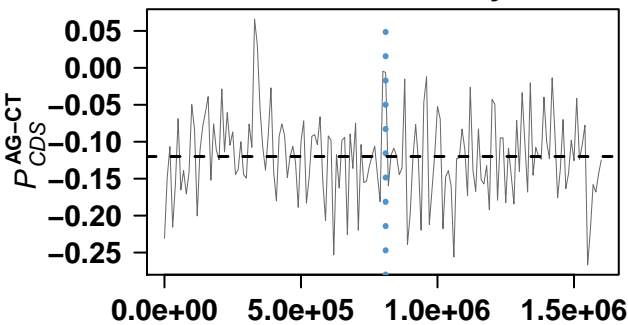
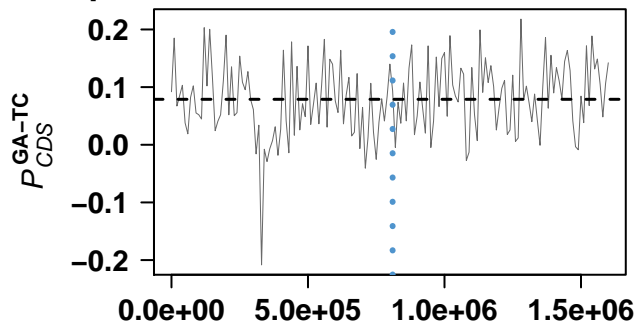


Diagrams (gray curve) and fitted linear models (red thick line) for dinucleotide odds-ratio skews ($P_{\text{CDS}}^{\text{AG-CT}}$, $P_{\text{CDS}}^{\text{GA-TC}}$, $P_{\text{CDS}}^{\text{GG-CC}}$, $P_{\text{CDS}}^{\text{AA-TT}}$, $P_{\text{CDS}}^{\text{AC-GT}}$ and $P_{\text{CDS}}^{\text{CA-TG}}$) along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

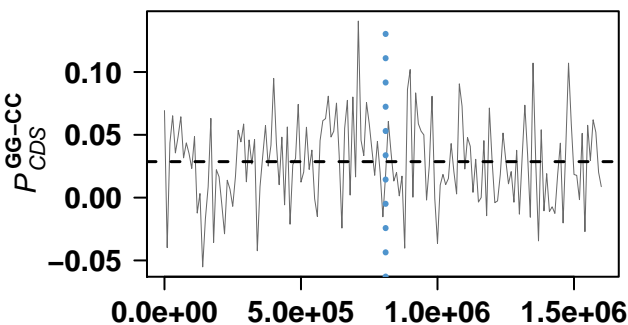
Mycobacterium leprae TN



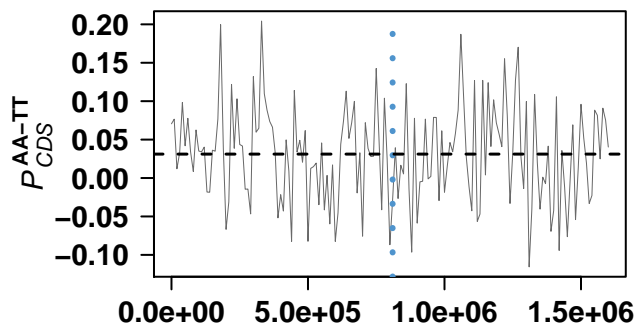
genome coordinates



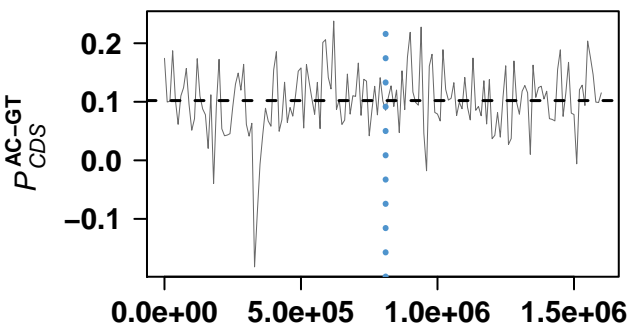
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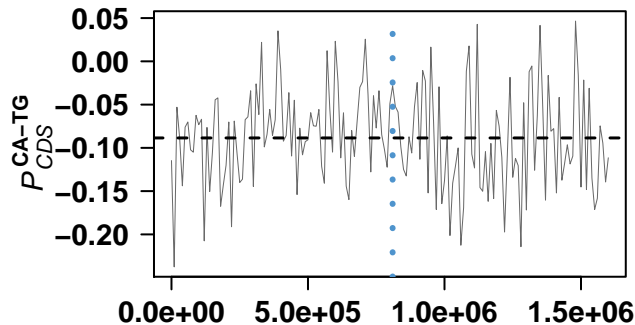
genome coordinates



genome coordinates

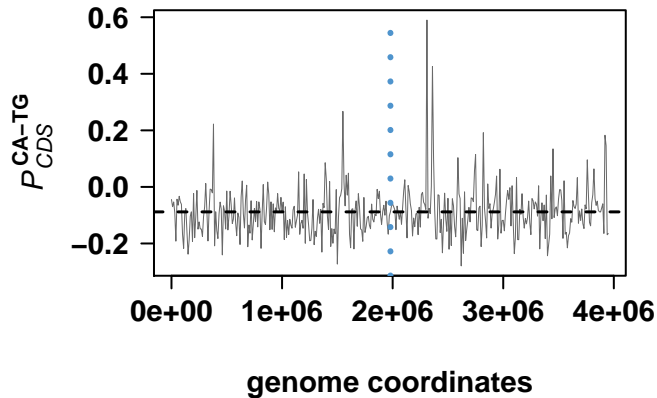
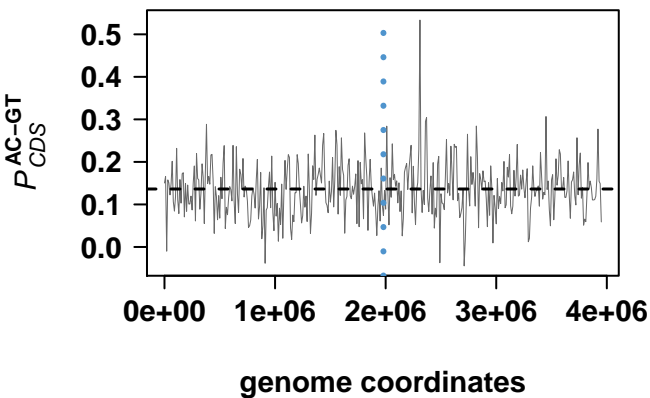
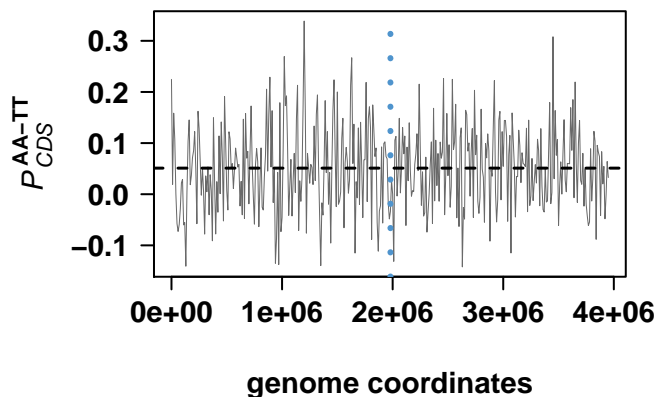
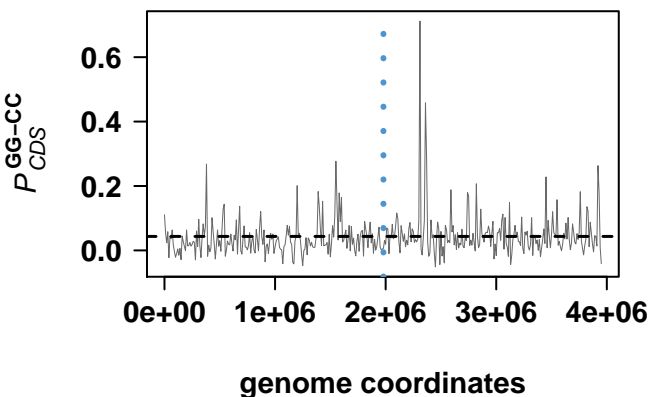
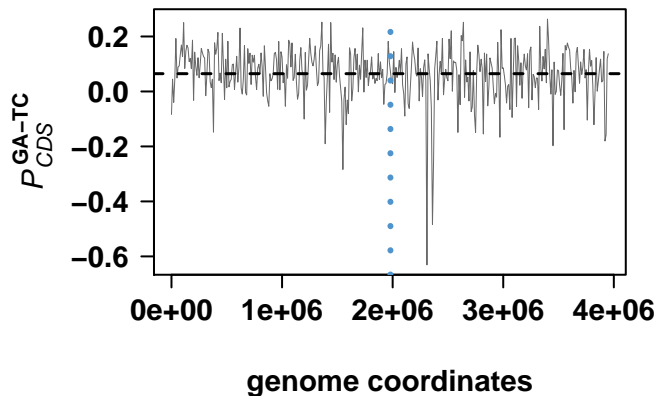
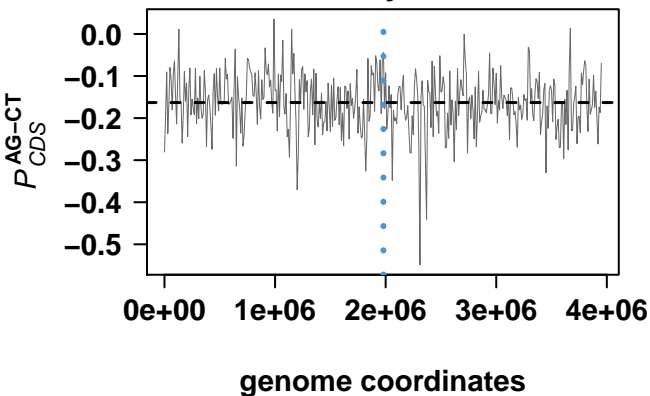


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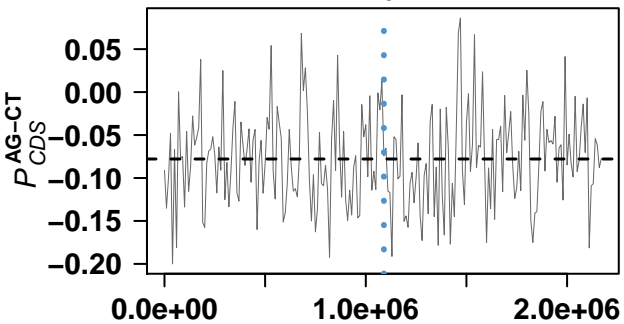


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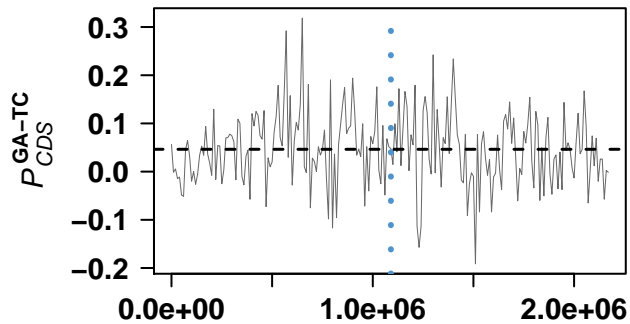
Mycobacterium tuberculosis CDC1551



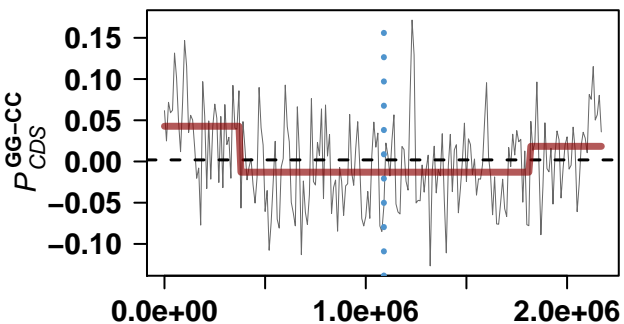
Corynebacterium diphtheriae NCTC 13129



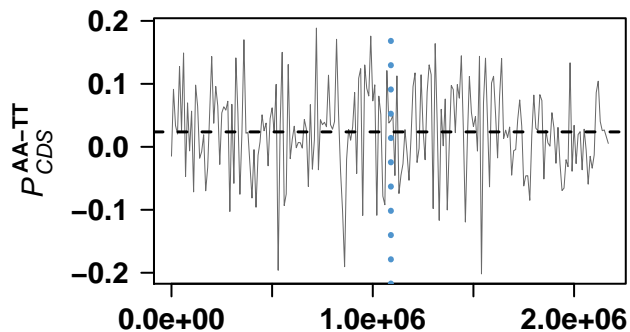
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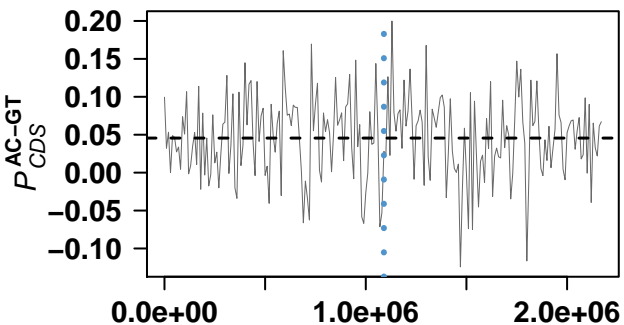
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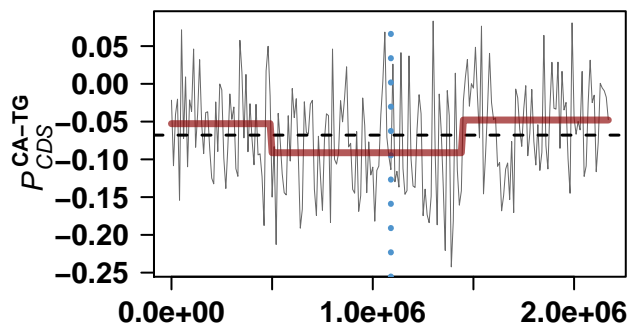
genome coordinates



genome coordinates

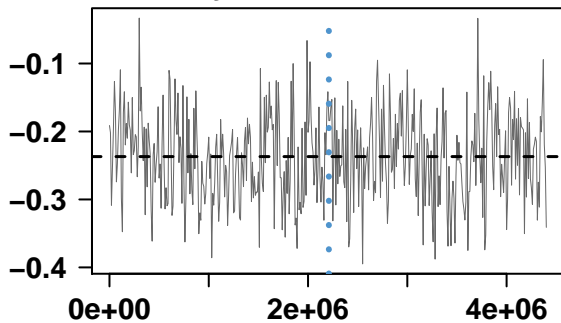


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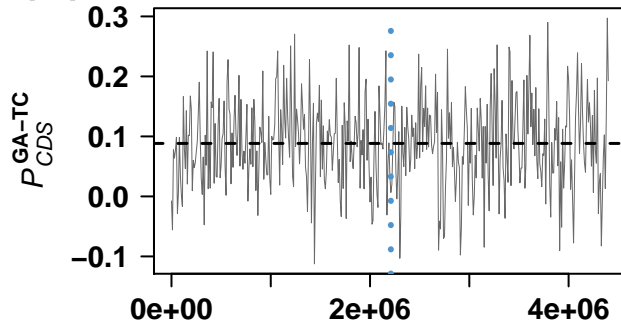


genome coordinates

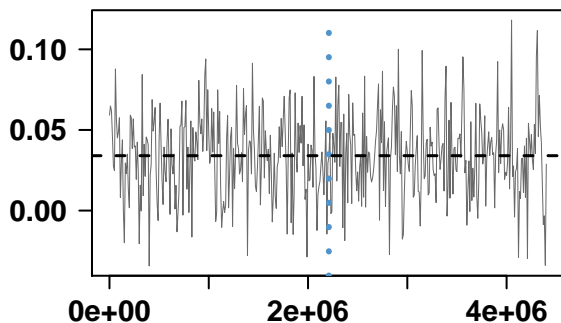
Mycobacterium avium subsp. paratuberculosis K-10



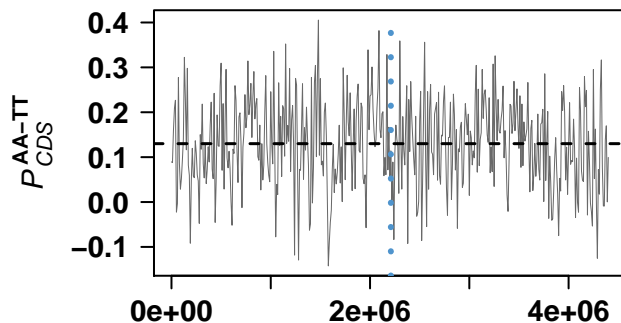
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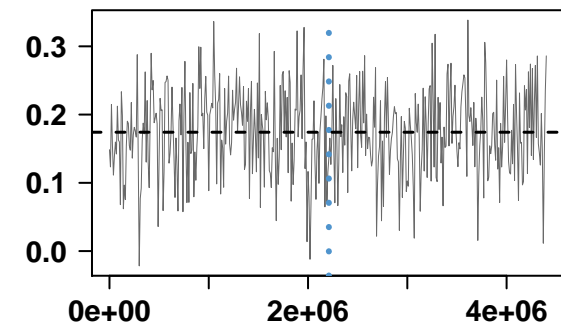
genome coordinates



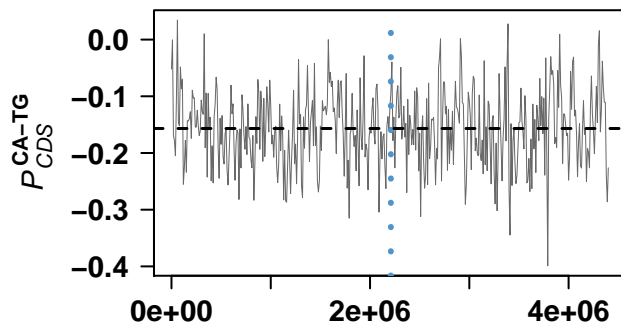
genome coordinates



genome coordinates

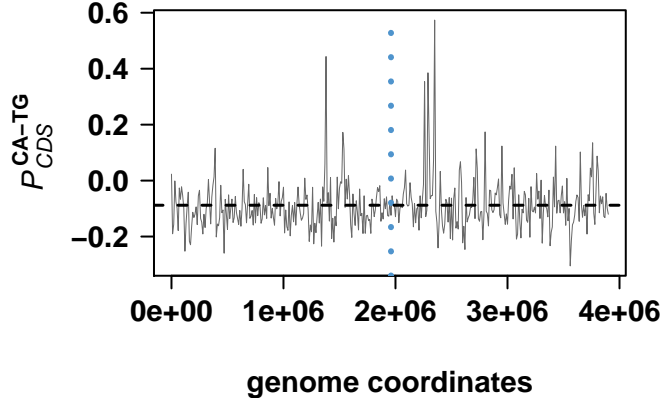
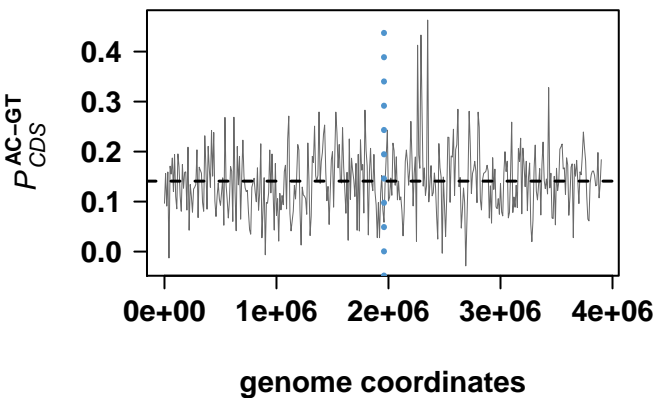
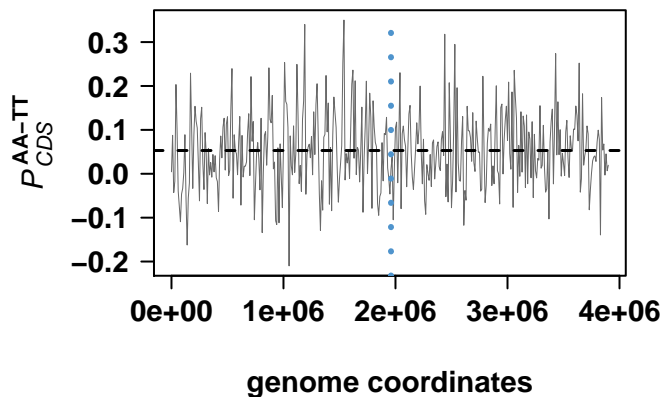
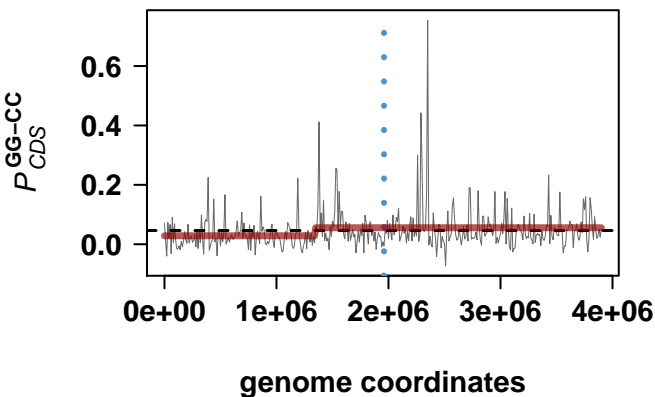
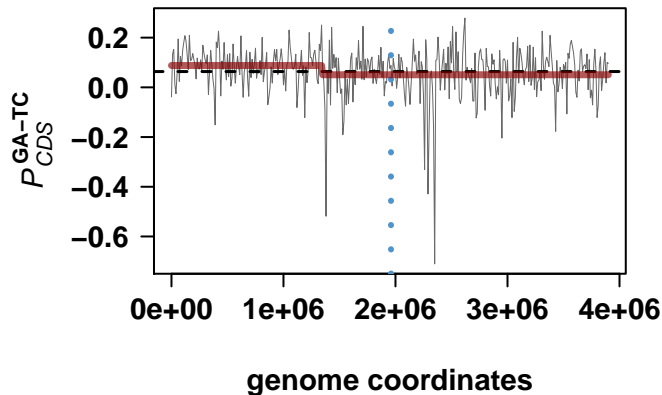
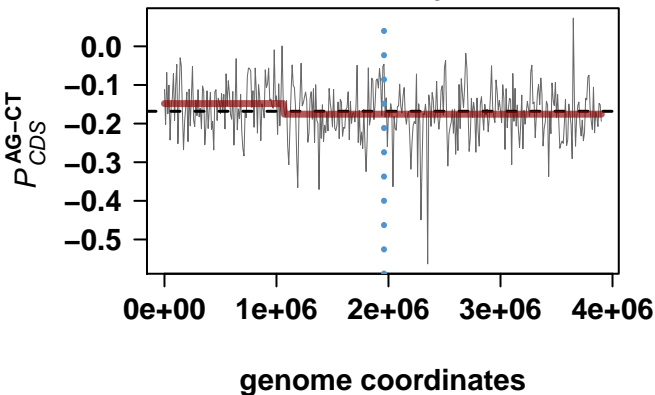


genome coordinates

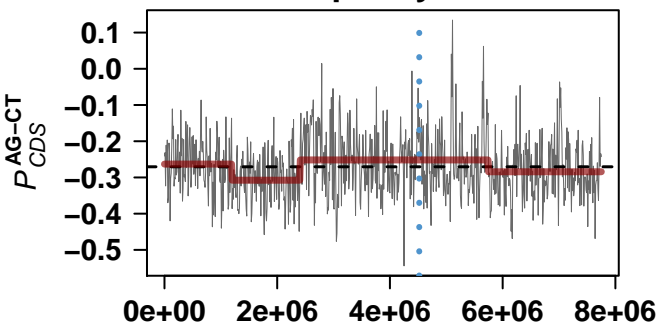


genome coordinates

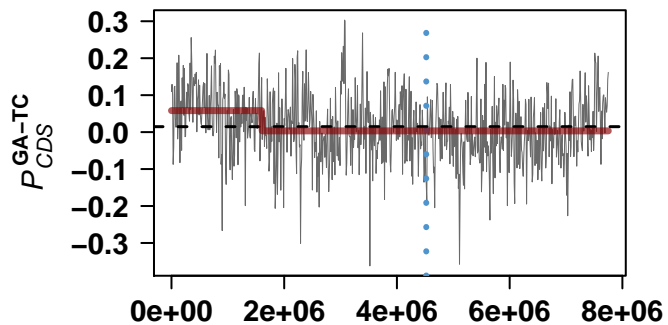
Mycobacterium bovis AF2122/97



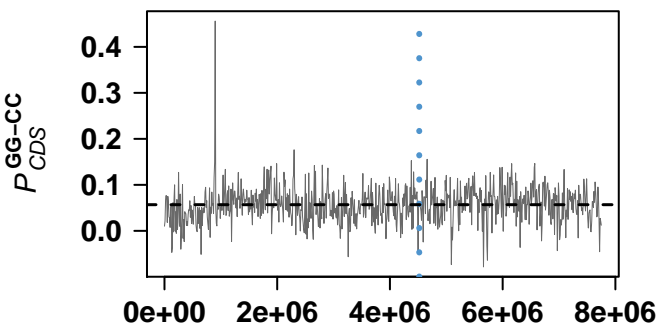
Streptomyces avermitilis MA-4680 = NBRC 14893



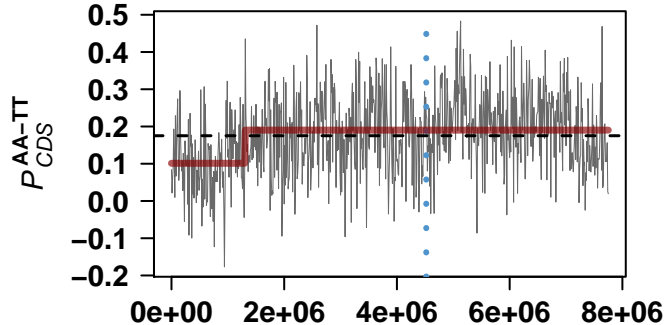
genome coordinates



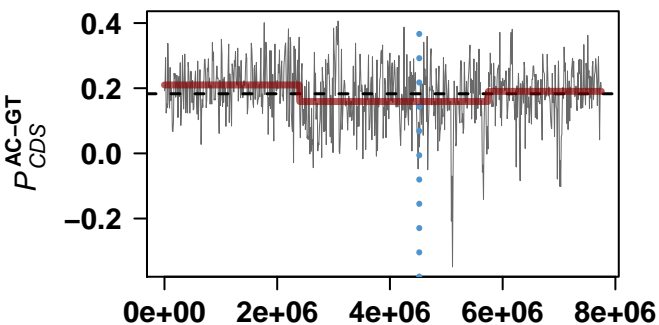
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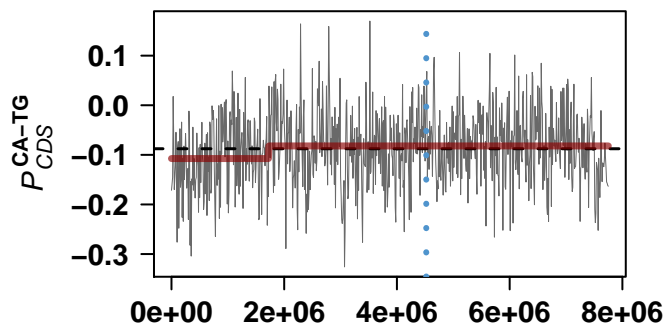
genome coordinates



genome coordinates

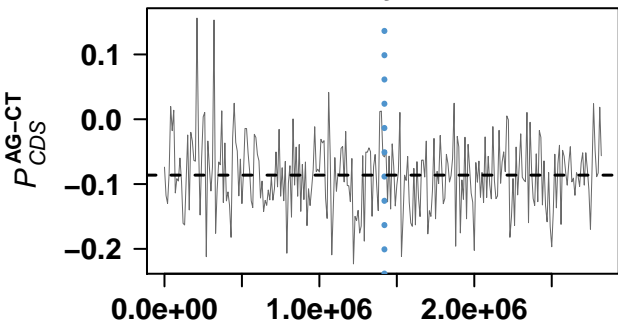


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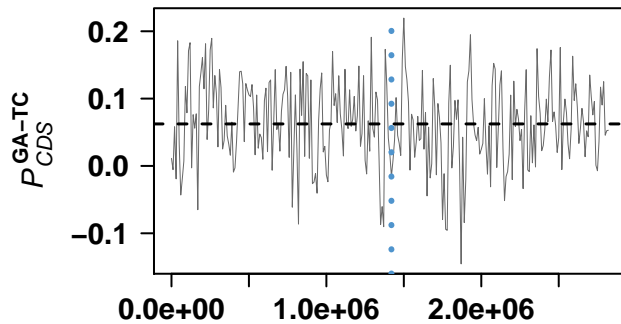


genome coordinates

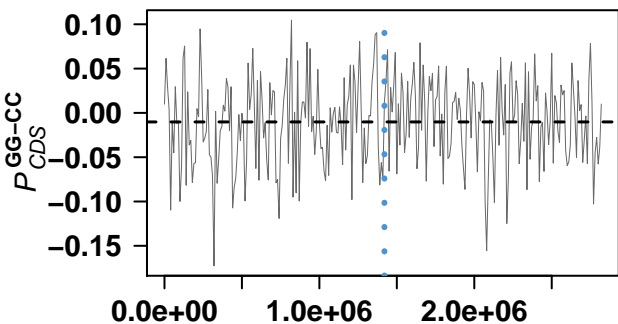
Corynebacterium glutamicum ATCC 13032



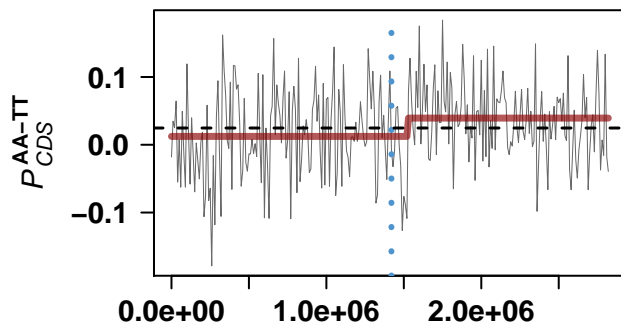
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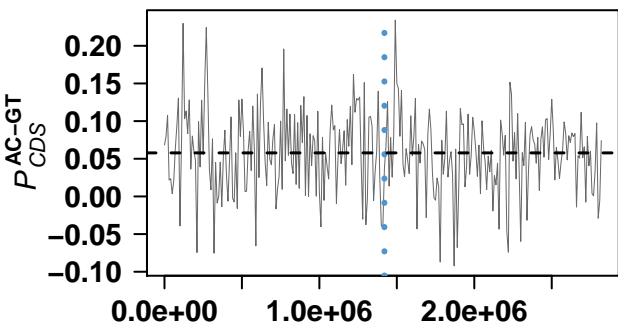
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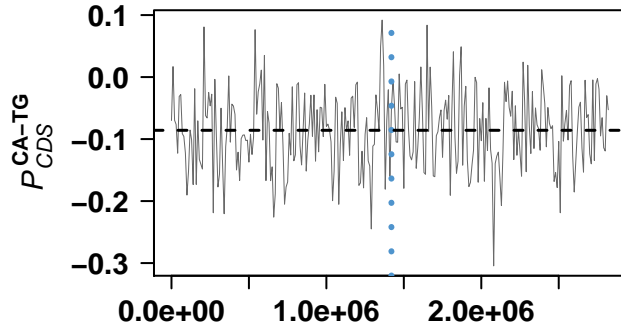
genome coordinates



genome coordinates

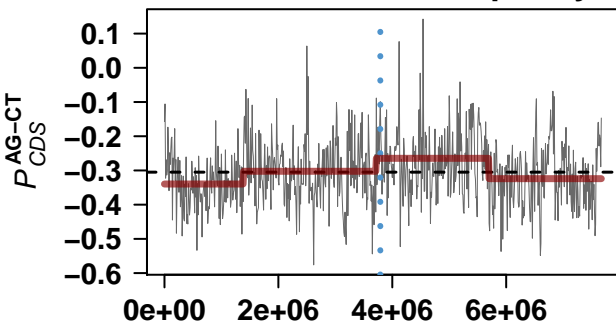


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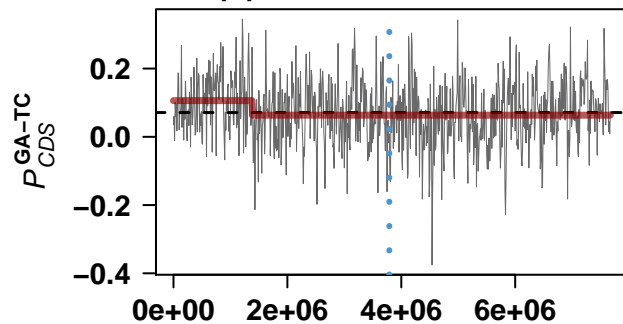


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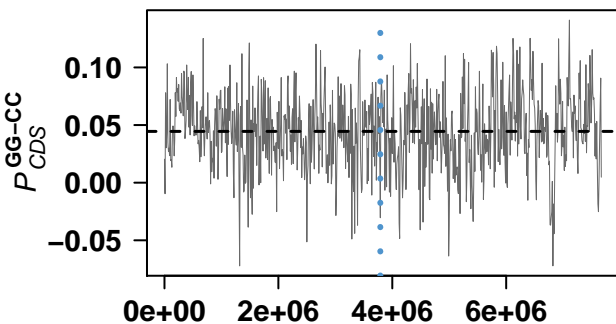
Streptomyces coelicolor A3(2)



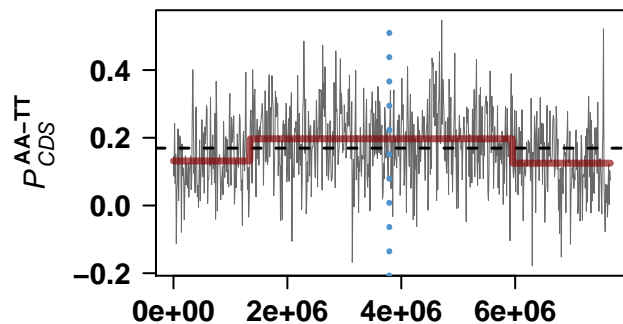
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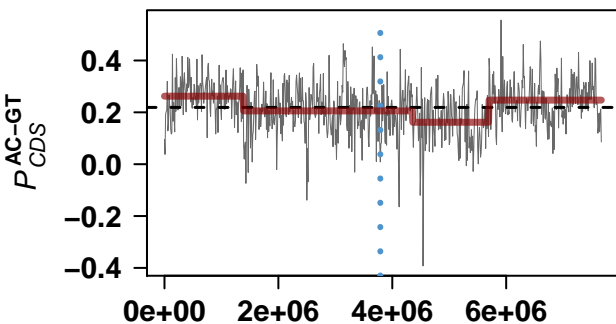
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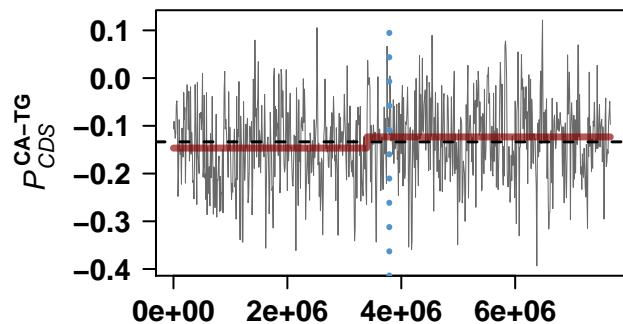
genome coordinates



genome coordinates

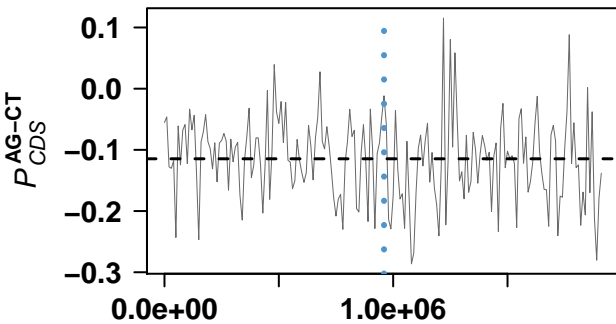


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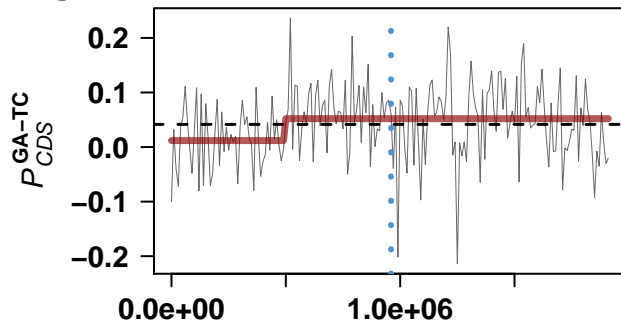


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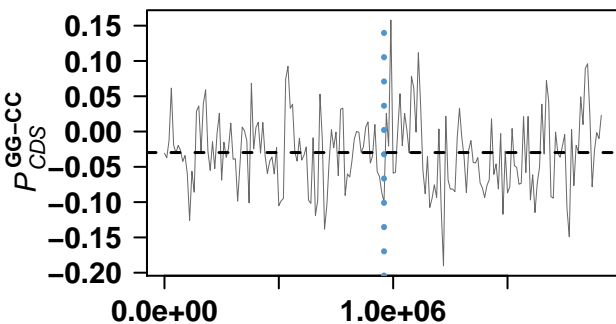
Bifidobacterium longum NCC2705



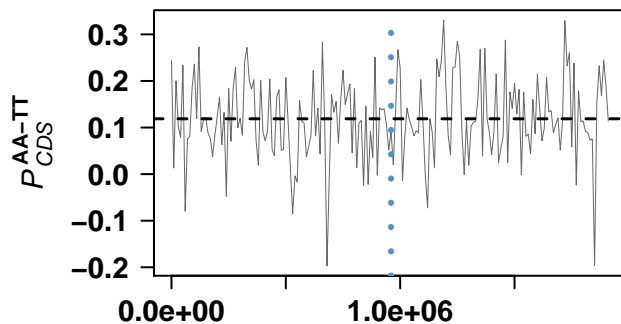
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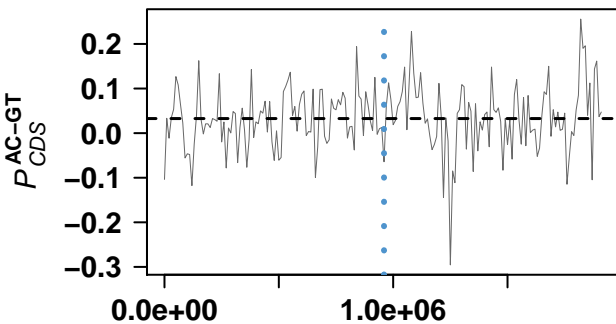
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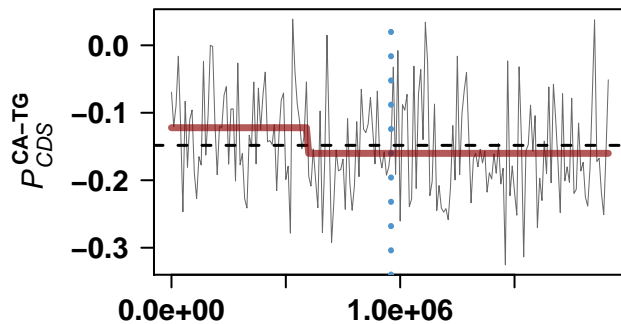
genome coordinates



genome coordinates

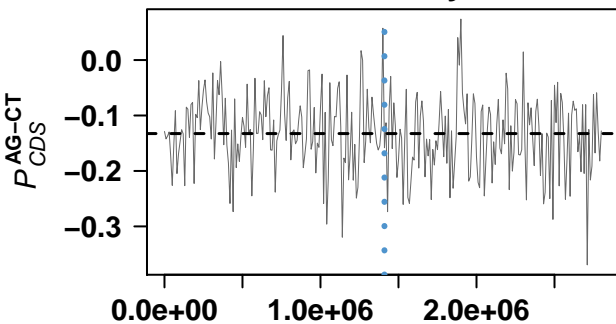


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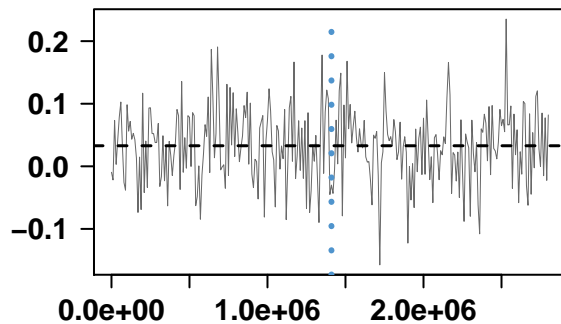


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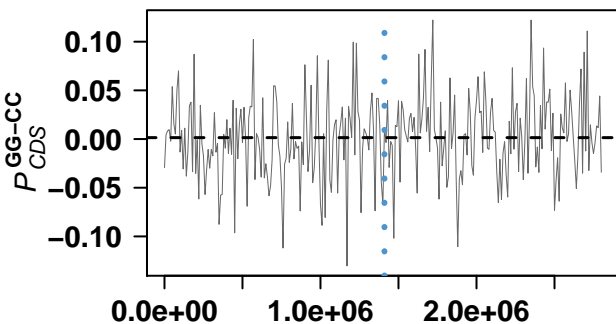
Corynebacterium efficiens YS-314



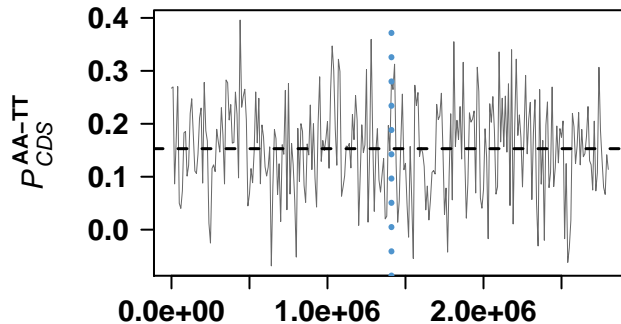
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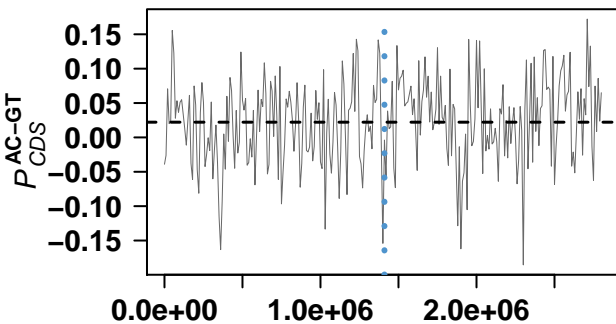
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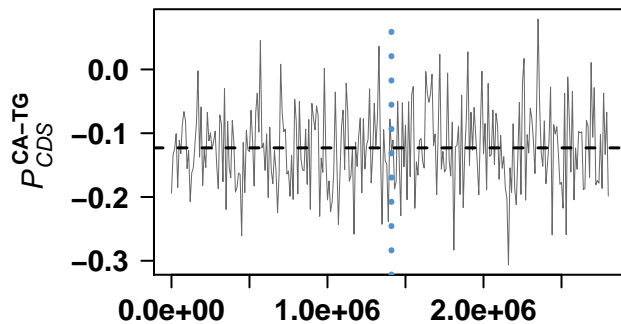
genome coordinates



genome coordinates

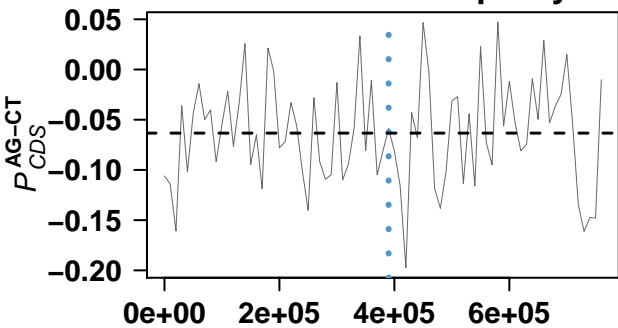


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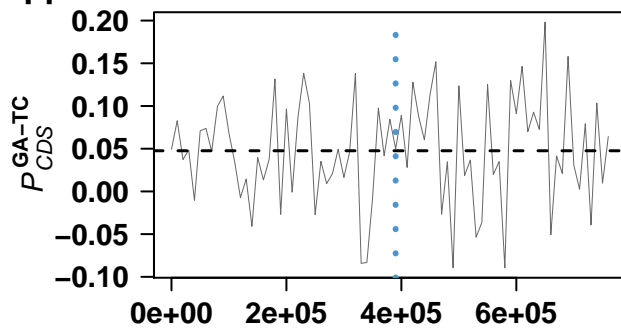


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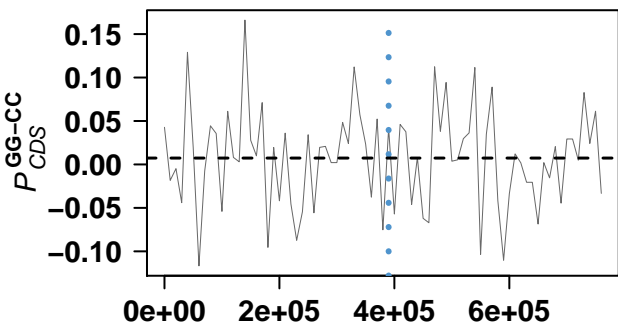
Tropheryma whippelii TW08/27



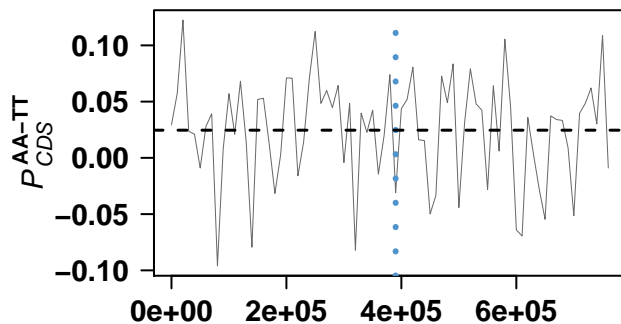
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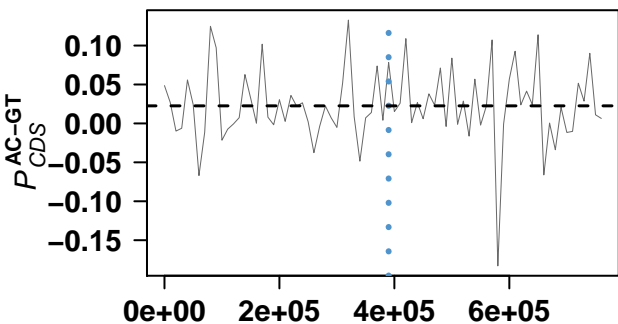
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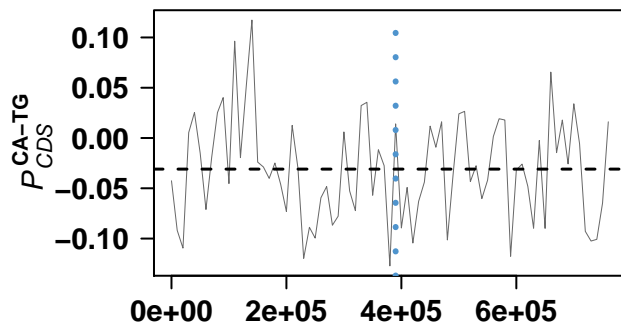
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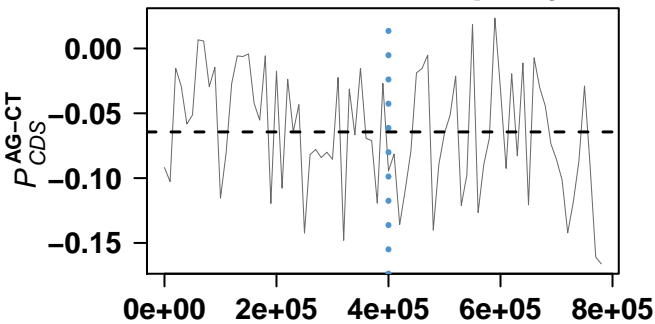


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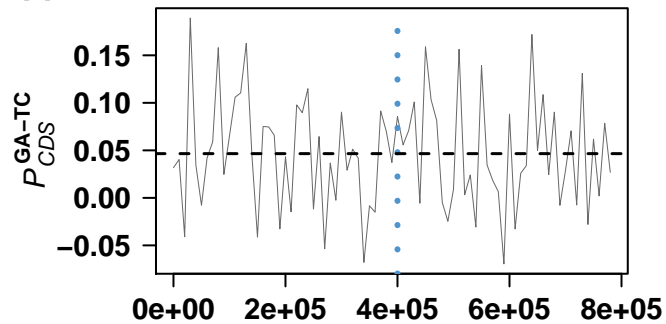


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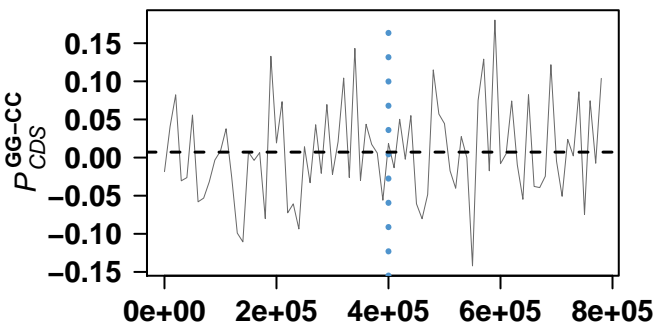
Tropheryma whipplei str. Twist



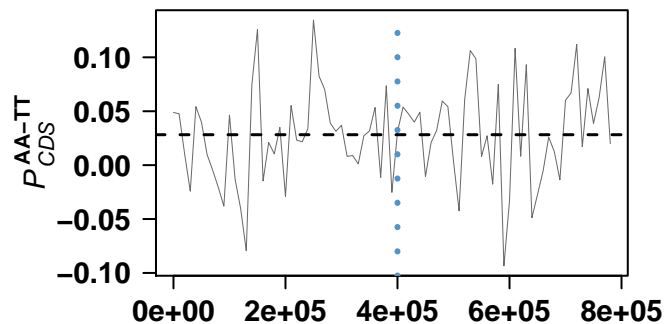
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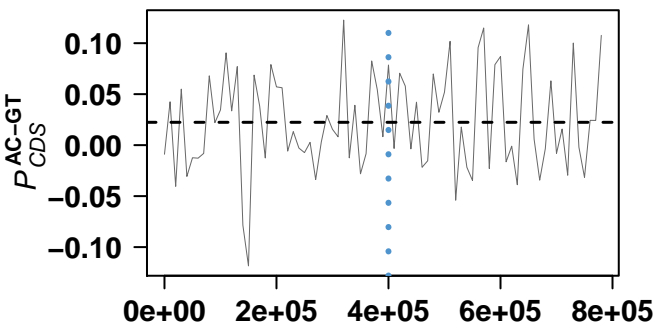
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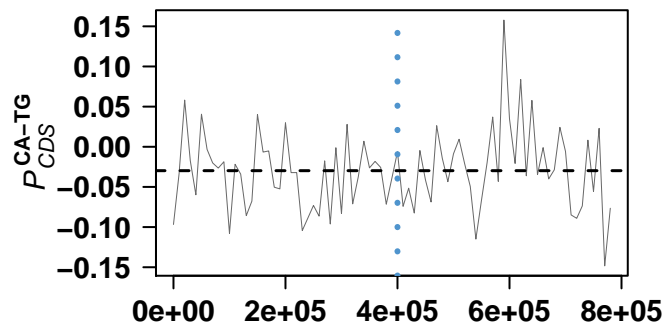
genome coordinates



genome coordinates

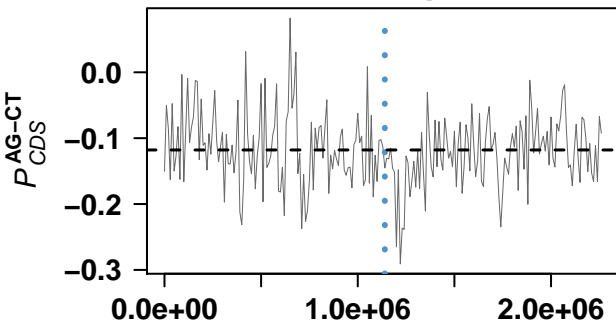


genome coordinates

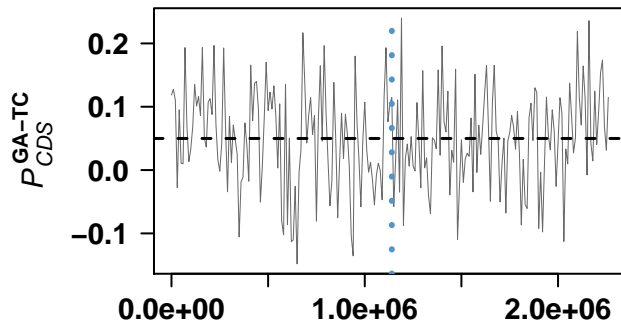


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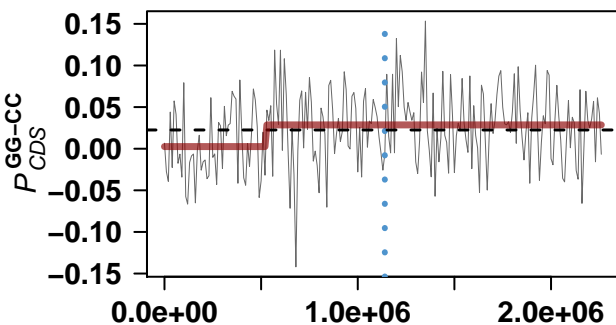
Propionibacterium acnes KPA171202



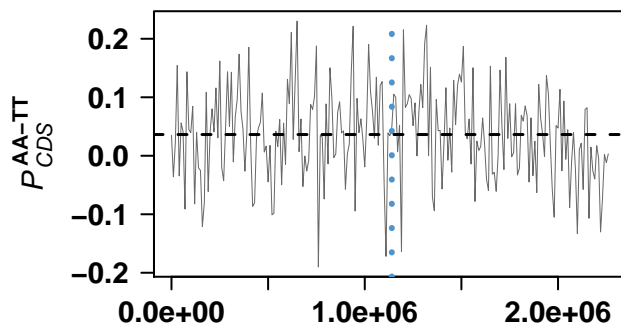
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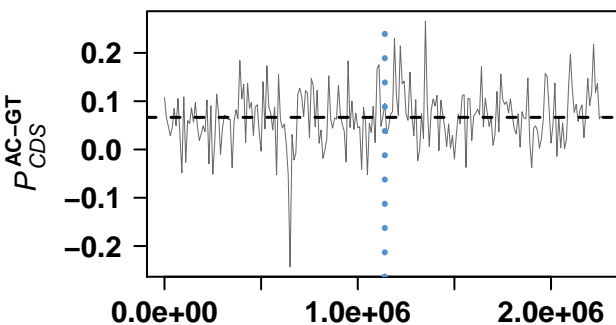
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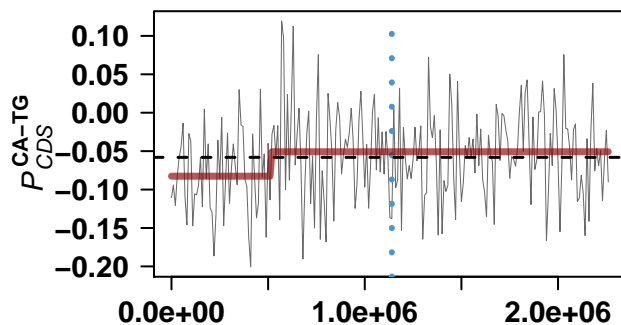
genome coordinates



genome coordinates

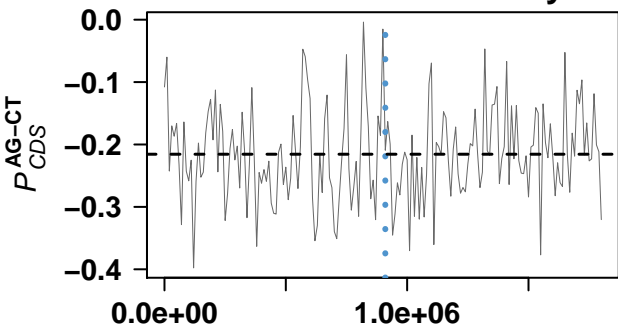


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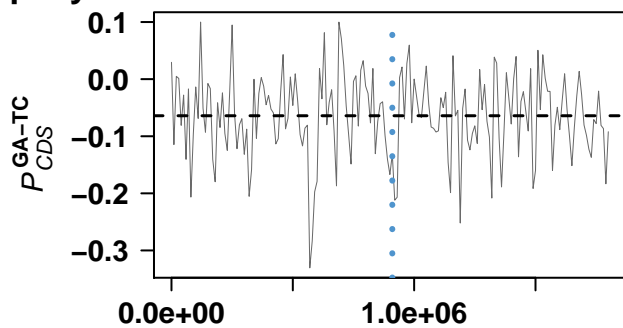


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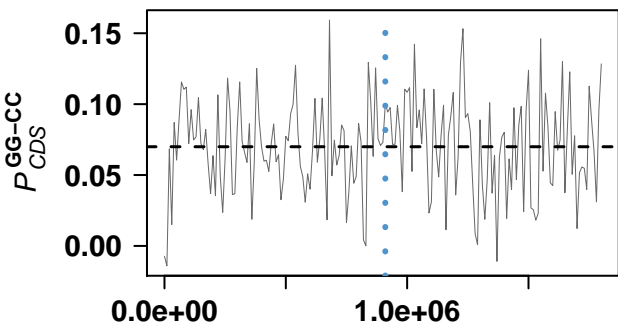
Leifsonia xyli subsp. xyli str. CTCB07



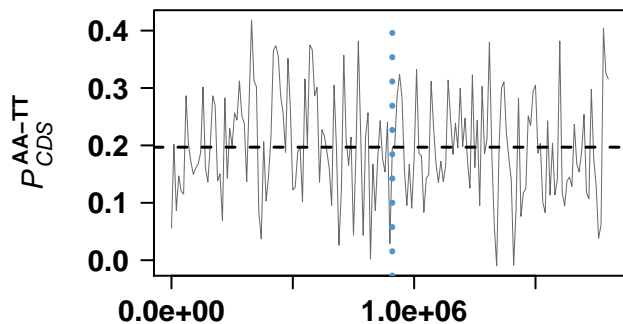
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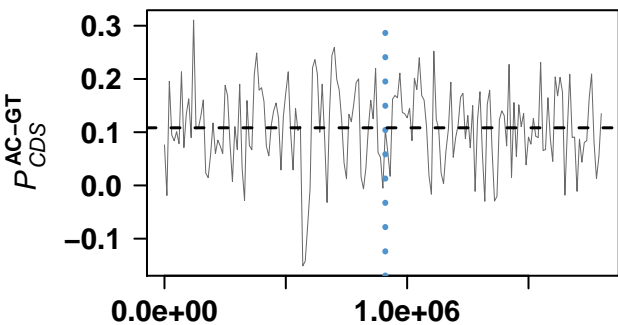
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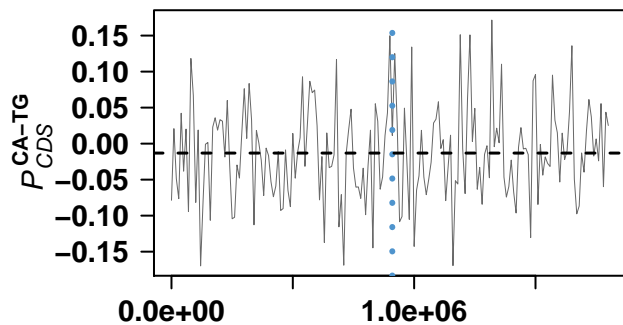
genome coordinates



genome coordinates

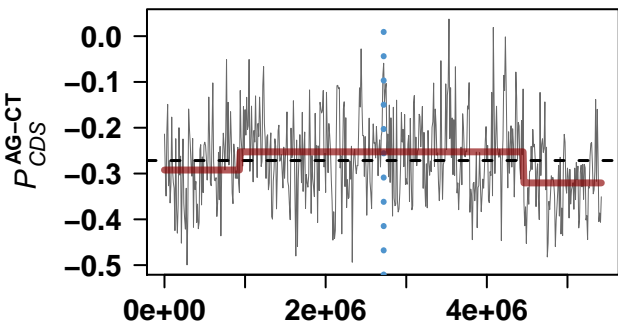


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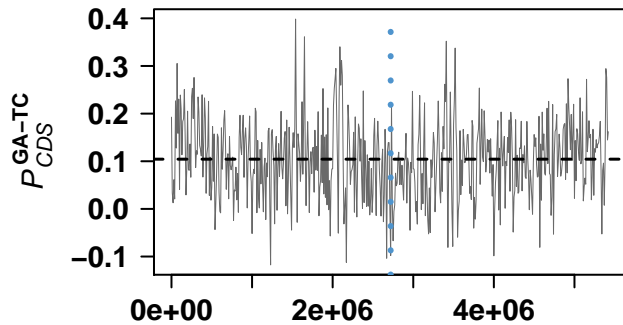


genome coordinates

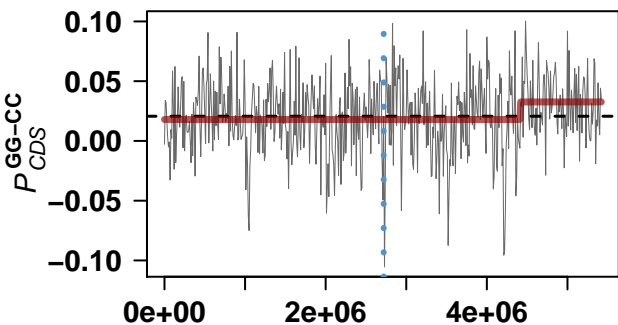
Nocardia farcinica IFM 10152



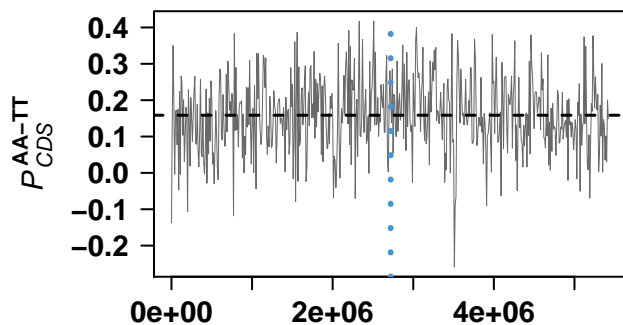
genome coordinates



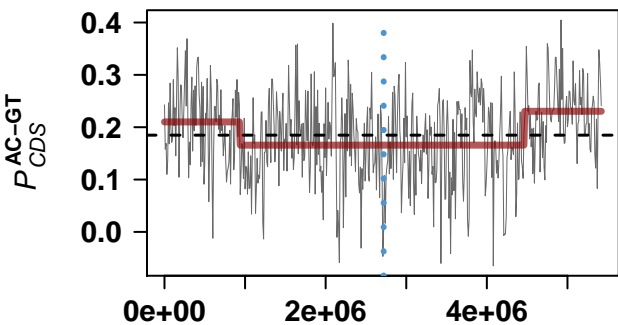
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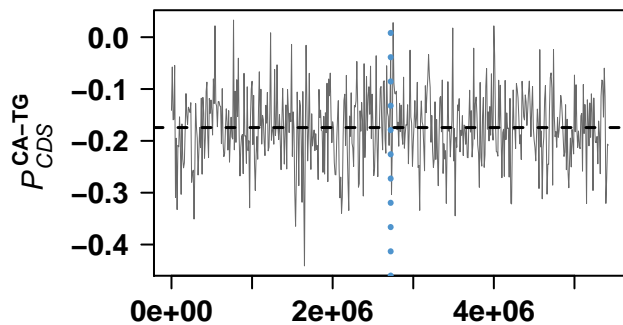
genome coordinates



genome coordinates

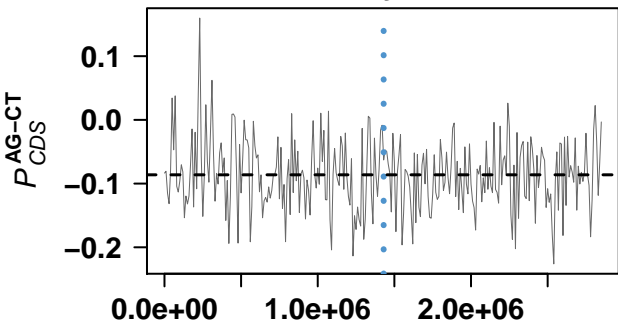


genome coordinates

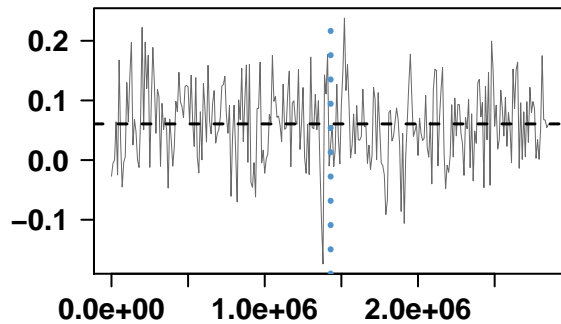


genome coordinates

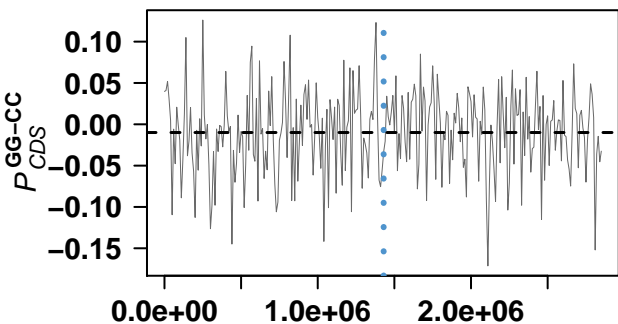
Corynebacterium glutamicum ATCC 13032



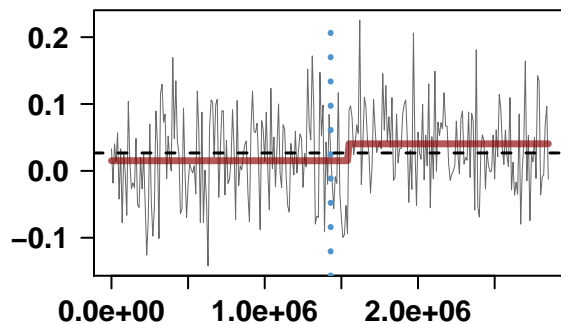
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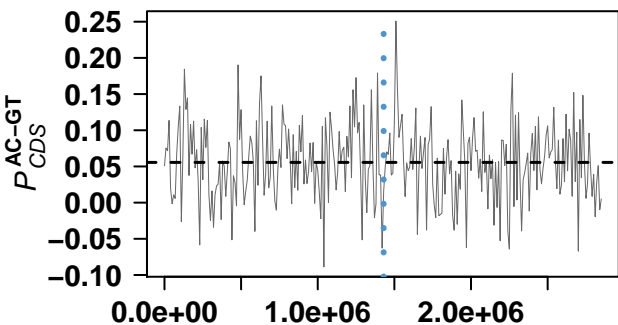
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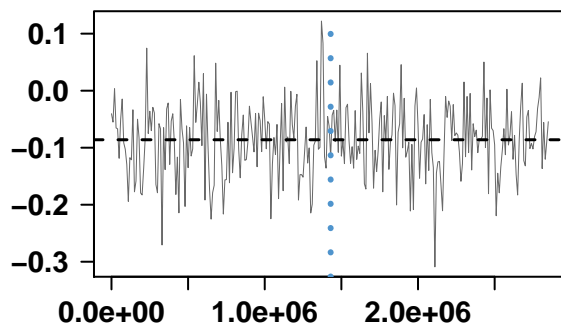
genome coordinates



genome coordinates

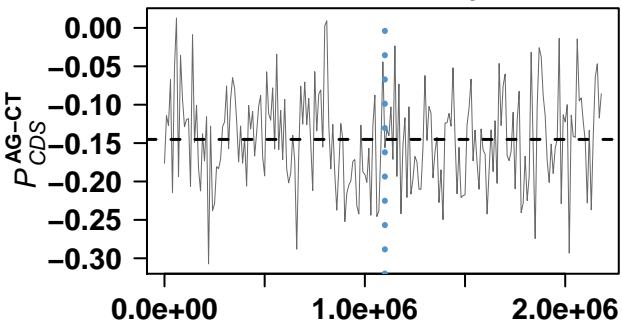


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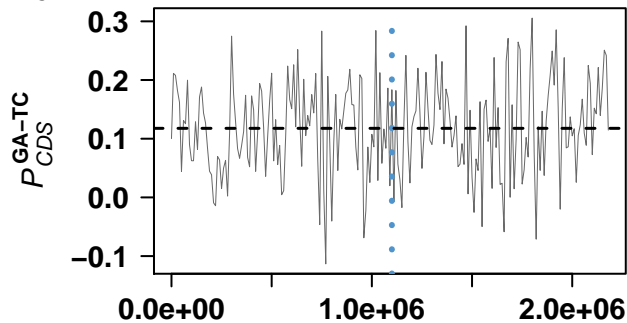


genome coordinates

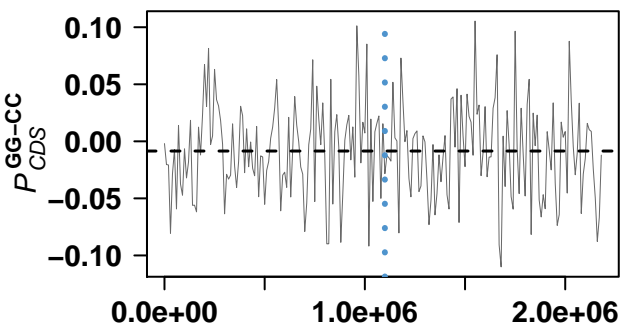
Corynebacterium jeikeium K411



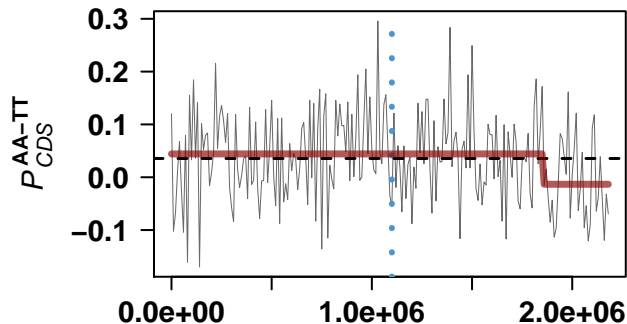
genome coordinates



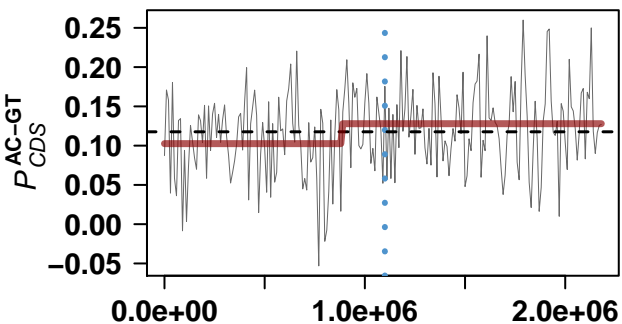
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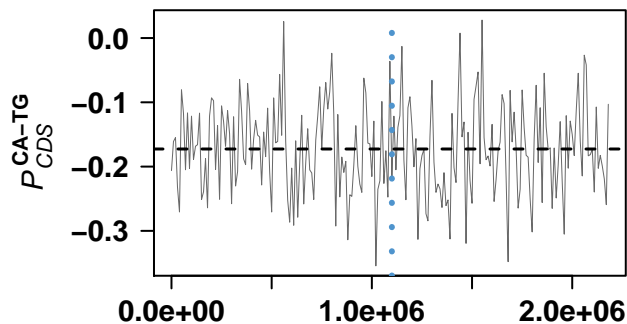
genome coordinates



genome coordinates

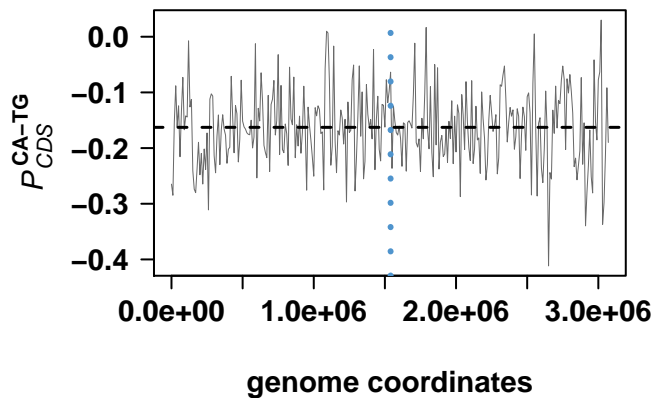
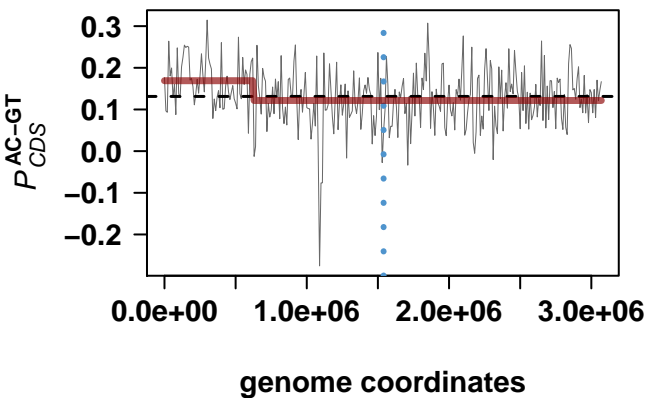
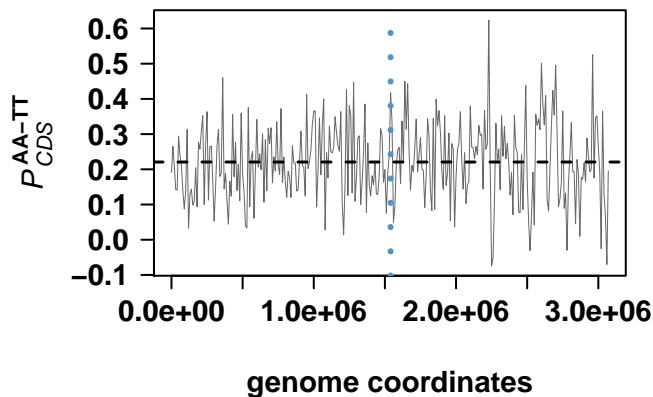
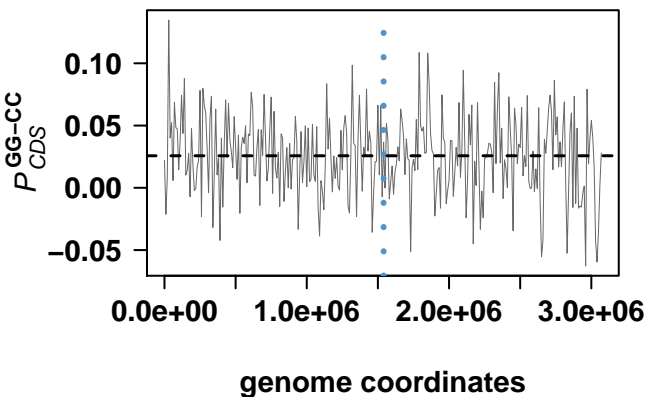
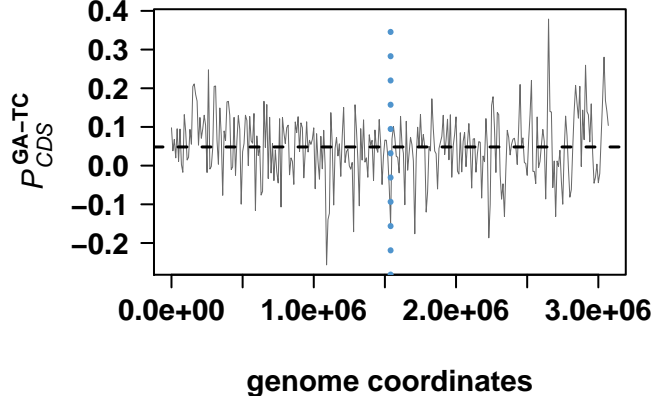
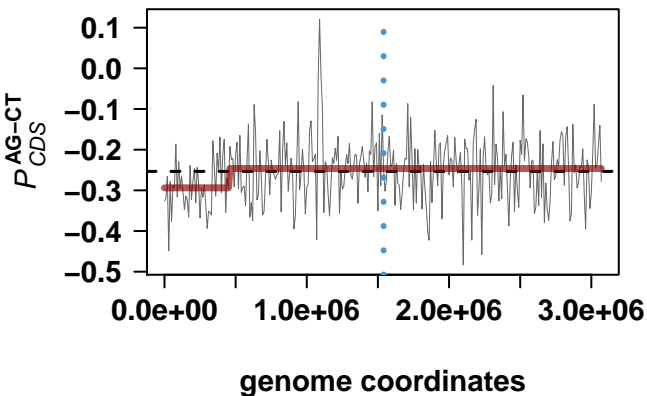


