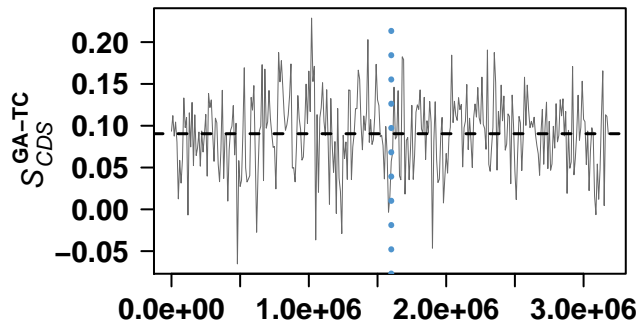


genome coordinates

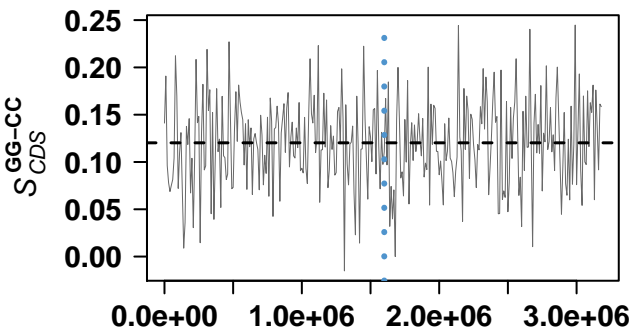
Shigella dysenteriae Sd197



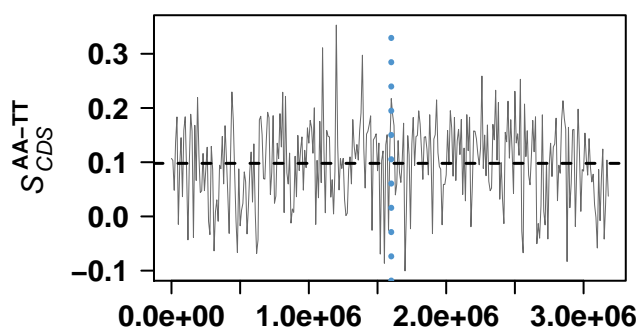
genome coordinates



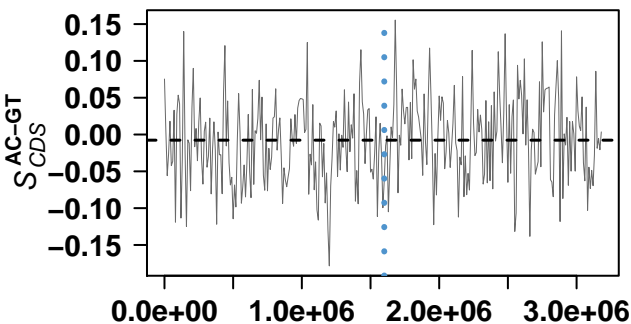
genome coordinates



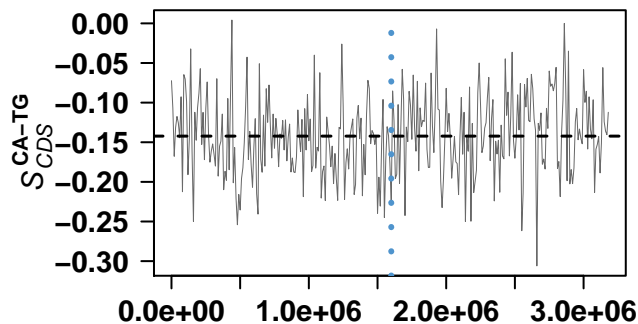
genome coordinates



genome coordinates

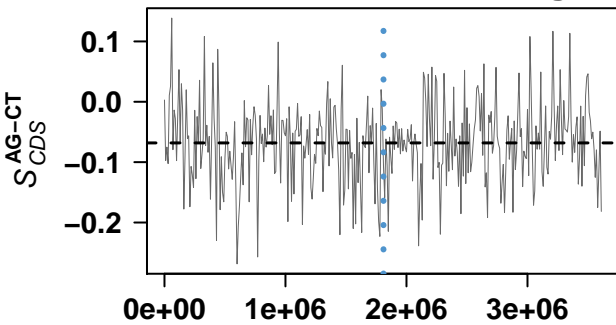


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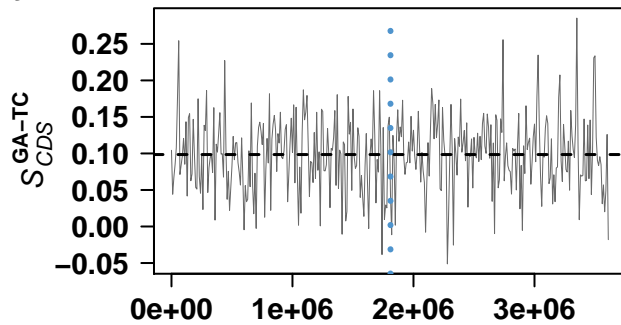


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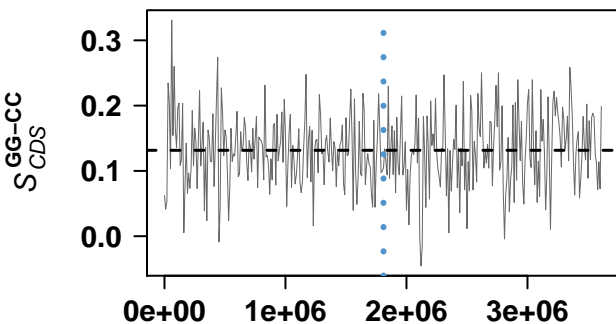
Shigella boydii Sb227



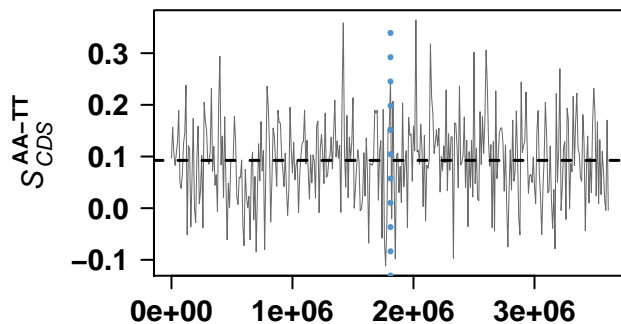
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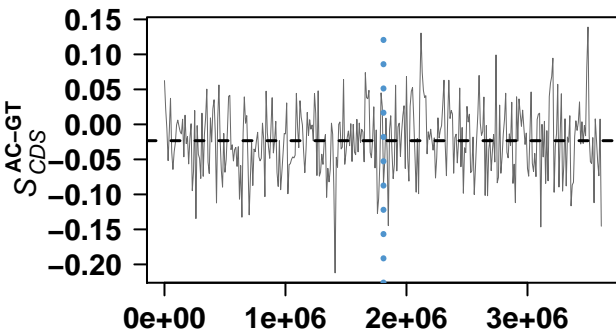
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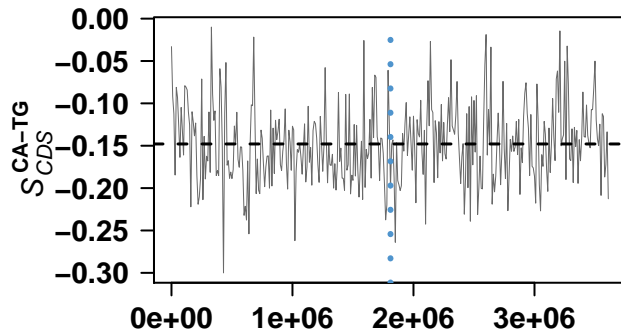
genome coordinates



genome coordinates

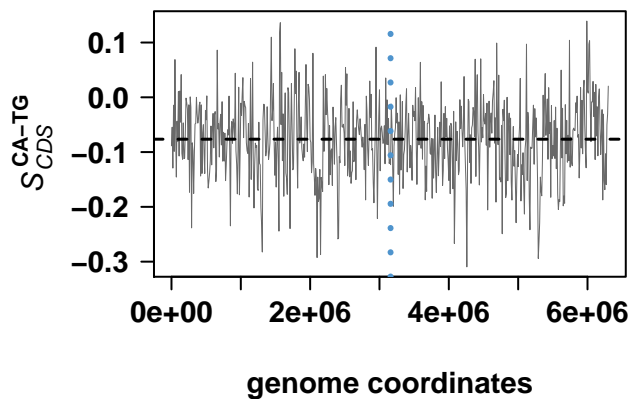
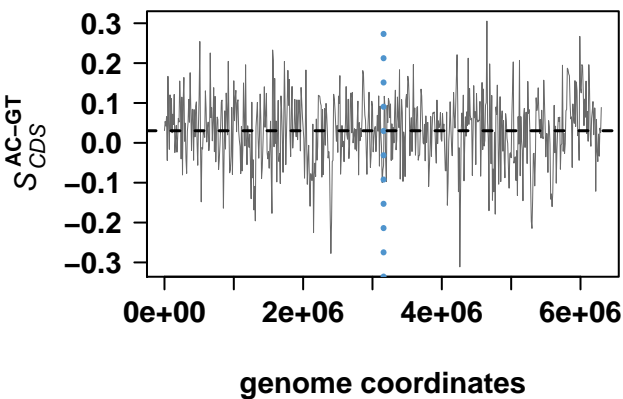
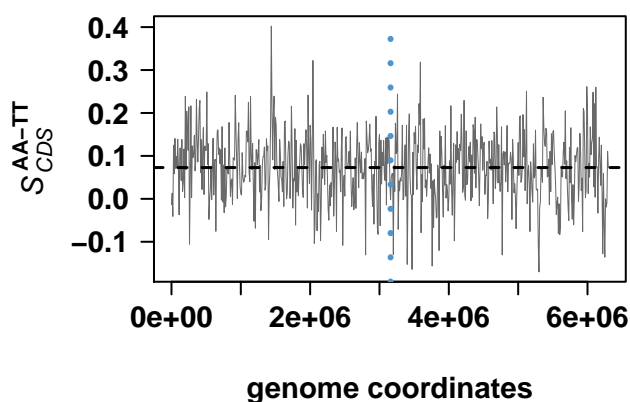
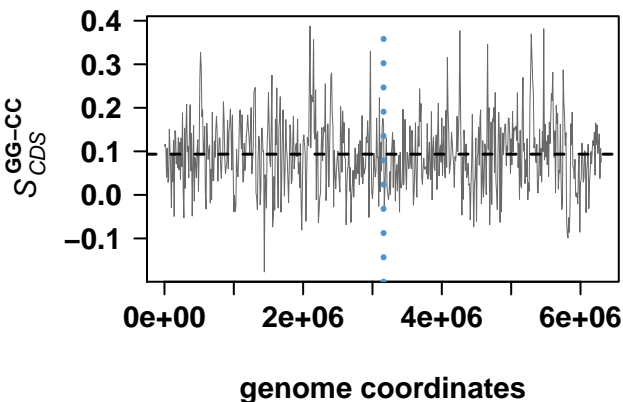
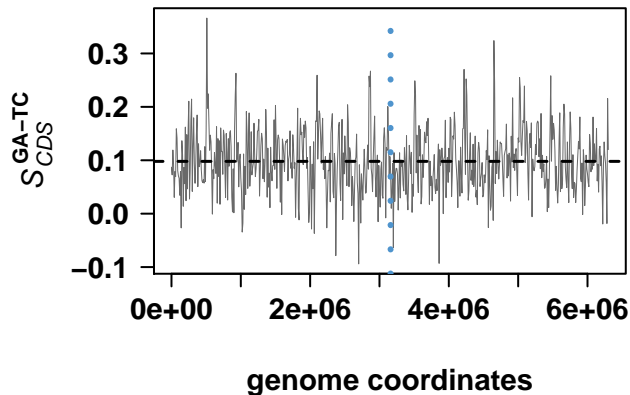
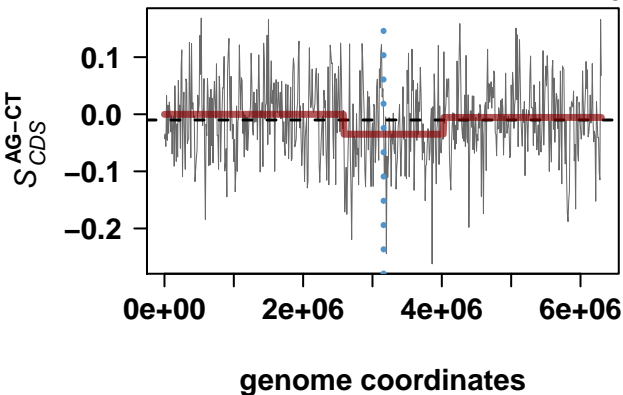


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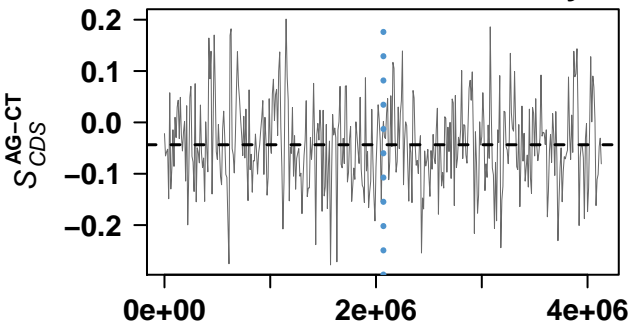


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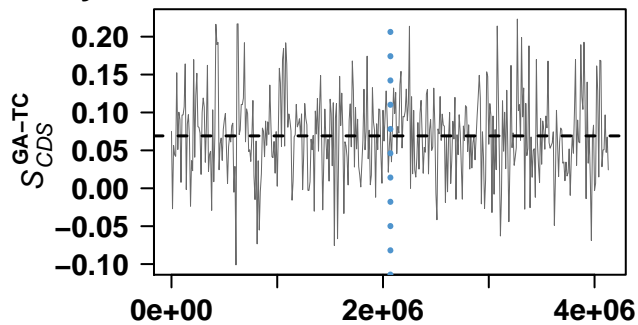
Hahella chejuensis KCTC 2396



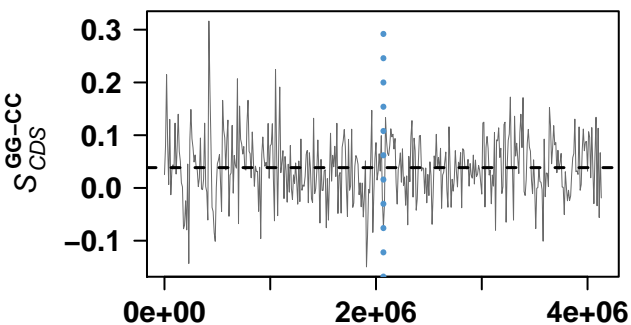
Xanthomonas oryzae pv. oryzae MAFF 311018



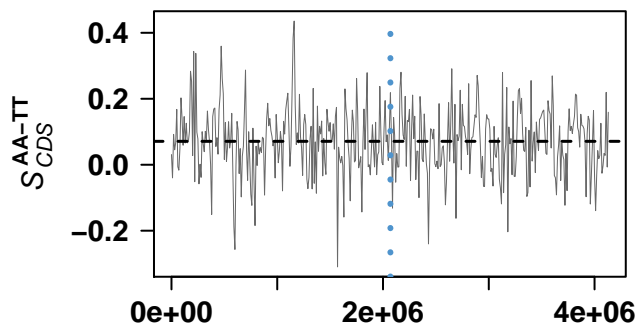
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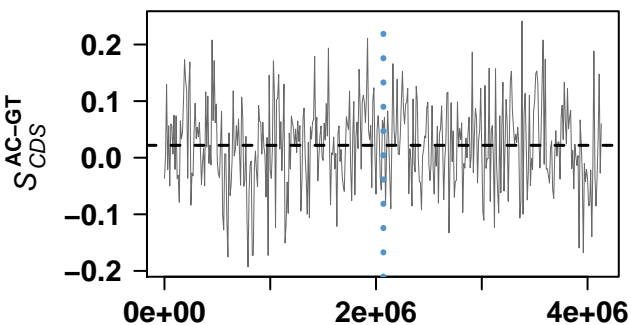
genome coordinates



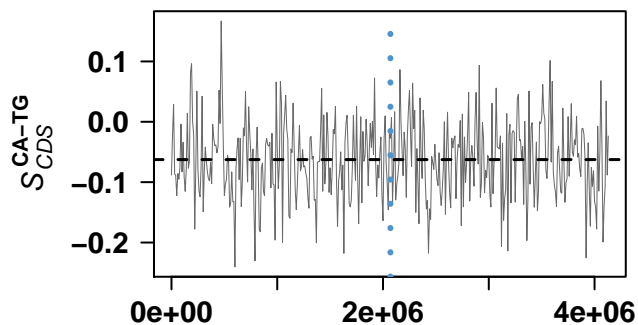
genome coordinates



genome coordinates

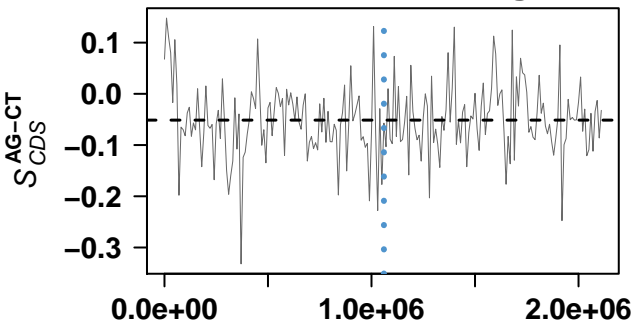


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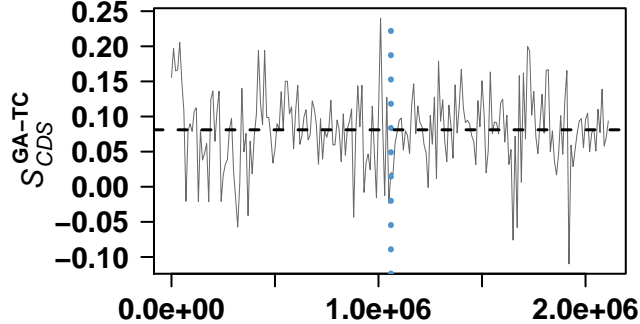


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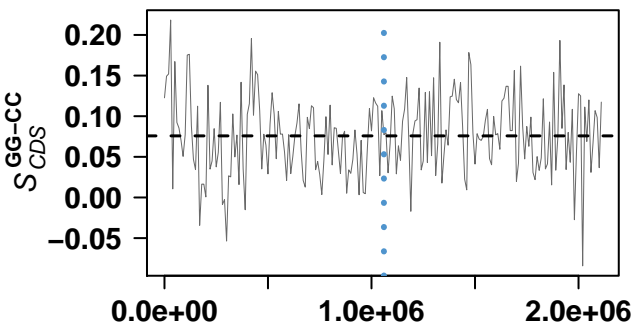
Sodalis glossinidius str. 'morsitans'



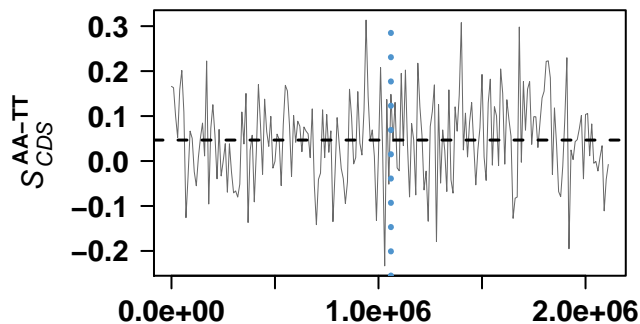
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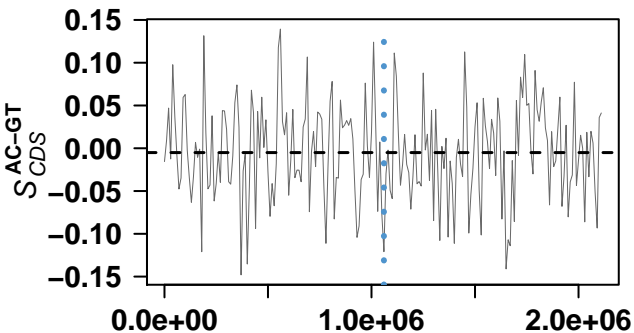
genome coordinates



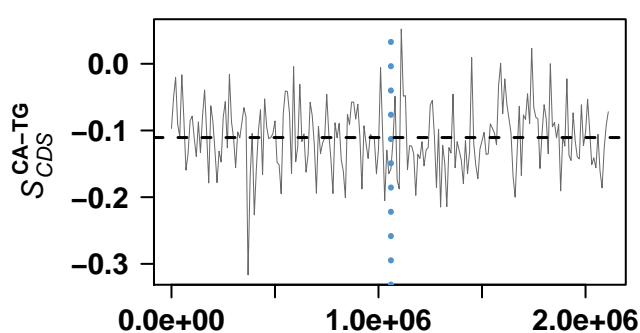
genome coordinates



genome coordinates

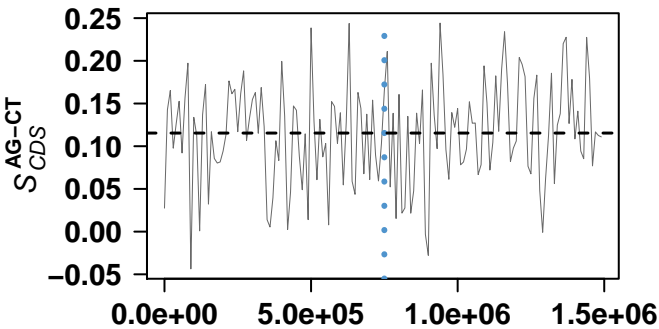


genome coordinates

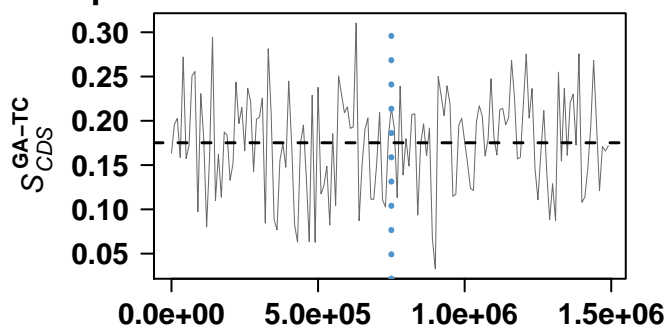


genome coordinates

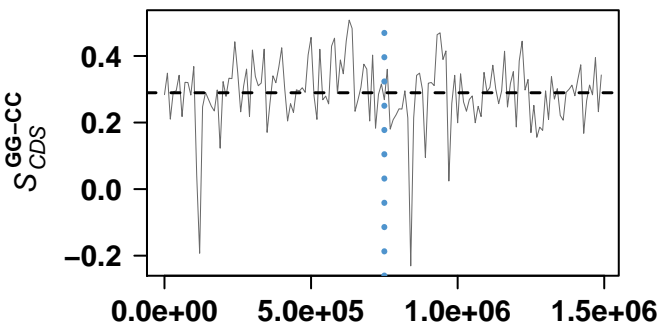
Francisella tularensis subsp. holarctica LVS