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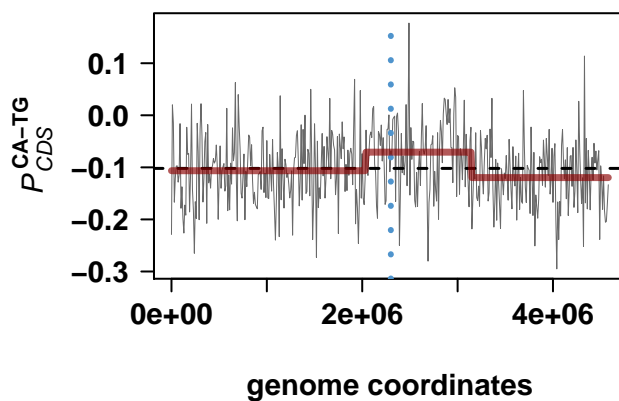
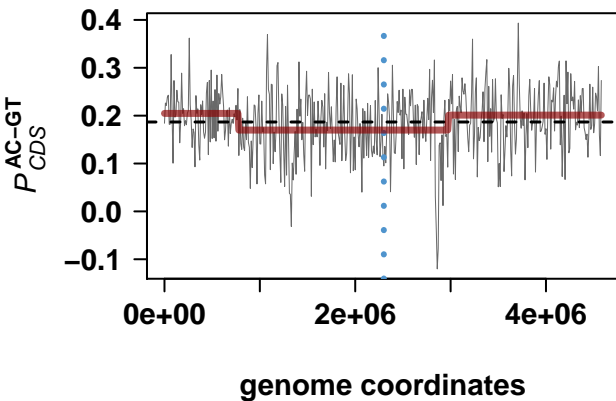
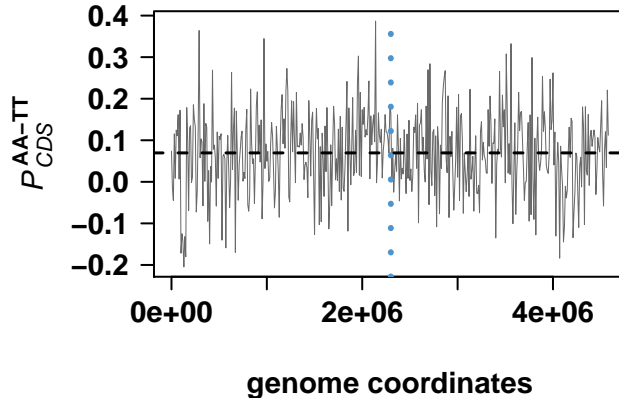
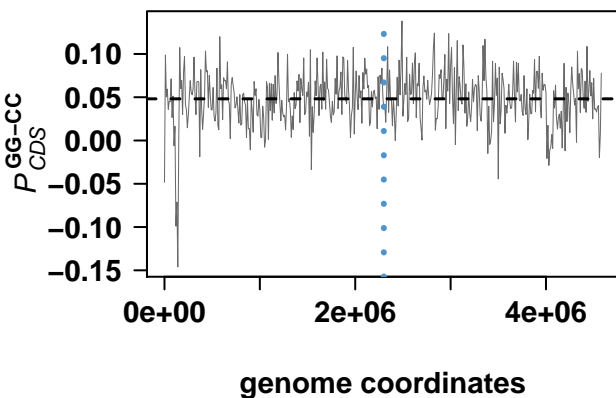
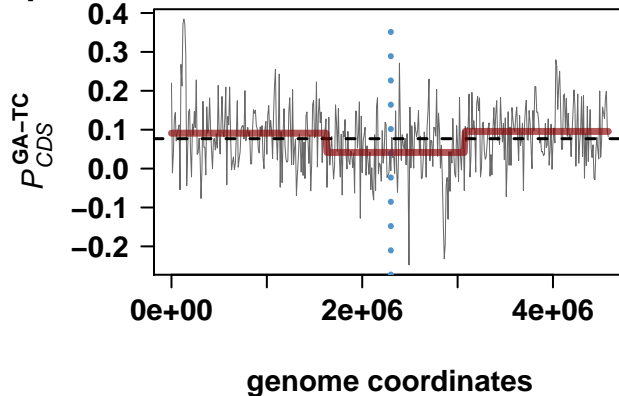
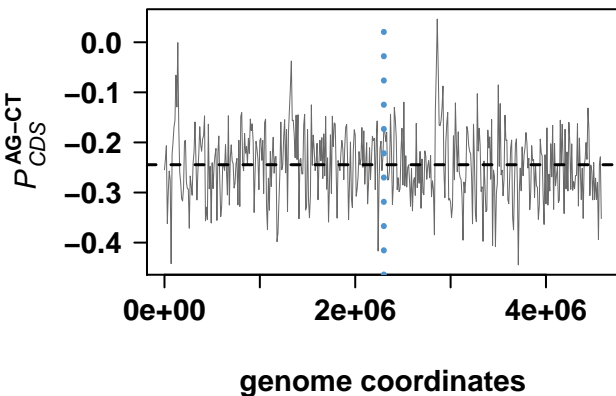


genome coordinates

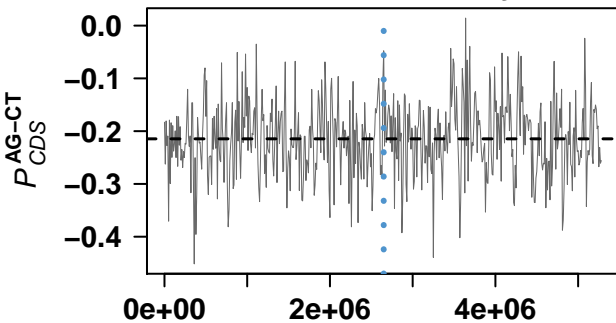
Thermobifida fusca YX



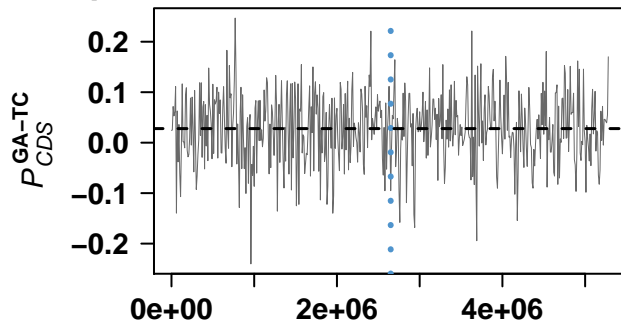
Frankia sp. Ccl3



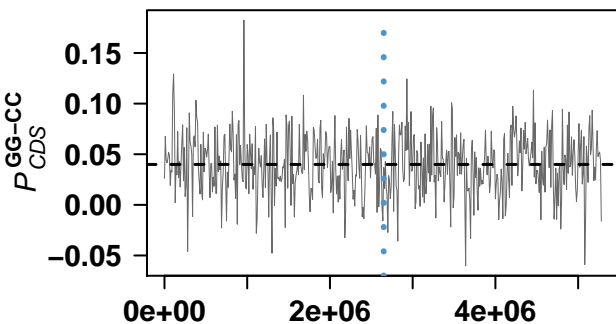
Mycobacterium sp. MCS



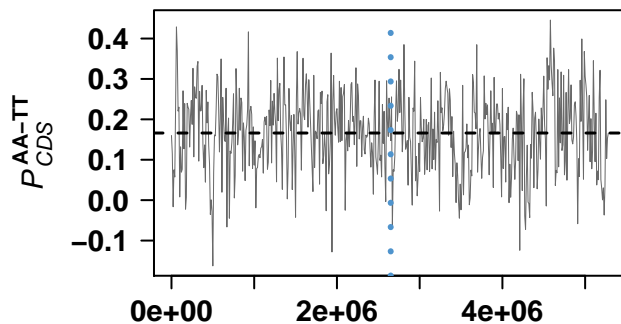
genome coordinates



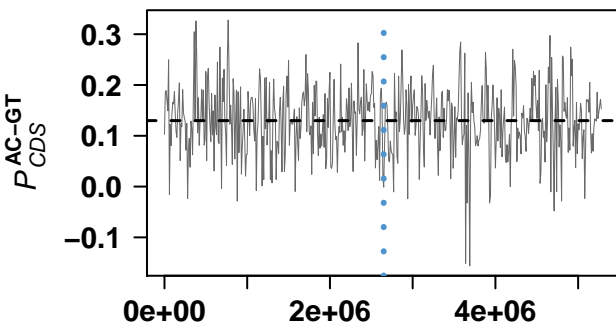
genome coordinates



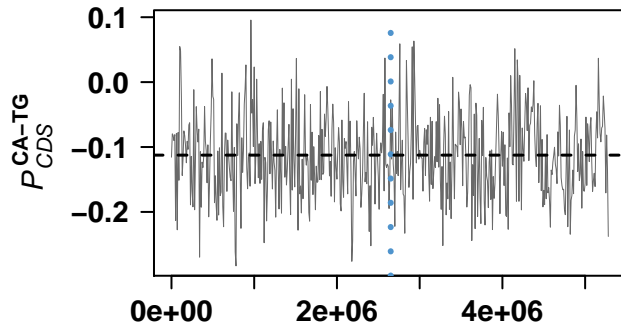
genome coordinates



genome coordinates

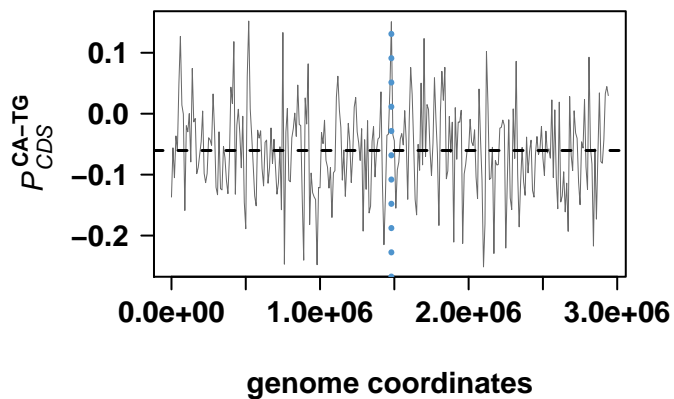
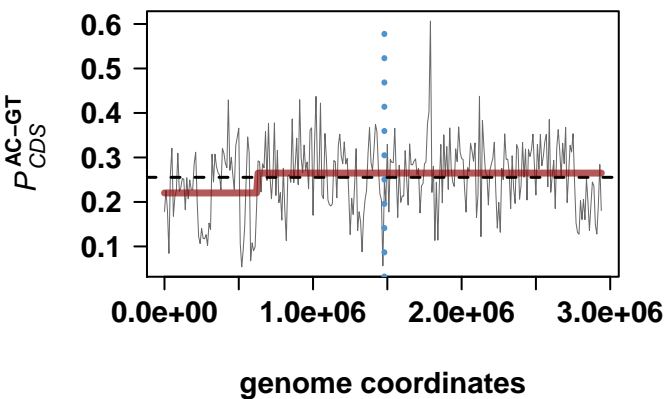
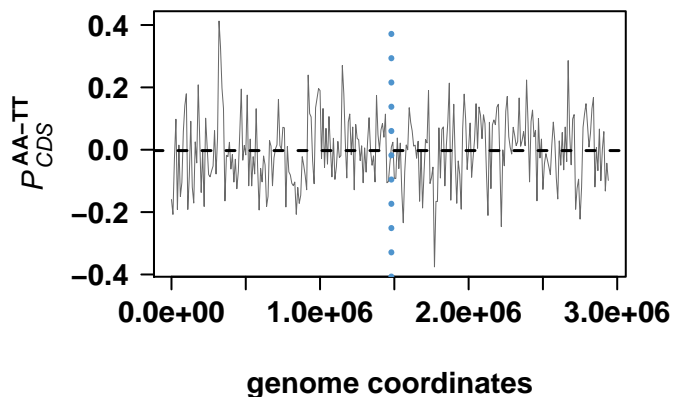
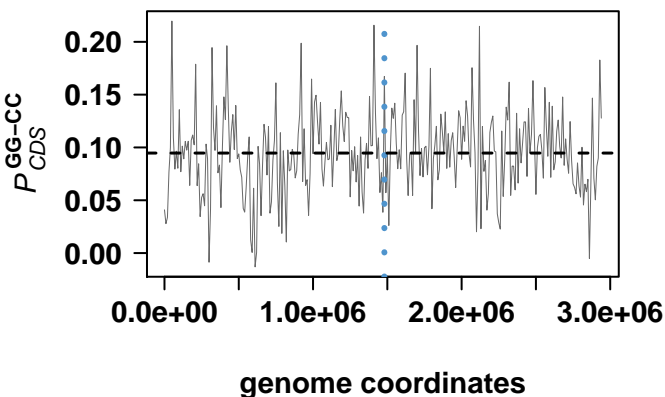
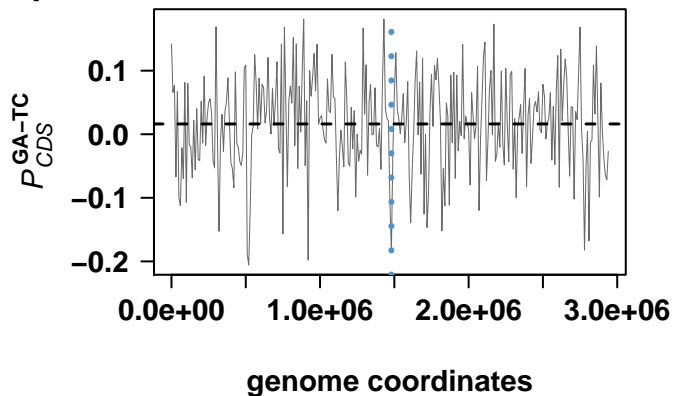
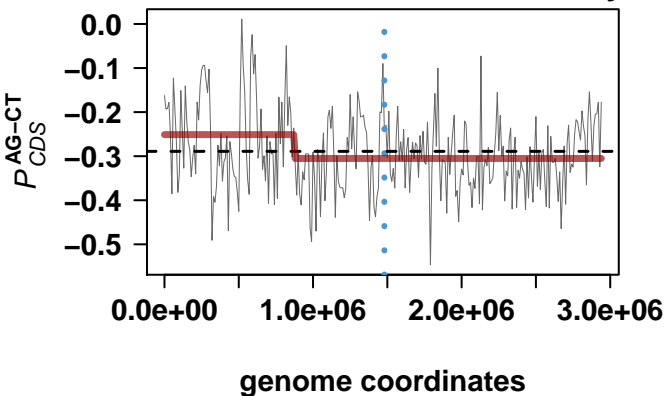


genome coordinates

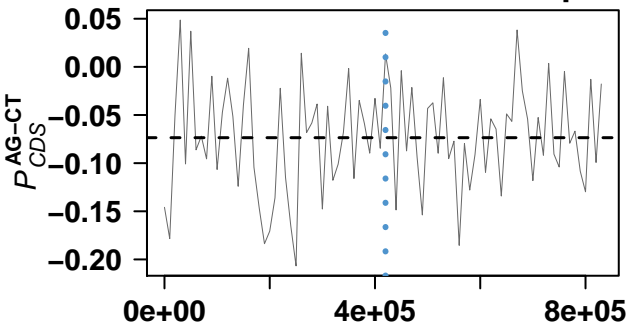


genome coordinates

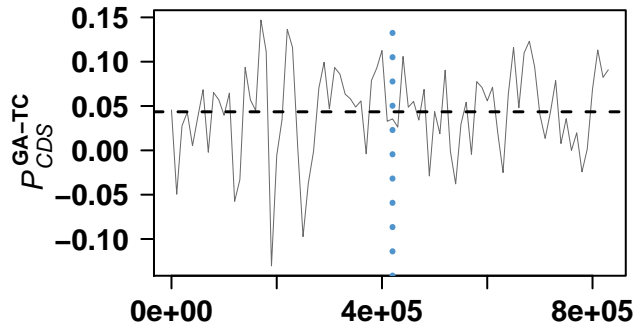
Rubrobacter xylanophilus DSM 9941



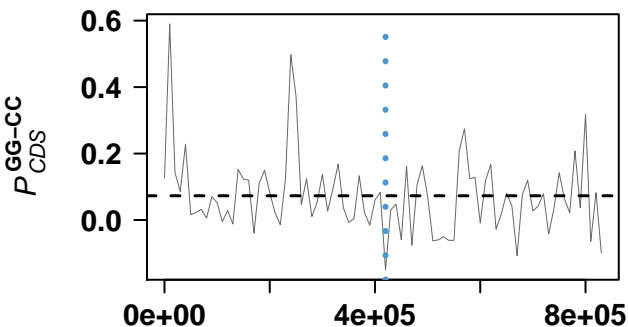
Rickettsia prowazekii str. Madrid E



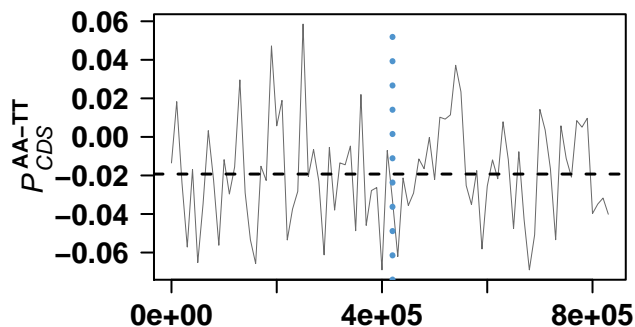
genome coordinates



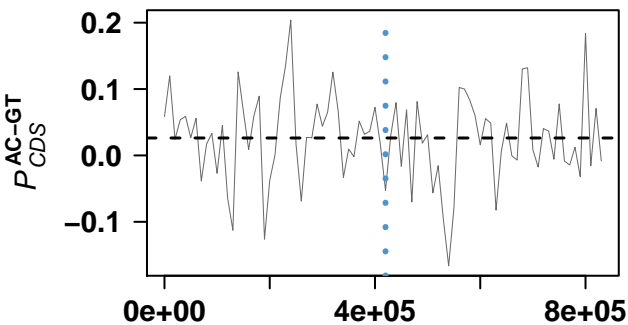
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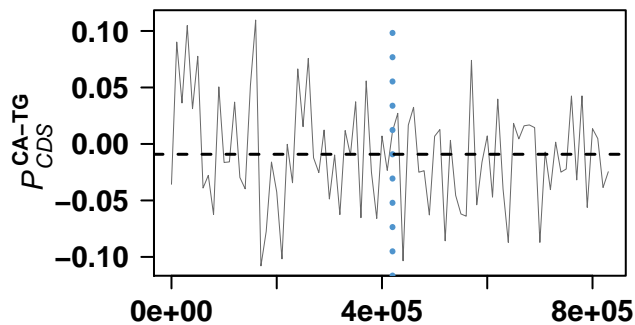
genome coordinates



genome coordinates

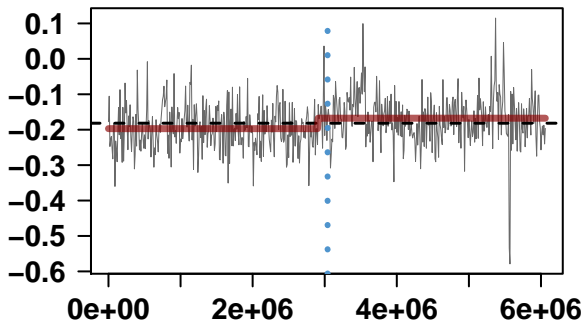


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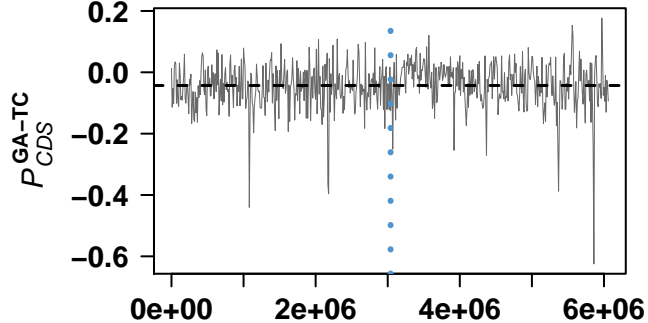


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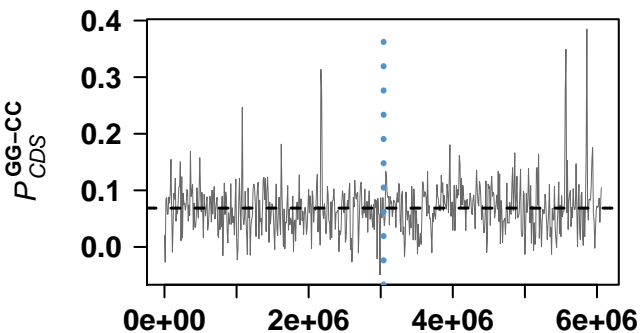
Mesorhizobium loti MAFF303099



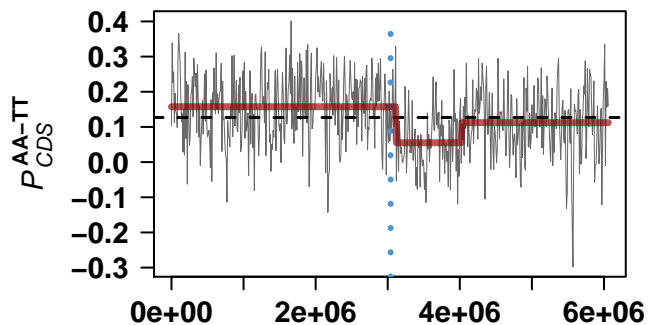
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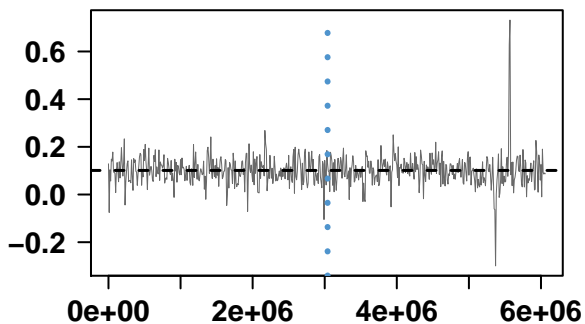
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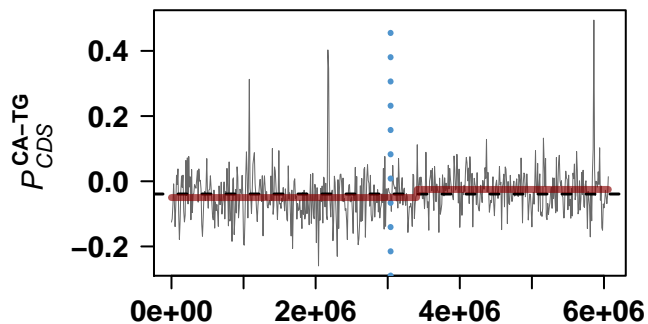
genome coordinates



genome coordinates

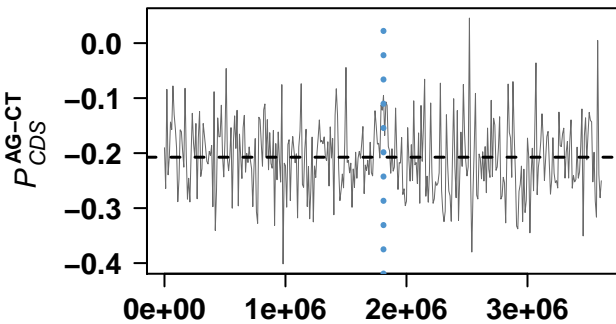


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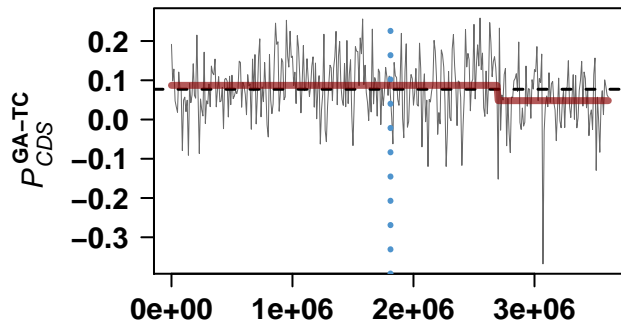


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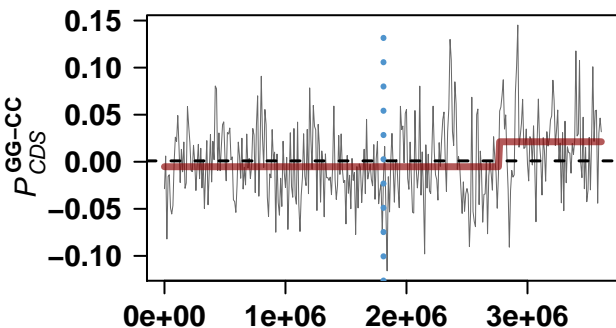
Caulobacter crescentus CB15



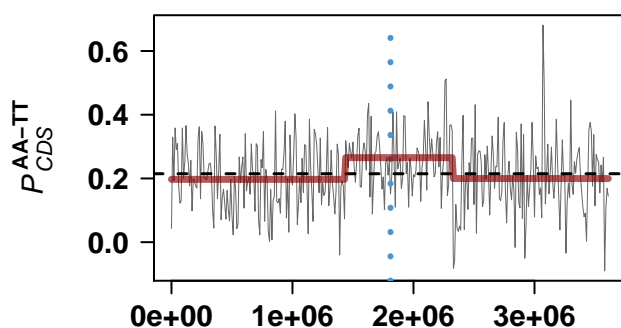
genome coordinates



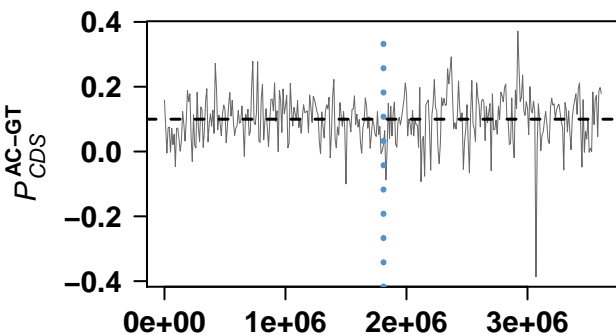
genome coordinates



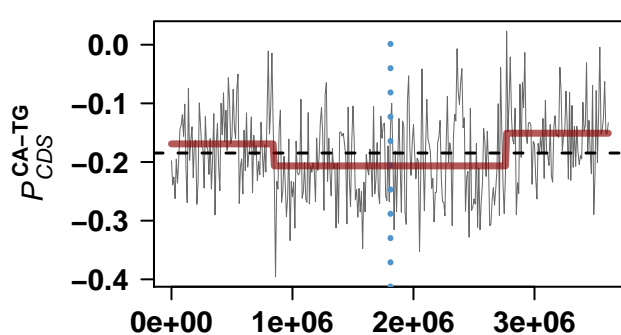
genome coordinates



genome coordinates

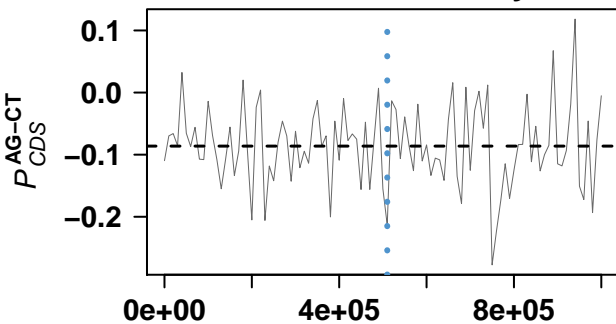


genome coordinates

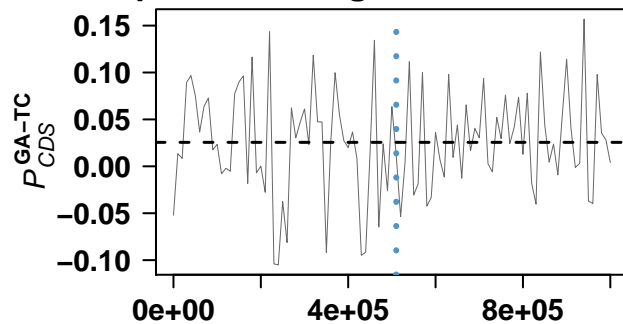


genome coordinates

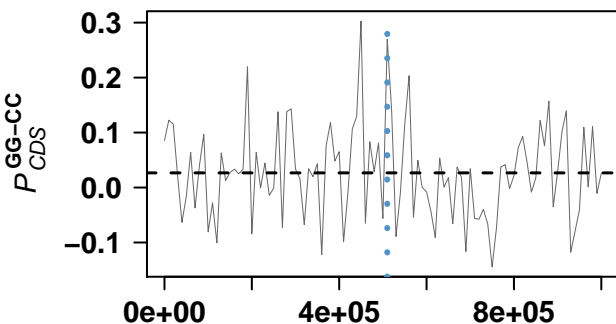
Wolbachia endosymbiont of *Drosophila melanogaster*



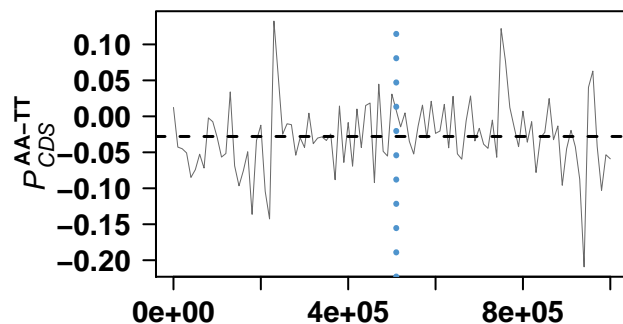
genome coordinates



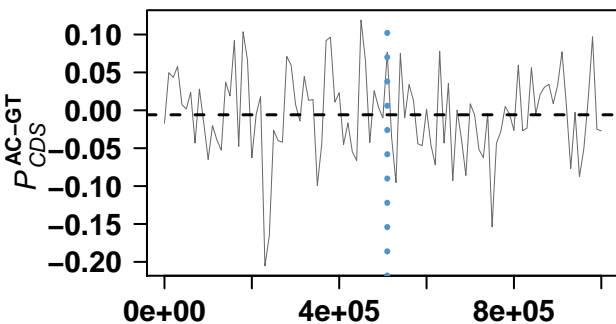
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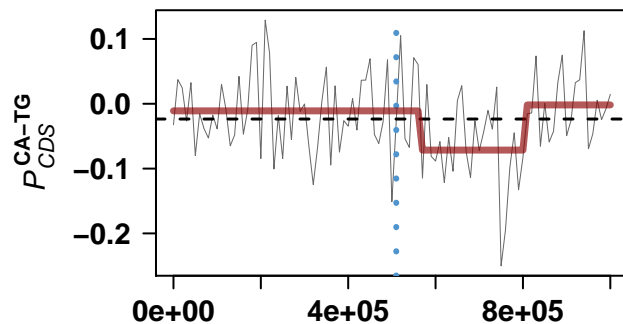
genome coordinates



genome coordinates

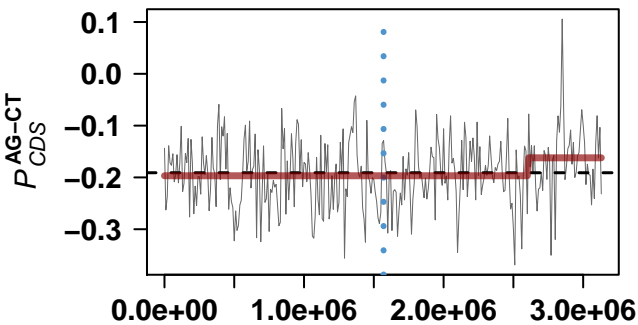


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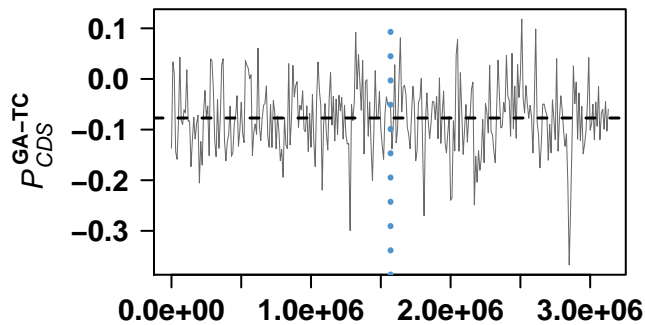


genome coordinates

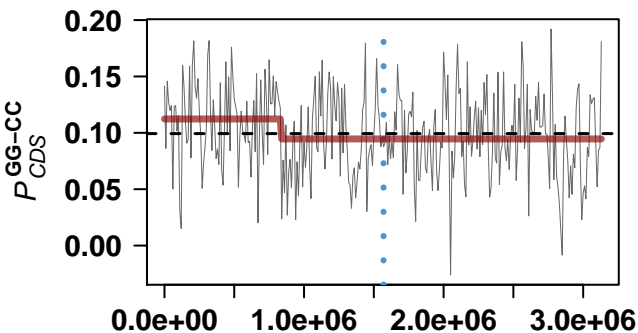
Sinorhizobium meliloti 1021



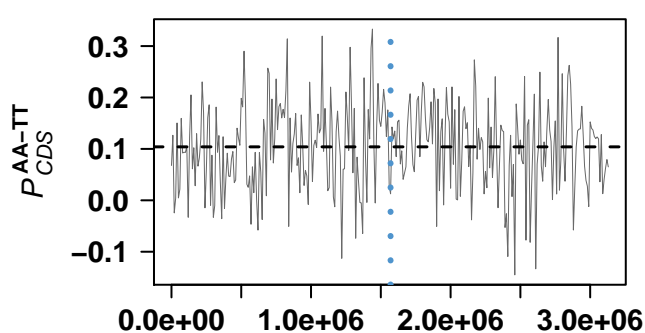
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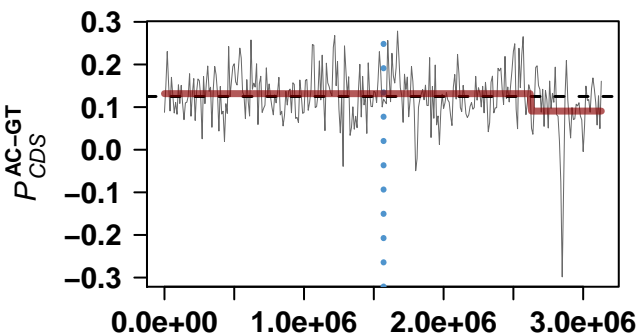
genome coordinates



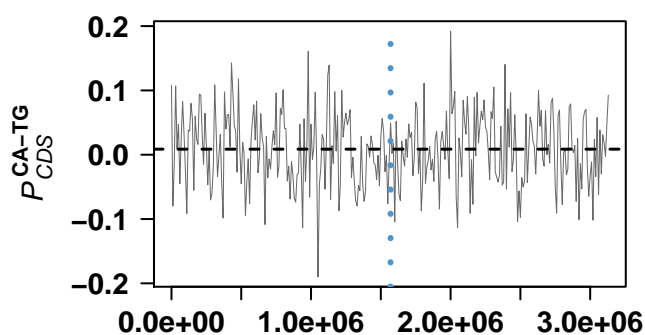
genome coordinates



genome coordinates

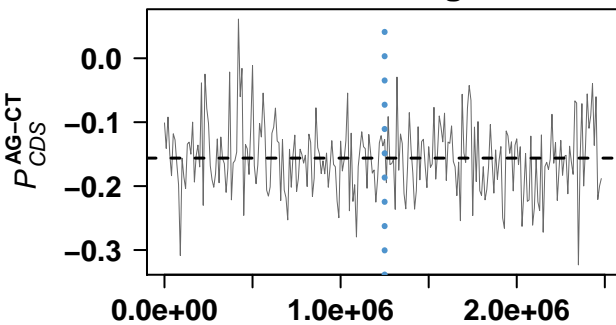


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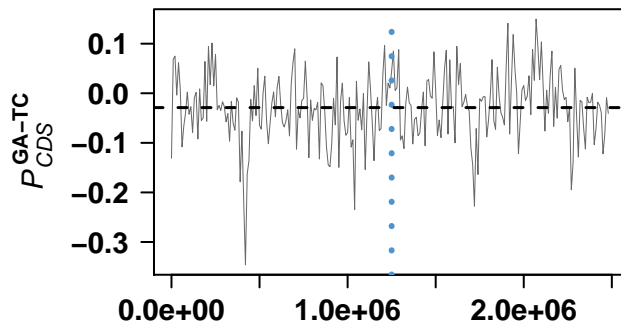


genome coordinates

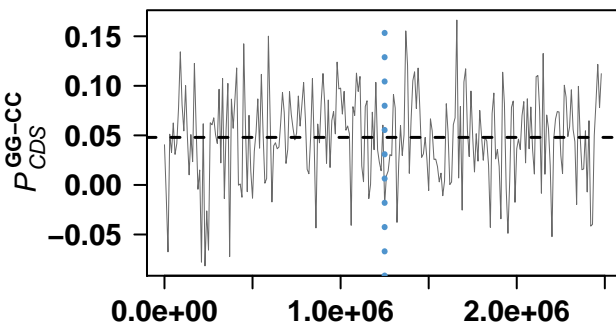
Agrobacterium fabrum str. C58



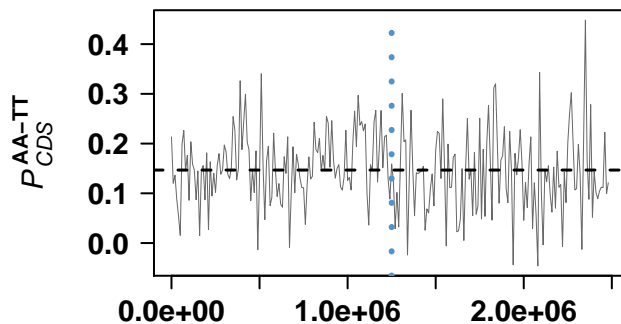
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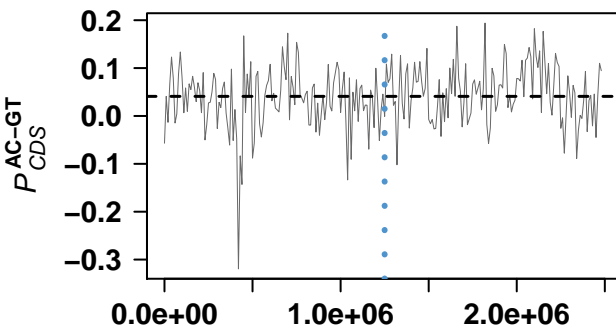
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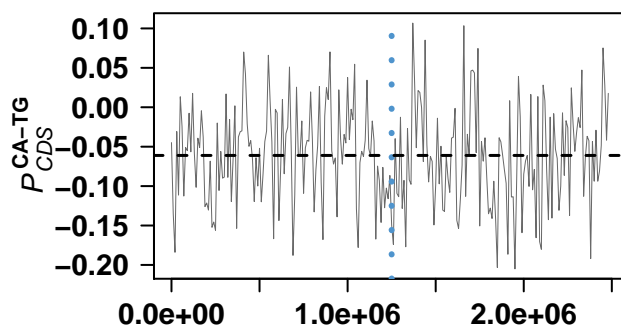
genome coordinates



genome coordinates

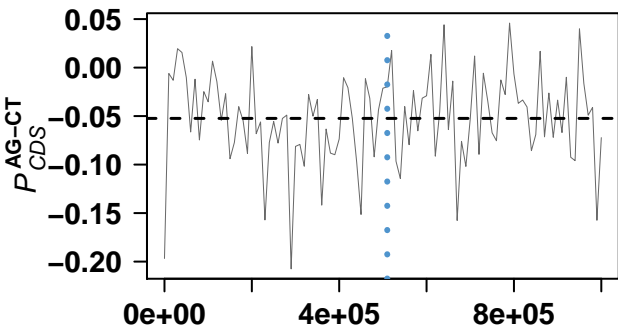


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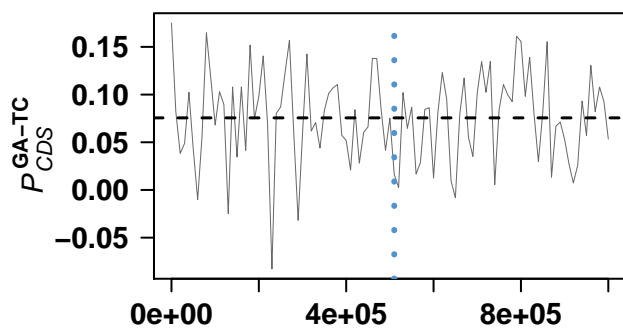


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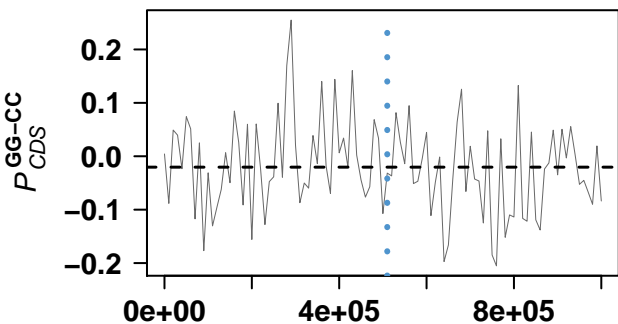
Rickettsia conorii str. Malish 7



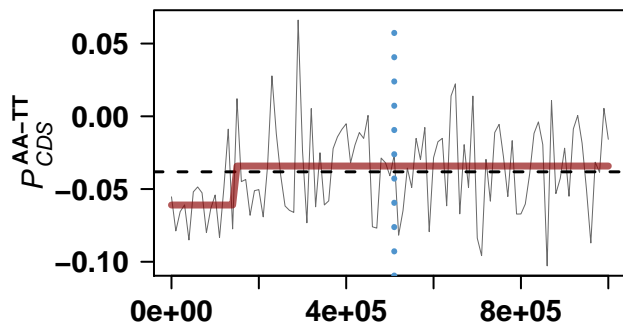
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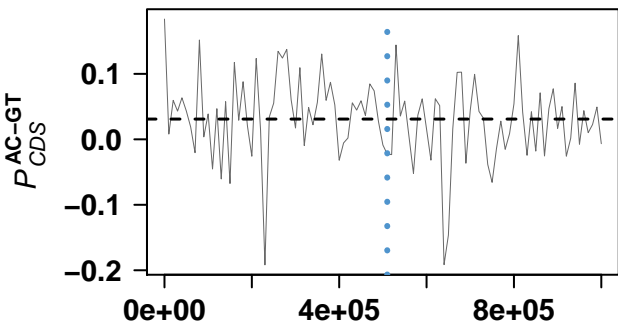
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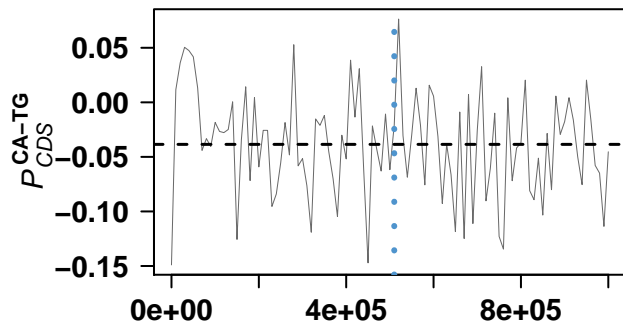
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genome coordinates

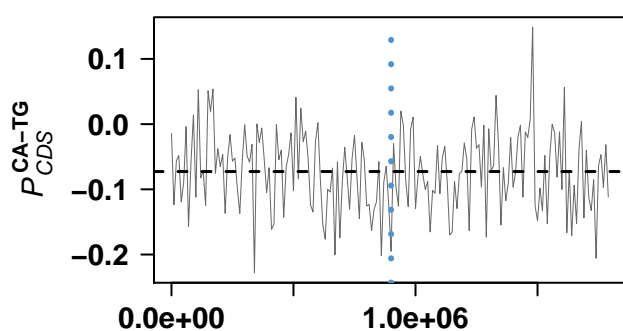
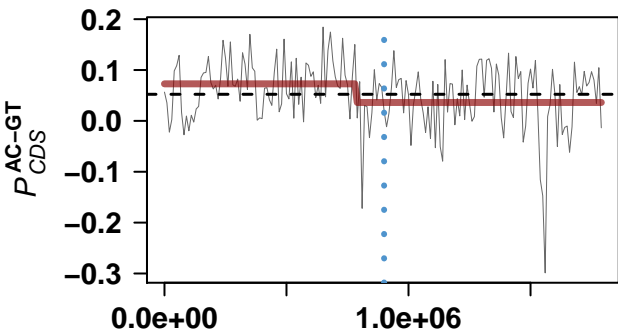
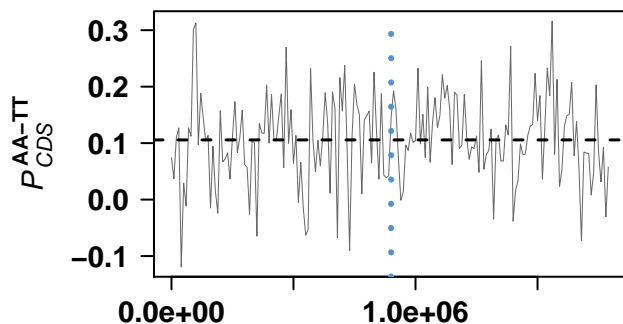
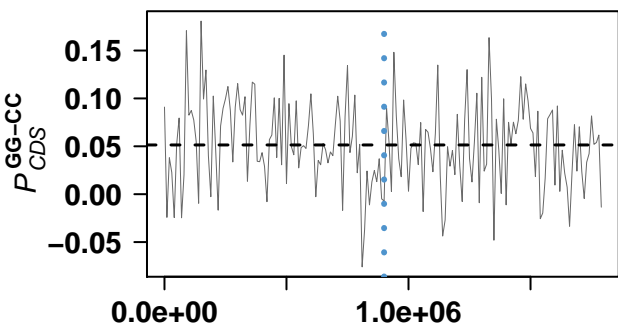
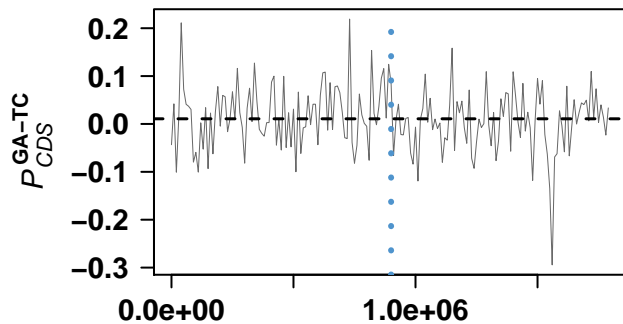
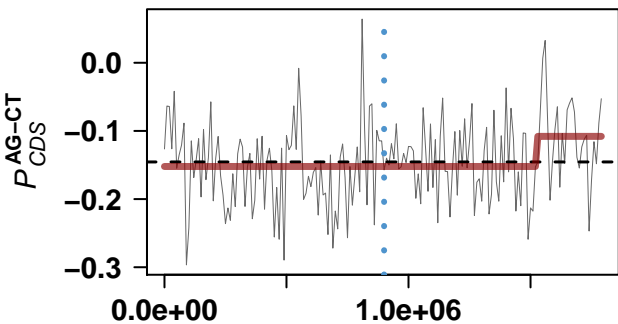


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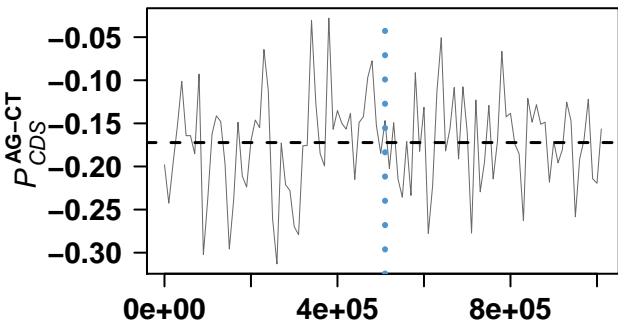


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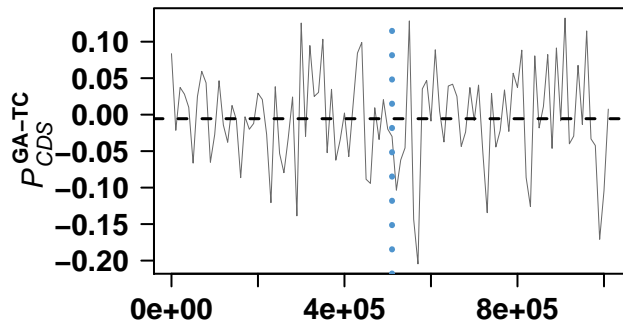
Brucella melitensis bv. 1 str. 16M



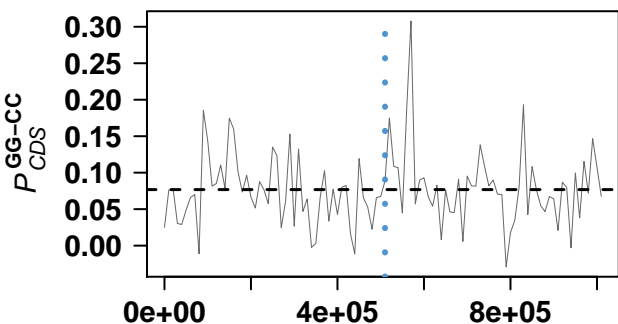
Brucella melitensis bv. 1 str. 16M



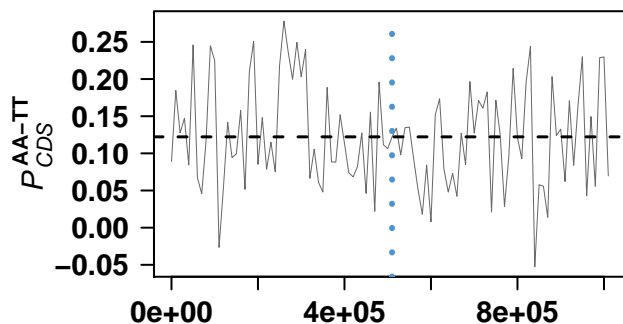
genome coordinates



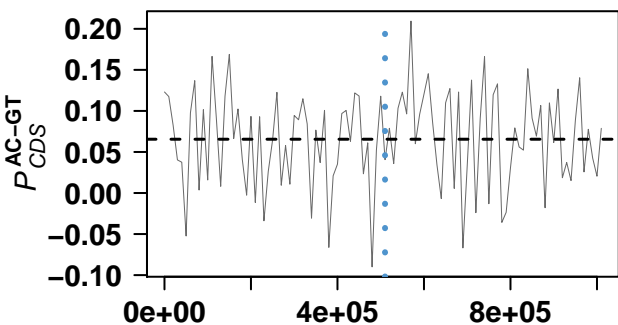
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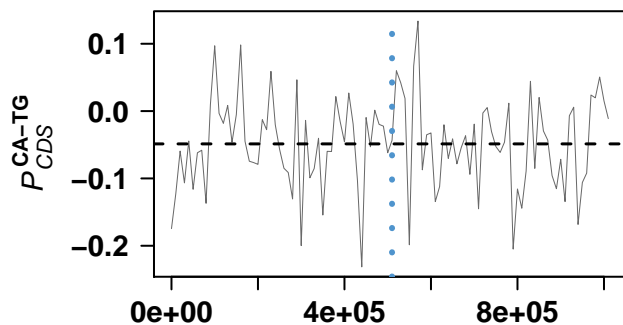
genome coordinates



genome coordinates

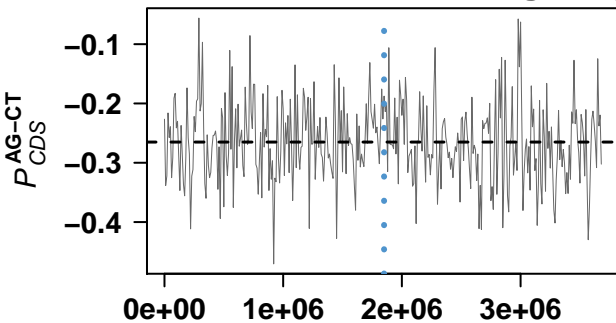


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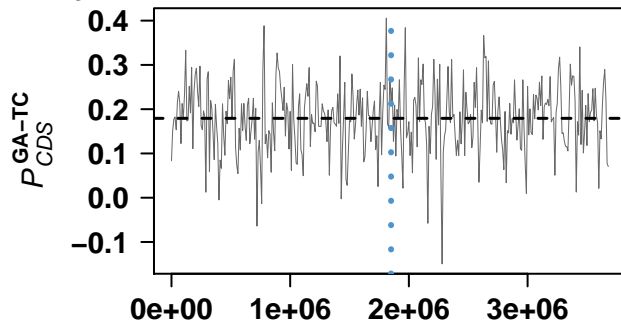


genome coordinates

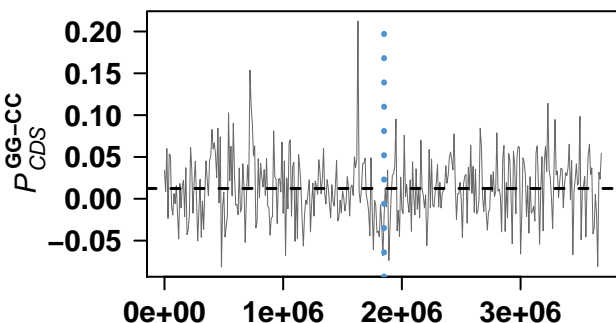
Ruegeria pomeroyi DSS-3



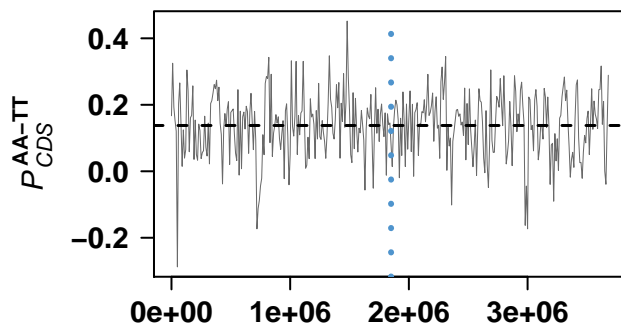
genome coordinates



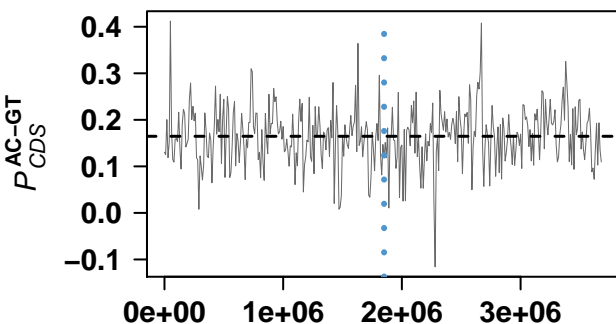
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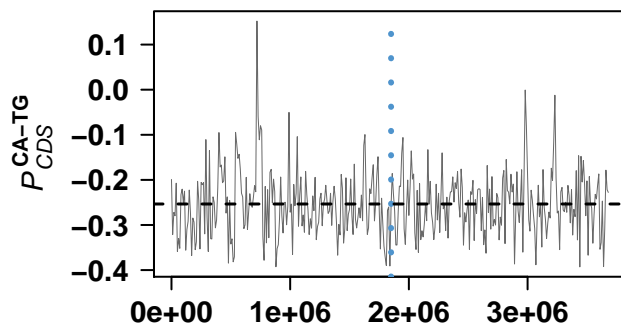
genome coordinates



genome coordinates

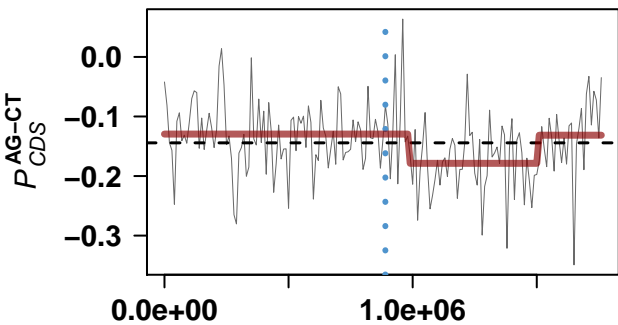


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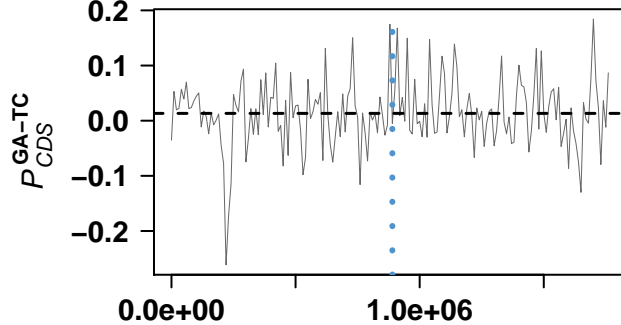


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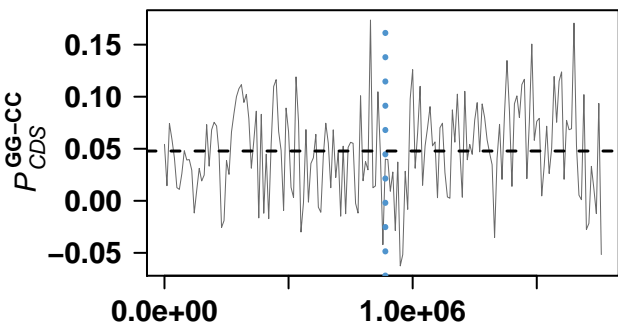
Brucella suis 1330



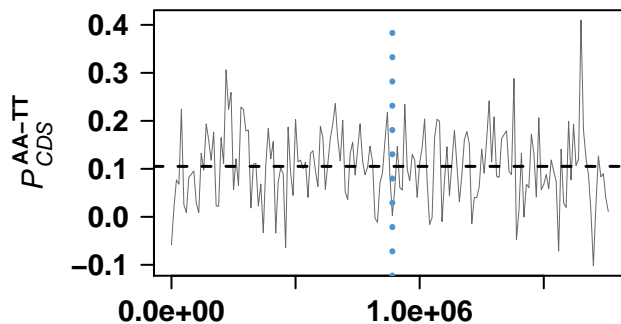
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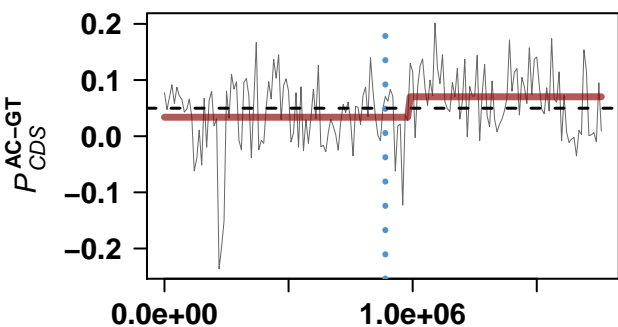
genome coordinates



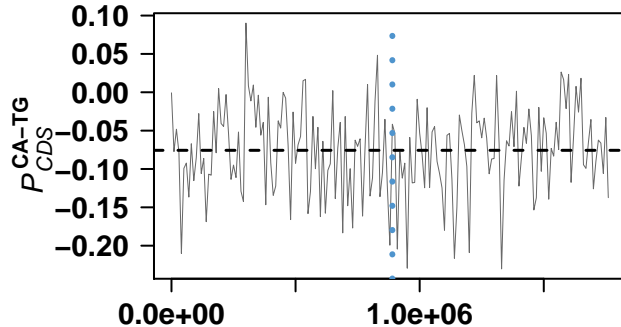
genome coordinates



genome coordinates

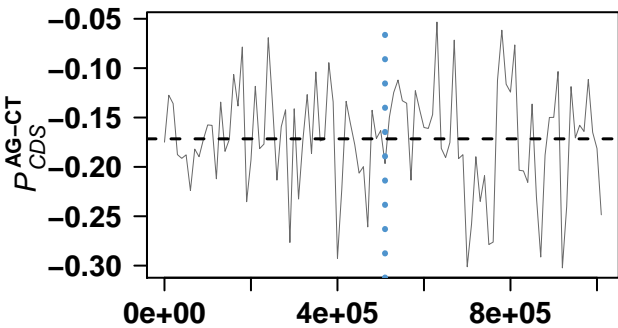


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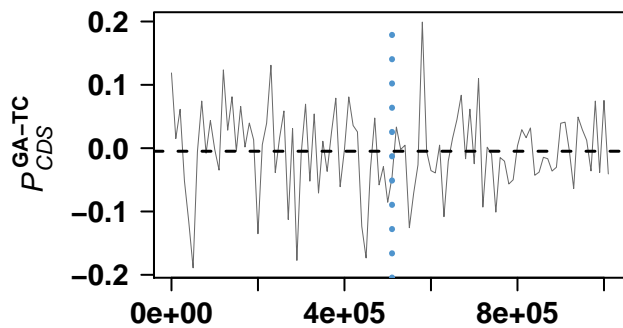


genome coordinates

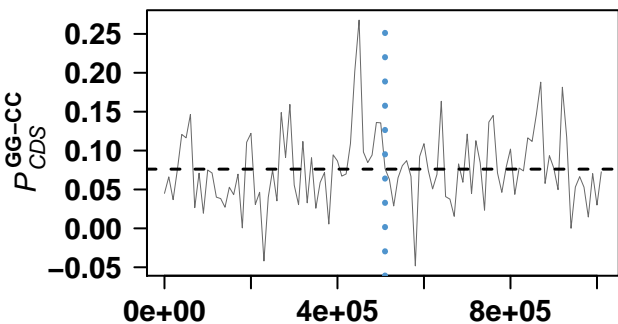
Brucella suis 1330



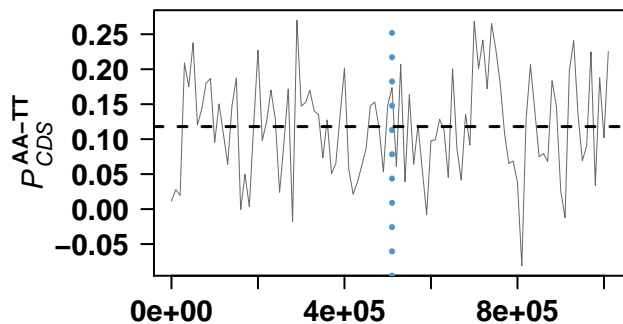
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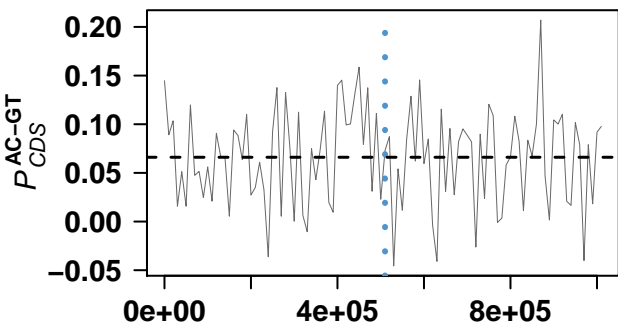
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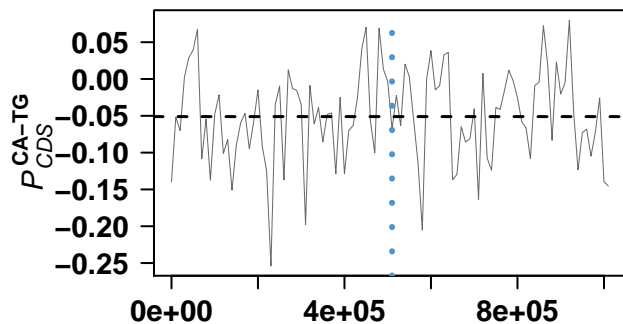
genome coordinates



genome coordinates

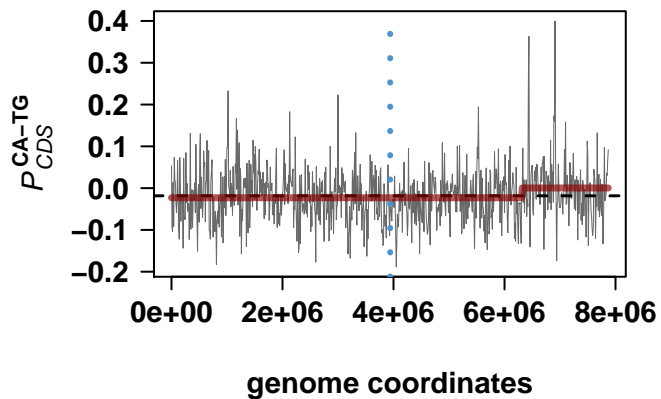
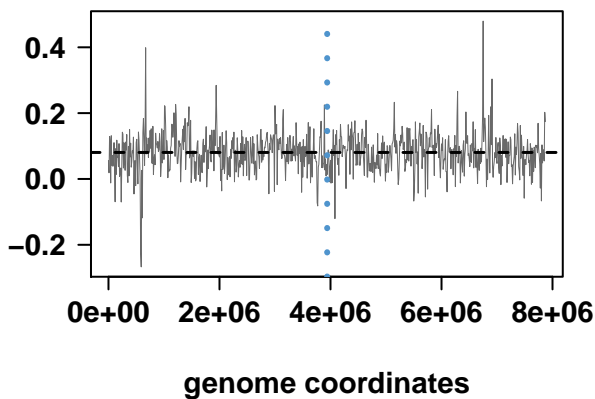
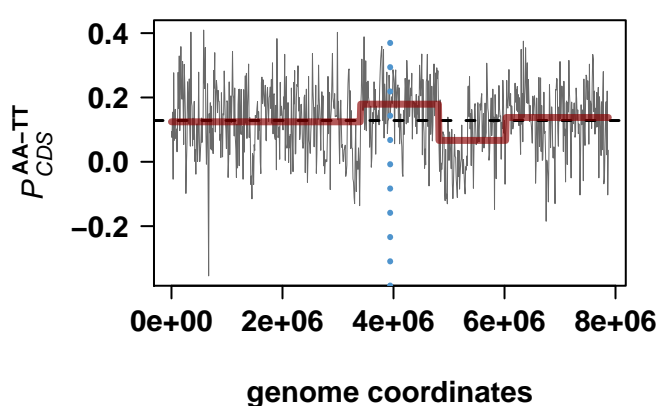
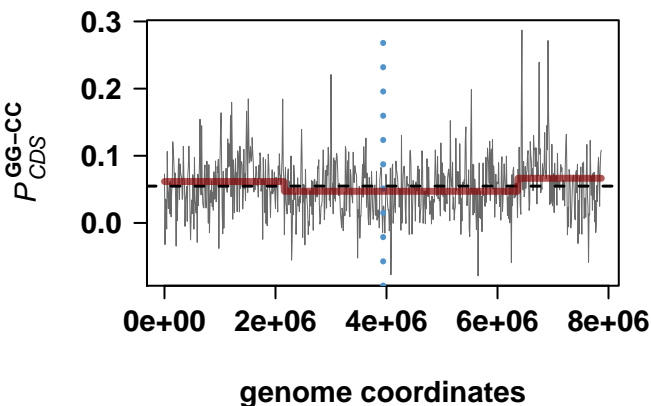
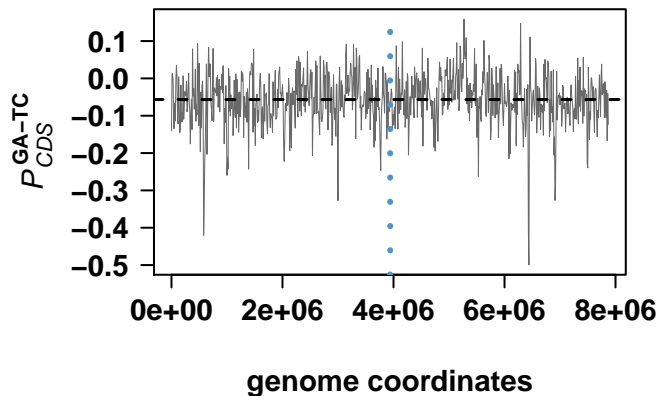
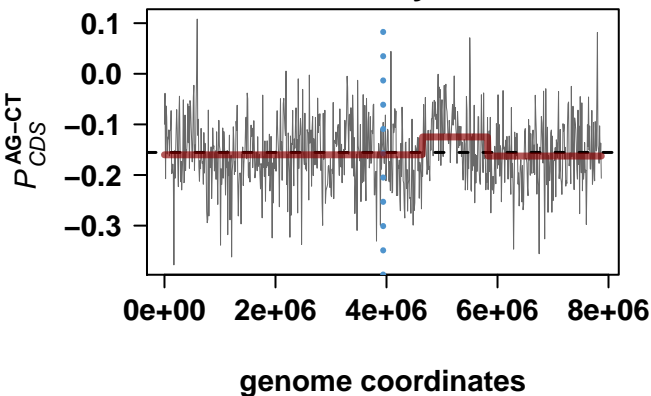


genome coordinates

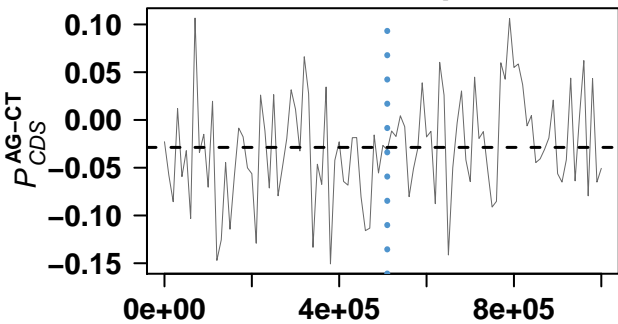


genome coordinates

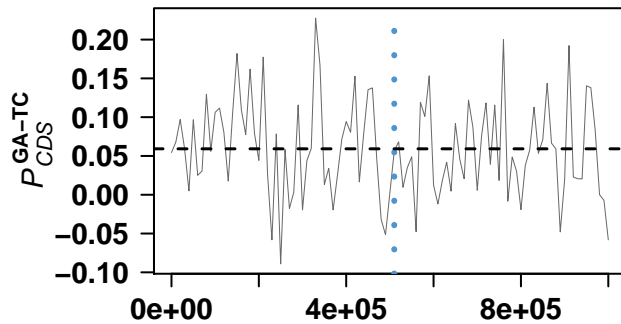
Bradyrhizobium diazoefficiens USDA 110



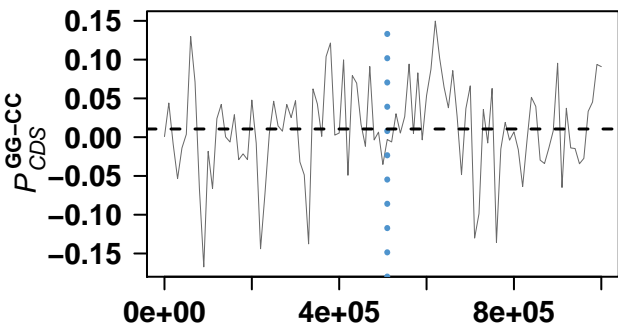
Anaplasma marginale str. St. Maries



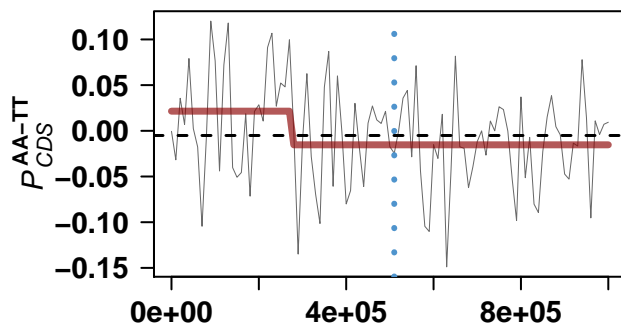
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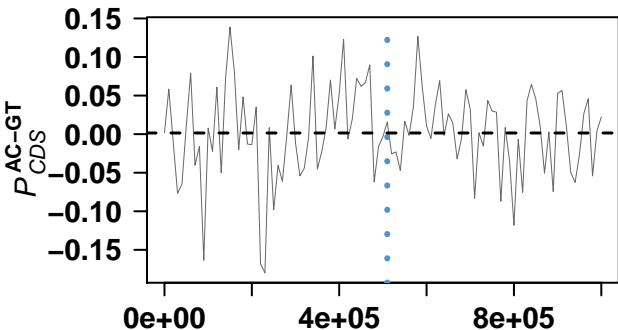
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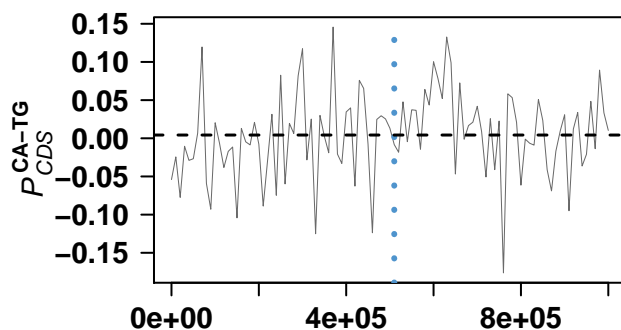
genome coordinates



genome coordinates

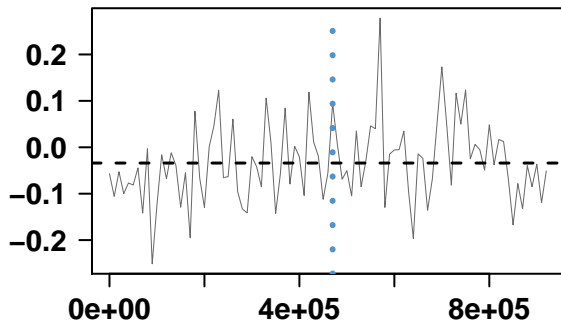


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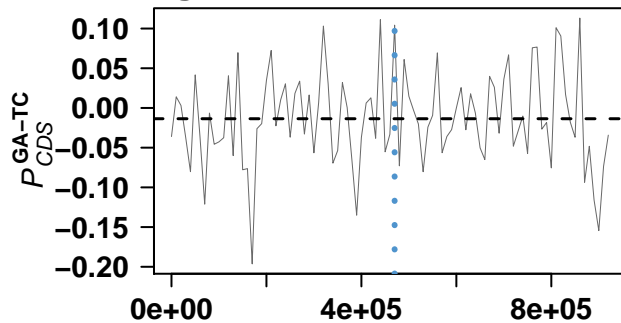


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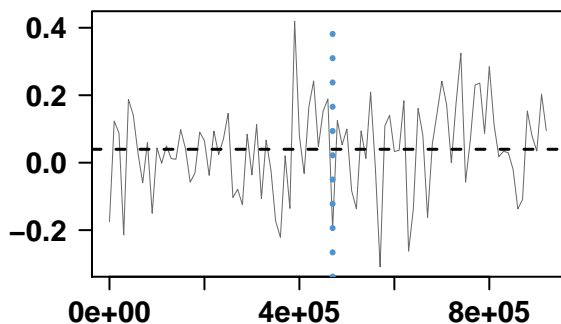
Ehrlichia ruminantium str. Welgevonden



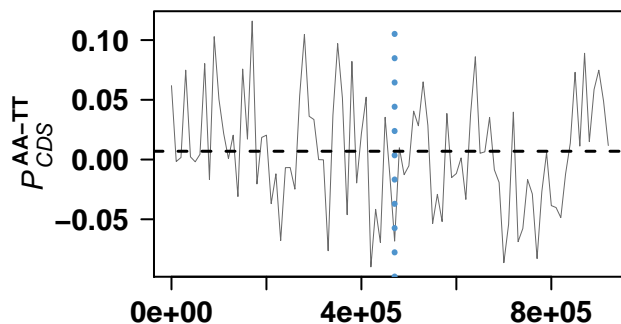
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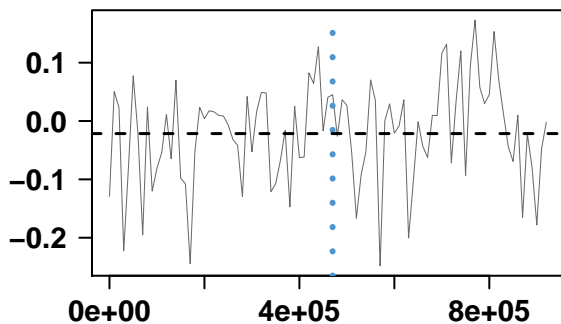
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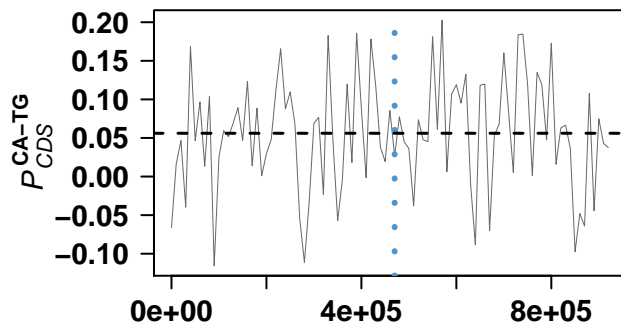
genome coordinates



genome coordinates

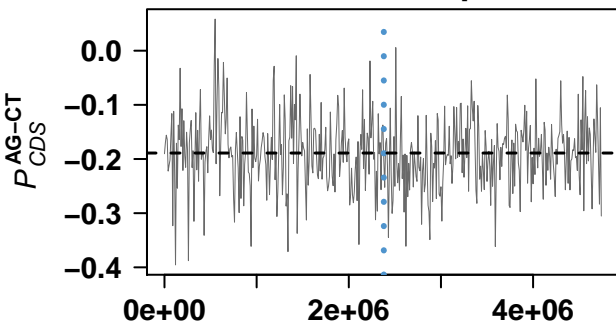


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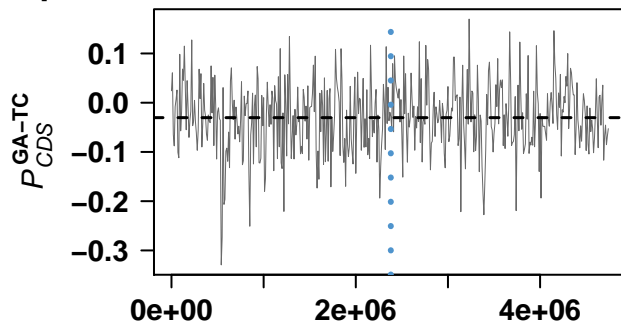


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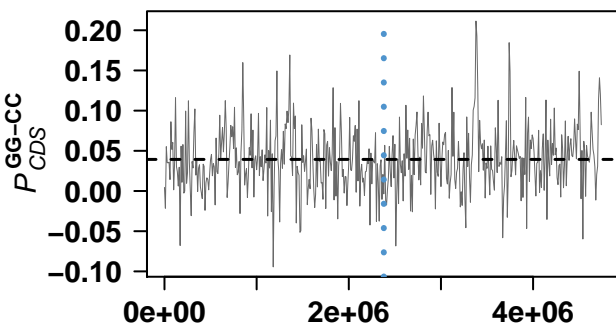
Rhodospseudomonas palustris CGA009



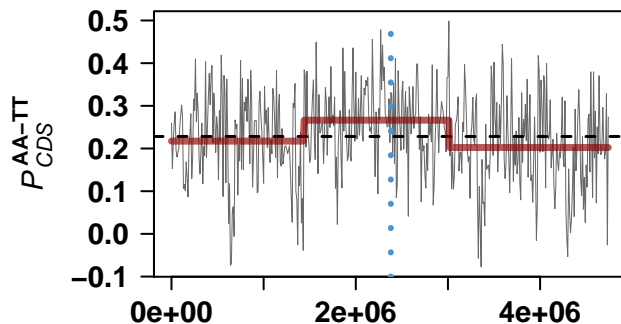
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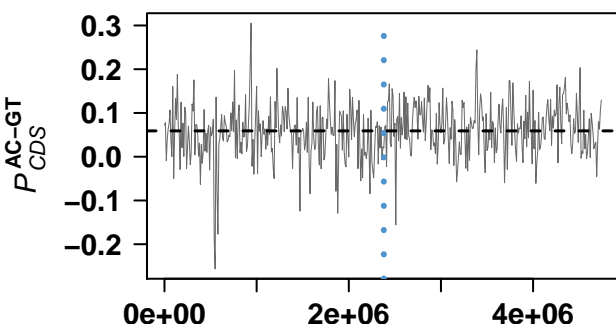
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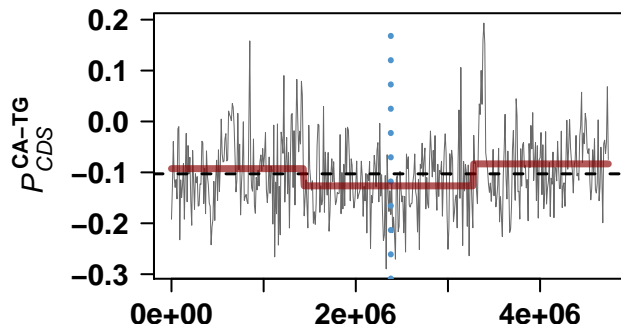
genome coordinates



genome coordinates

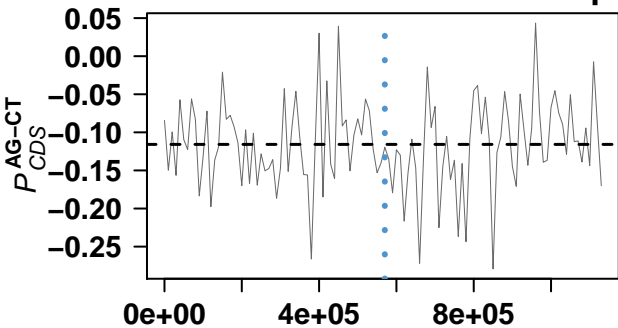


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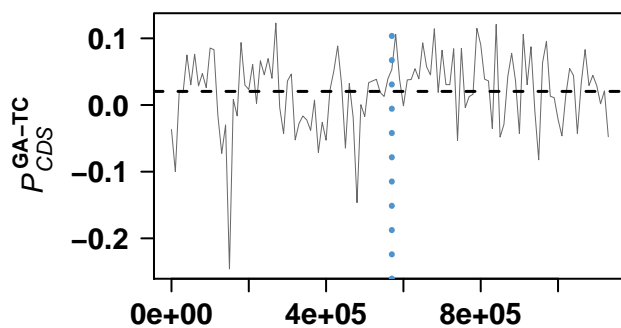


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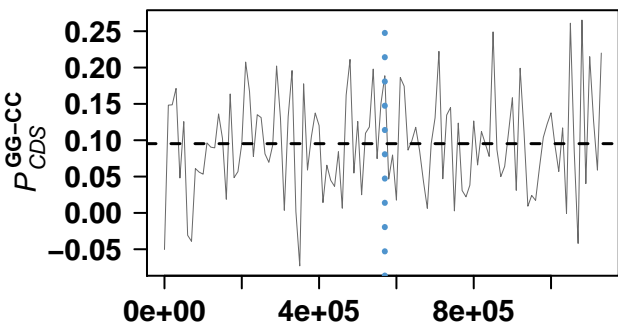
Bartonella quintana str. Toulouse



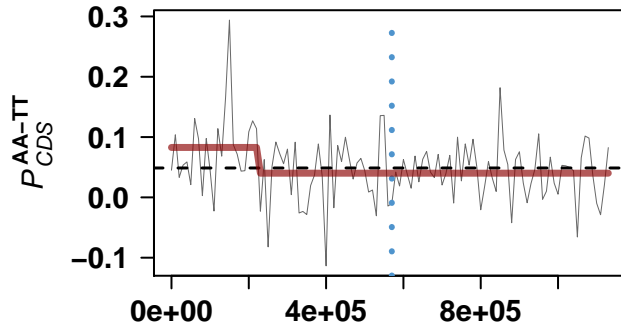
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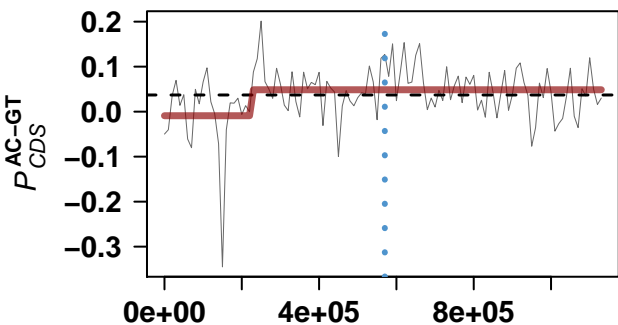
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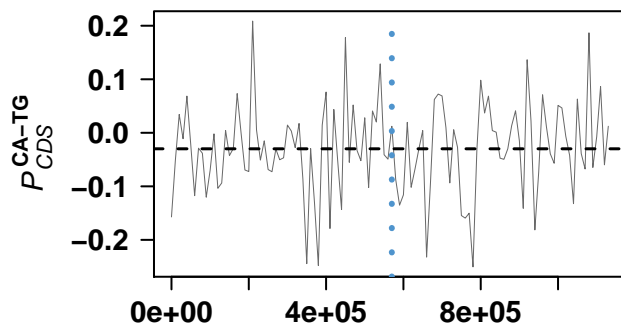
genome coordinates



genome coordinates

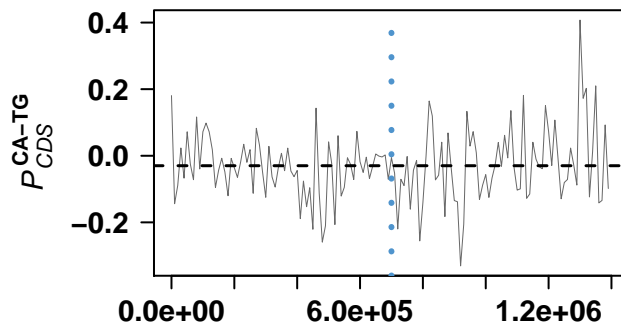
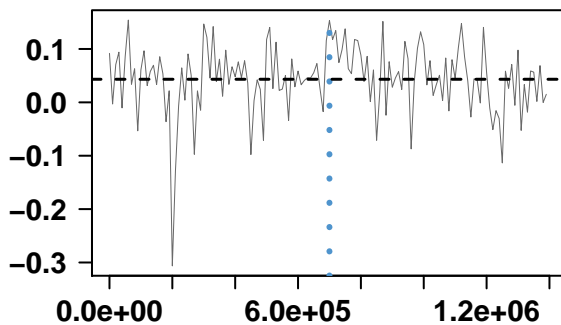
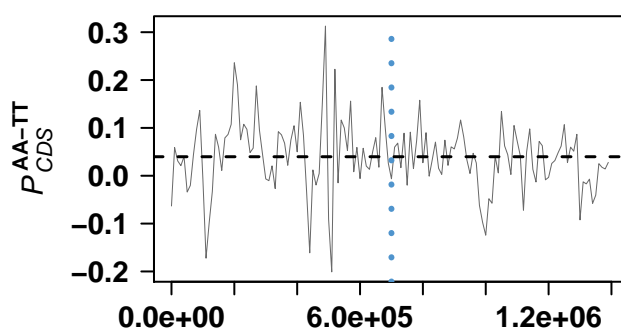
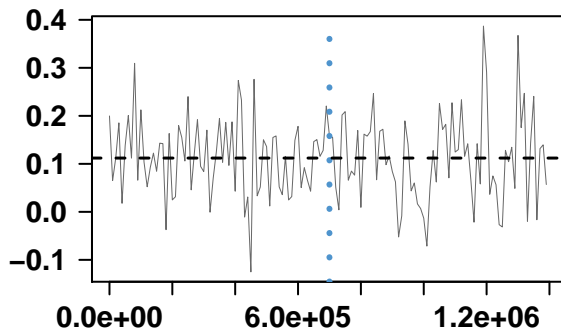
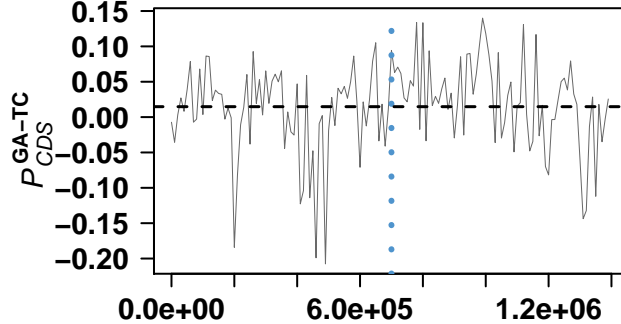
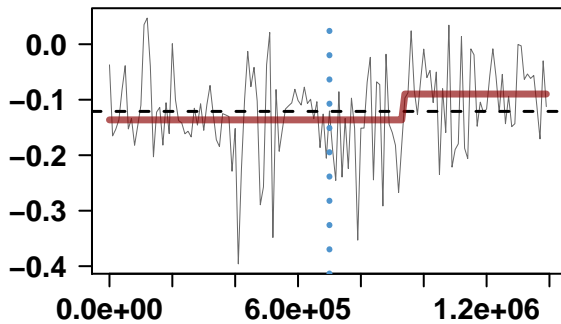


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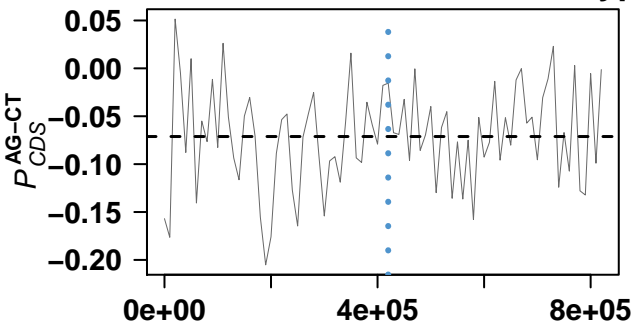


genome coordinates

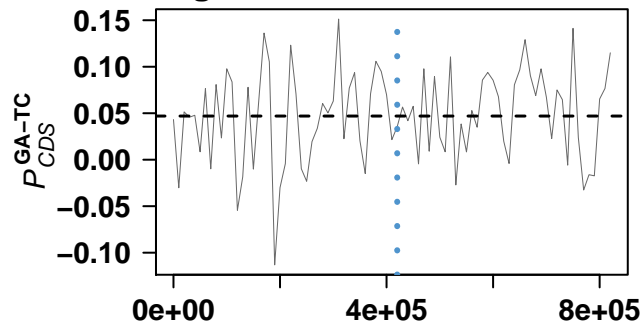
Bartonella henselae str. Houston-1



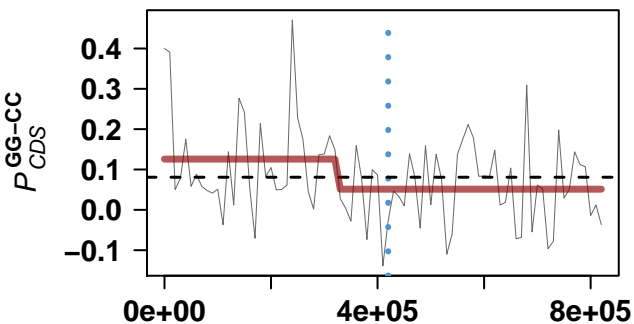
Rickettsia typhi str. Wilmington



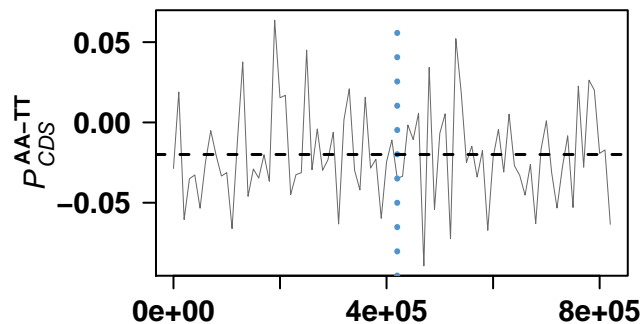
genome coordinates



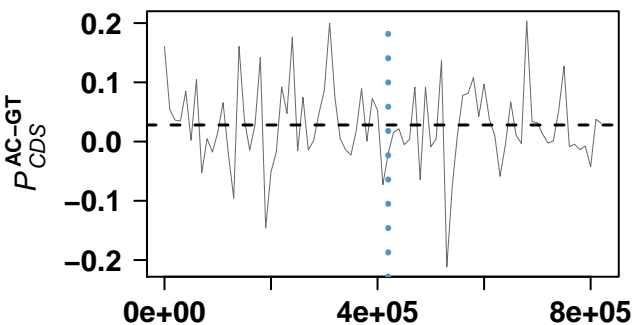
genome coordinates



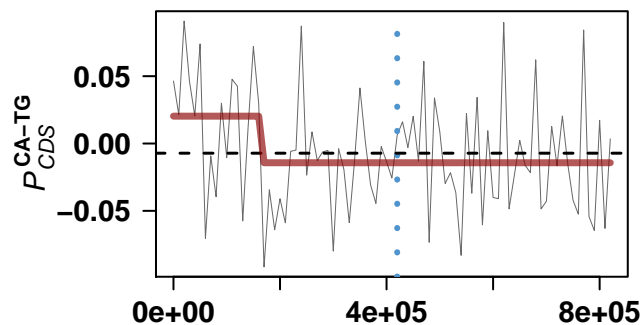
genome coordinates



genome coordinates

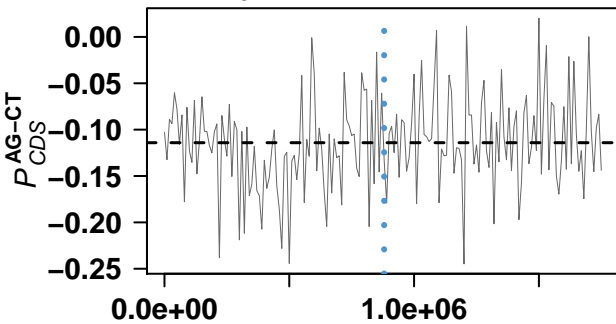


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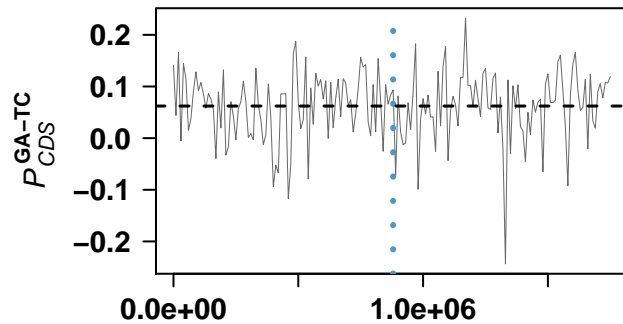


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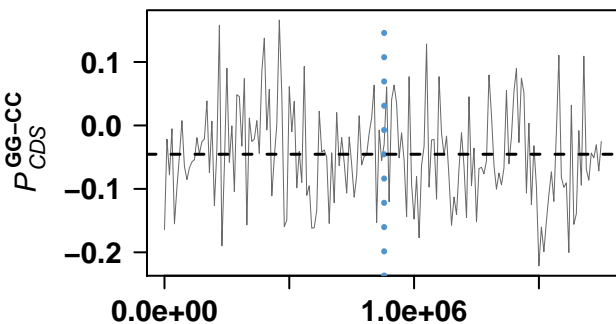
Zymomonas mobilis subsp. mobilis ZM4 = ATCC 31821



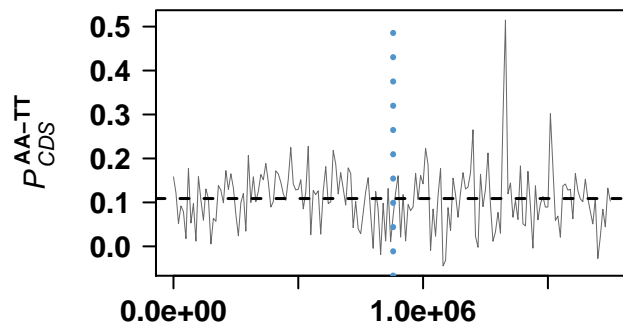
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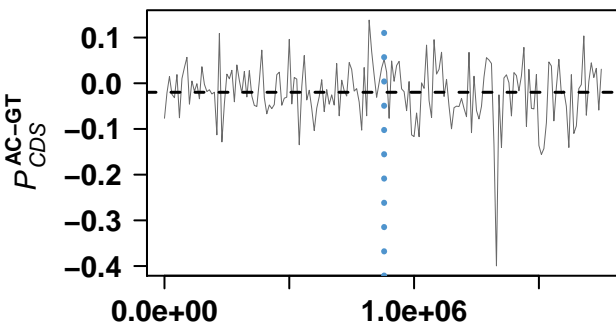
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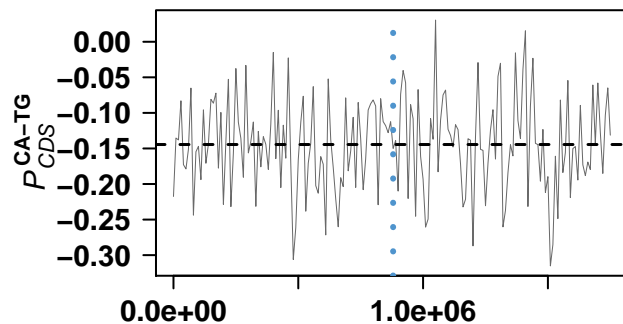
genome coordinates



genome coordinates

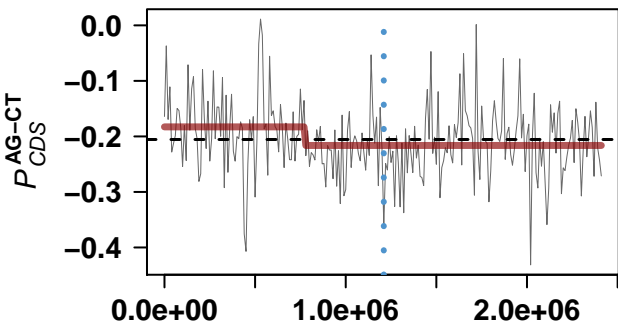


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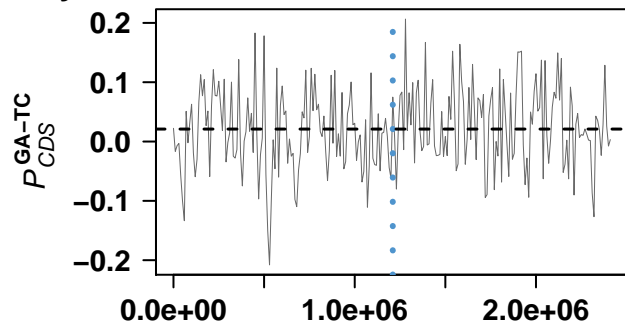