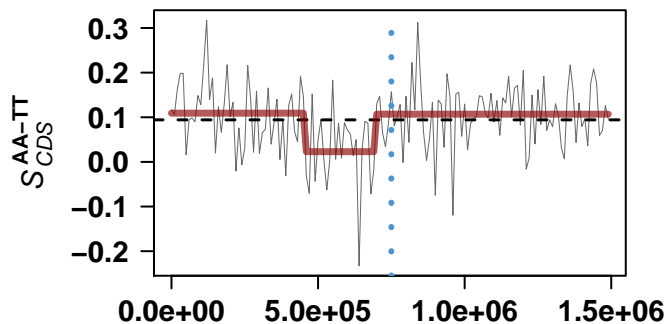
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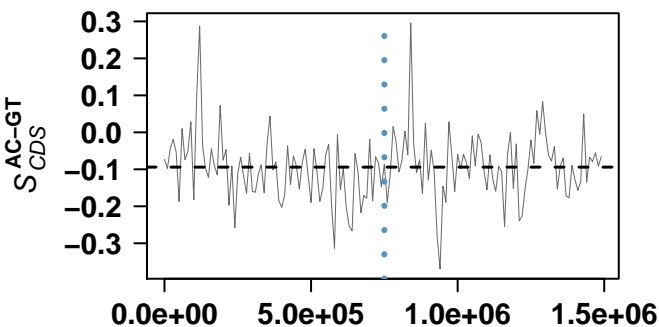
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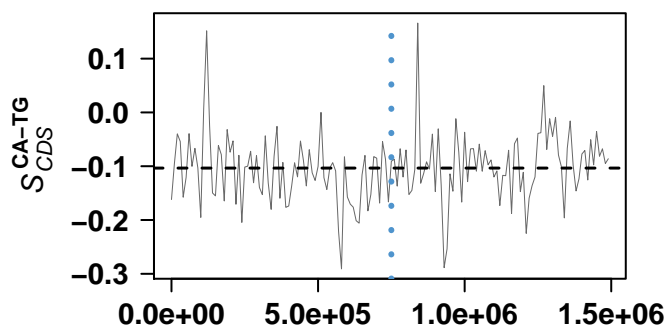
genome coordinates



genome coordinates

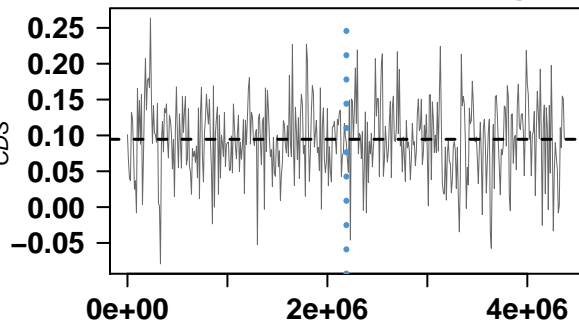


genome coordinates

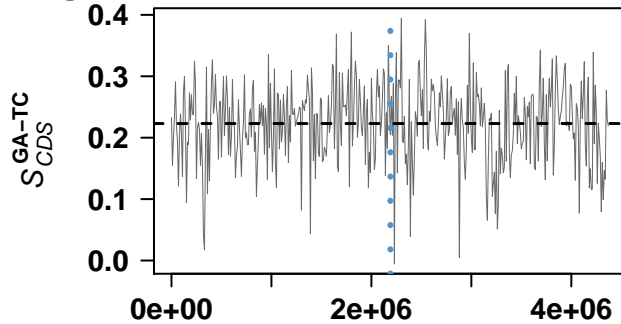


genome coordinates

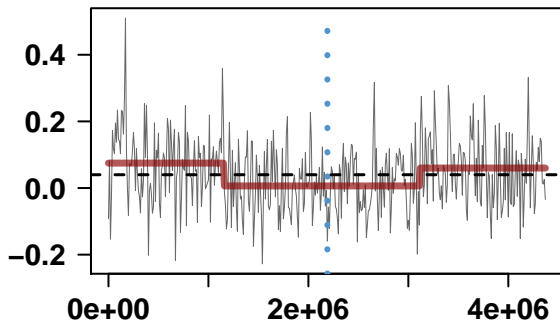
Saccharophagus degradans 2-40



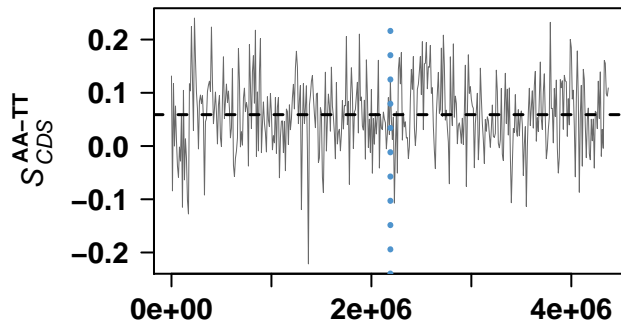
genome coordinates



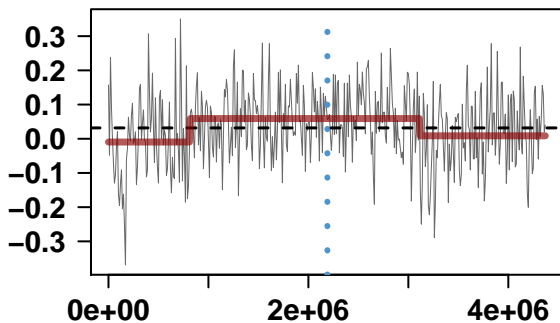
genome coordinates



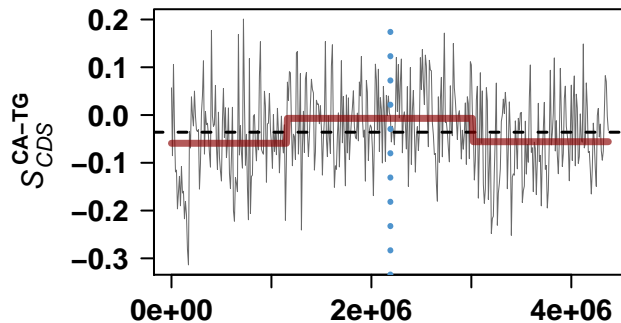
genome coordinates



genome coordinates

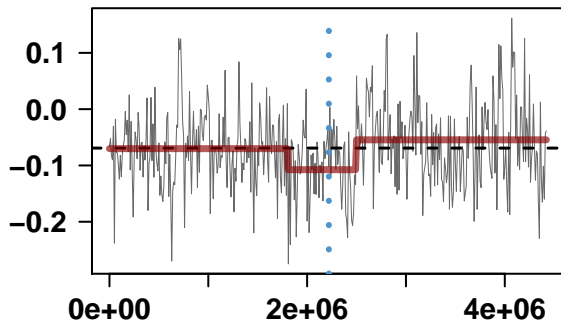


genome coordinates

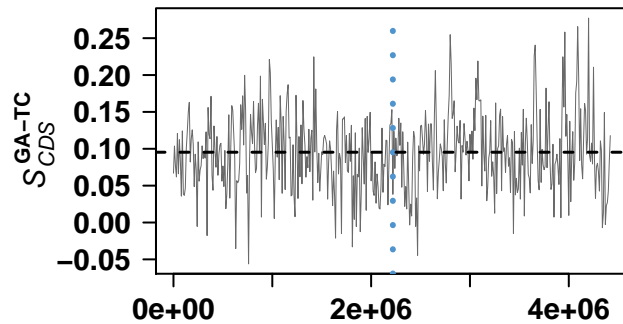


genome coordinates

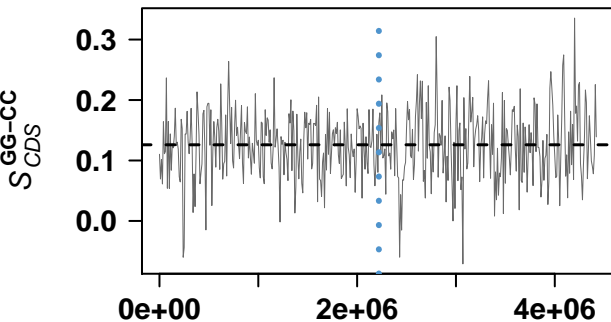
Escherichia coli UTI89



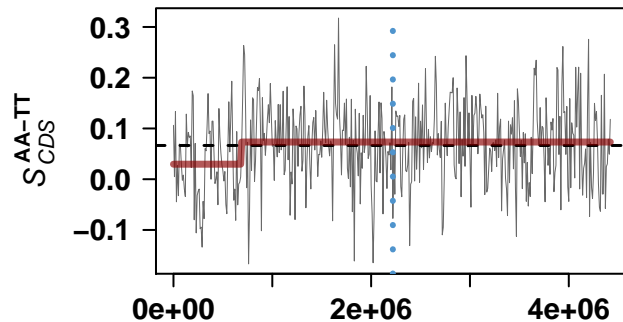
genome coordinates



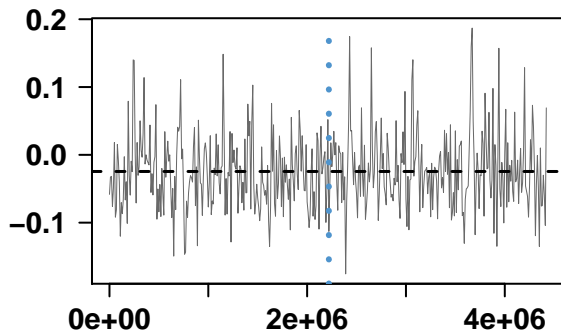
genome coordinates



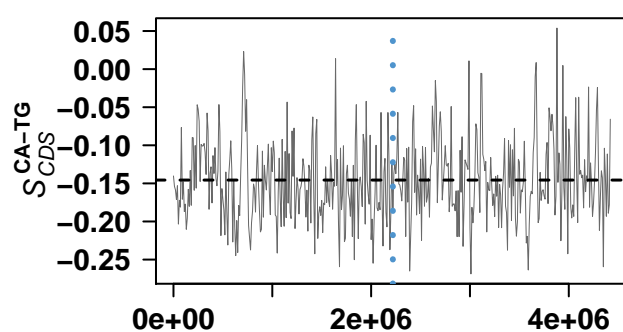
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genome coordinates

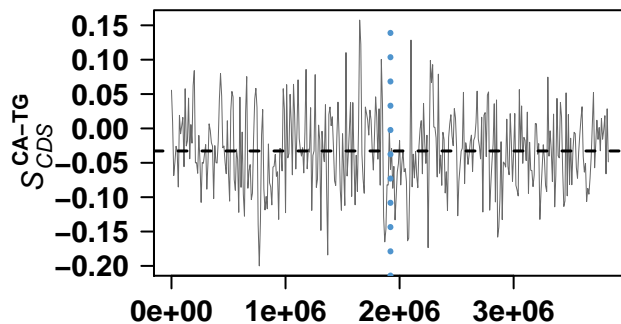
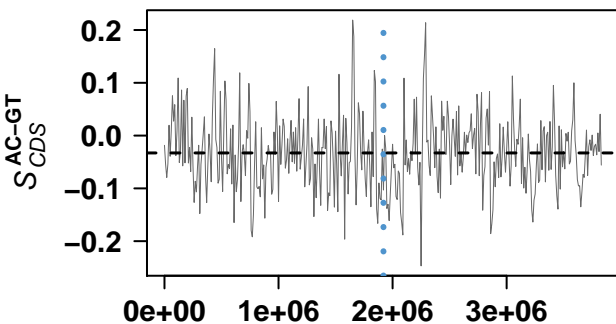
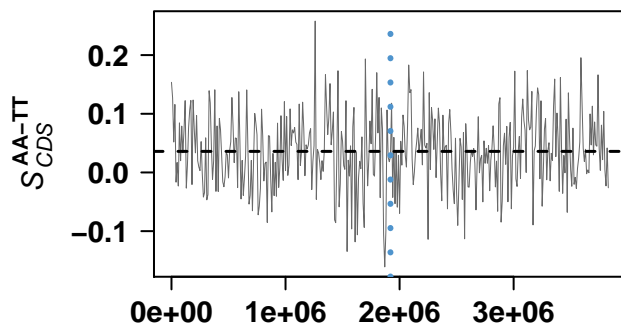
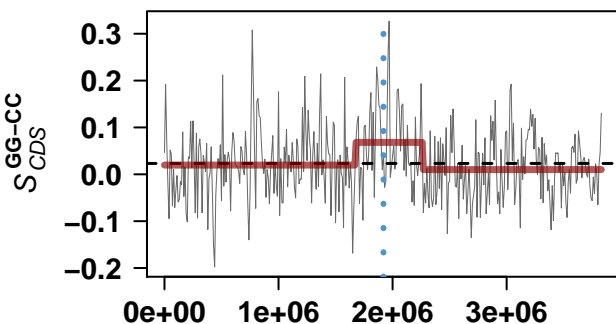
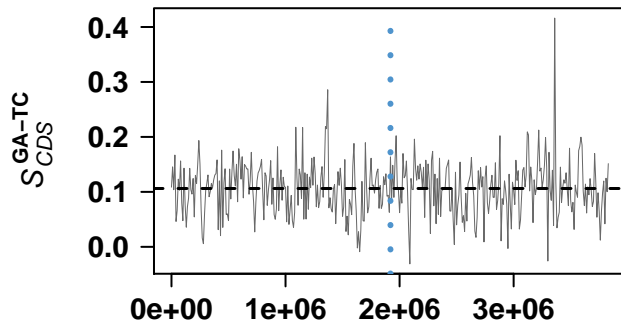
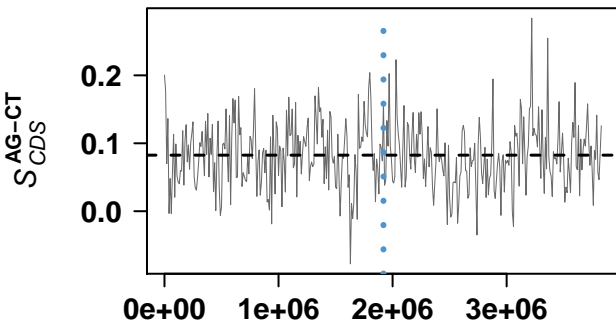


genome coordinates

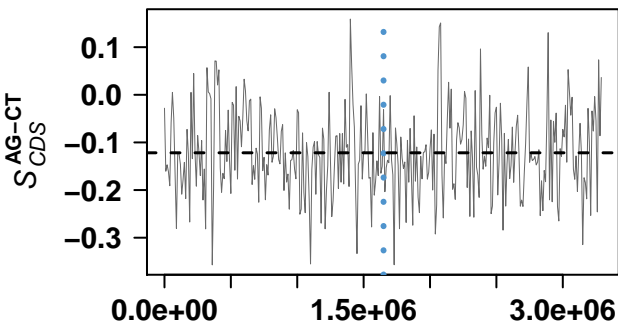


genome coordinates

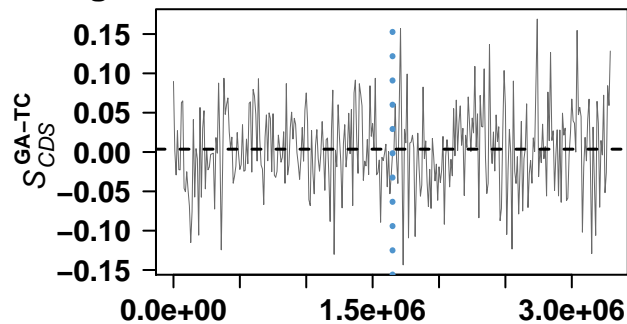
Shewanella denitrificans OS217



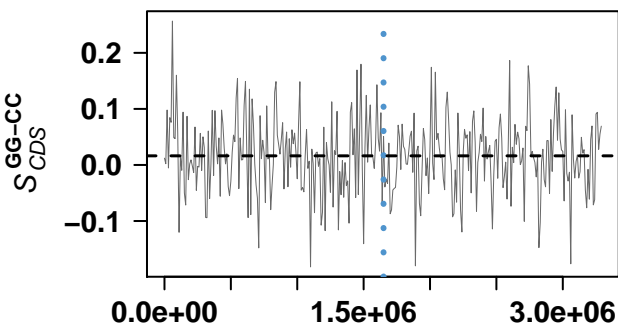
Chromohalobacter salexigens DSM 3043



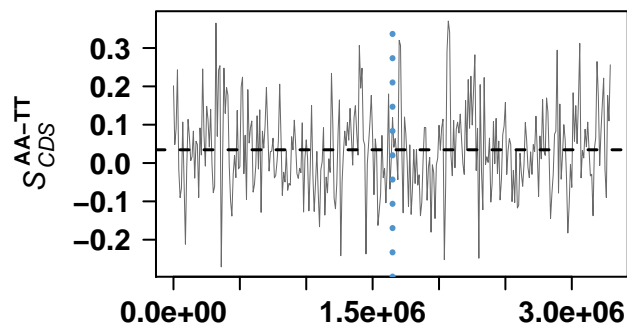
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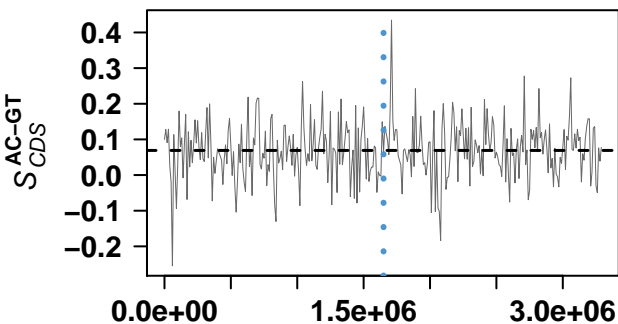
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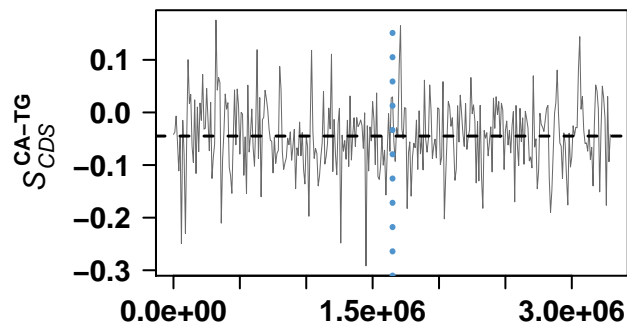
genome coordinates



genome coordinates

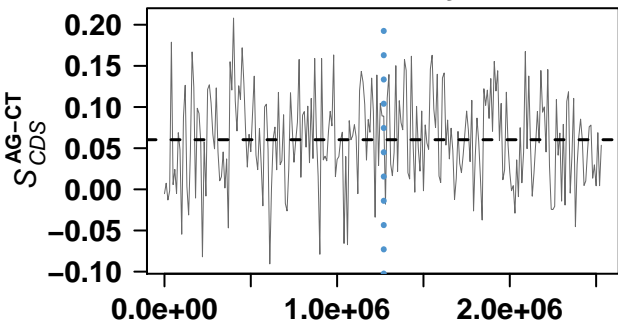


genome coordinates

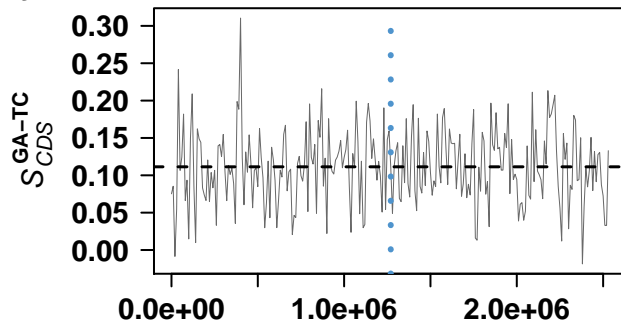


genome coordinates

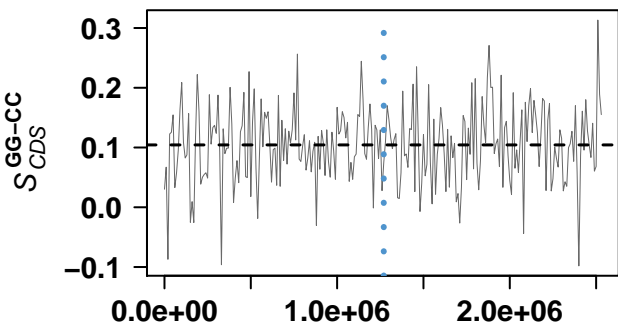
Psychrobacter cryohalolentis K5



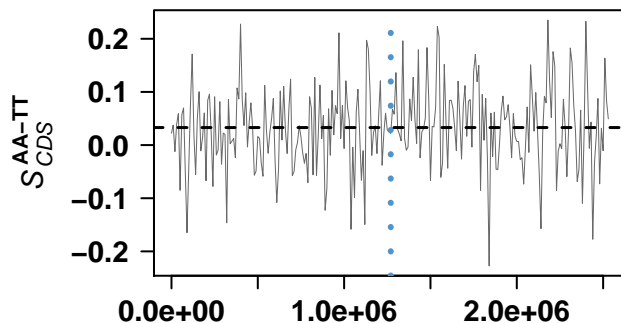
genome coordinates



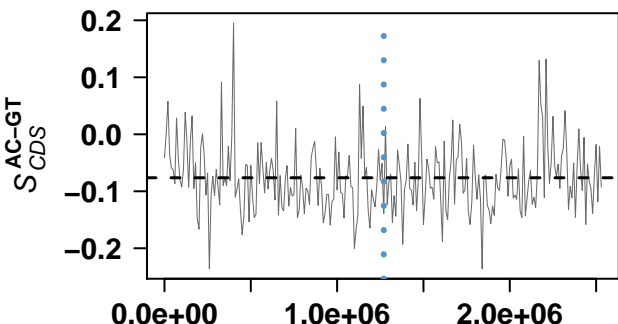
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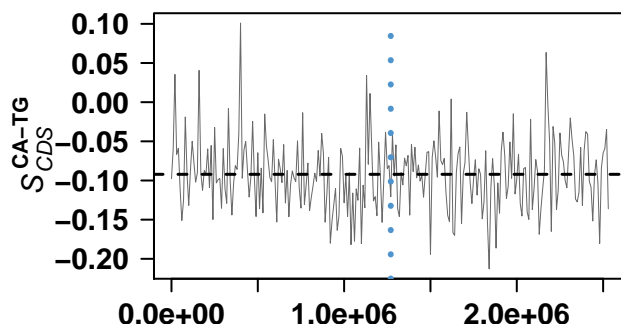
genome coordinates



genome coordinates

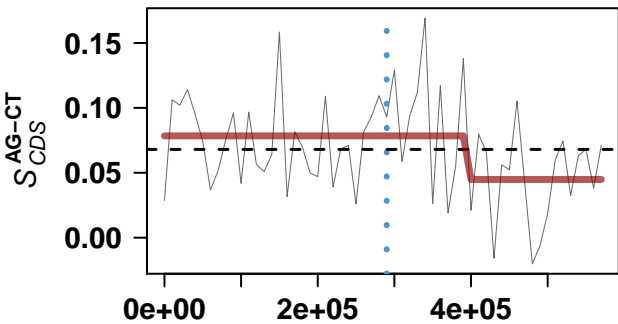


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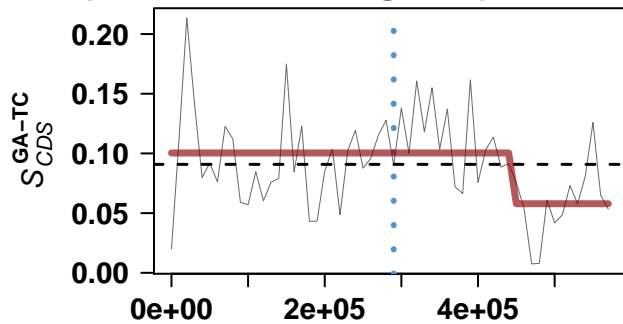


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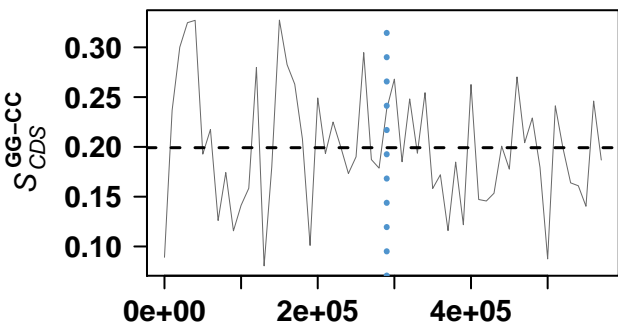
Baumannia cicadellinicola str. Hc (Homalodisca coagulata)



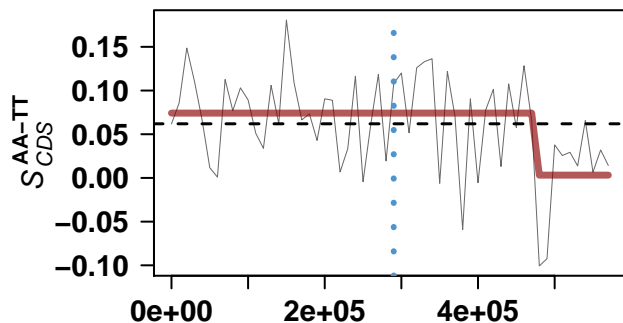
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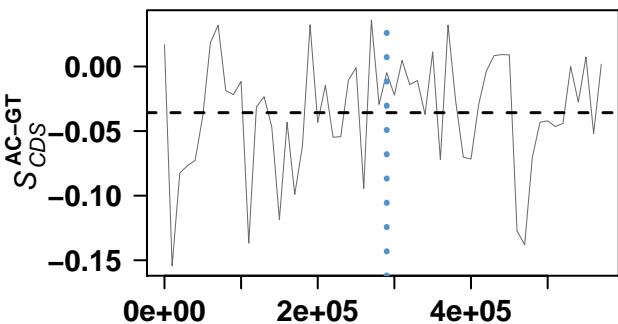
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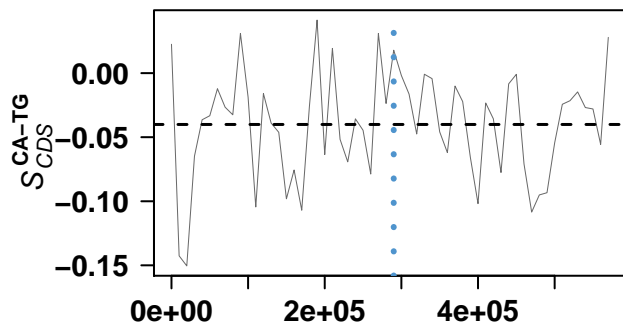
genome coordinates



genome coordinates

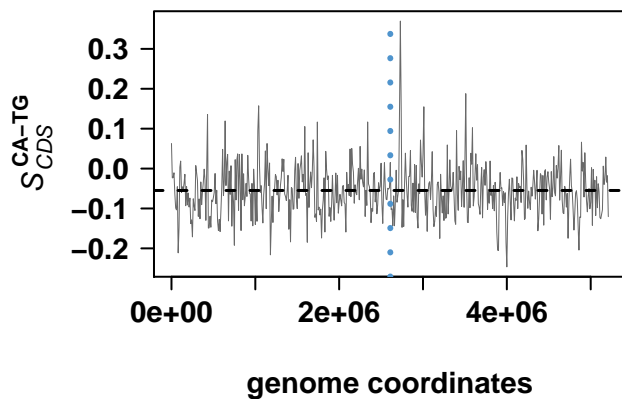
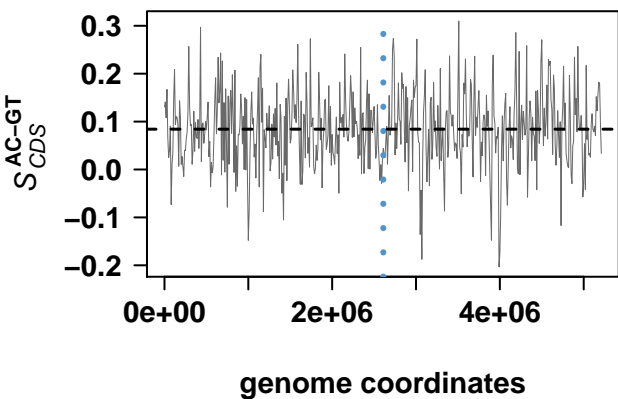
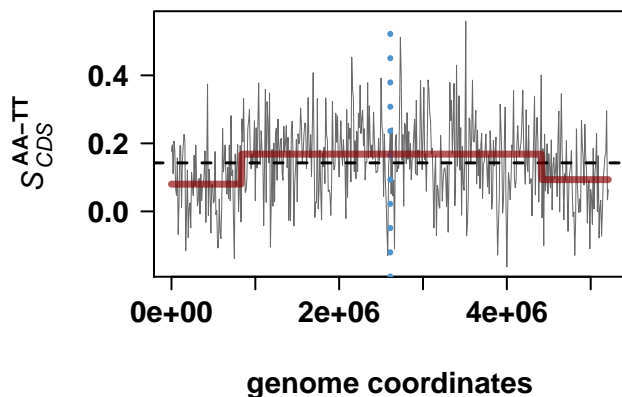
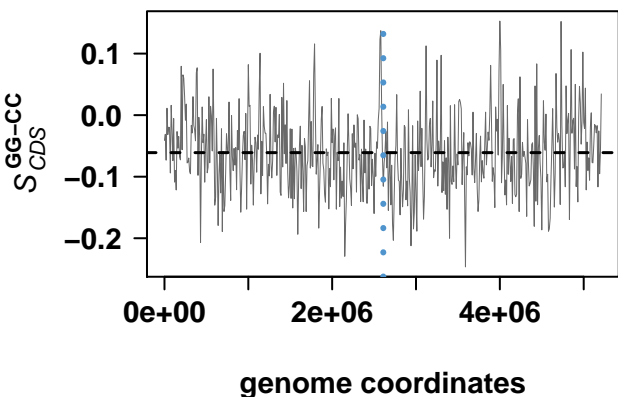
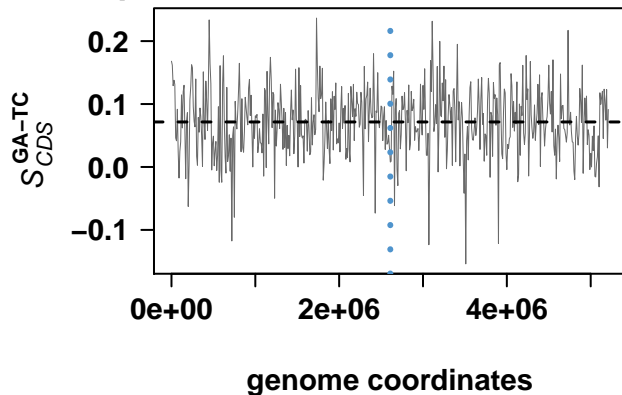
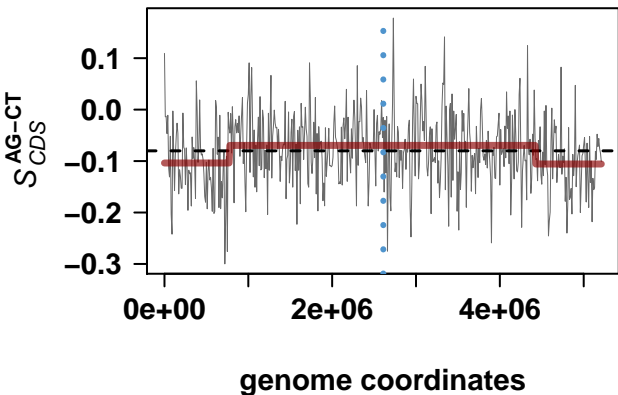


genome coordinates

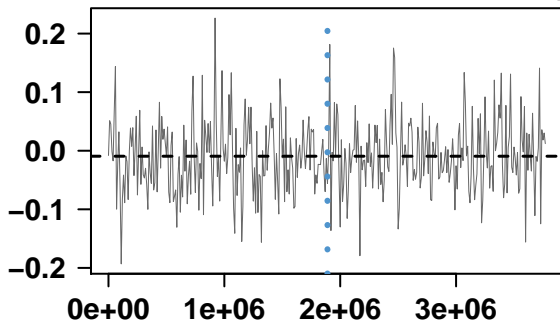


genome coordinates

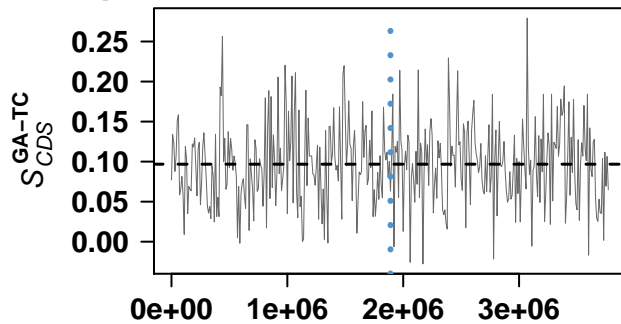
Pseudomonas entomophila L48



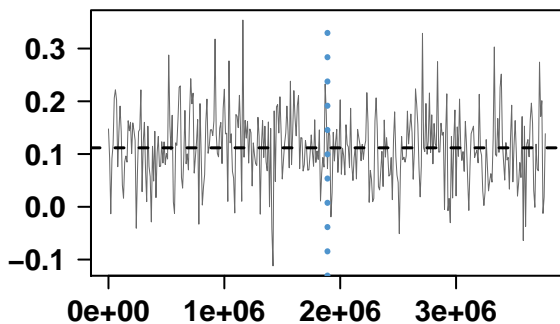
Yersinia pestis Nepal516



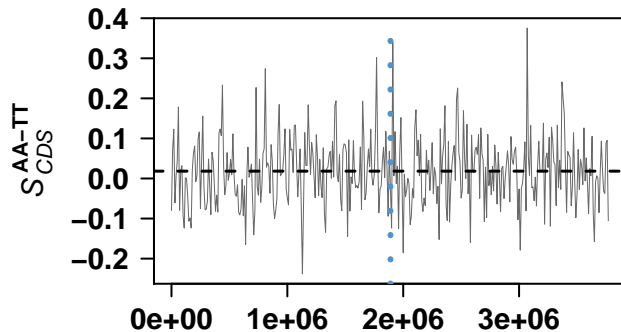
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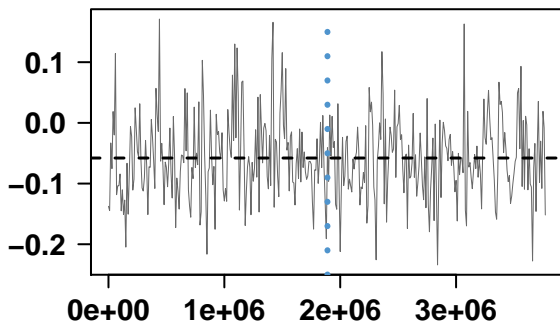
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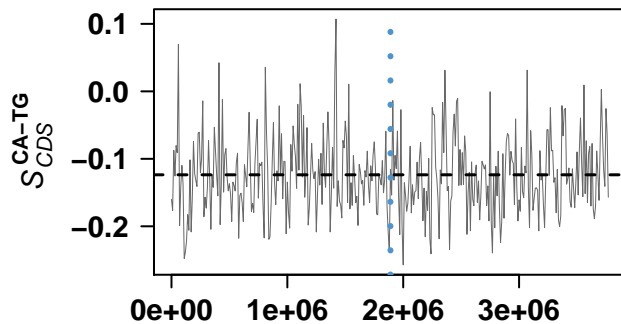
genome coordinates



genome coordinates

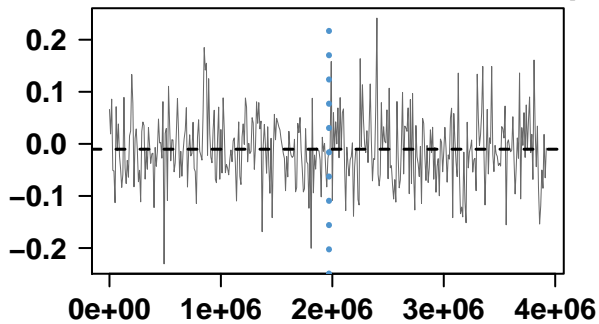


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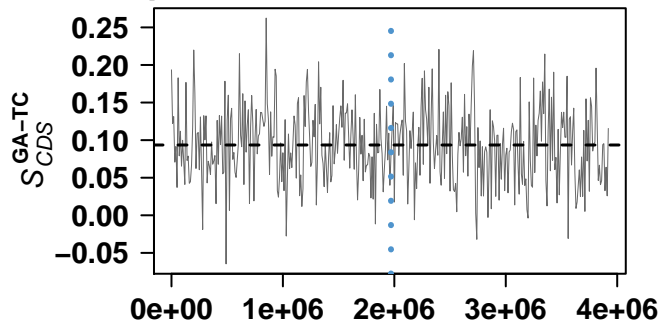


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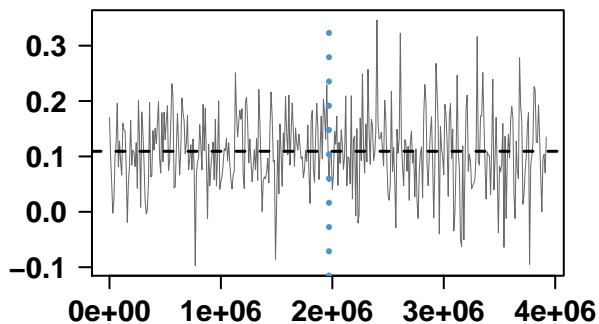
Yersinia pestis Antiqua



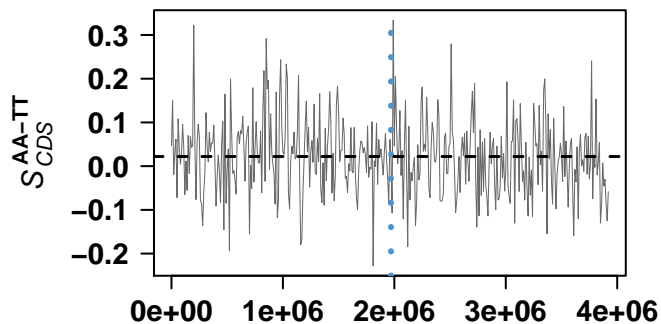
genome coordinates



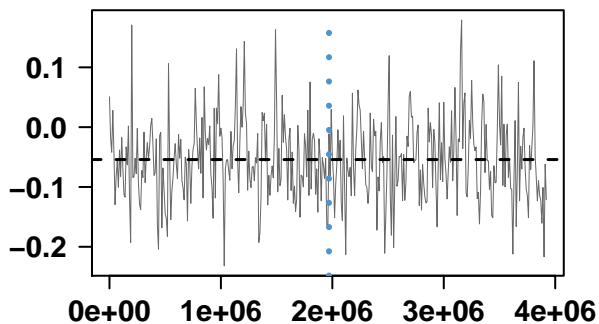
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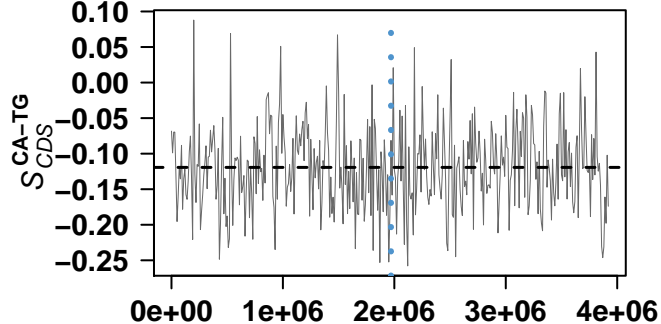
genome coordinates



genome coordinates

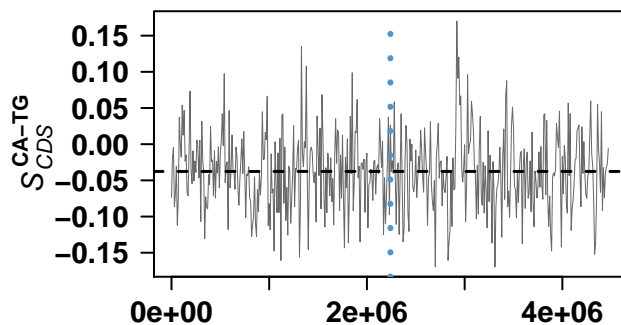
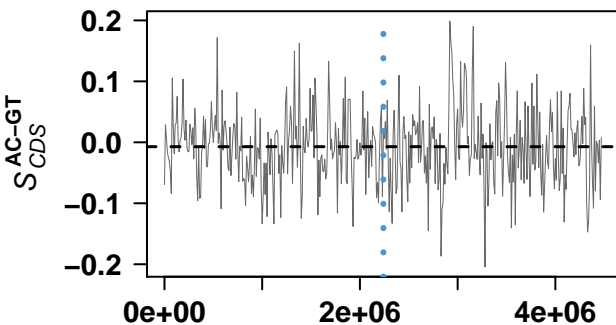
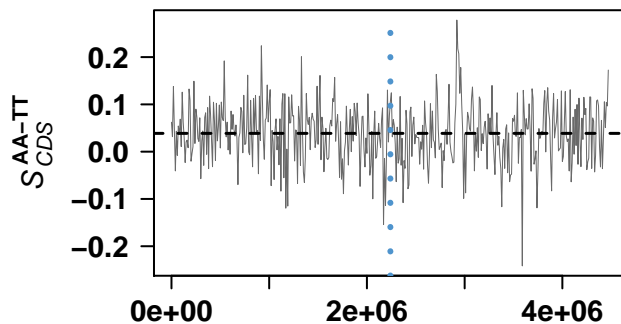
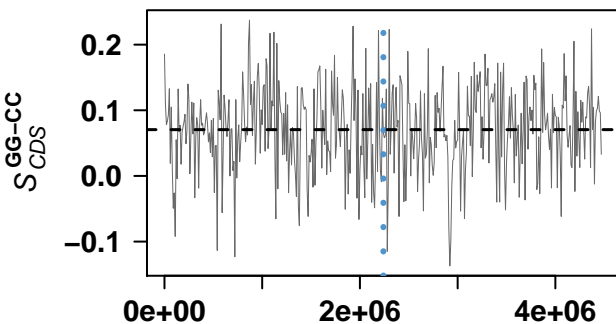
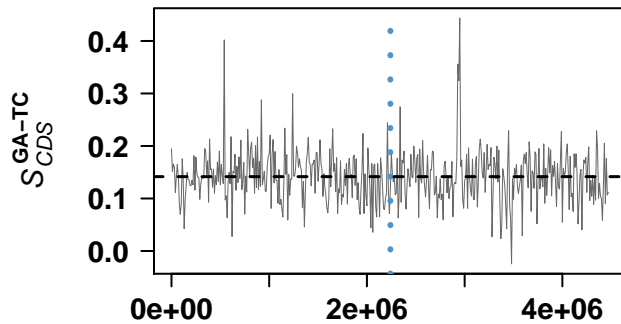
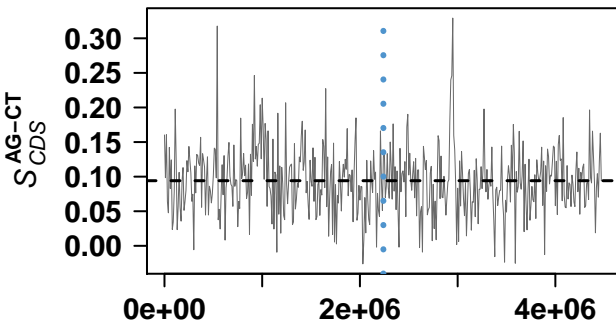