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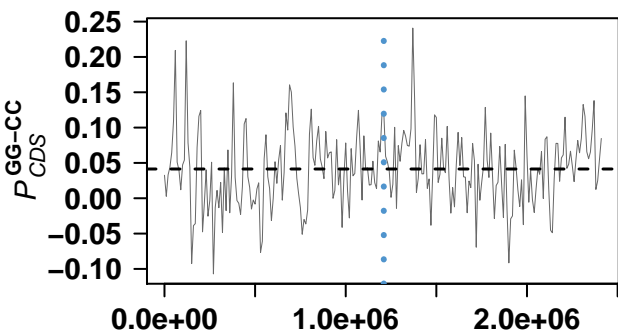
Gluconobacter oxydans 621H



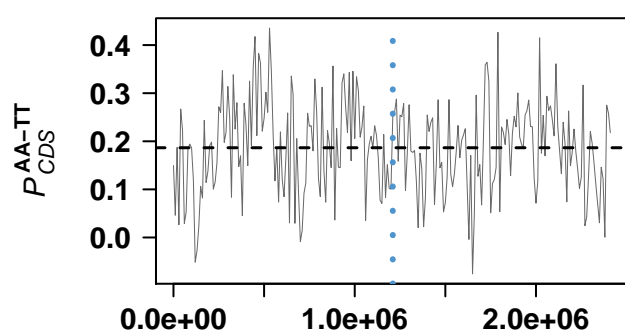
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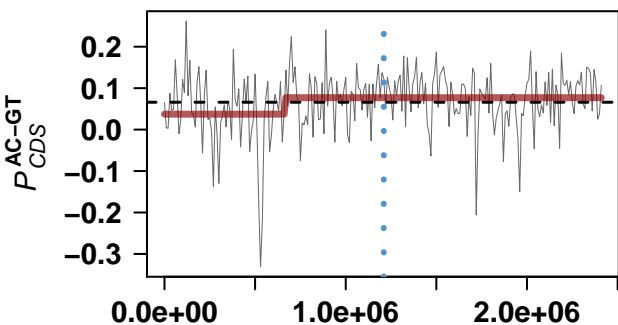
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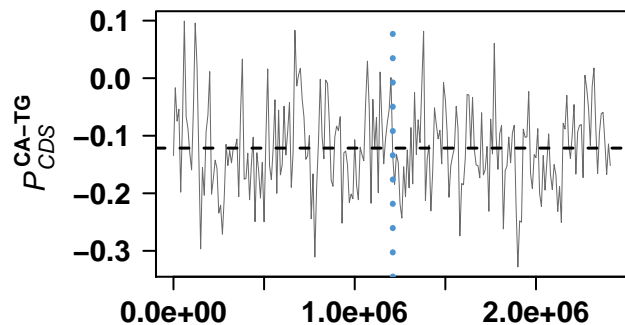
genome coordinates



genome coordinates

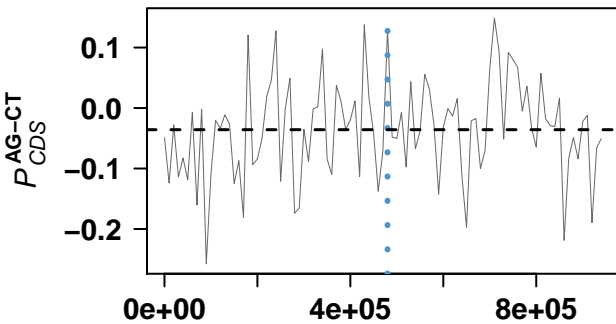


genome coordinates

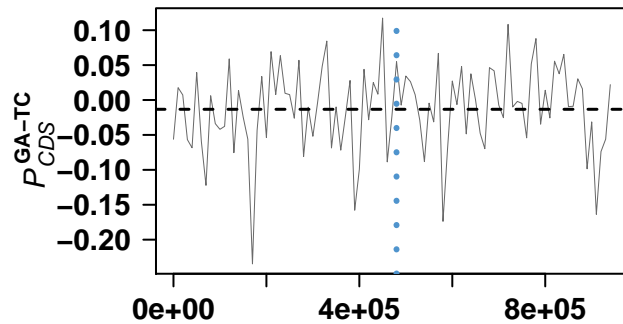


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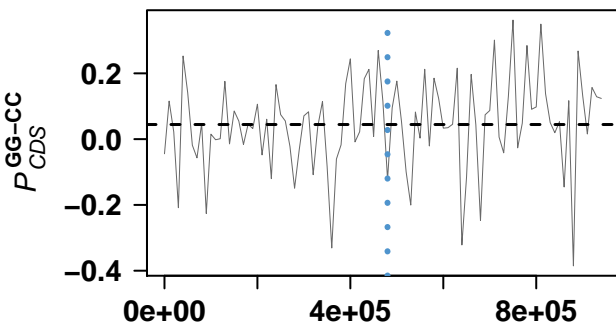
Ehrlichia ruminantium str. Gardel



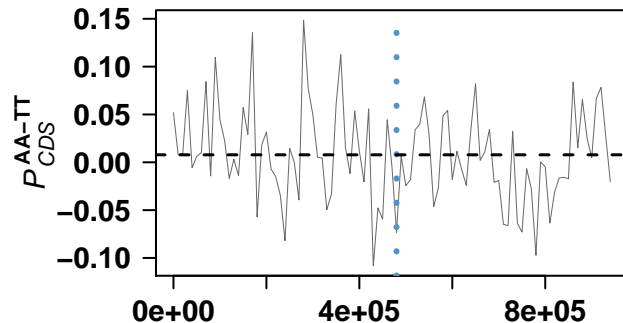
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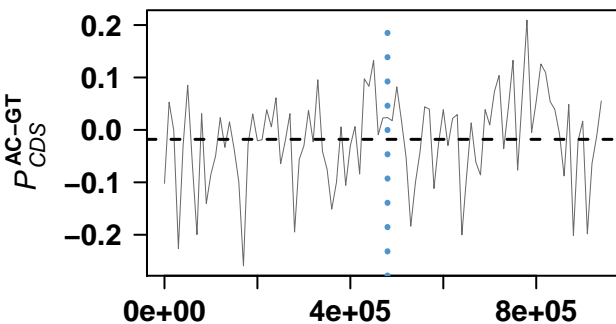
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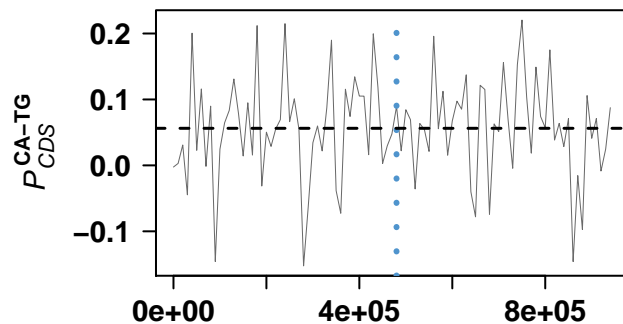
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genome coordinates

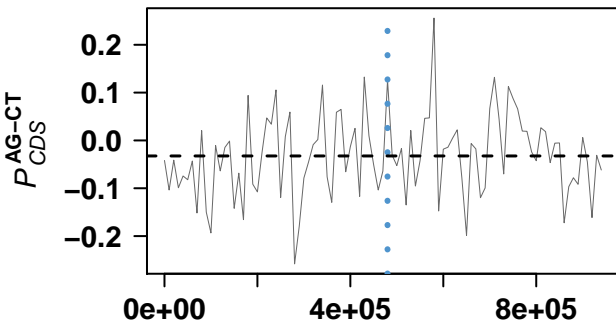


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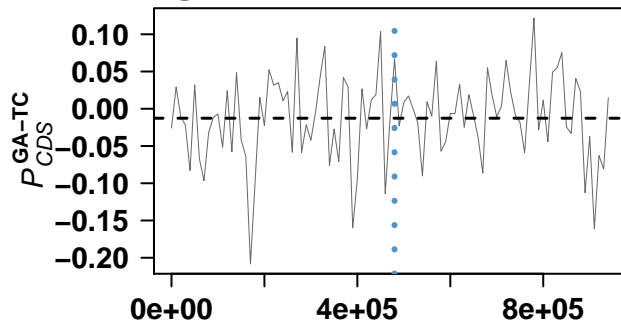


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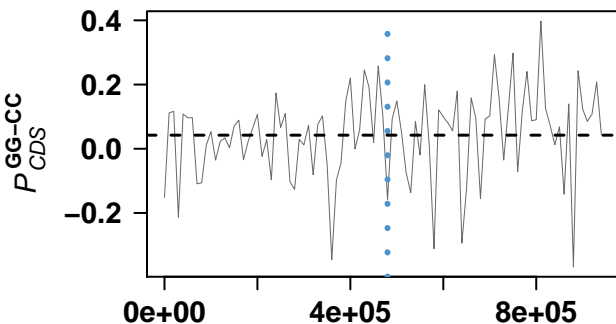
Ehrlichia ruminantium str. Welgevonden



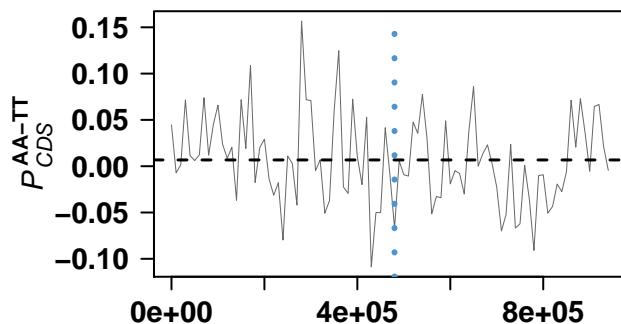
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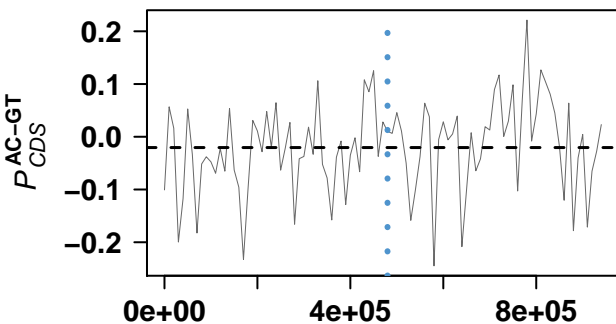
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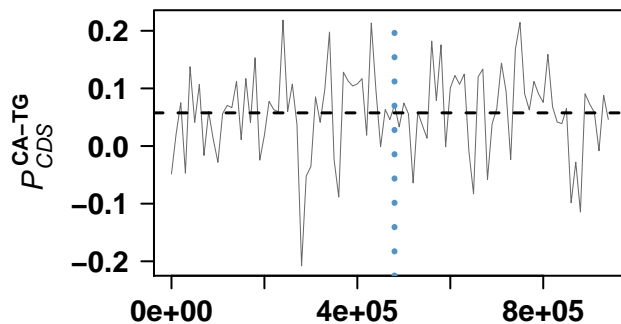
genome coordinates



genome coordinates

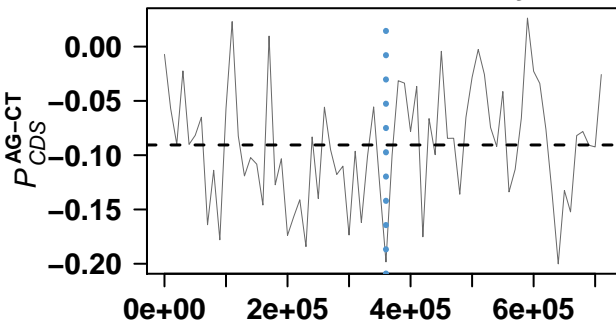


genome coordinates

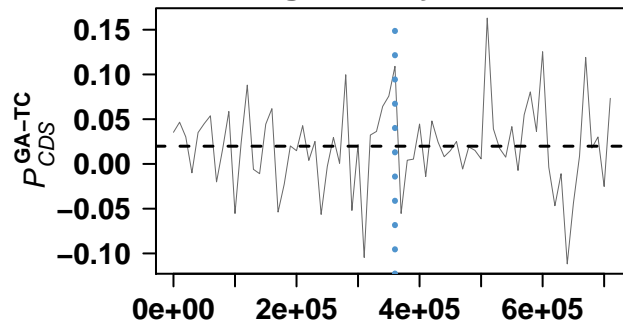


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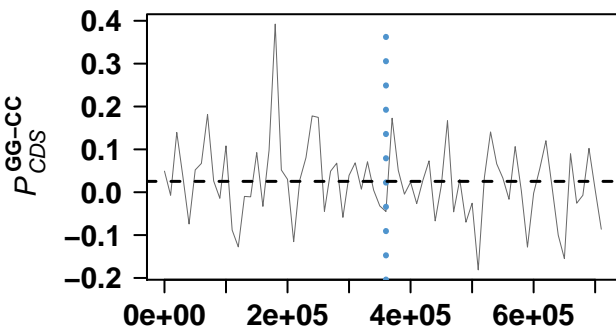
Wolbachia endosymbiont strain TRS of *Brugia malayi*



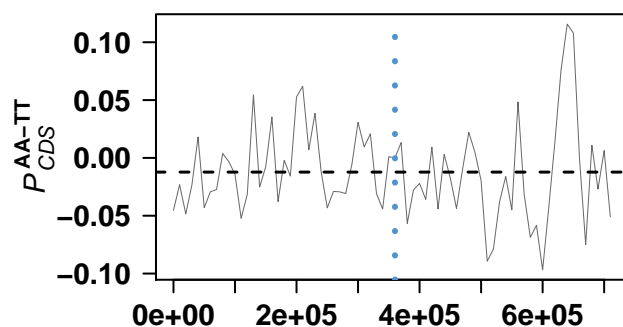
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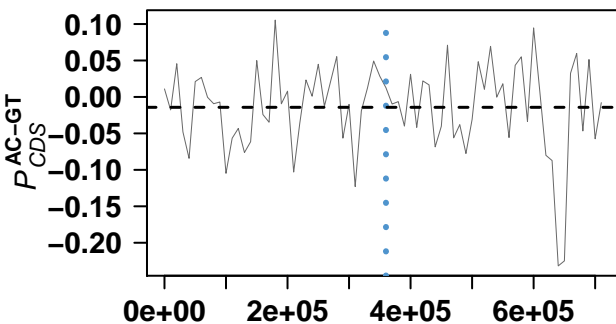
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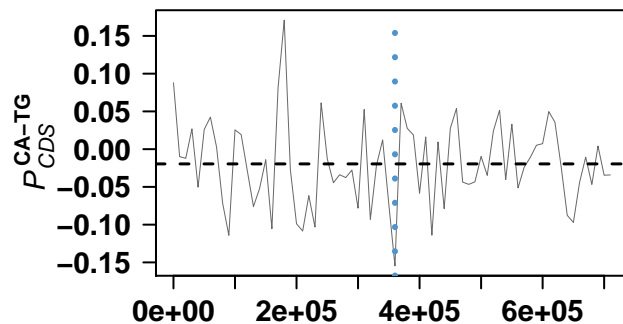
genome coordinates



genome coordinates

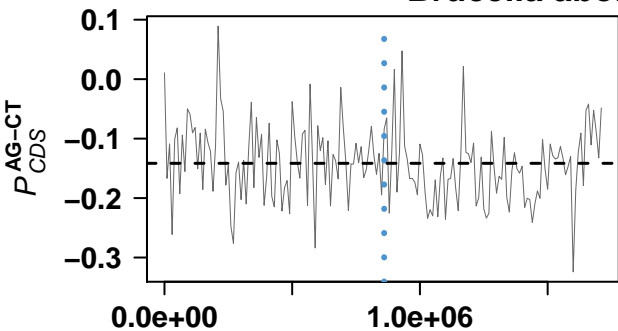


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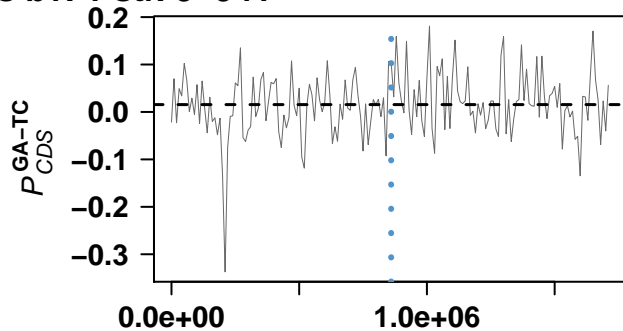


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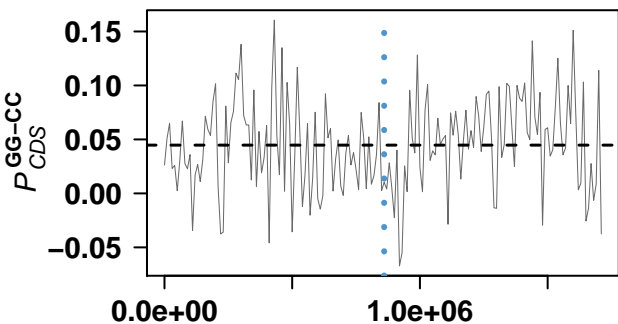
Brucella abortus bv. 1 str. 9-941



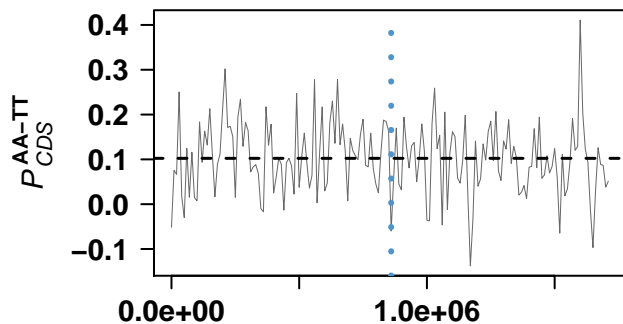
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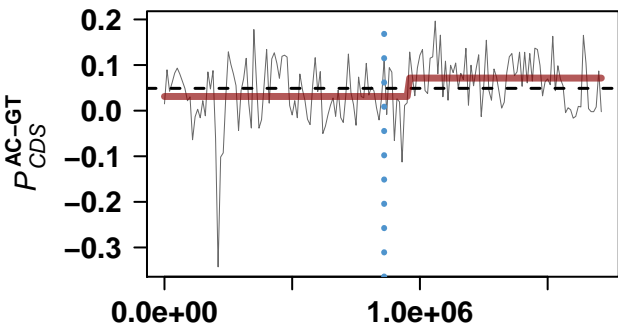
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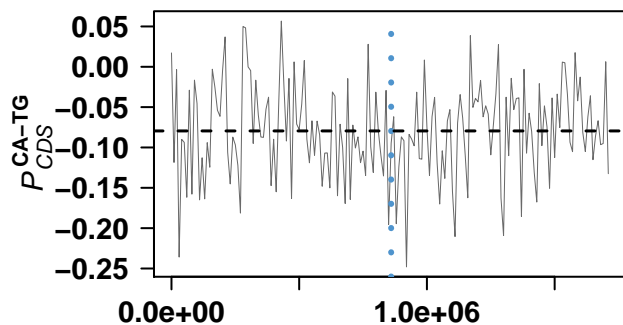
genome coordinates



genome coordinates

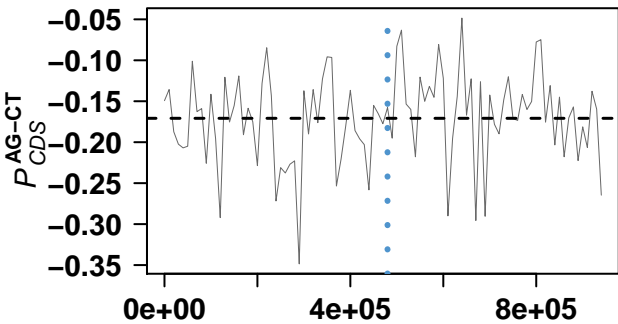


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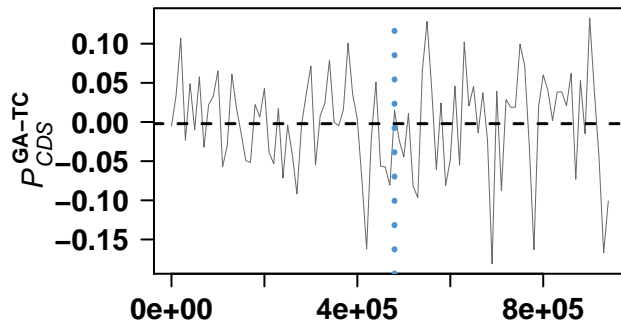


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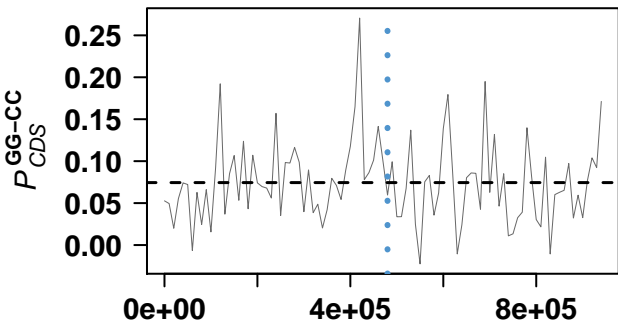
Brucella abortus bv. 1 str. 9-941



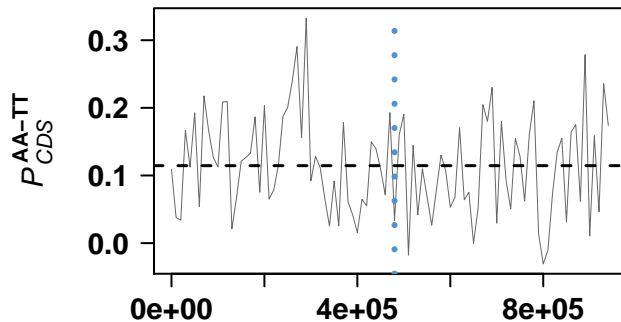
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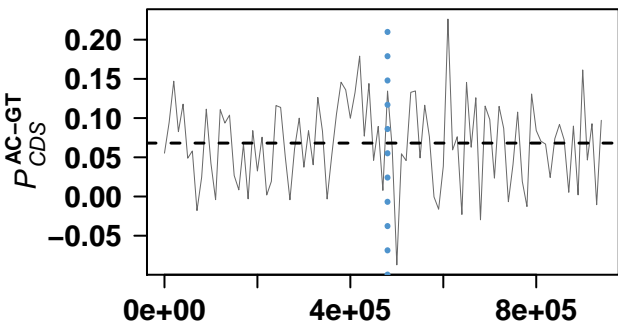
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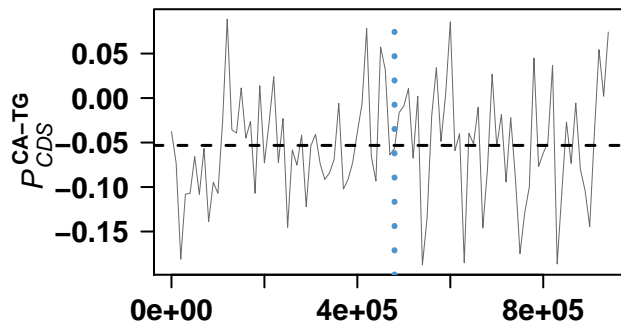
genome coordinates



genome coordinates

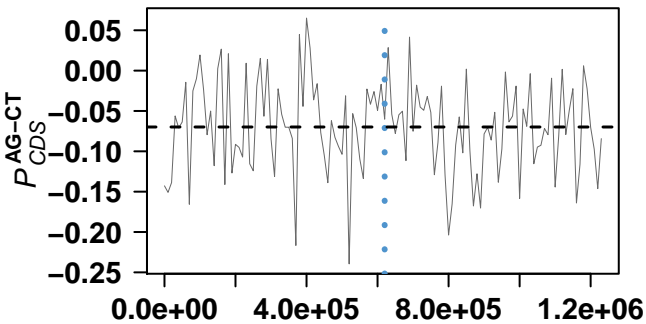


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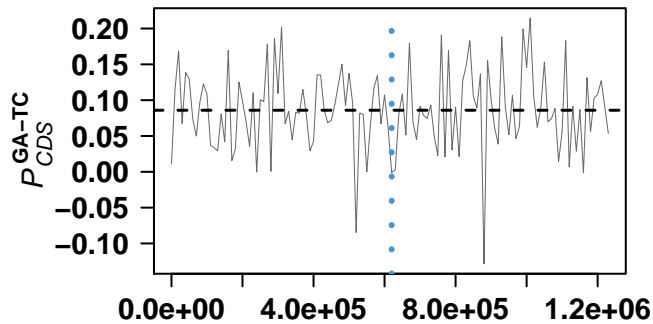


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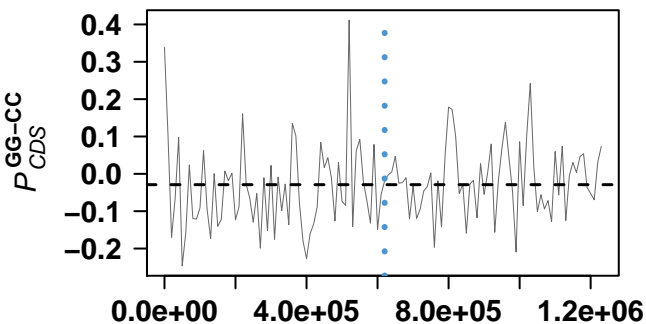
Rickettsia felis URRWXCa12



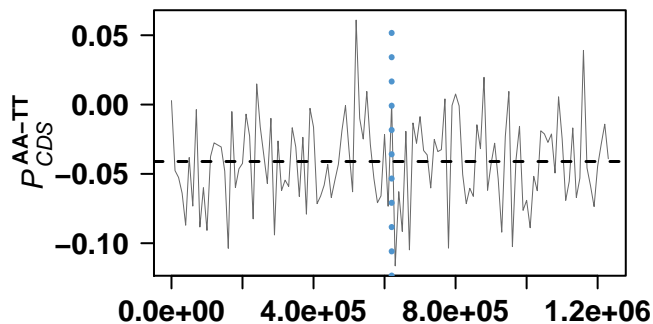
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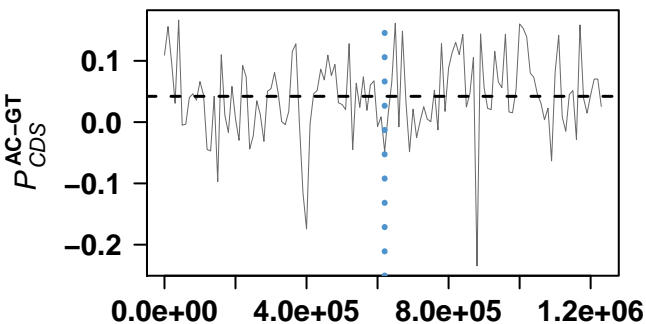
genome coordinates



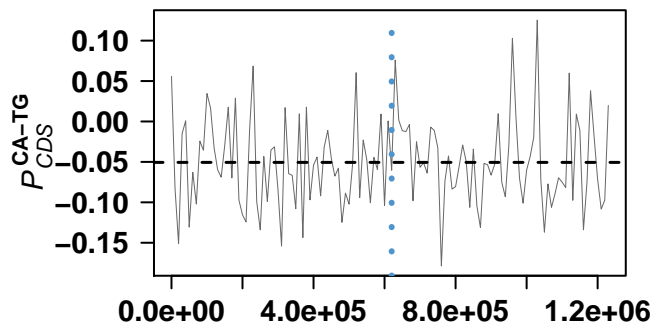
genome coordinates



genome coordinates

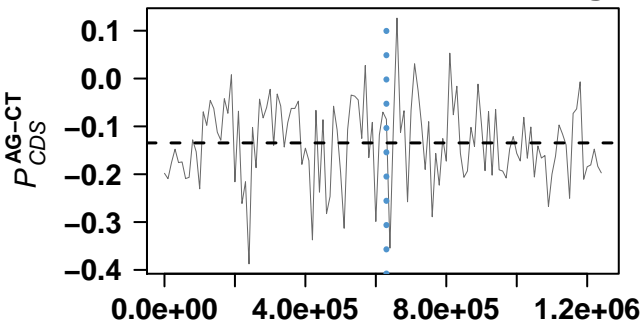


genome coordinates

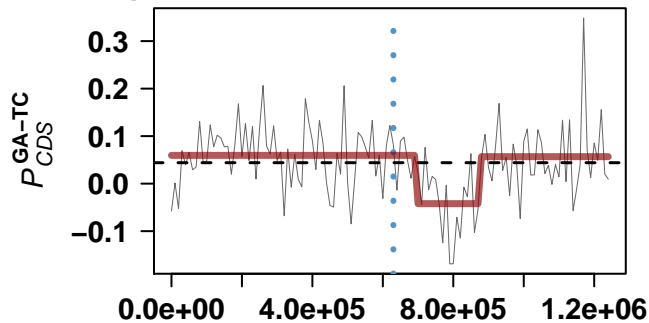


genome coordinates

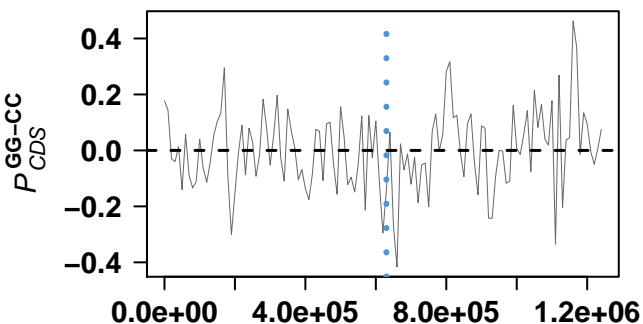
Candidatus Pelagibacter ubique HTCC1062



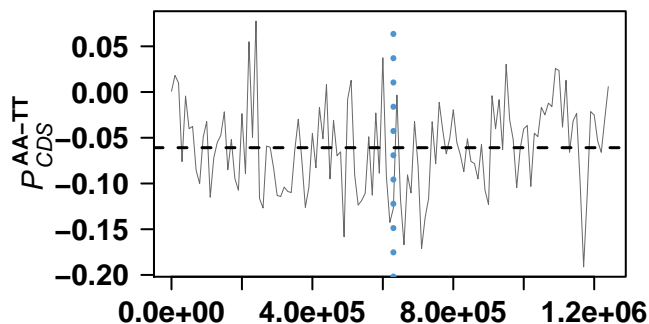
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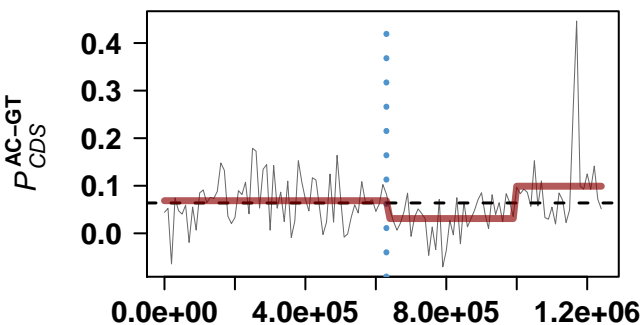
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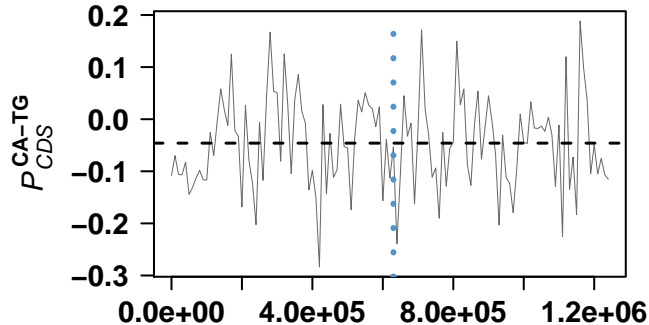
genome coordinates



genome coordinates

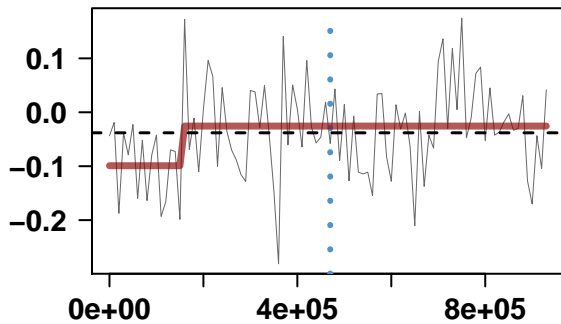


genome coordinates

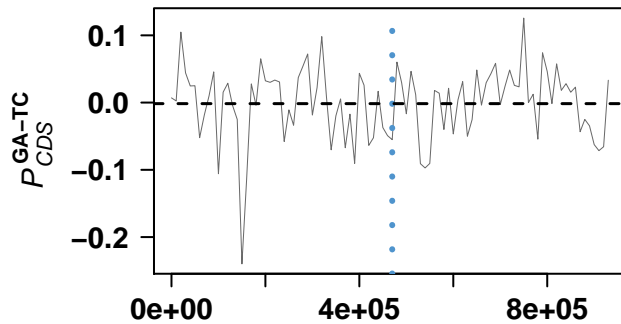


genome coordinates

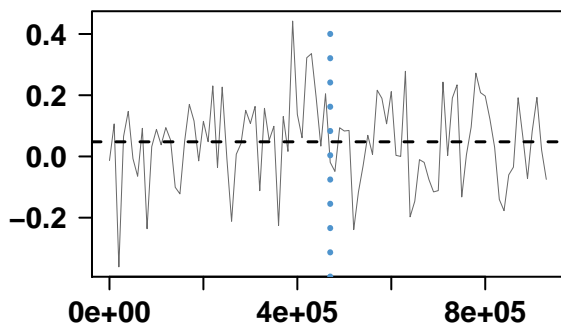
Ehrlichia canis str. Jake



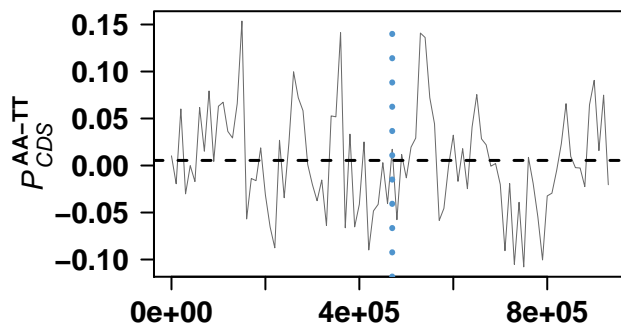
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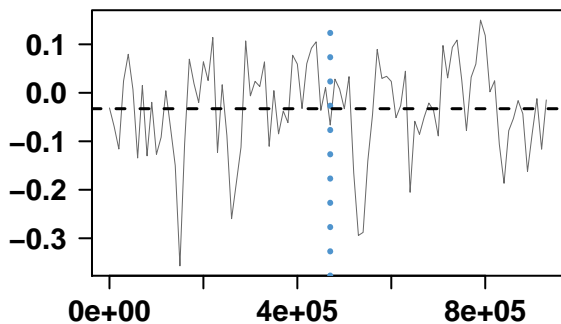
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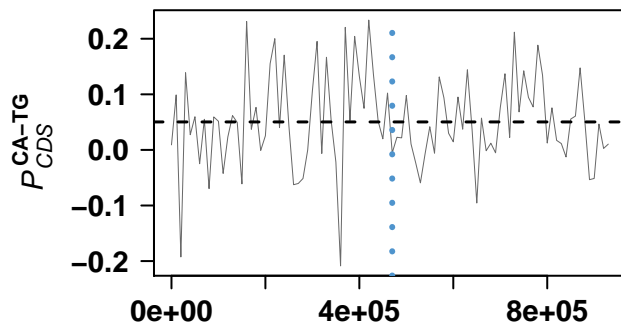
genome coordinates



genome coordinates

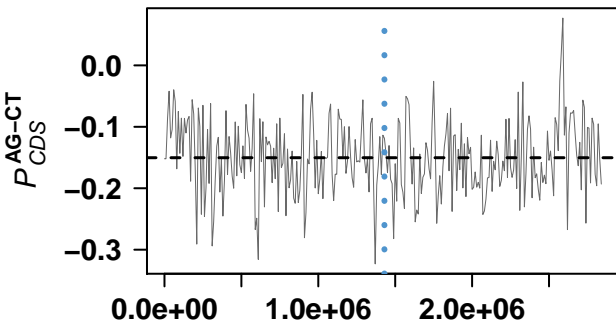


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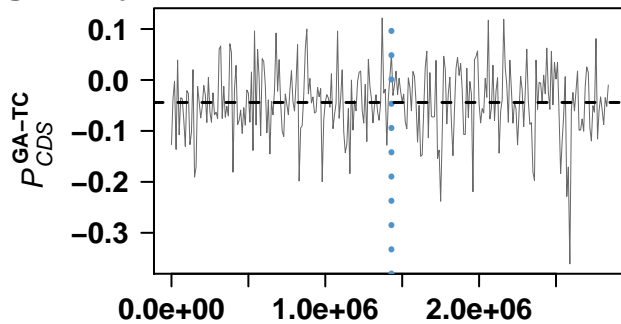


genome coordinates

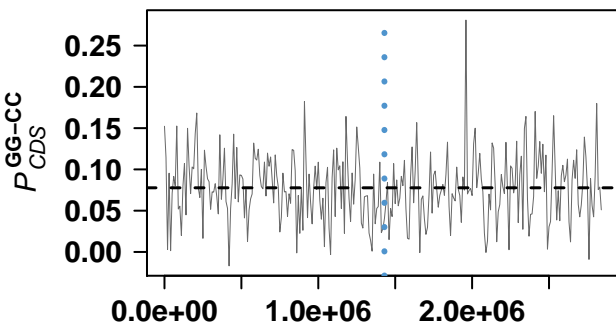
Nitrobacter winogradskyi Nb-255



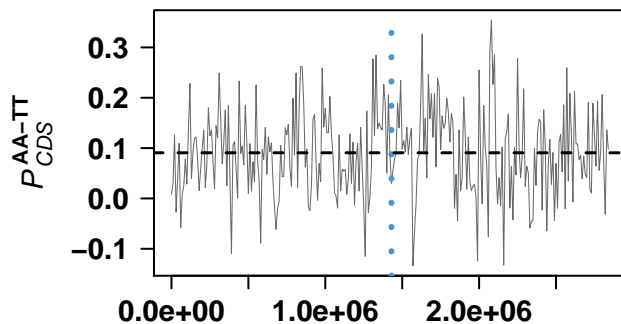
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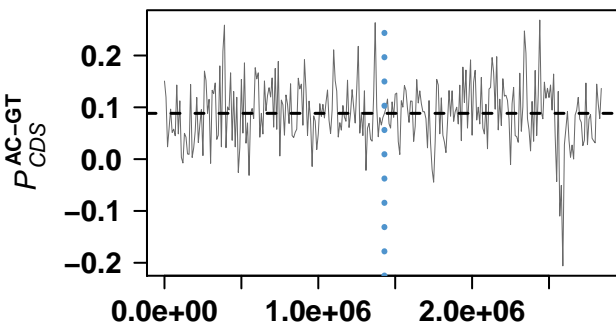
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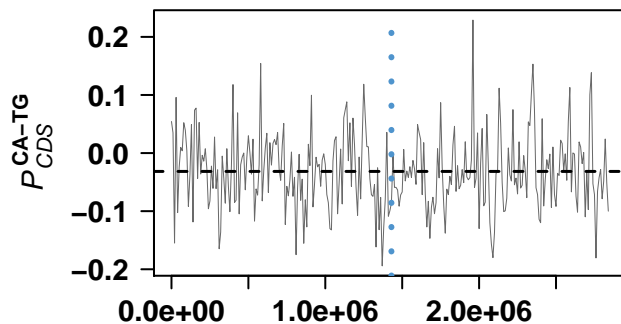
genome coordinates



genome coordinates

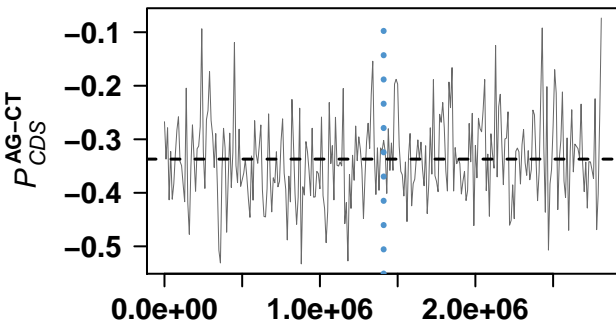


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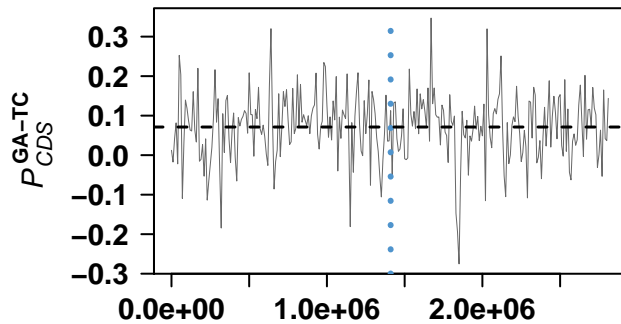


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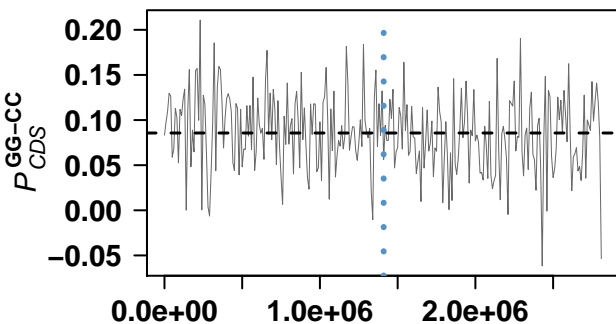
Rhodobacter sphaeroides 2.4.1



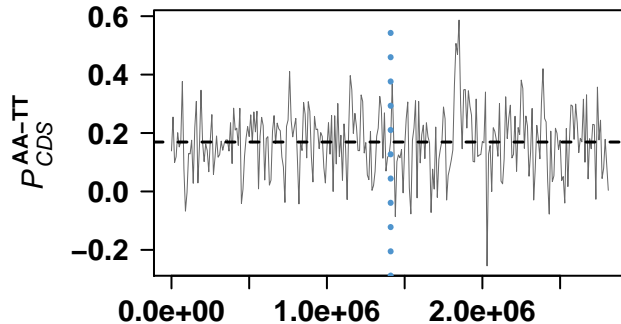
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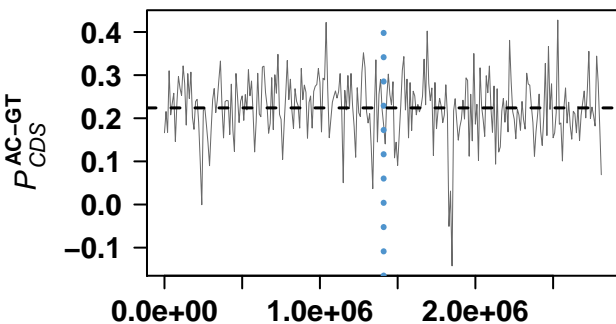
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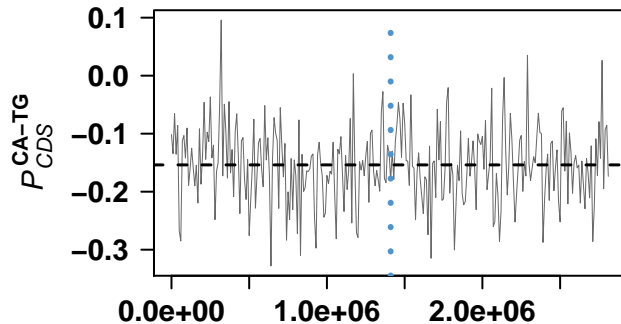
genome coordinates



genome coordinates

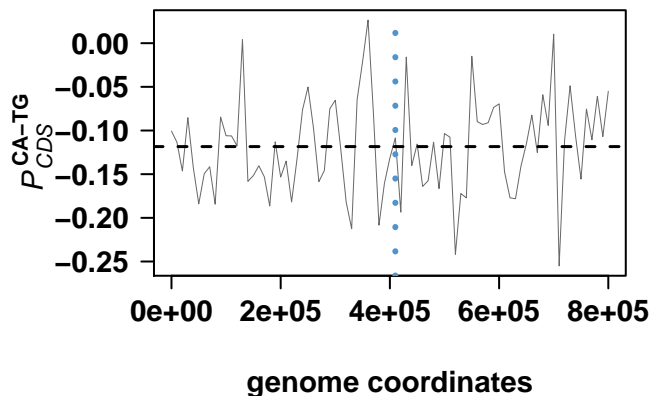
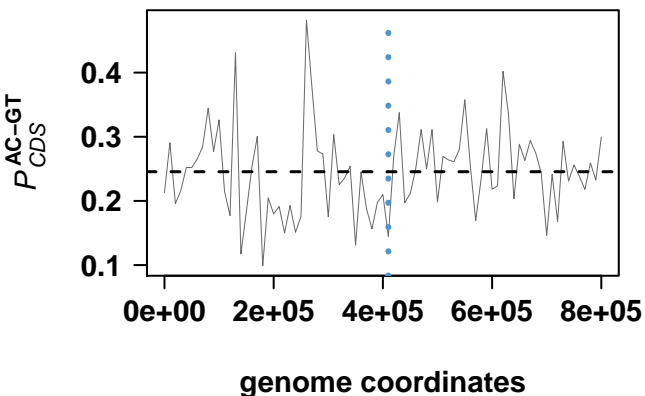
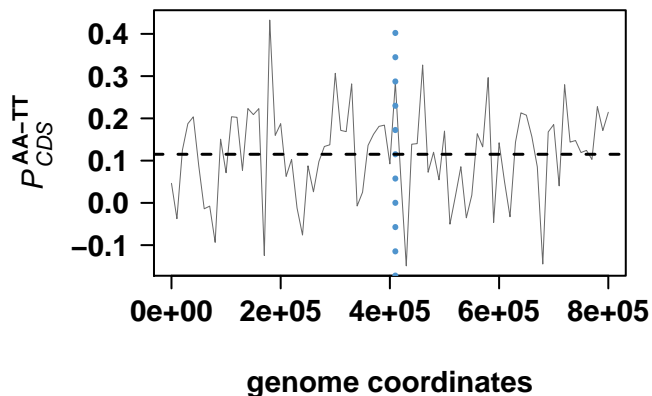
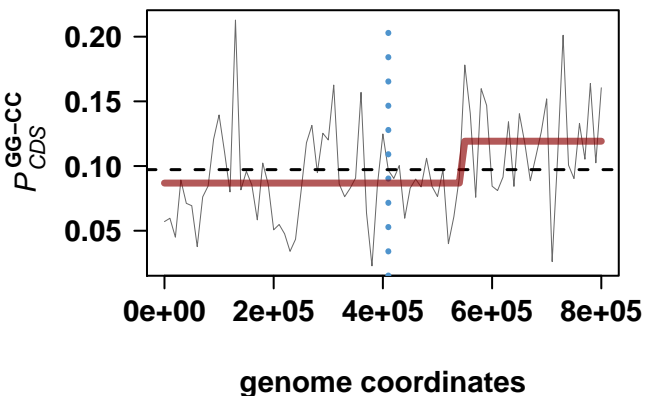
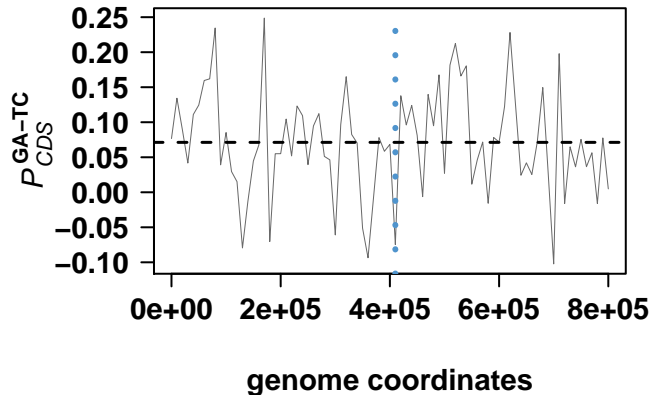
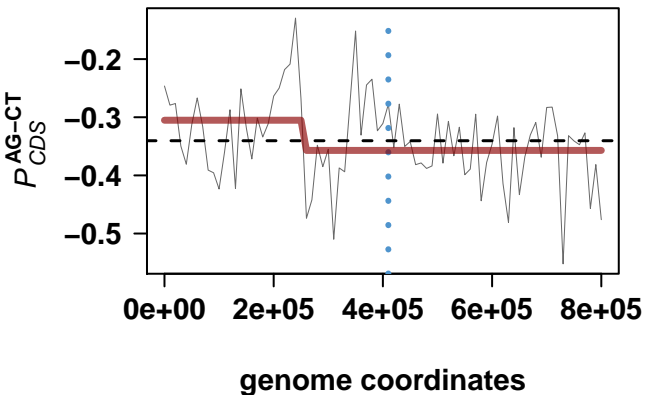


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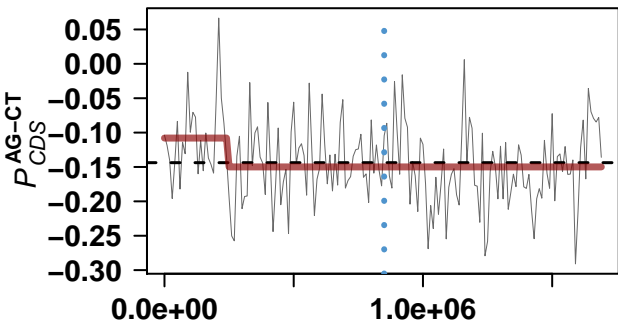


genome coordinates

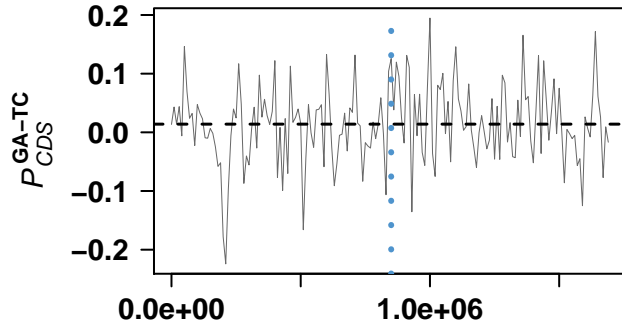
Rhodobacter sphaeroides 2.4.1



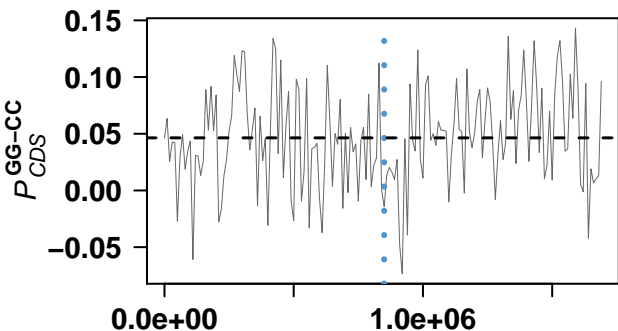
Brucella abortus 2308



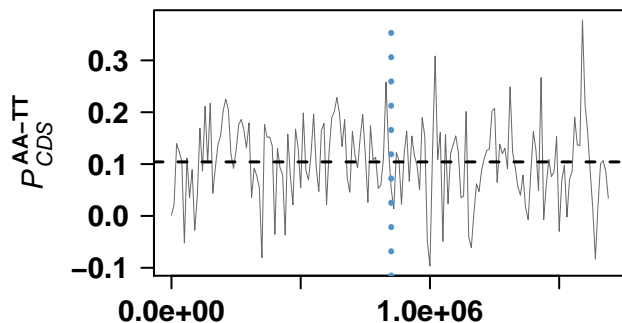
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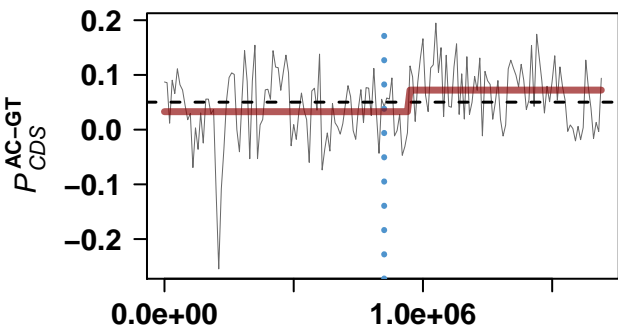
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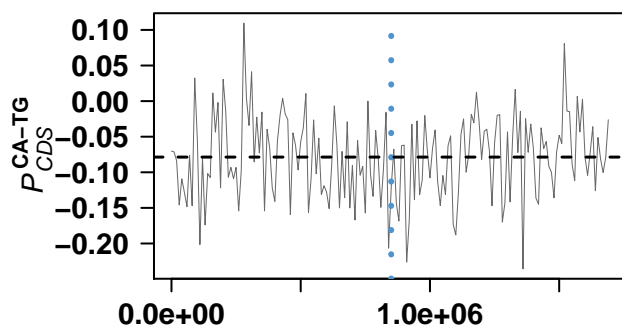
genome coordinates



genome coordinates

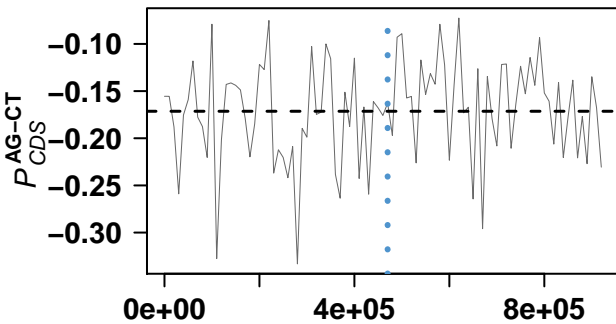


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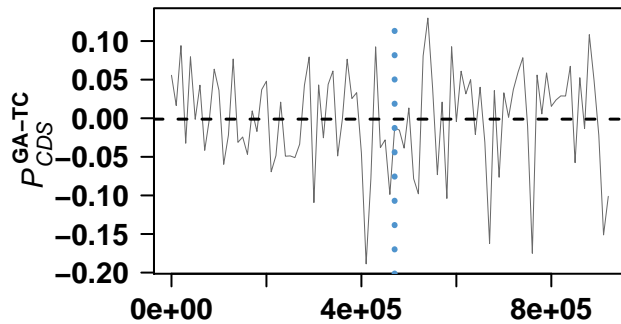


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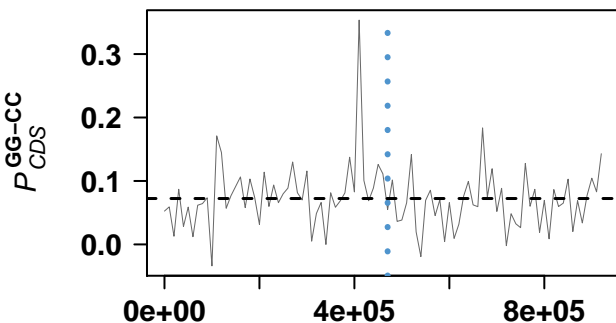
Brucella abortus 2308



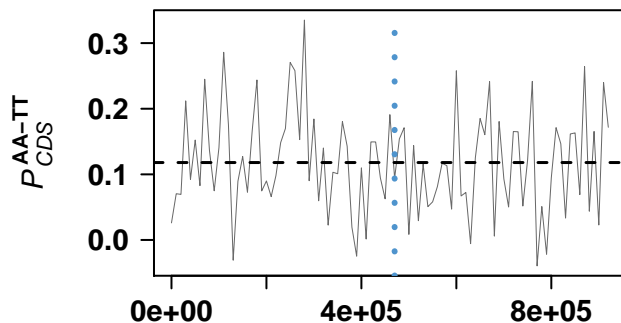
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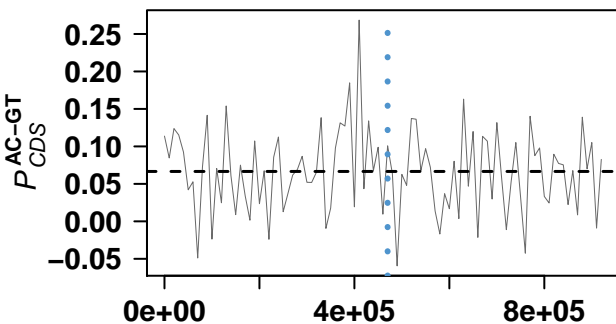
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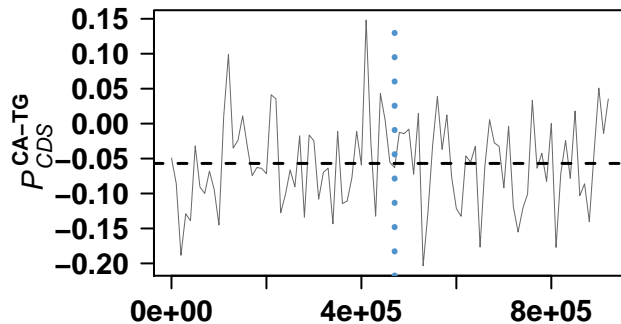
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genome coordinates

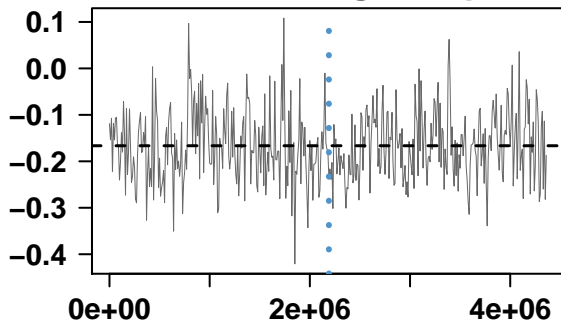


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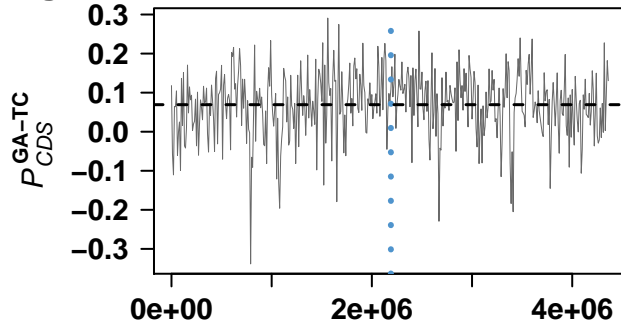


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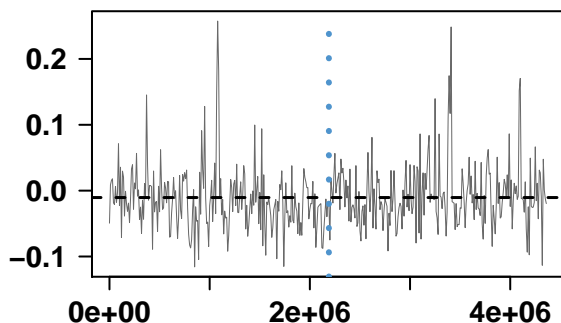
Magnetospirillum magneticum AMB-1



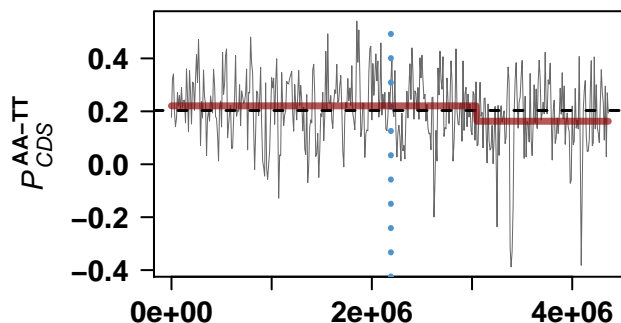
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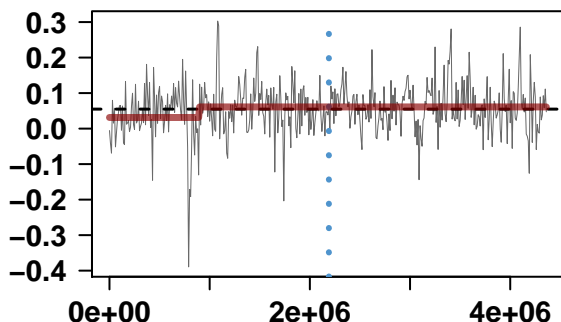
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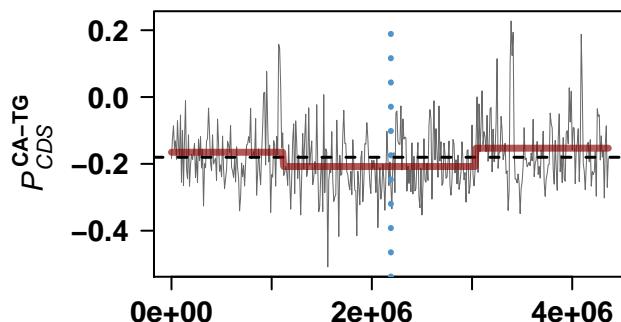
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genome coordinates

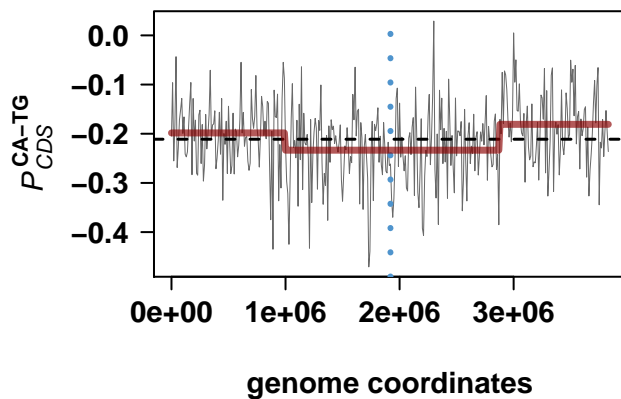
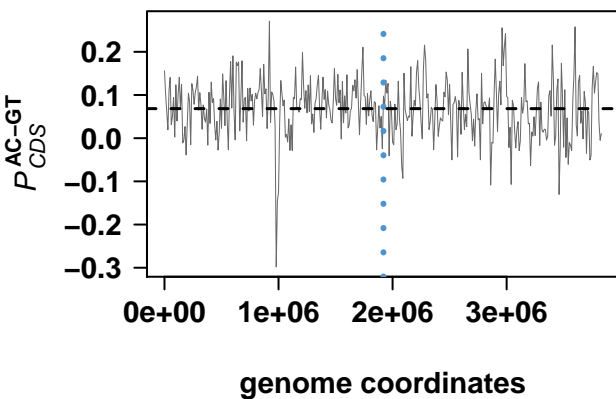
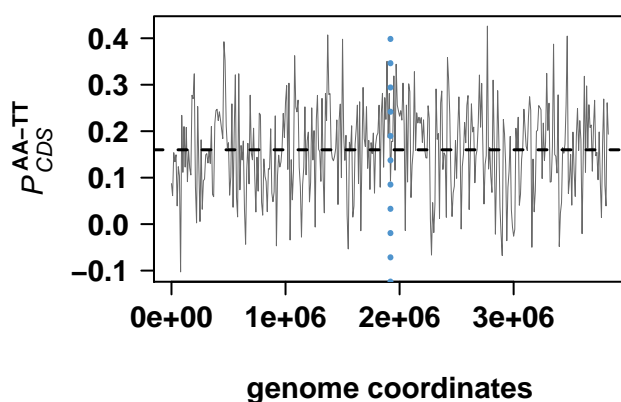
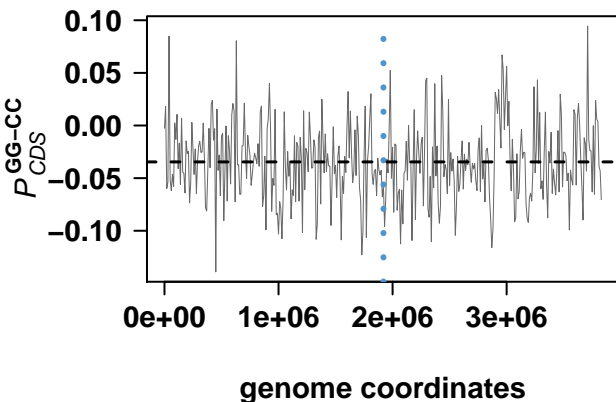
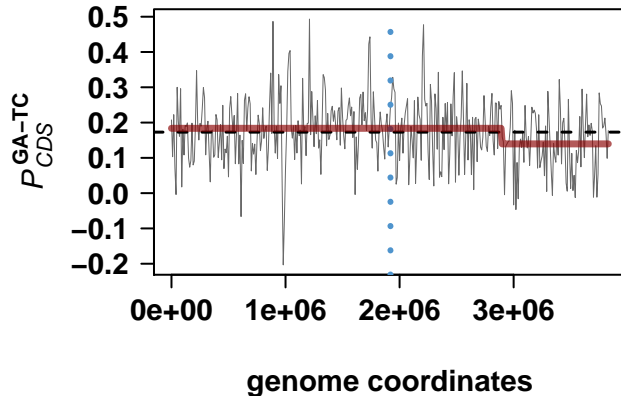
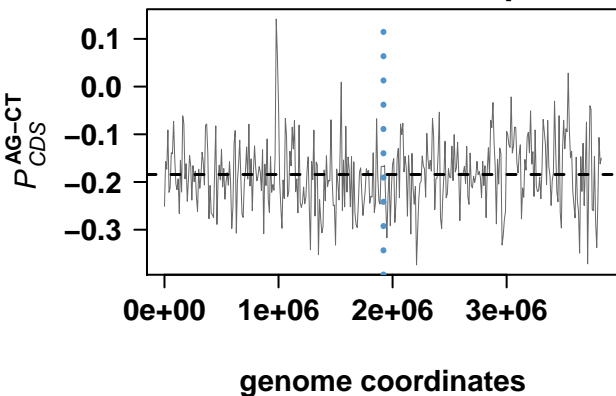


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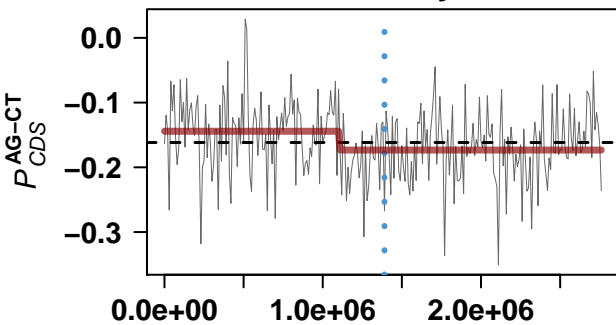


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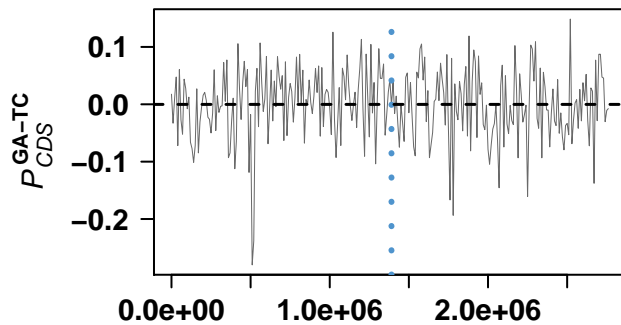
Rhodospirillum rubrum ATCC 11170



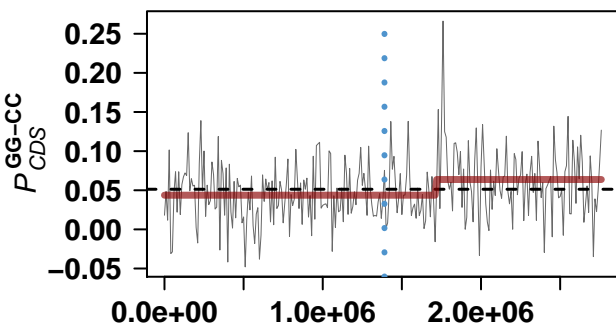
Erythrobacter litoralis HTCC2594



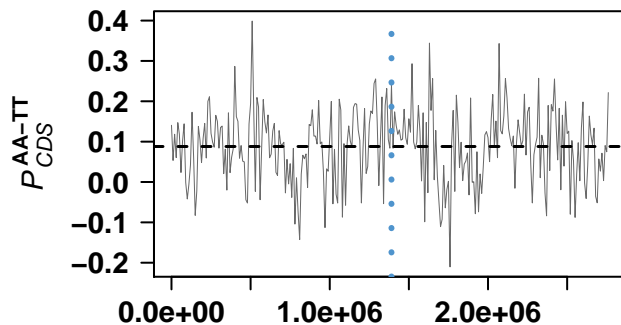
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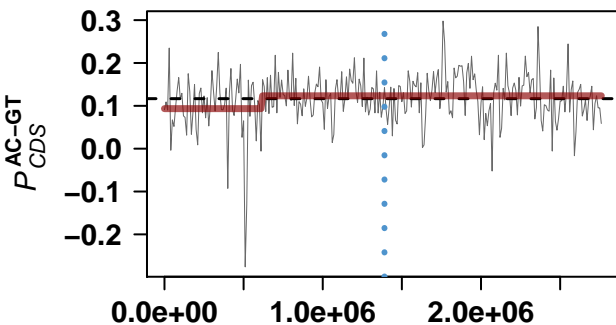
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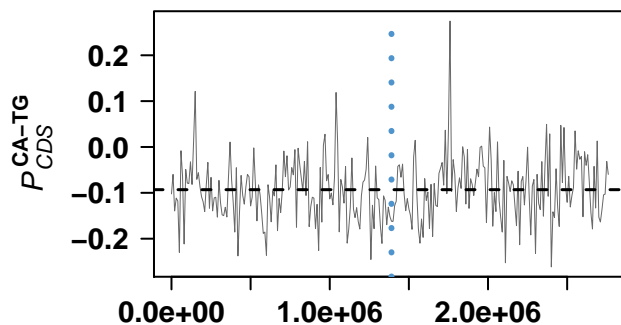
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genome coordinates

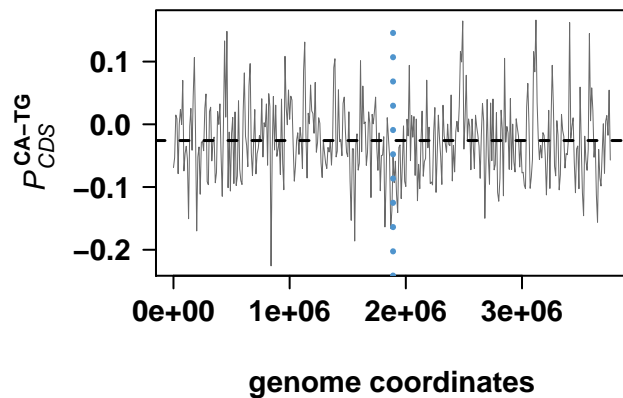
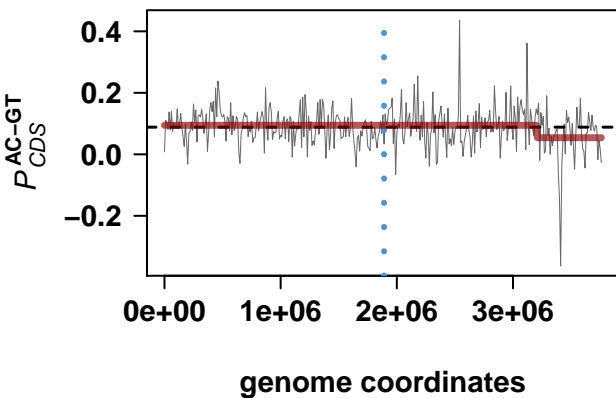
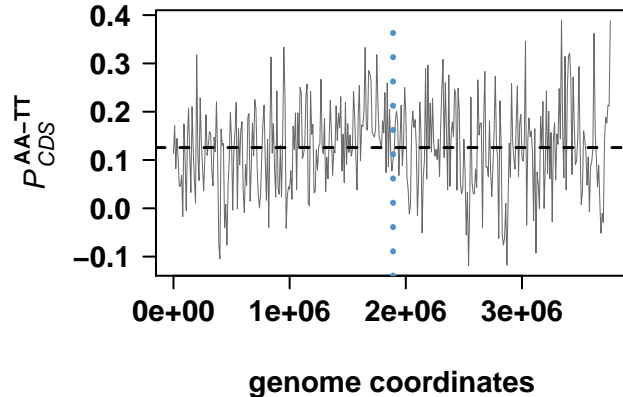
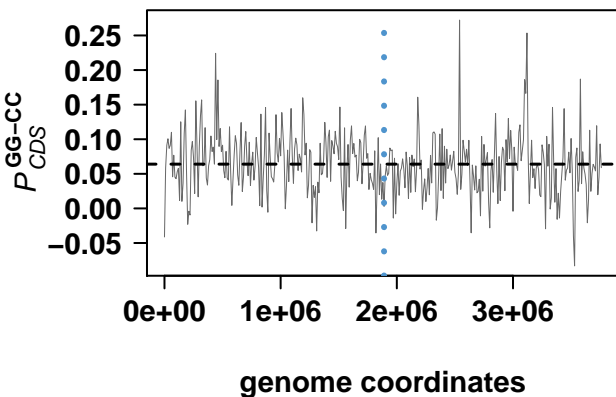
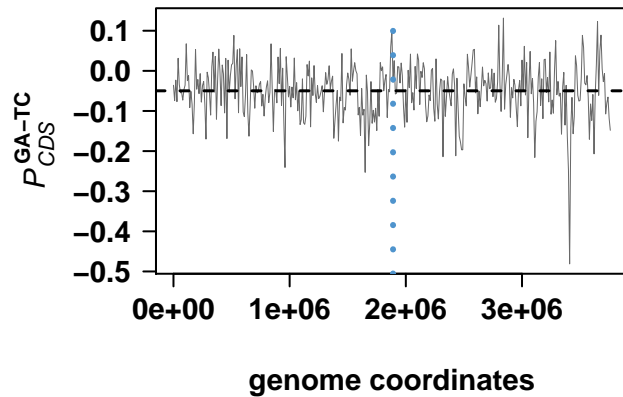
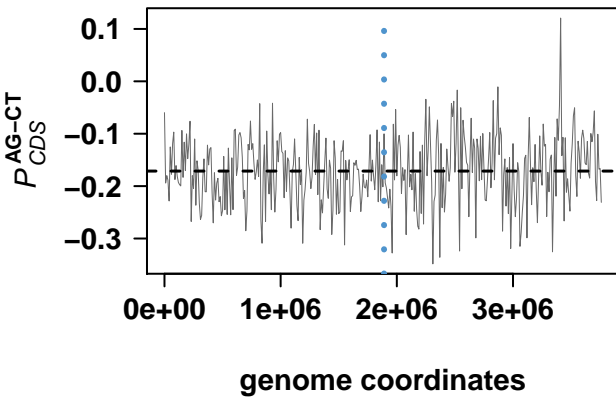


genome coordinates

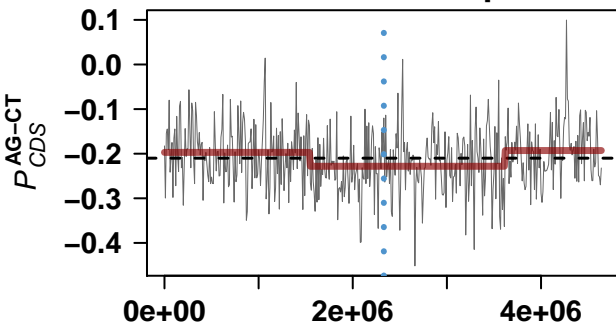


genome coordinates

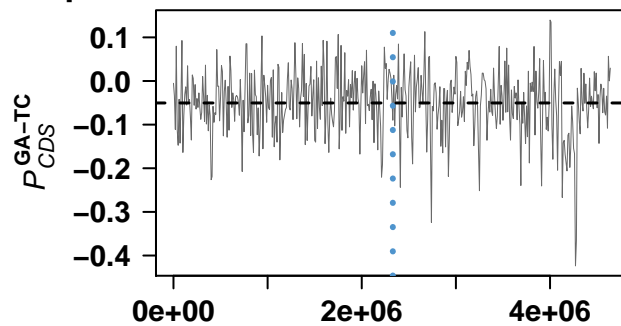
Rhizobium etli CFN 42



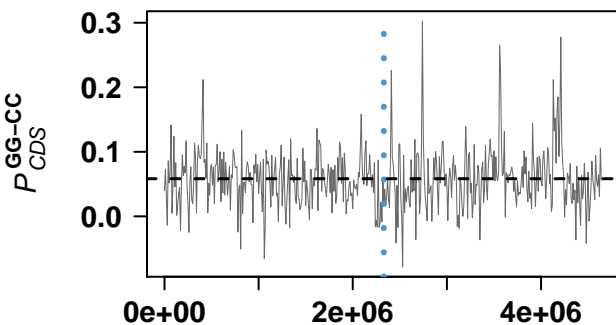
Rhodospseudomonas palustris HaA2



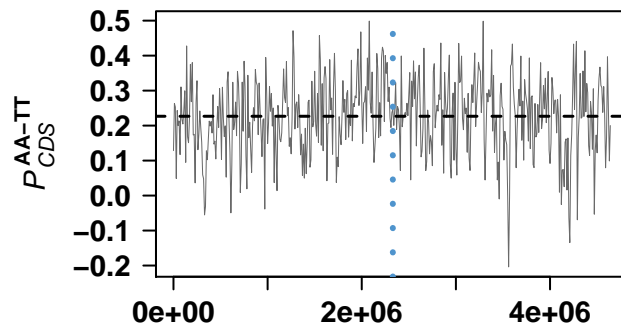
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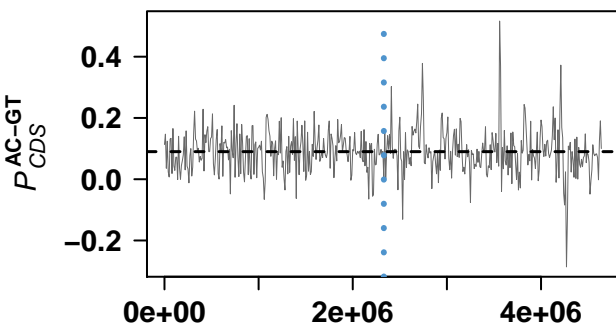
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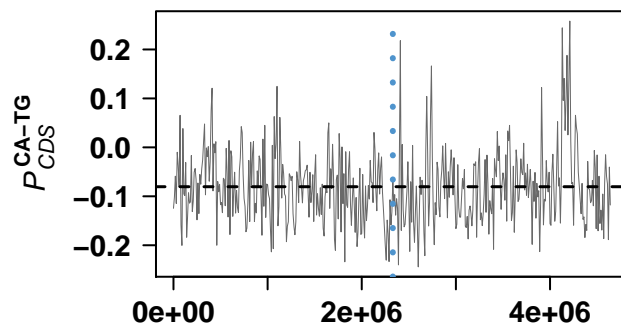
genome coordinates



genome coordinates

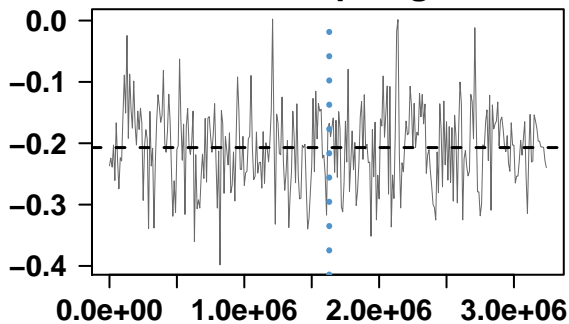


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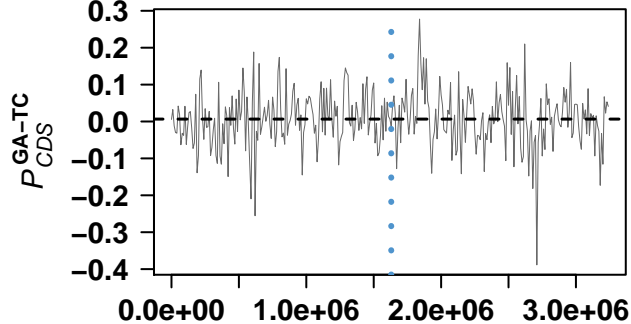


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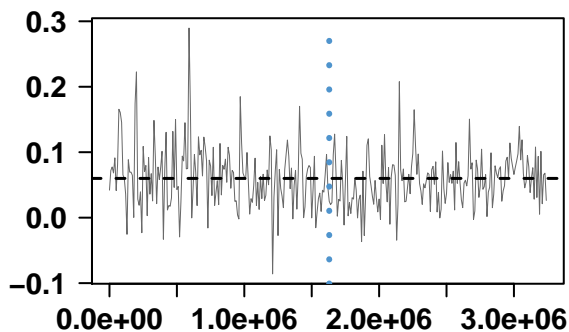
Novosphingobium aromaticivorans DSM 12444



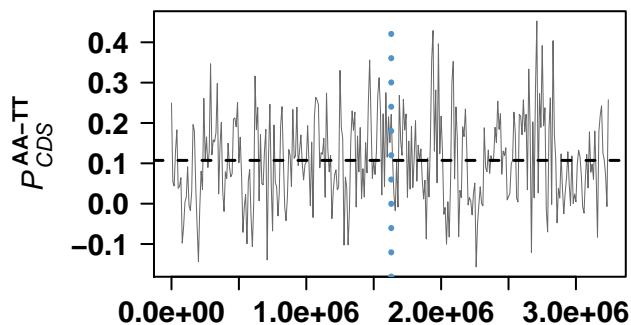
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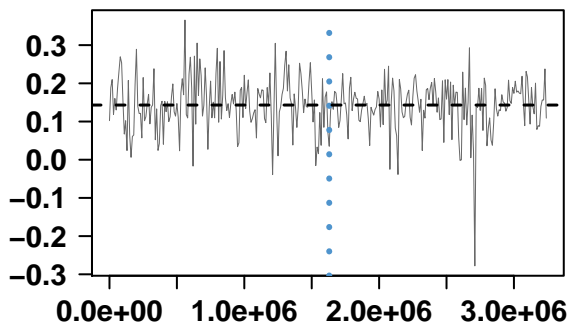
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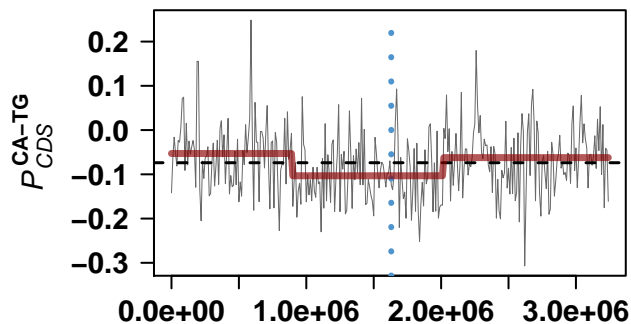
genome coordinates



genome coordinates

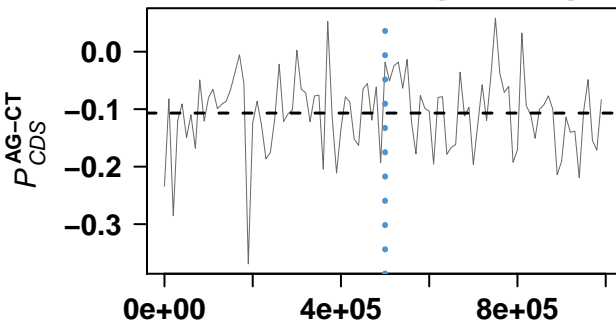


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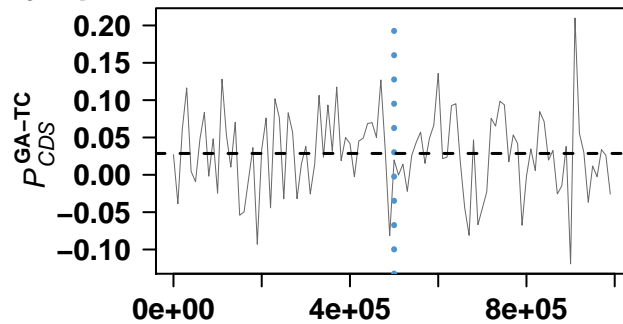


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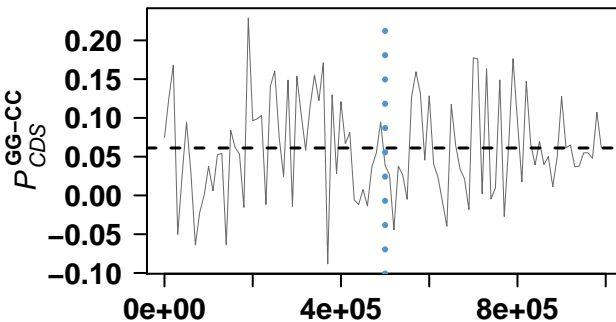
Anaplasma phagocytophilum str. HZ



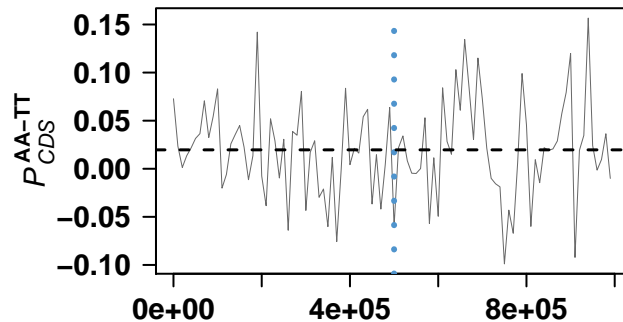
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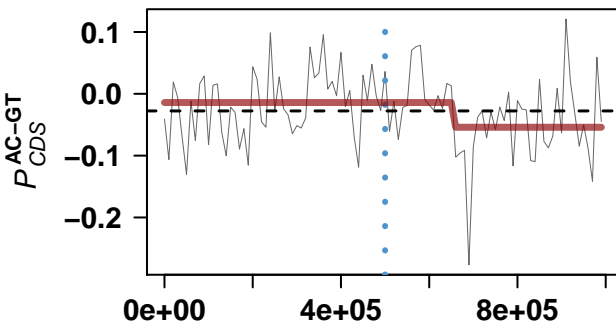
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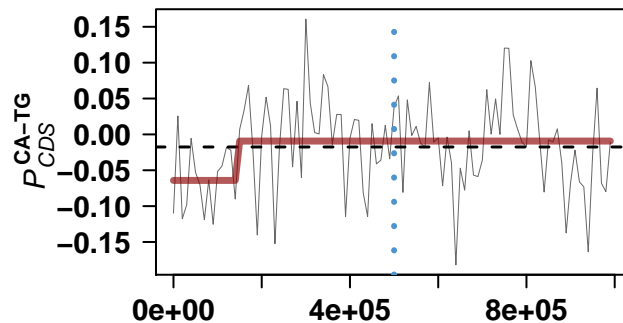
genome coordinates



genome coordinates

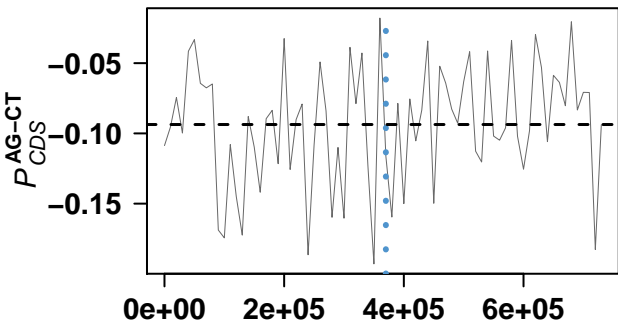


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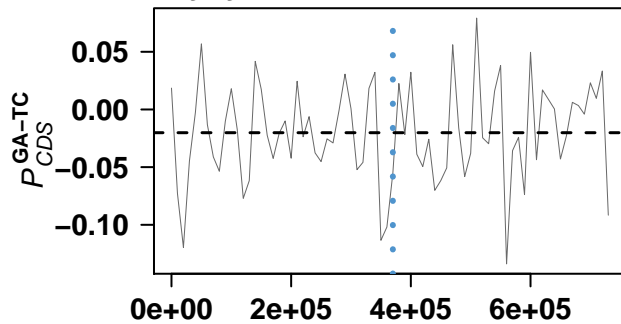


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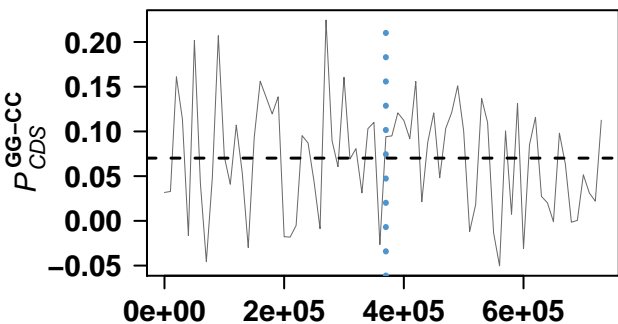
Neorickettsia sennetsu str. Miyayama



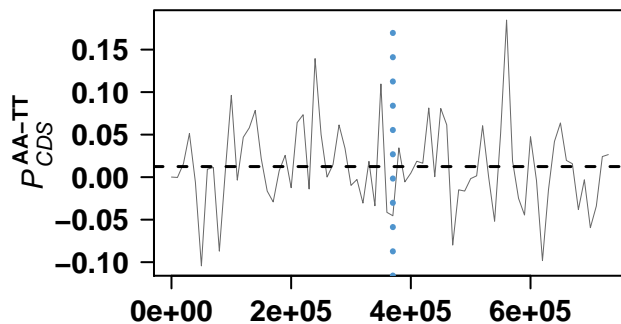
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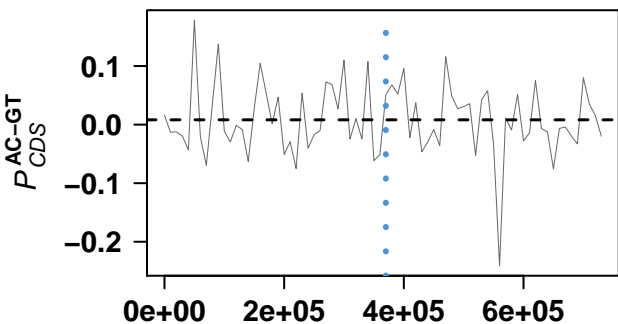
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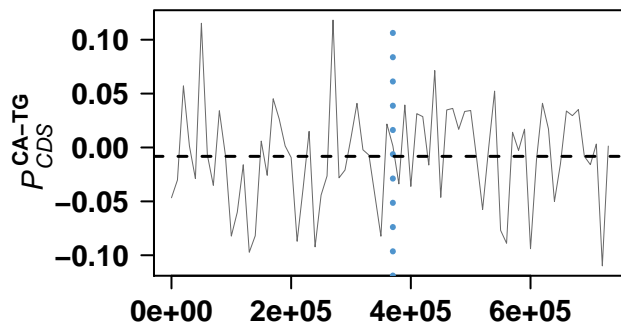
genome coordinates



genome coordinates

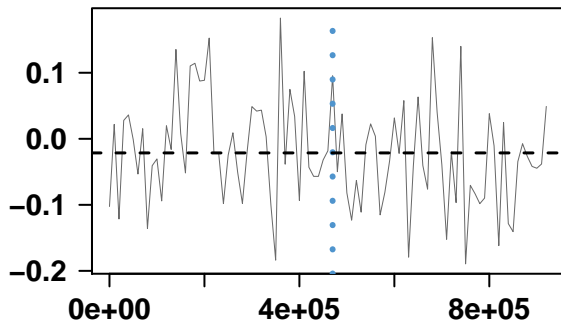


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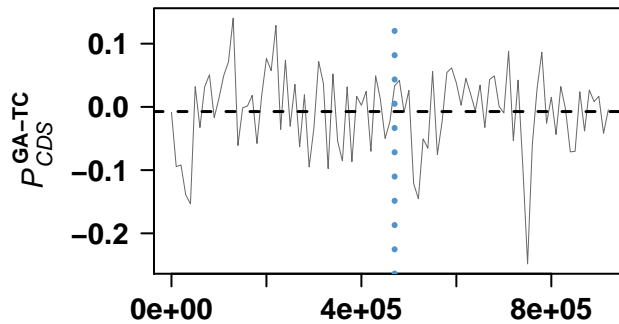


genome coordinates

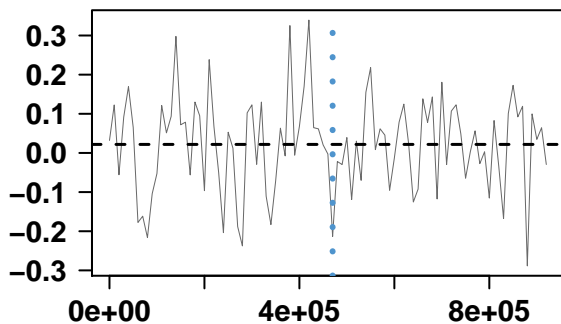
Ehrlichia chaffeensis str. Arkansas



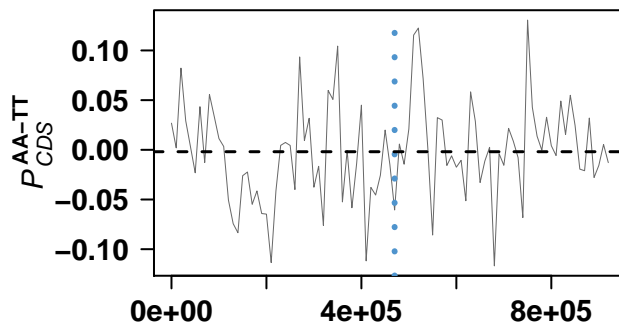
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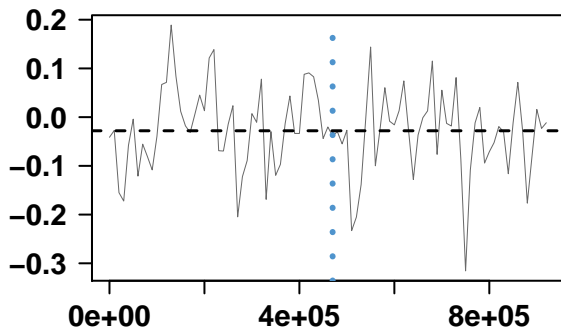
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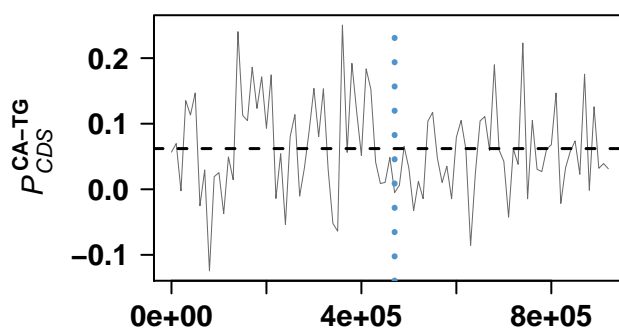
genome coordinates



genome coordinates

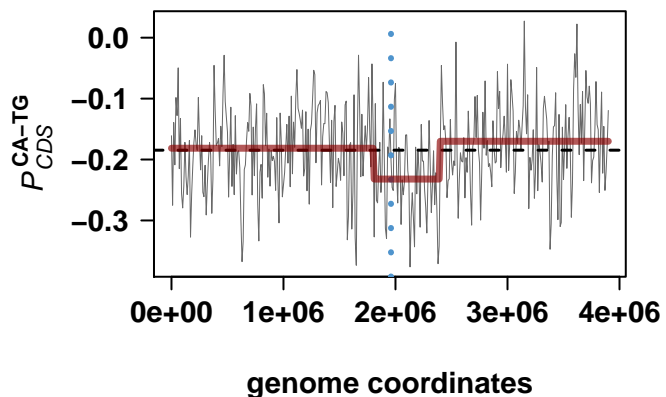
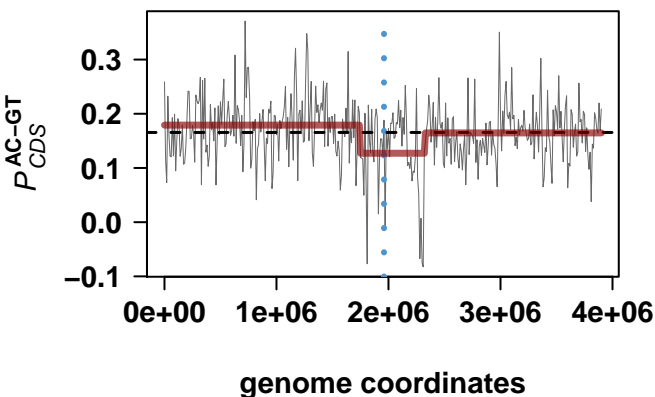
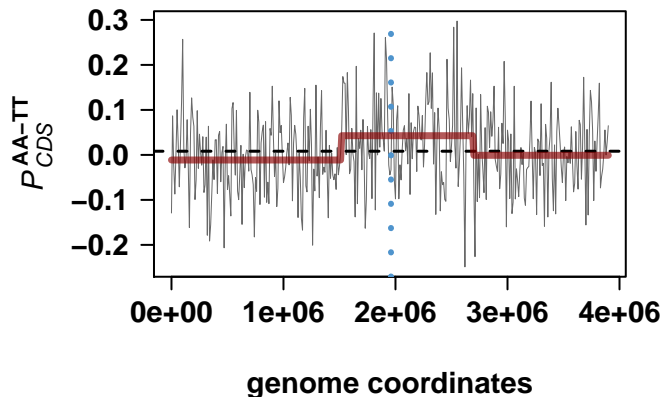
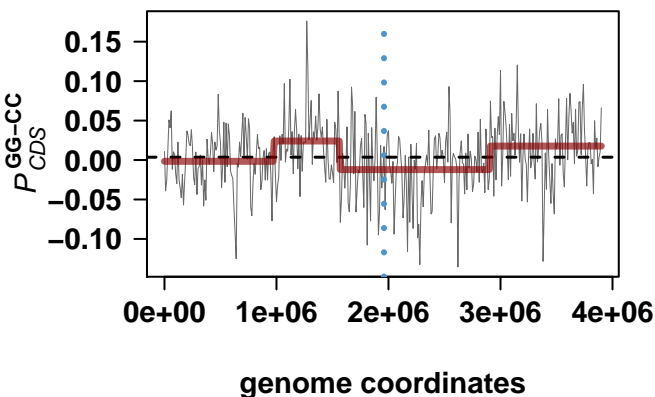
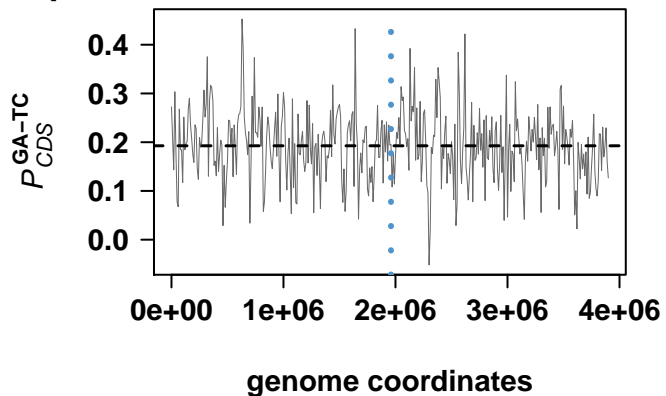
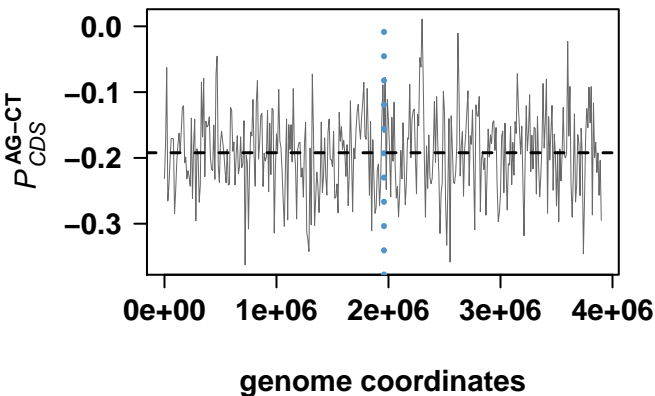


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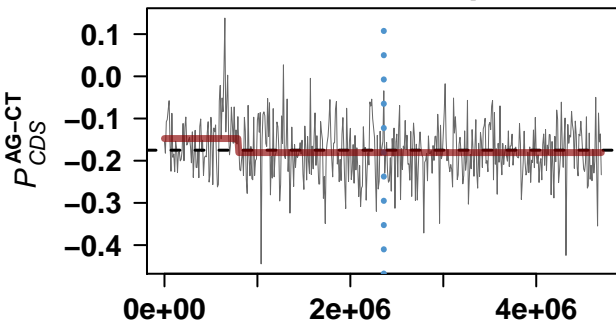


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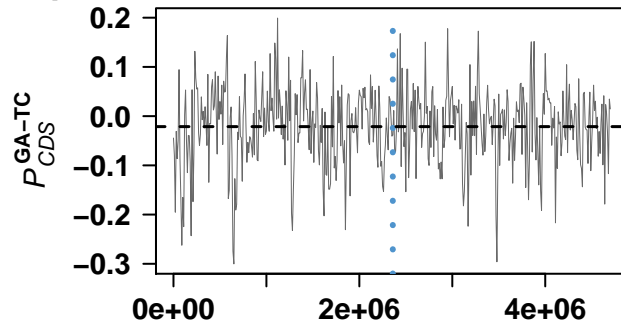
Jannaschia sp. CCS1



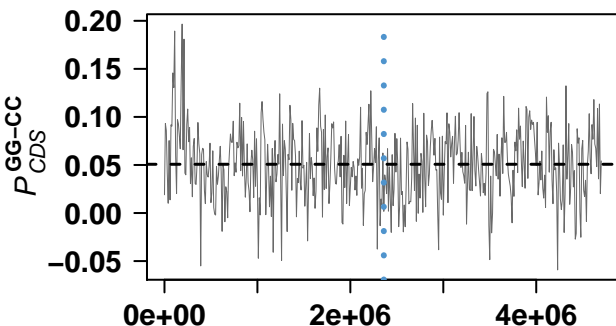
Rhodopseudomonas palustris BisB18



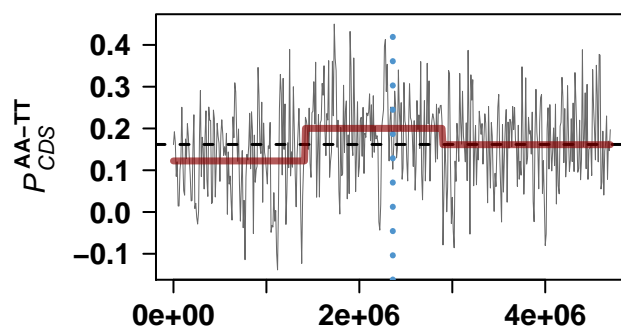
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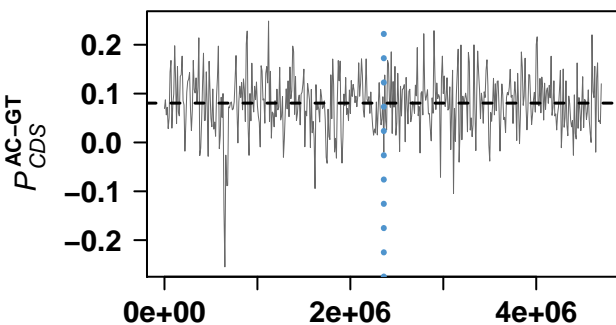
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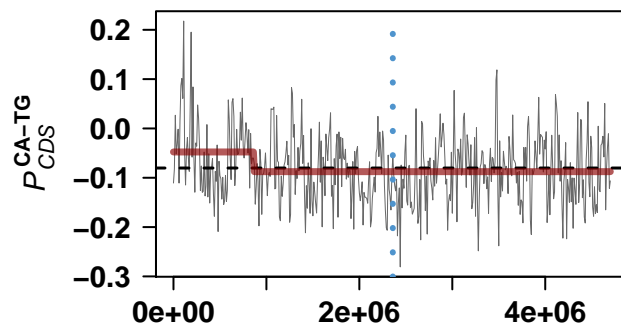
genome coordinates



genome coordinates

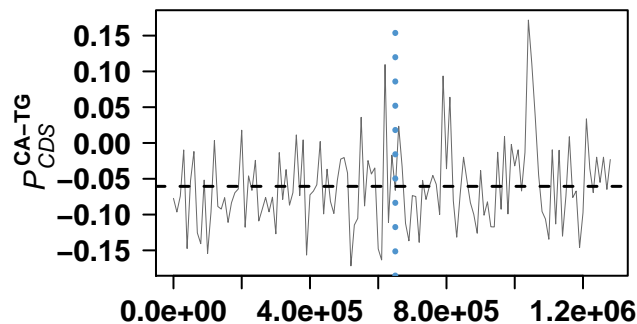
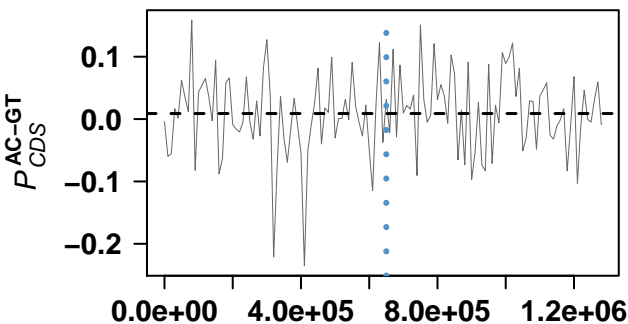
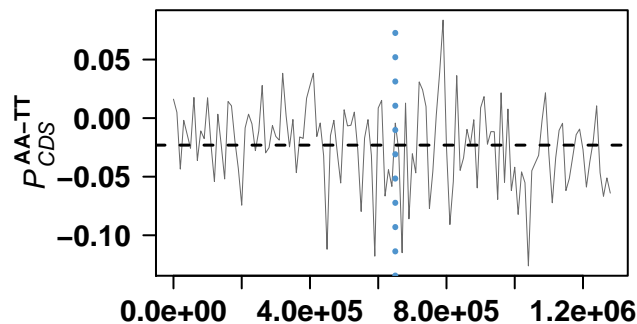
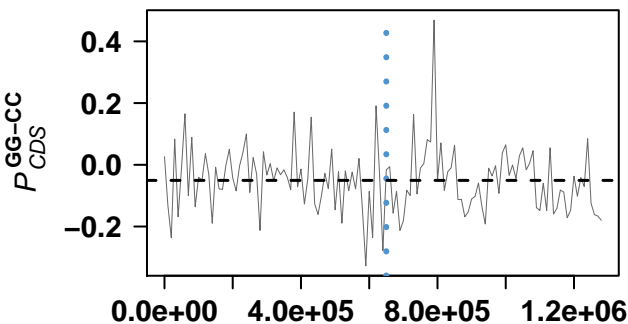
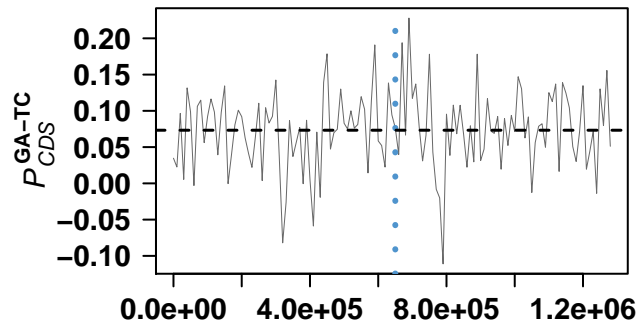
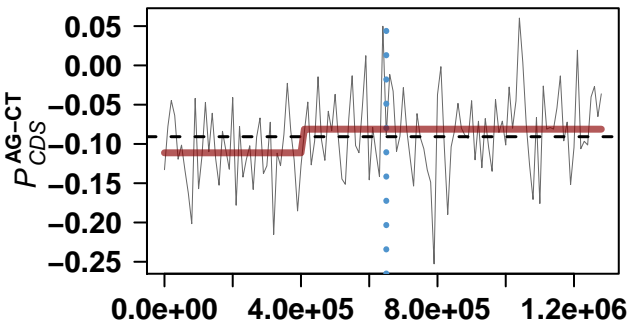


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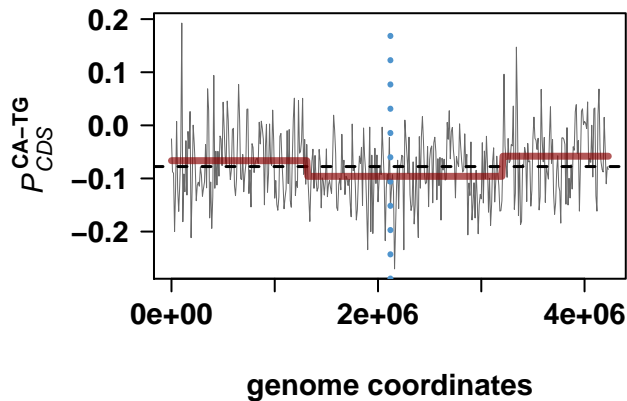
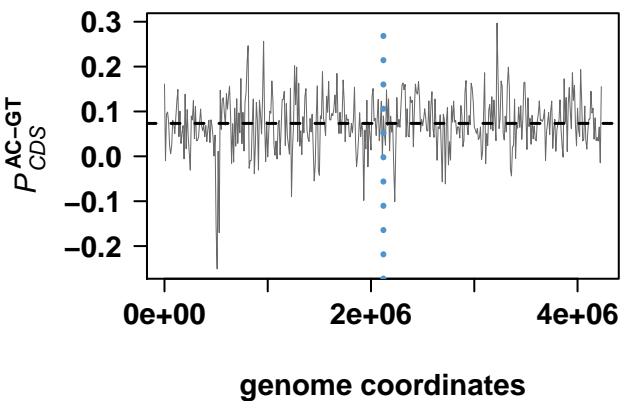
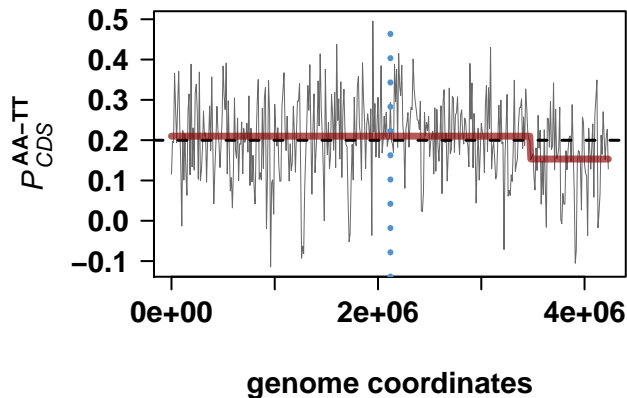
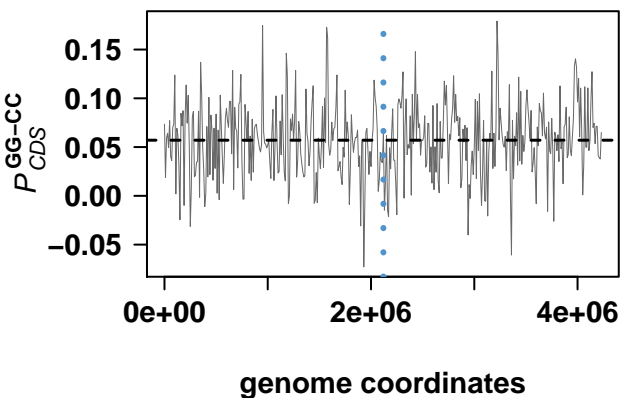
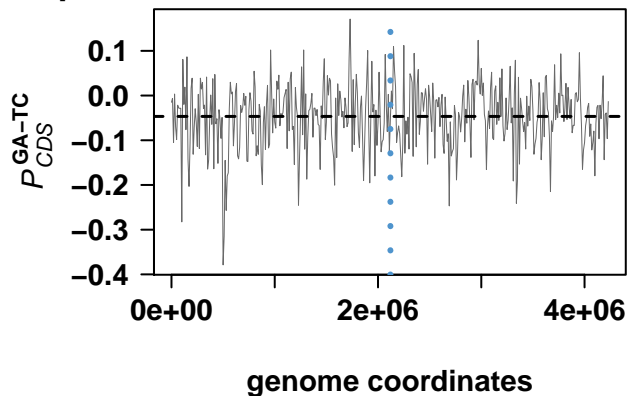
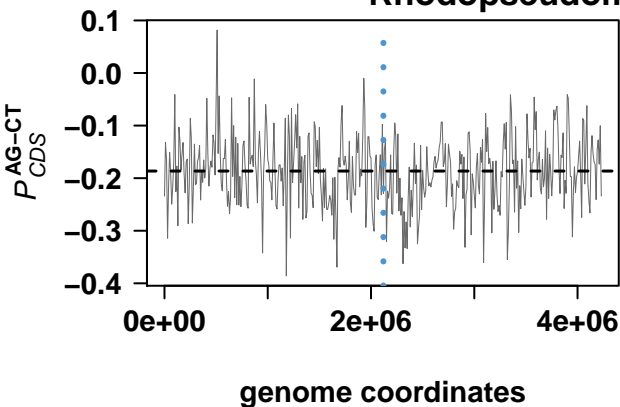


genome coordinates

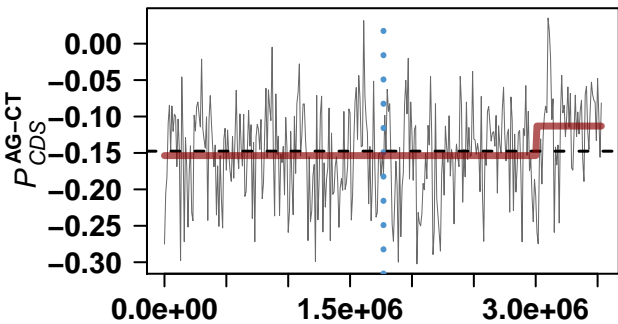
Rickettsia bellii RML369-C



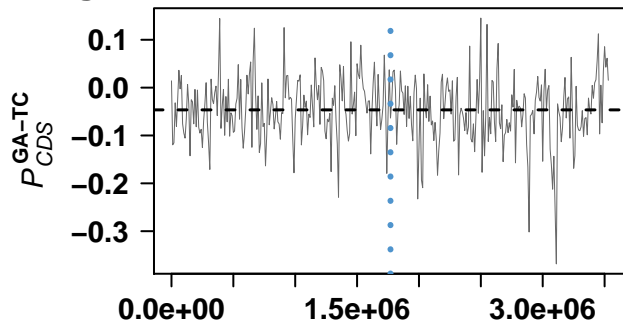
Rhodopseudomonas palustris BisB5



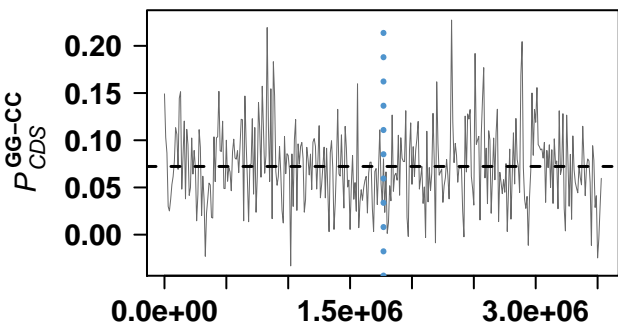
Nitrobacter hamburgensis X14



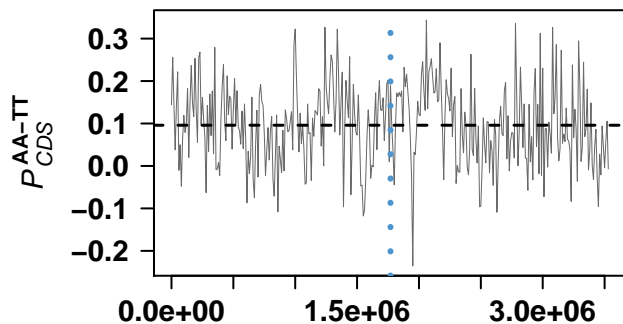
genome coordinates



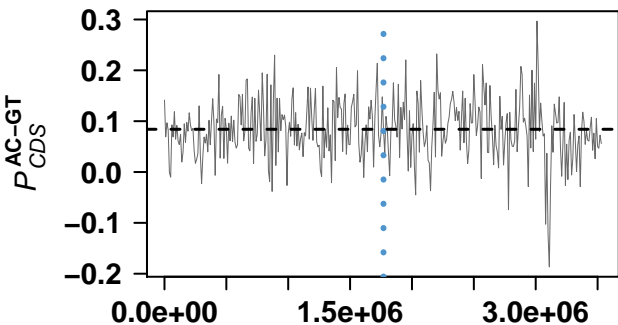
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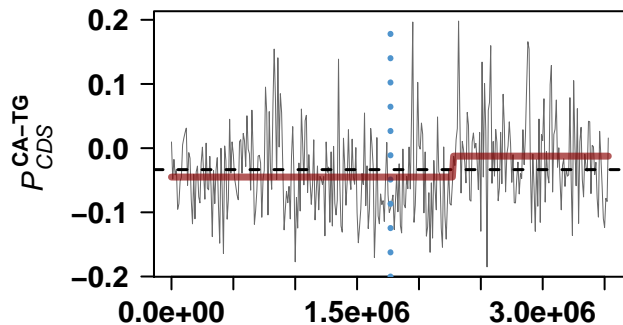
genome coordinates



genome coordinates

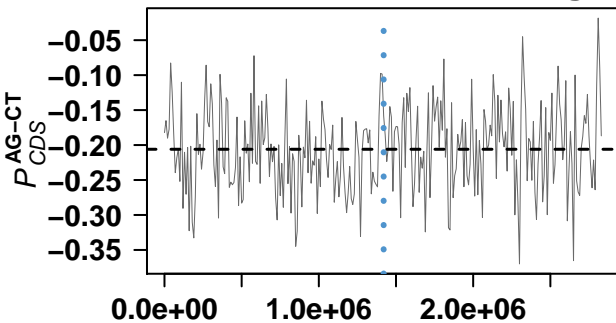


genome coordinates

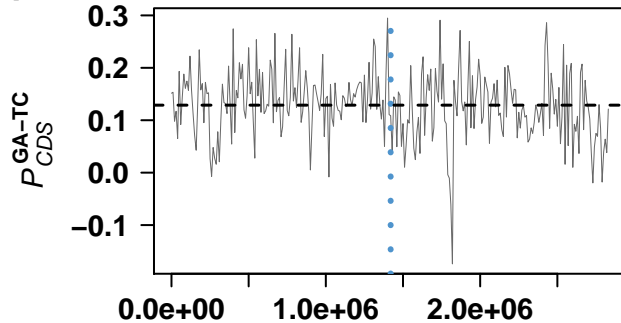


genome coordinates

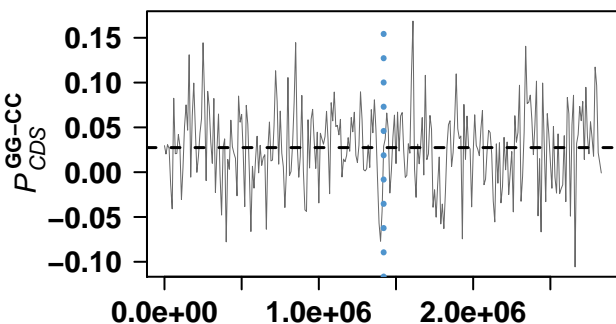
Ruegeria sp. TM1040



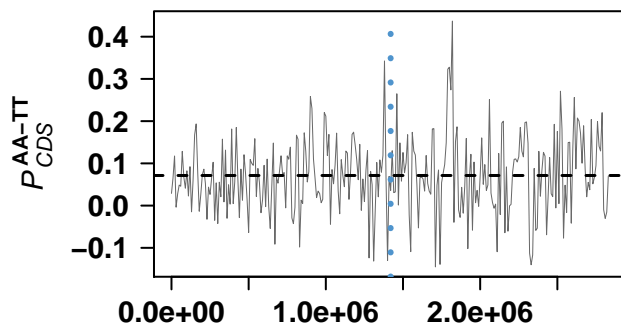
genome coordinates



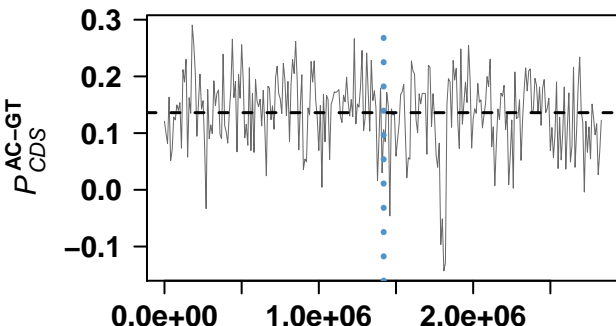
genome coordinates



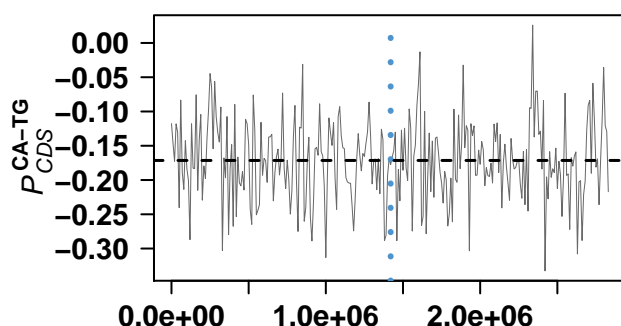
genome coordinates



genome coordinates

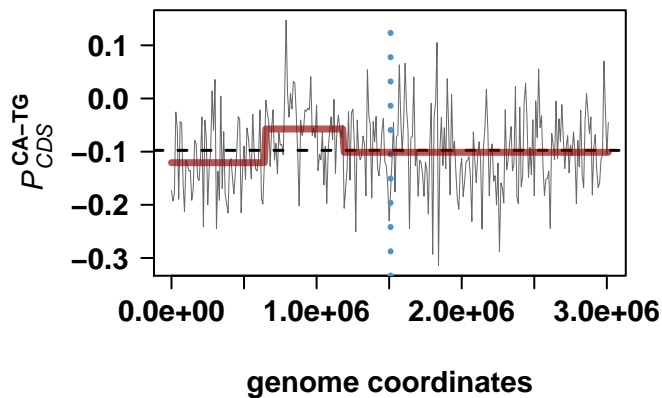
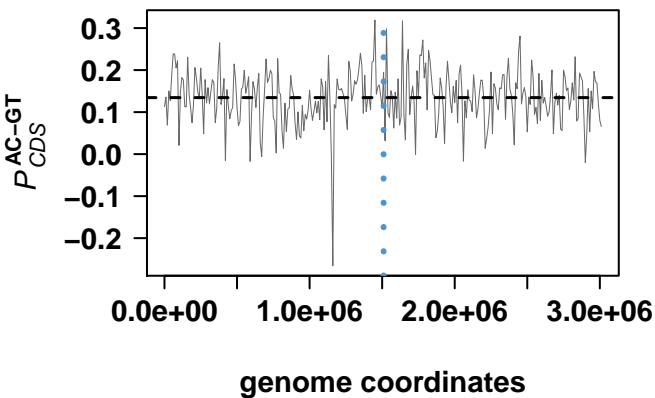
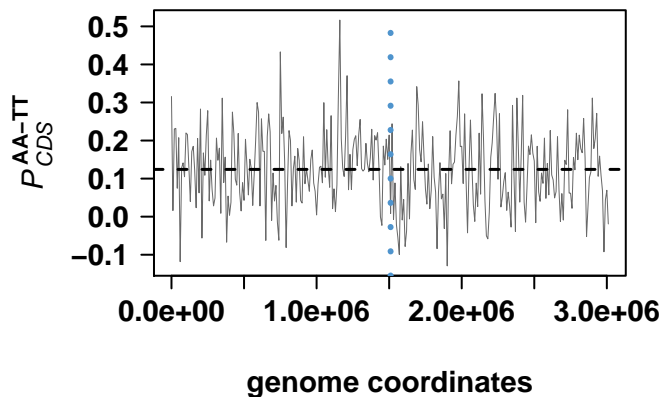
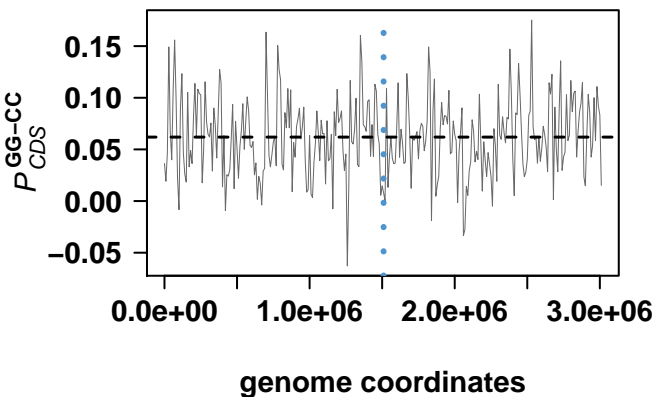
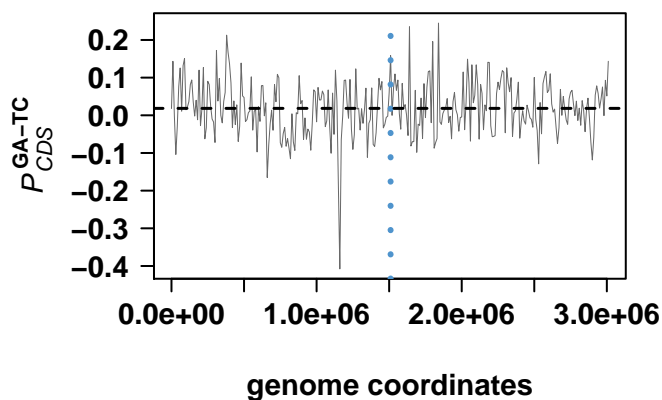
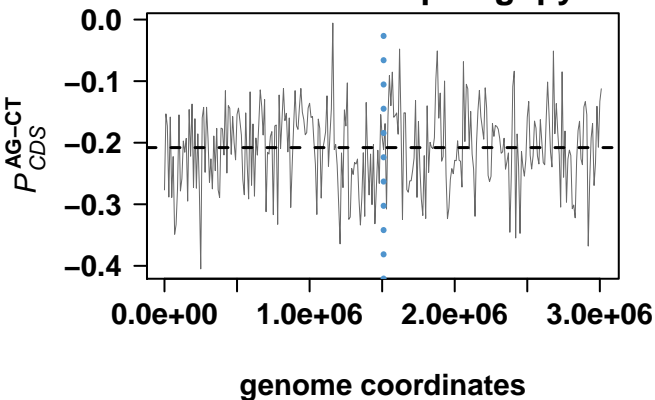


genome coordinates

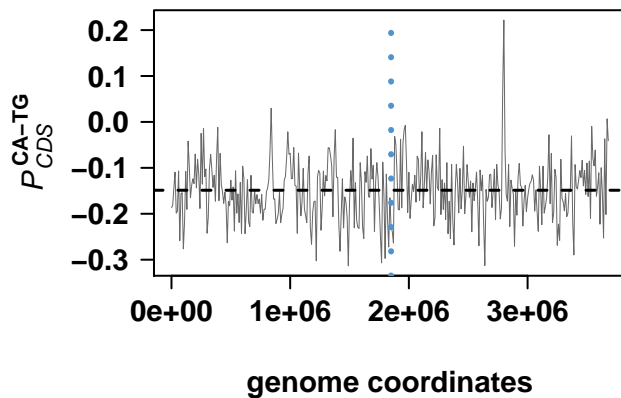
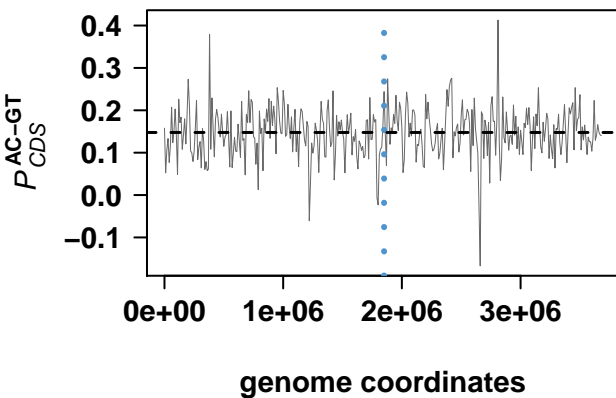
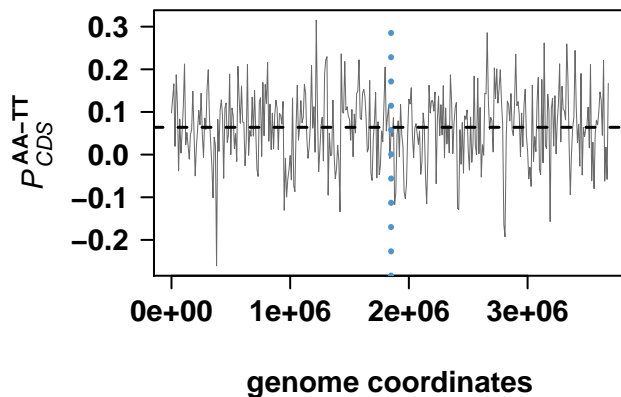
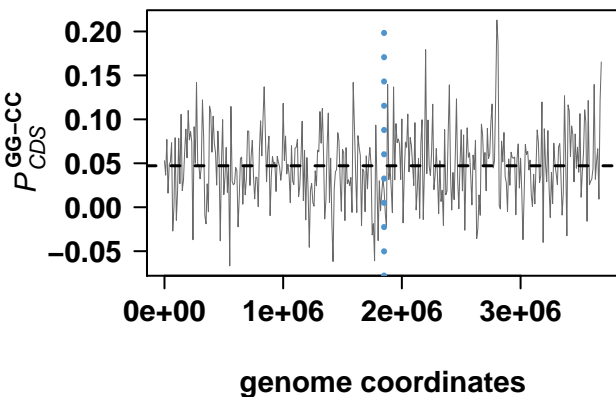
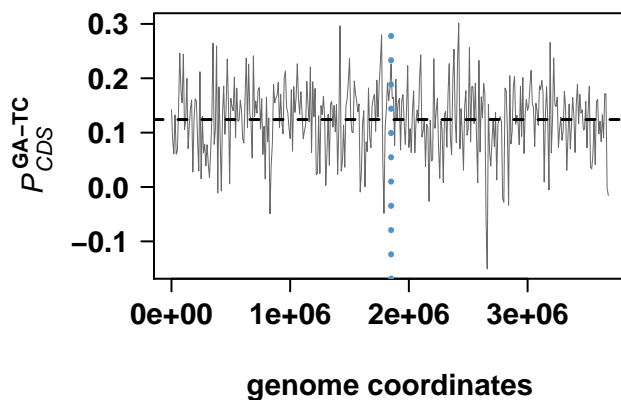
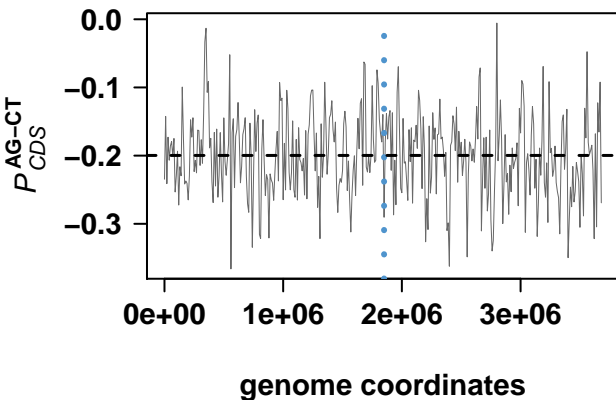


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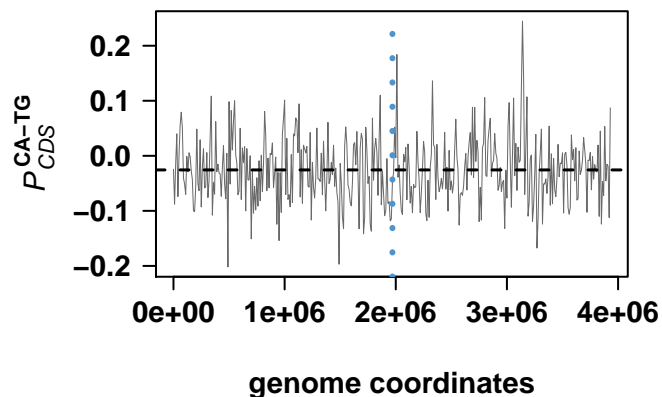
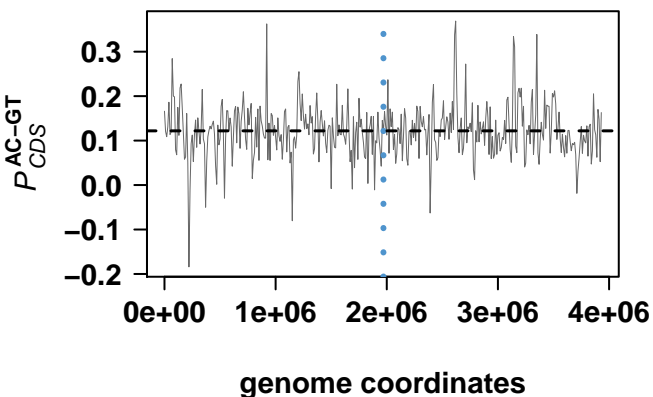
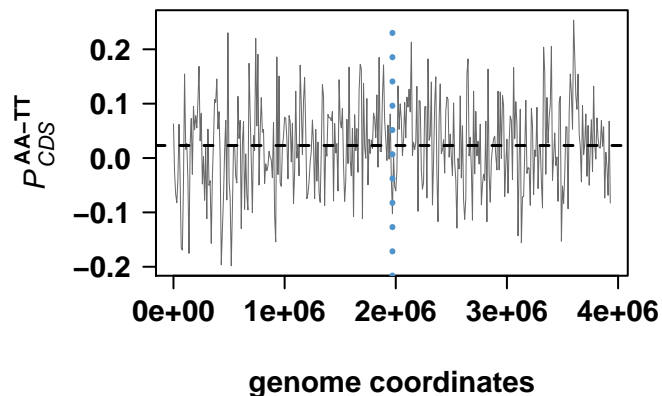
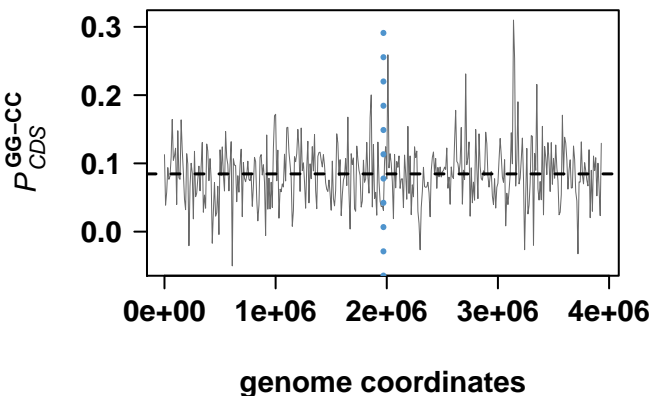
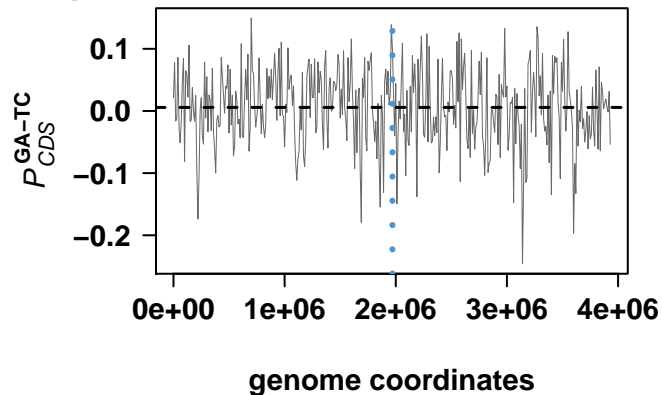
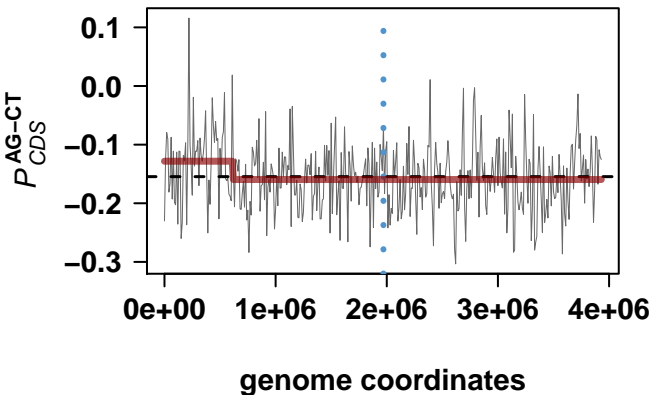
Spingopyxis alaskensis RB2256



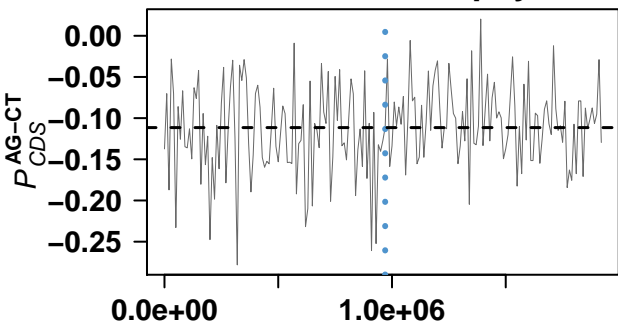
Roseobacter denitrificans OCh 114



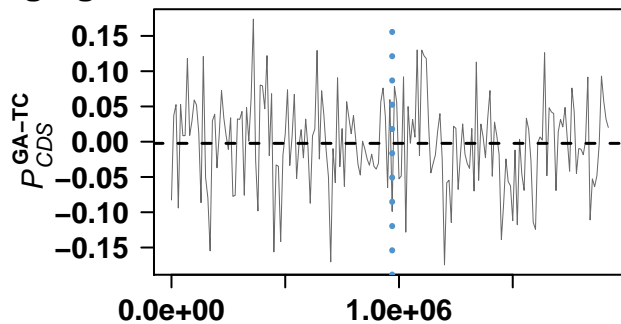
Chelativorans sp. BNC1



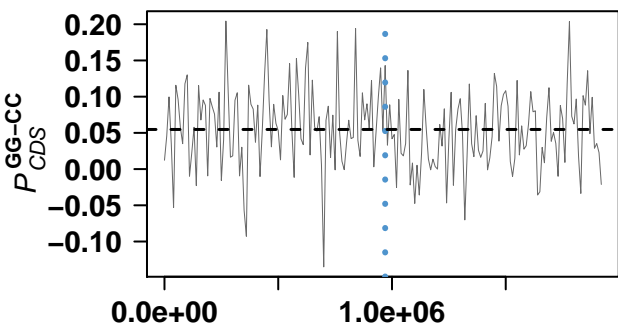
Porphyromonas gingivalis W83



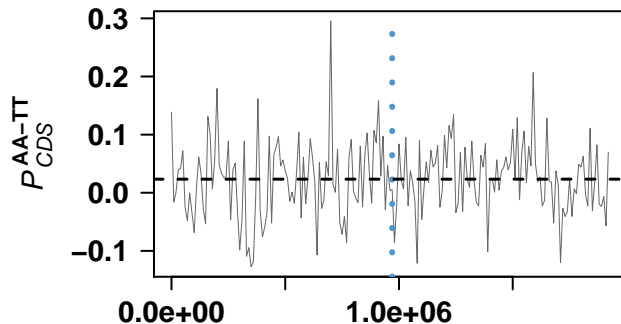
genome coordinates



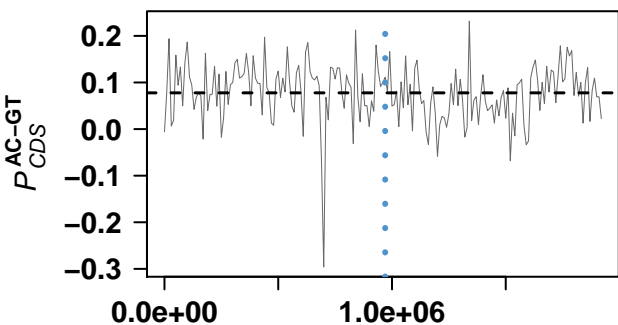
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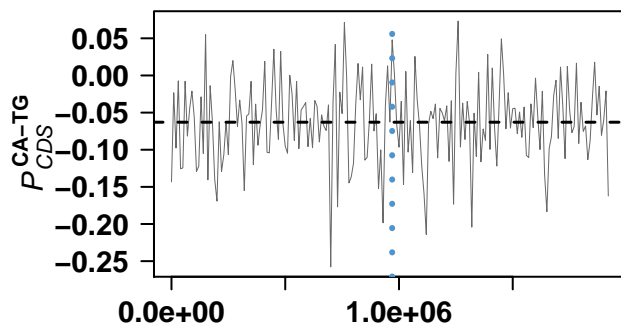
genome coordinates



genome coordinates

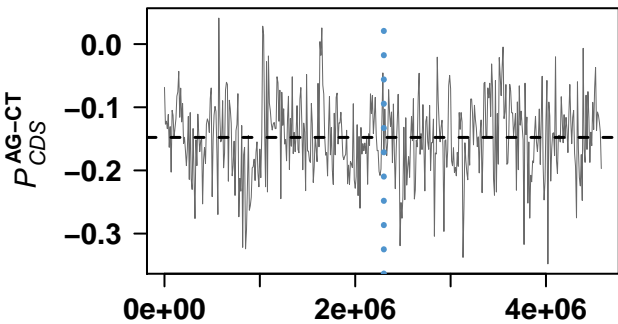


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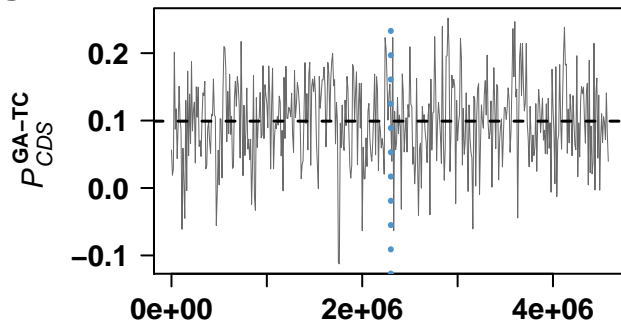


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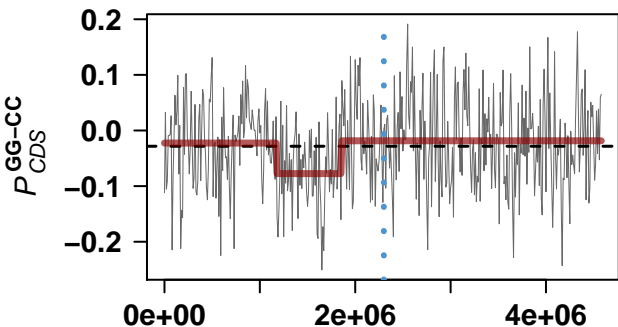
Bacteroides fragilis NCTC 9343



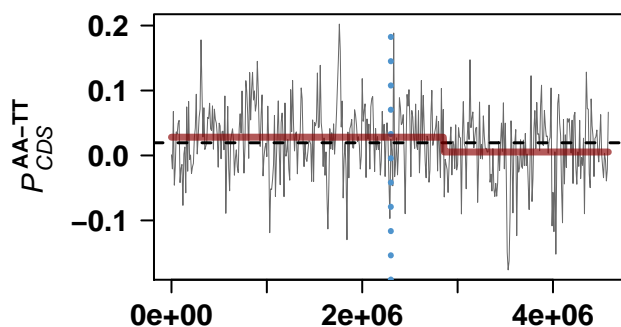
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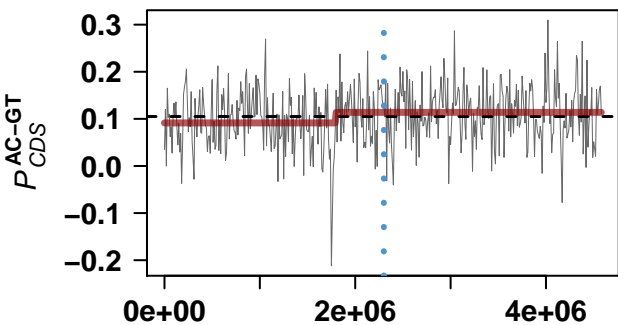
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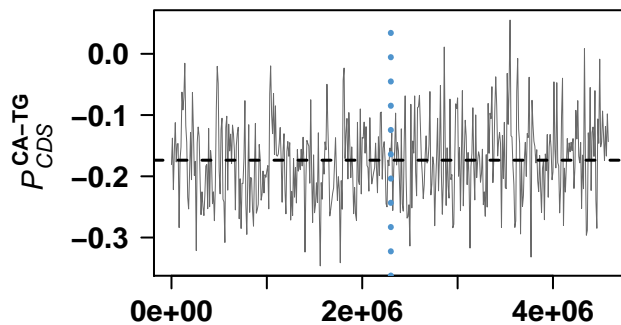
genome coordinates



genome coordinates

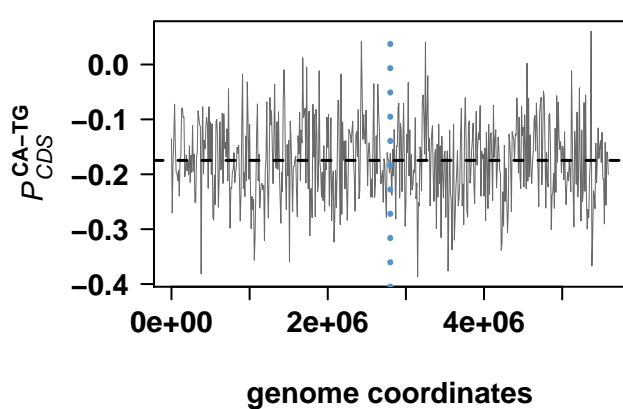
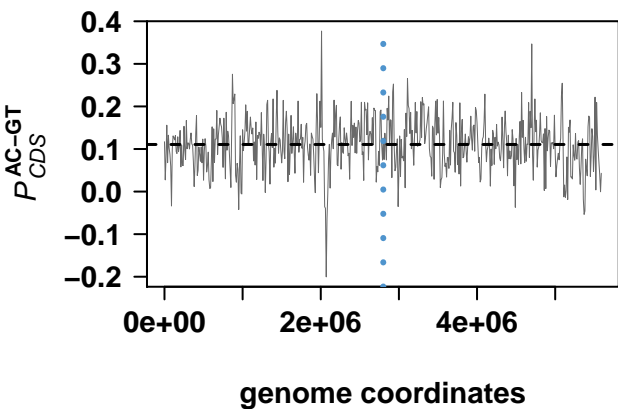
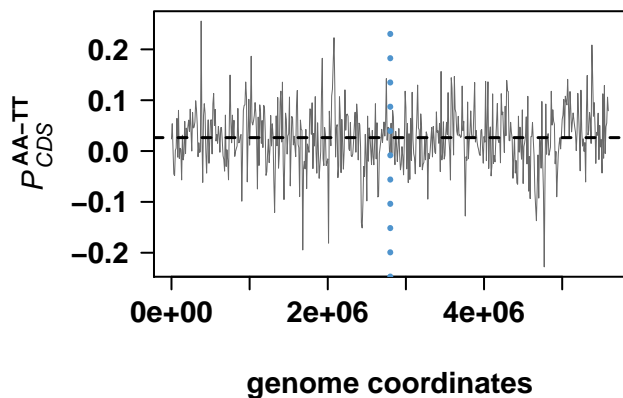
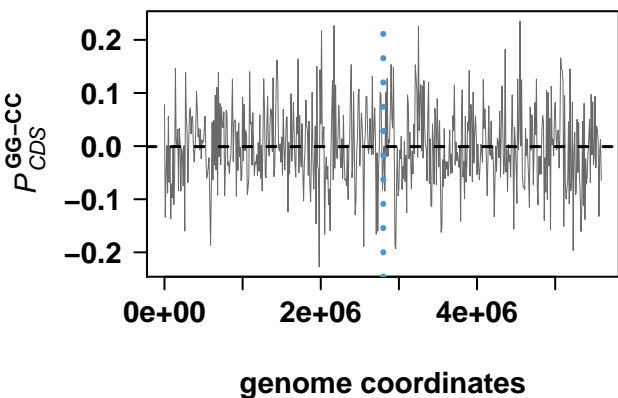
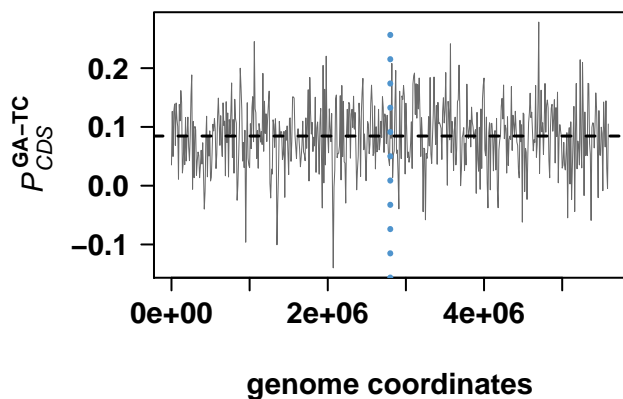
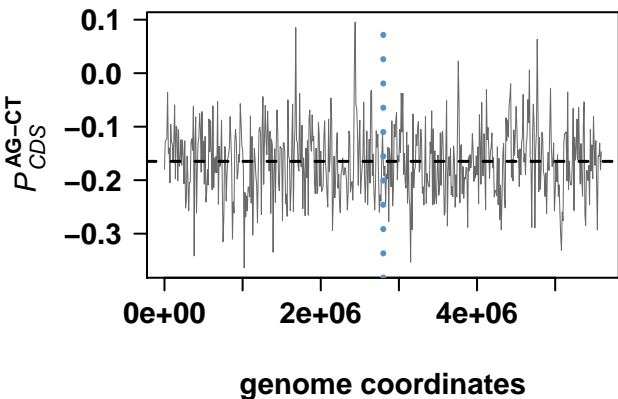


genome coordinates

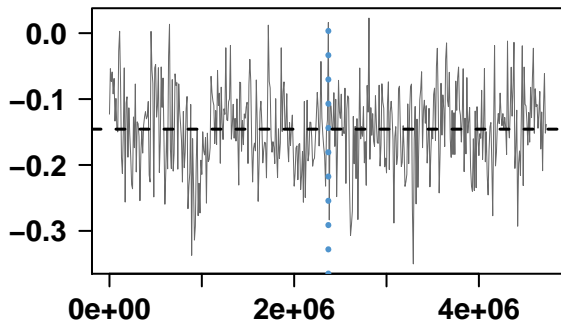


genome coordinates

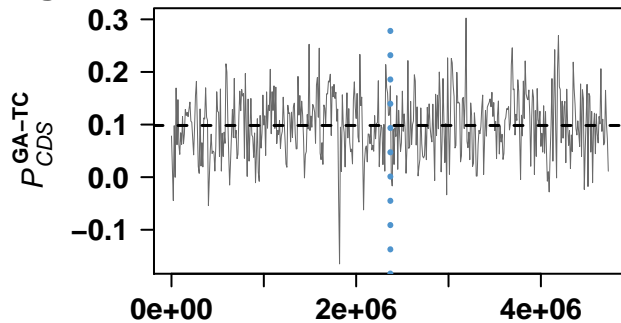
Bacteroides thetaiotaomicron VPI-5482



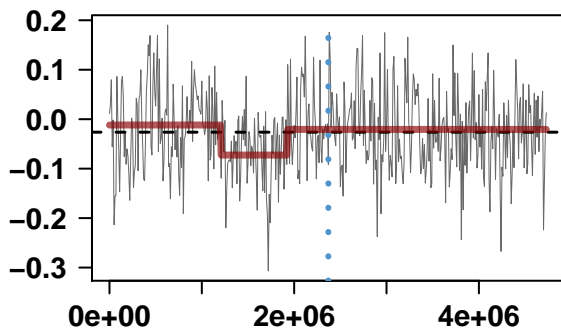
Bacteroides fragilis YCH46



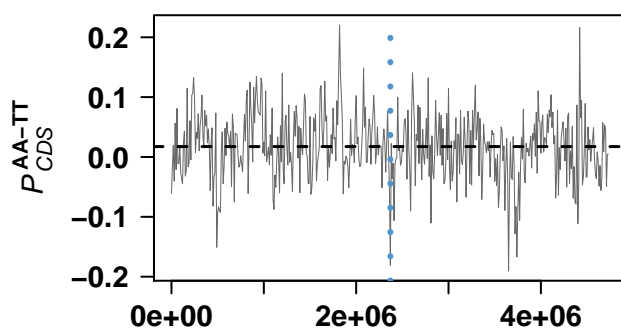
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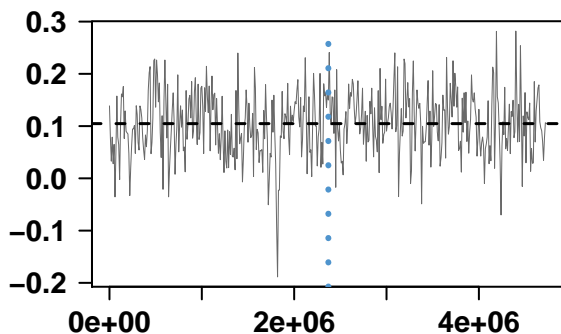
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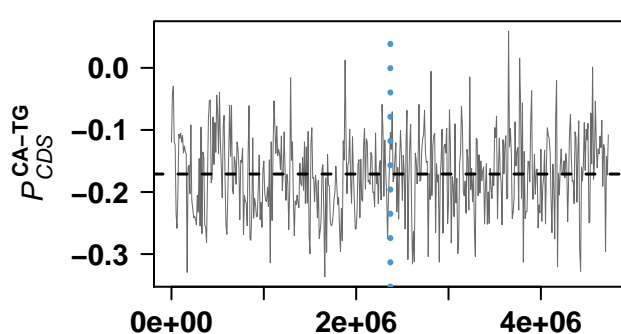
genome coordinates



genome coordinates

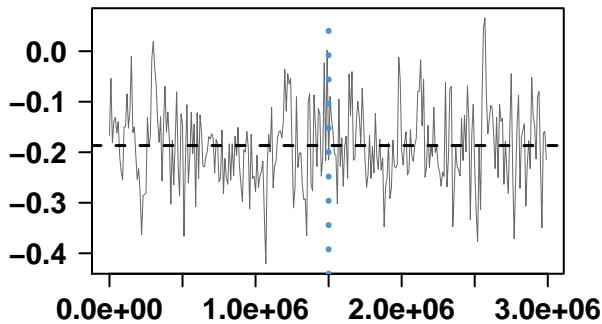


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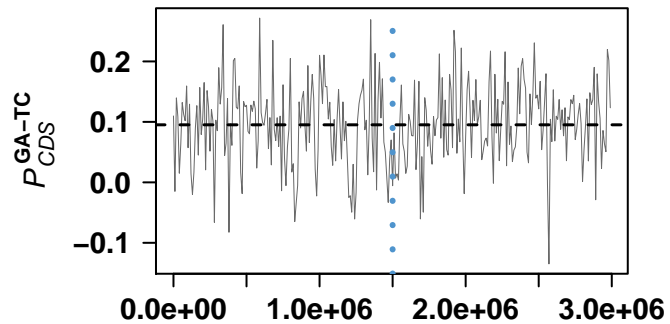


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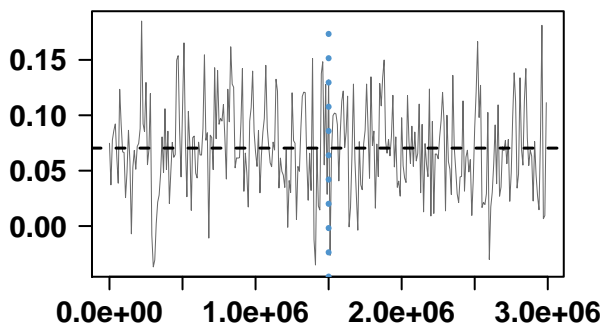
Salinibacter ruber DSM 13855



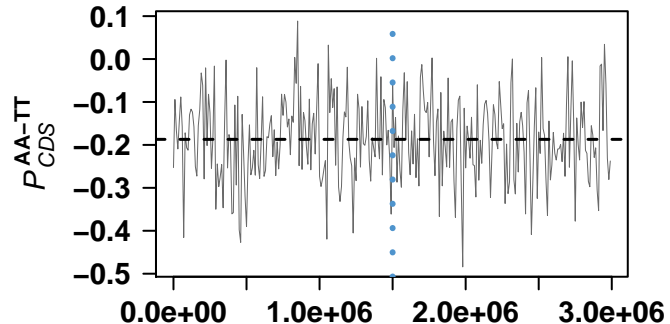
genome coordinates



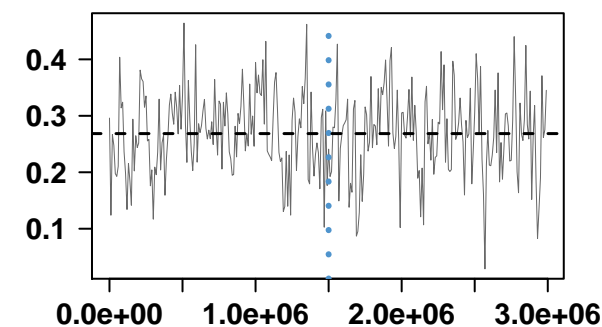
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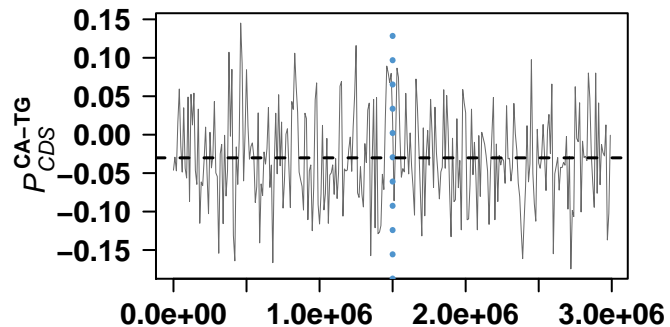
genome coordinates



genome coordinates

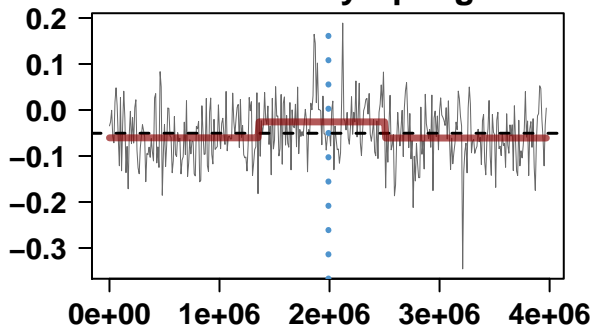


genome coordinates

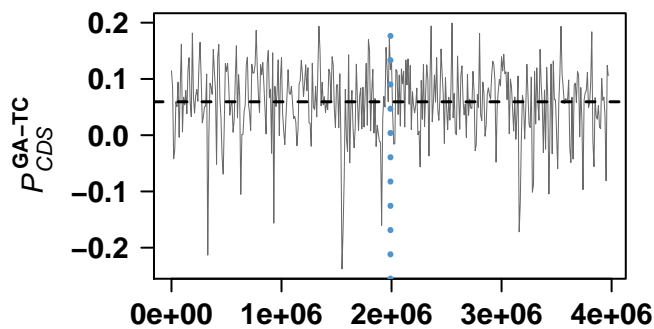


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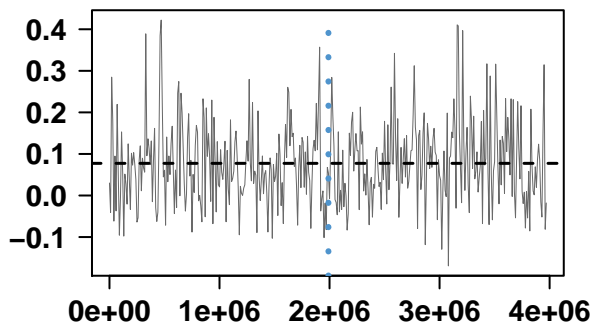
Cytophaga hutchinsonii ATCC 33406



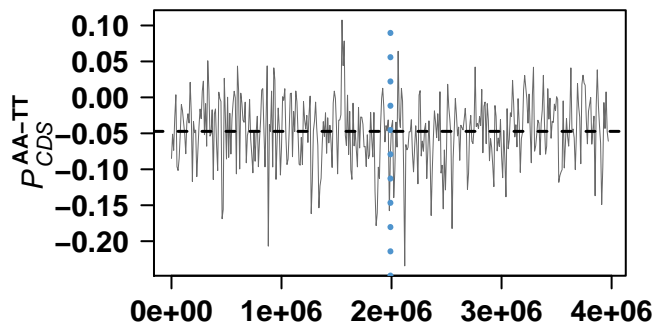
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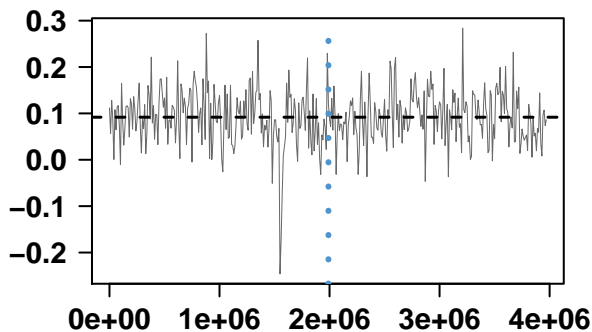
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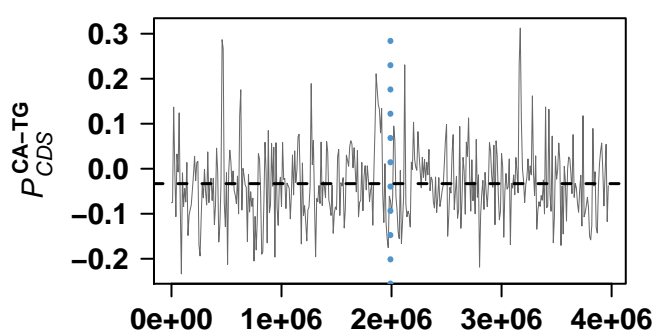
genome coordinates



genome coordinates

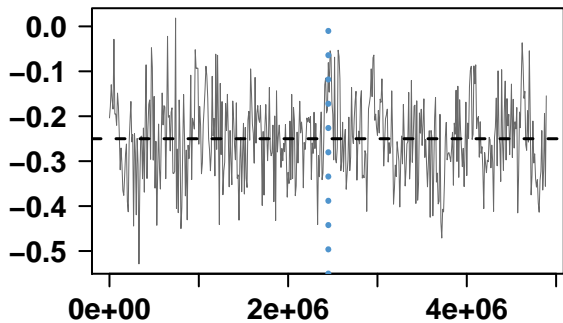


genome coordinates

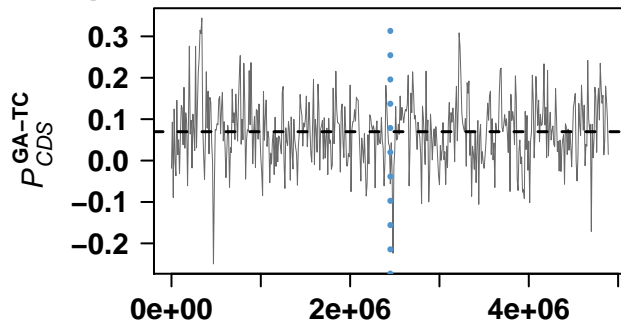


genome coordinates

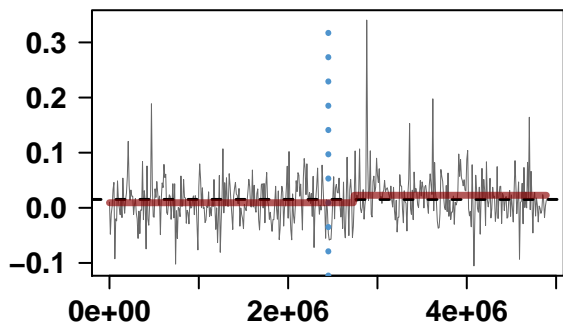
Bordetella bronchiseptica RB50



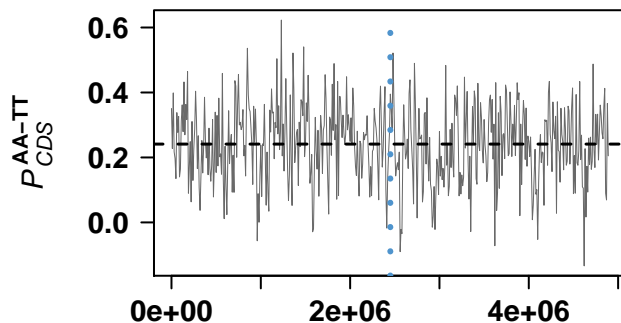
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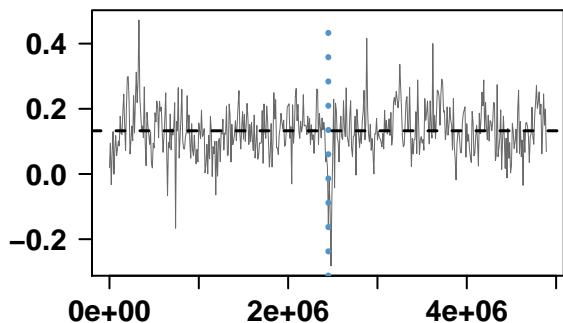
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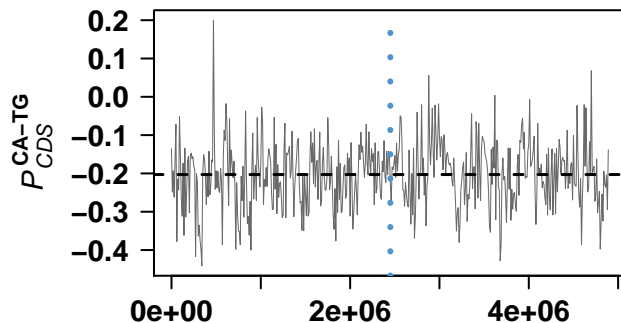
genome coordinates



genome coordinates

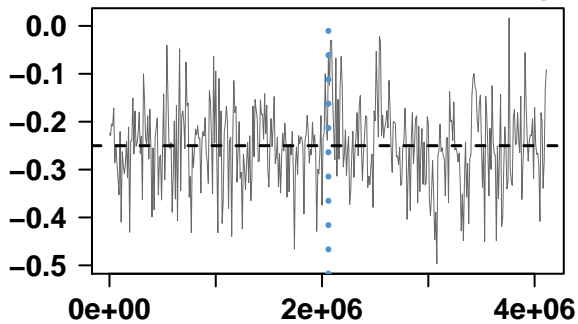


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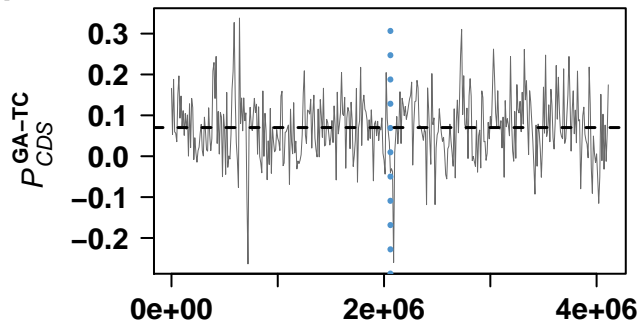


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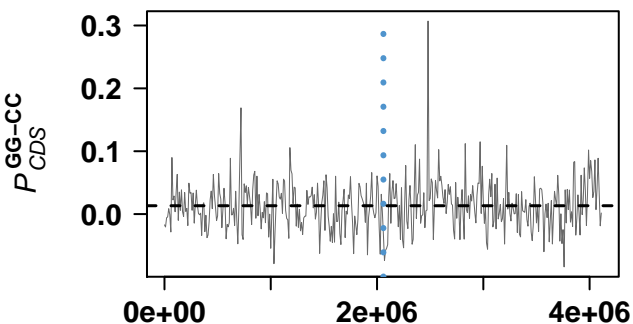
Bordetella parapertussis 12822



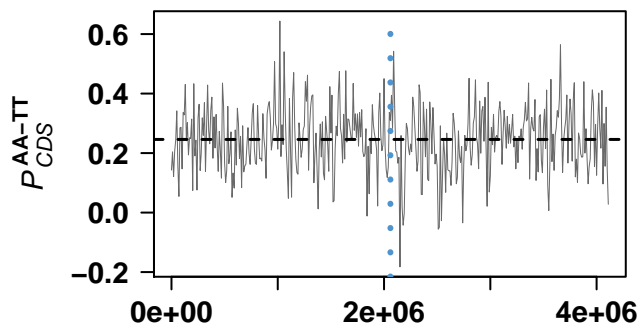
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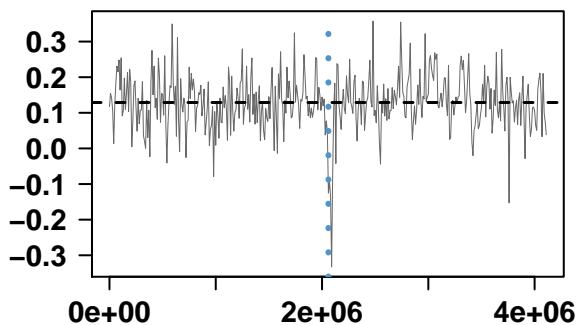
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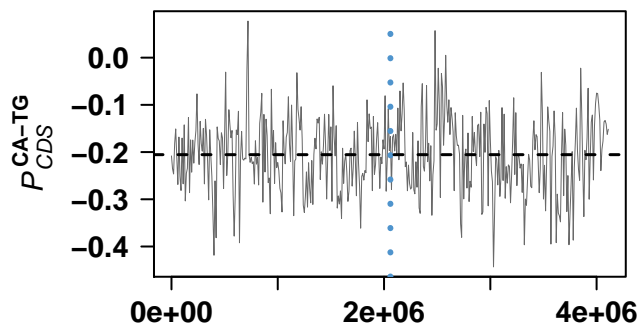
genome coordinates



genome coordinates

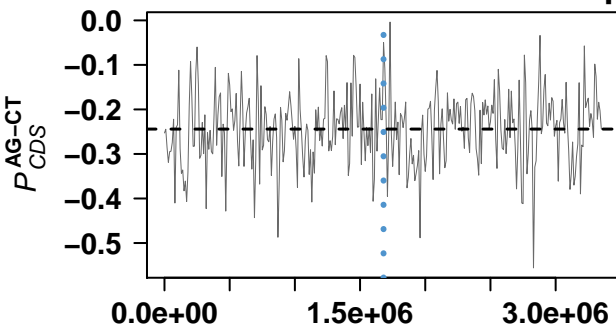


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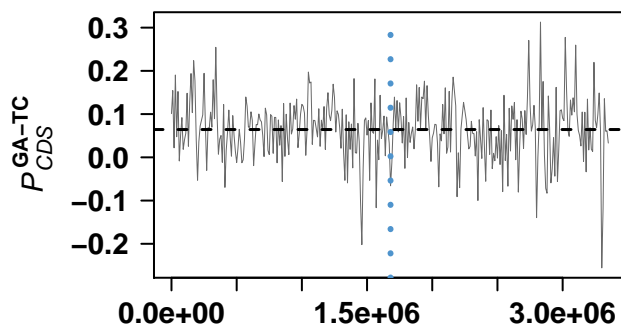


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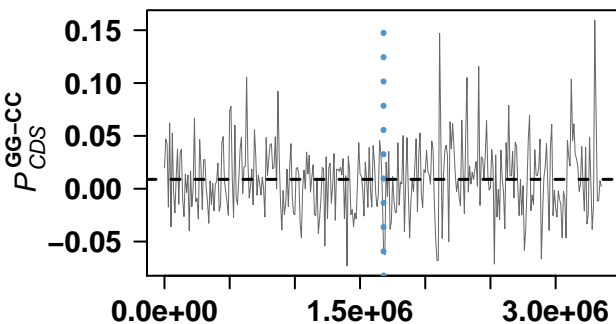
Bordetella pertussis Tohama I