genome coordinates

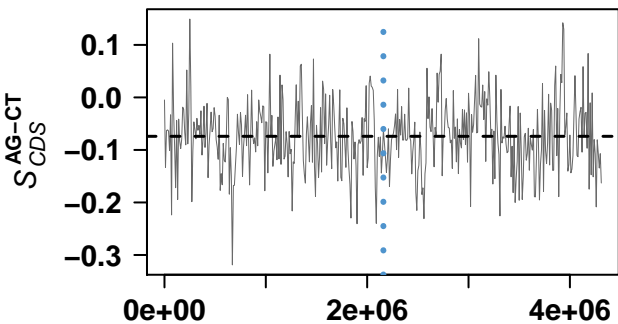


genome coordinates

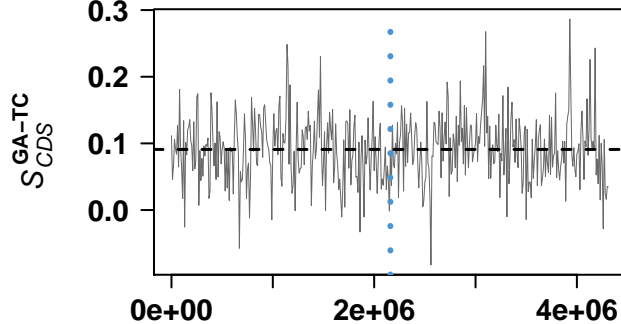
Pseudoalteromonas atlantica T6c



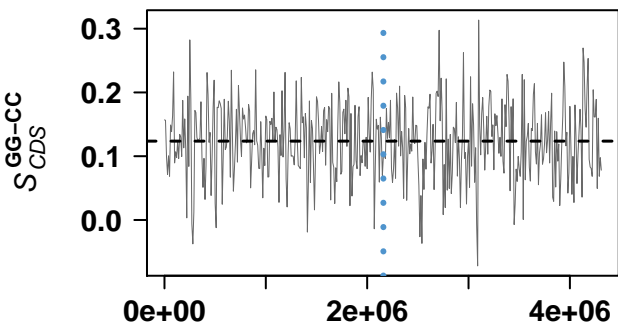
Escherichia coli 536



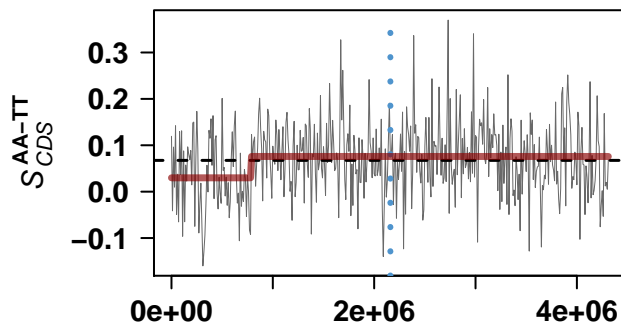
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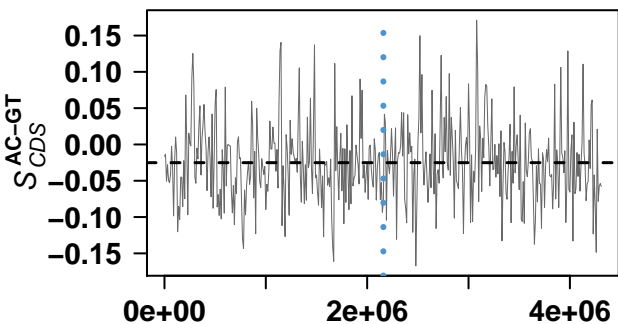
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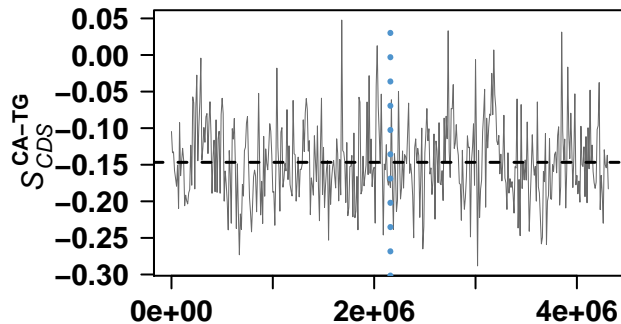
genome coordinates



genome coordinates

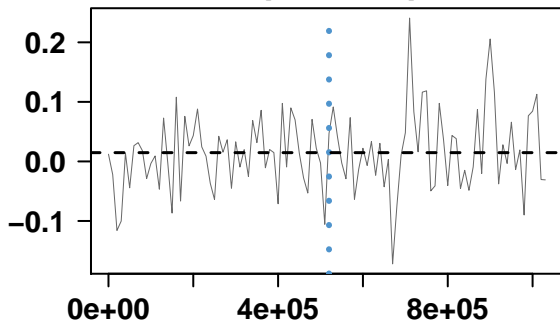


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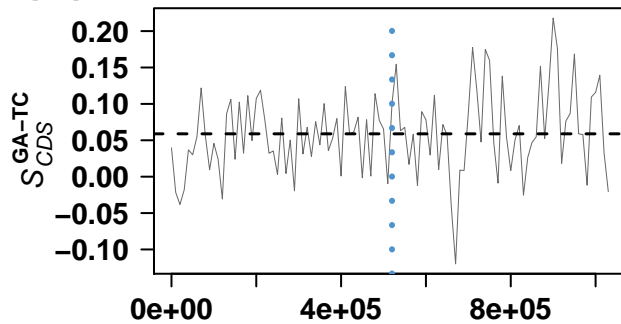


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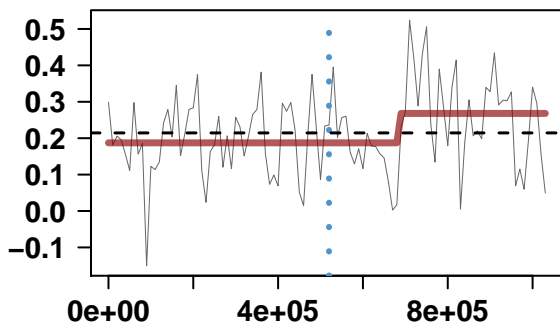
Treponema pallidum subsp. pallidum str. Nichols



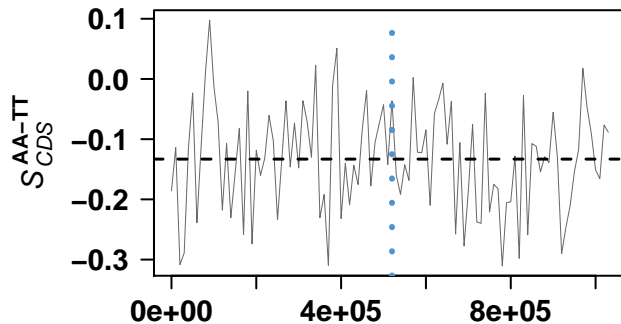
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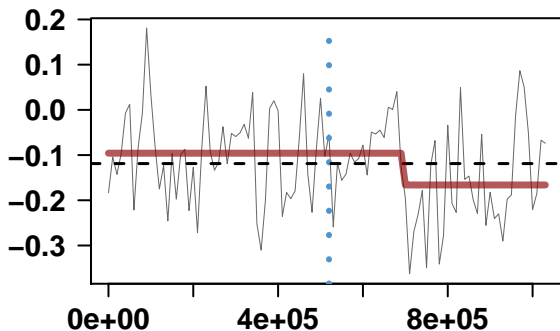
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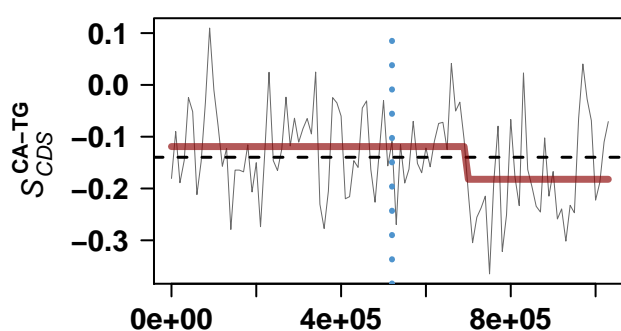
genome coordinates



genome coordinates

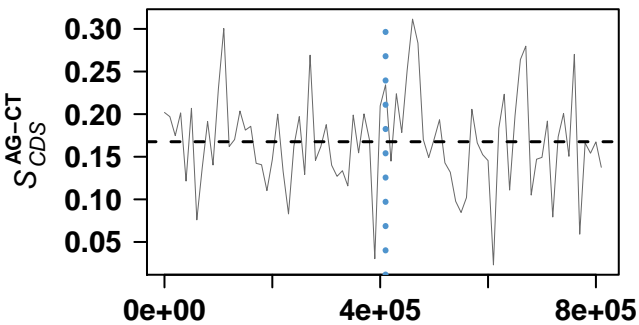


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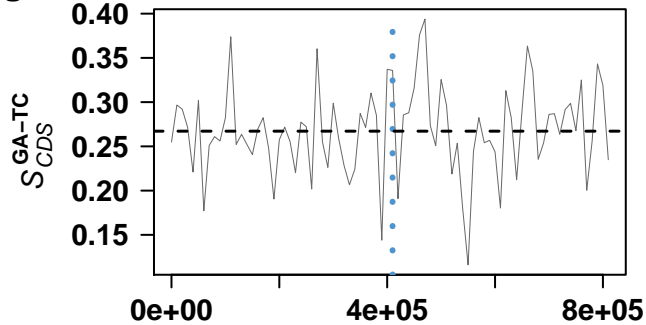


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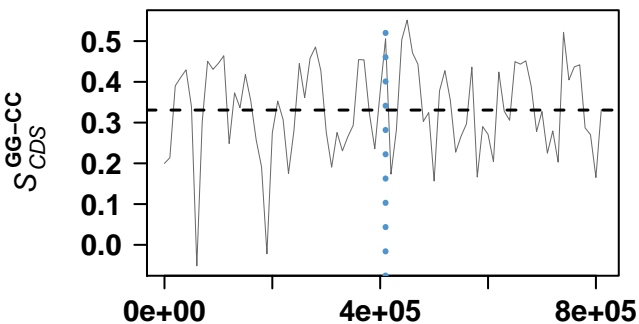
Borrelia burgdorferi B31



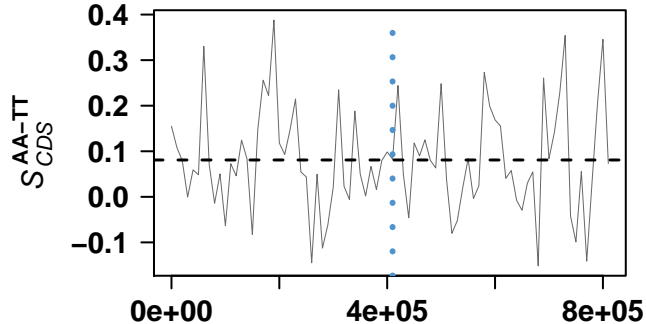
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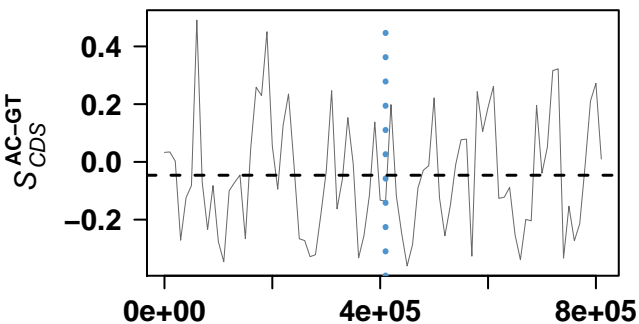
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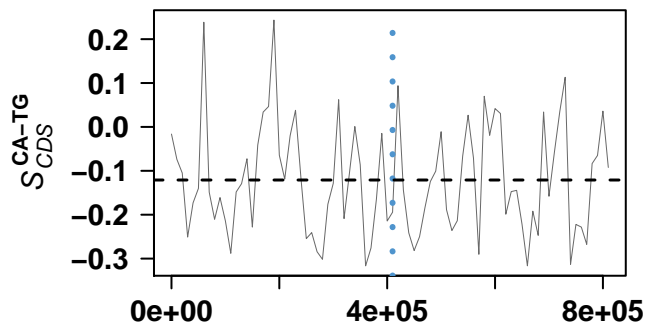
genome coordinates



genome coordinates

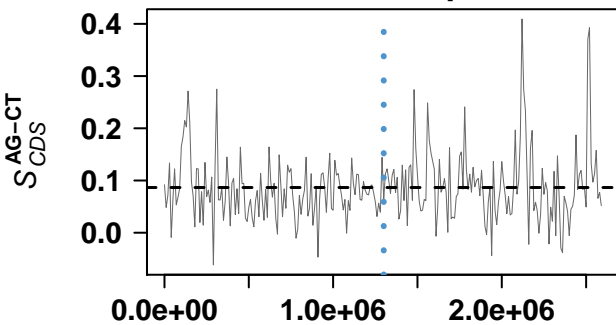


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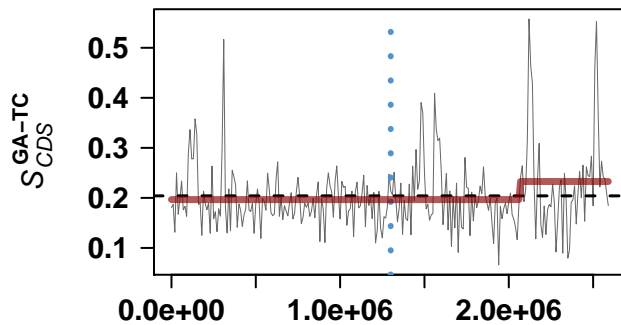


genome coordinates

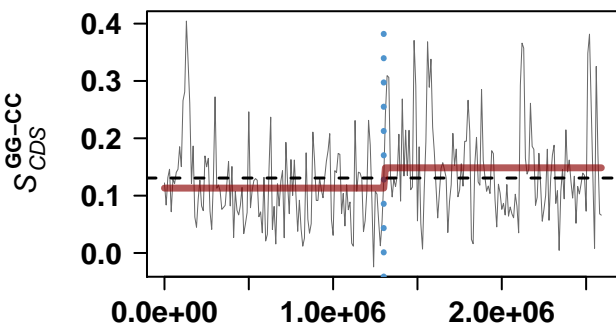
Treponema denticola ATCC 35405



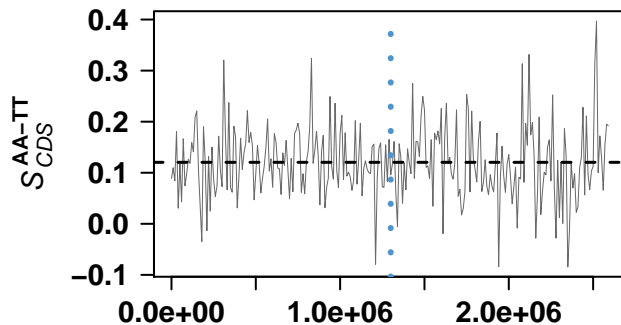
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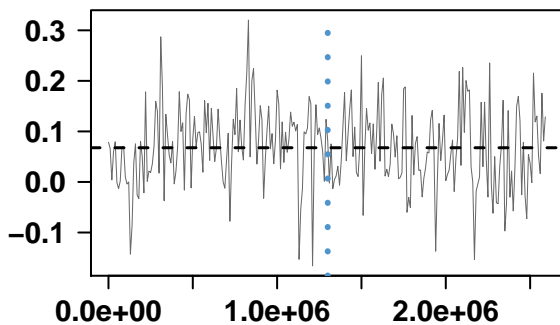
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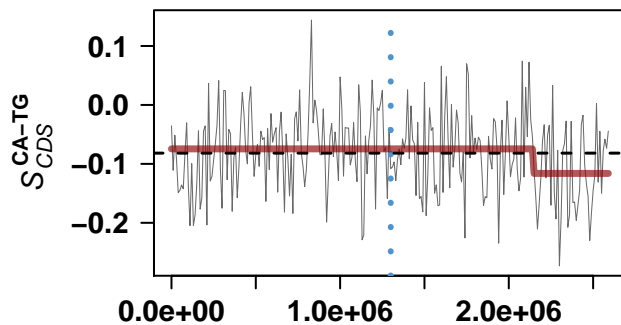
genome coordinates



genome coordinates

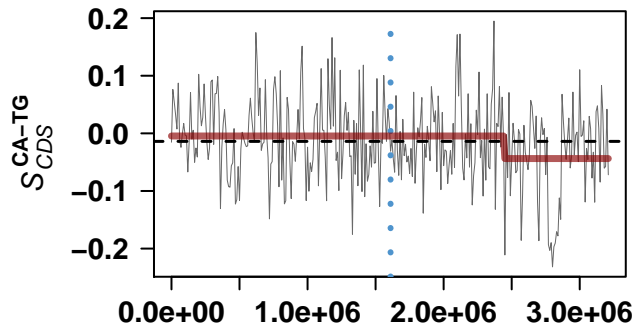
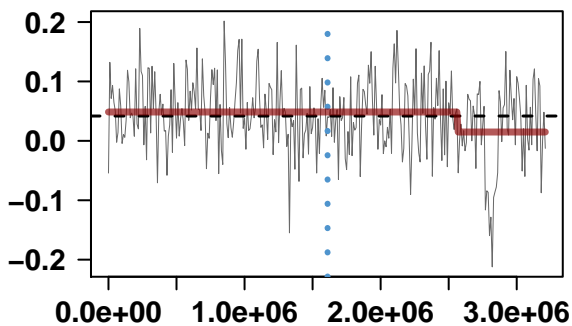
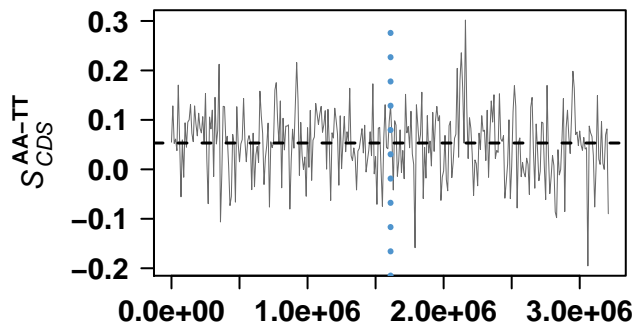
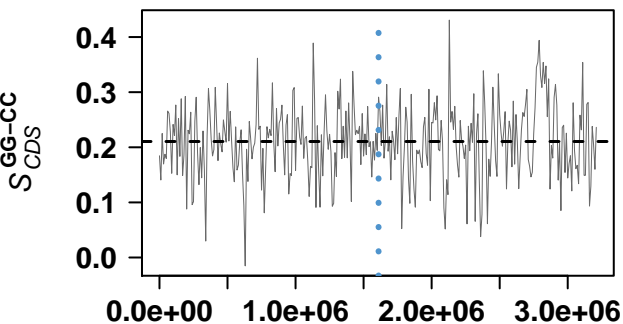
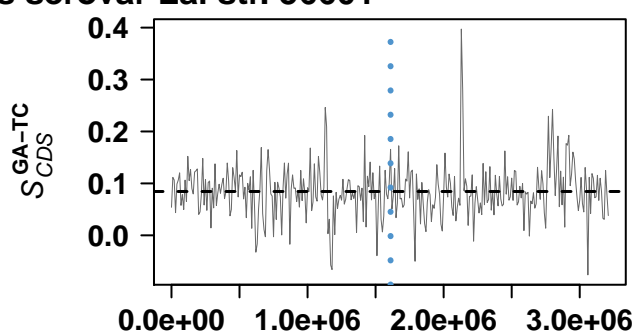
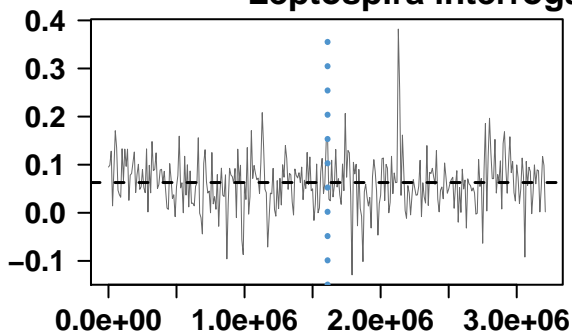


genome coordinates

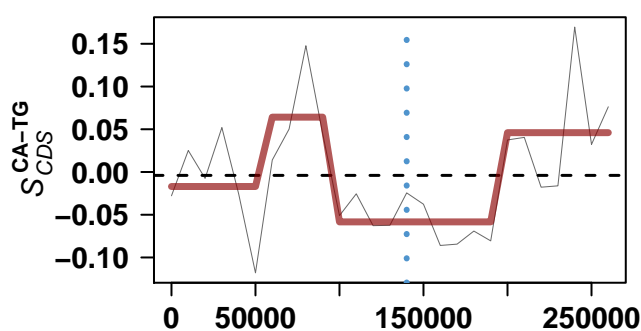
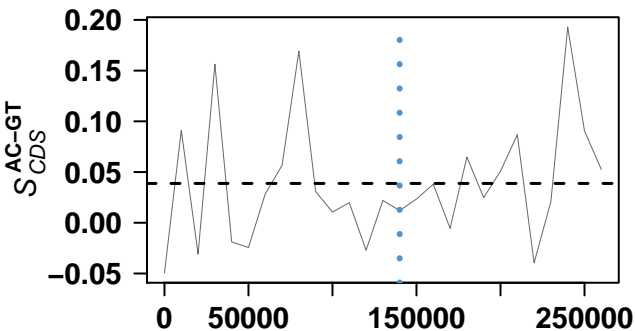
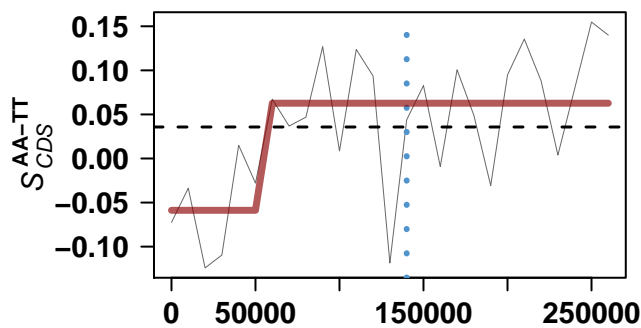
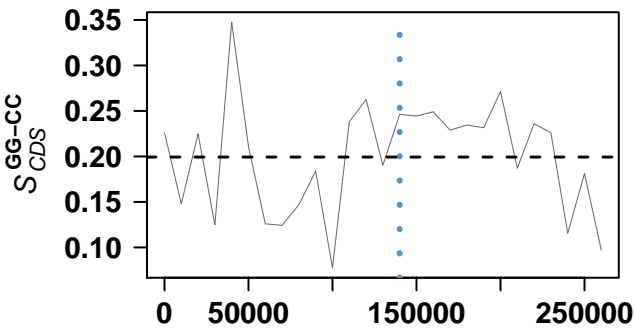
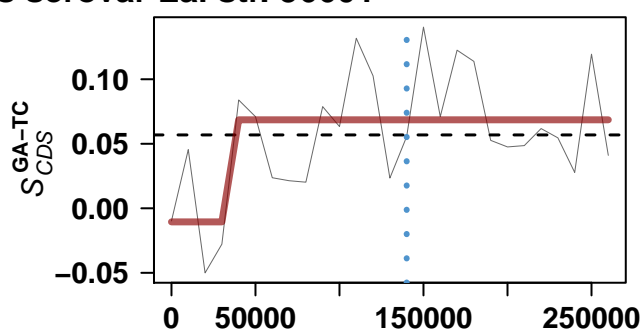
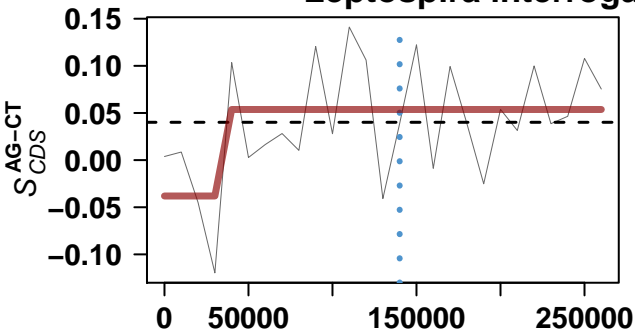


genome coordinates

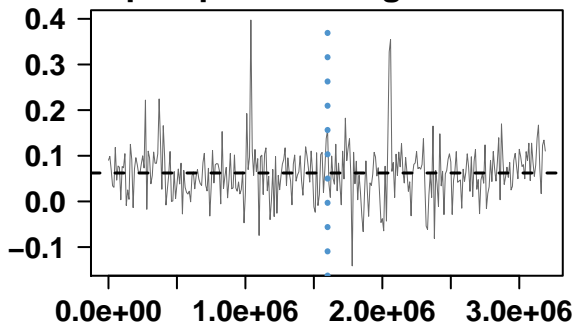
Leptospira interrogans serovar Lai str. 56601



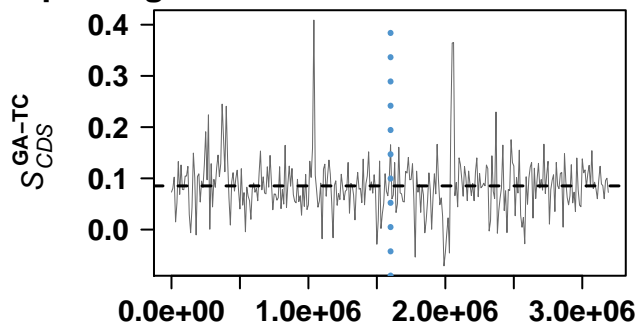
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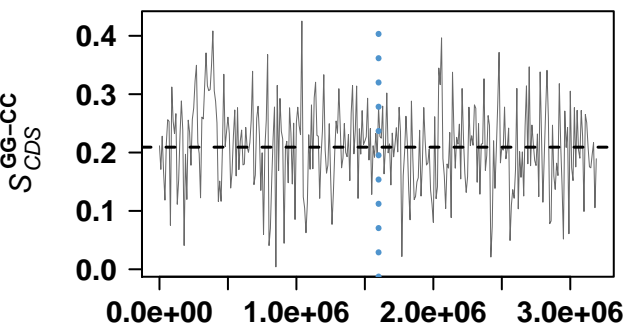
Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130



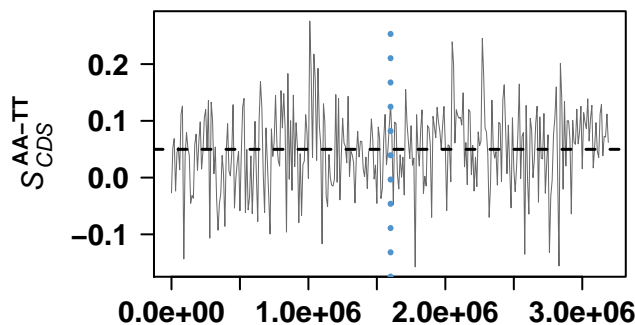
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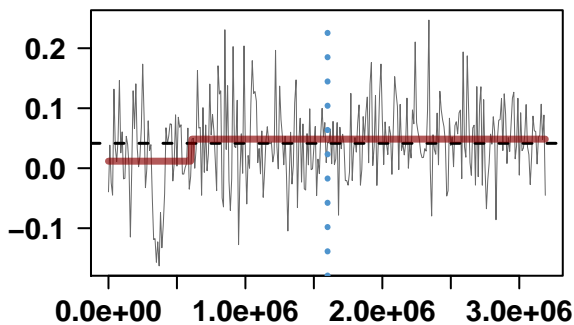
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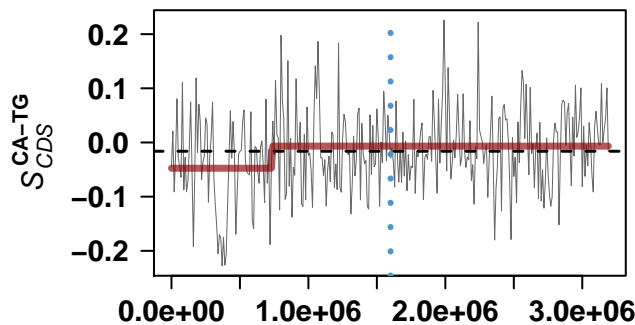
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genome coordinates

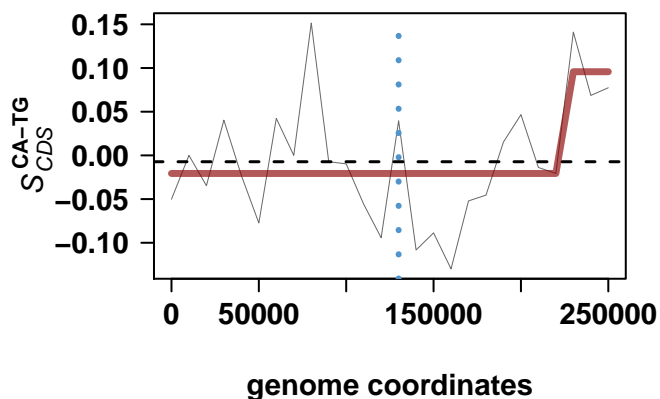
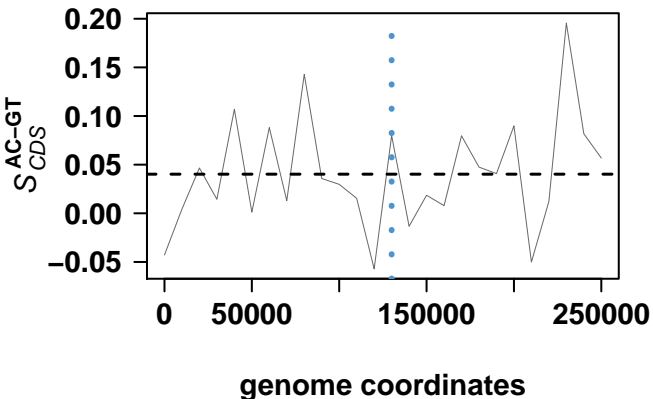
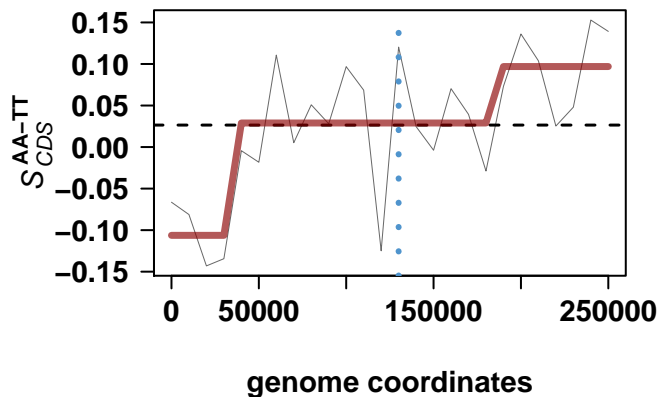
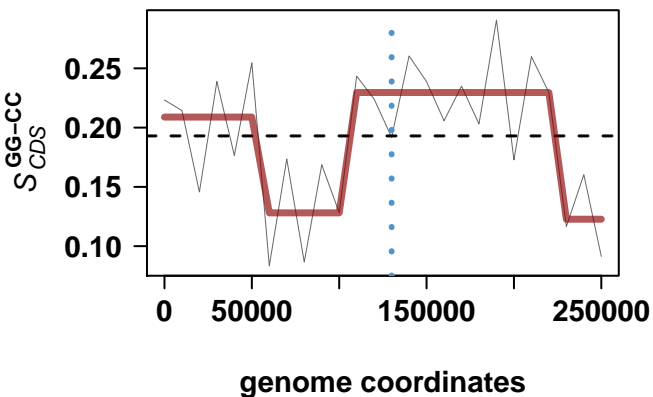
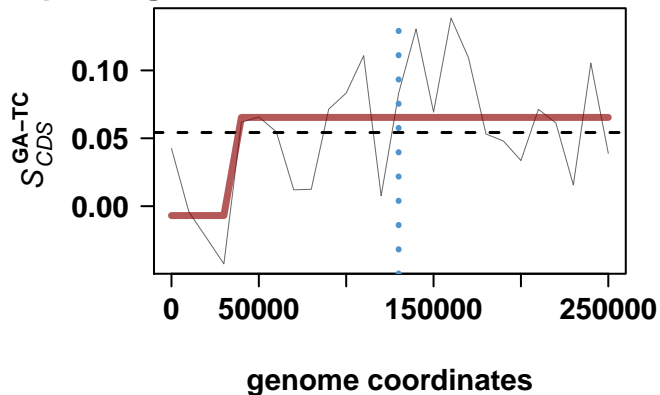
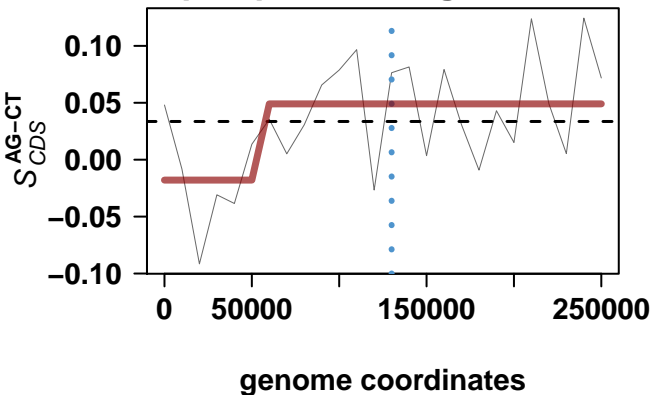


genome coordinates

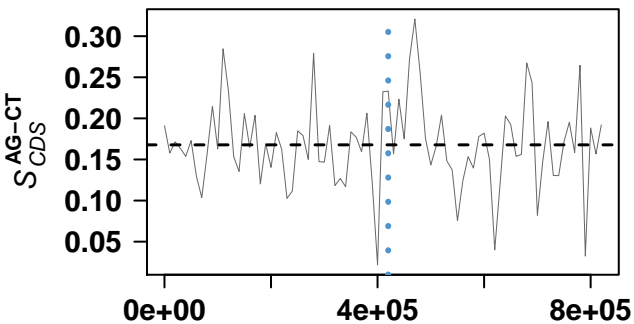


genome coordinates

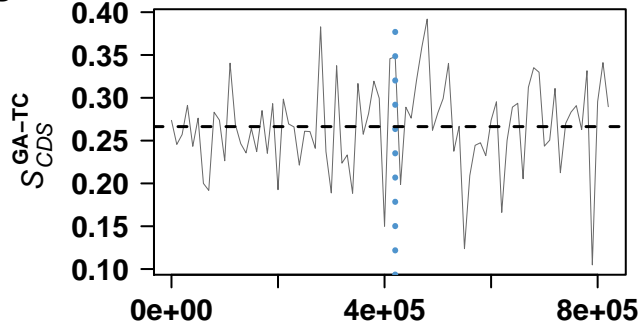
Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130



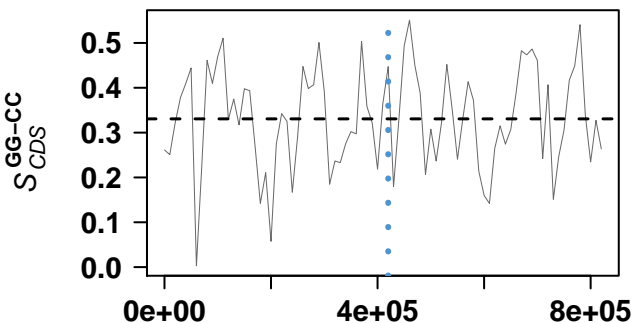
Borrelia garinii PBI



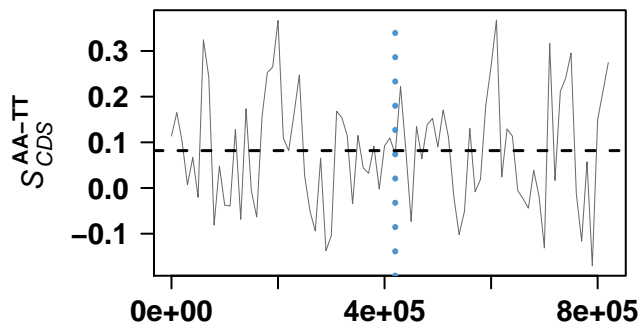
genome coordinates



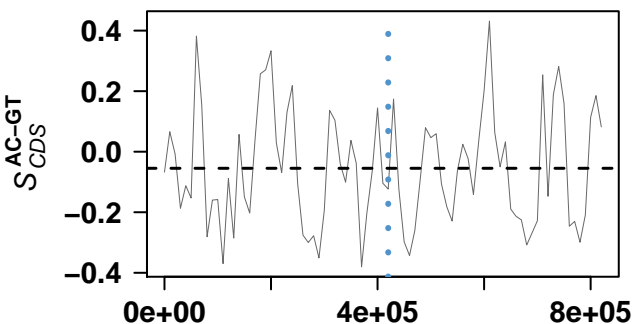
genome coordinates



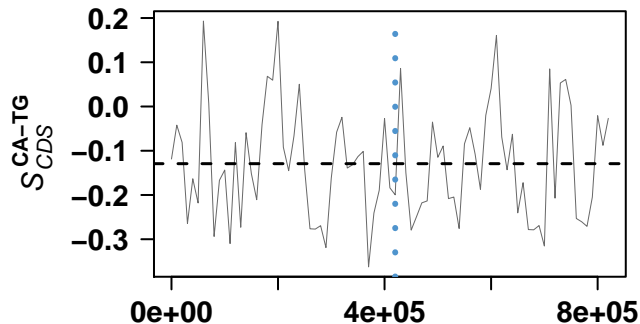
genome coordinates



genome coordinates

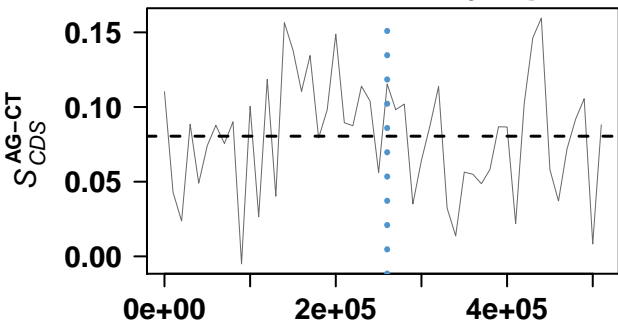


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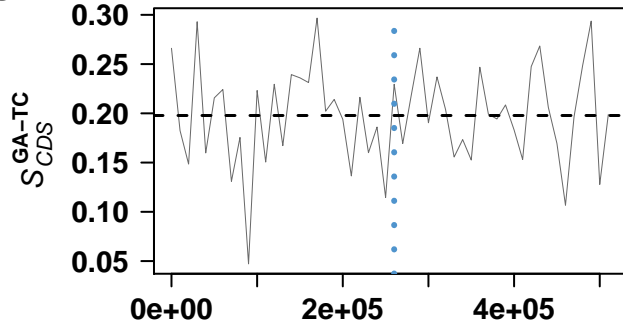