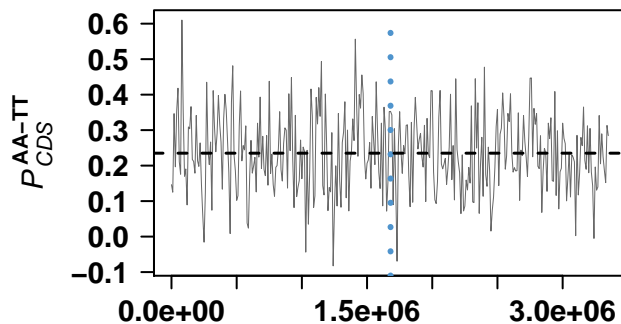
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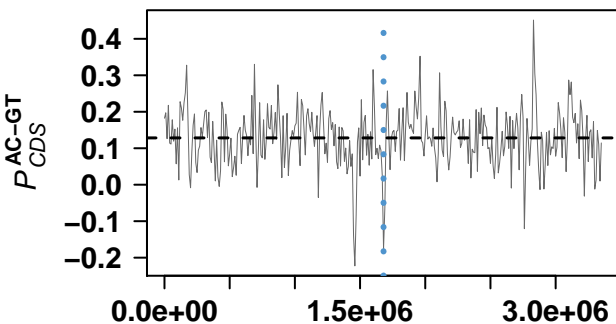
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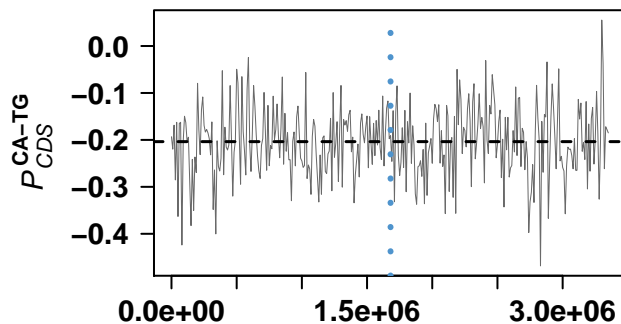
genome coordinates



genome coordinates

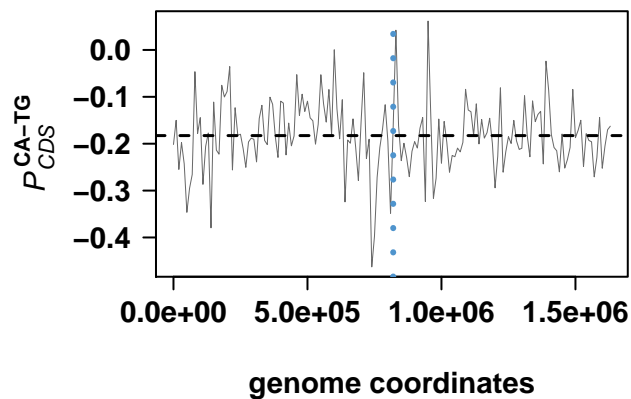
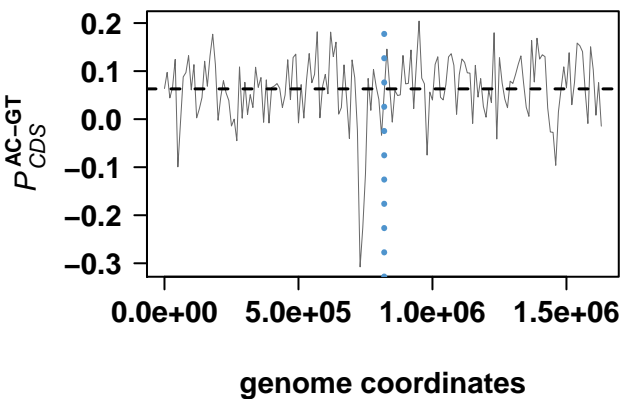
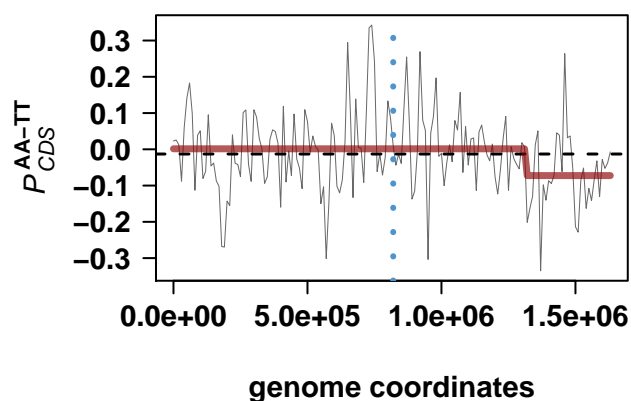
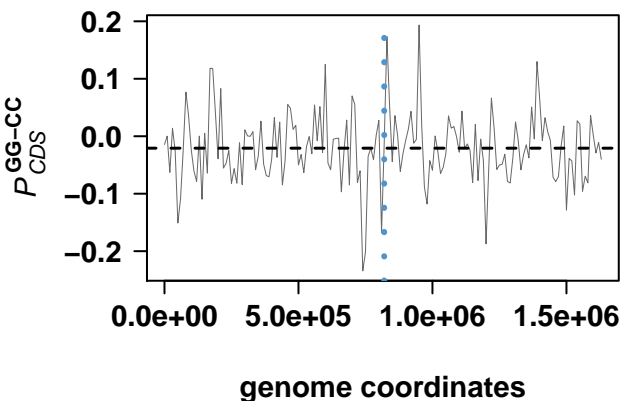
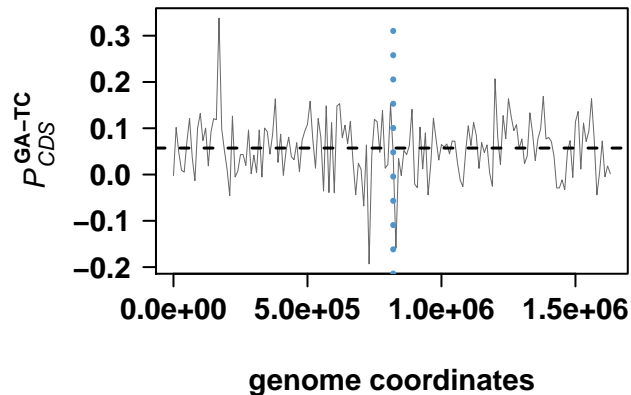
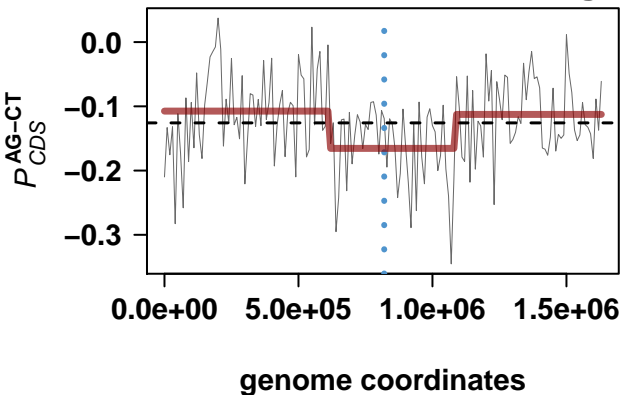


genome coordinates

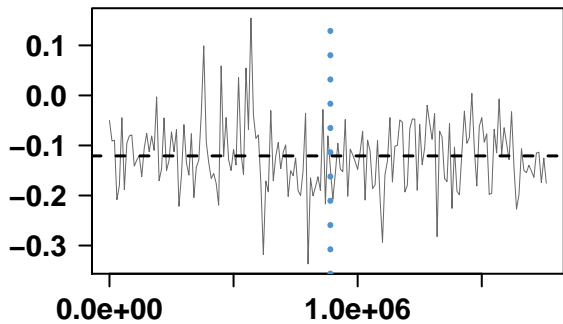


genome coordinates

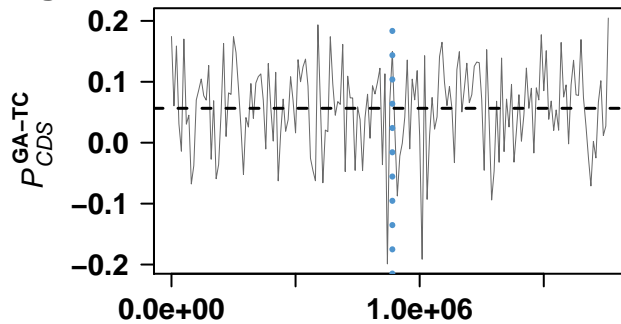
Neisseria gonorrhoeae FA 1090



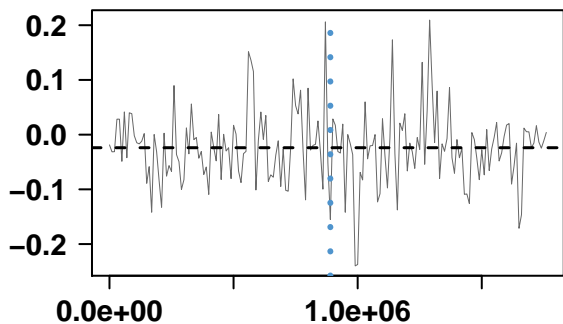
Neisseria meningitidis MC58



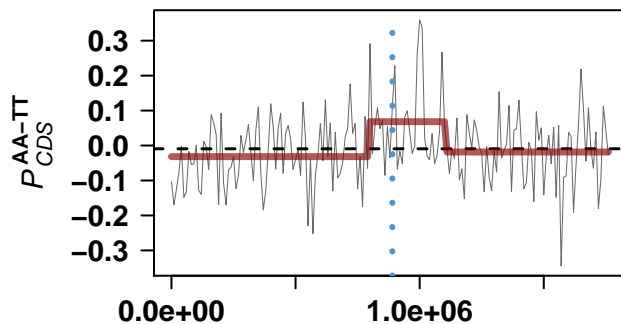
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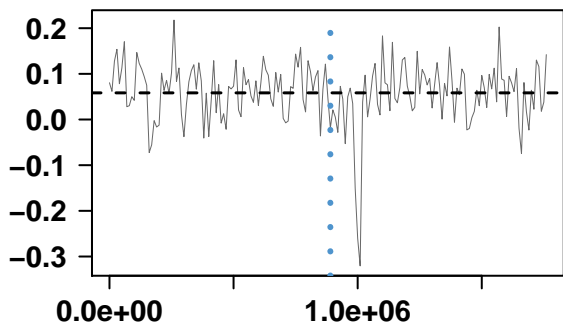
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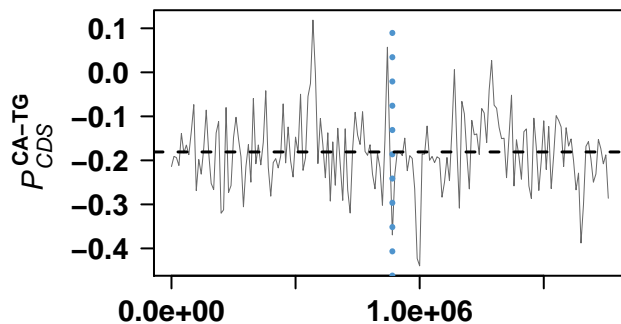
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genome coordinates

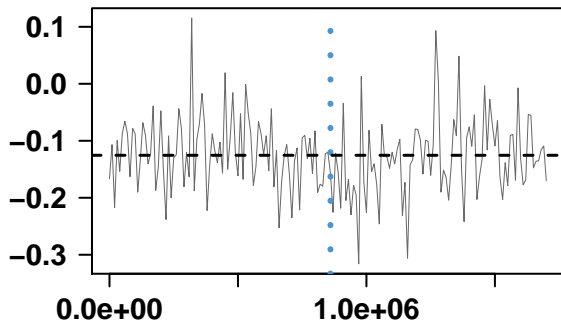


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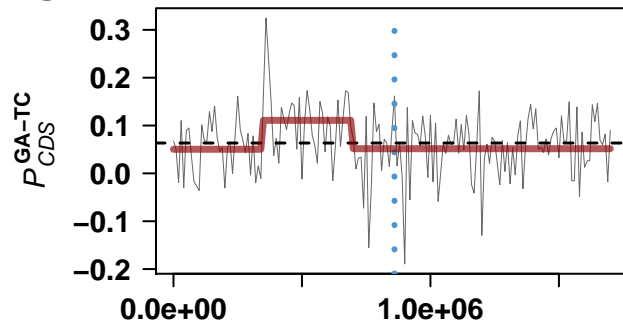


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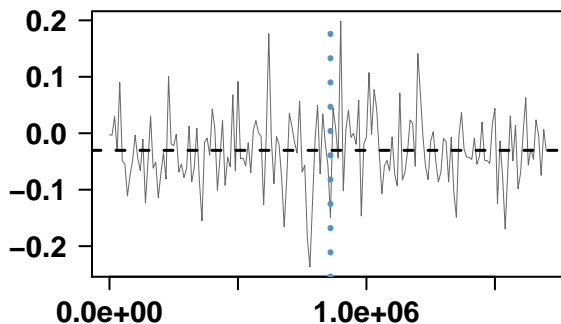
Neisseria meningitidis Z2491



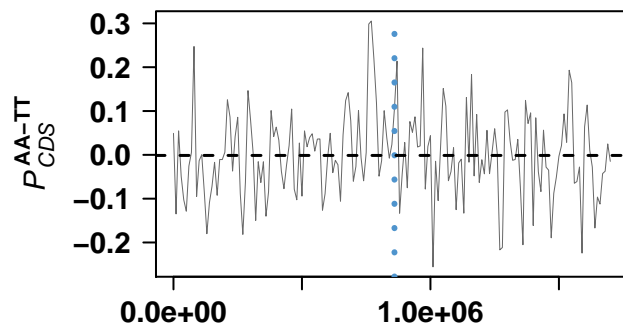
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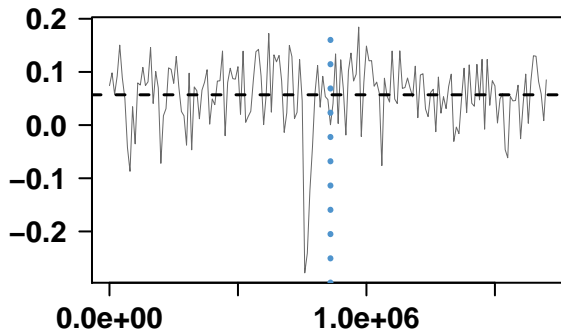
genome coordinates



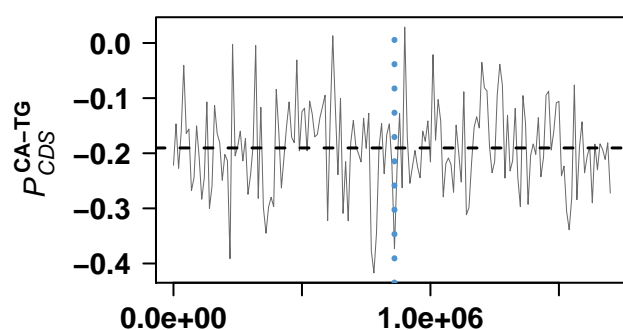
genome coordinates



genome coordinates

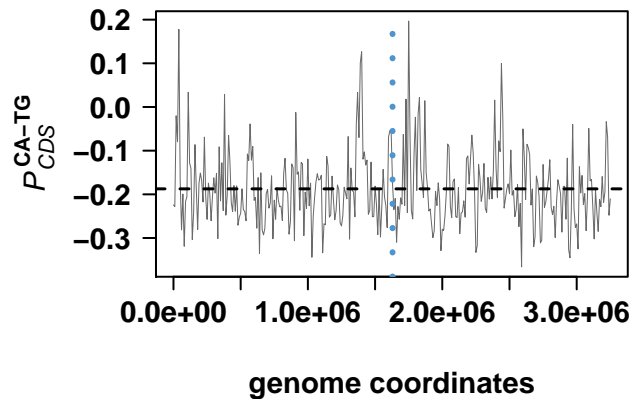
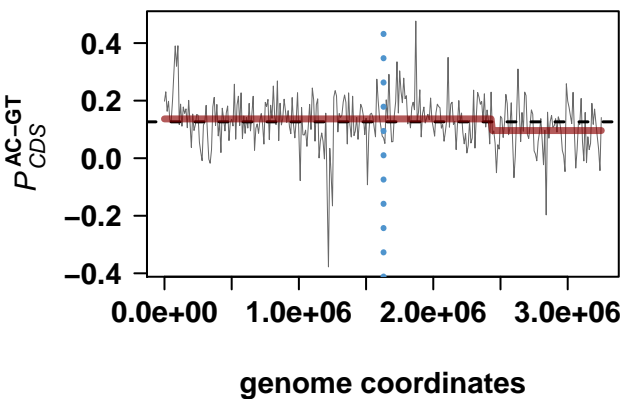
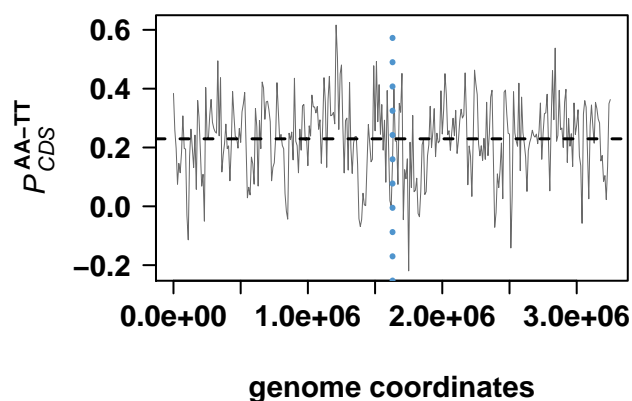
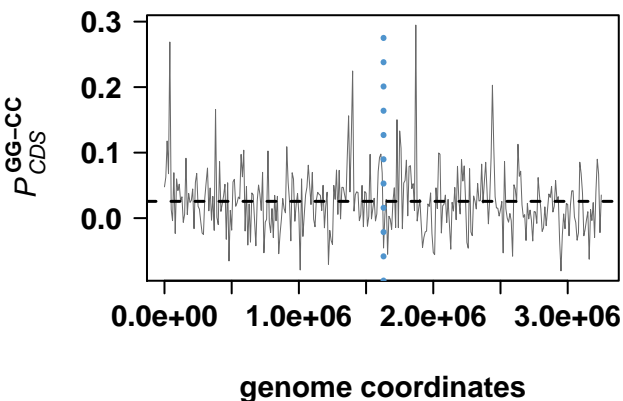
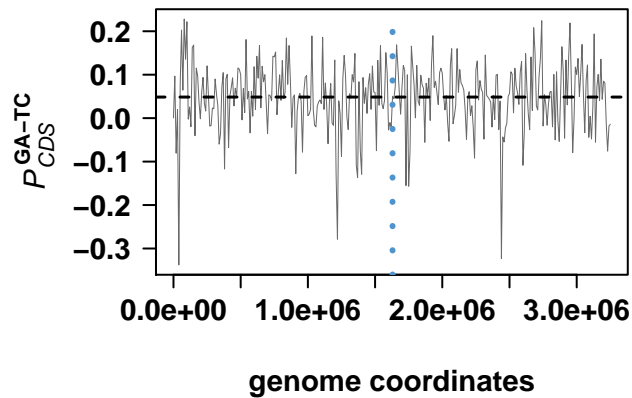
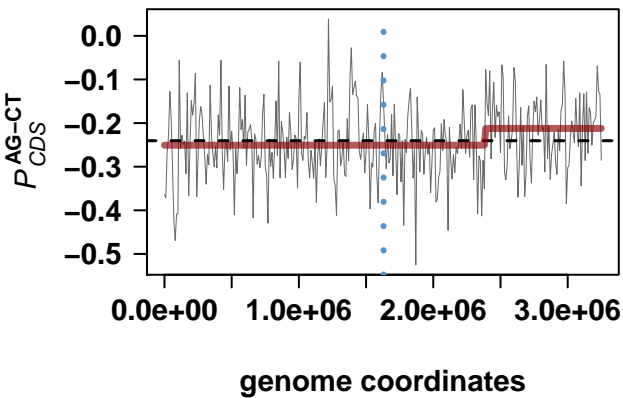


genome coordinates

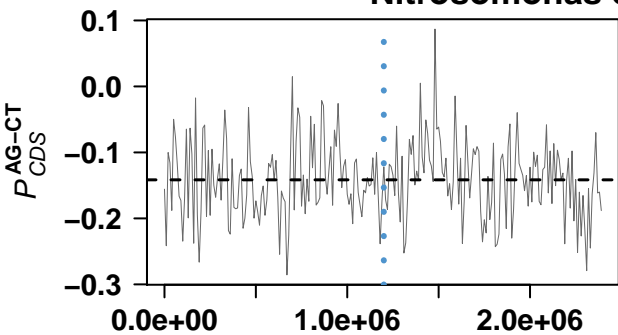


genome coordinates

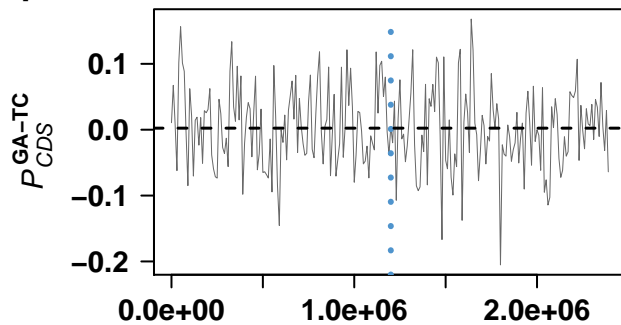
Ralstonia solanacearum GMI1000



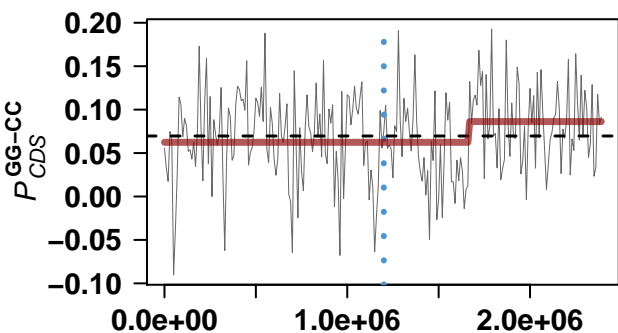
Nitrosomonas europaea ATCC 19718



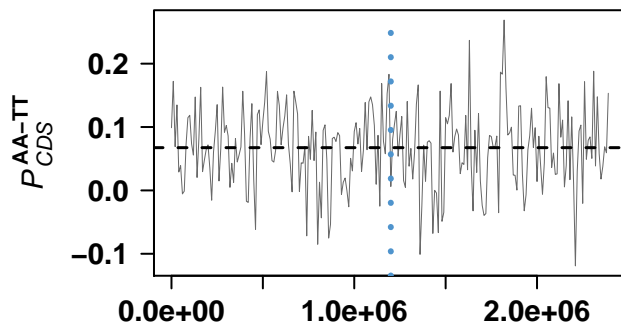
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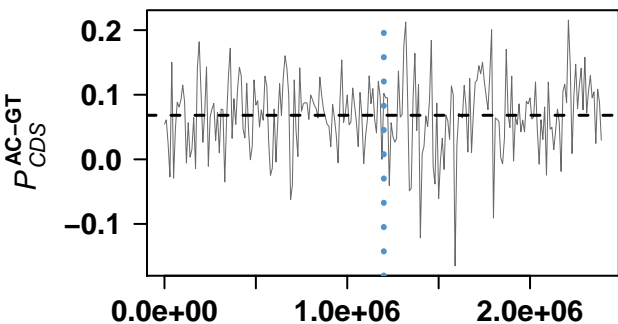
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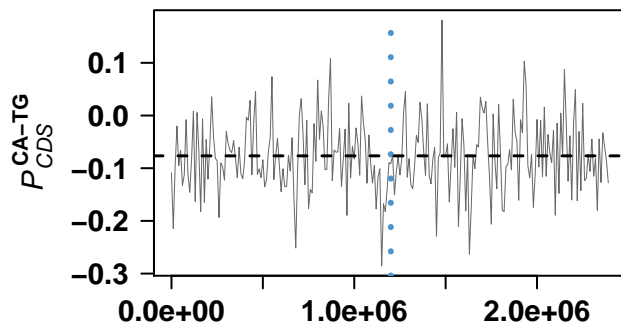
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genome coordinates

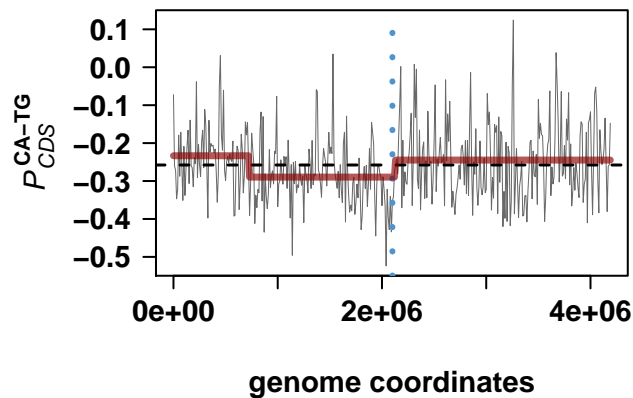
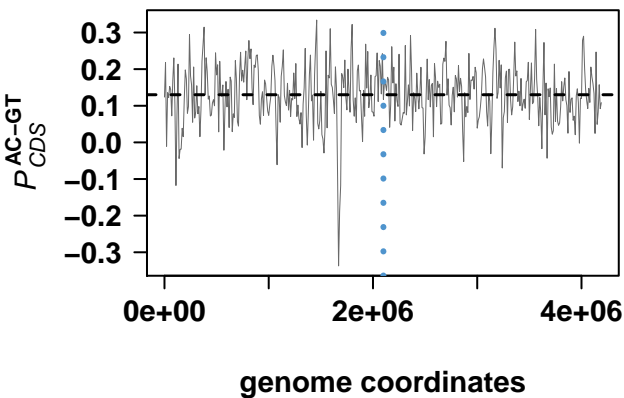
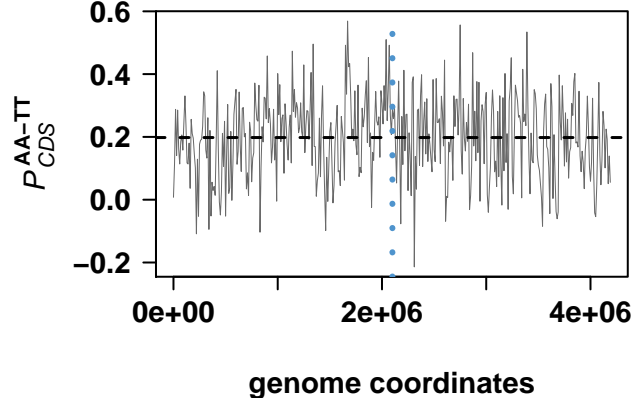
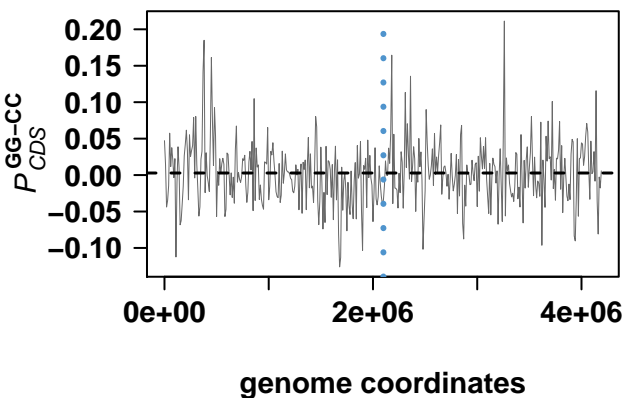
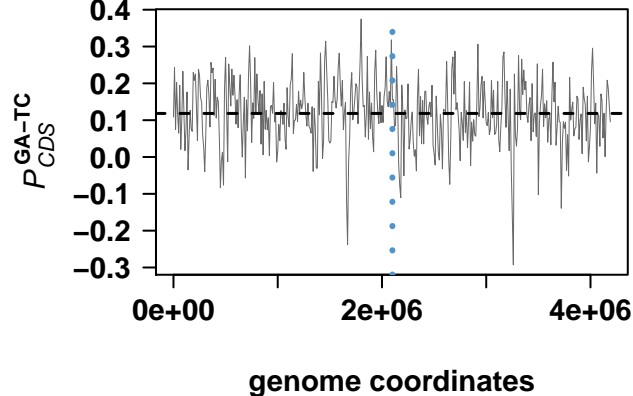
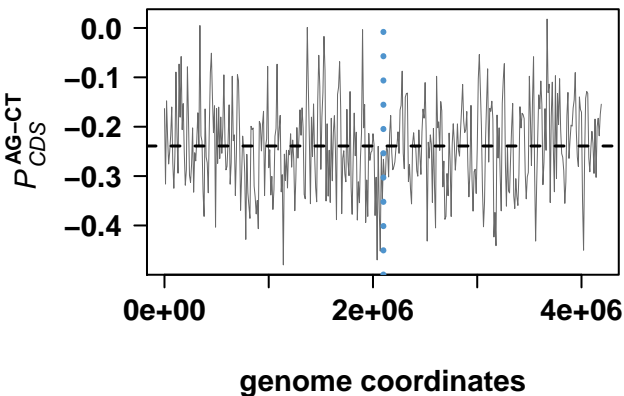


genome coordinates

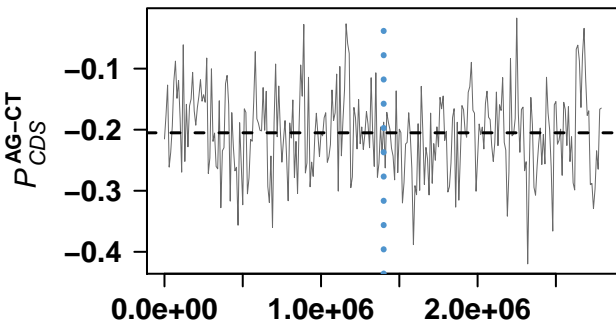


genome coordinates

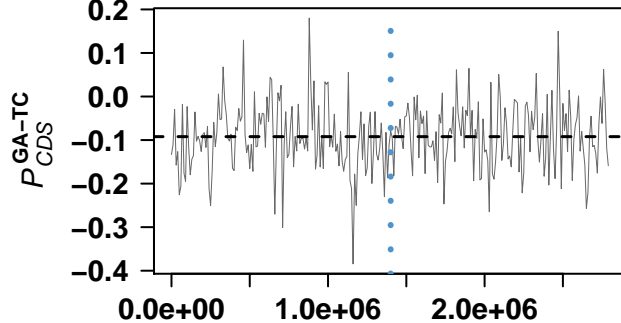
Chromobacterium violaceum ATCC 12472



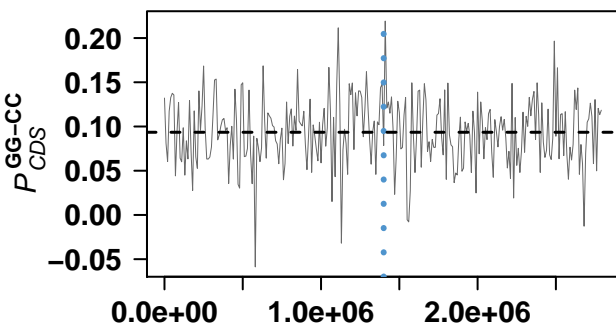
Burkholderia mallei ATCC 23344



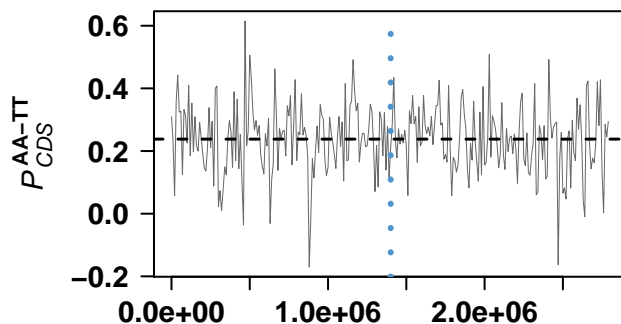
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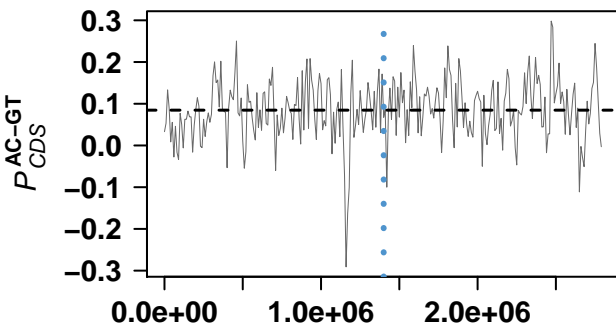
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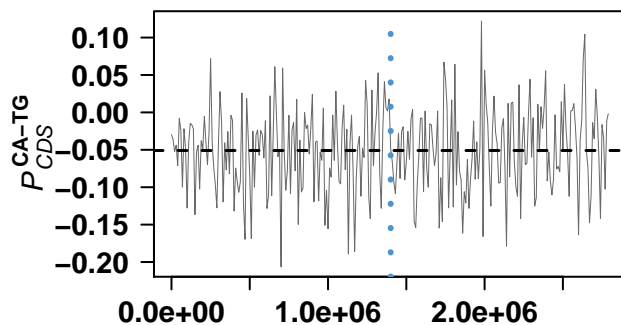
genome coordinates



genome coordinates

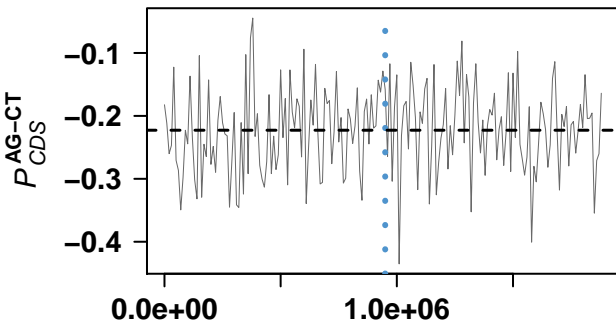


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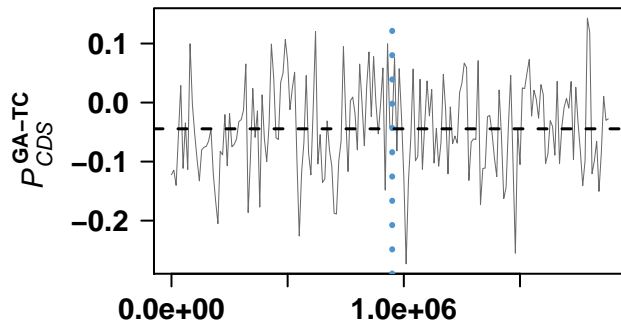


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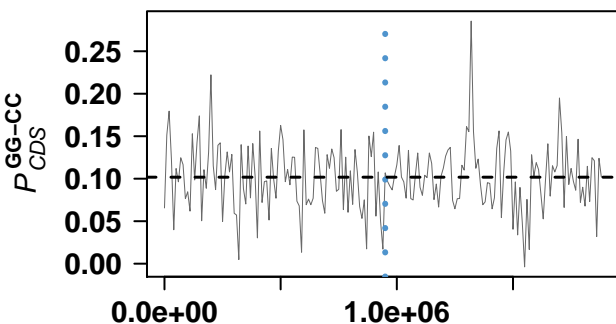
Burkholderia mallei ATCC 23344



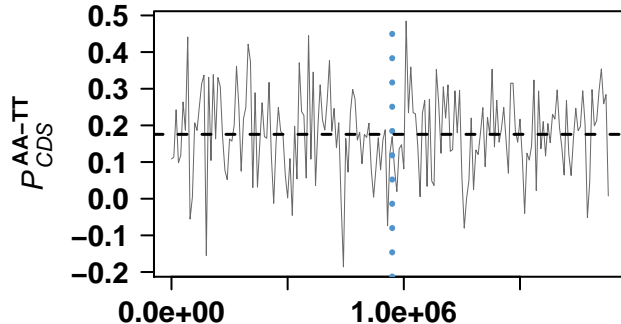
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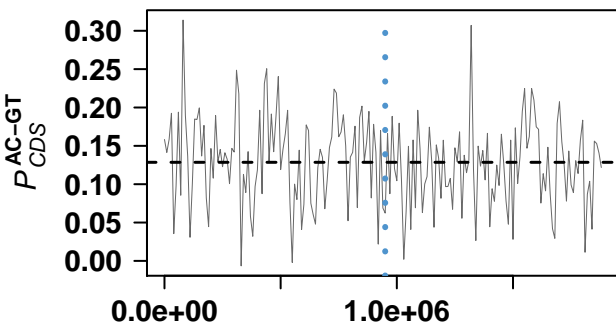
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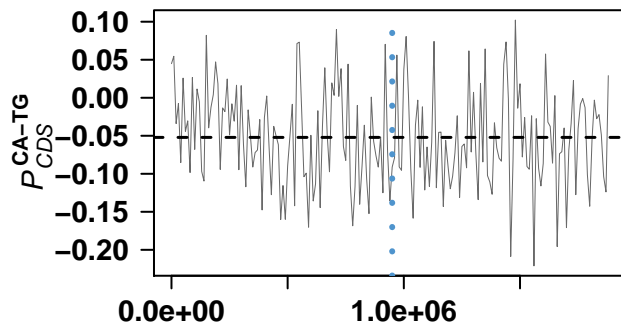
genome coordinates



genome coordinates

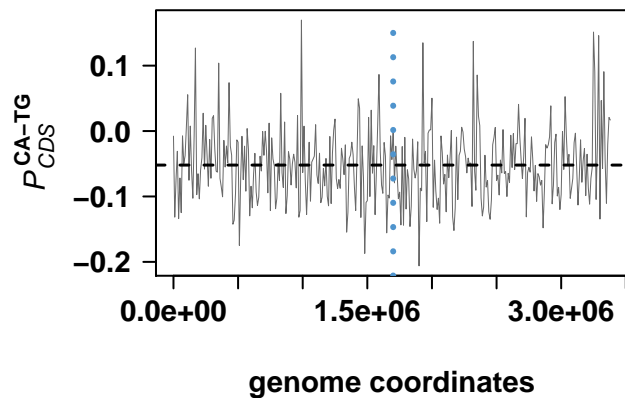
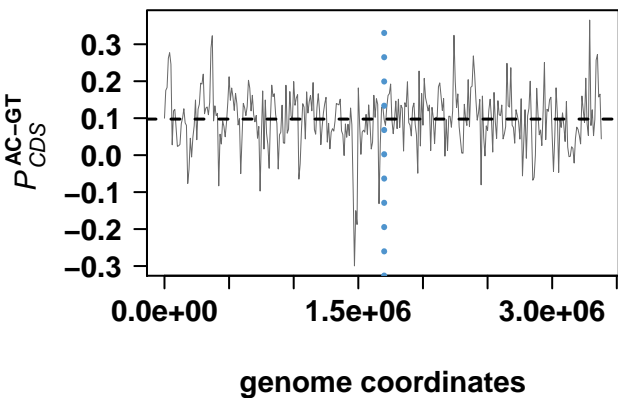
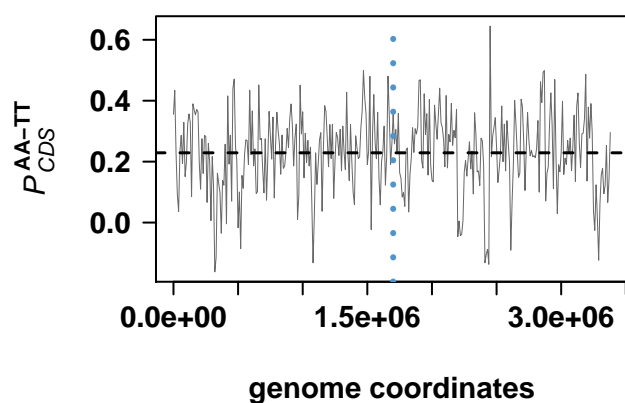
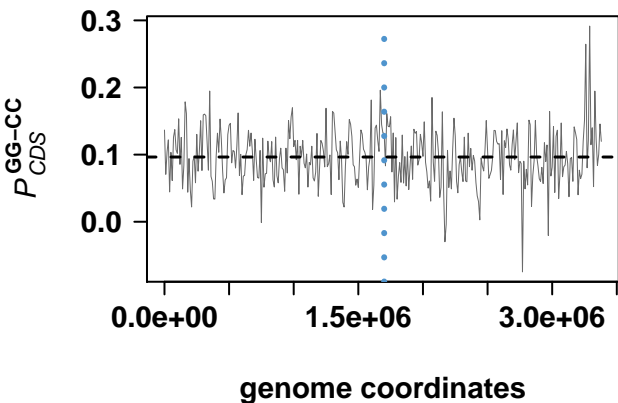
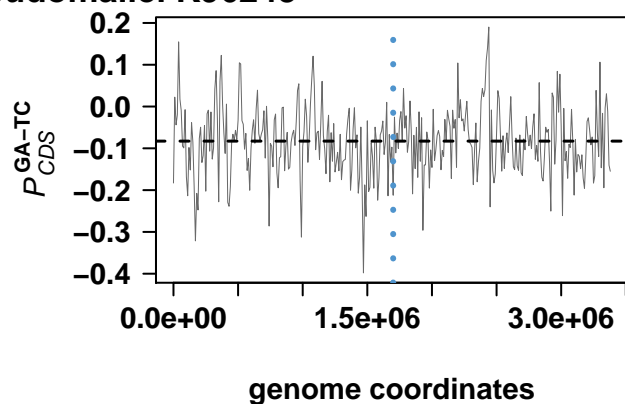
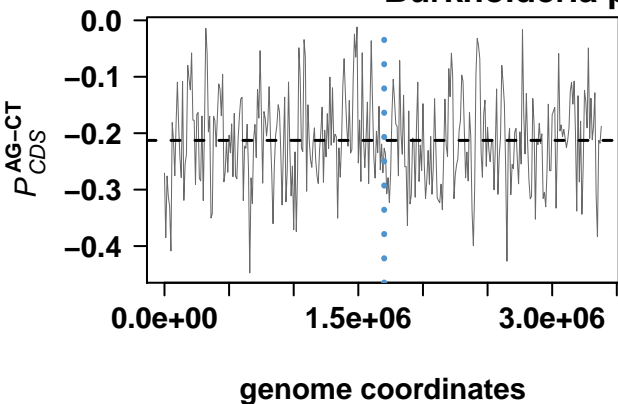


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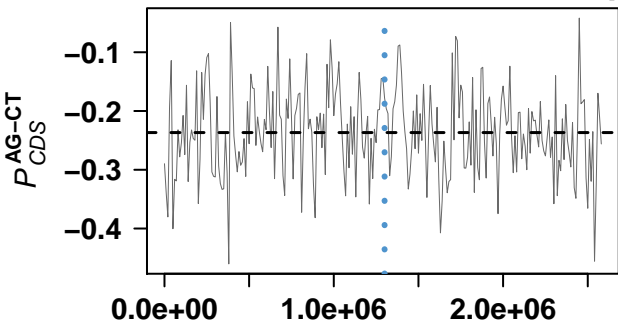


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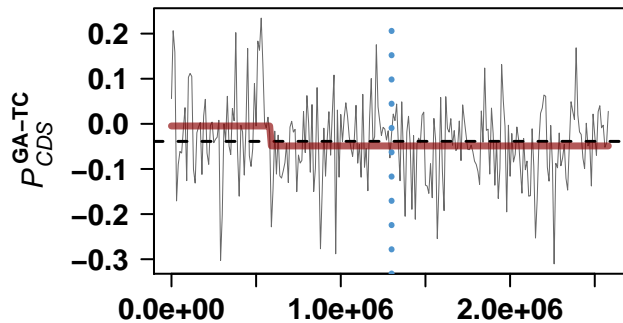
Burkholderia pseudomallei K96243



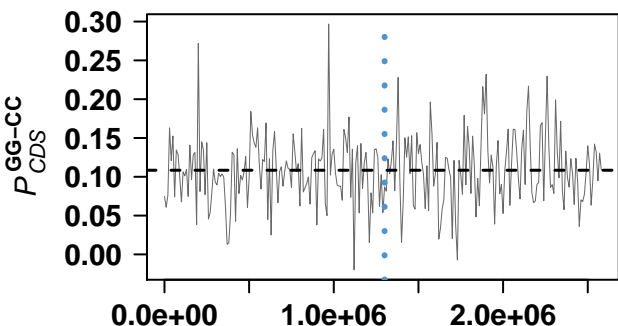
Burkholderia pseudomallei K96243



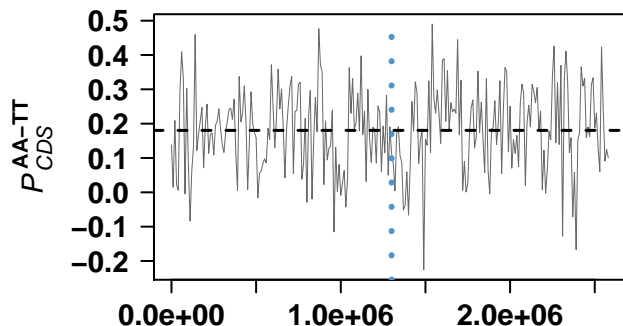
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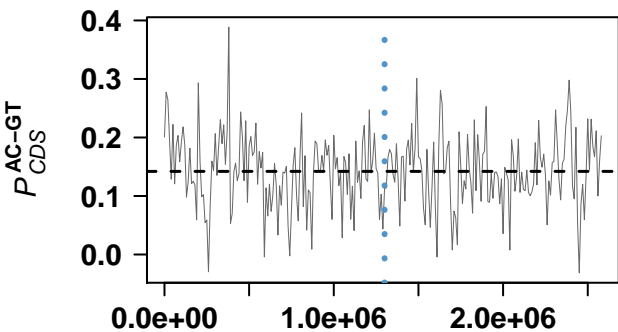
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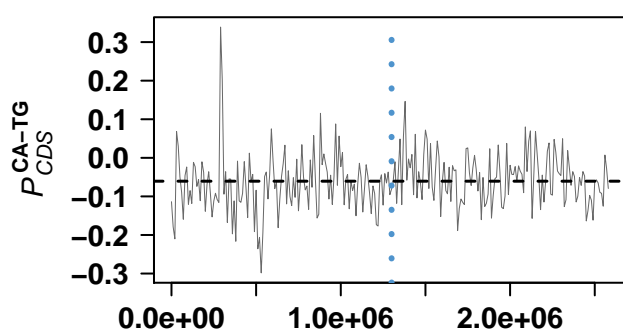
genome coordinates



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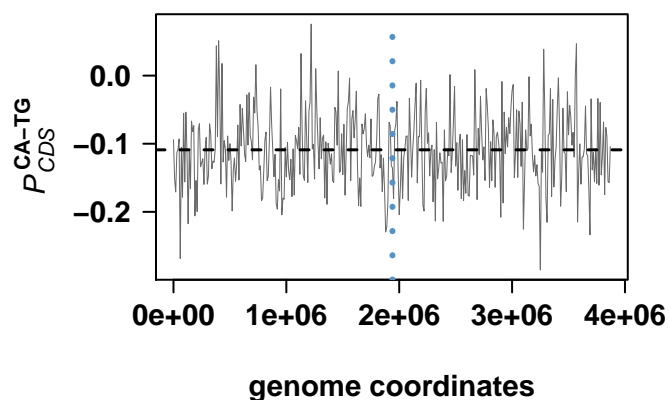
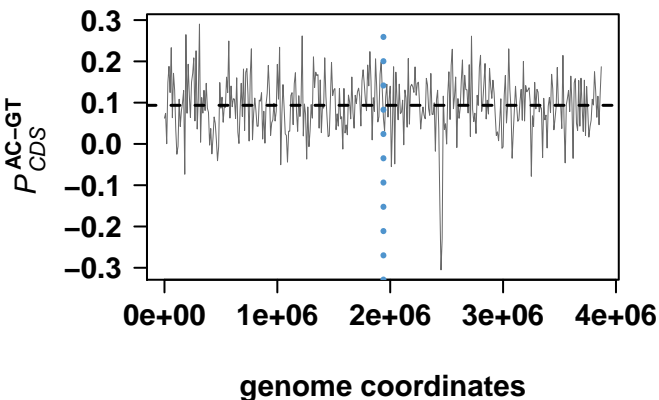
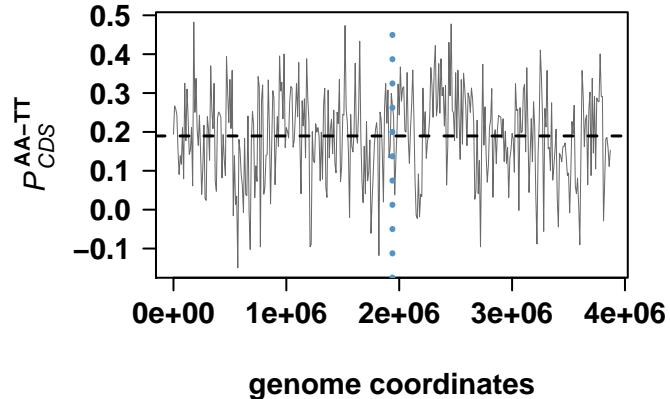
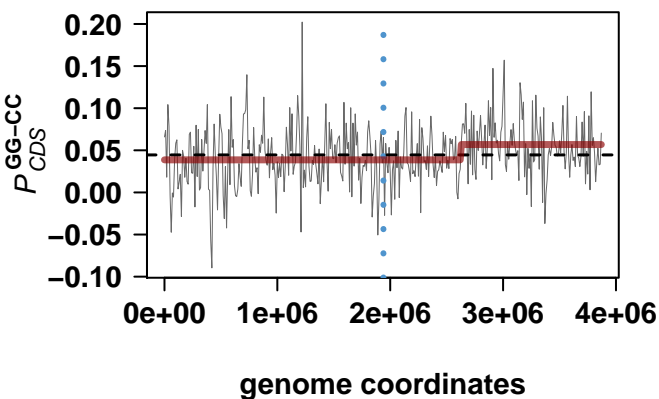
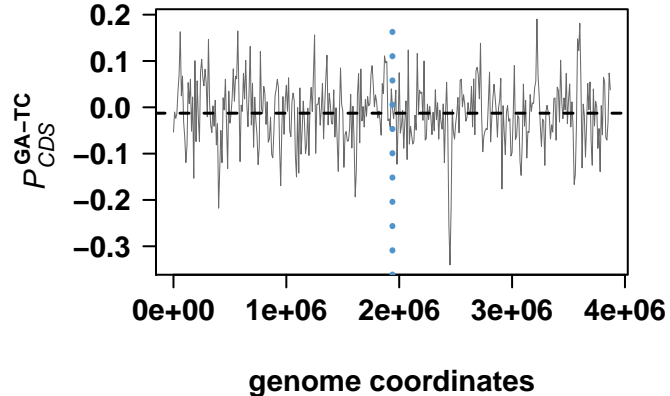
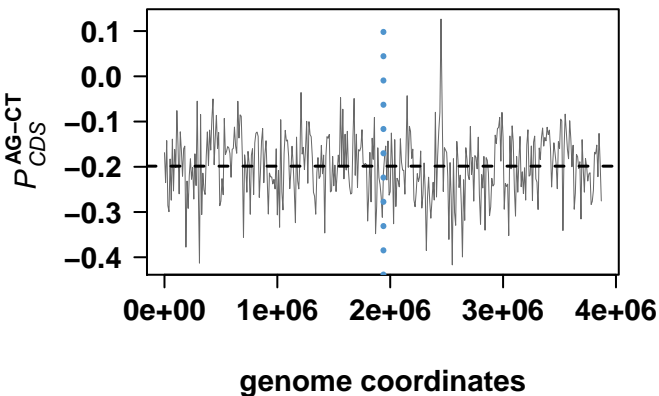


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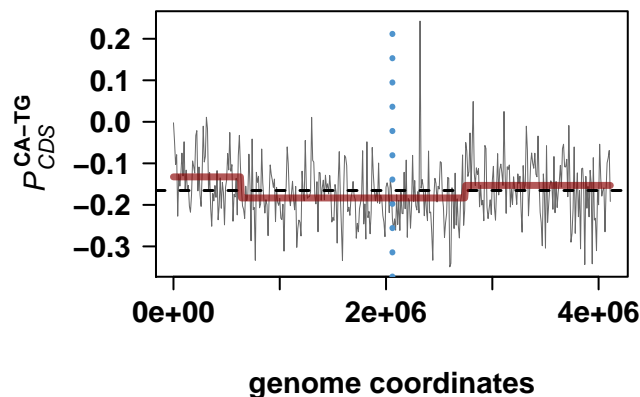
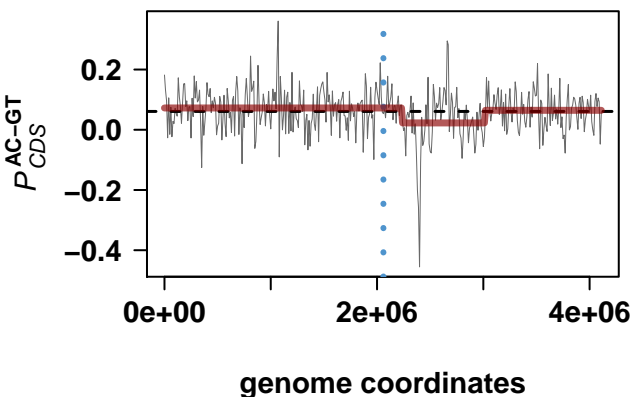
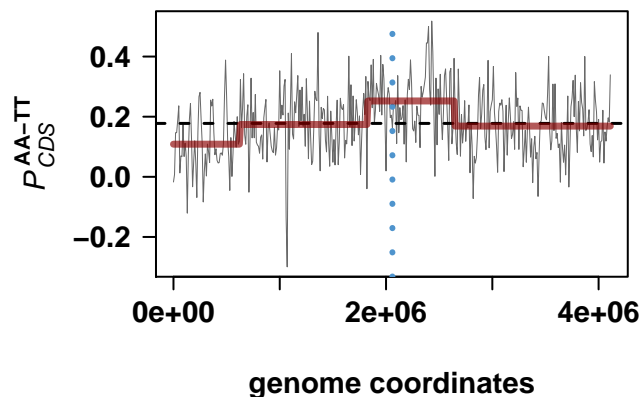
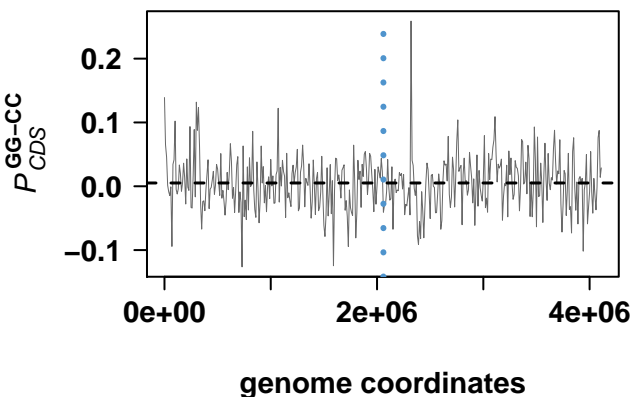
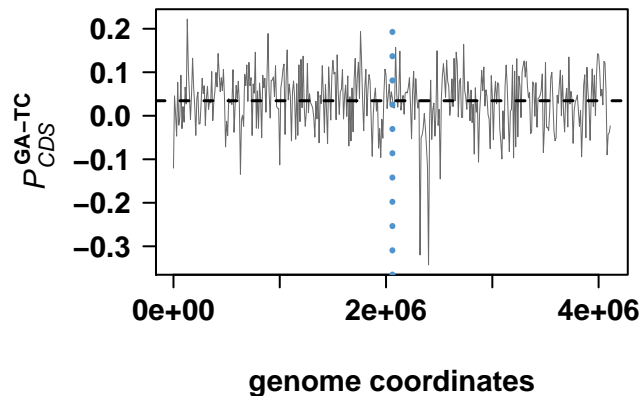
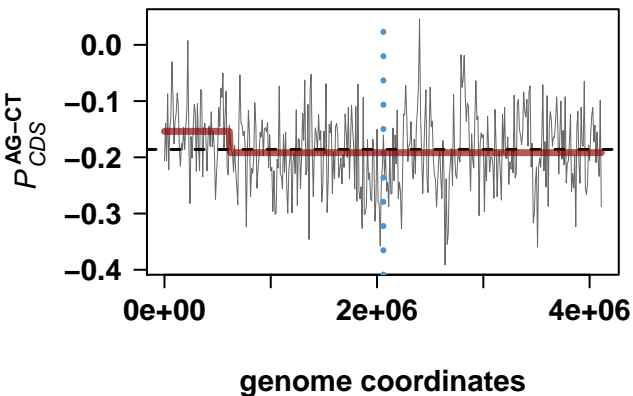


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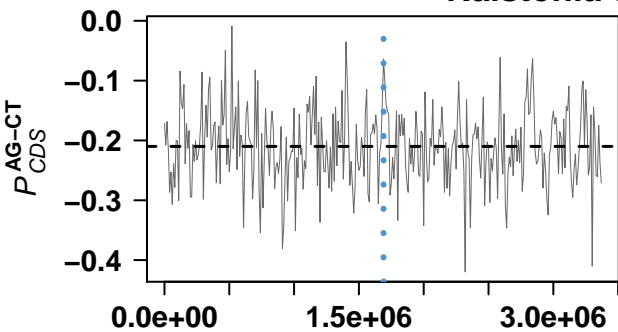
Aromatoleum aromaticum EbN1



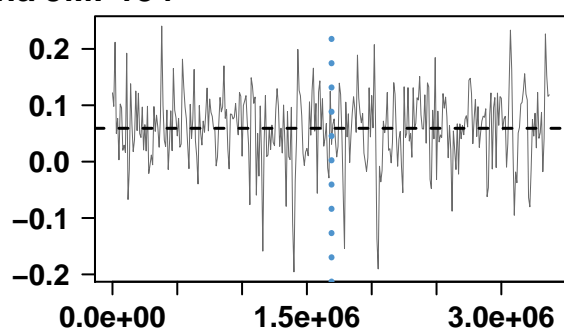
Dechloromonas aromatica RCB



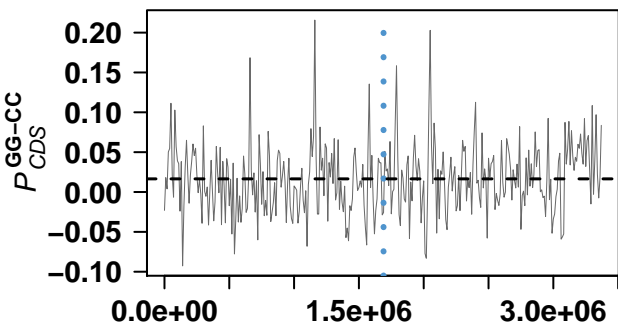
Ralstonia eutropha JMP134



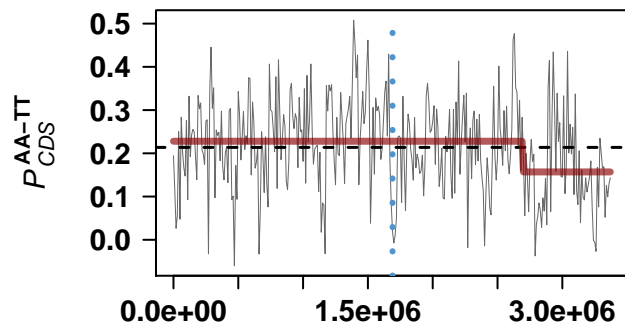
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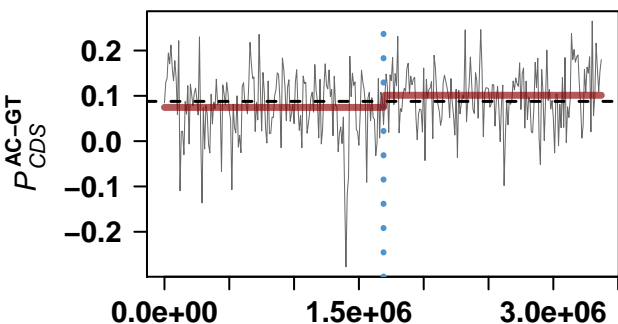
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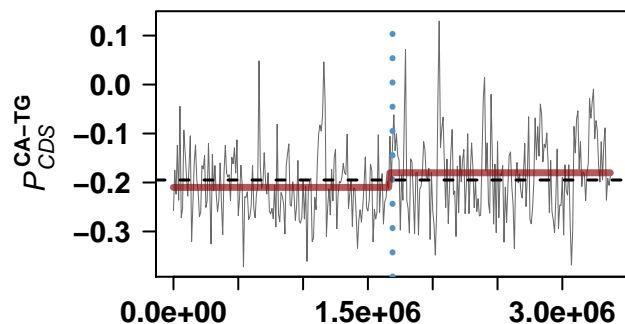
genome coordinates



genome coordinates

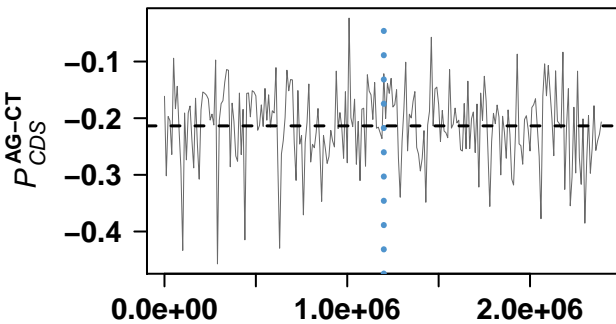


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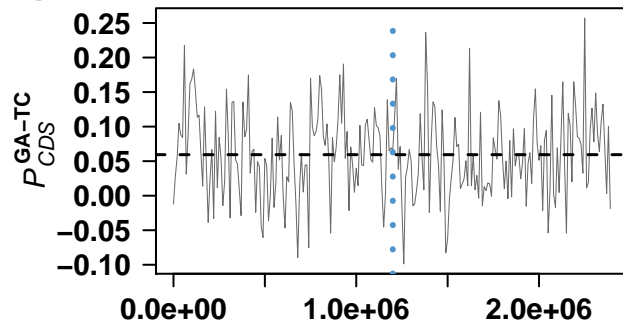


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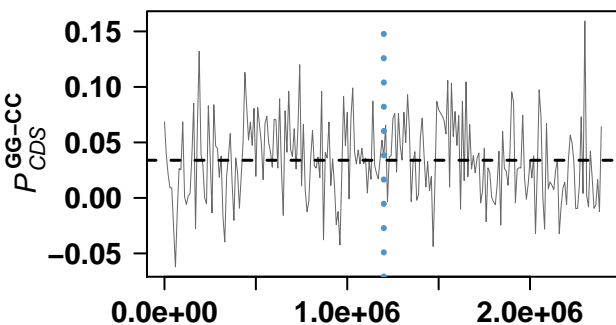
Ralstonia eutropha JMP134



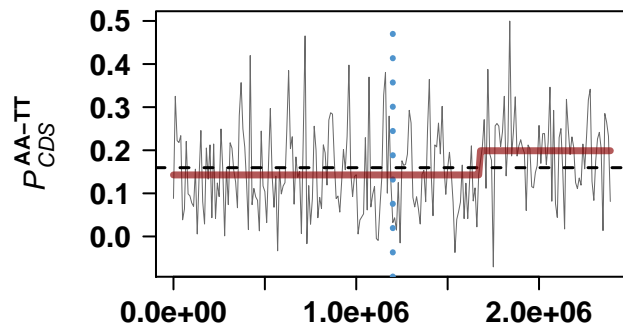
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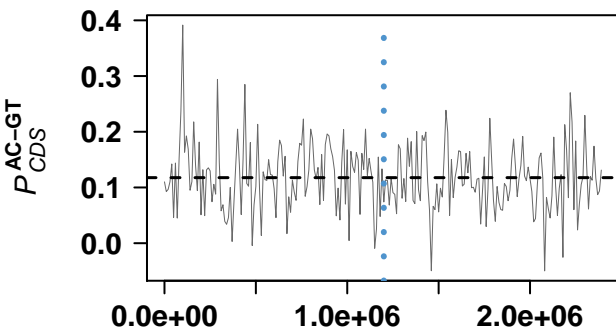
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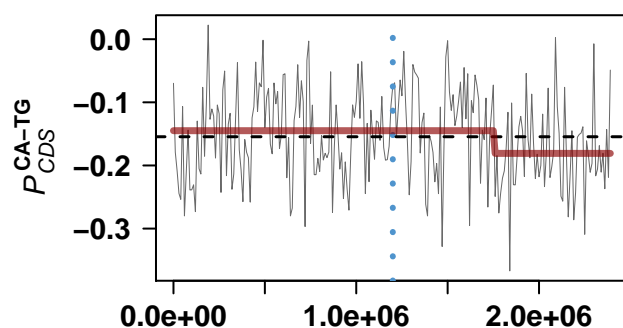
genome coordinates



genome coordinates

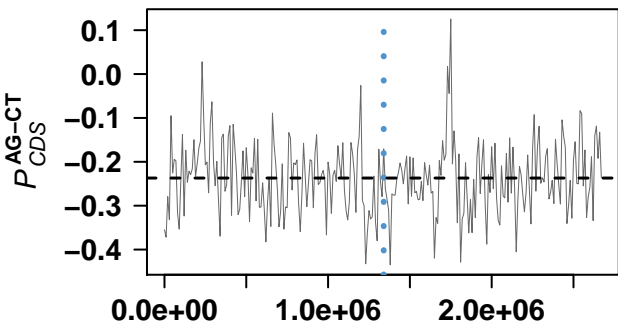


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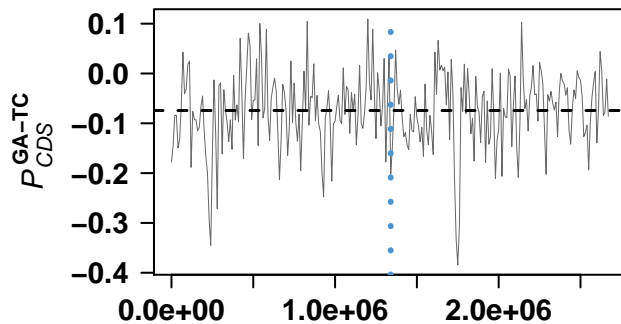


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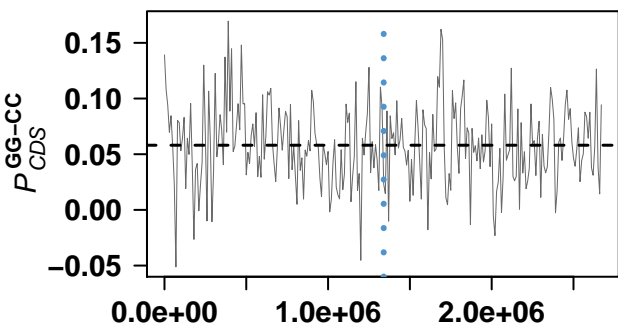
Thiobacillus denitrificans ATCC 25259



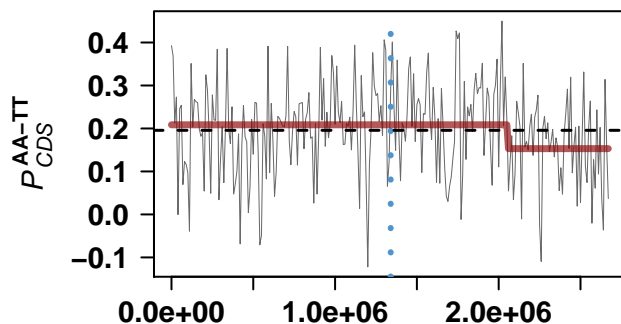
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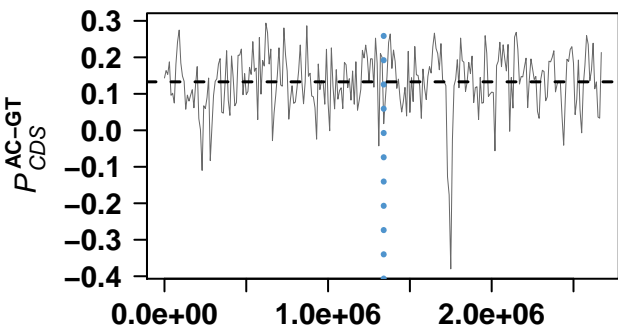
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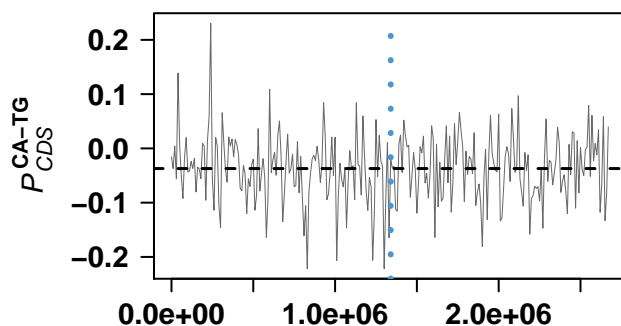
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genome coordinates

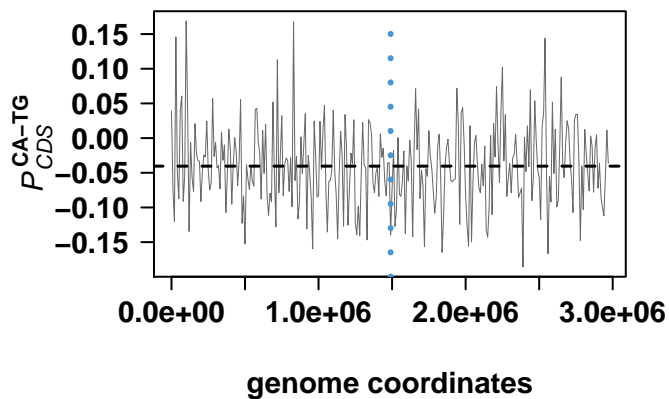
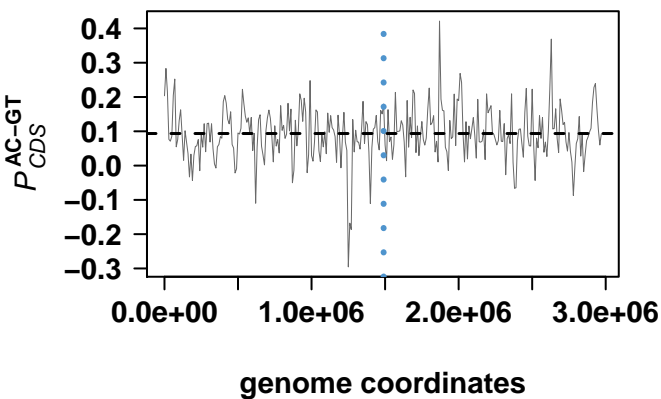
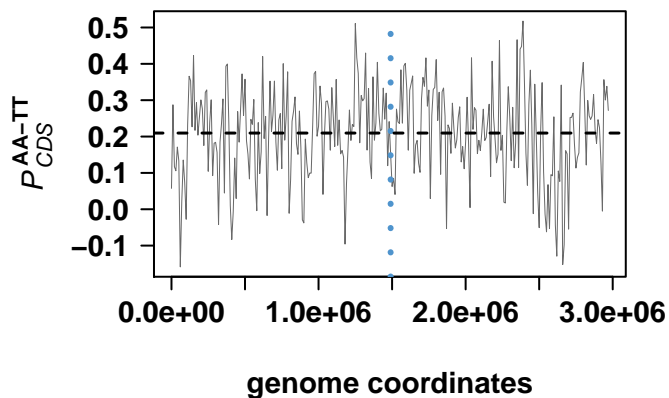
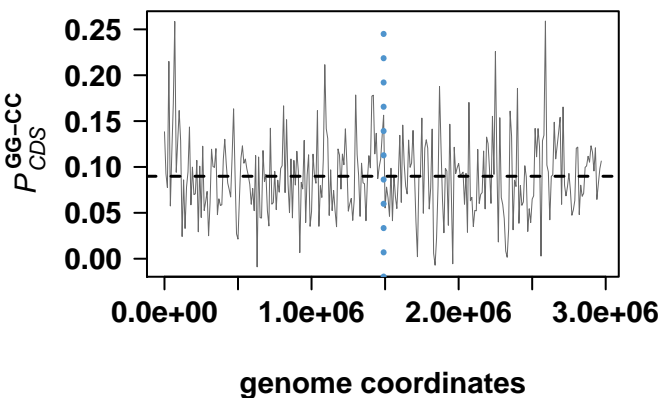
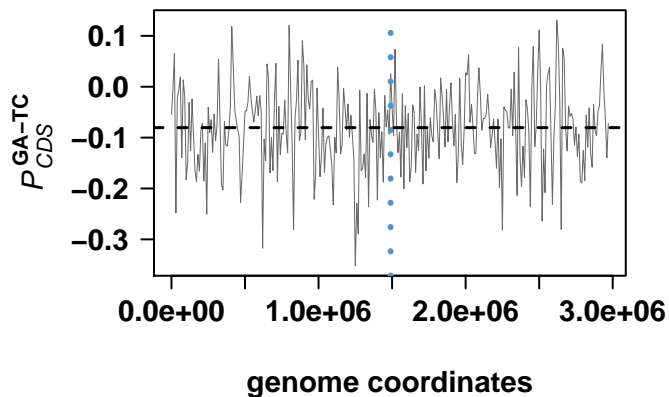
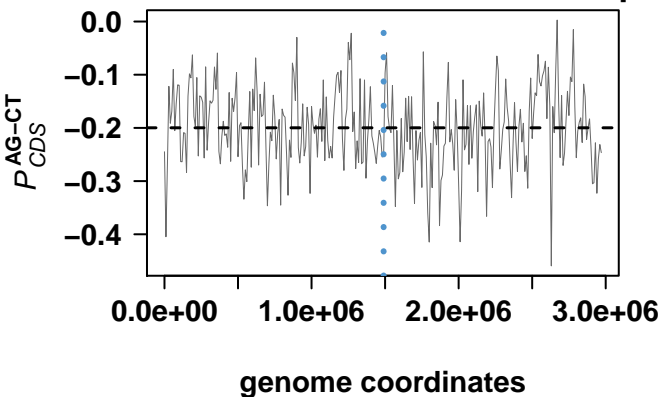


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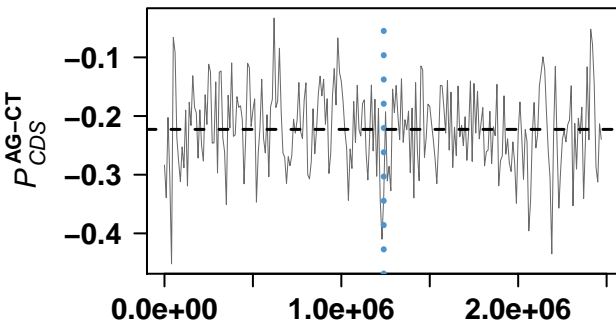


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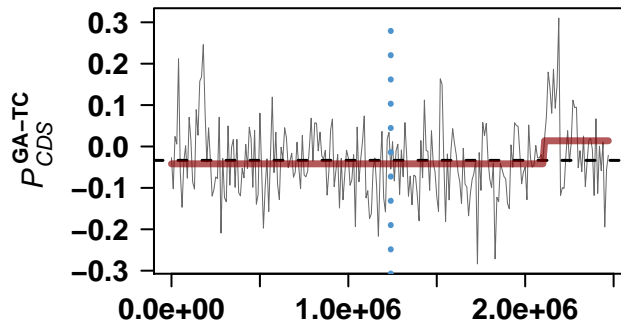
Burkholderia pseudomallei 1710b



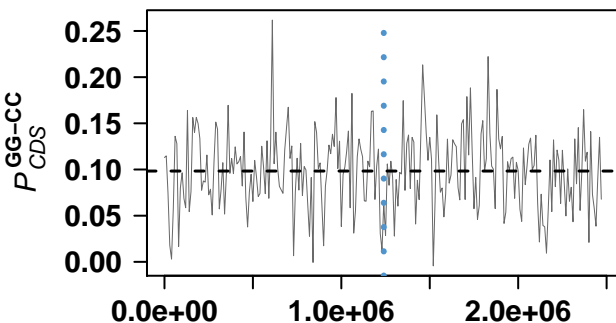
Burkholderia pseudomallei 1710b



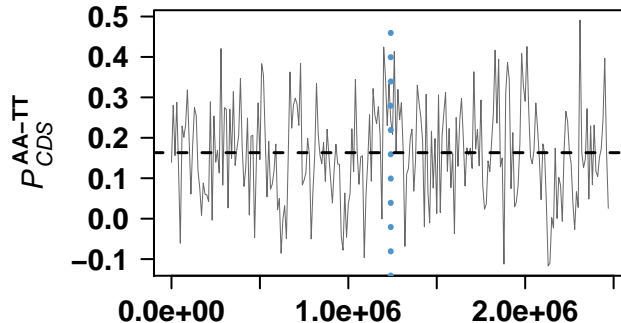
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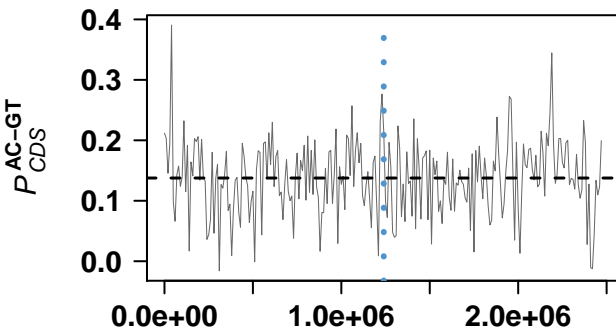
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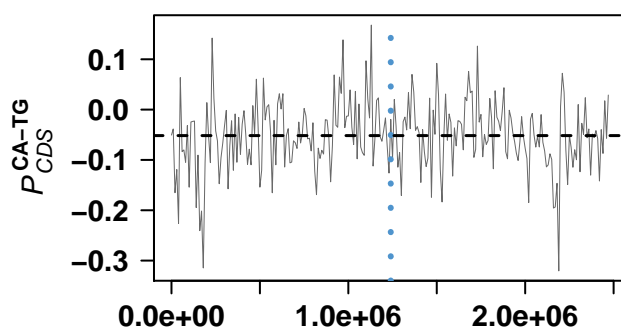
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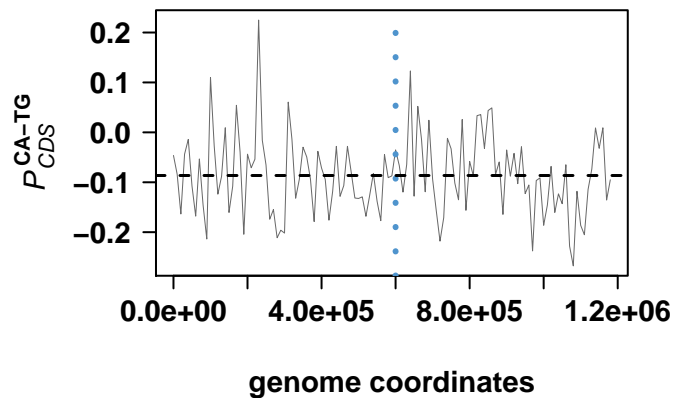
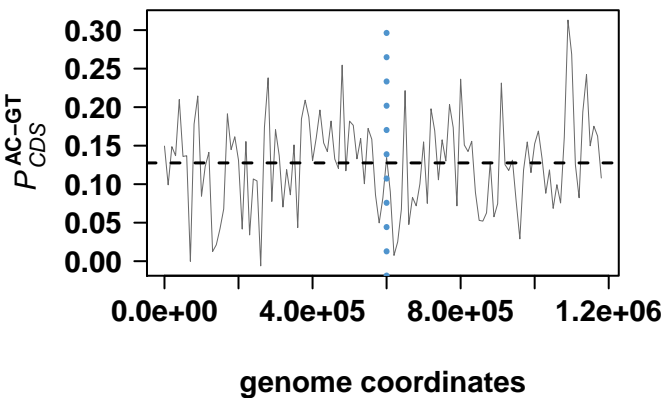
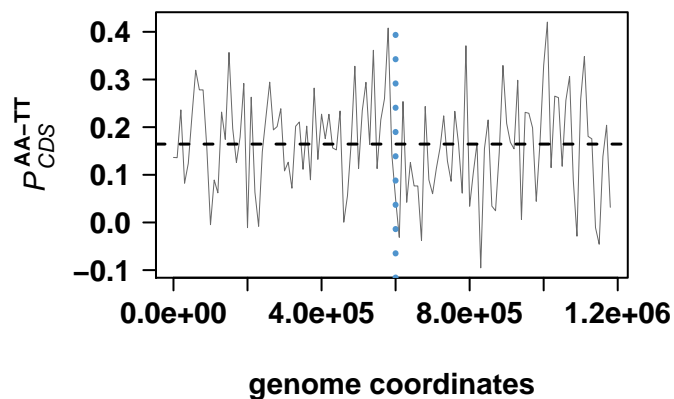
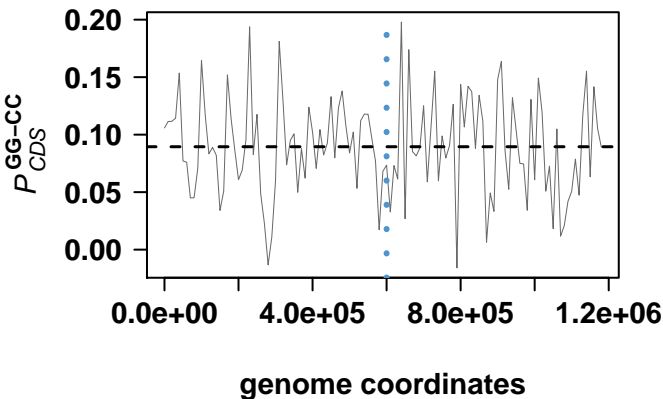
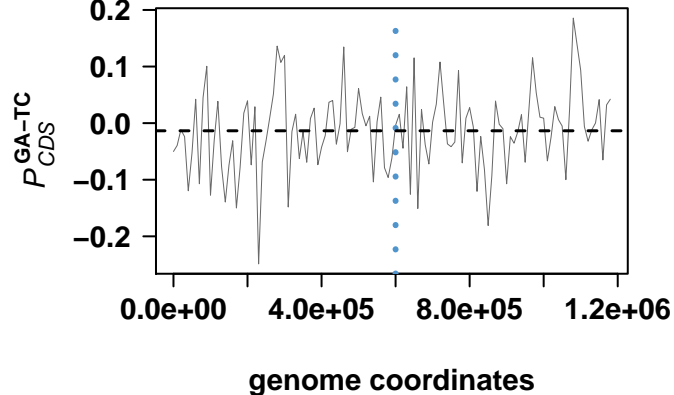
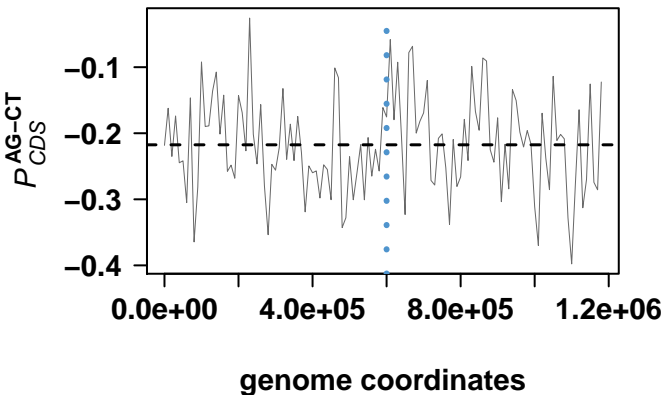


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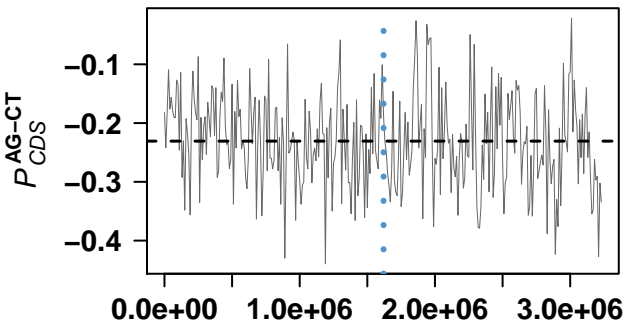


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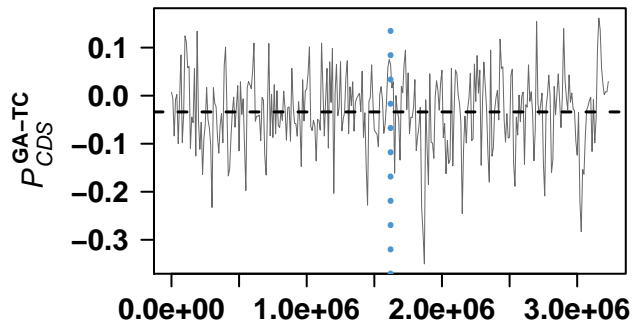
Burkholderia lata



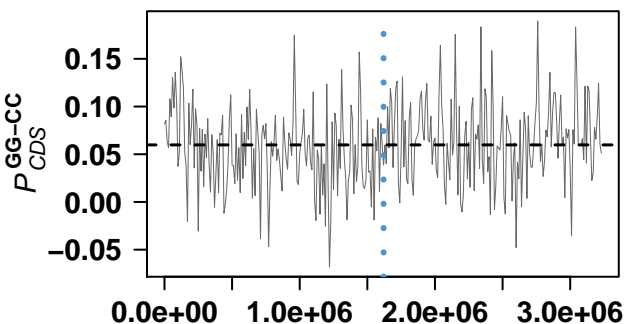
Burkholderia lata



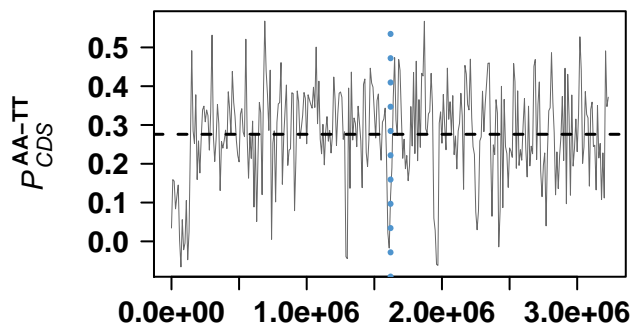
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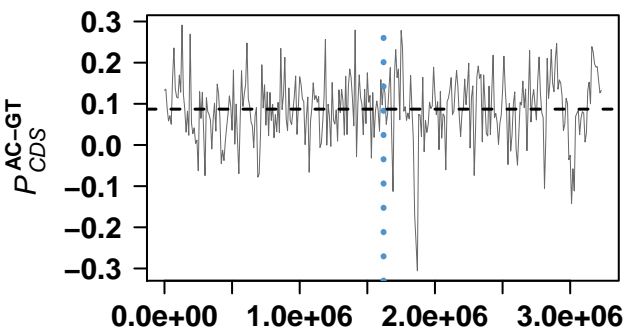
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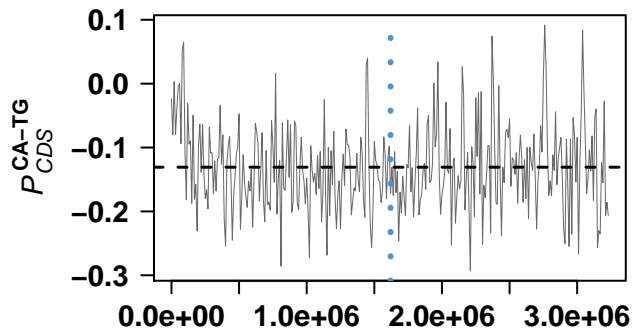
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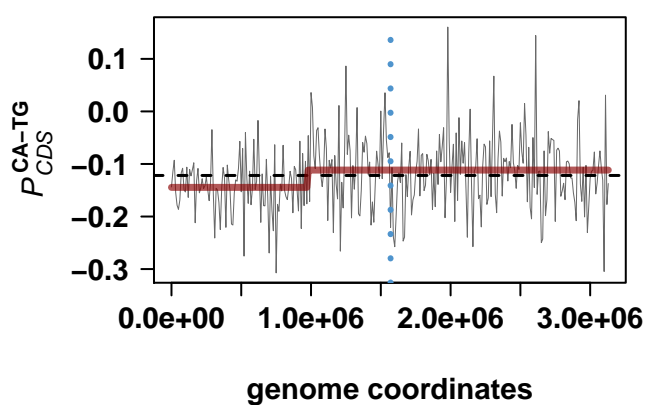
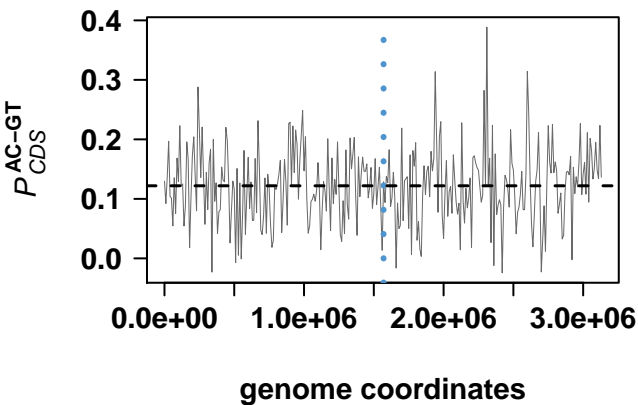
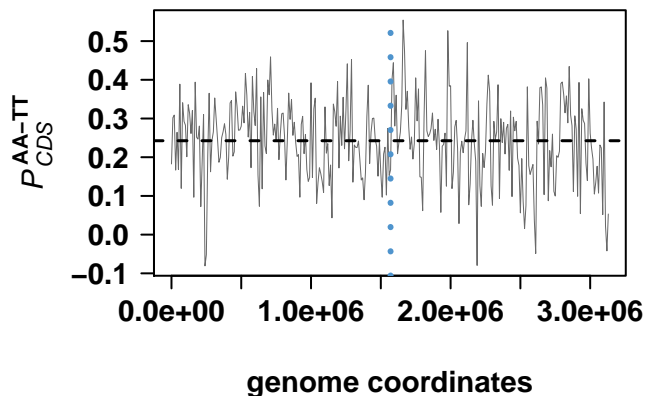
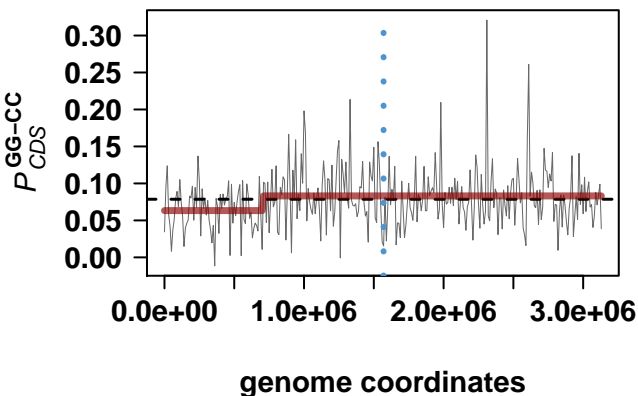
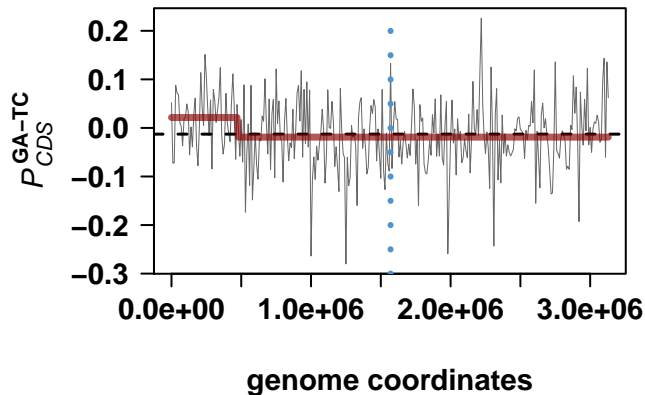
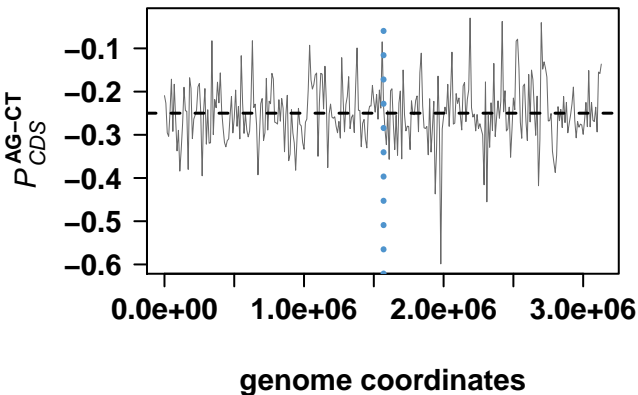