genome coordinates

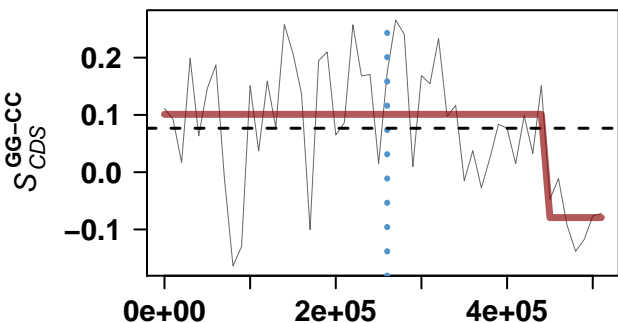
Mycoplasma genitalium G37



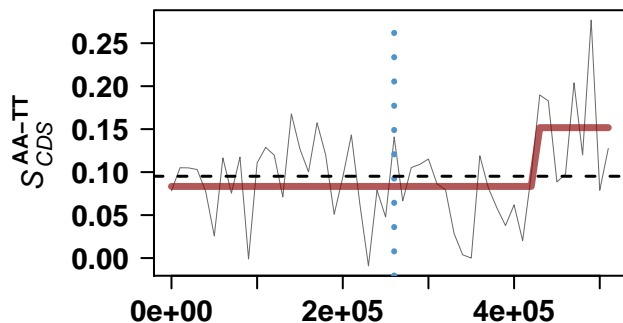
genome coordinates



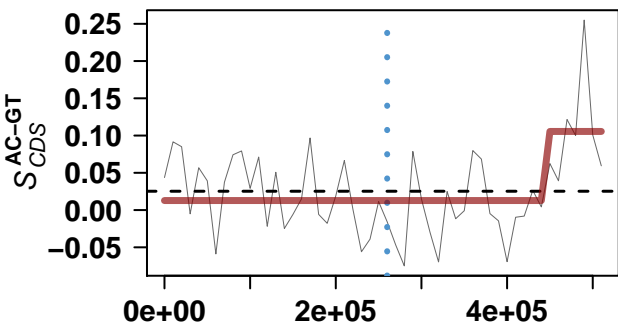
genome coordinates



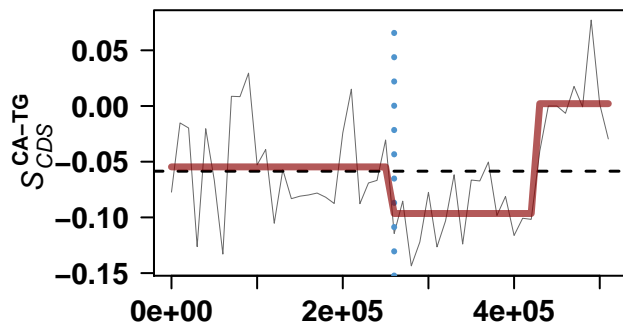
genome coordinates



genome coordinates

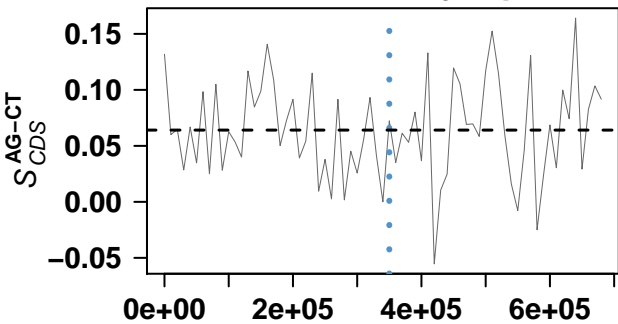


genome coordinates

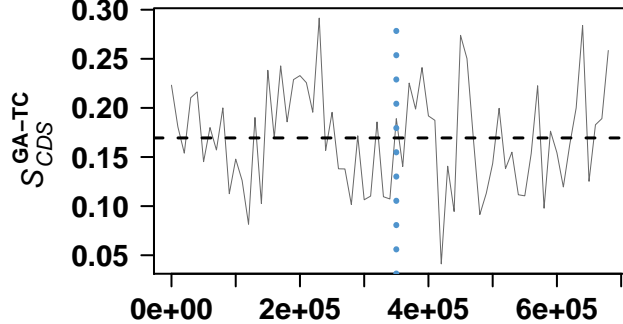


genome coordinates

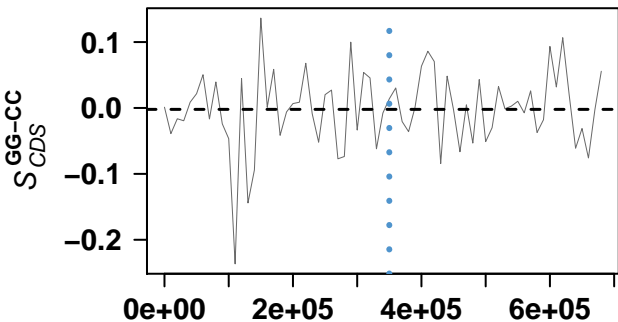
Mycoplasma pneumoniae M129



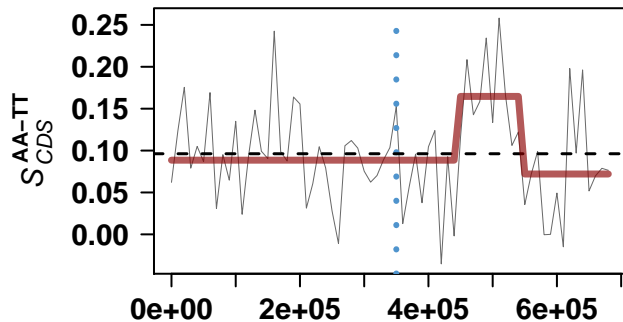
genome coordinates



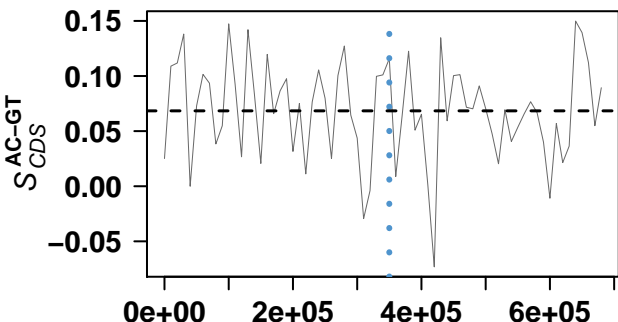
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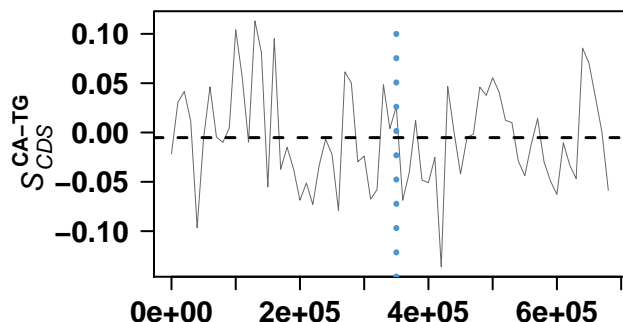
genome coordinates



genome coordinates

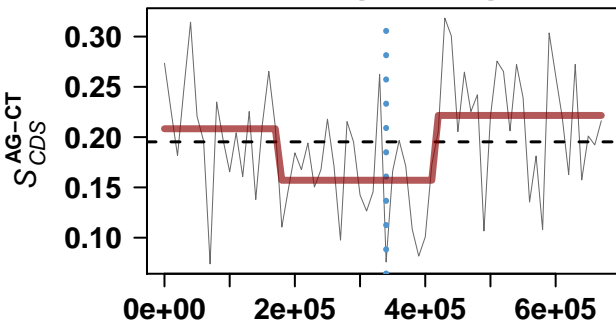


genome coordinates

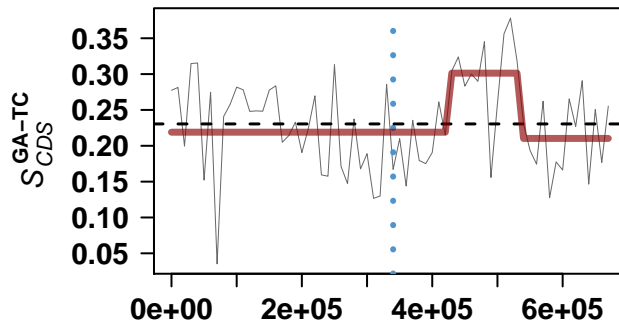


genome coordinates

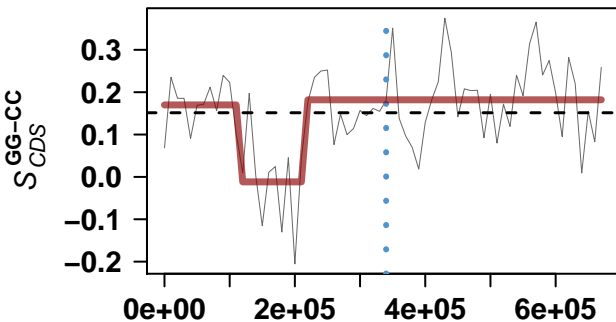
Ureaplasma parvum serovar 3 str. ATCC 700970



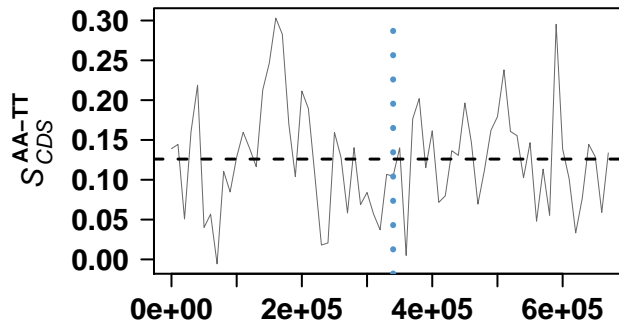
genome coordinates



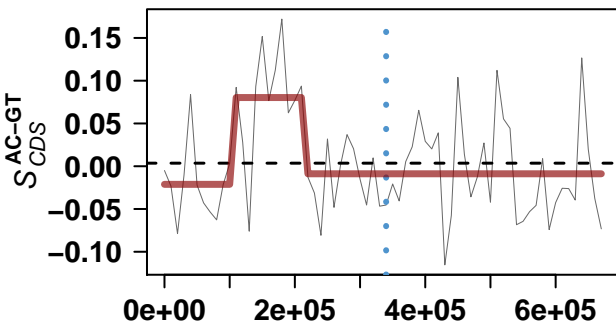
genome coordinates



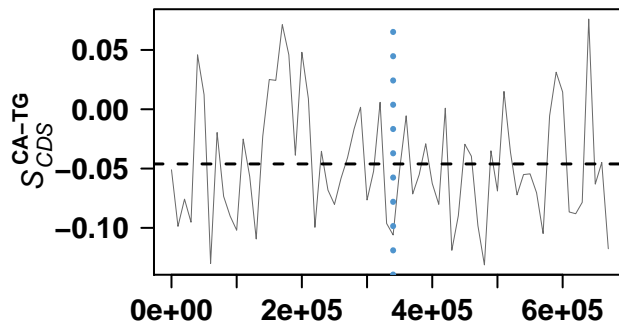
genome coordinates



genome coordinates

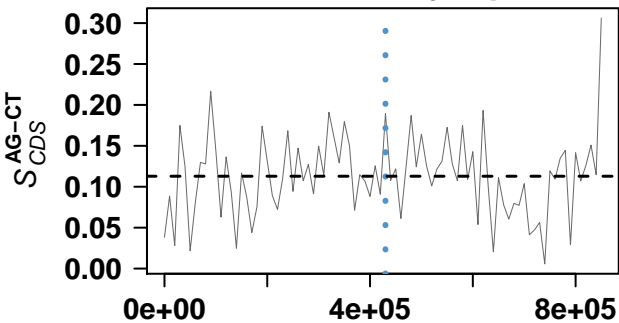


genome coordinates

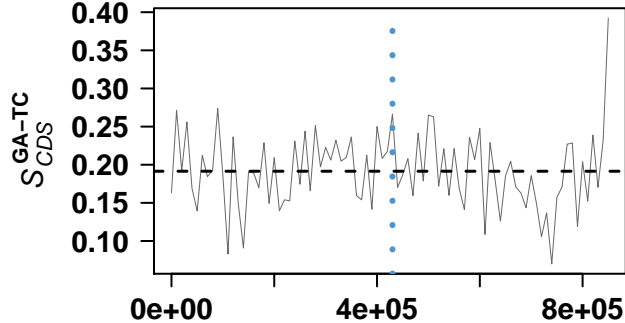


genome coordinates

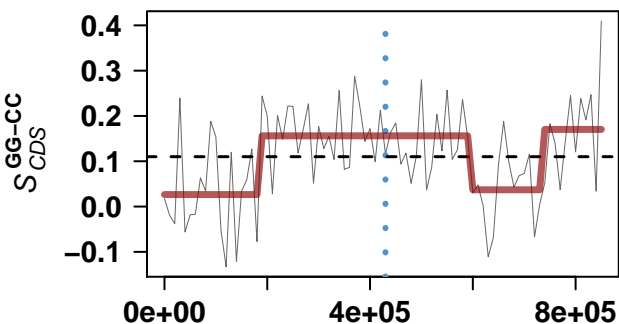
Mycoplasma pulmonis UAB CTIP



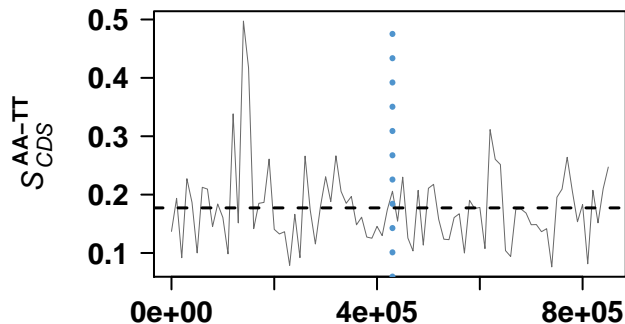
genome coordinates



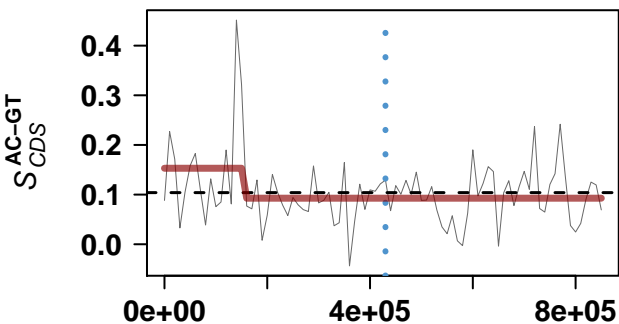
genome coordinates



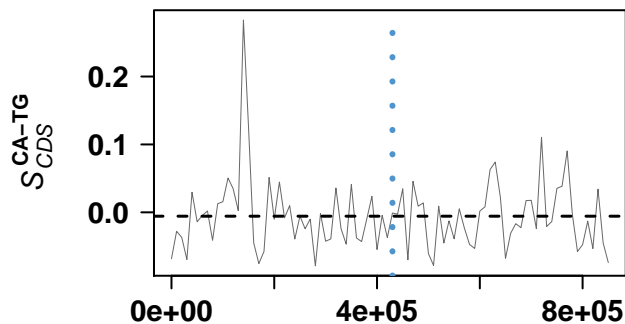
genome coordinates



genome coordinates

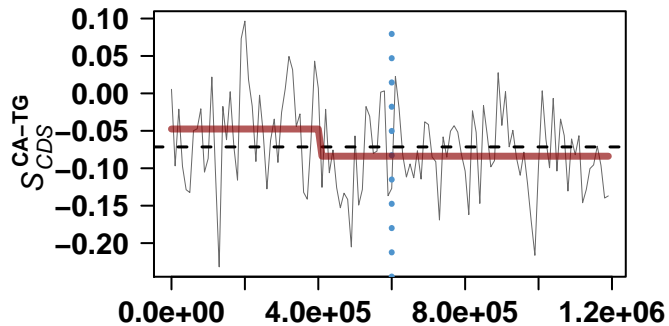
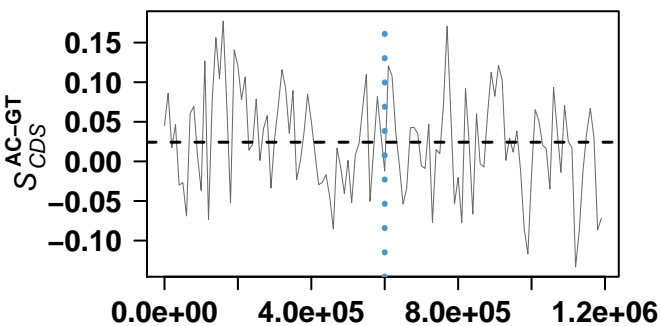
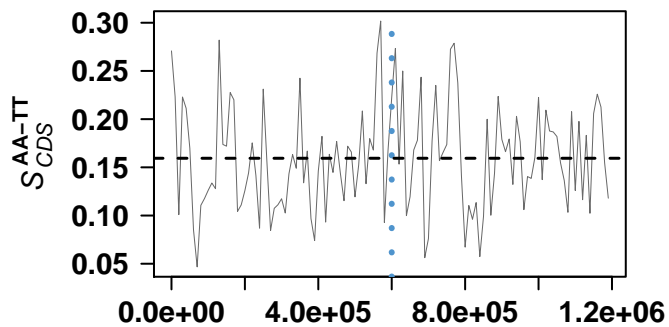
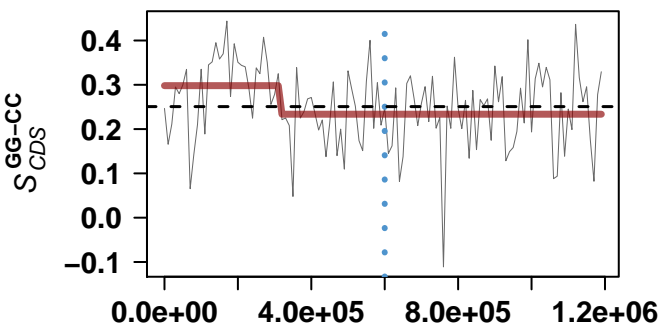
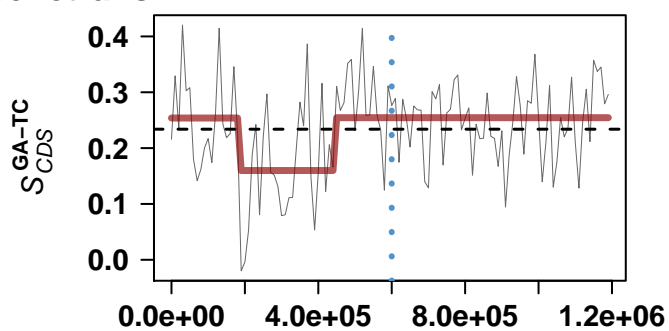
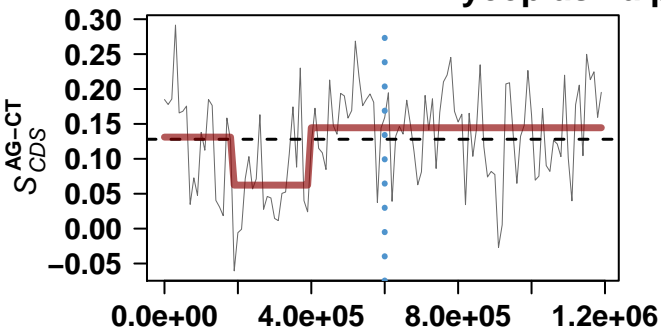


genome coordinates

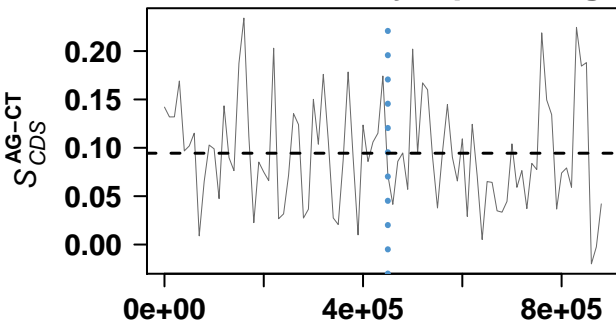


genome coordinates

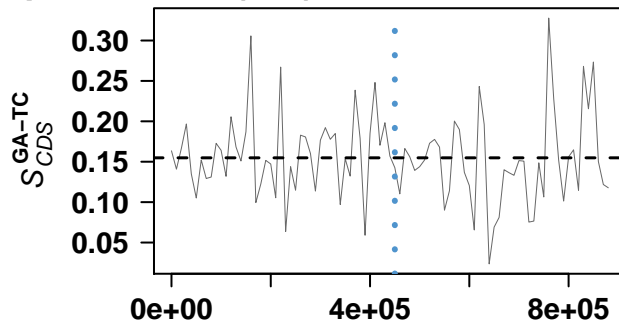
Mycoplasma penetrans HF-2



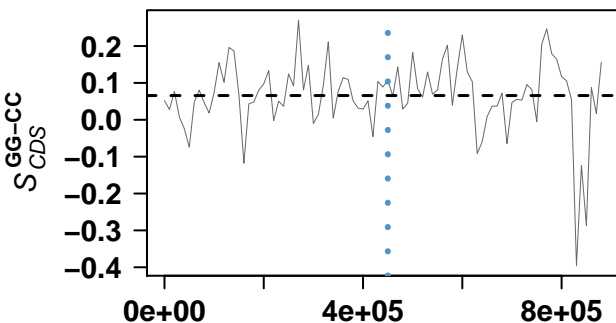
Mycoplasma gallisepticum str. R(low)



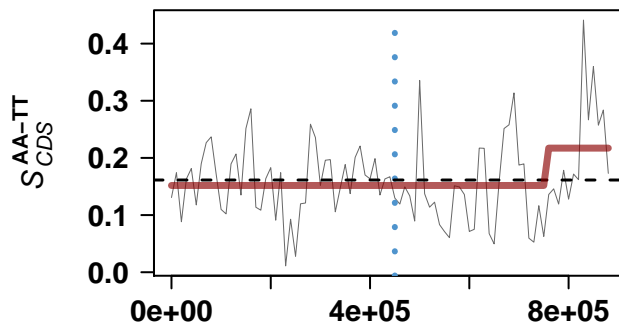
genome coordinates



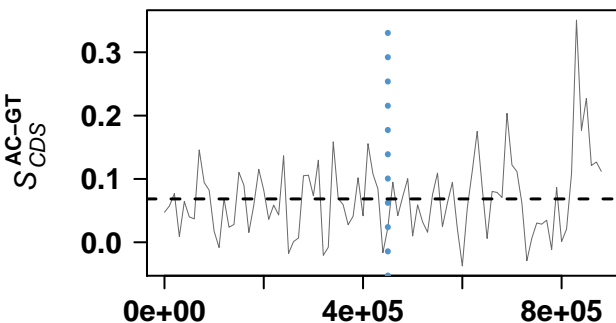
genome coordinates



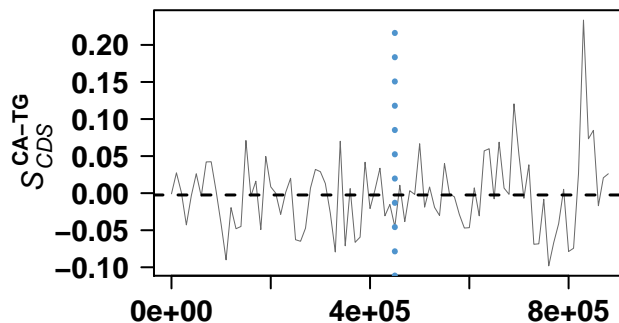
genome coordinates



genome coordinates

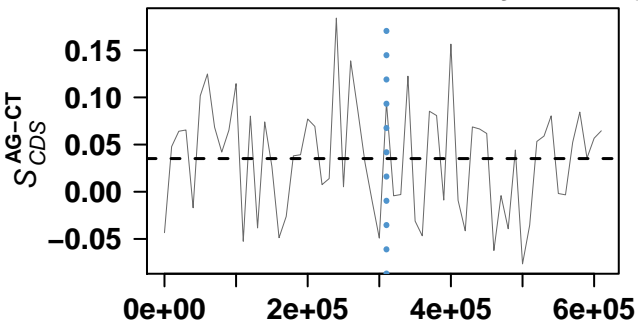


genome coordinates

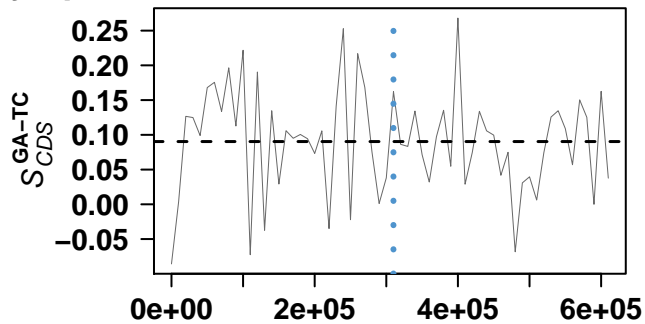


genome coordinates

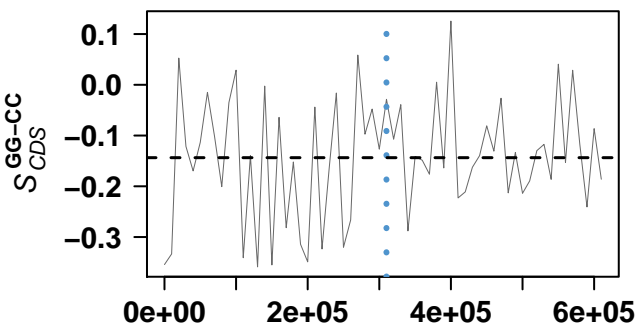
Onion yellows phytoplasma OY-M



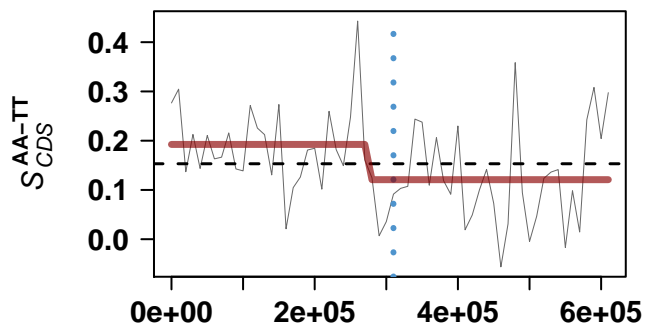
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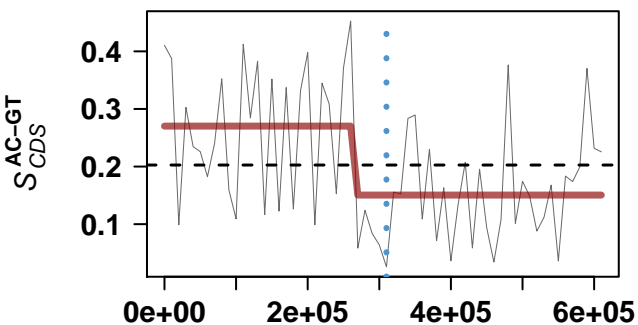
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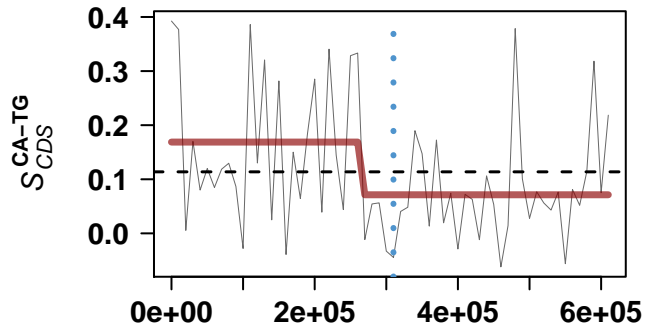
genome coordinates