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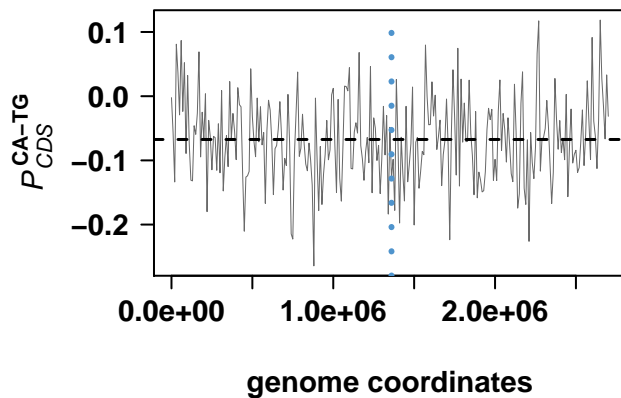
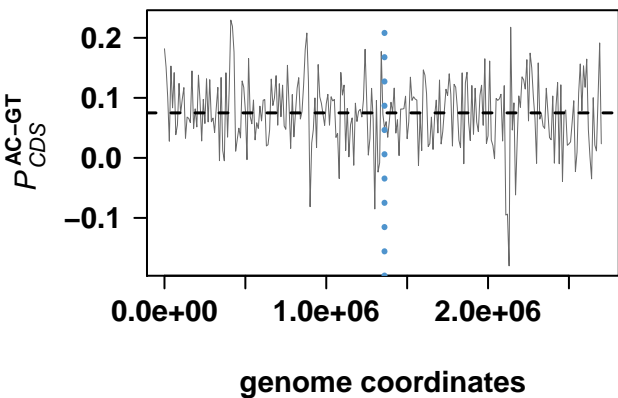
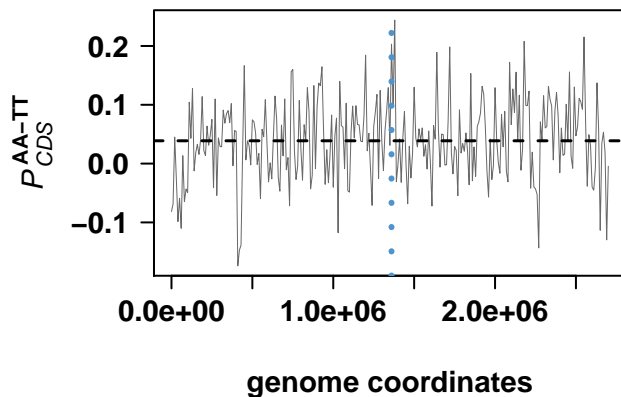
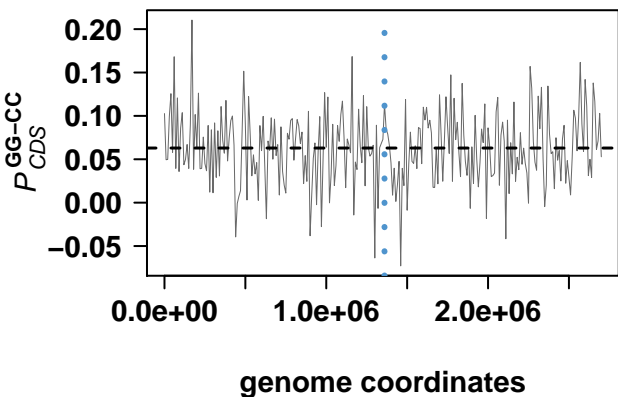
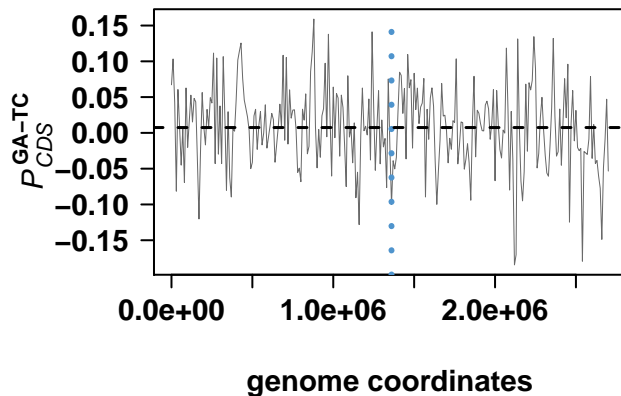
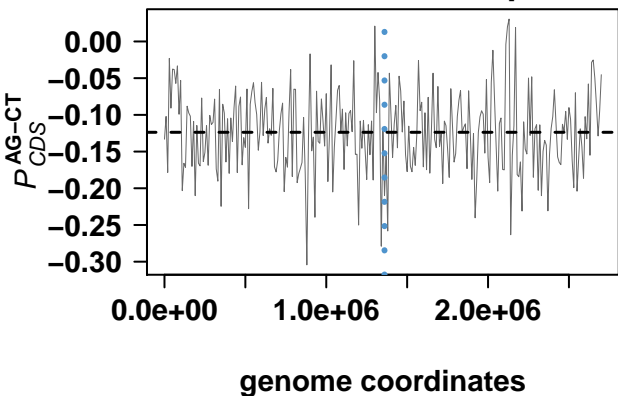


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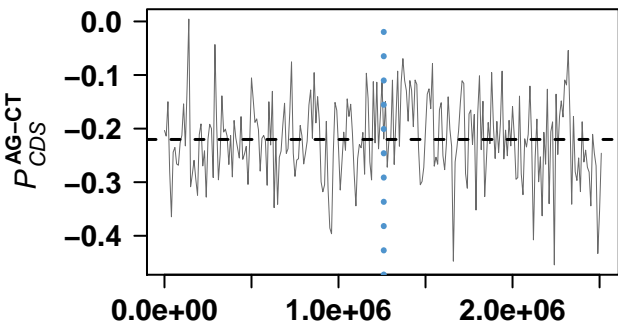
Burkholderia lata



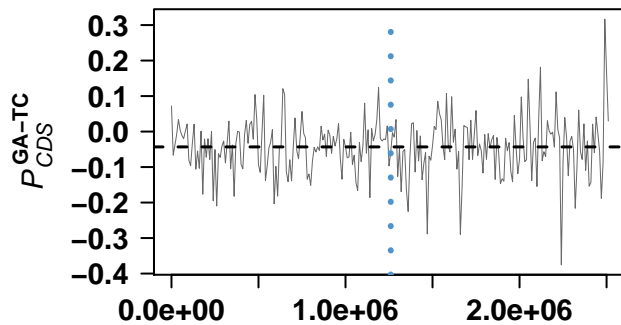
Nitrosospira multiformis ATCC 25196



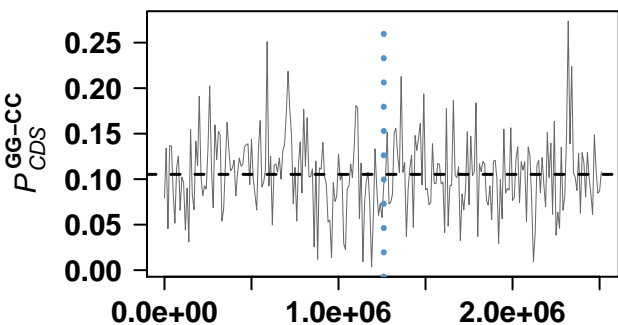
Burkholderia thailandensis E264



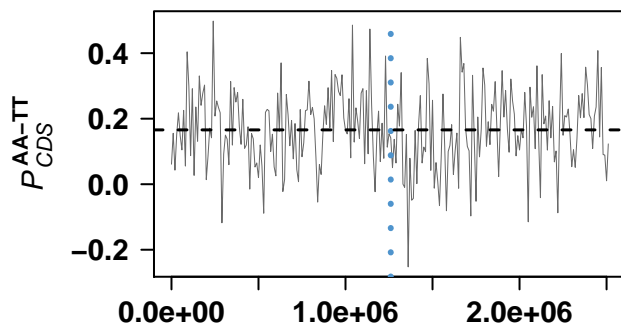
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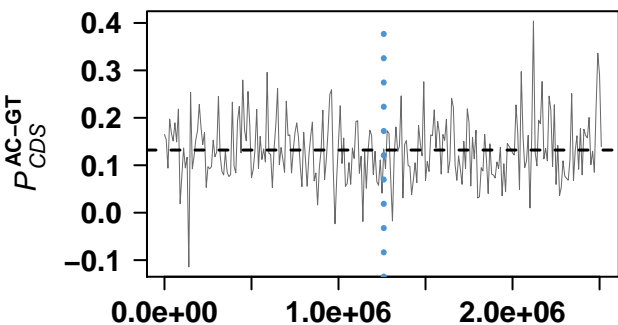
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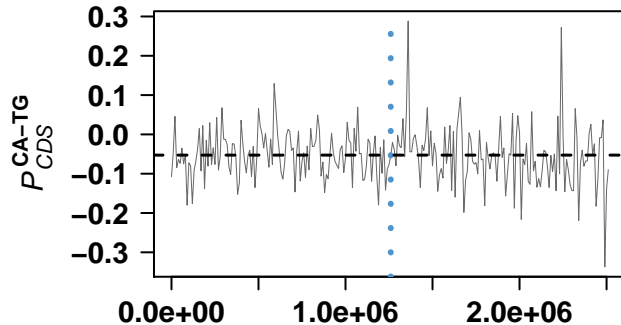
genome coordinates



genome coordinates

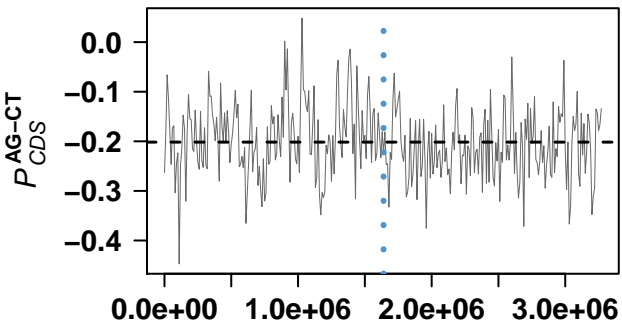


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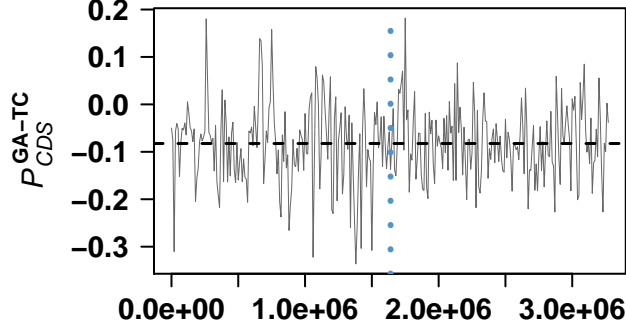


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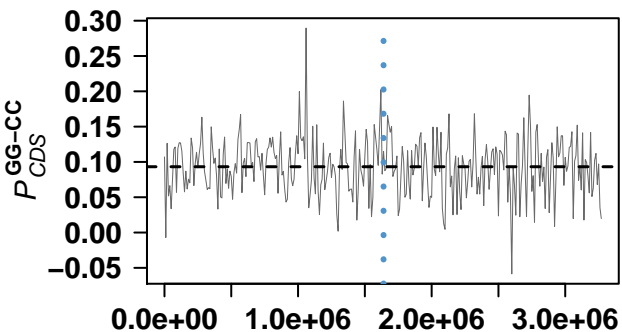
Burkholderia thailandensis E264



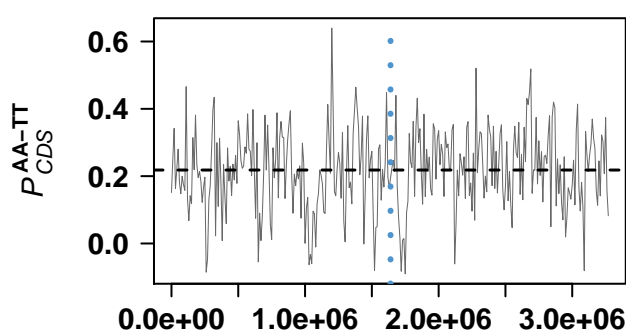
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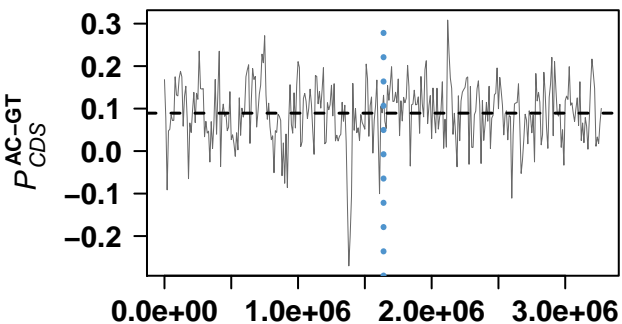
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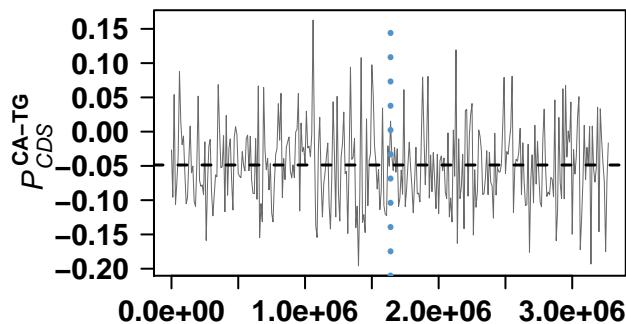
genome coordinates



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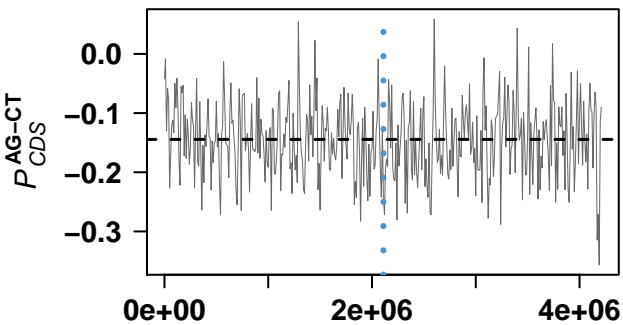


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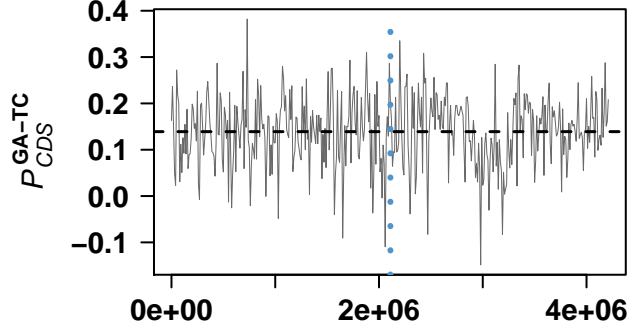


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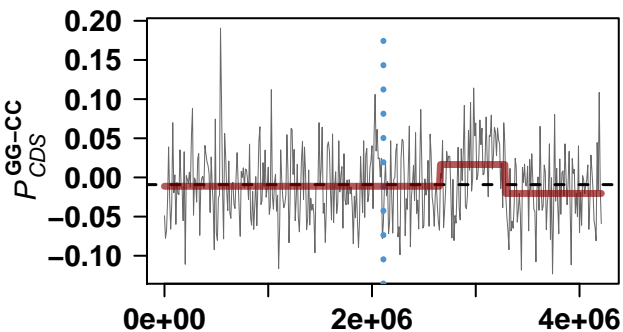
Albidiferax ferrireducens T118



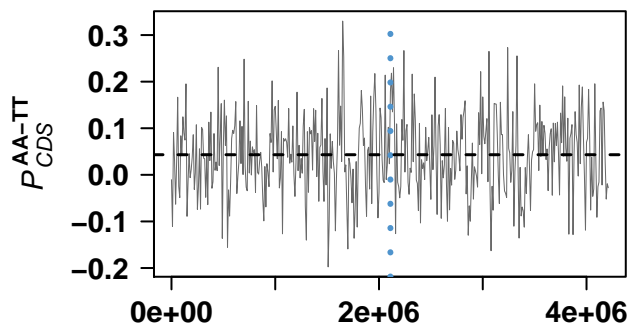
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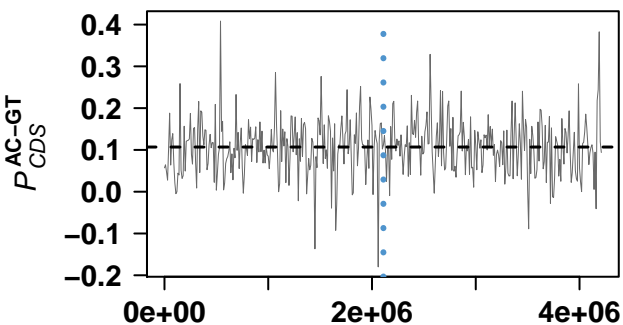
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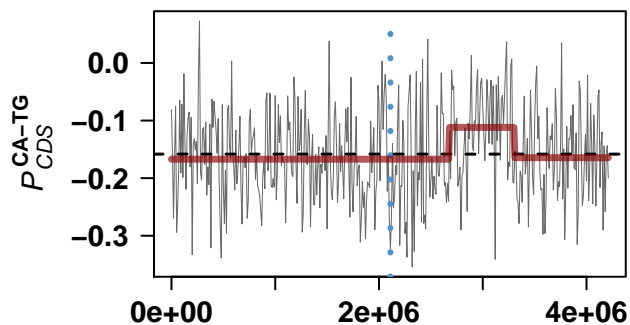
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genome coordinates

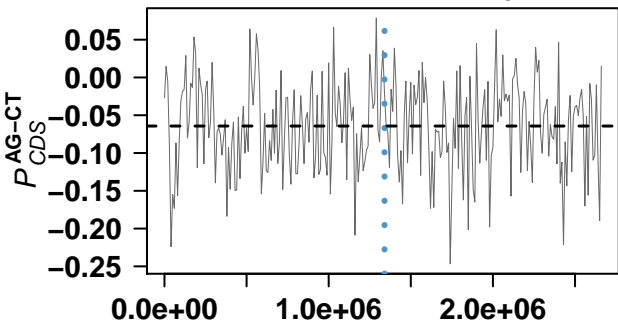


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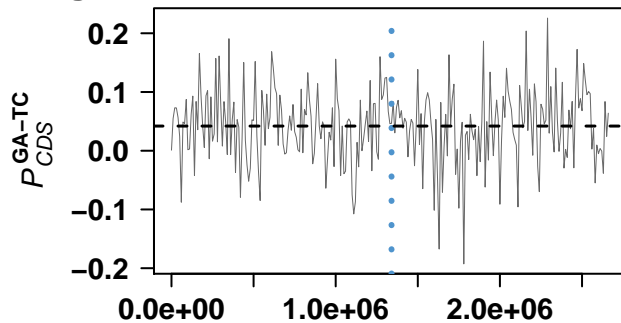


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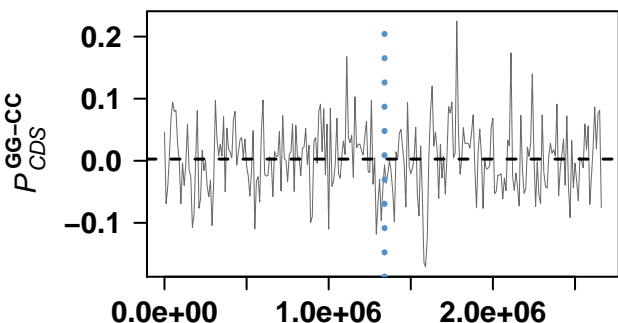
Methylobacillus flagellatus KT



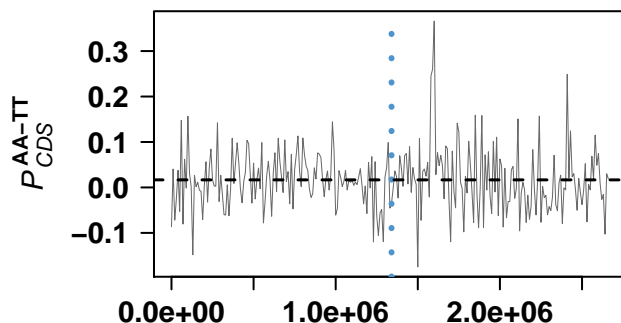
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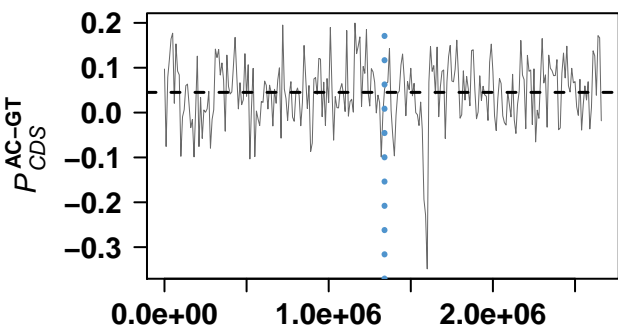
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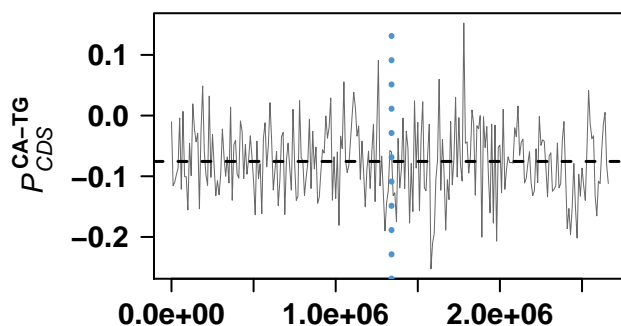
genome coordinates



genome coordinates

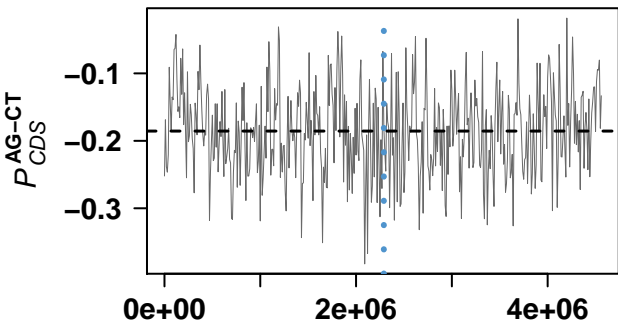


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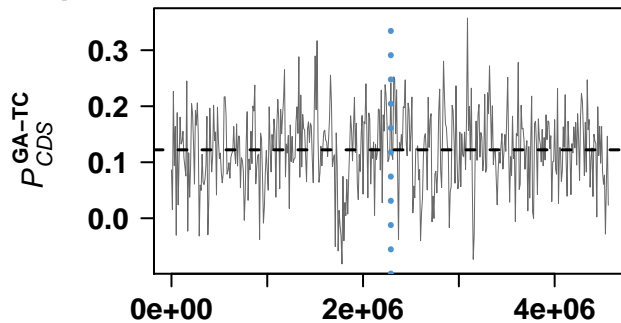


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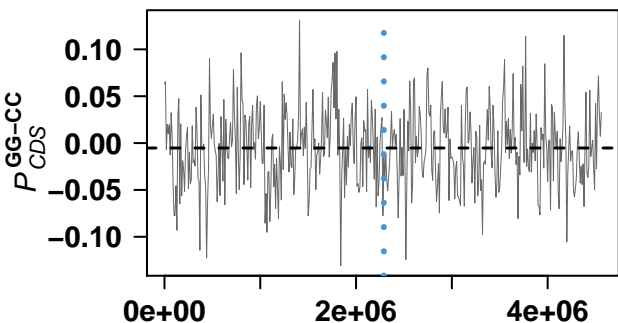
Polaromonas sp. JS666



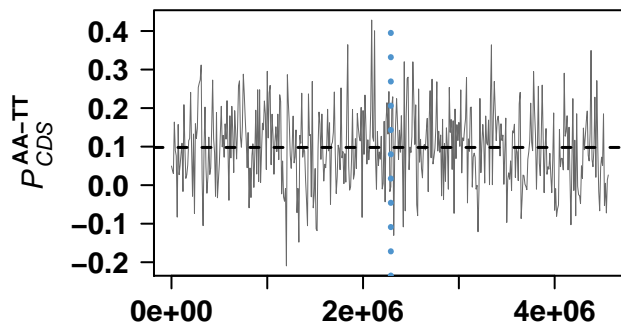
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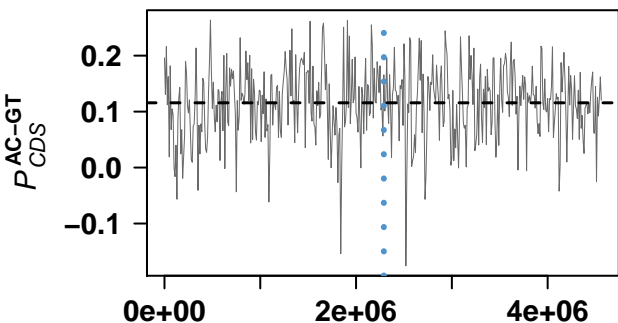
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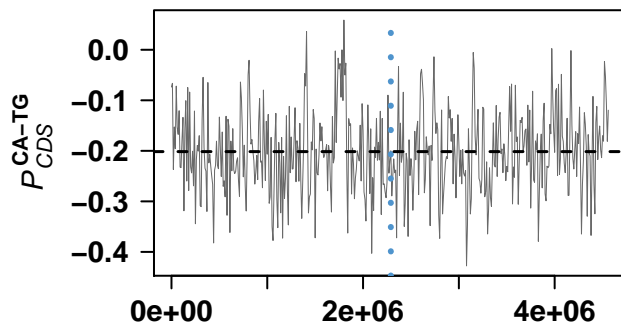
genome coordinates



genome coordinates

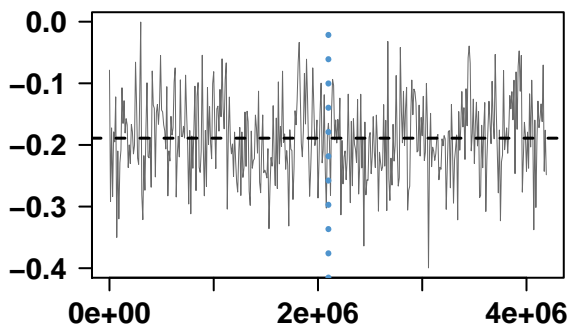


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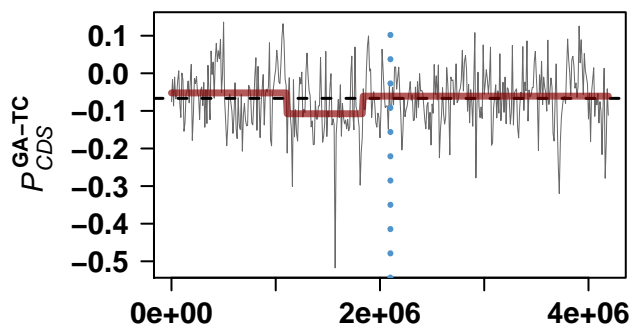


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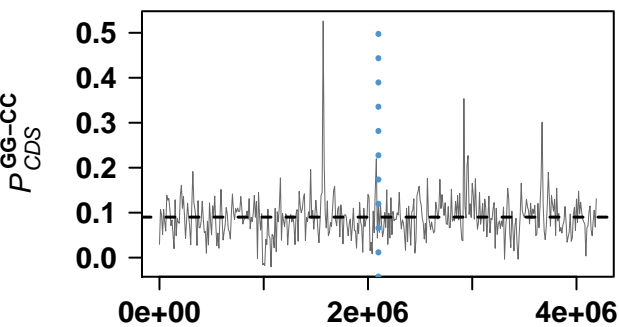
Burkholderia xenovorans LB400



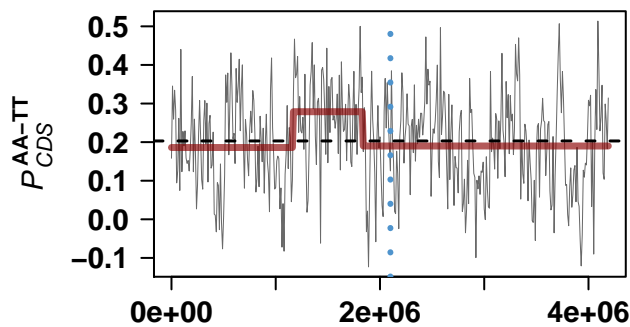
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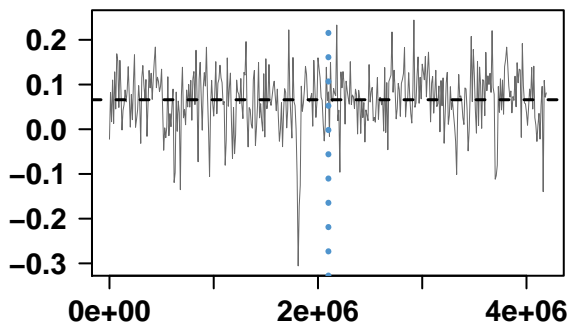
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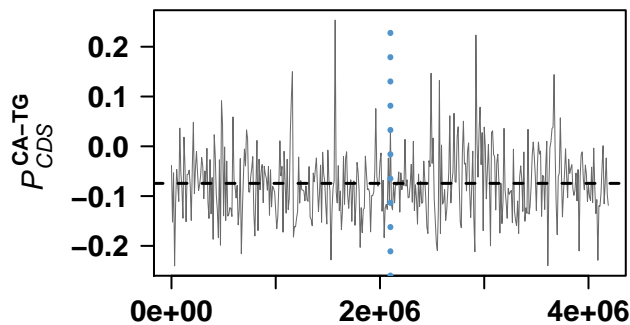
genome coordinates



genome coordinates

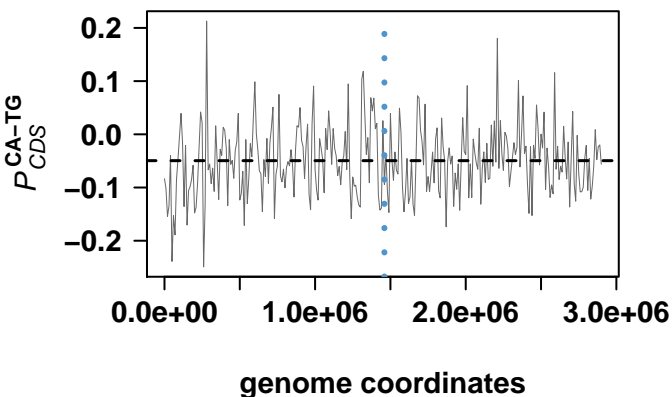
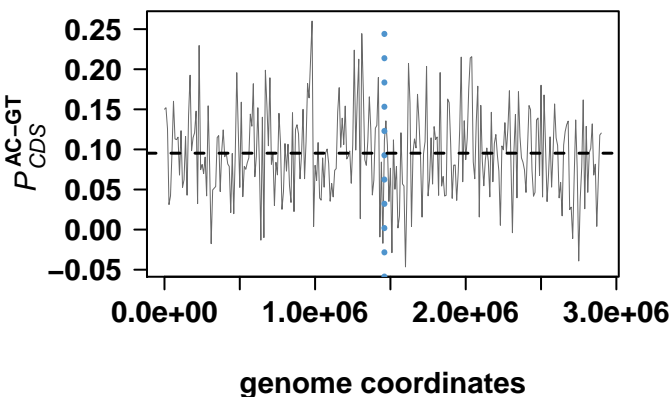
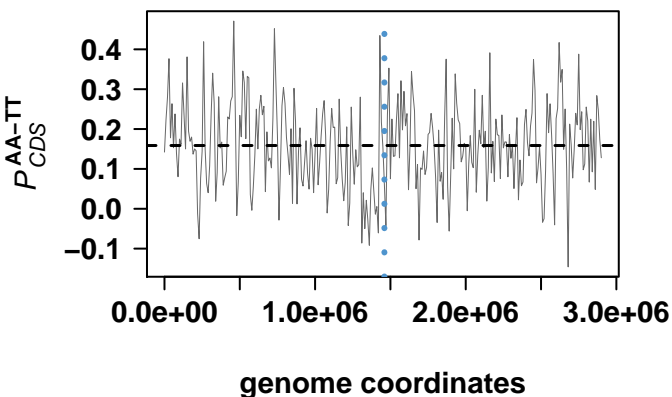
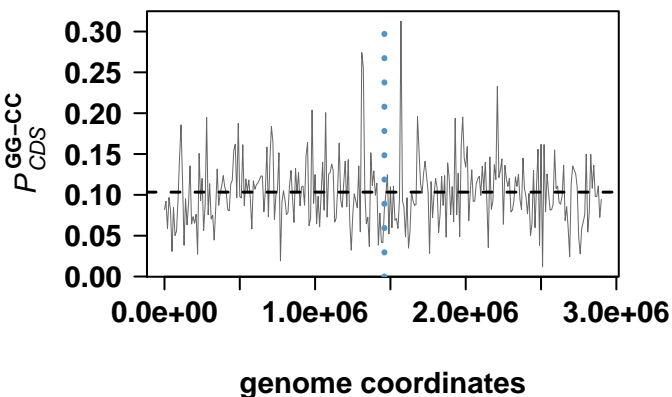
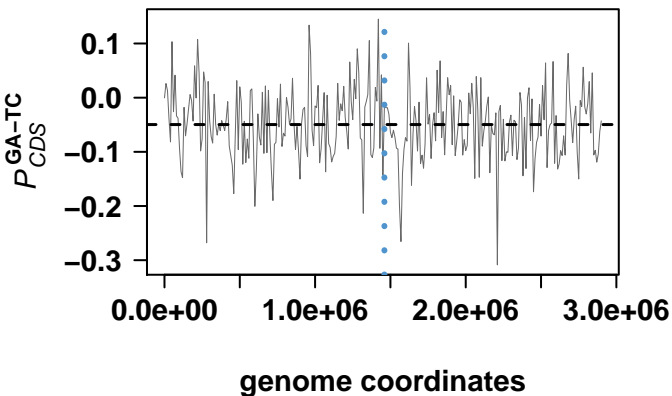
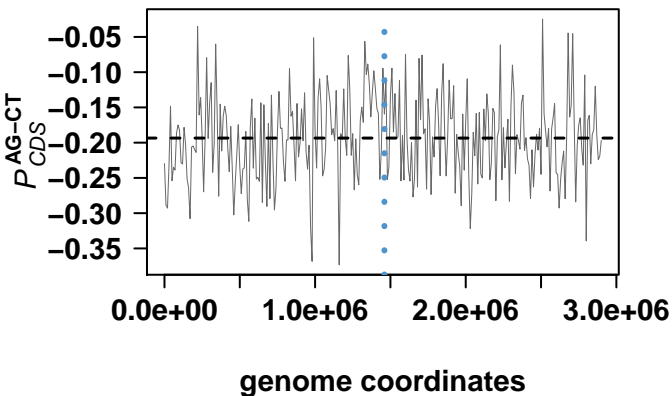


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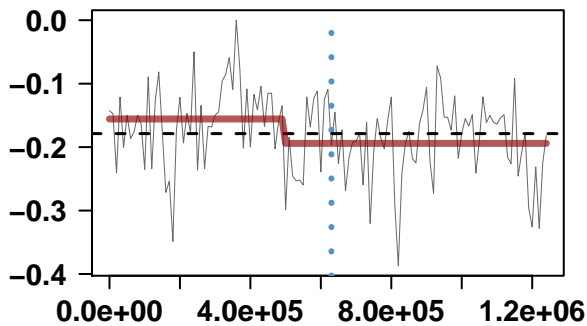


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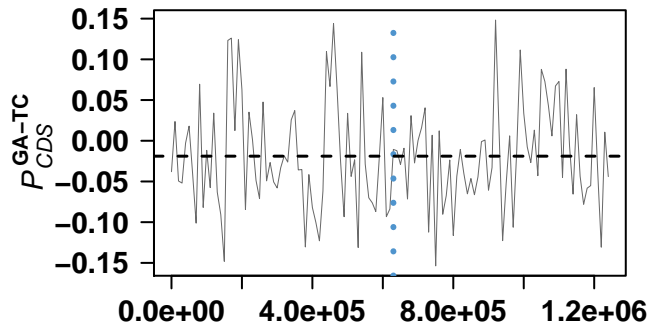
Burkholderia xenovorans LB400



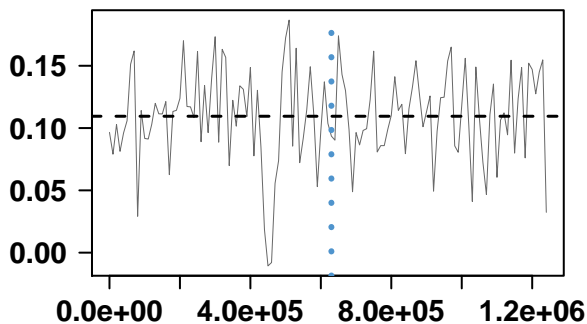
Burkholderia xenovorans LB400



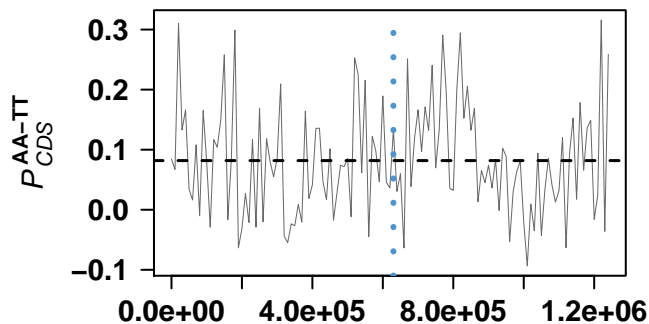
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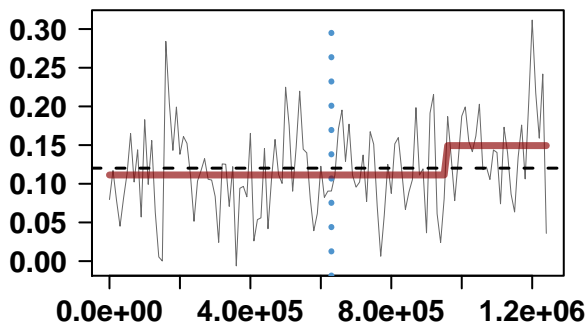
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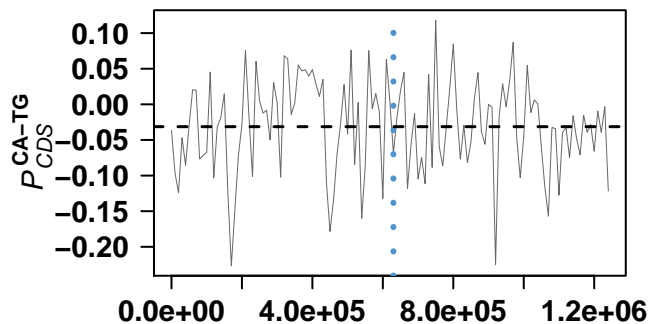
genome coordinates



genome coordinates

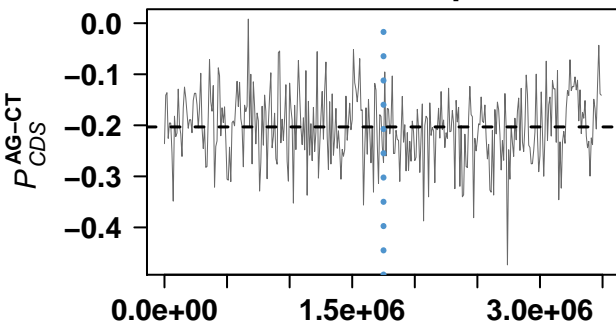


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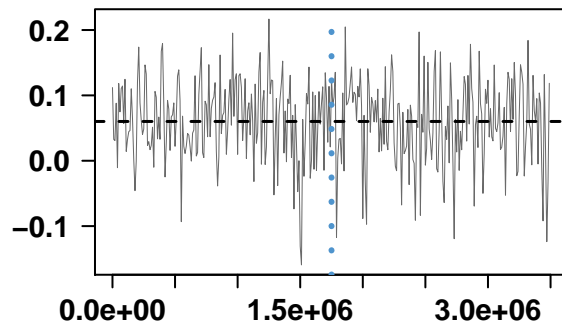


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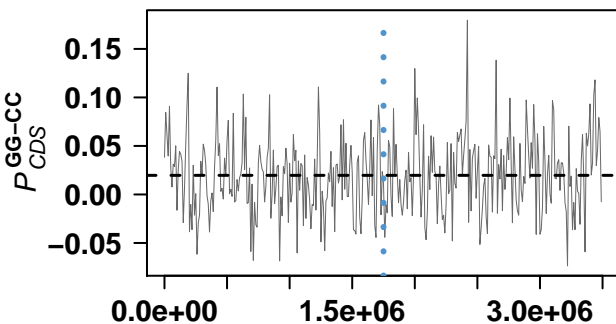
Cupriavidus metallidurans CH34



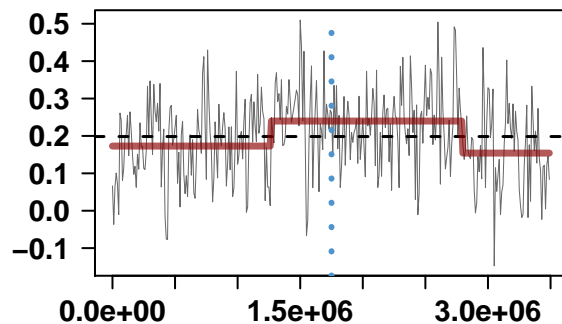
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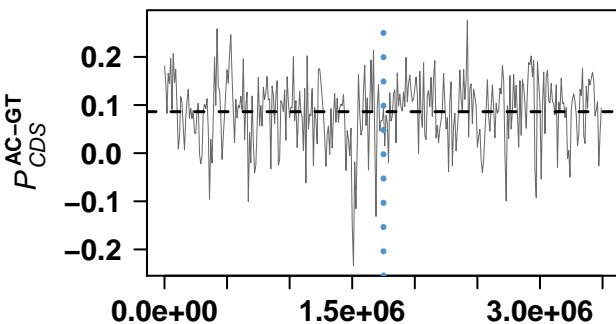
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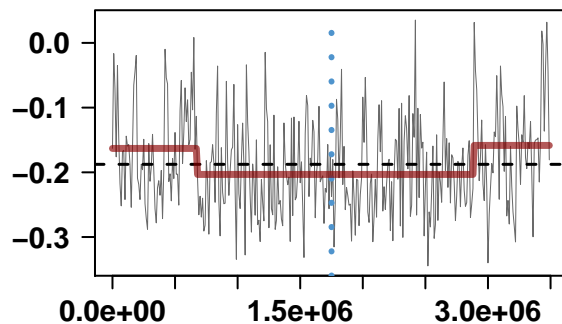
genome coordinates



genome coordinates

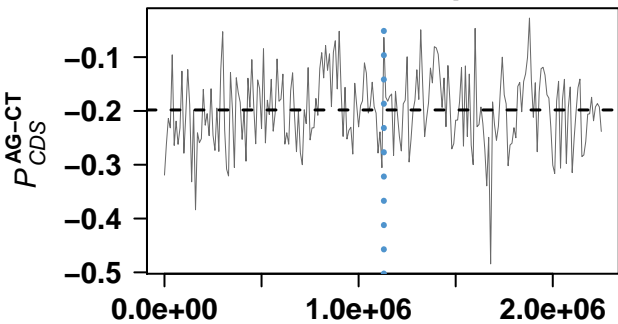


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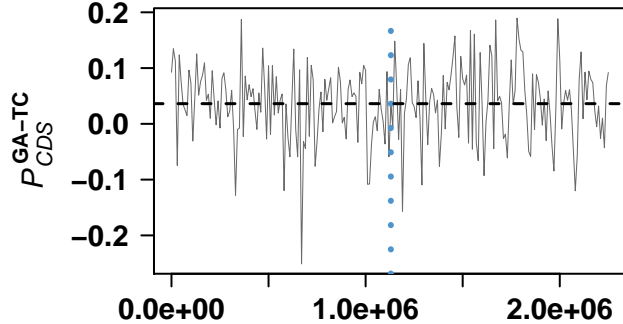


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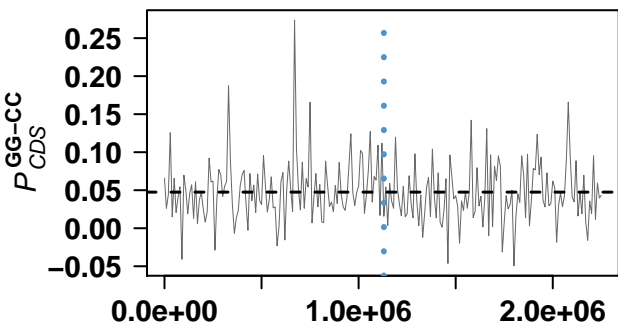
Cupriavidus metallidurans CH34



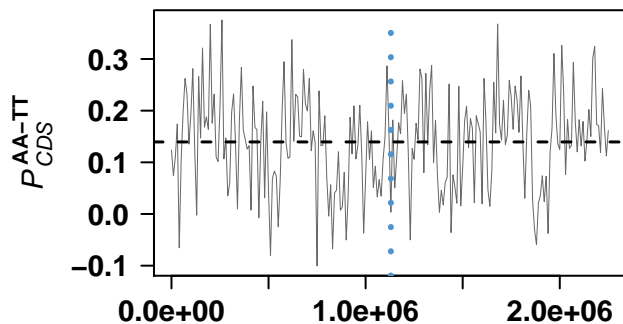
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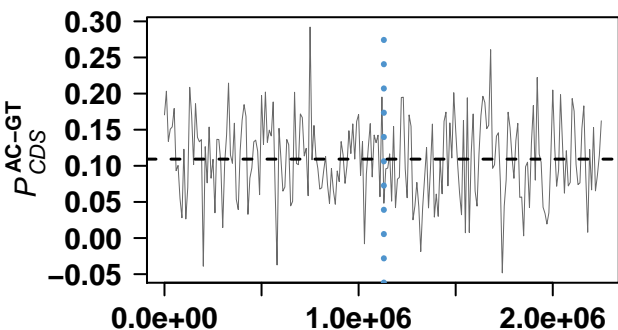
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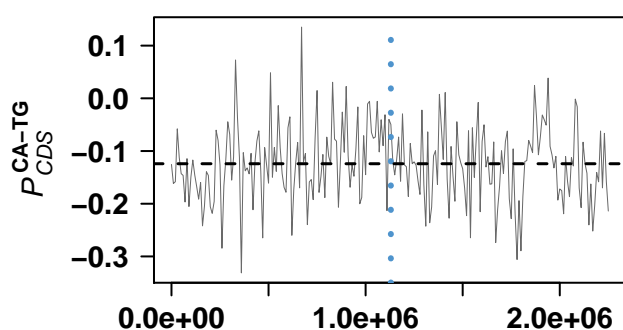
genome coordinates



genome coordinates

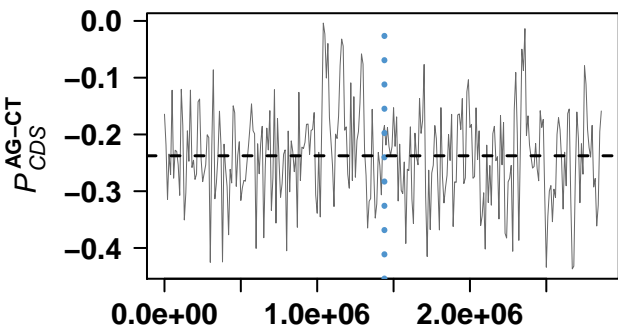


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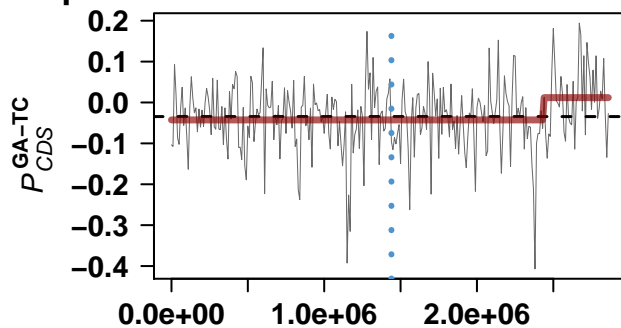


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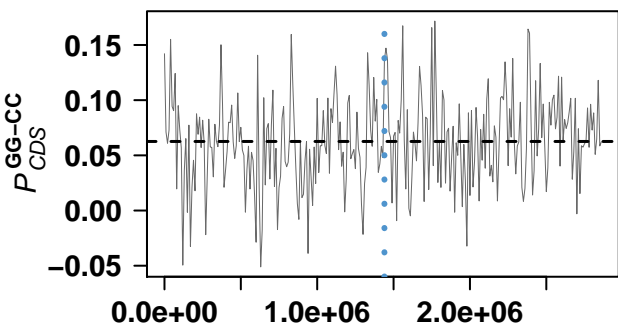
Burkholderia cenocepacia AU 1054



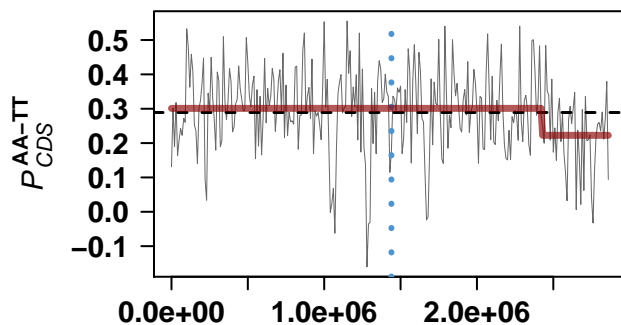
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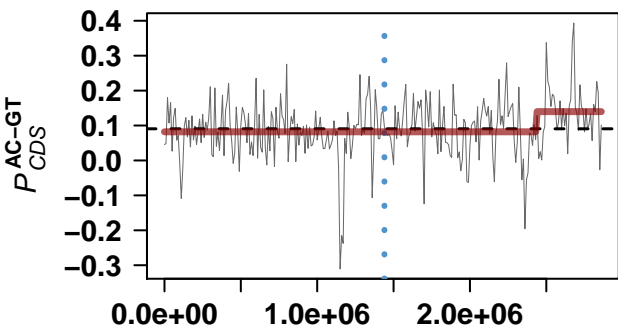
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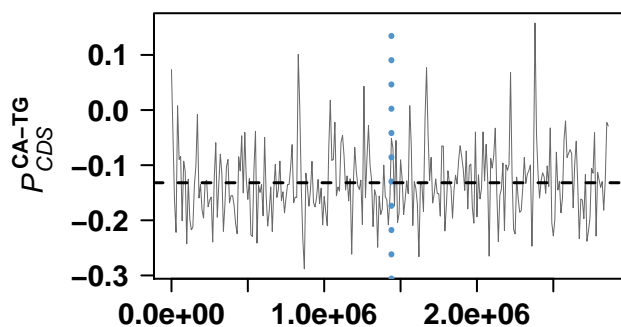
genome coordinates



genome coordinates

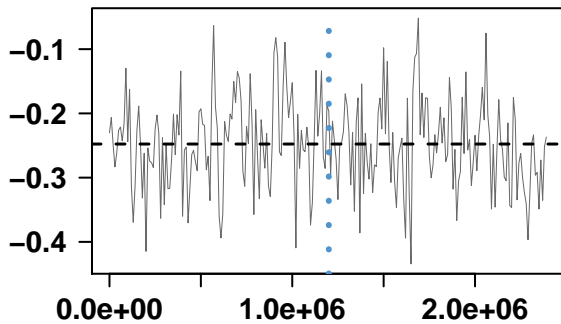


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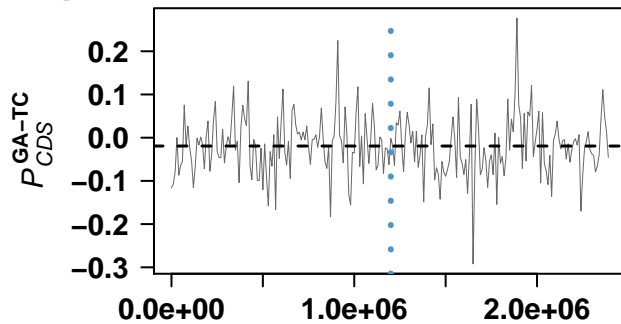


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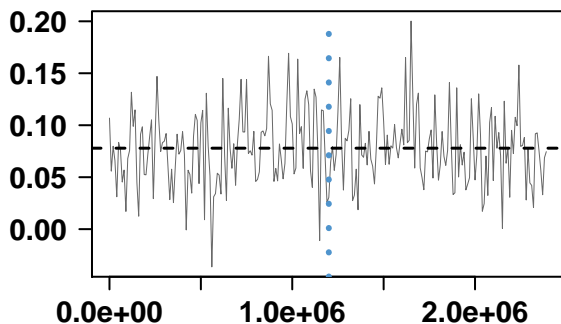
Burkholderia cenocepacia AU 1054



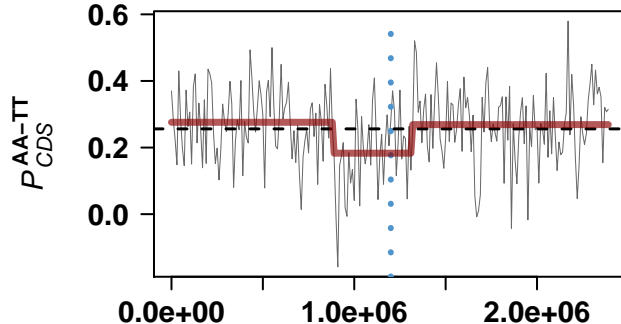
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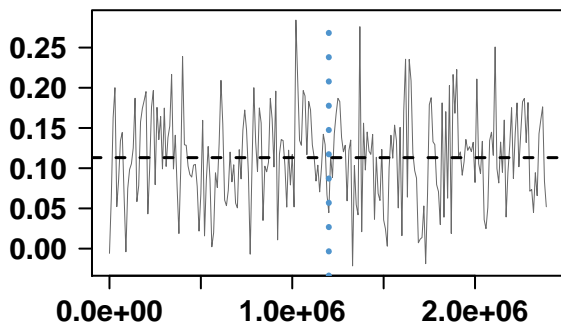
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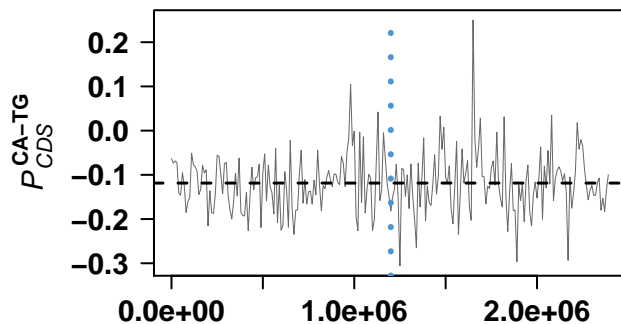
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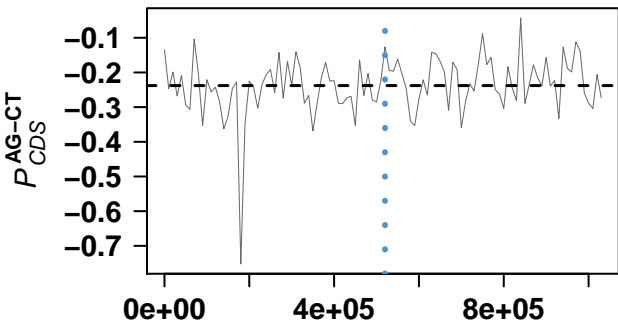


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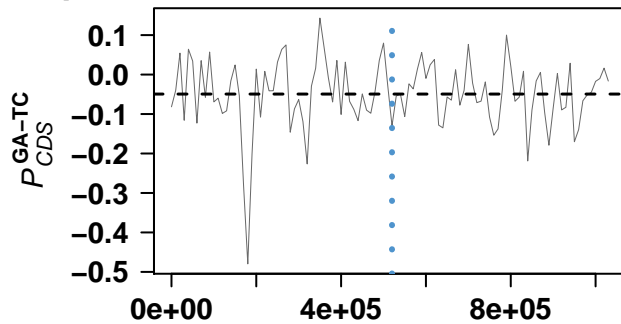


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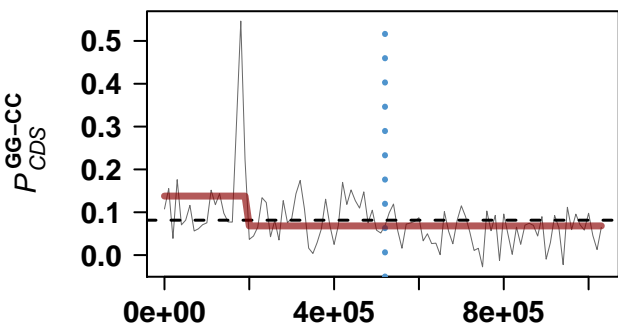
Burkholderia cenocepacia AU 1054



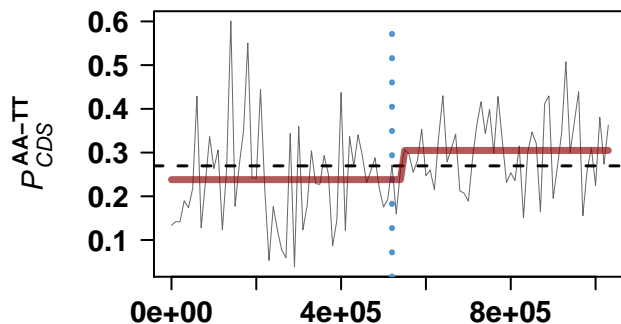
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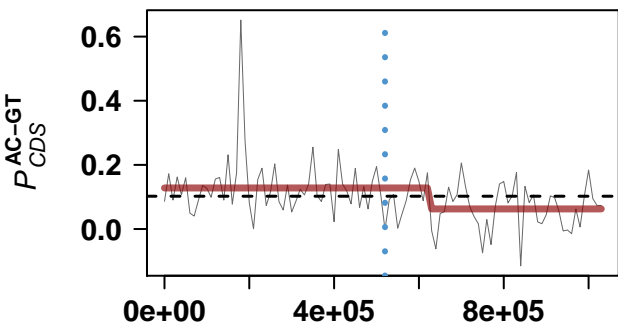
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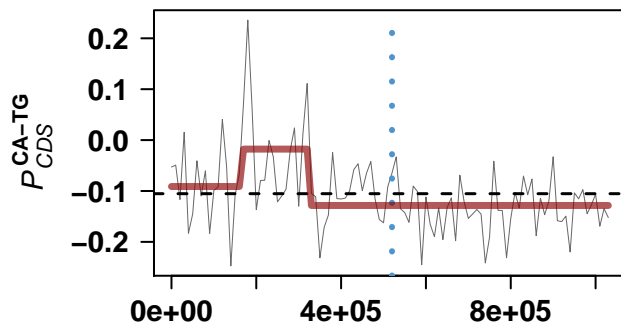
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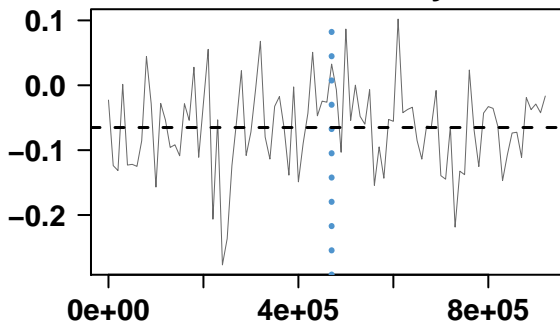


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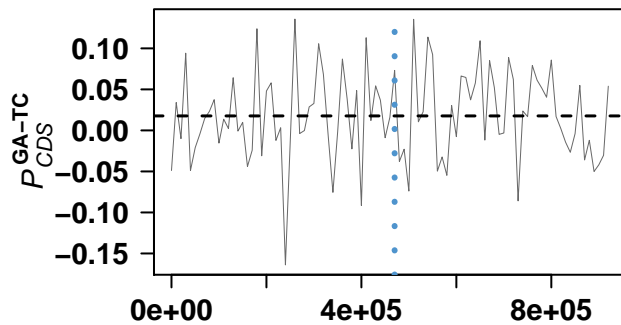


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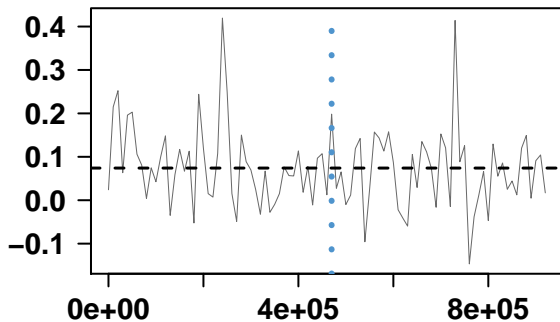
Chlamydia trachomatis D/UW-3/CX



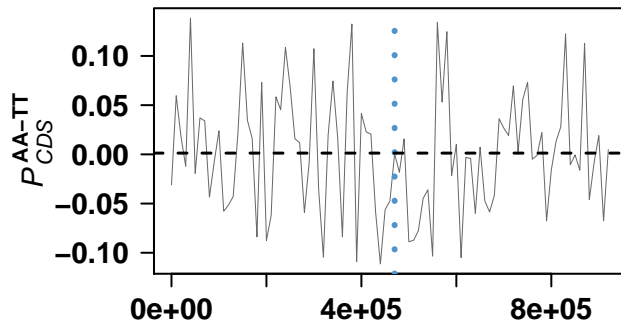
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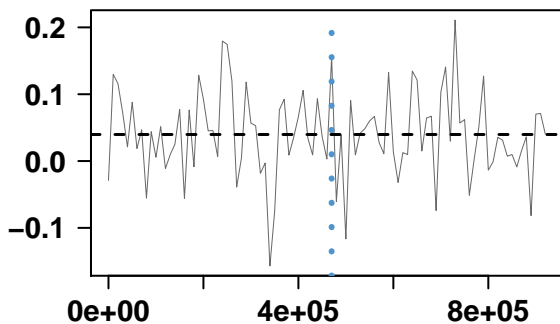
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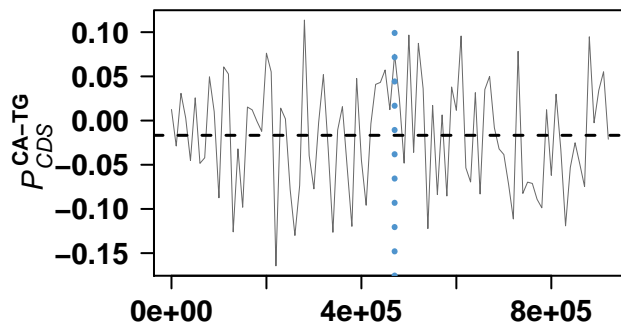
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genome coordinates

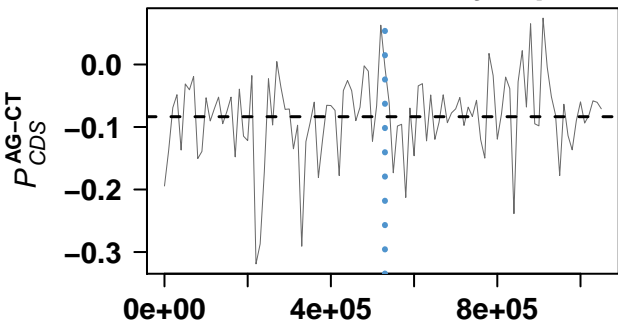


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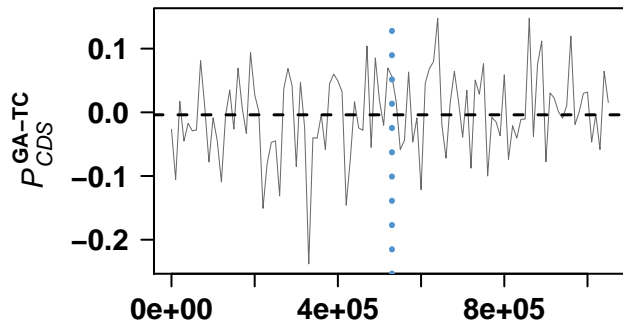


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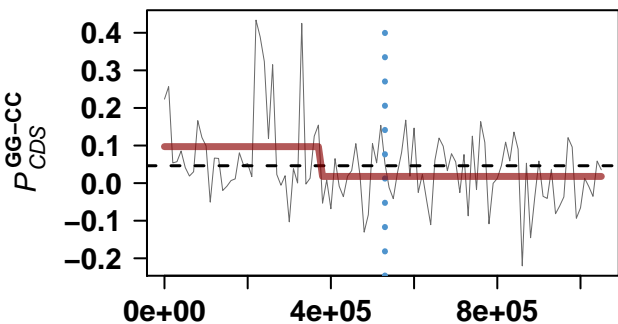
Chlamydophila pneumoniae CWL029



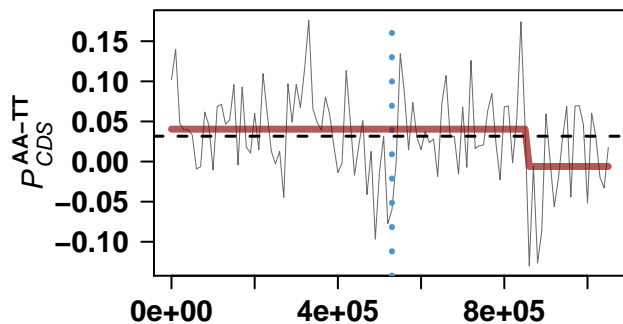
genome coordinates



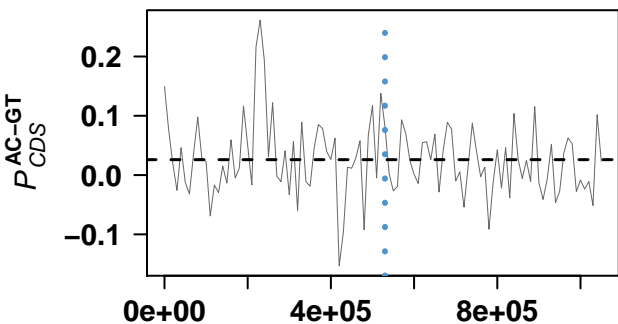
genome coordinates



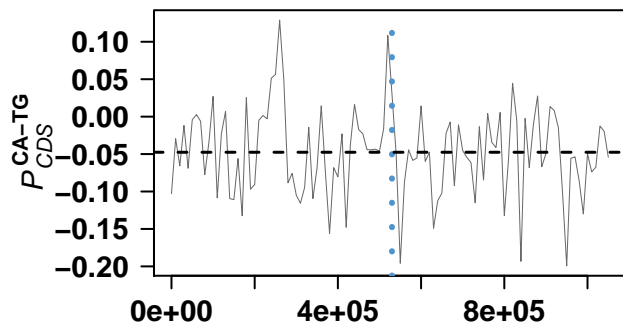
genome coordinates



genome coordinates

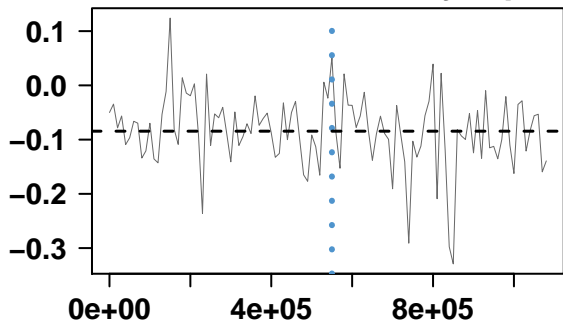


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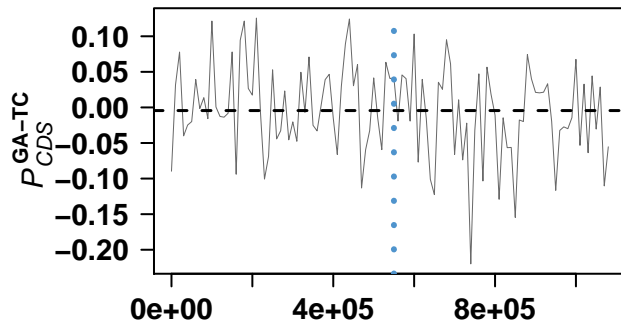


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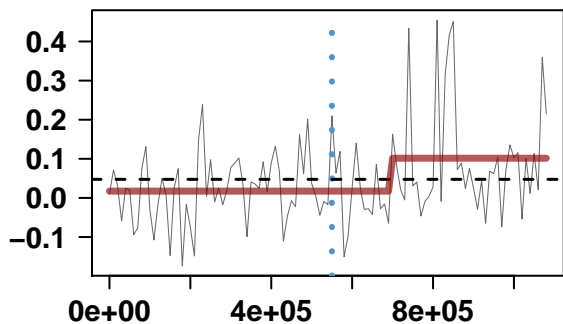
Chlamydophila pneumoniae AR39



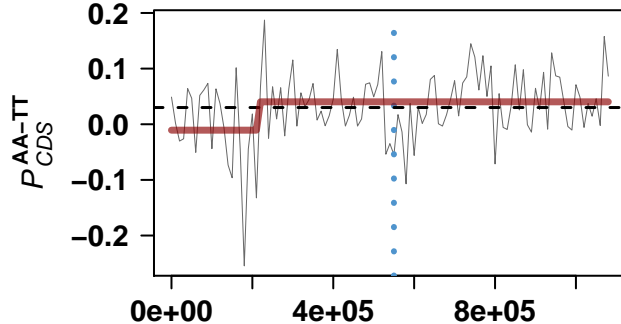
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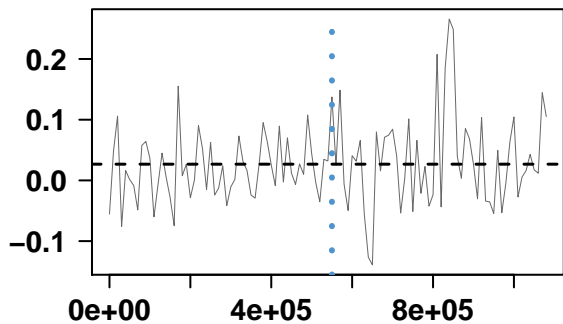
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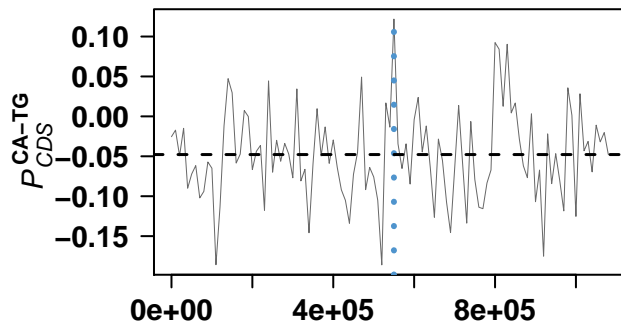
genome coordinates



genome coordinates

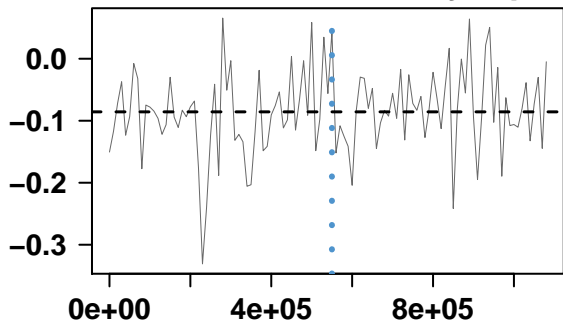


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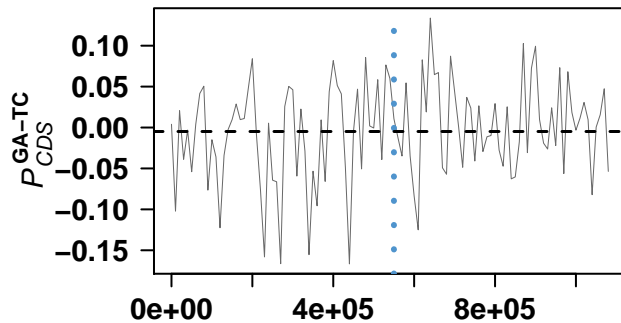


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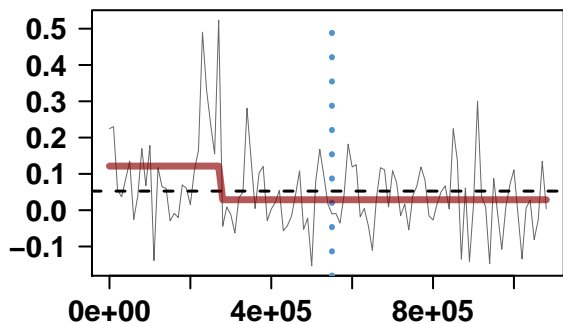
Chlamydomophila pneumoniae J138



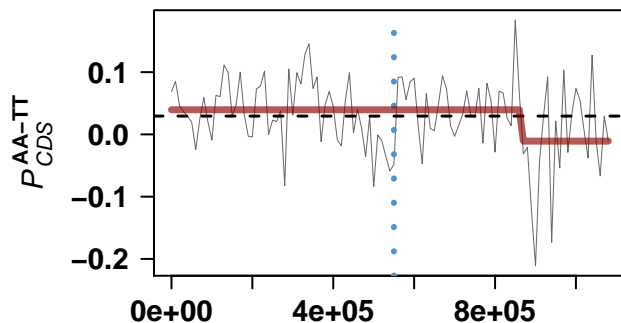
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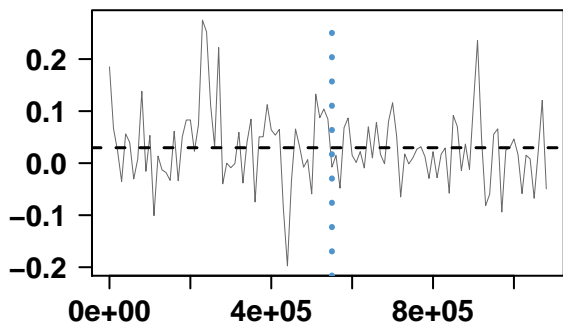
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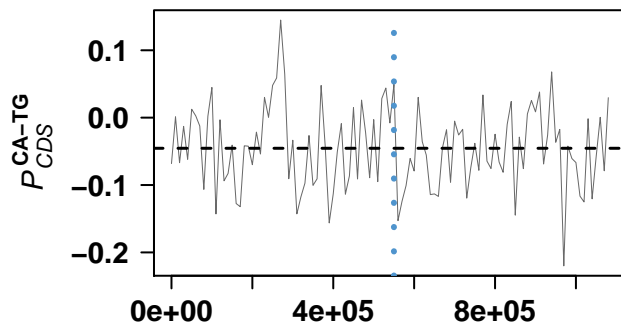
genome coordinates



genome coordinates

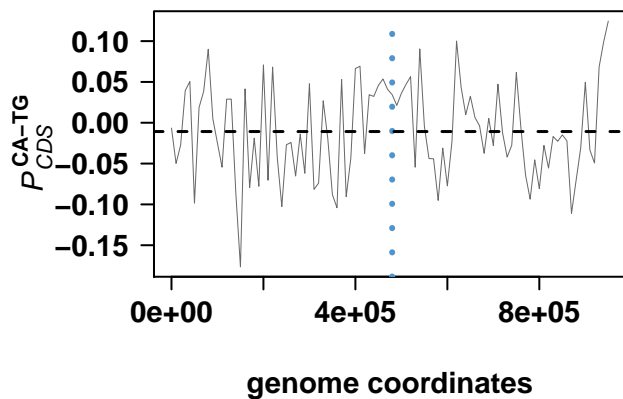
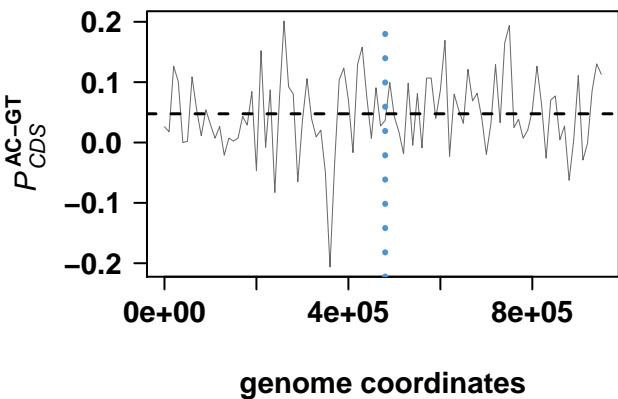
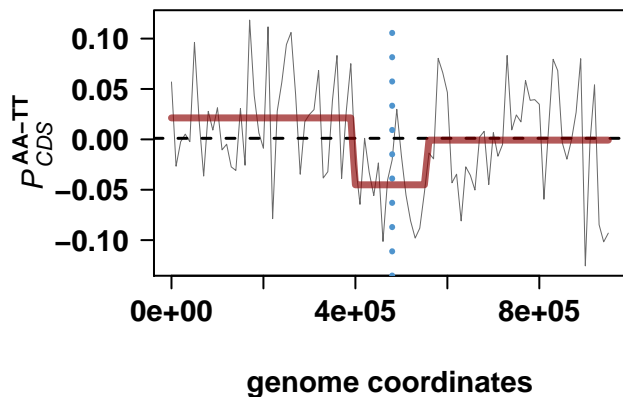
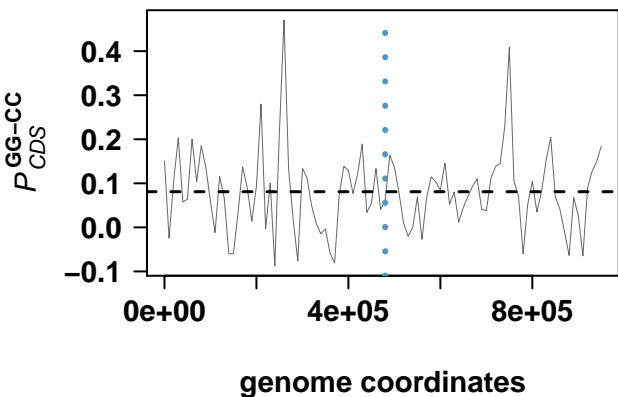
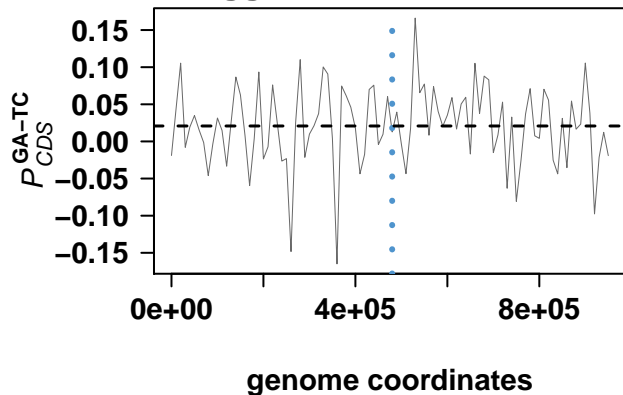
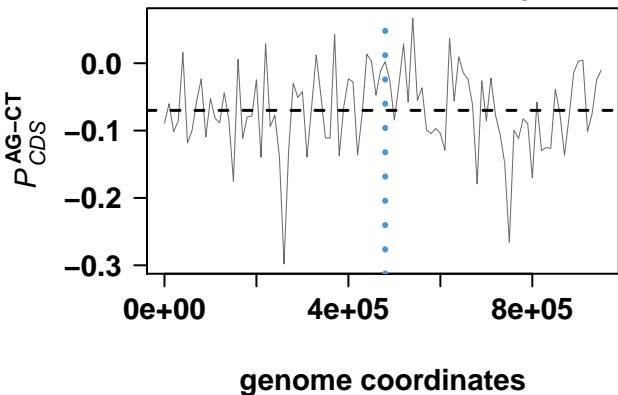


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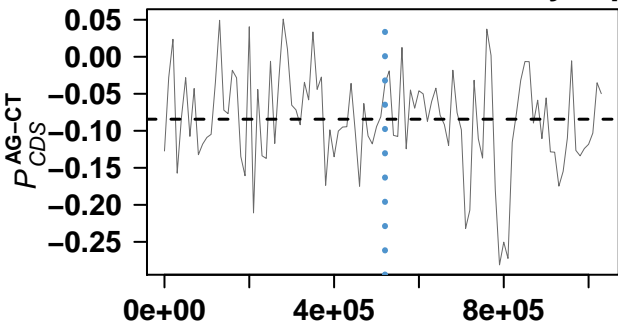


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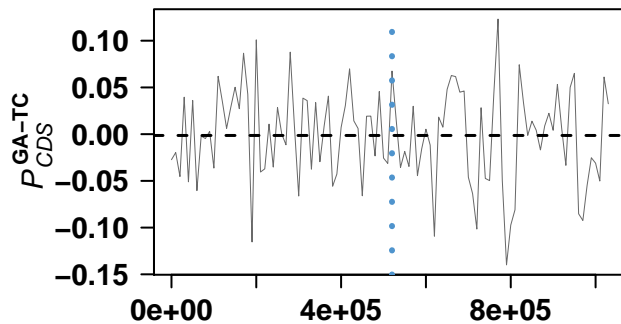
Chlamydia muridarum str. Nigg



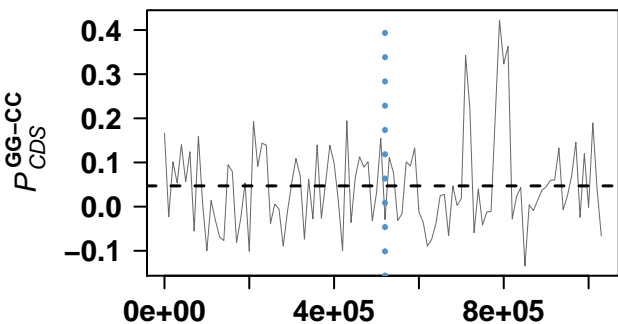
Chlamydomonas reinhardtii GPIC



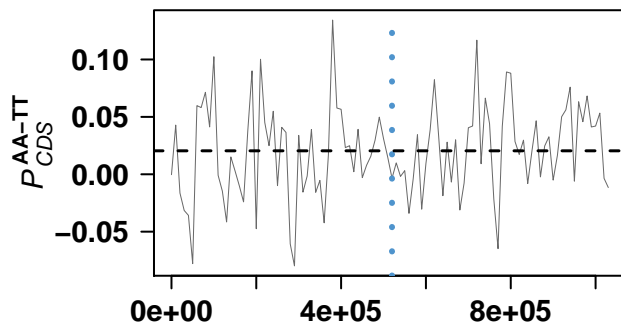
genome coordinates



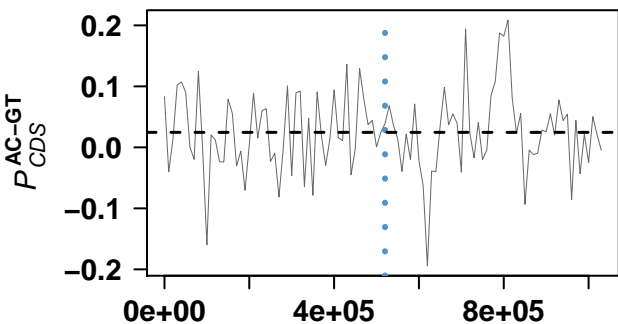
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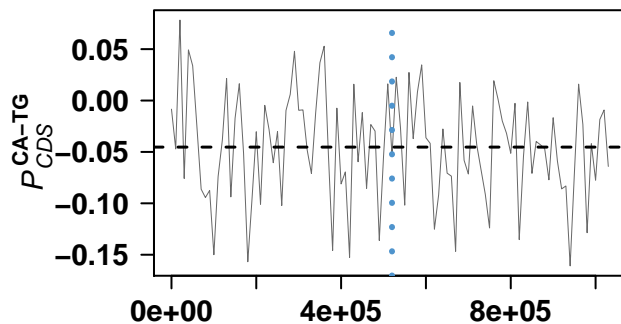
genome coordinates



genome coordinates

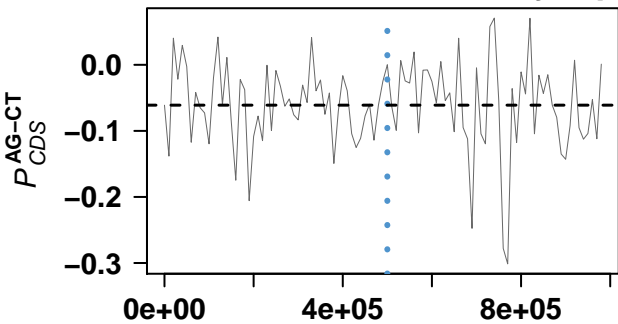


genome coordinates

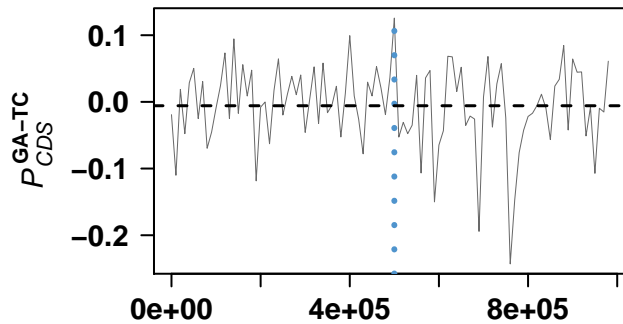


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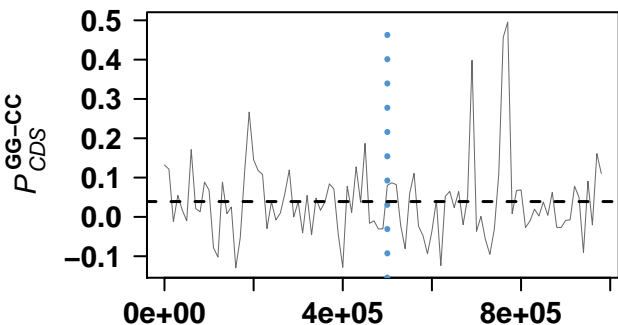
Chlamydomonas abortus S26/3



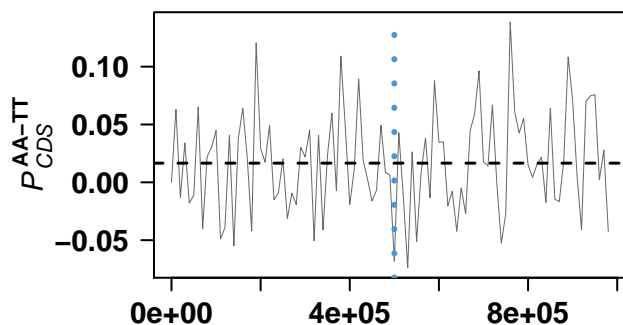
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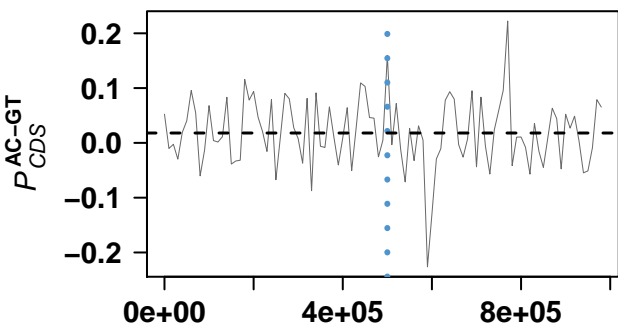
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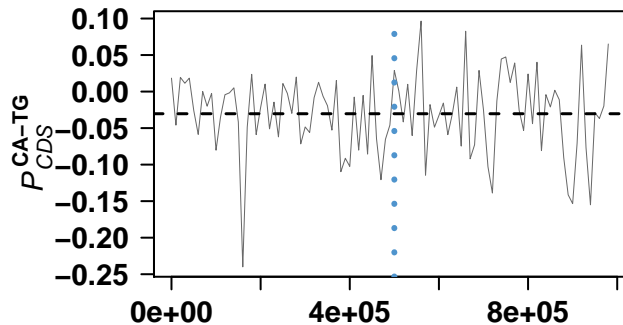
genome coordinates



genome coordinates

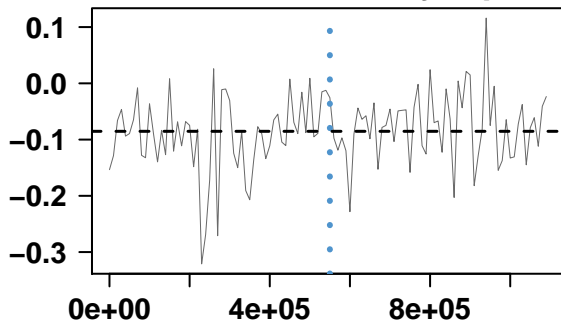


genome coordinates

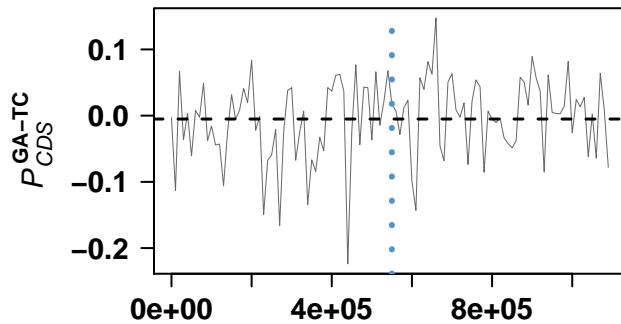


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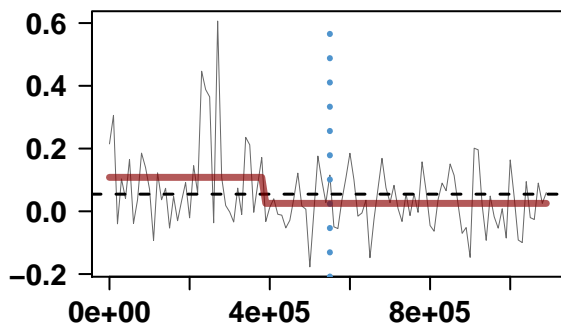
Chlamydophila pneumoniae TW-183



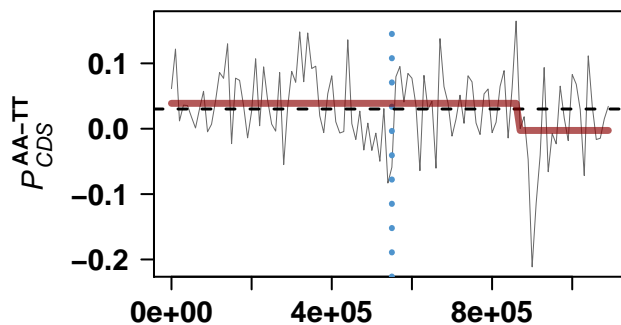
genome coordinates



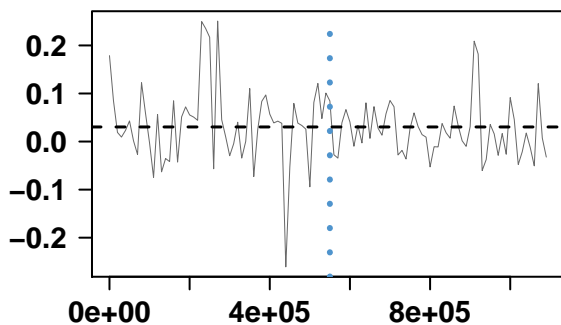
genome coordinates



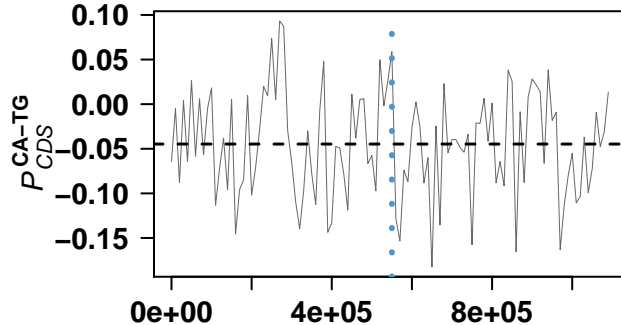
genome coordinates



genome coordinates

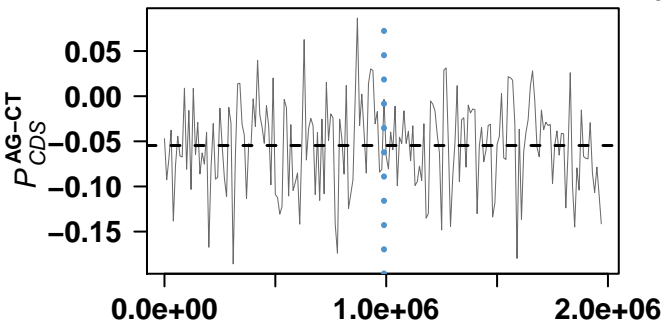


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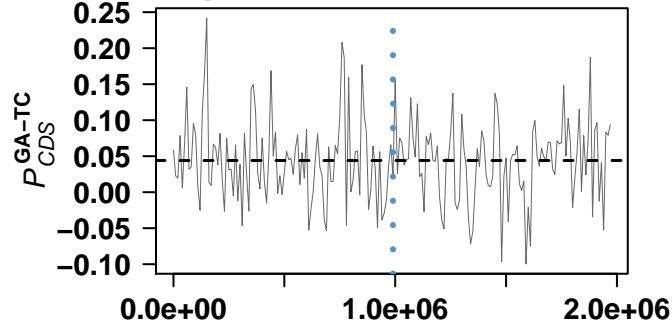


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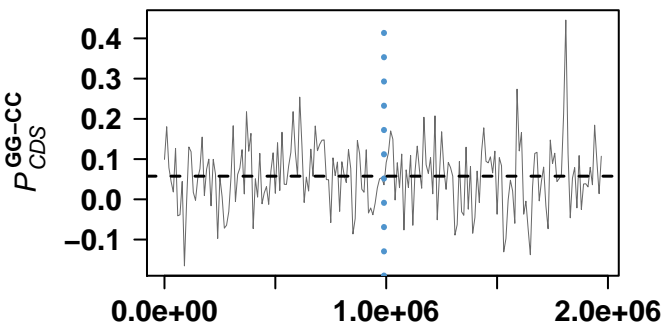
Candidatus Protochlamydia amoebophila UWE25



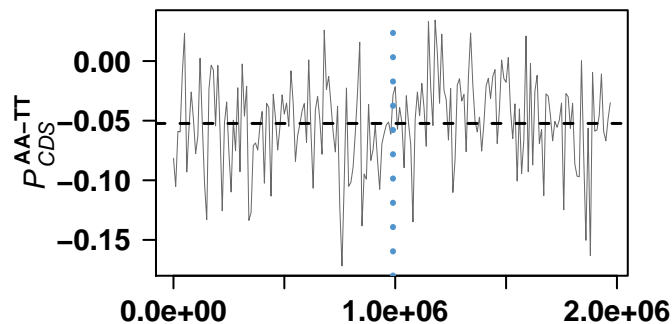
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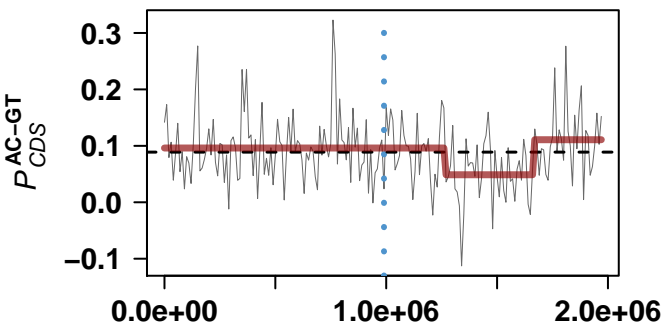
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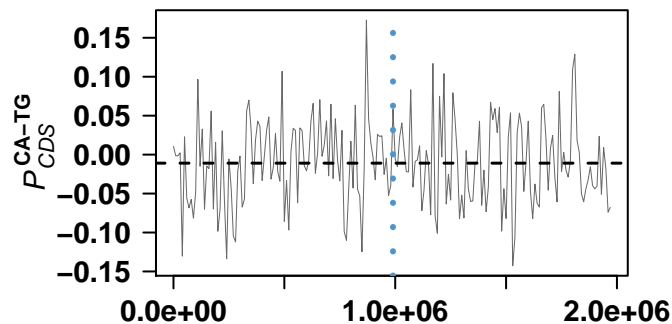
genome coordinates



genome coordinates

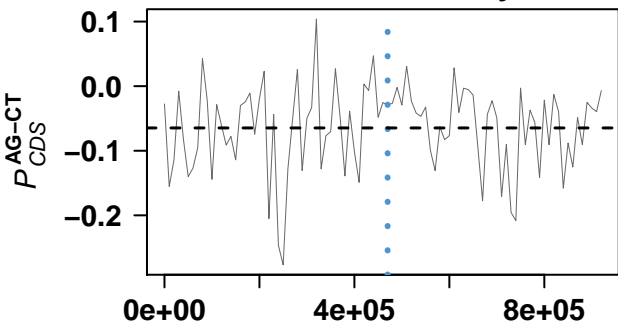


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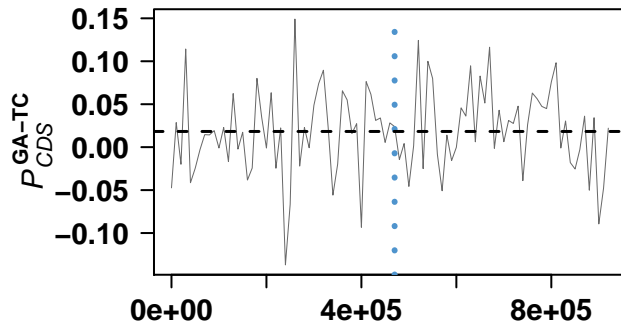


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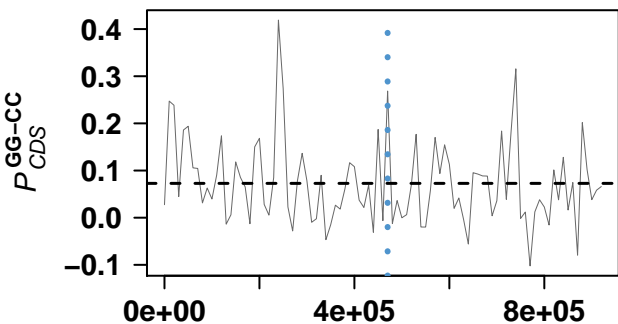
Chlamydia trachomatis A/HAR-13



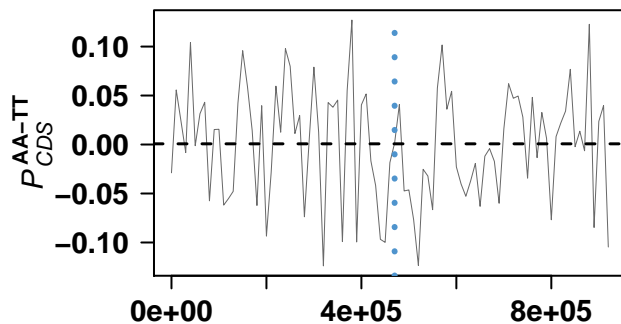
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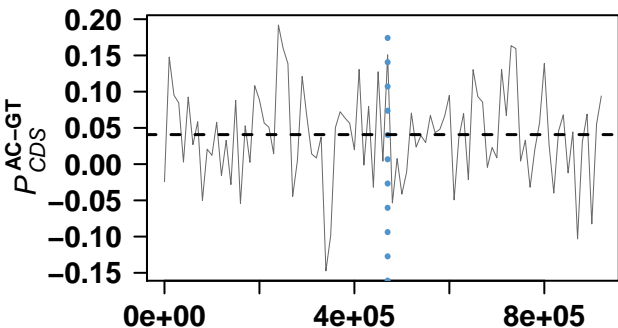
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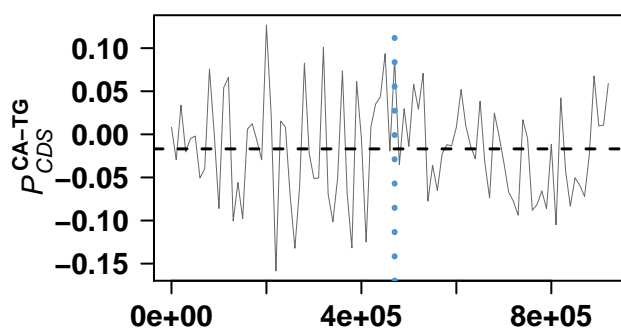
genome coordinates



genome coordinates

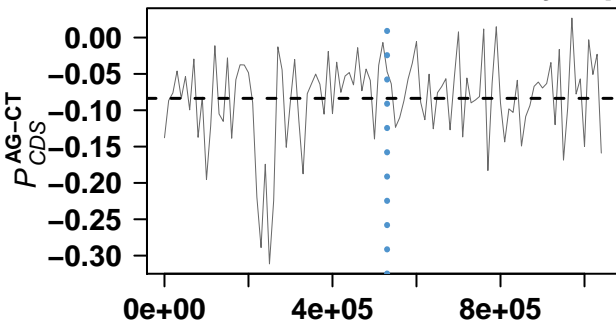


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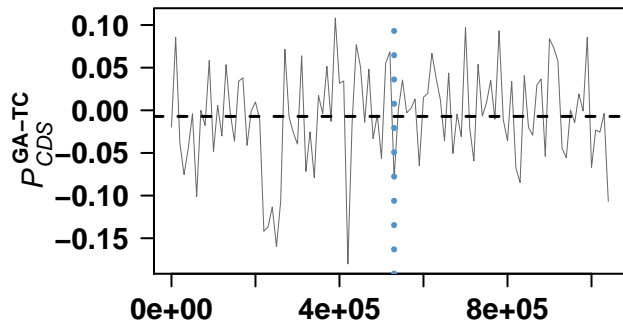


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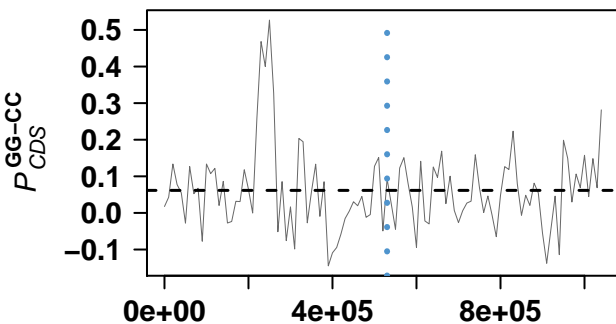
Chlamydophila felis Fe/C-56



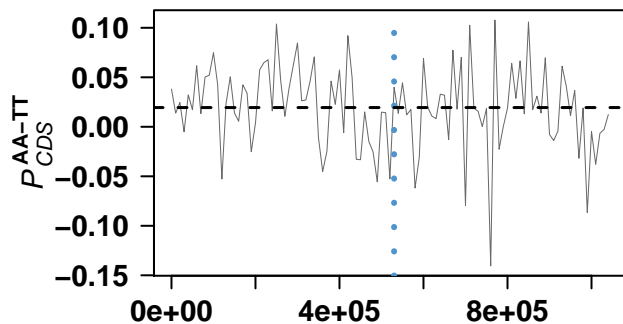
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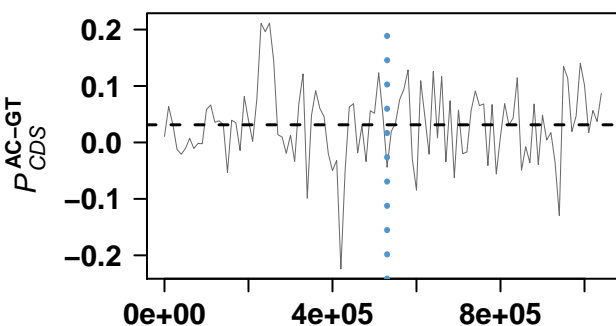
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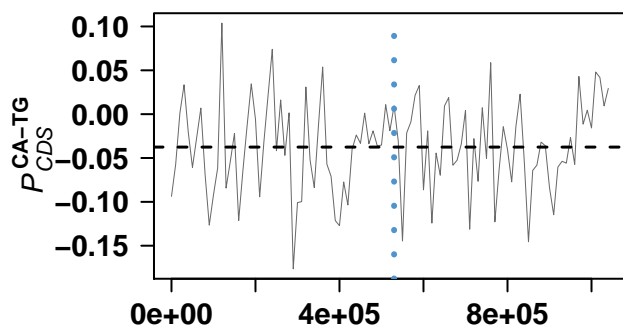
genome coordinates



genome coordinates

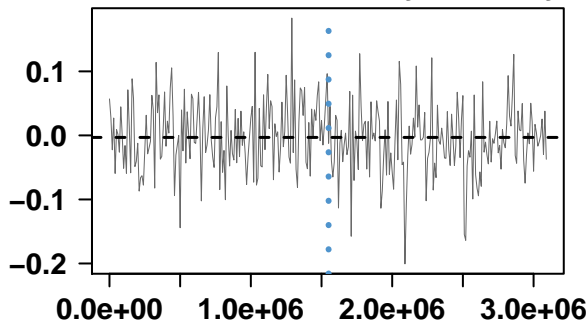


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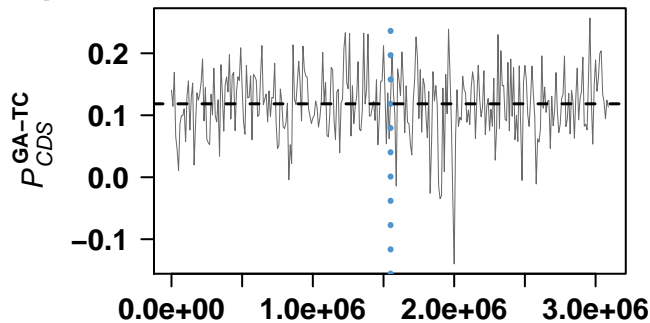


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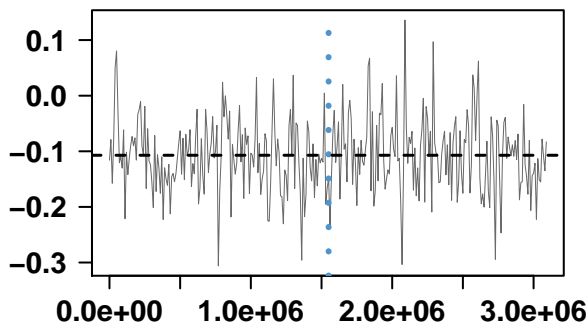
Synechocystis sp. PCC 6803



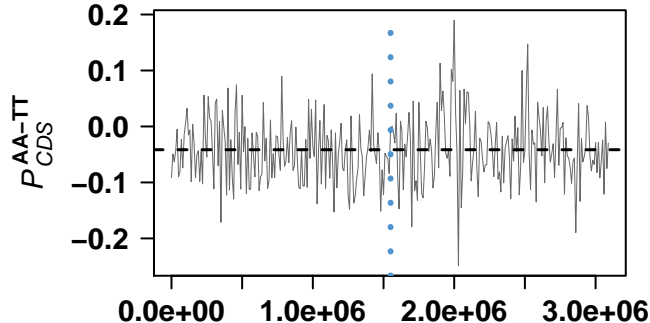
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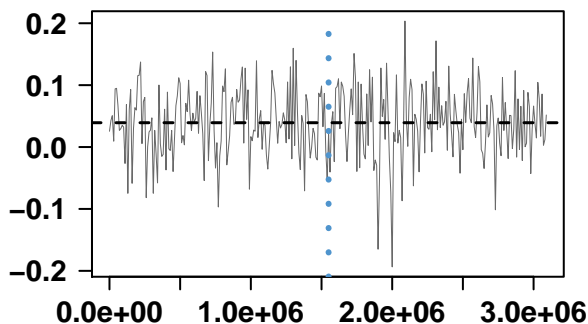
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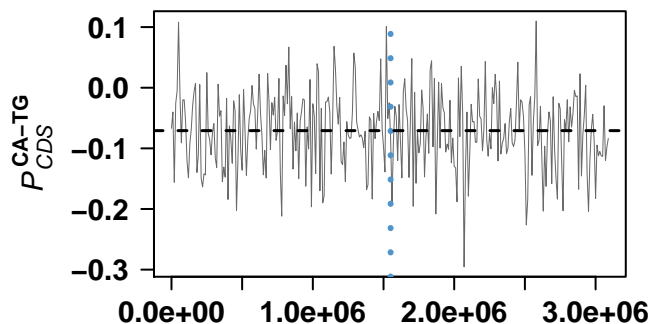
genome coordinates



genome coordinates

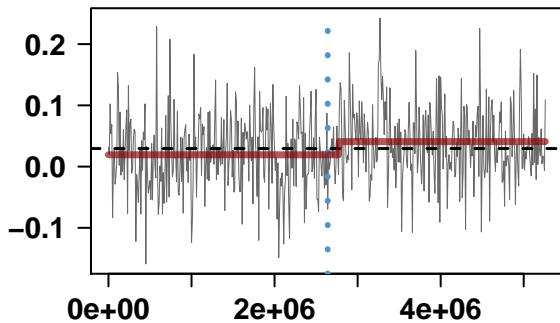


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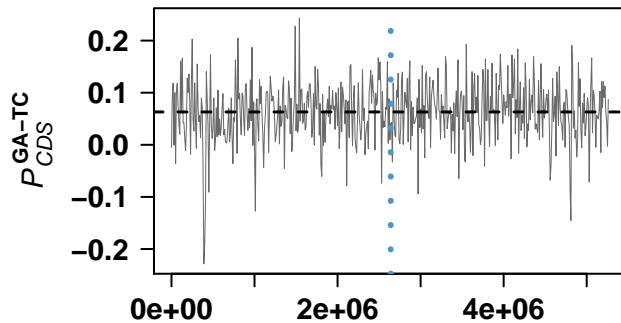


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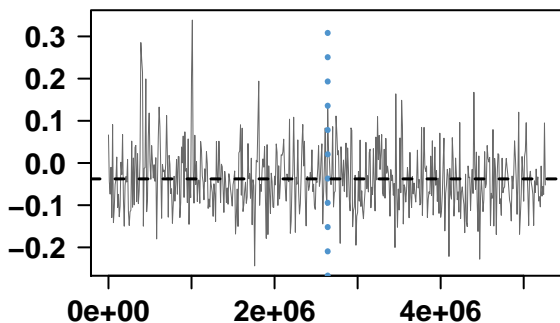
Nostoc sp. PCC 7120



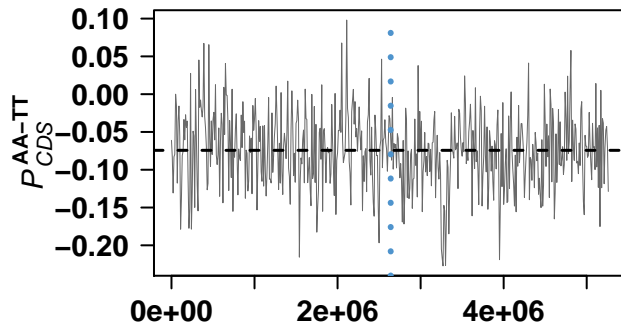
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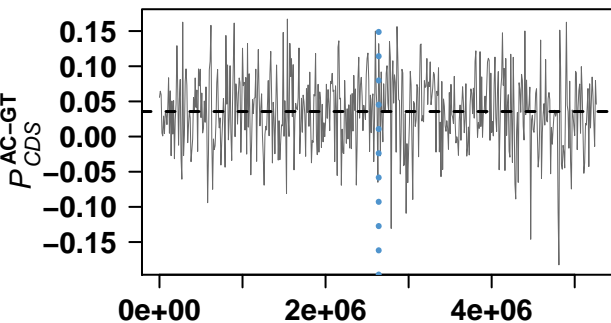
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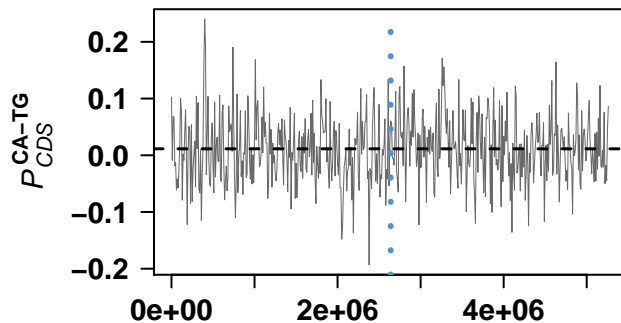
genome coordinates



genome coordinates

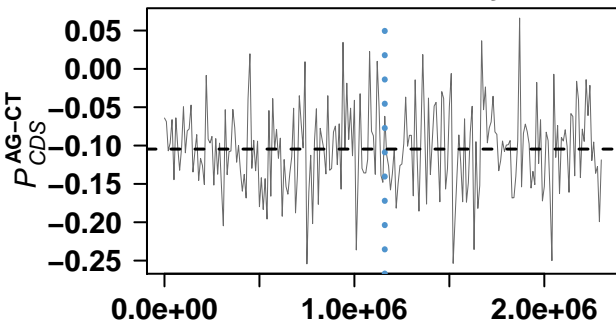


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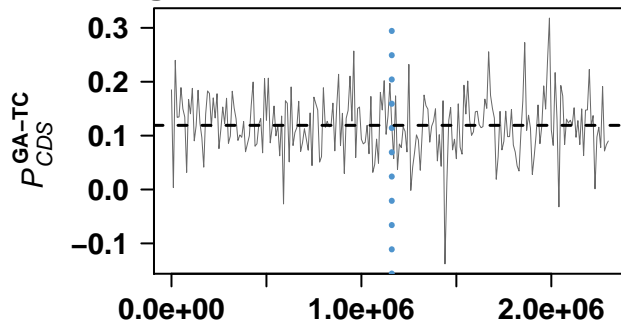


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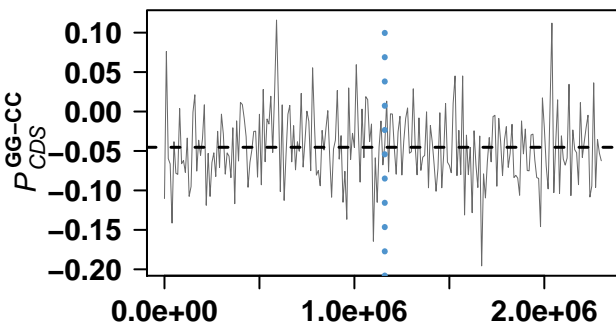
Thermosynechococcus elongatus BP-1



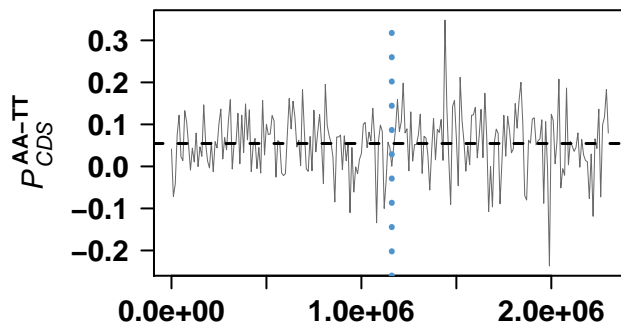
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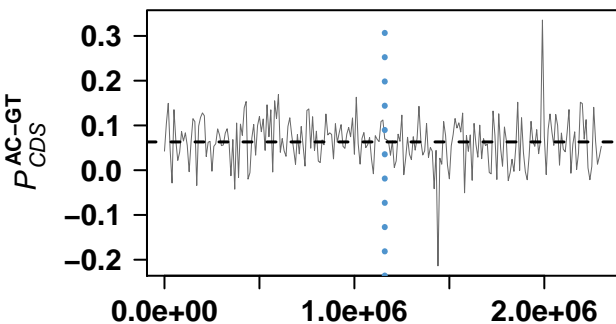
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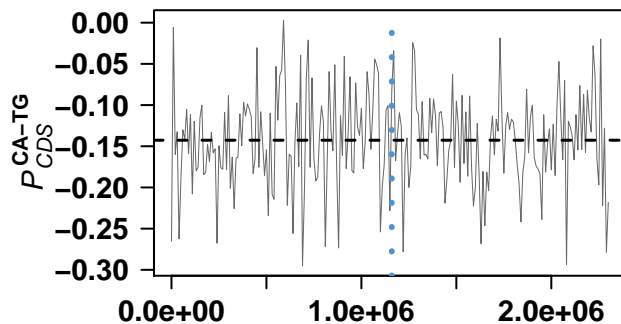
genome coordinates



genome coordinates

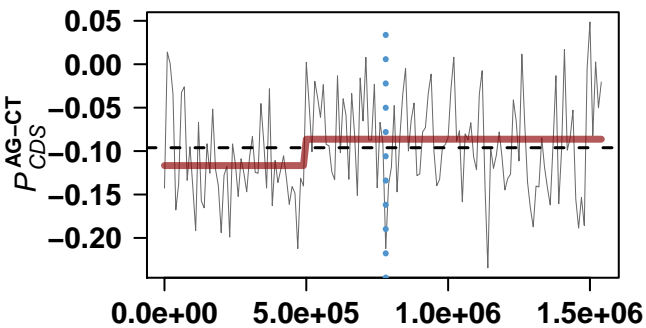


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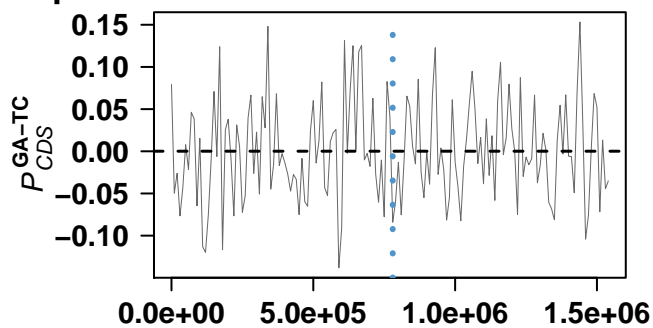


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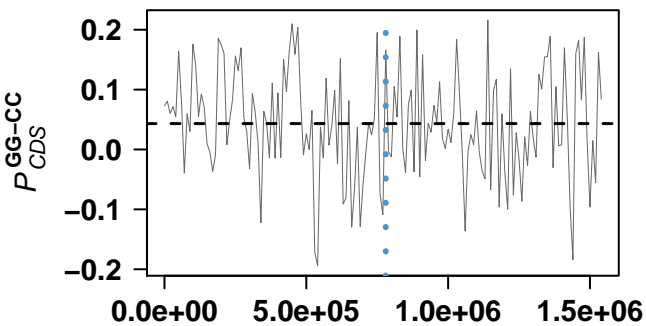
Prochlorococcus marinus subsp. marinus str. CCMP1375



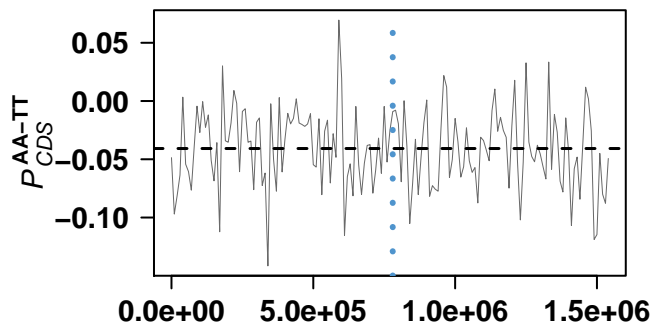
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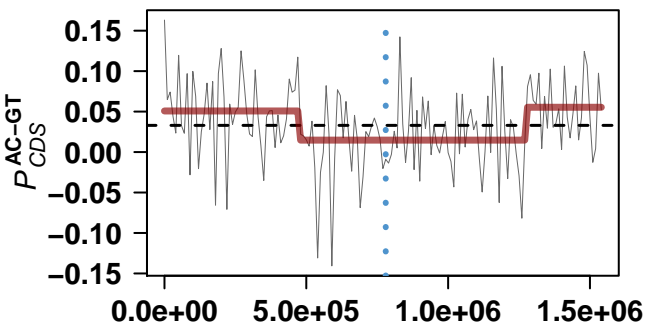
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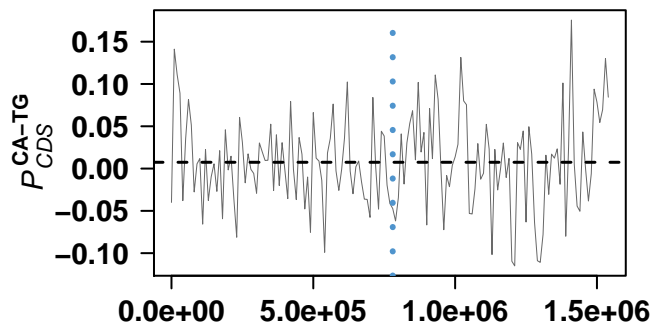
genome coordinates



genome coordinates

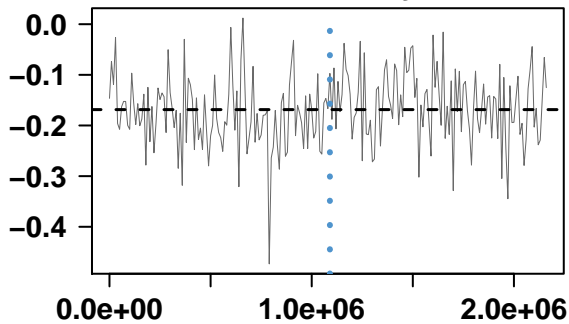


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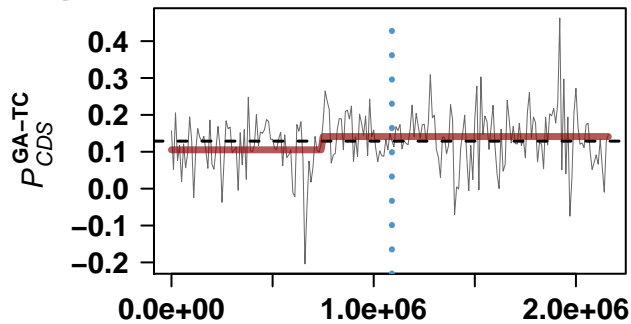


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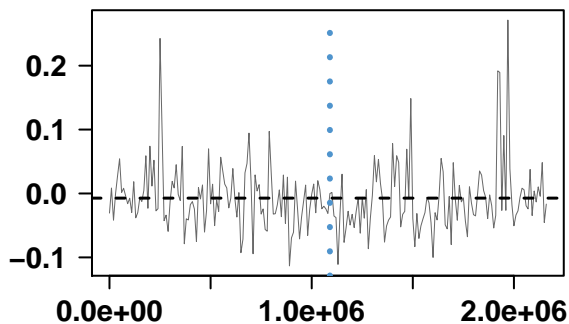
Synechococcus sp. WH 8102



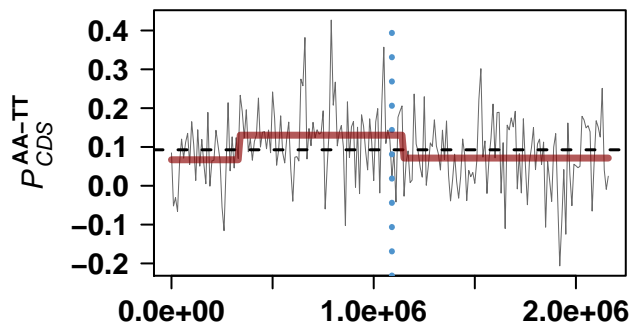
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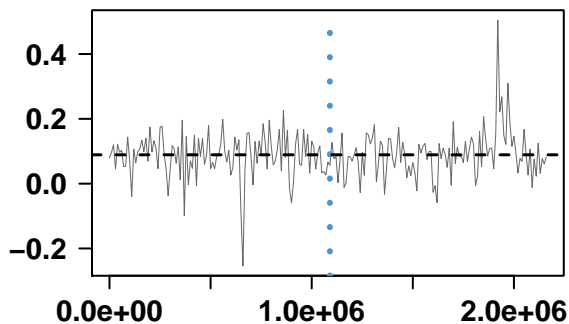
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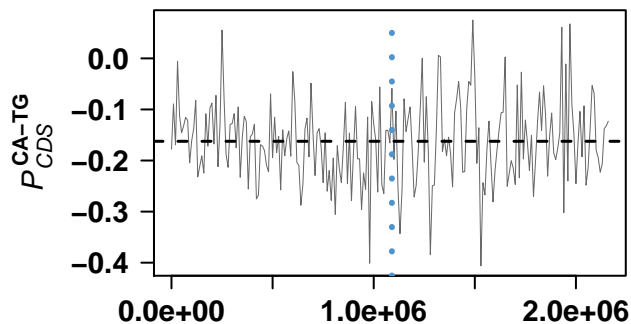
genome coordinates



genome coordinates

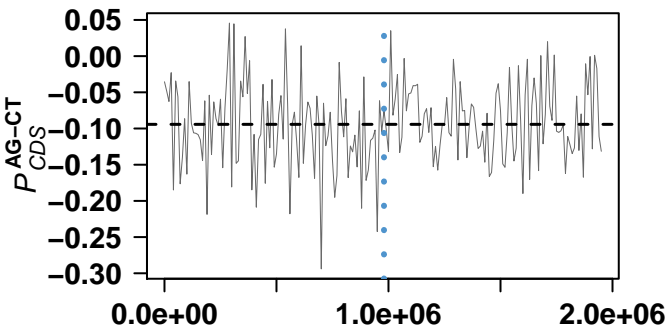


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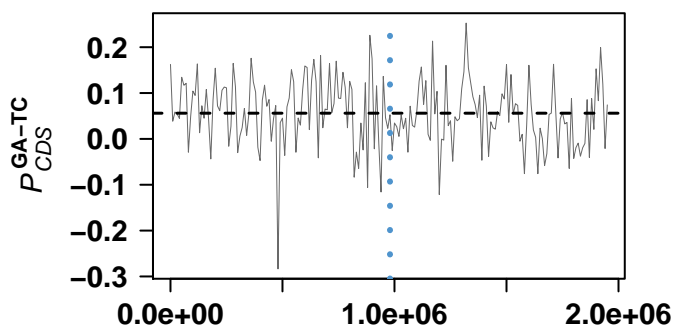


genome coordinates

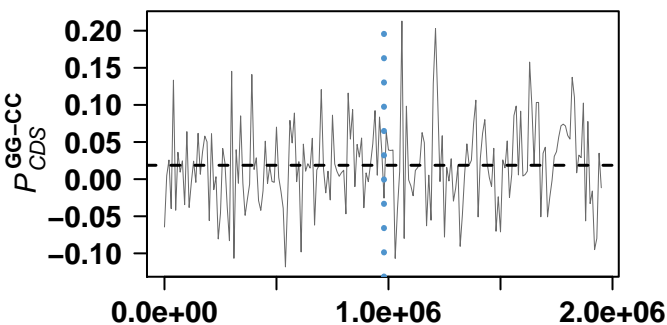
Prochlorococcus marinus str. MIT 9313



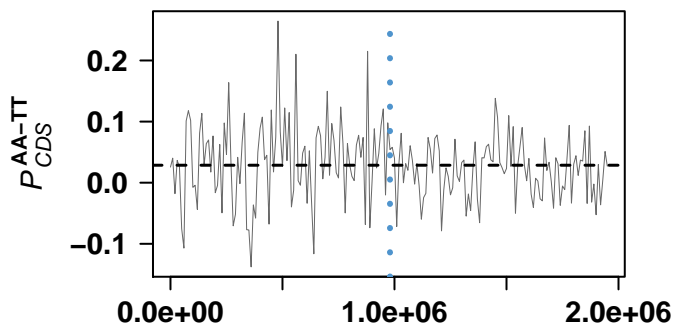
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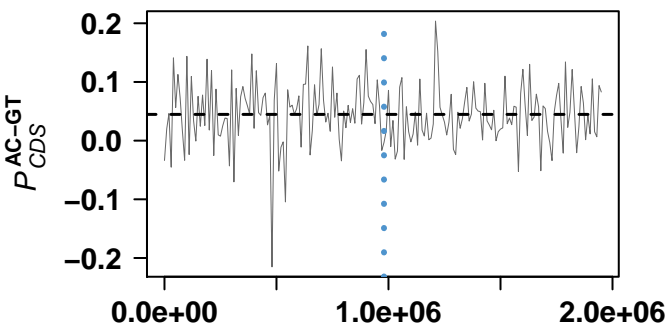
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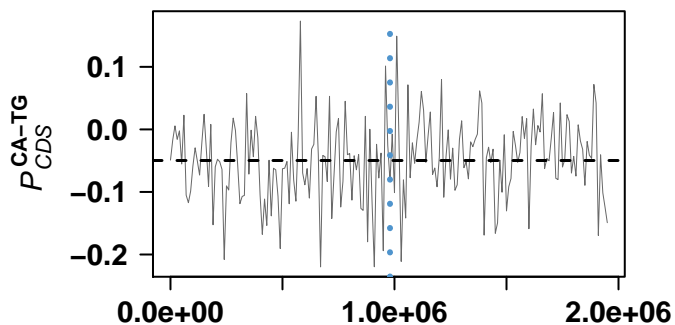
genome coordinates



genome coordinates

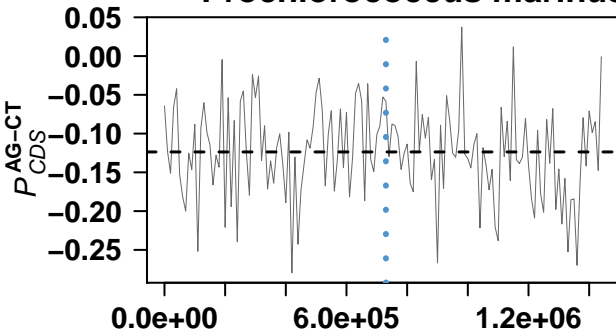


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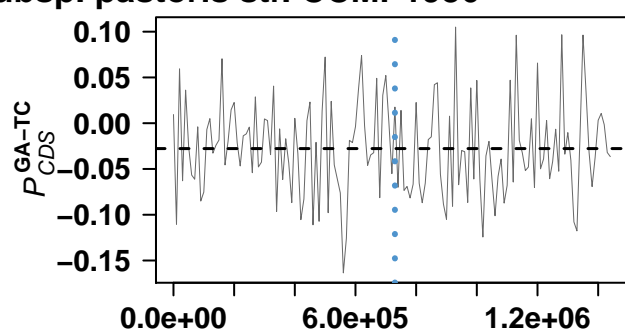


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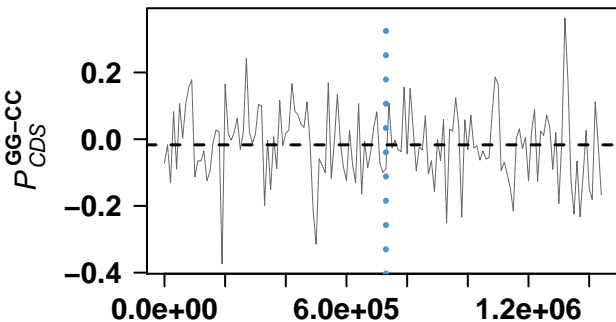
Prochlorococcus marinus subsp. pastoris str. CCMP1986



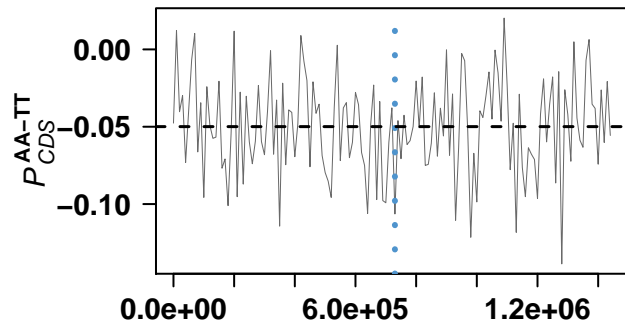
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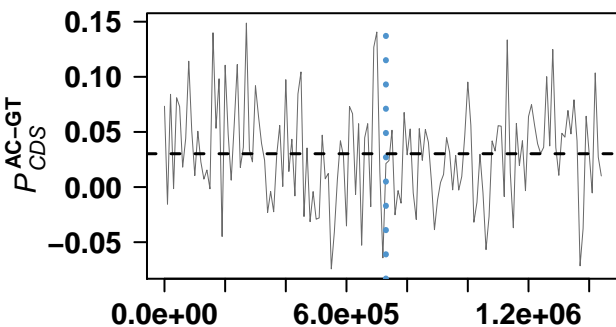
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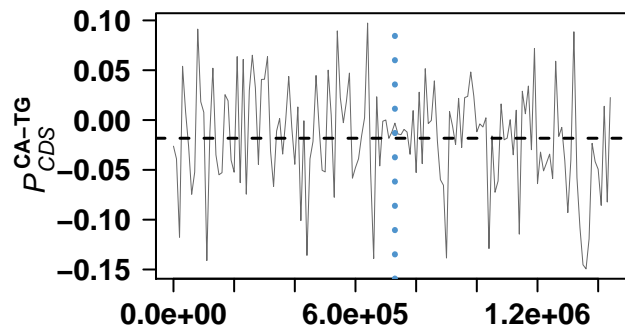
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genome coordinates

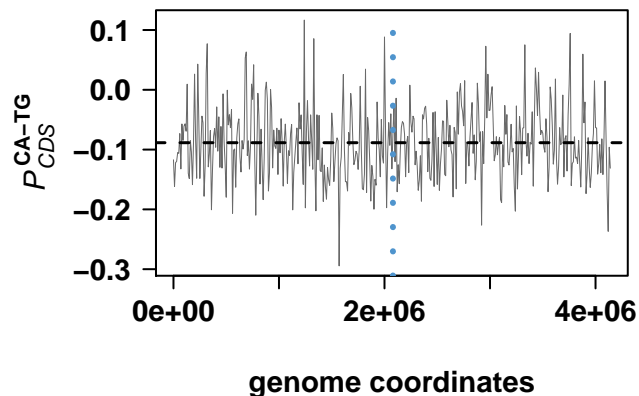
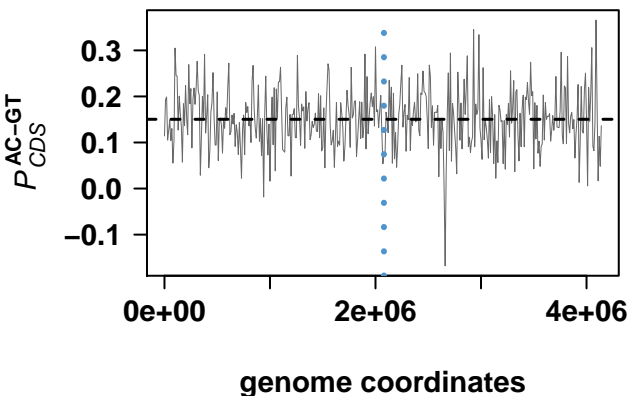
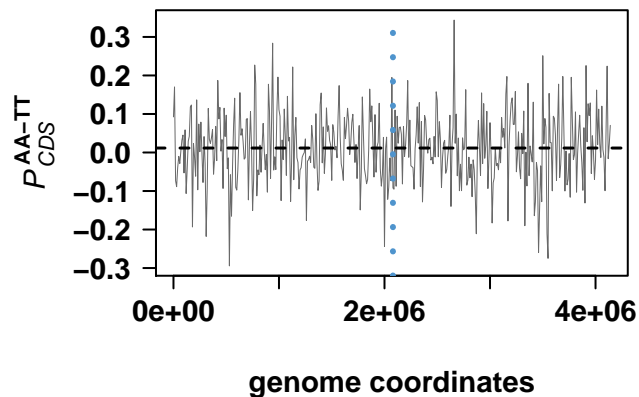
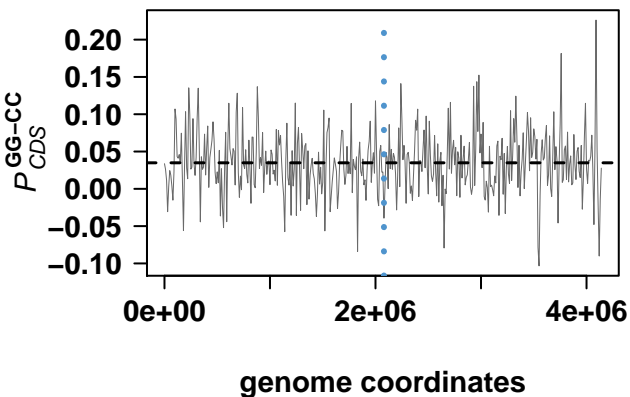
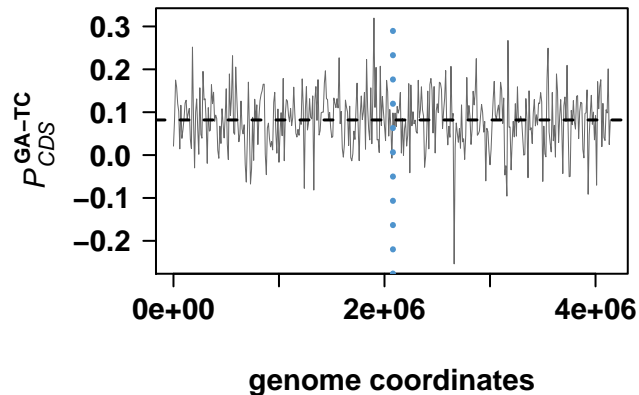
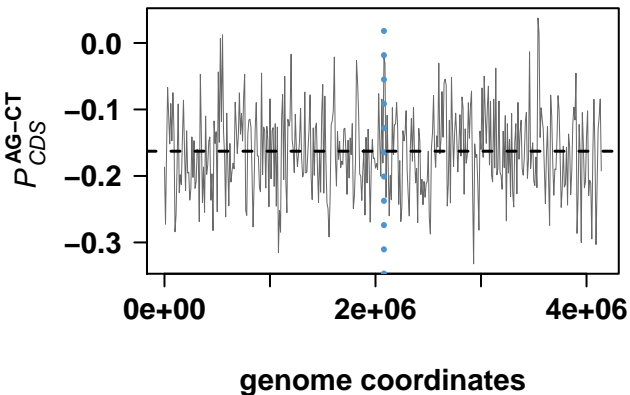


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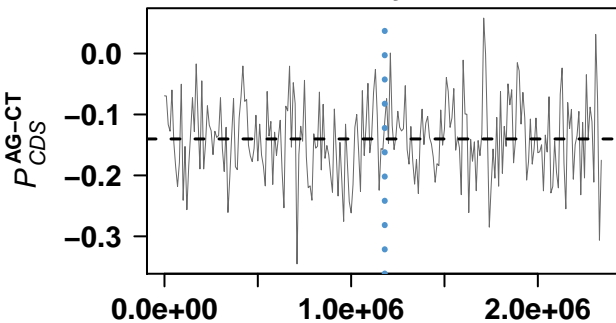


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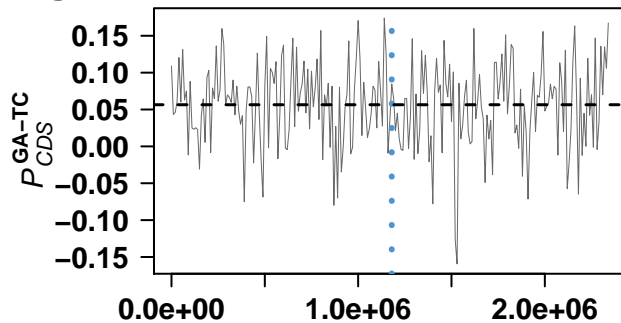
Gloeobacter violaceus PCC 7421



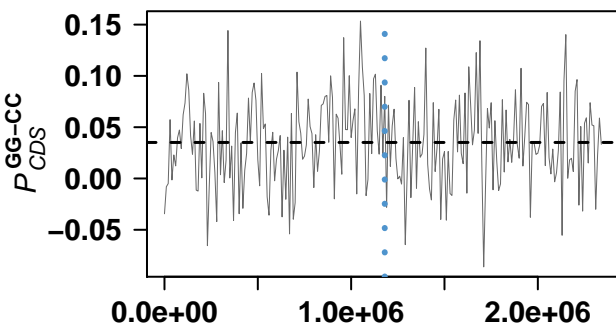
Synechococcus elongatus PCC 6301



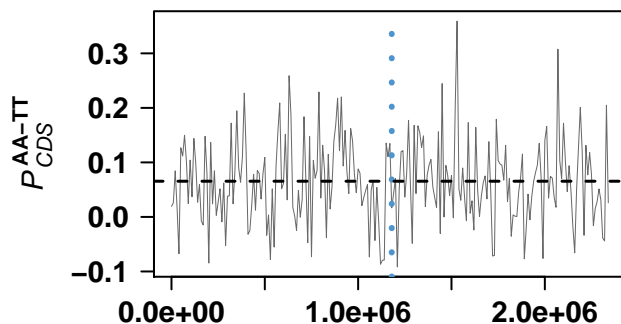
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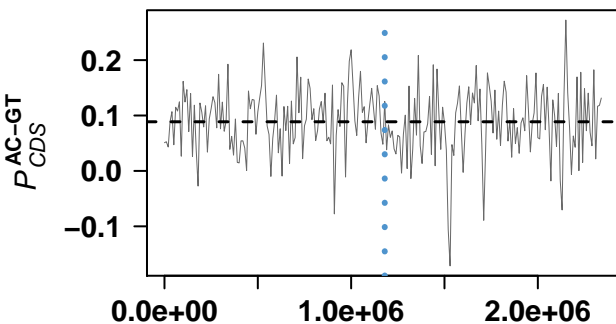
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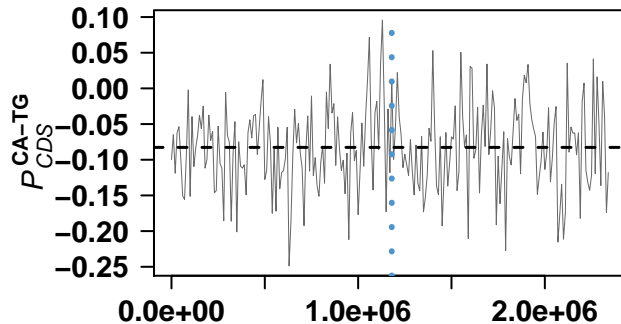
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genome coordinates

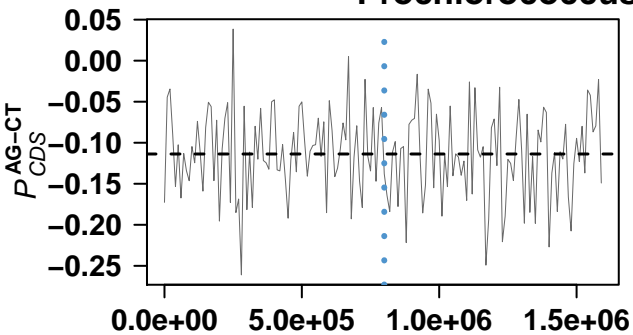


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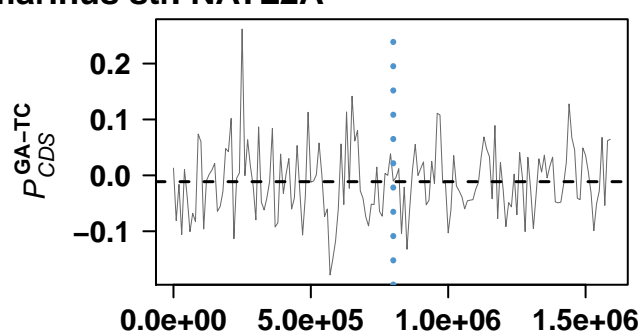


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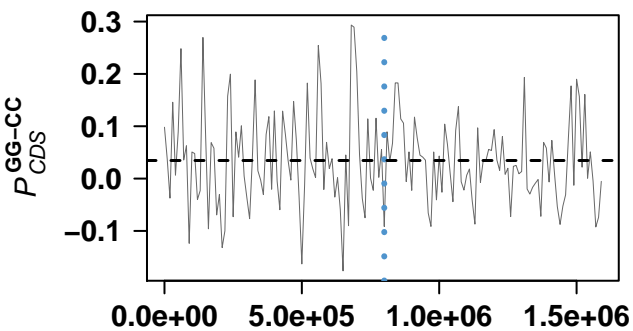
Prochlorococcus marinus str. NATL2A



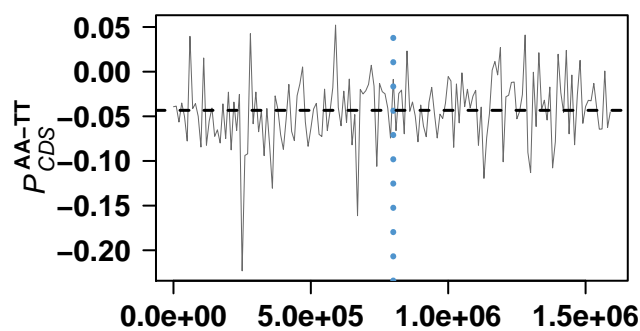
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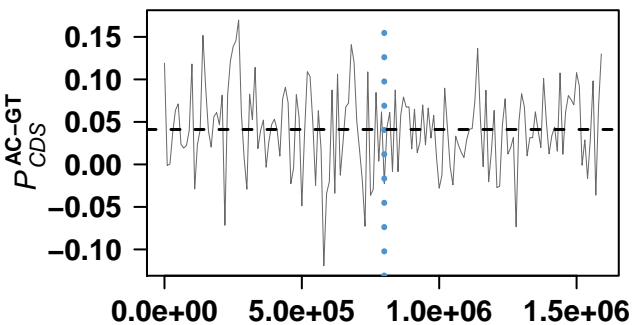
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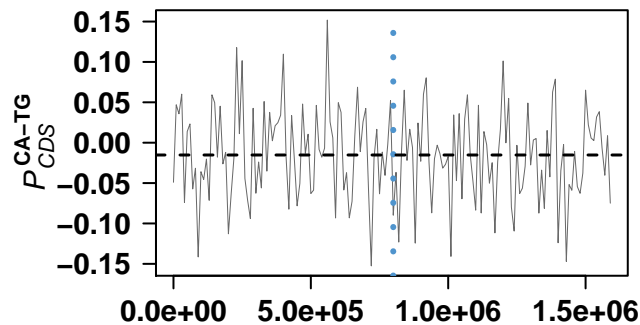
genome coordinates



genome coordinates

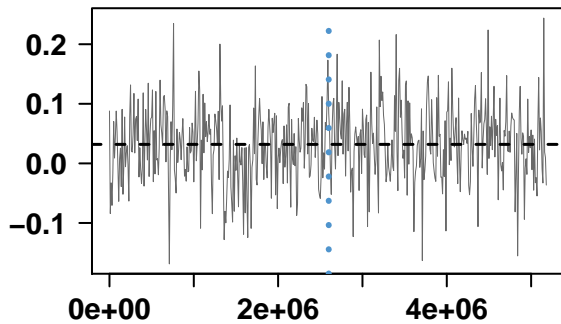


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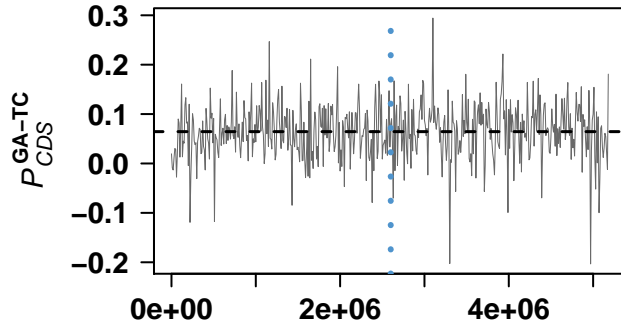


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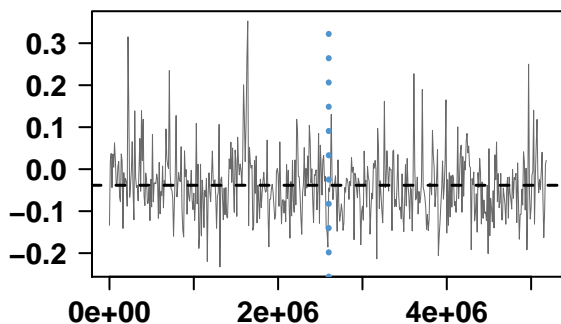
Anabaena variabilis ATCC 29413



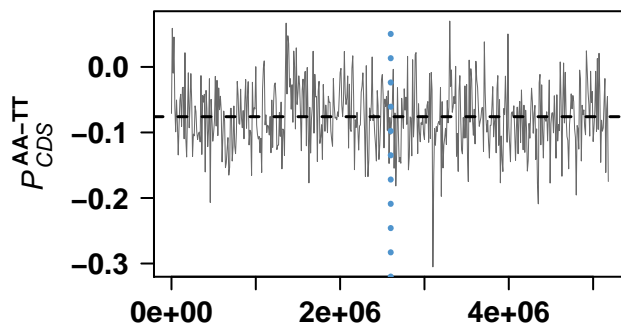
genome coordinates



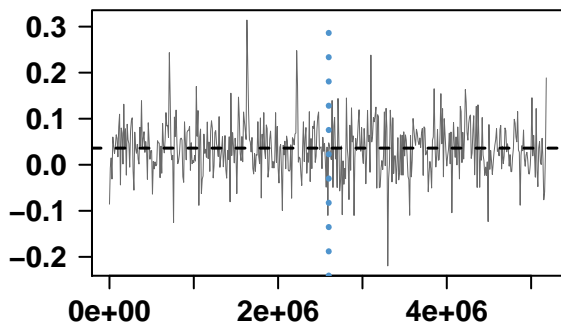
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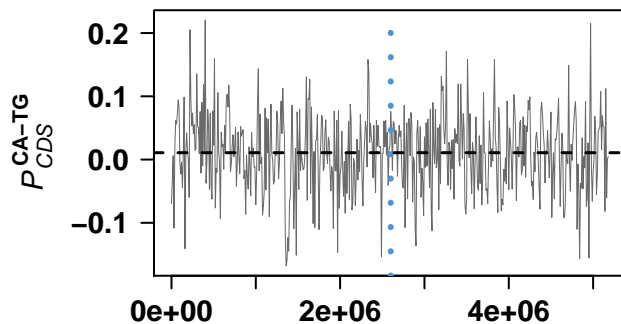
genome coordinates



genome coordinates

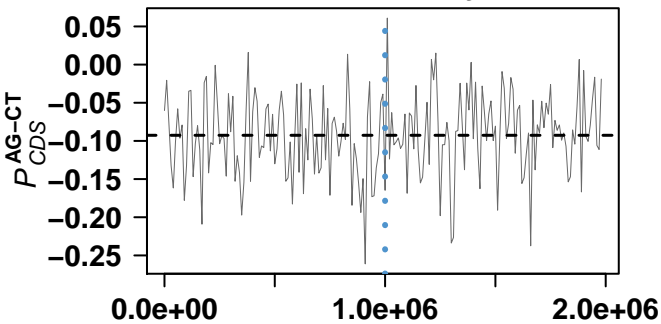


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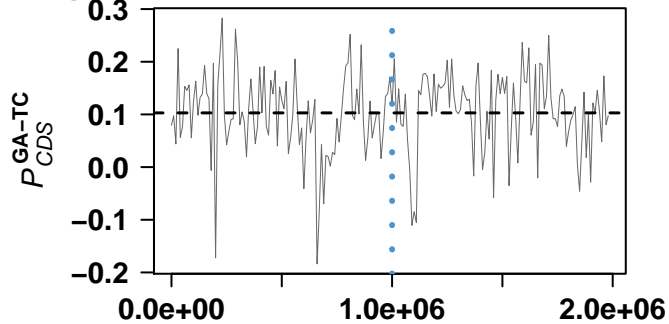


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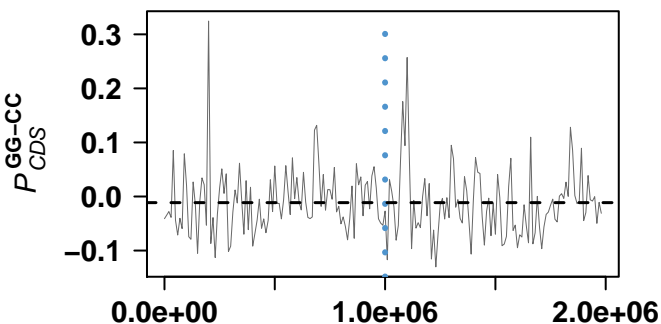
Synechococcus sp. CC9902



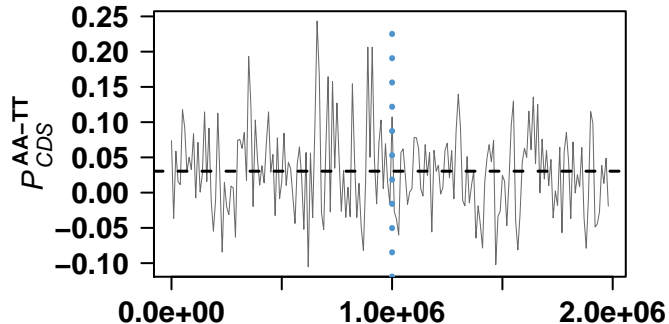
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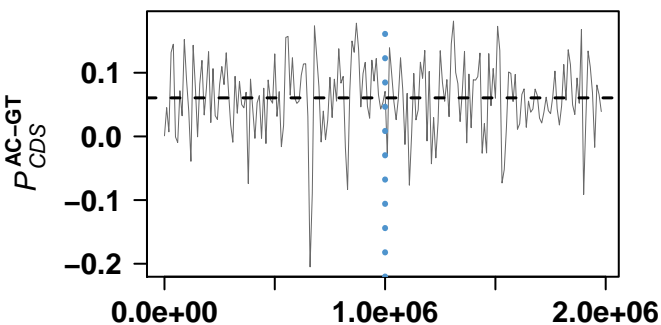
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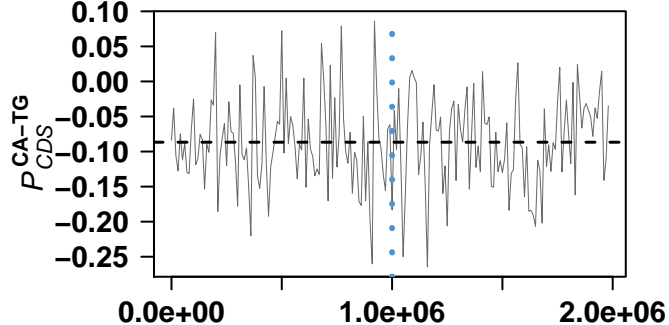
genome coordinates



genome coordinates

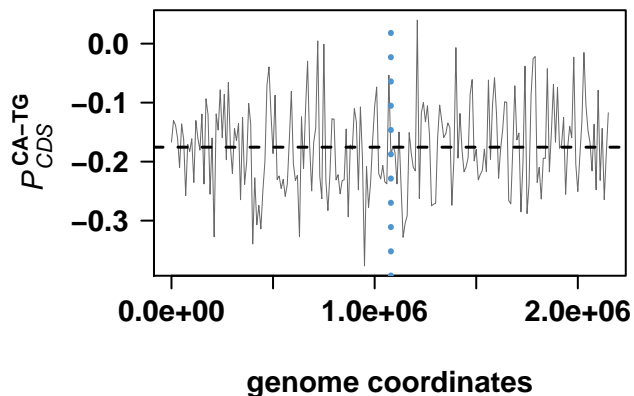
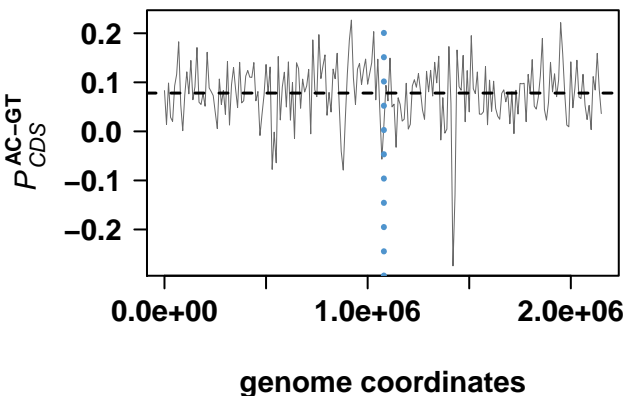
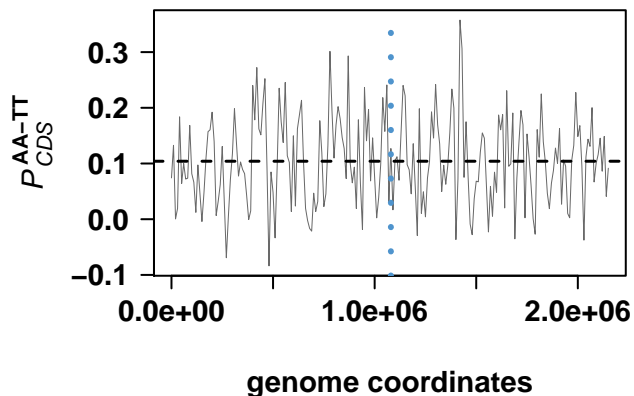
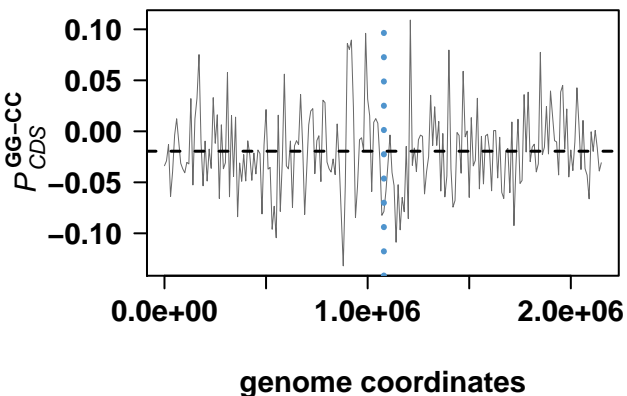
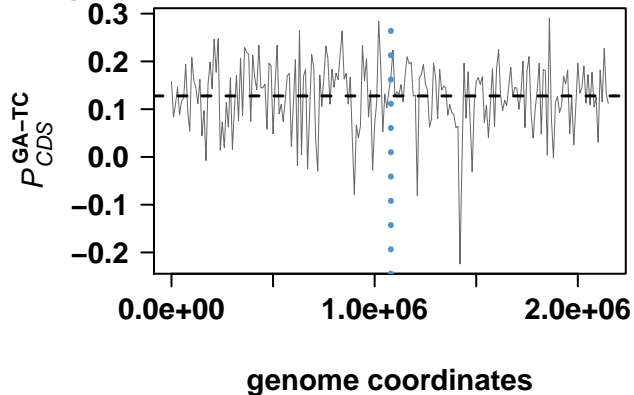
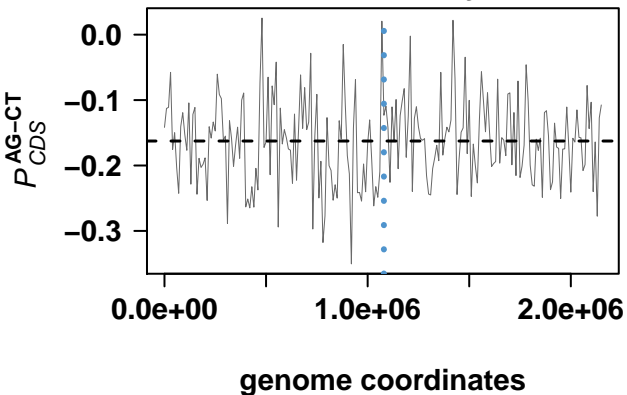


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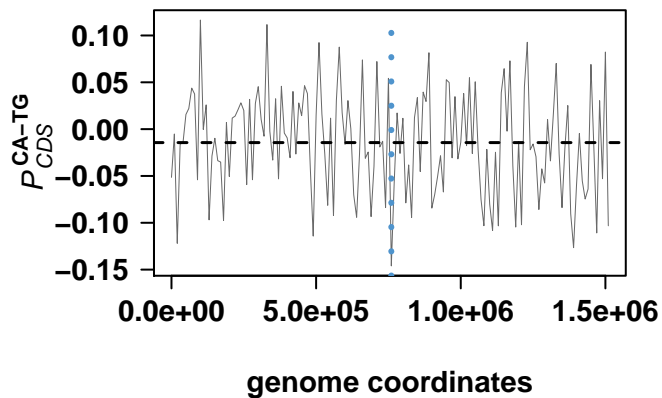
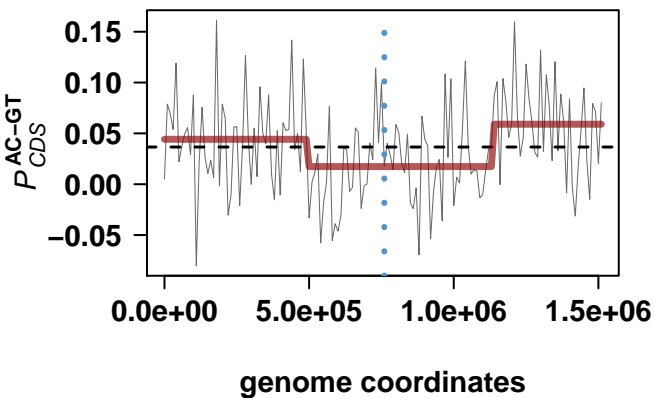
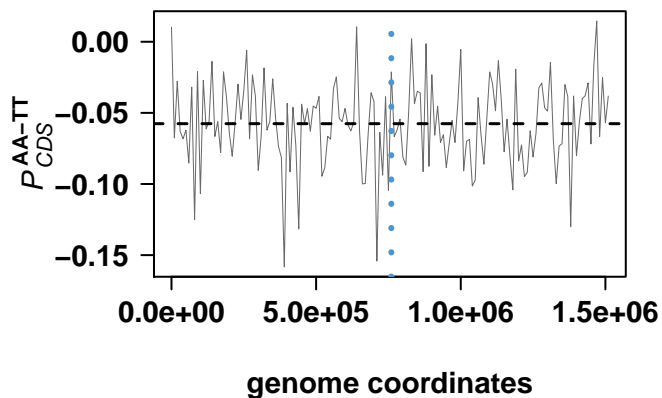
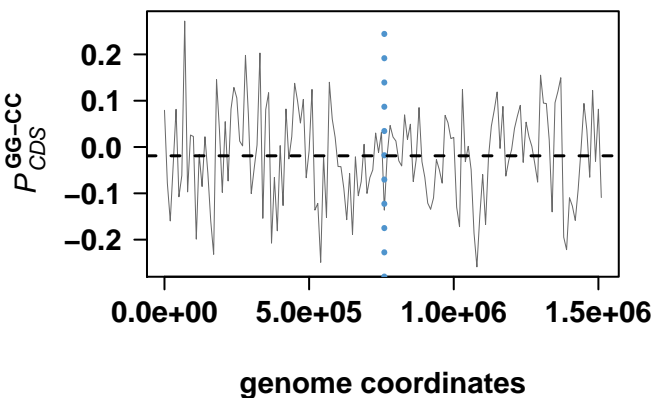
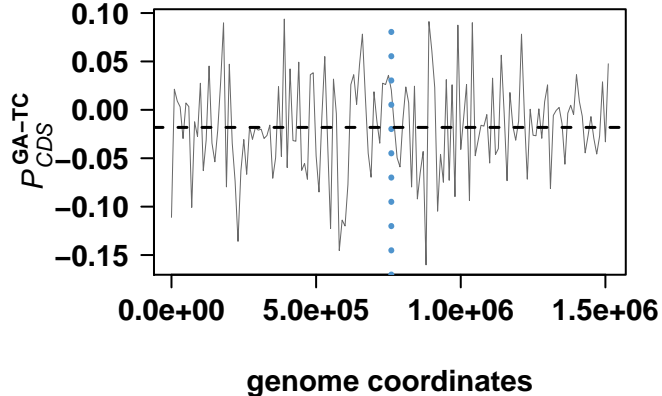
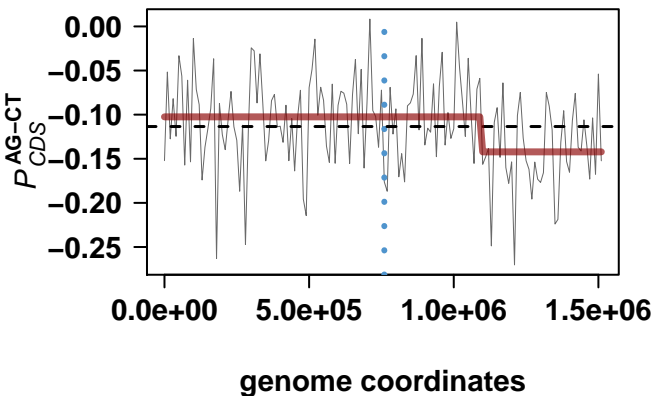


genome coordinates

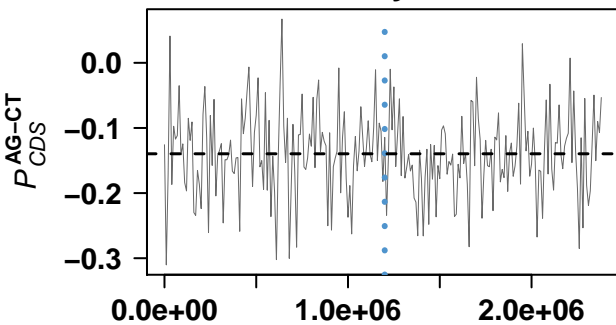
Synechococcus sp. CC9605



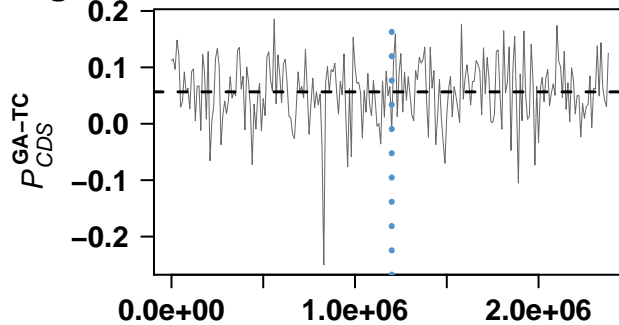
Prochlorococcus marinus str. MIT 9312



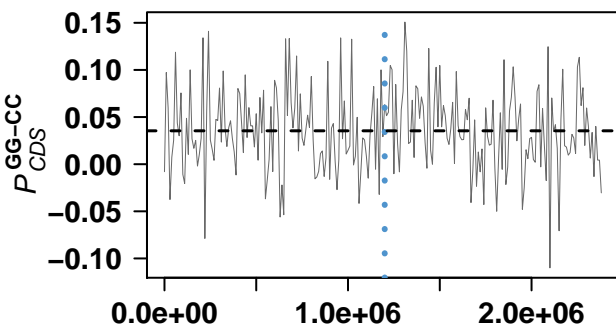
Synechococcus elongatus PCC 7942



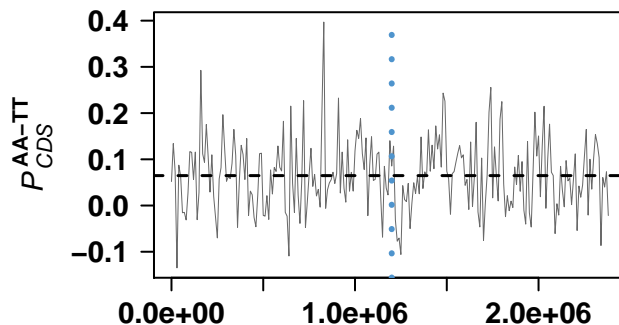
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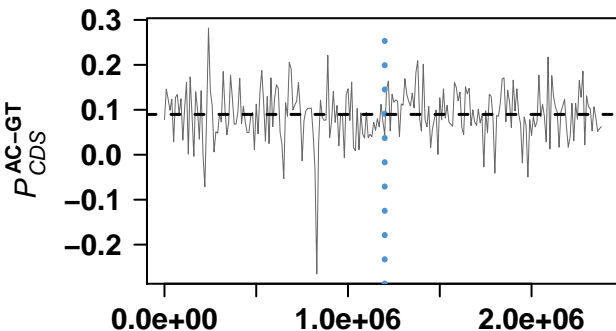
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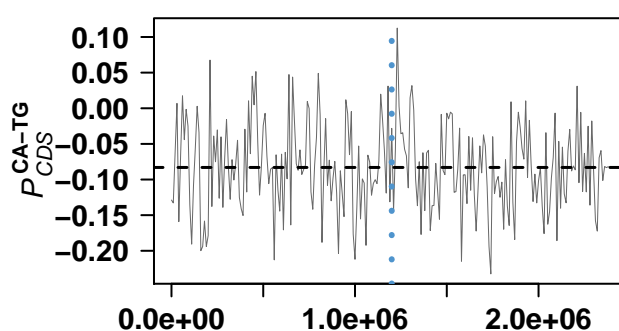
genome coordinates



genome coordinates

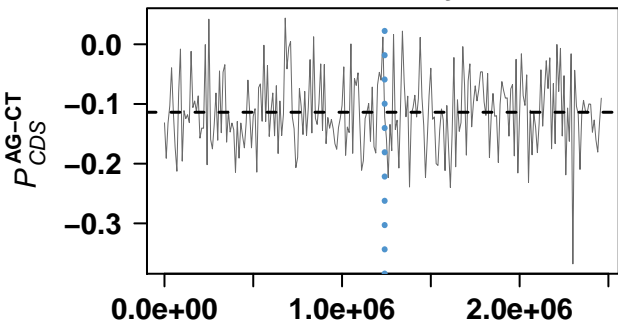


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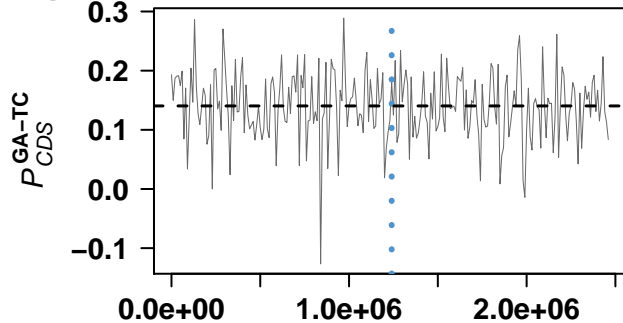


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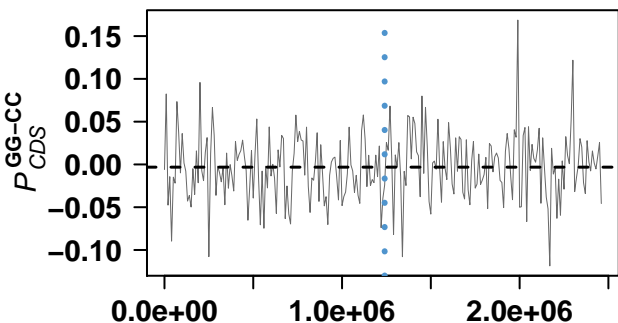
Synechococcus sp. JA-3-3Ab