genome coordinates

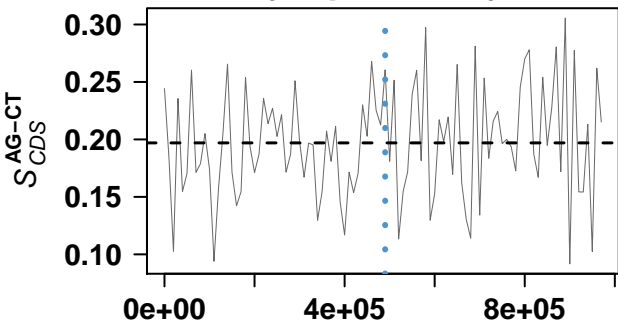


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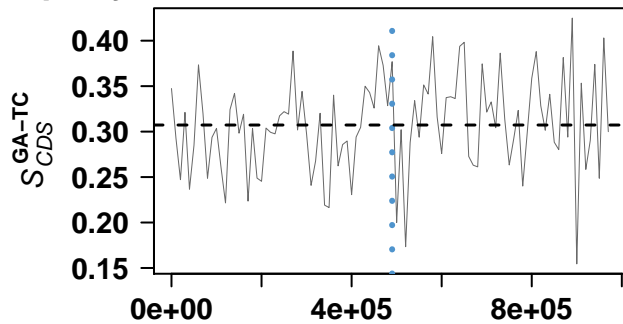


genome coordinates

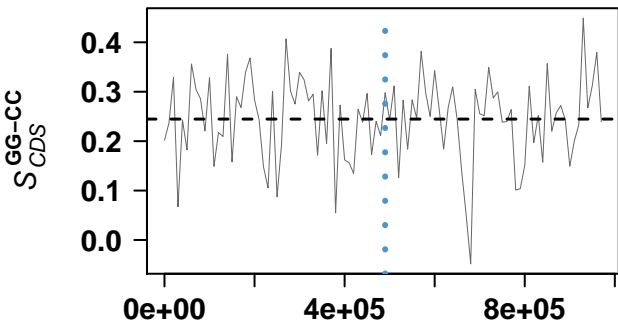
Mycoplasma mycoides subsp. *mycoides* SC str. PG1



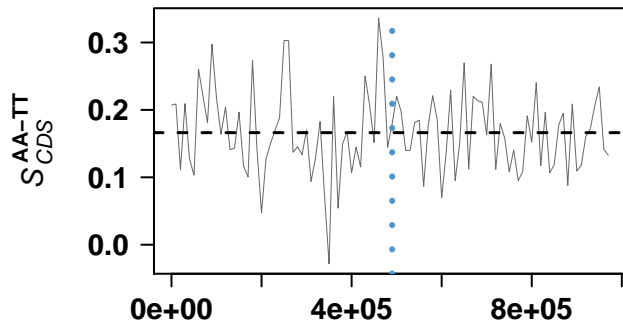
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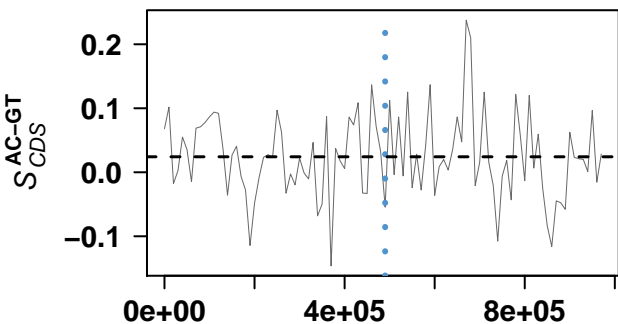
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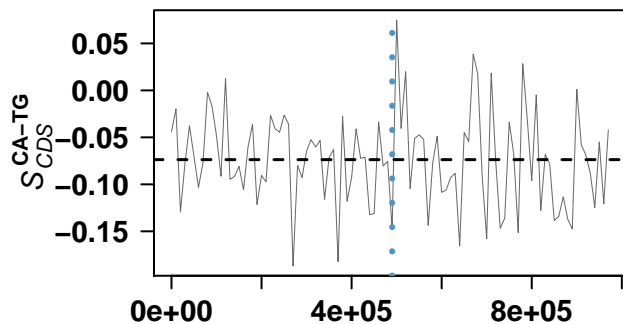
genome coordinates



genome coordinates

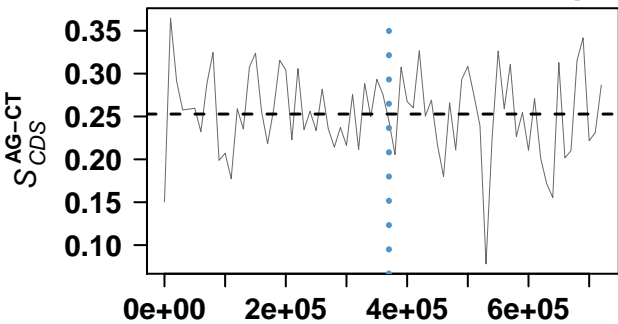


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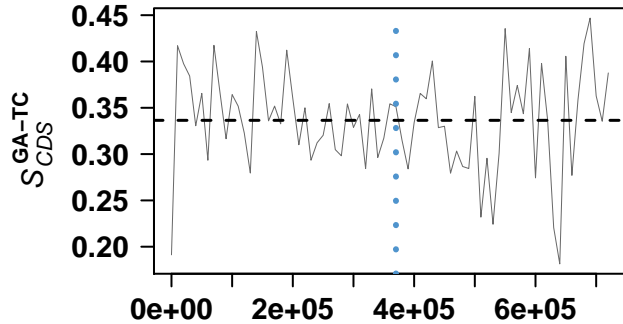


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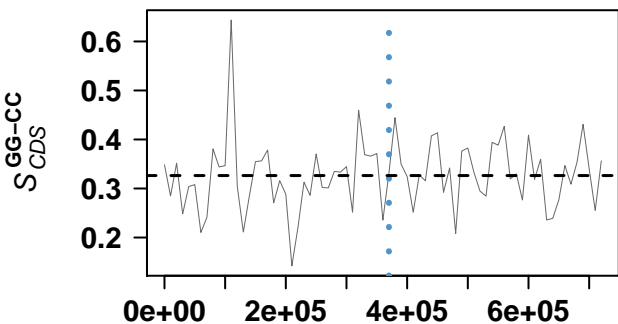
Mesoplasma florum L1



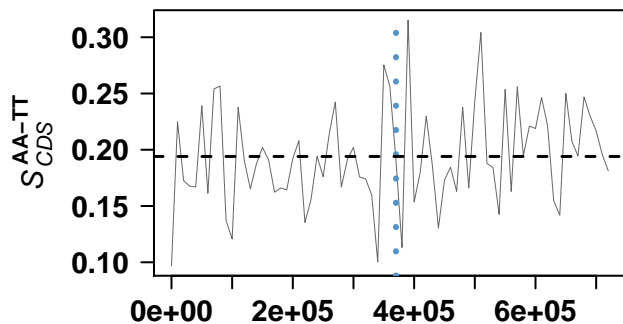
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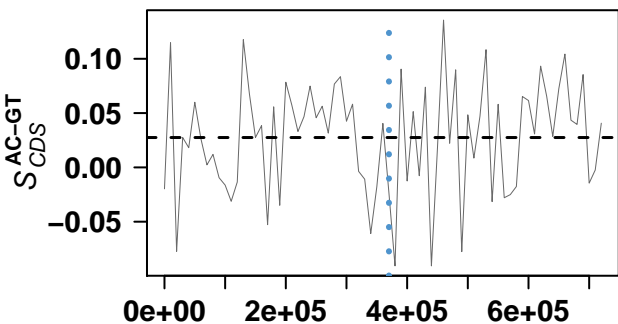
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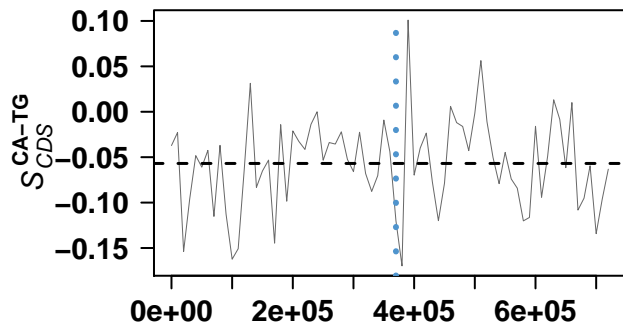
genome coordinates



genome coordinates

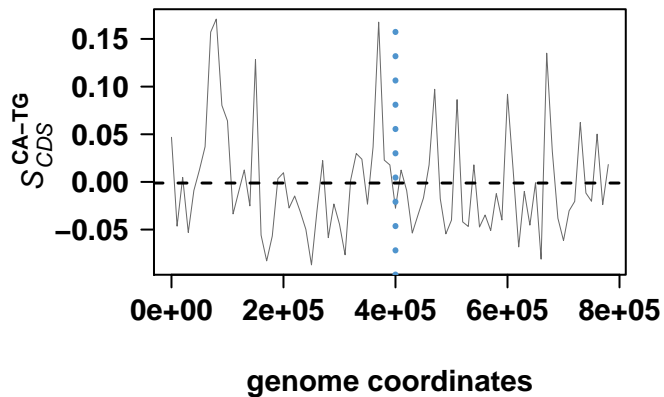
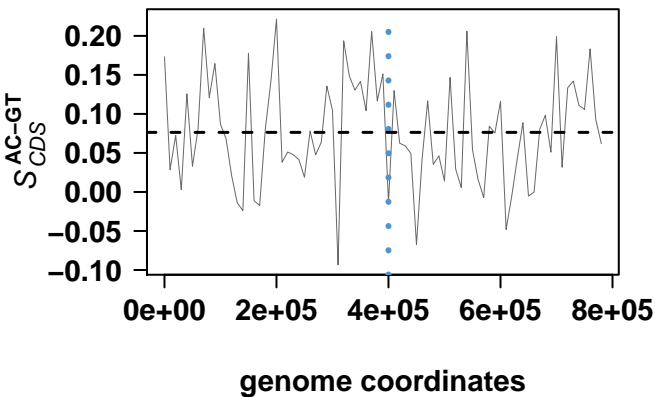
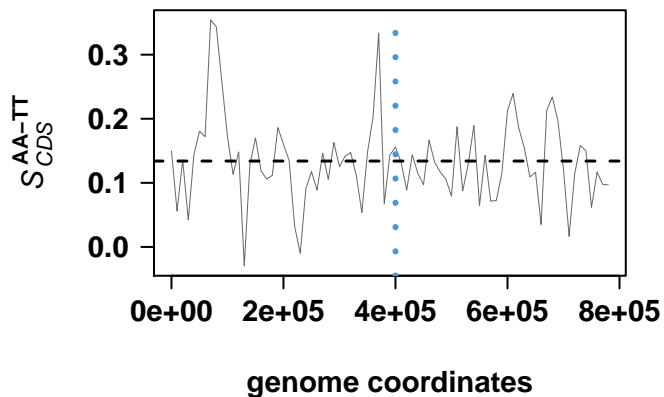
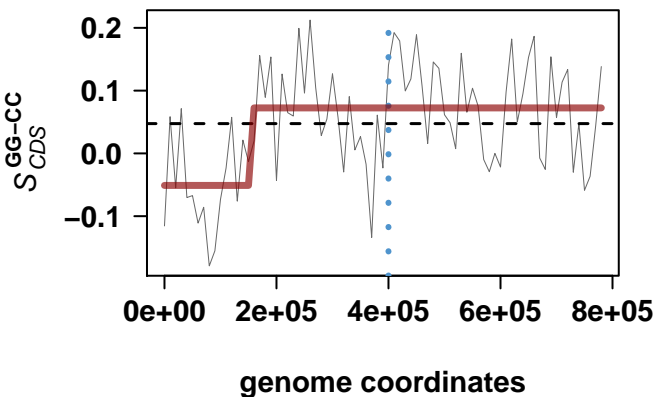
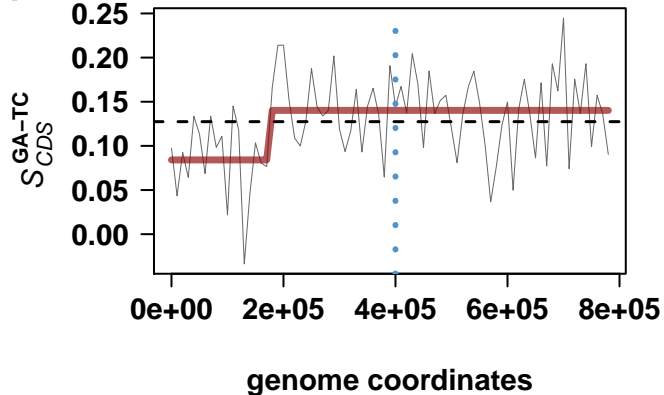
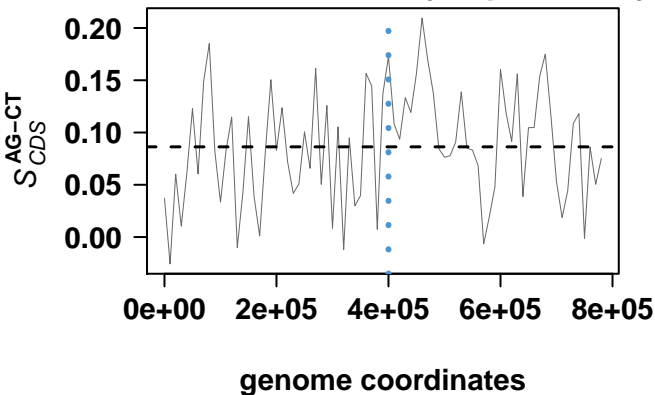


genome coordinates

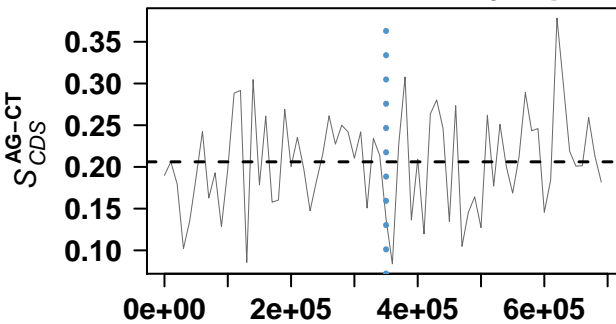


genome coordinates

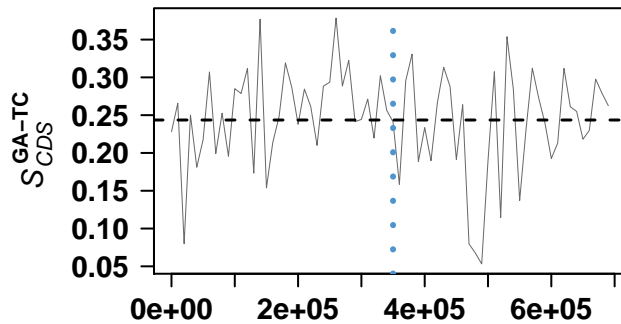
Mycoplasma hyopneumoniae 232



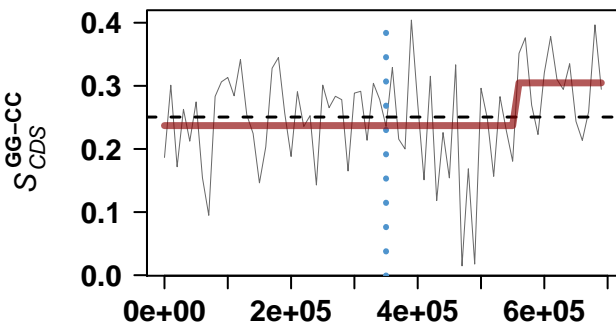
Mycoplasma mobile 163K



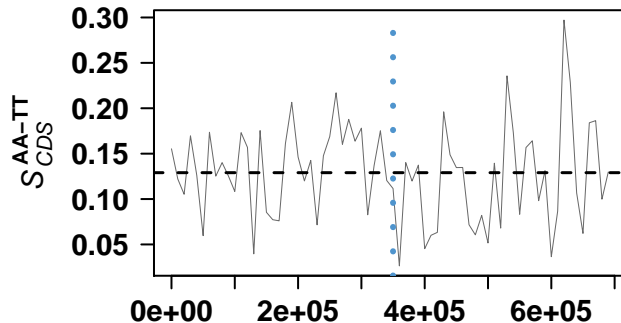
genome coordinates



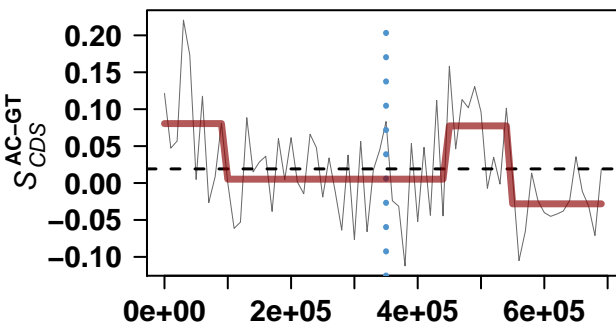
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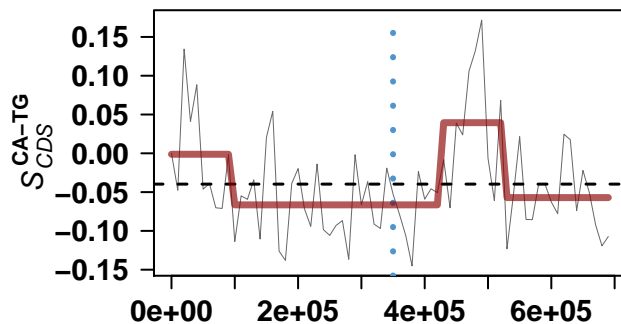
genome coordinates



genome coordinates

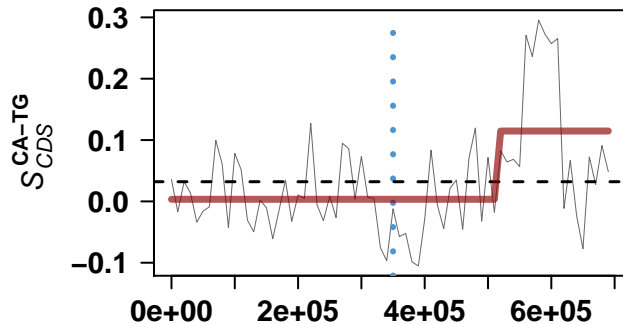
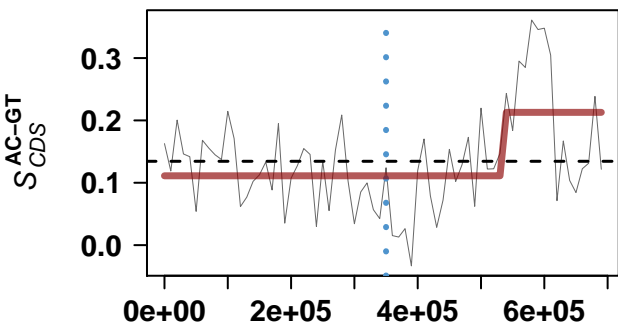
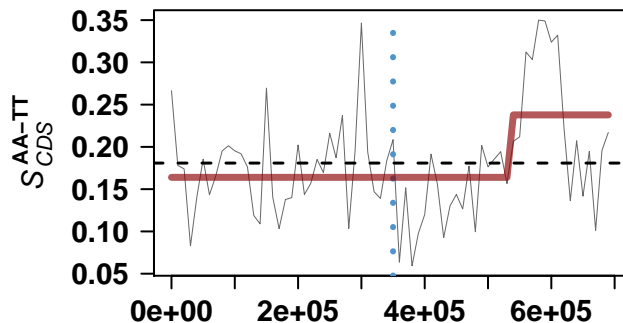
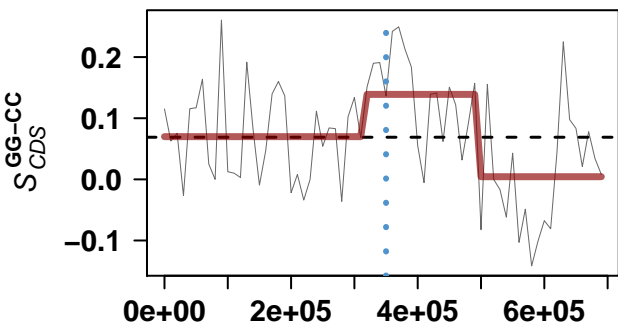
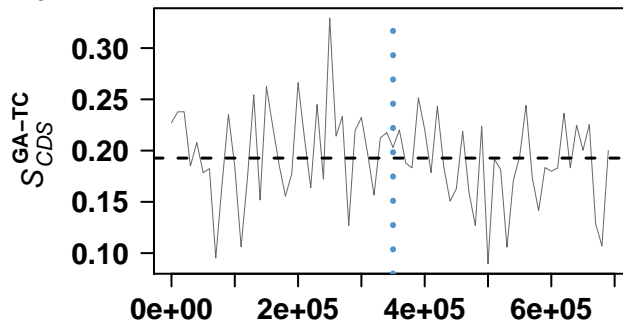
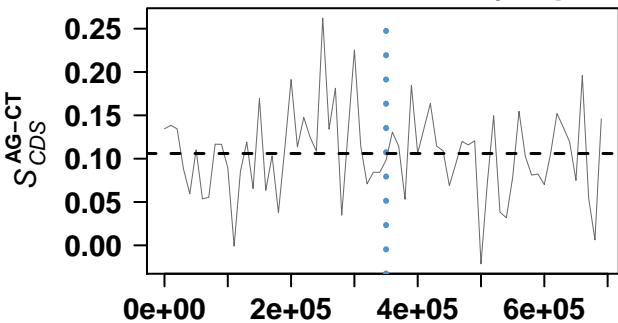


genome coordinates

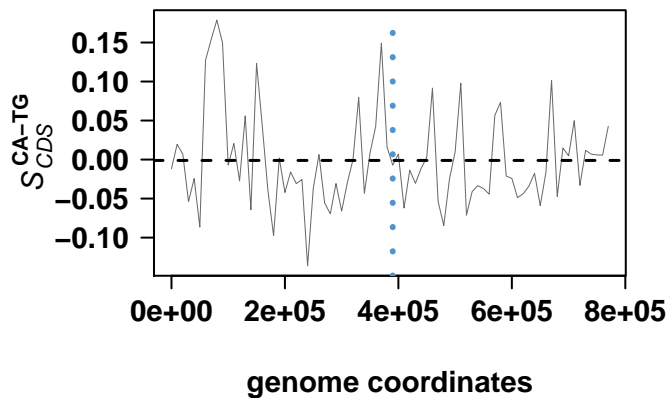
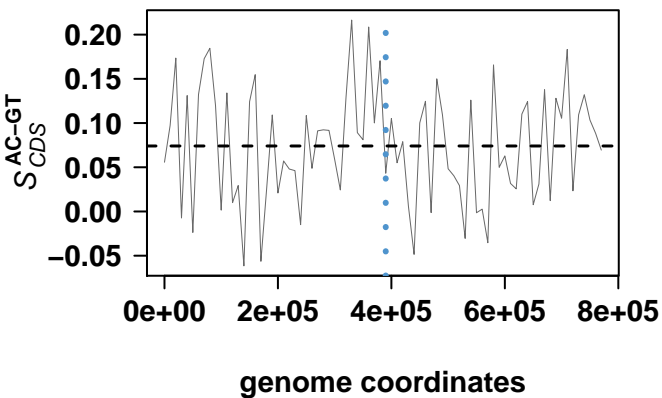
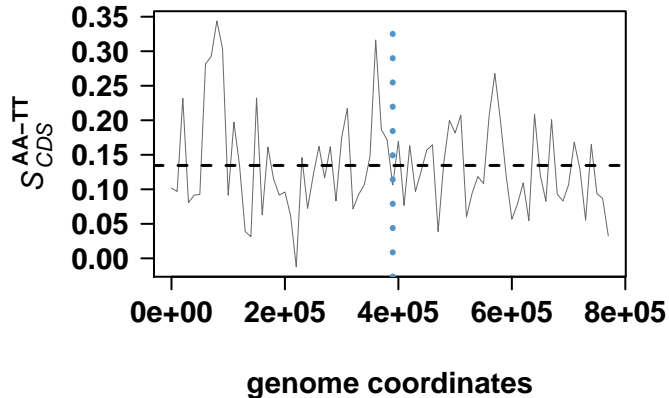
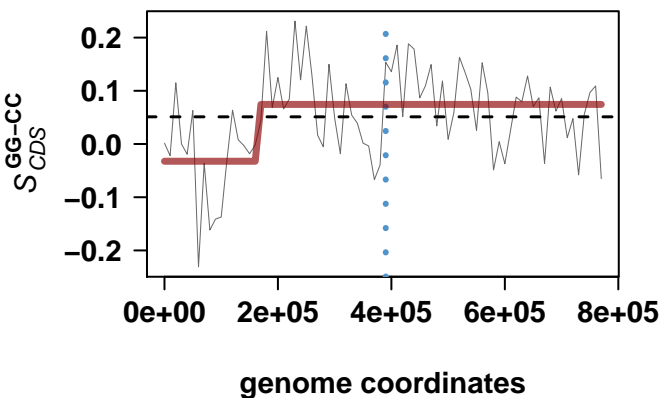
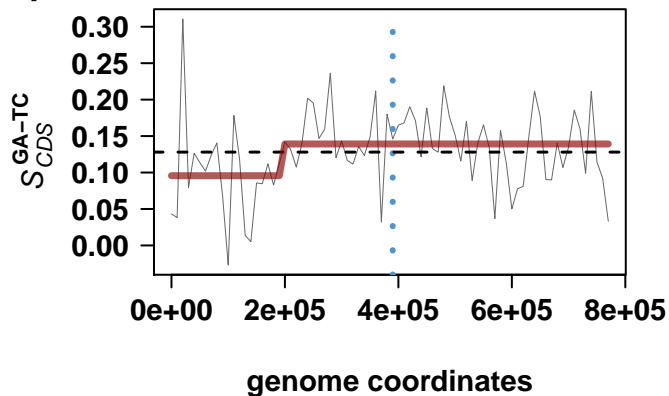
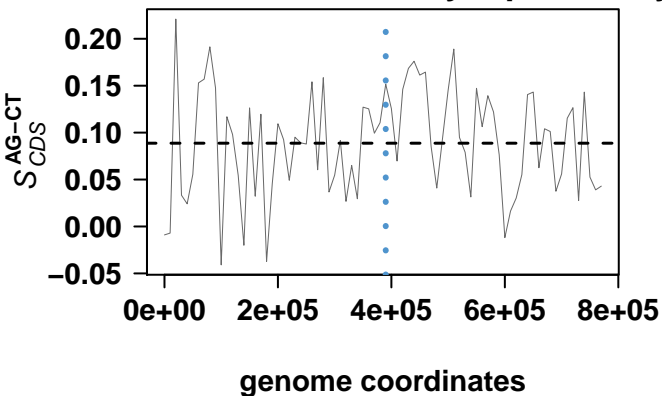


genome coordinates

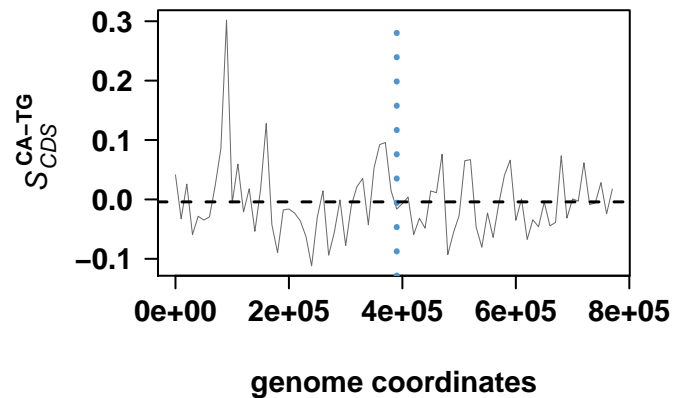
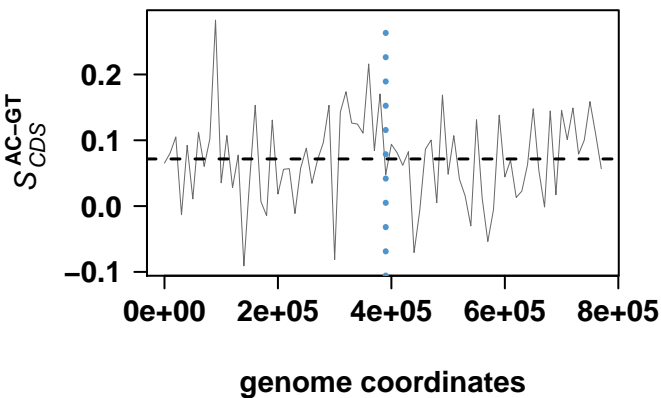
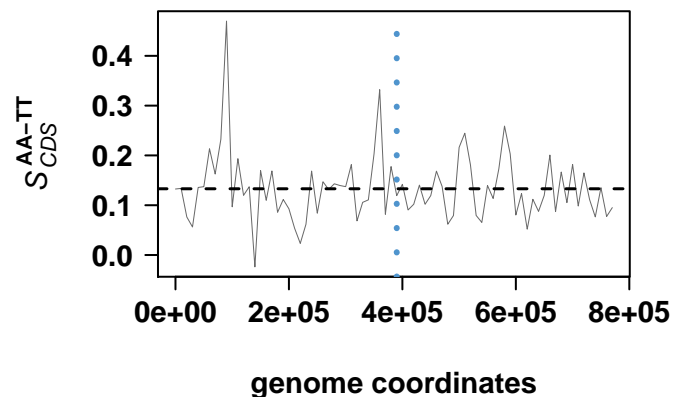
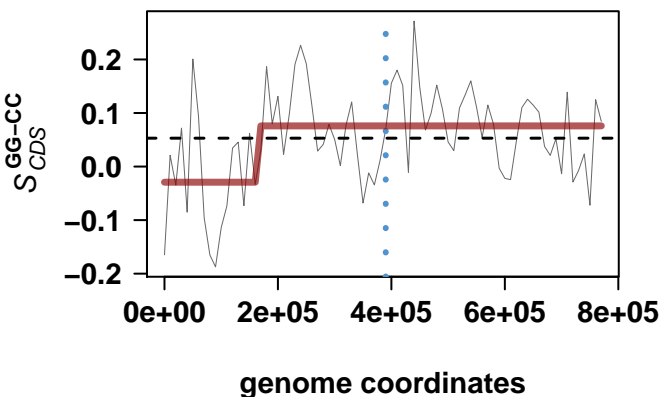
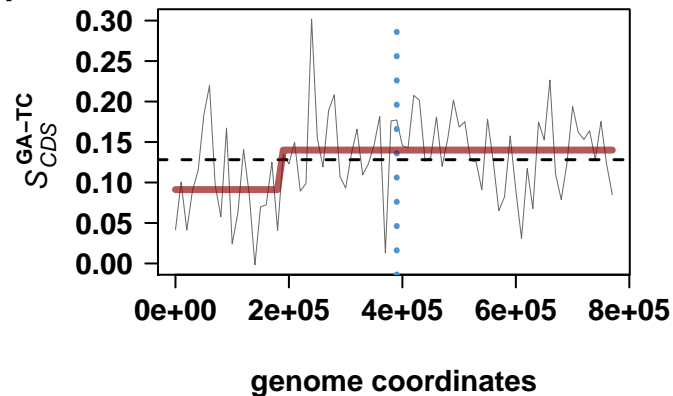
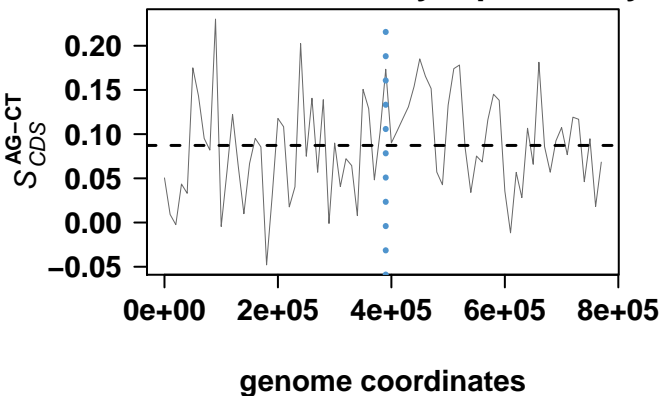
Mycoplasma synoviae 53



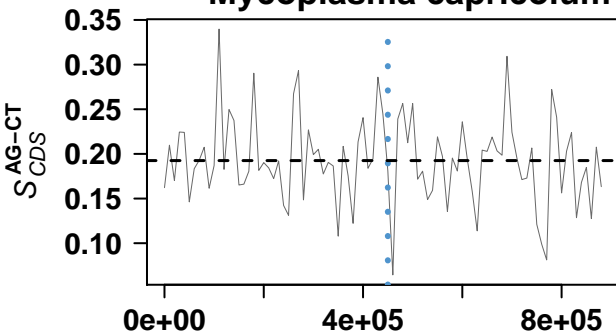
Mycoplasma hyopneumoniae J



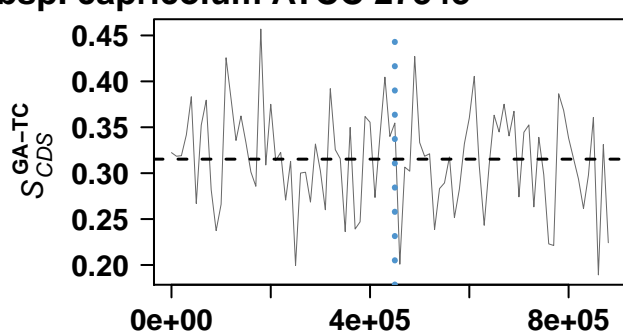
Mycoplasma hyopneumoniae 7448



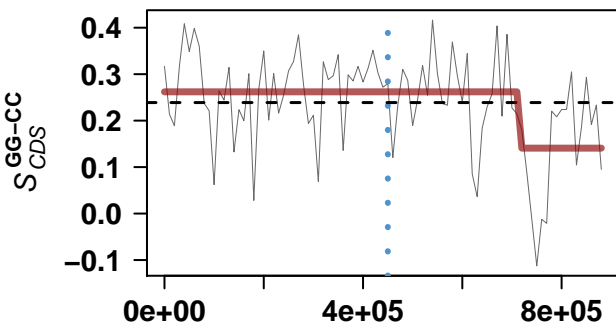
Mycoplasma capricolum subsp. *capricolum* ATCC 27343



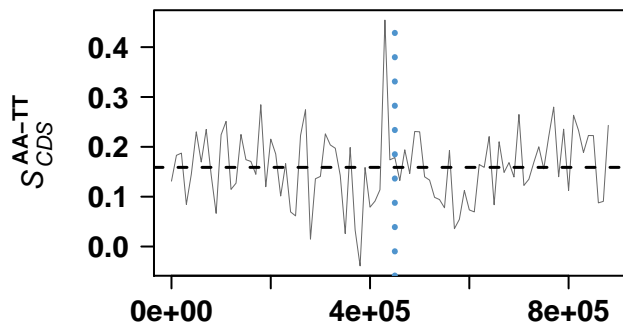
genome coordinates



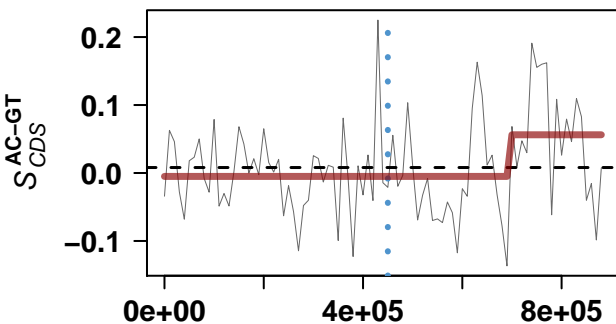
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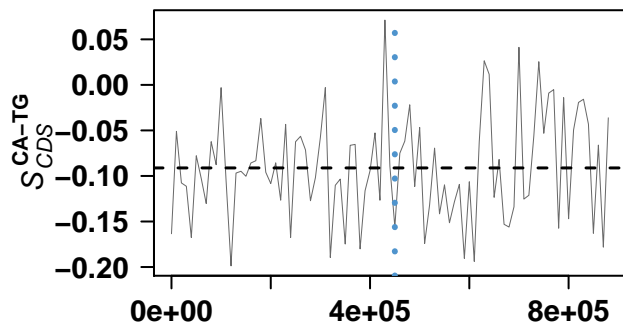
genome coordinates



genome coordinates

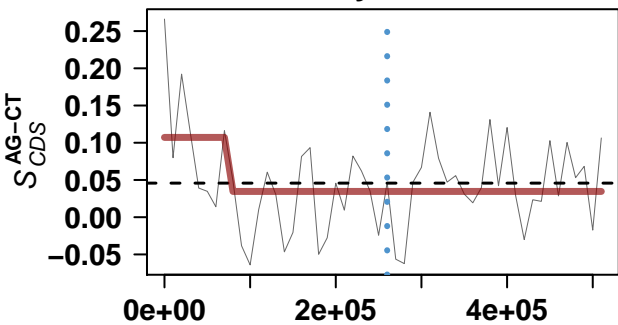


genome coordinates

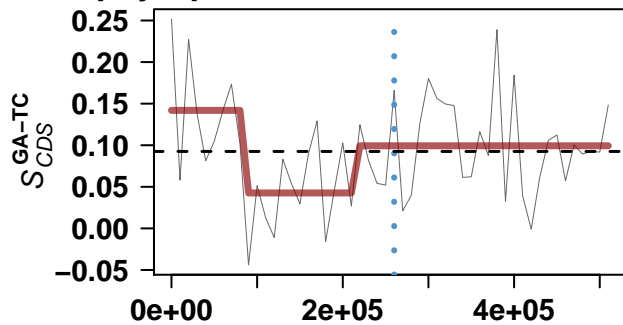


genome coordinates

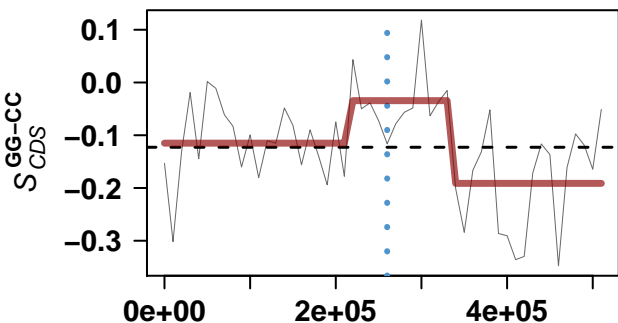
Aster yellows witches'-broom phytoplasma AYWB



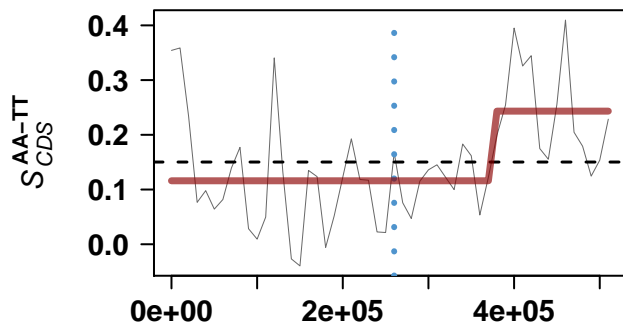
genome coordinates



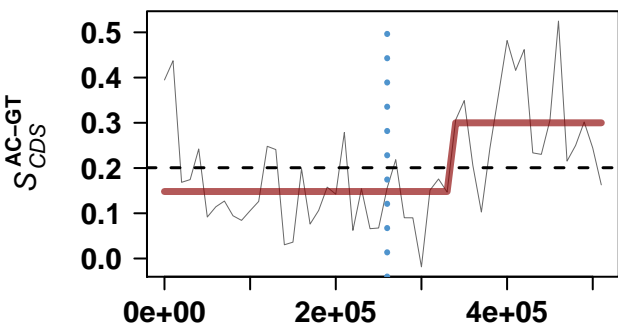
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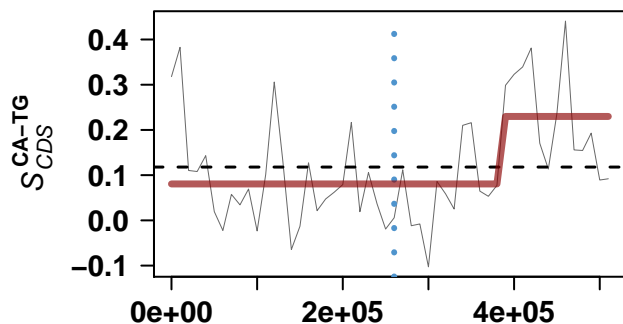
genome coordinates



genome coordinates



genome coordinates



genome coordinates