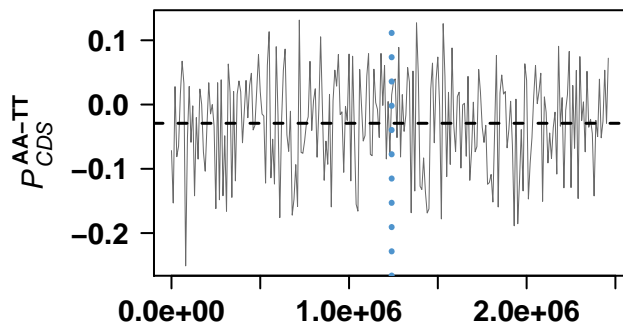
genome coordinates



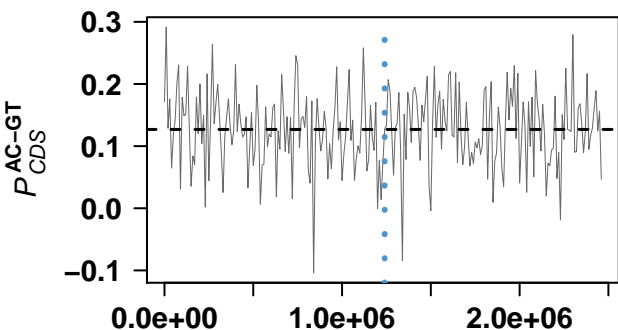
genome coordinates



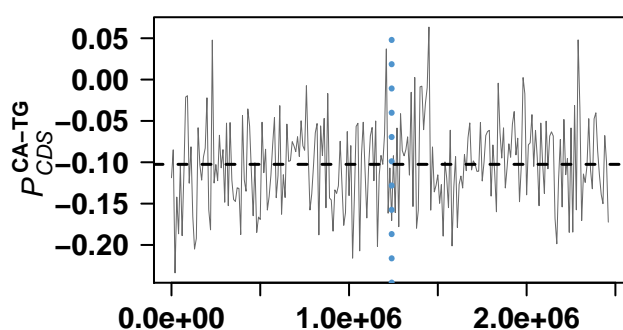
genome coordinates



genome coordinates

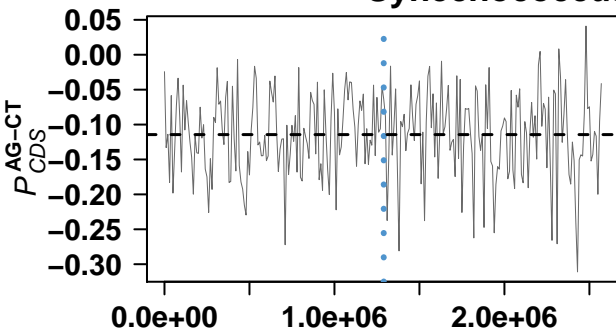


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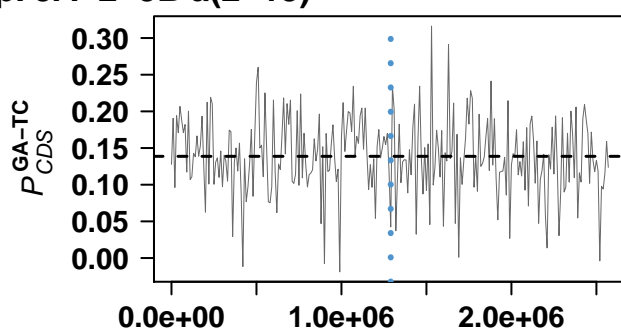


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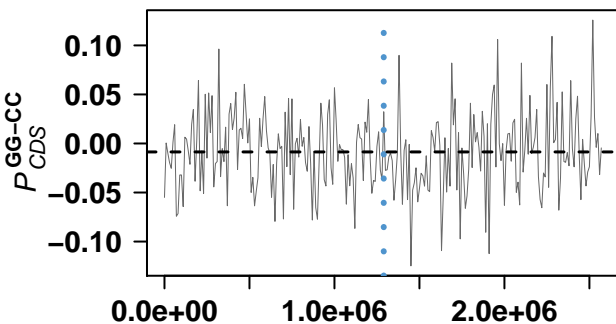
Synechococcus sp. JA-2-3B'a(2-13)



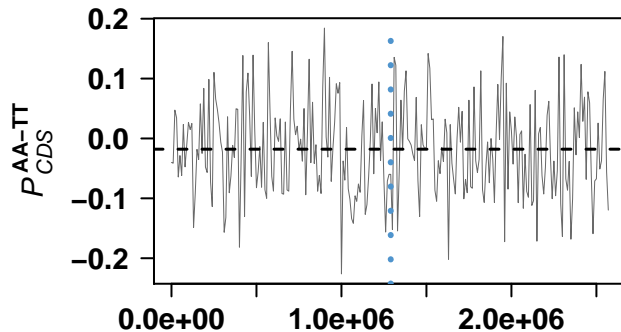
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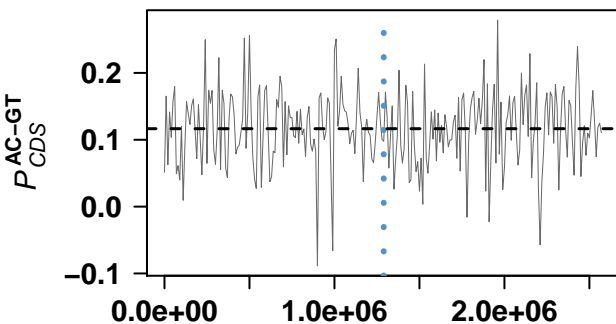
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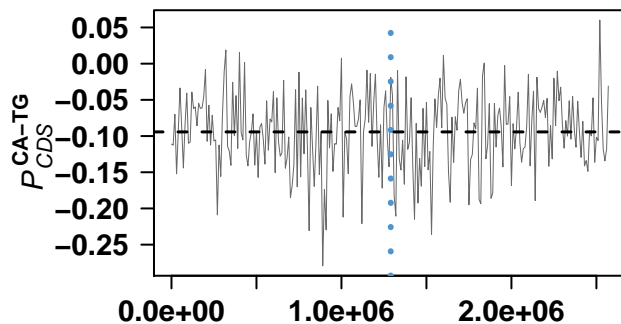
genome coordinates



genome coordinates

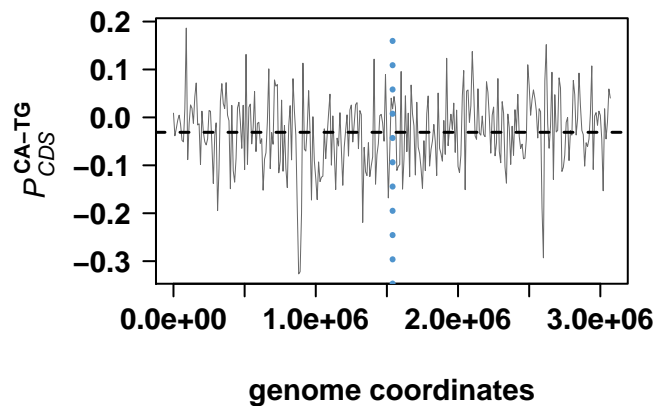
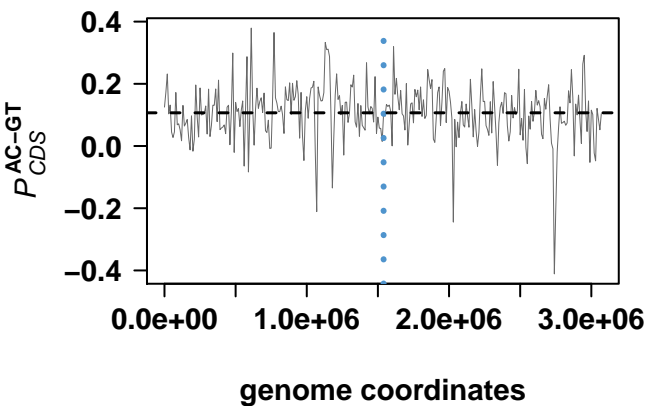
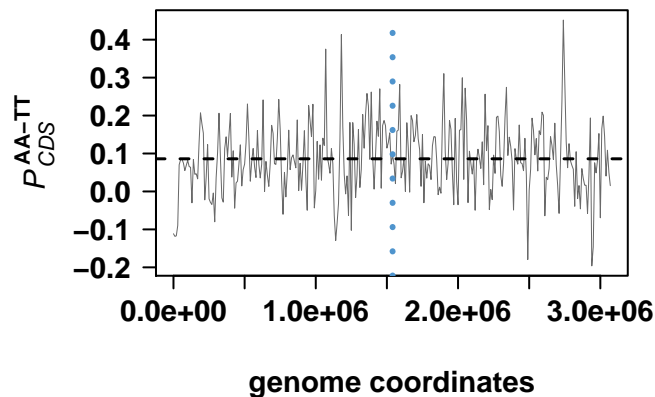
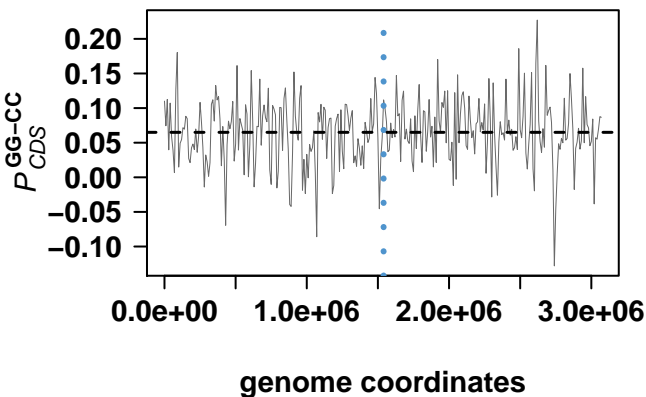
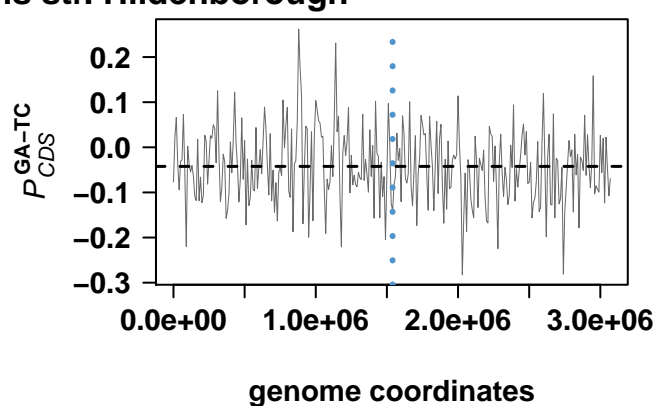
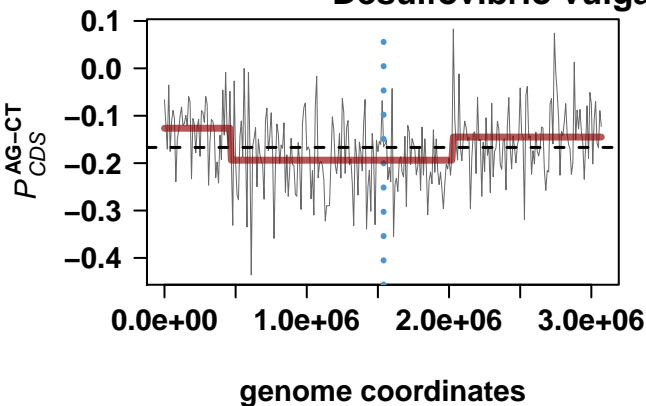


genome coordinates

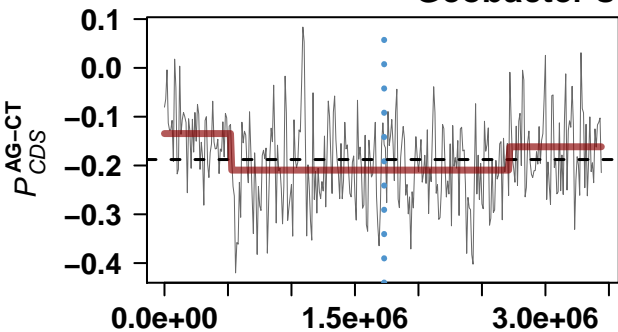


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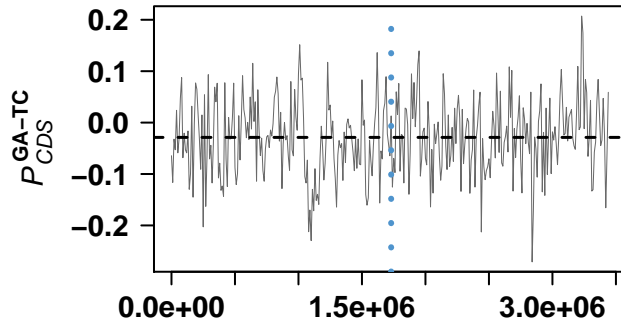
Desulfovibrio vulgaris str. Hildenborough



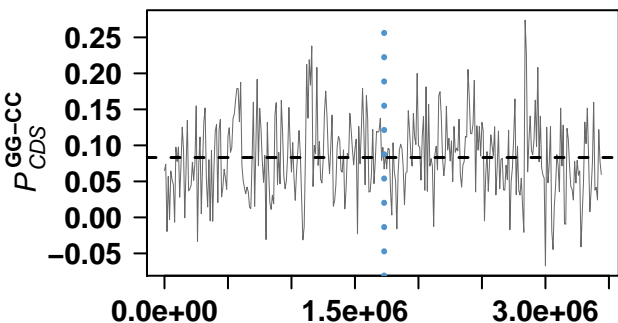
Geobacter sulfurreducens PCA



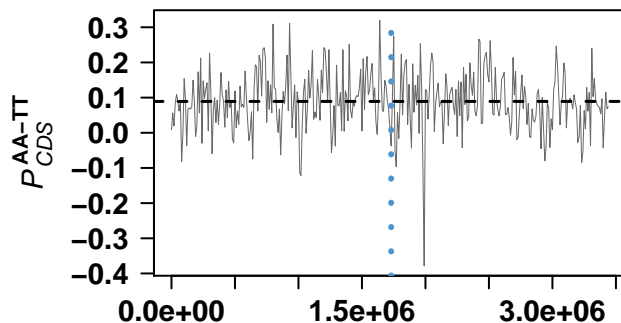
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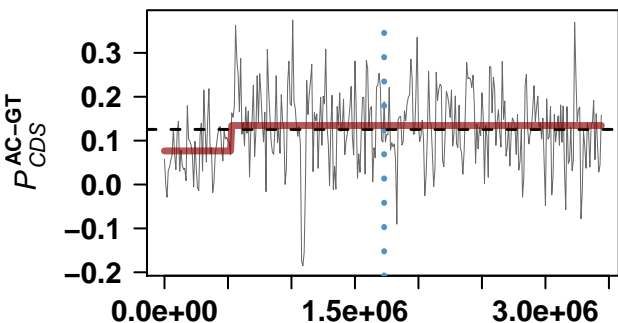
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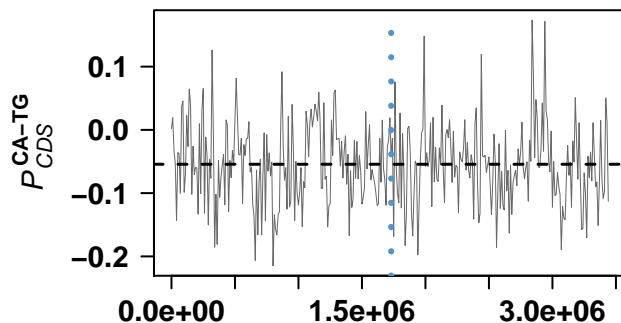
genome coordinates



genome coordinates

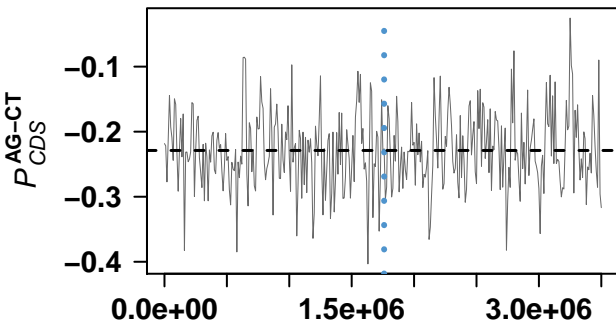


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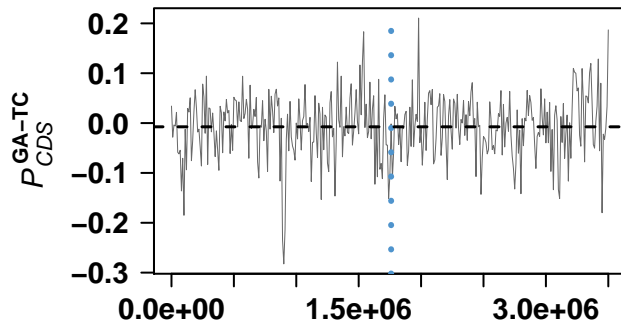


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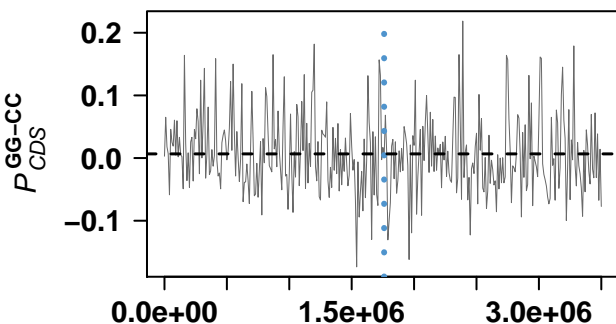
Bdellovibrio bacteriovorus HD100



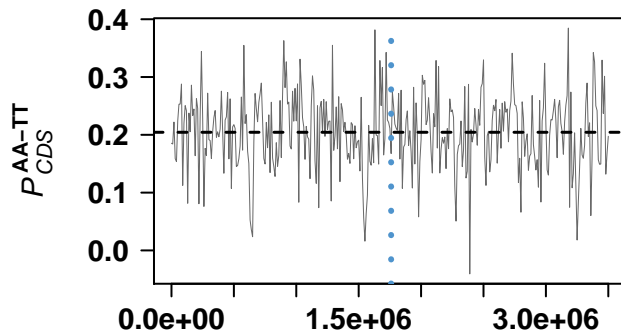
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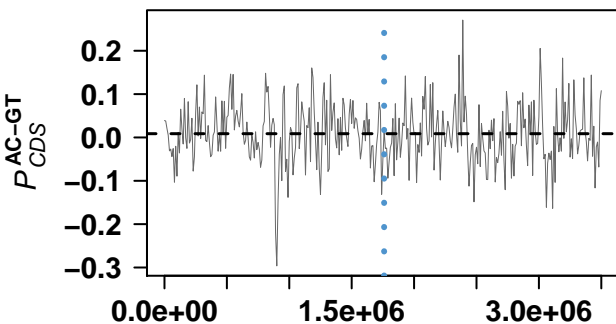
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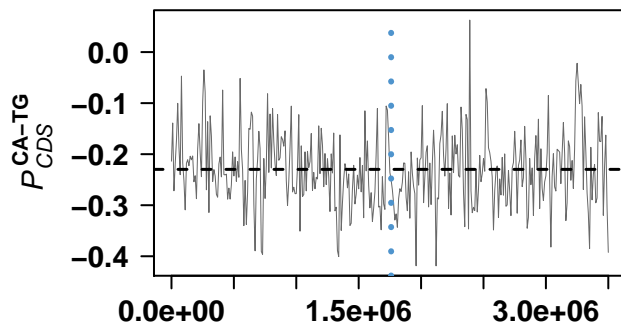
genome coordinates



genome coordinates

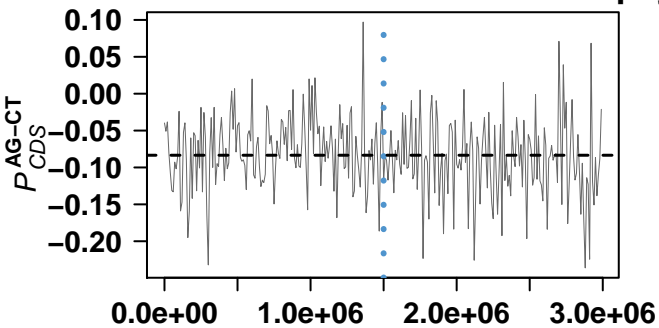


genome coordinates

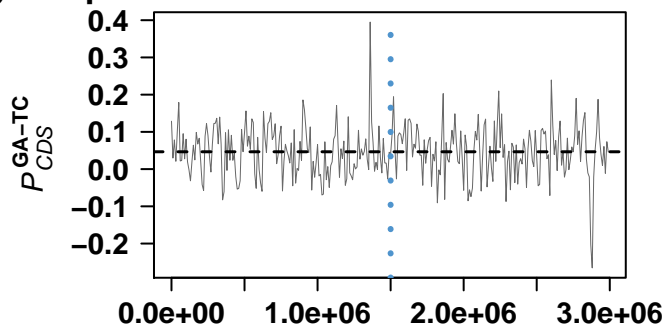


genome coordinates

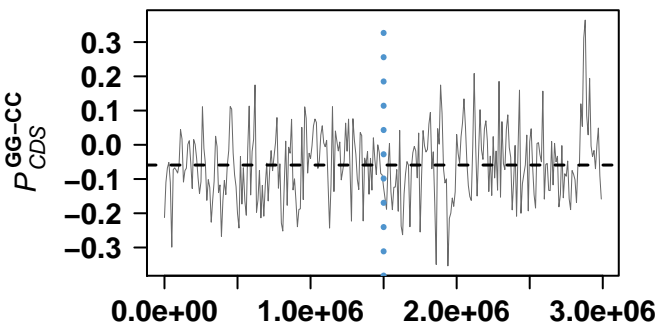
Desulfotalea psychrophila LSv54



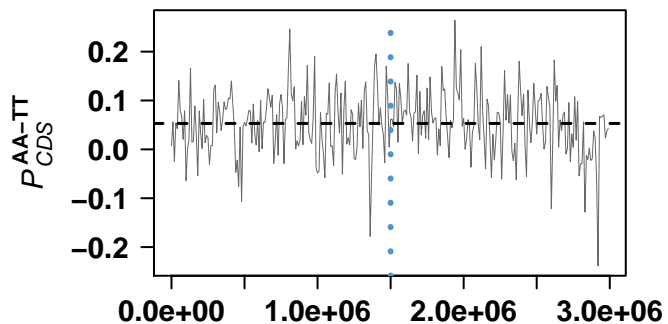
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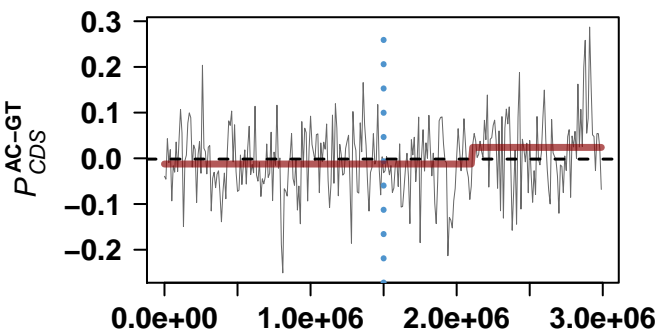
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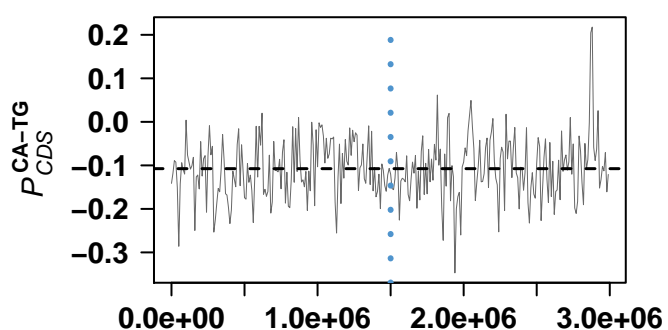
genome coordinates



genome coordinates

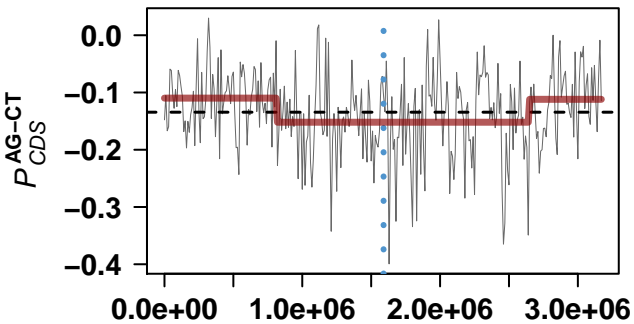


genome coordinates

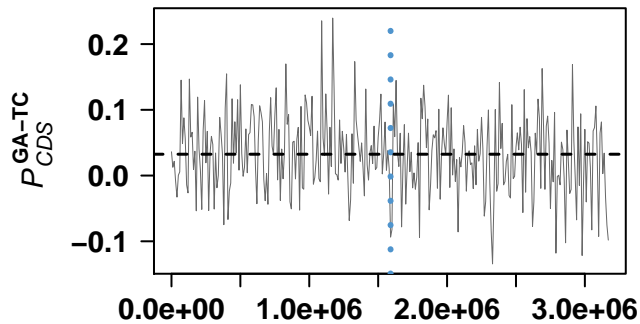


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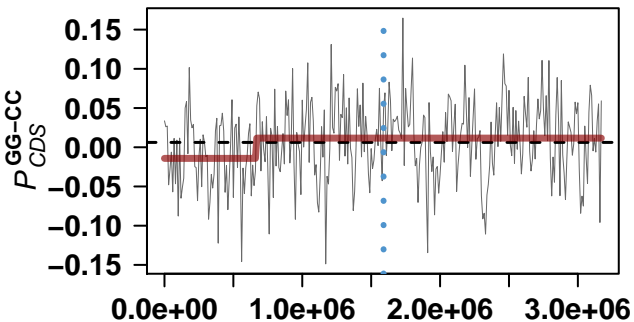
Pelobacter carbinolicus DSM 2380



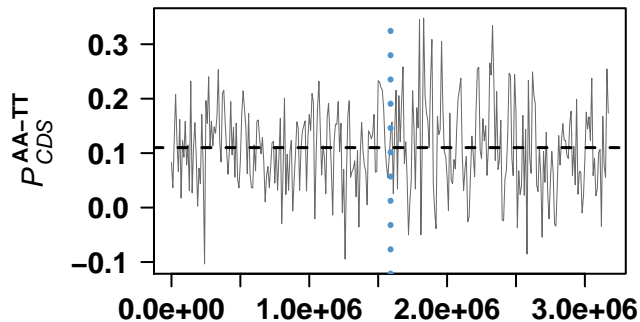
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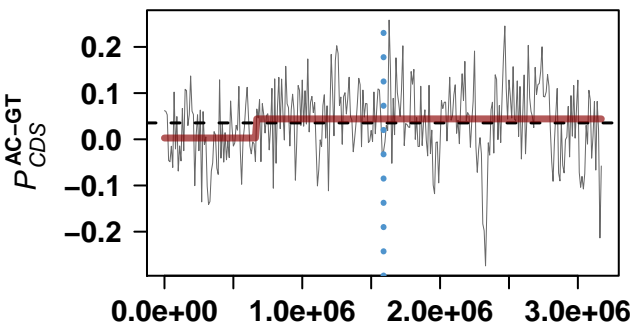
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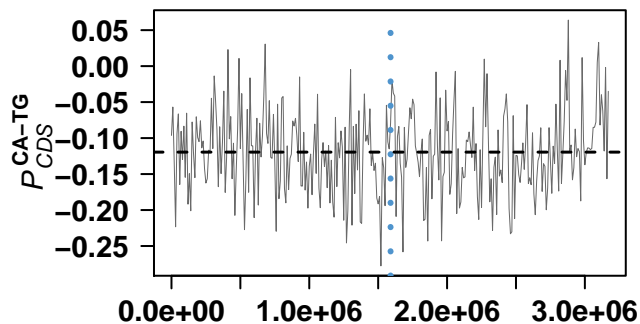
genome coordinates



genome coordinates

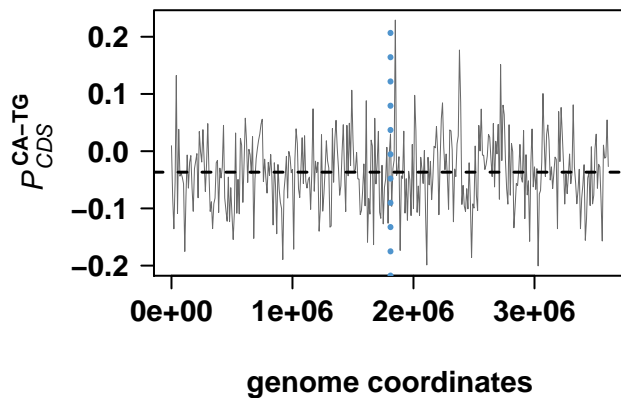
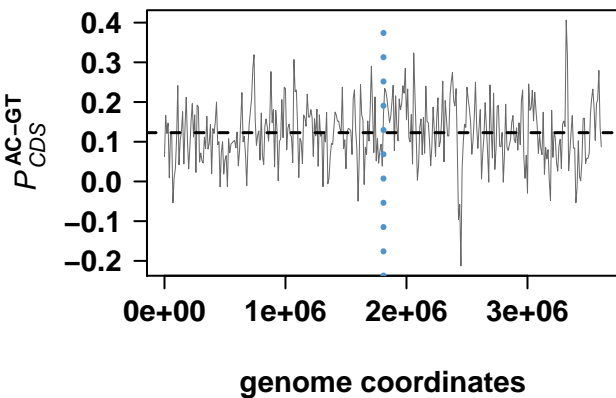
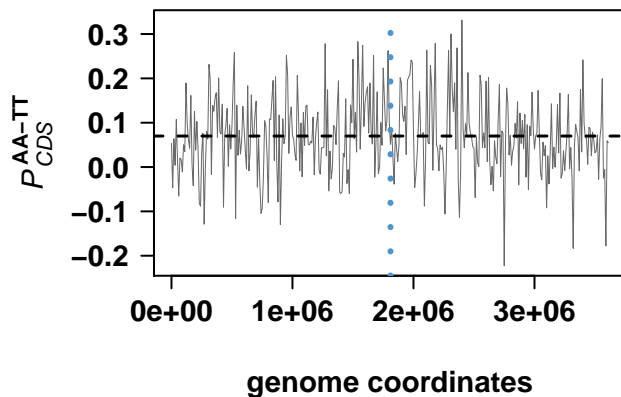
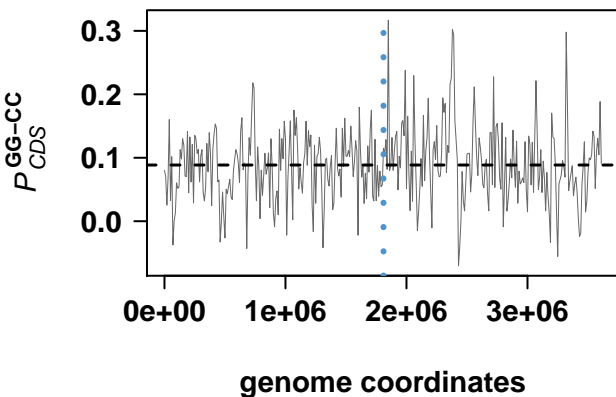
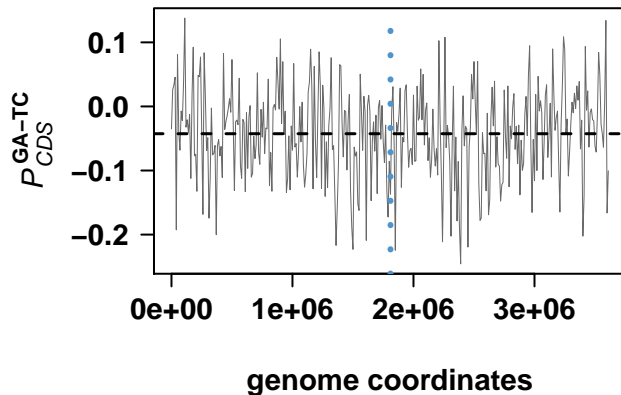
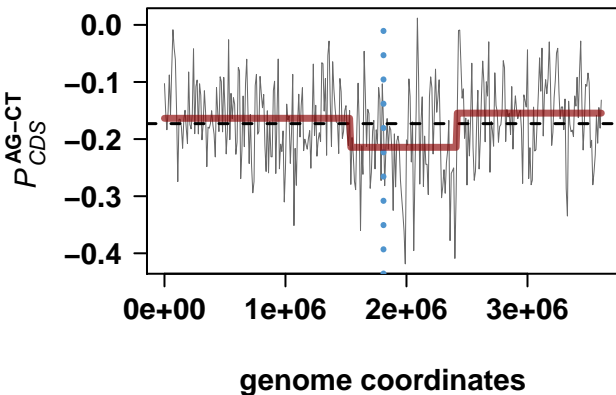


genome coordinates

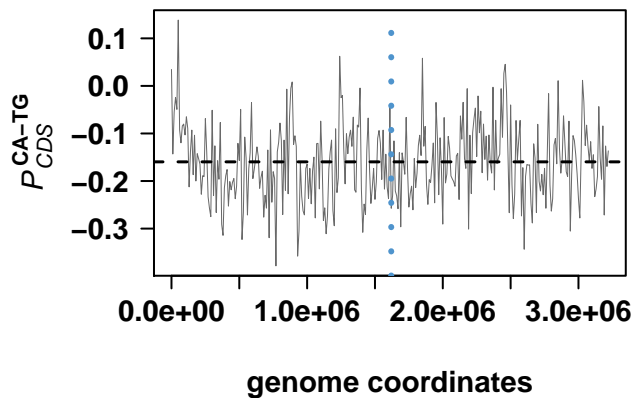
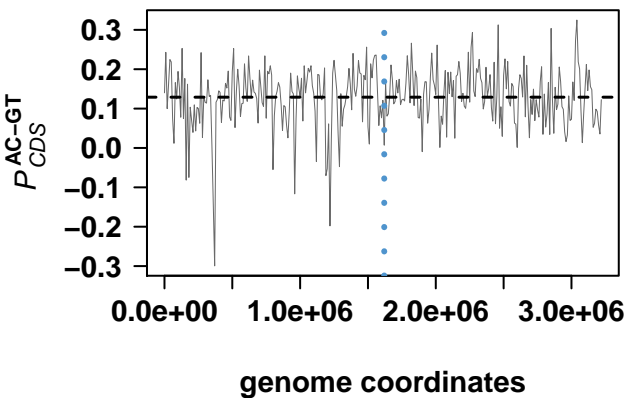
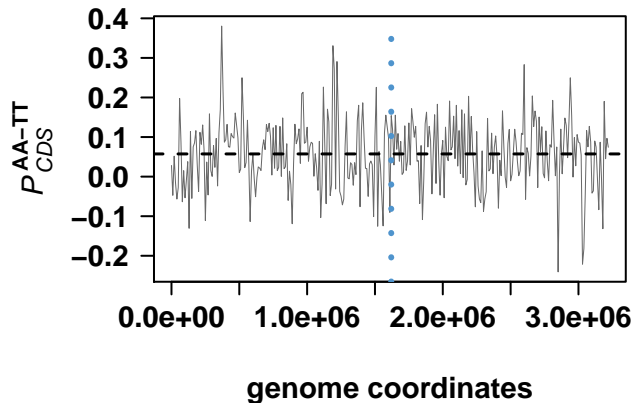
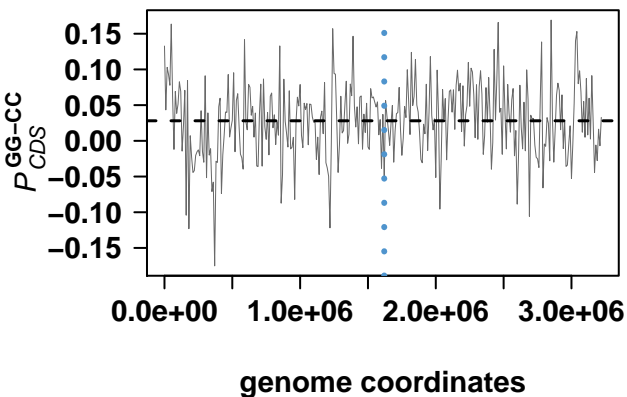
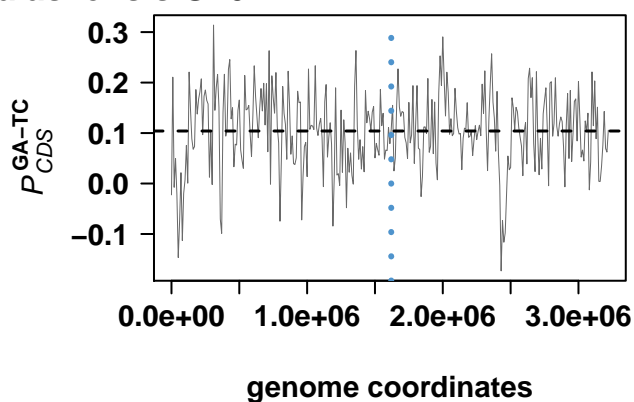
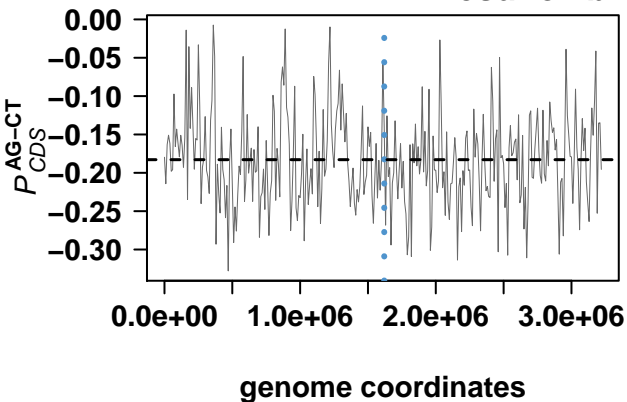


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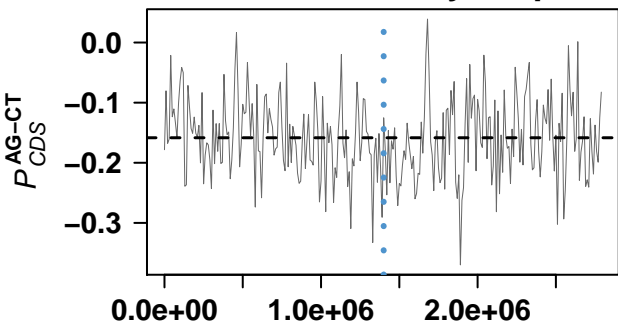
Geobacter metallireducens GS-15



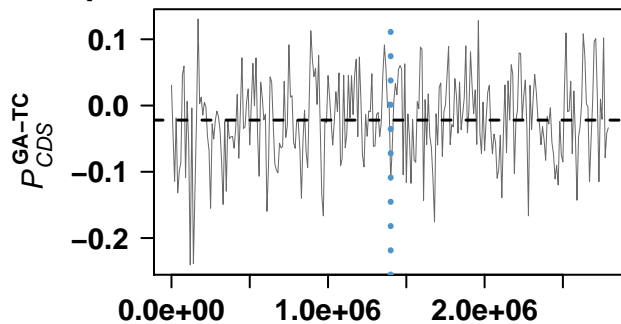
Desulfovibrio alaskensis G20



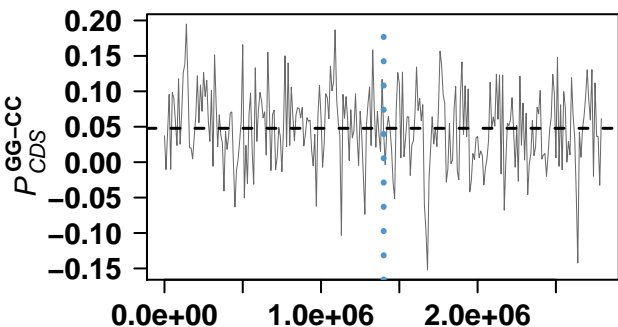
Syntrophus aciditrophicus SB



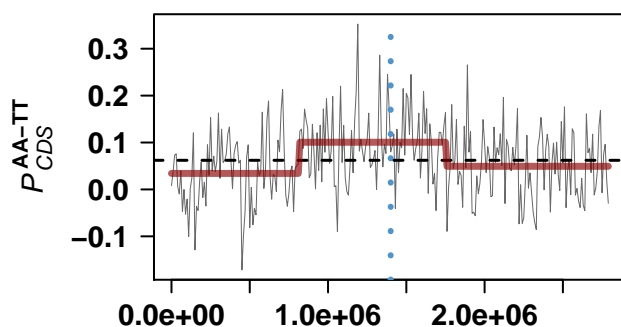
genome coordinates



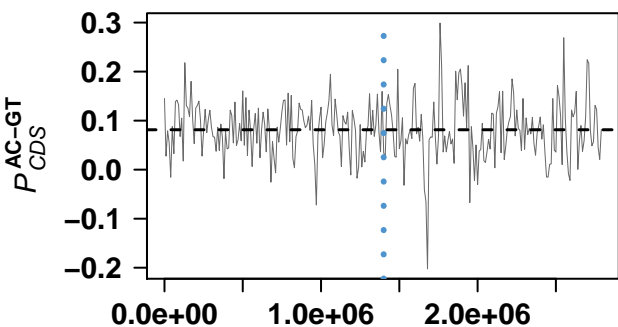
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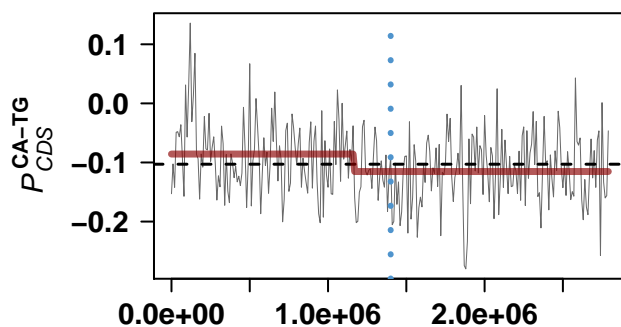
genome coordinates



genome coordinates

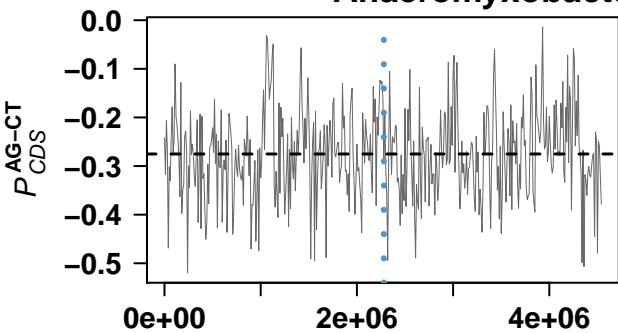


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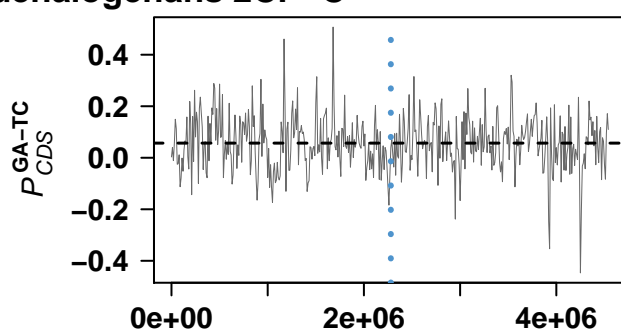


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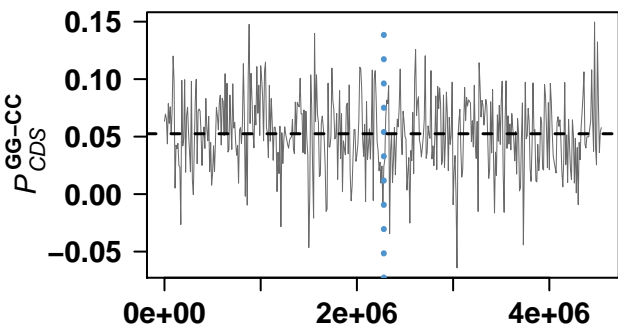
Anaeromyxobacter dehalogenans 2CP-C



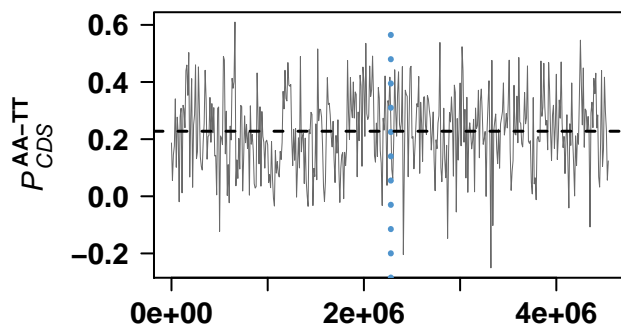
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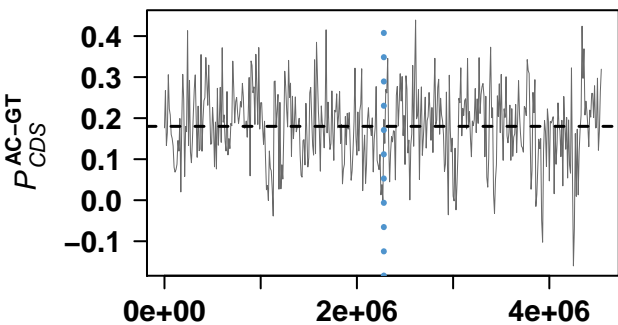
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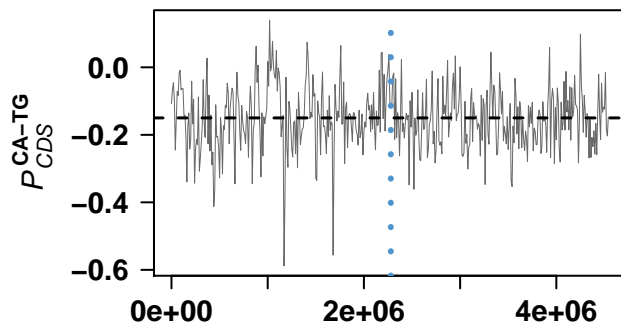
genome coordinates



genome coordinates

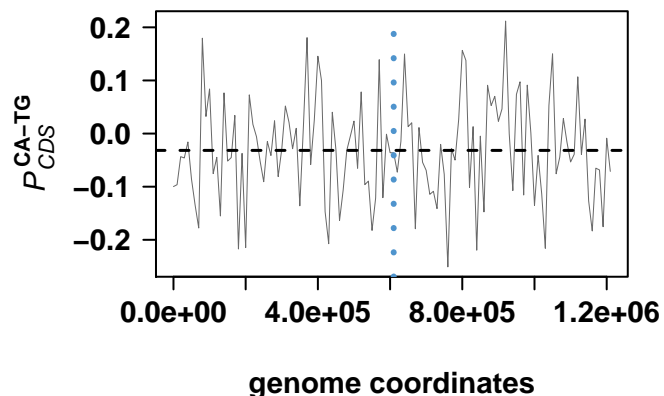
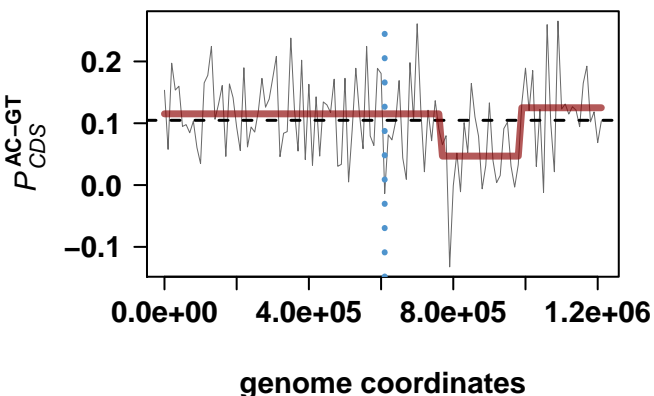
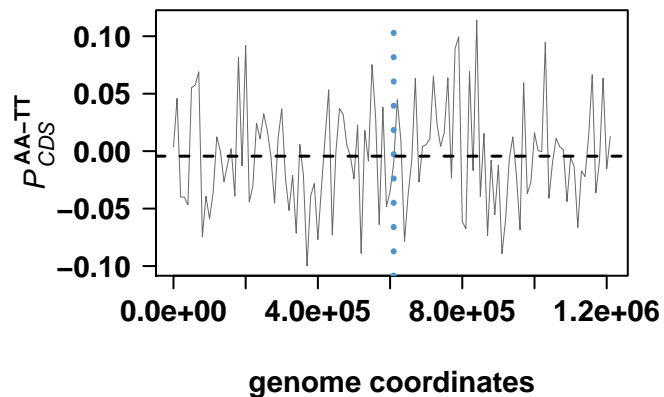
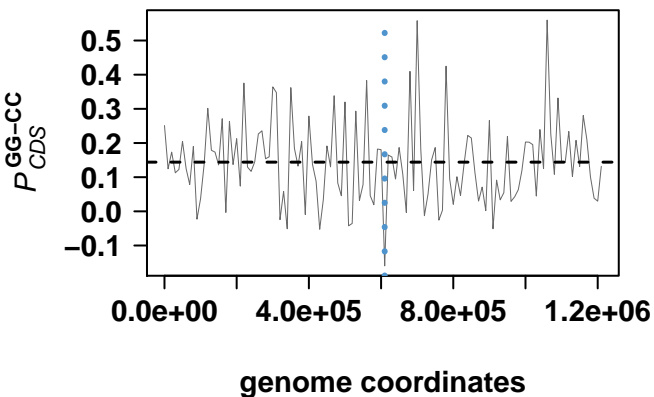
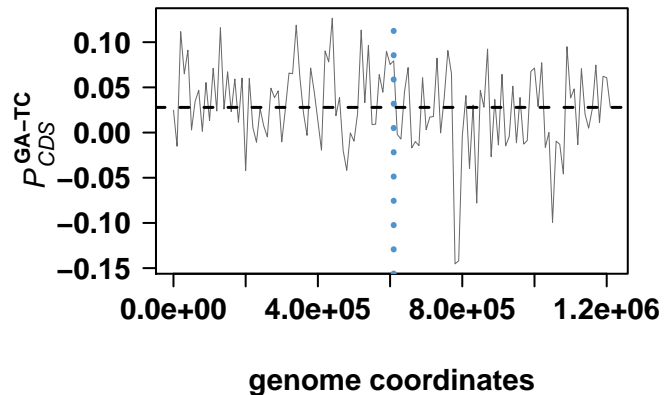
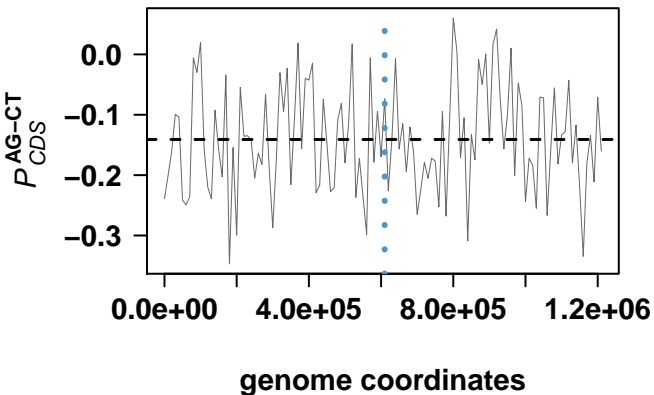


genome coordinates

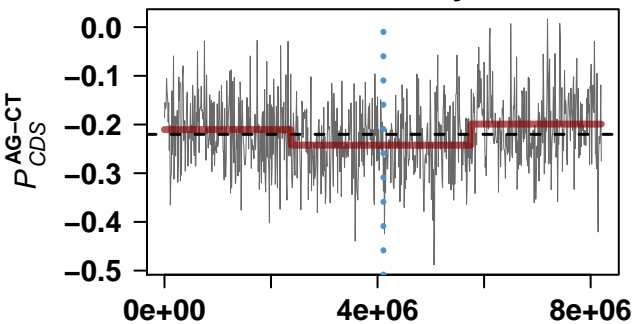


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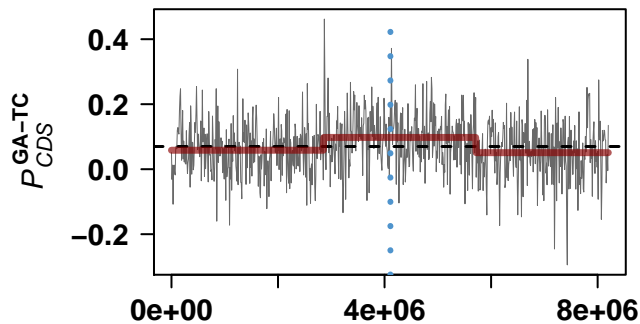
Lawsonia intracellularis PHE/MN1-00



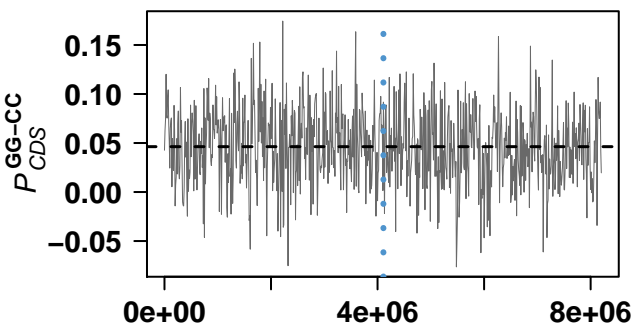
Myxococcus xanthus DK 1622



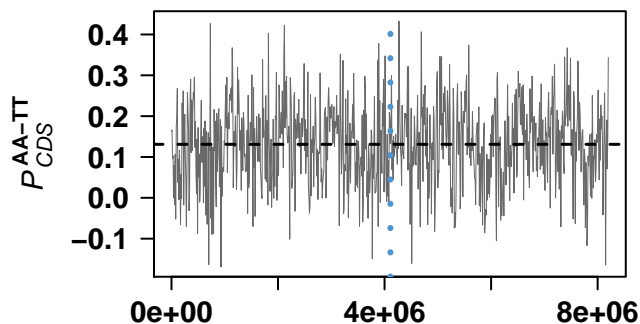
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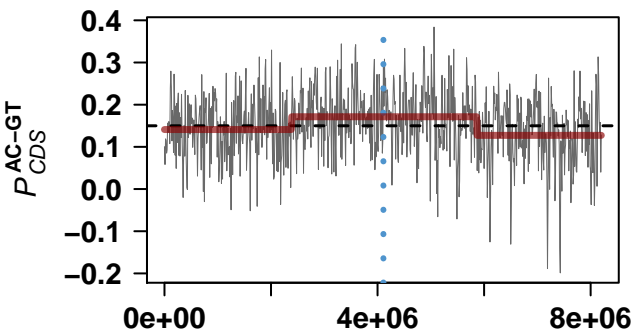
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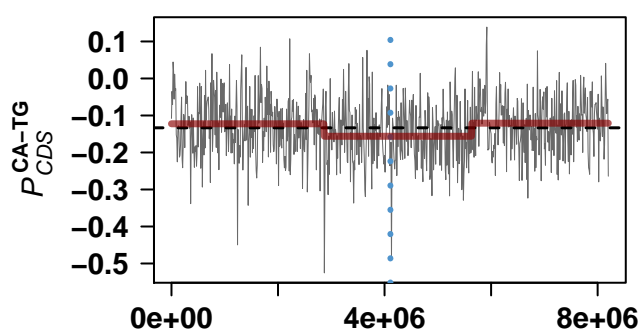
genome coordinates



genome coordinates

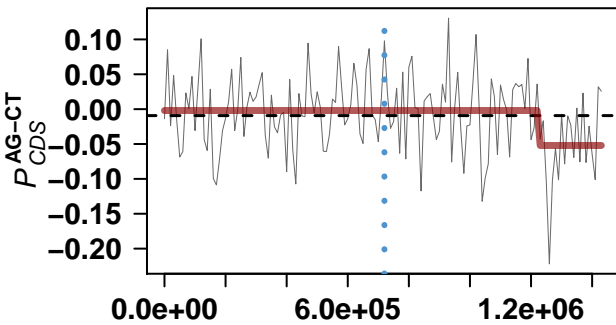


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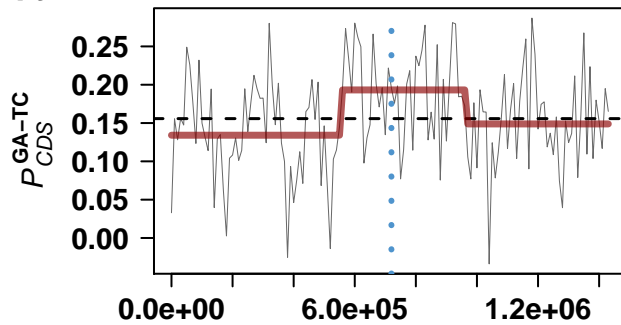


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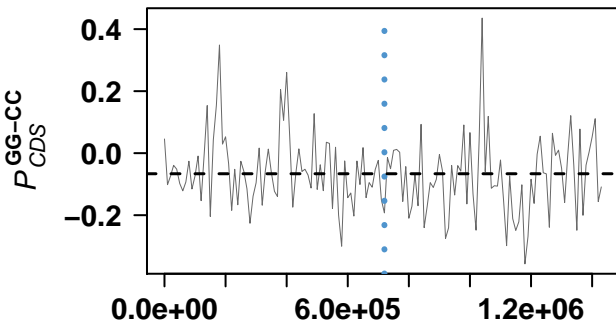
Helicobacter pylori 26695



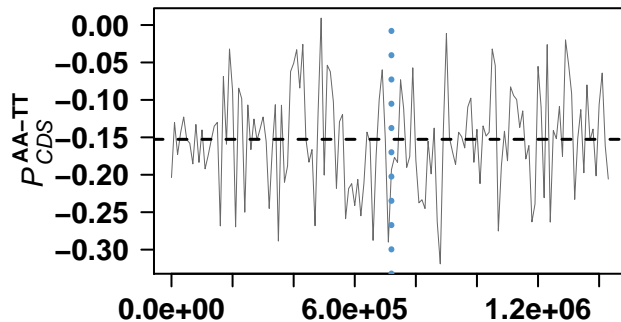
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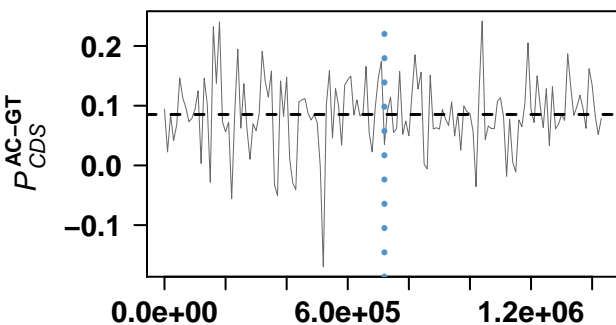
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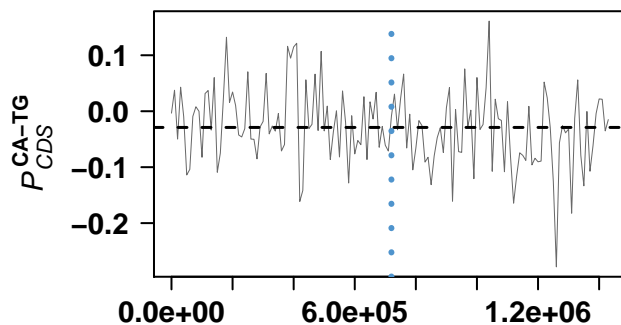
genome coordinates



genome coordinates

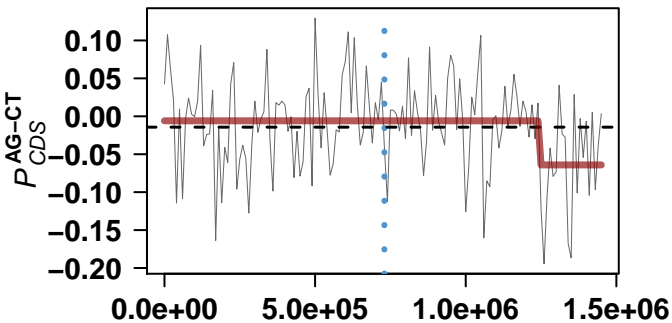


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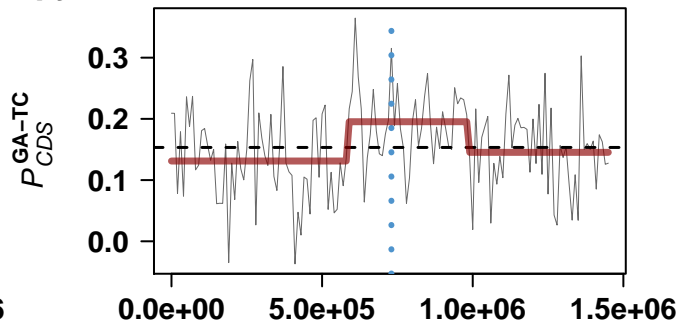


genome coordinates

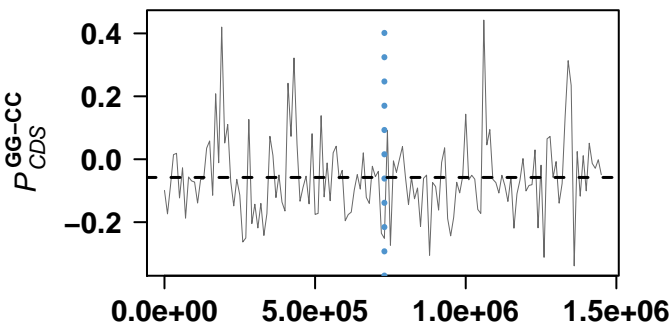
Helicobacter pylori J99



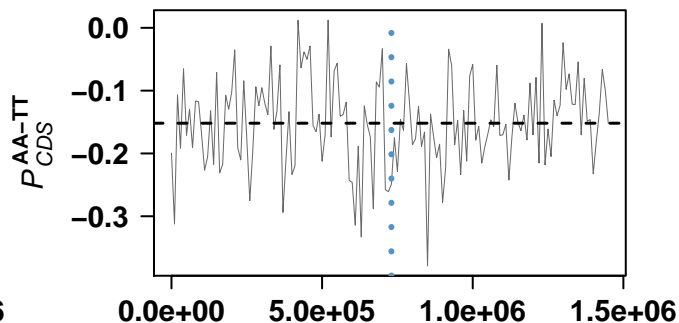
genome coordinates



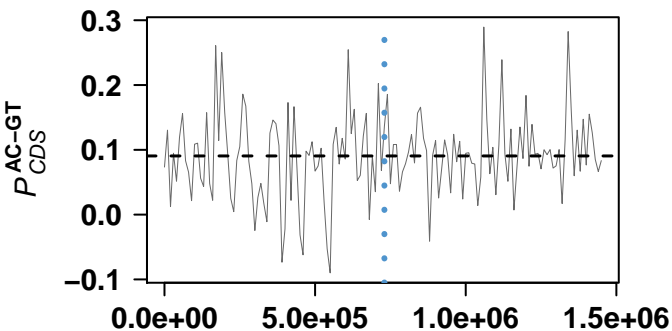
genome coordinates



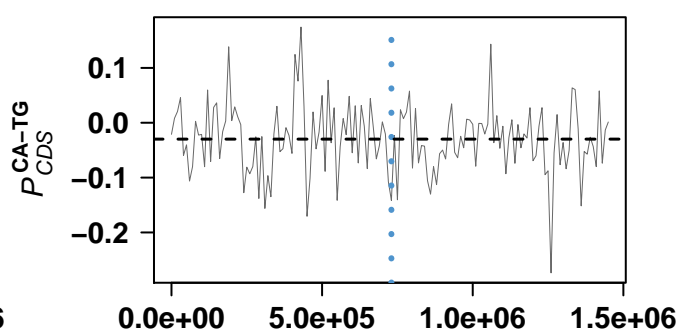
genome coordinates



genome coordinates

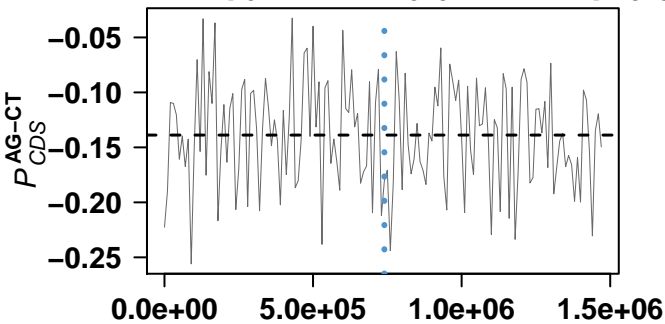


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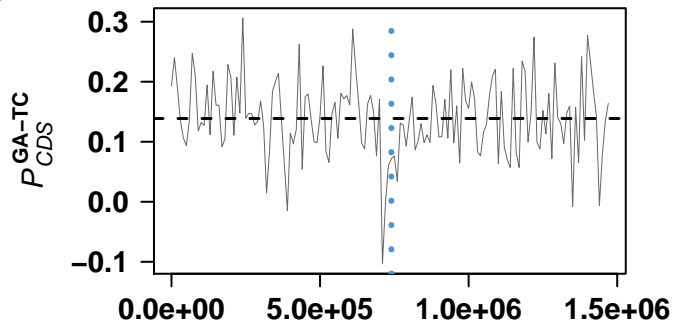


genome coordinates

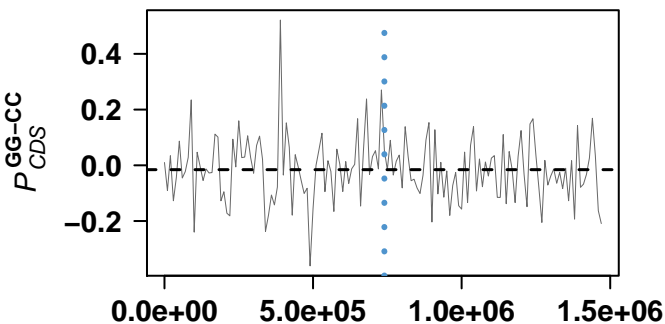
Campylobacter jejuni subsp. jejuni NCTC 11168 = ATCC 700819



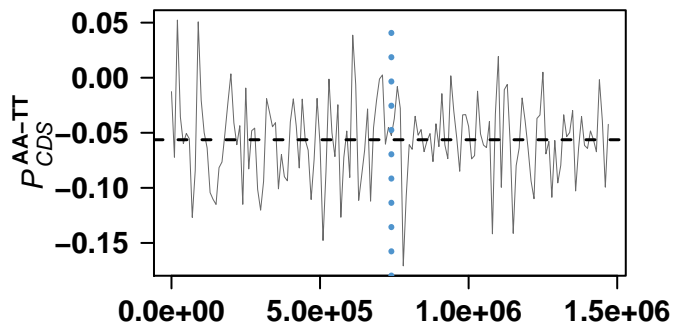
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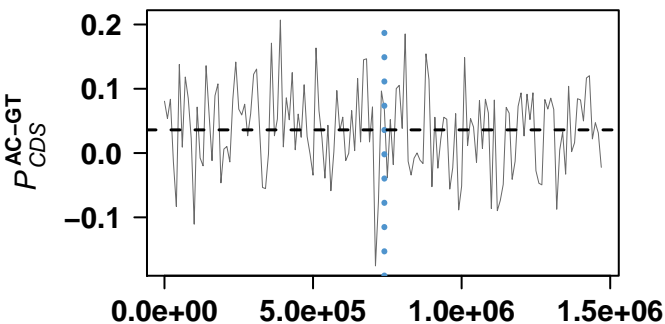
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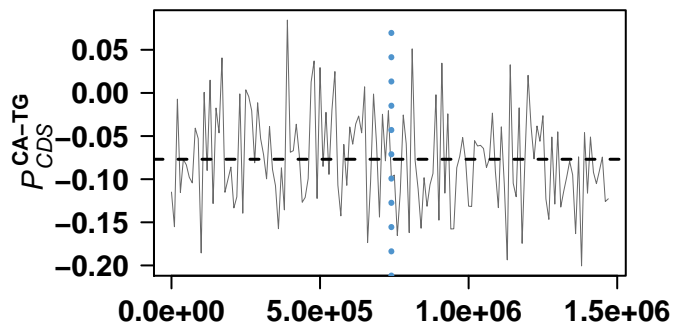
genome coordinates



genome coordinates

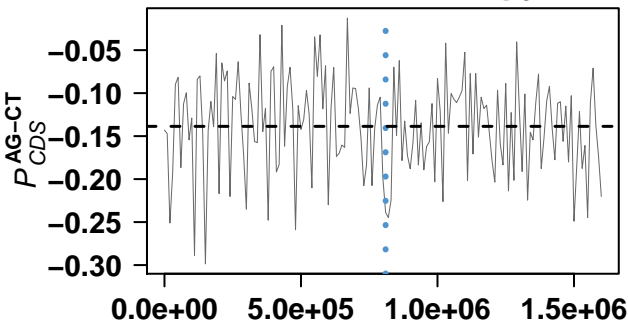


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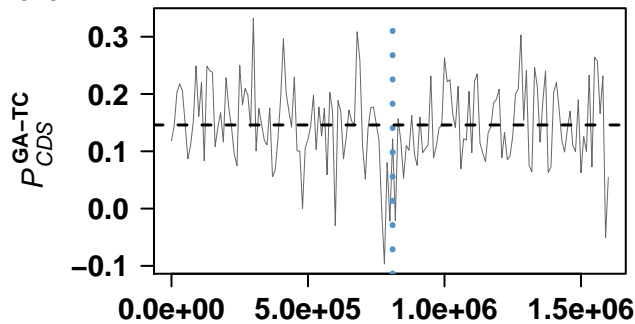


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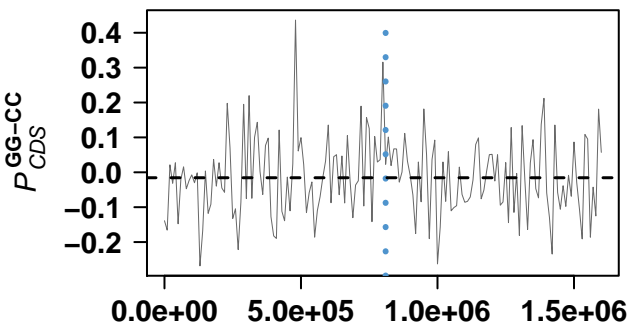
Campylobacter jejuni RM1221



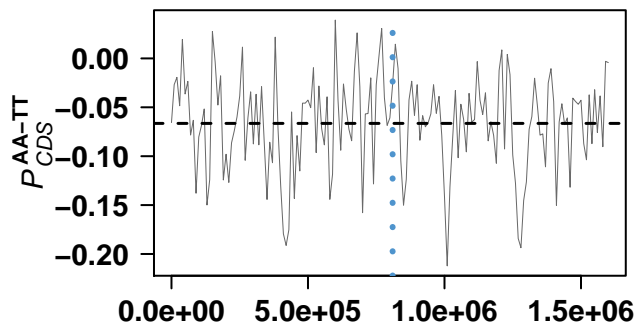
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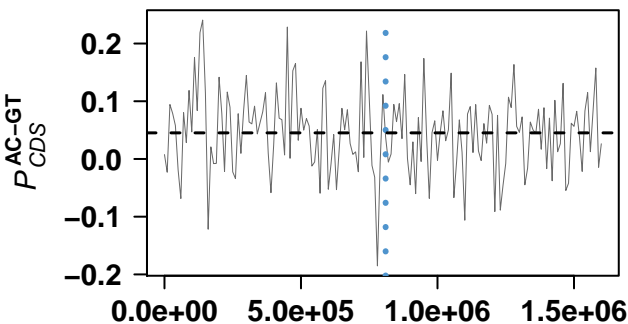
genome coordinates



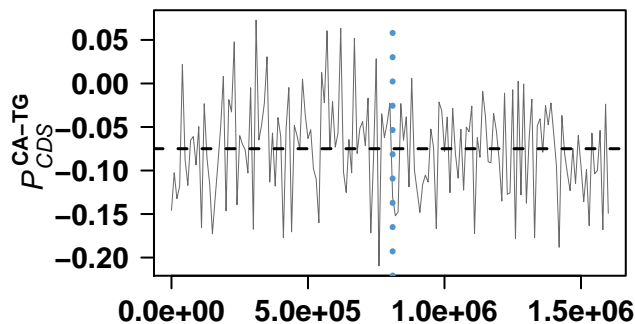
genome coordinates



genome coordinates

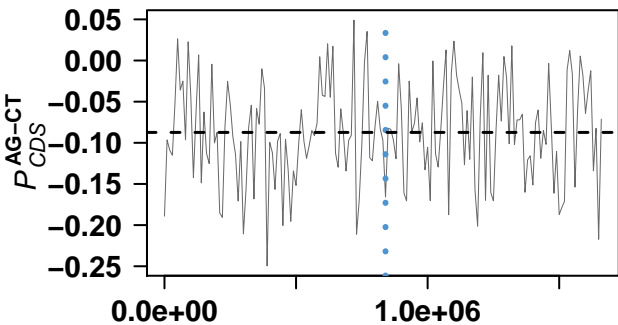


genome coordinates

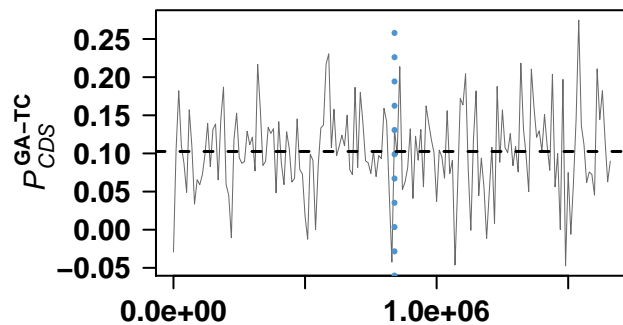


genome coordinates

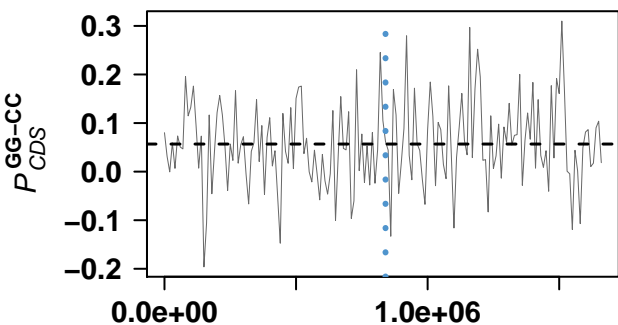
Helicobacter hepaticus ATCC 51449



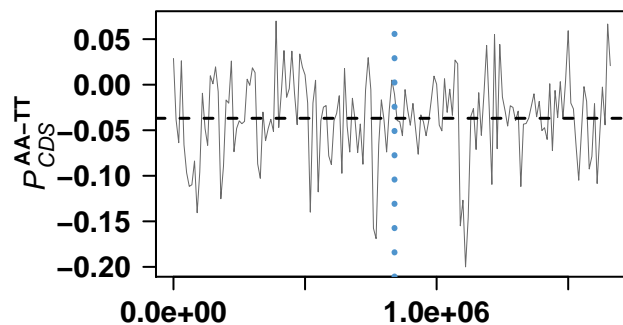
genome coordinates



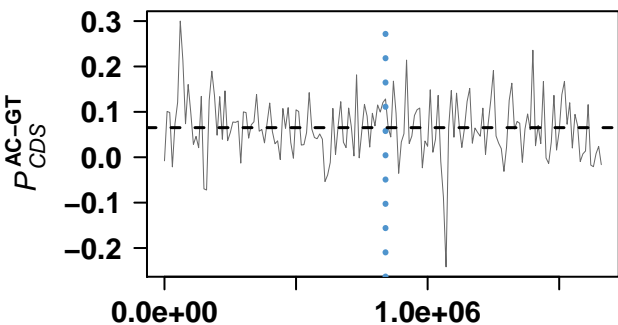
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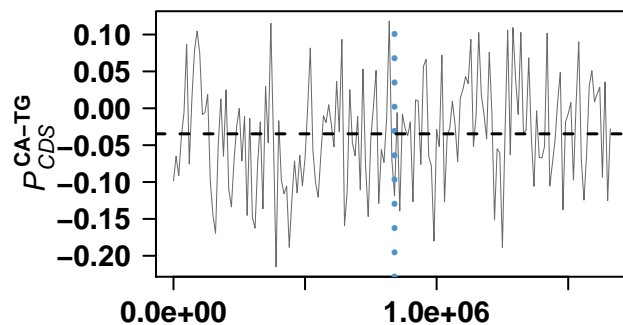
genome coordinates



genome coordinates

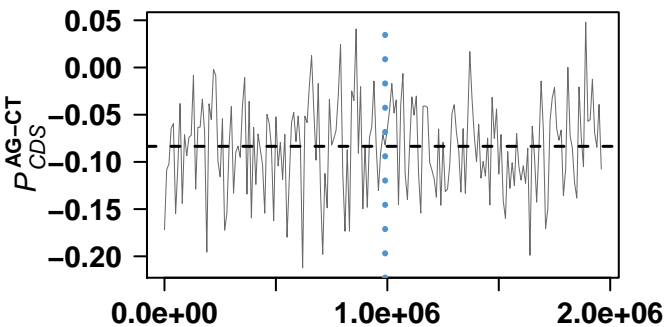


genome coordinates

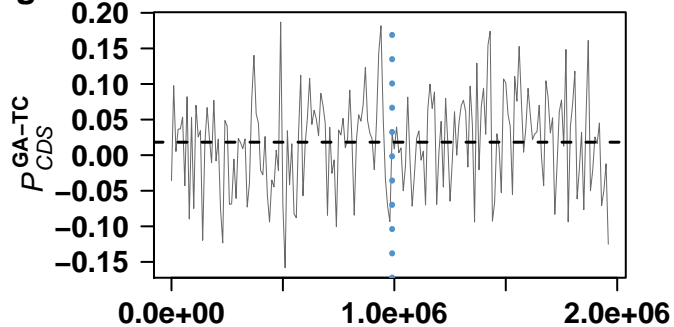


genome coordinates

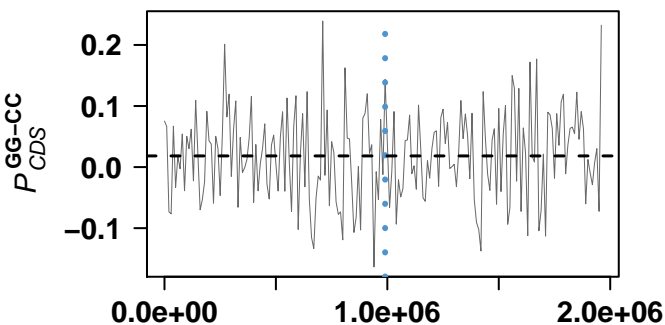
Wolinella succinogenes DSM 1740



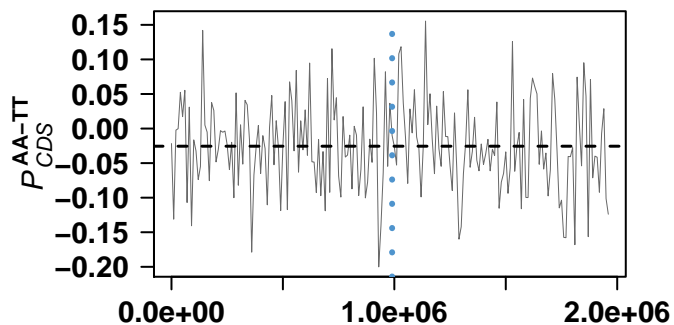
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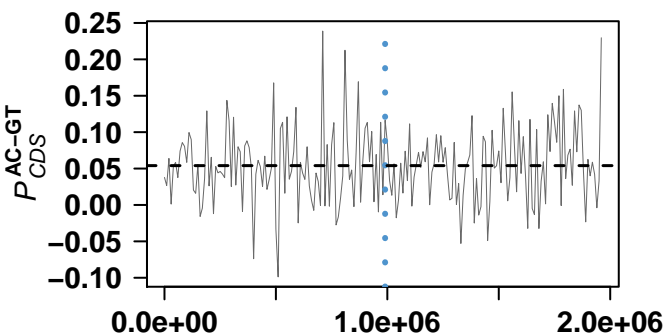
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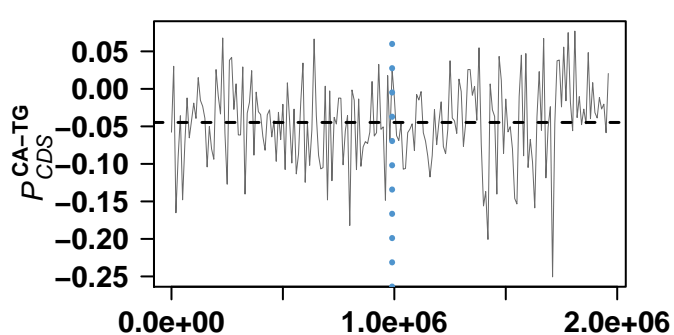
genome coordinates



genome coordinates

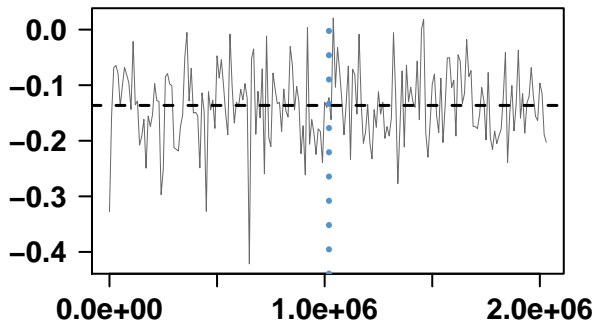


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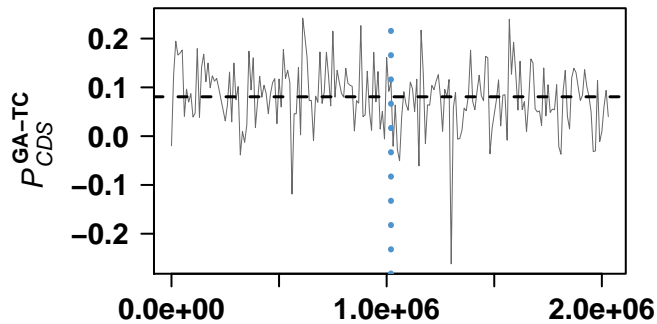


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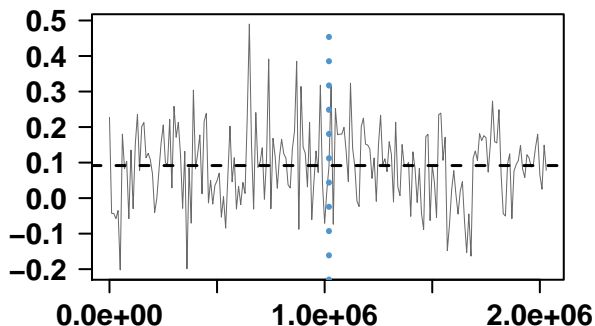
Sulfurimonas denitrificans DSM 1251



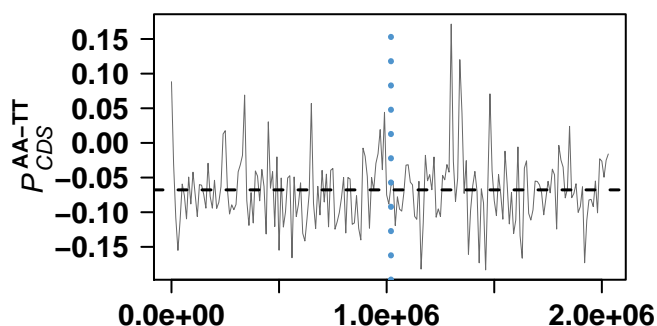
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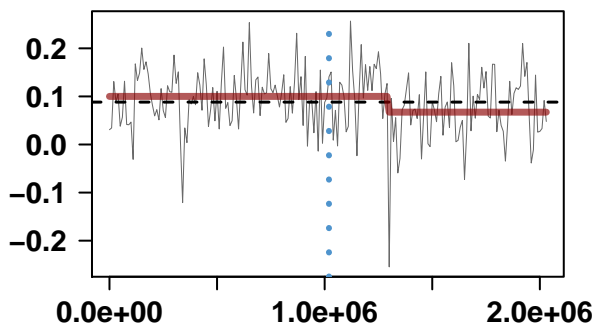
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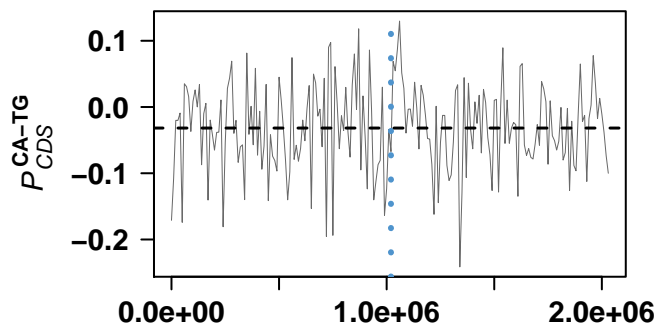
genome coordinates



genome coordinates

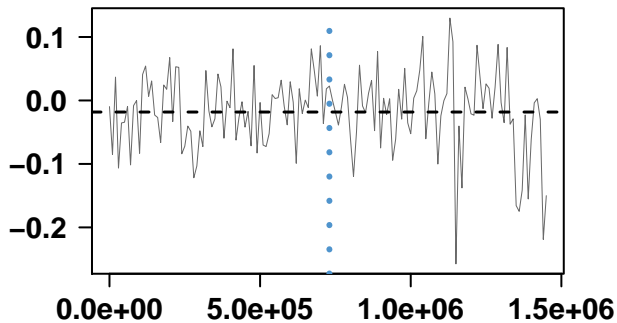


genome coordinates

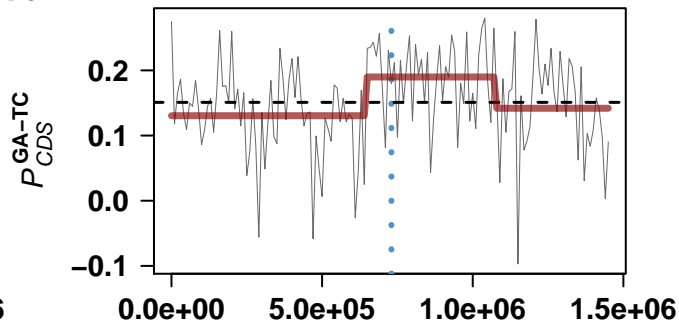


genome coordinates

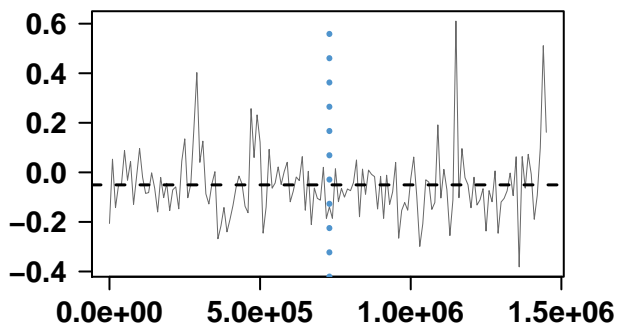
Helicobacter pylori HPAG1



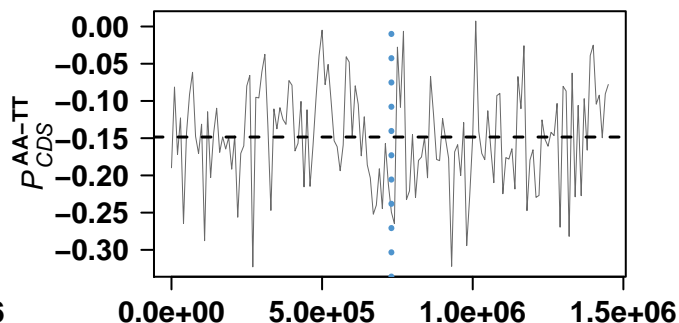
genome coordinates



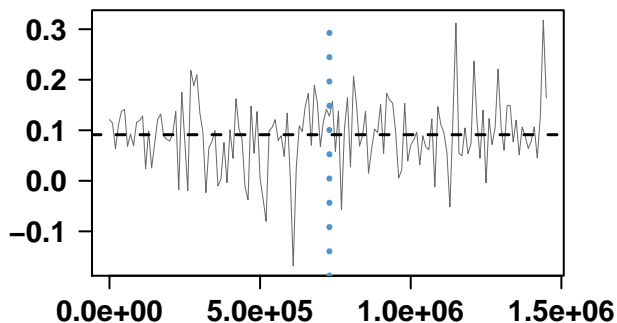
genome coordinates



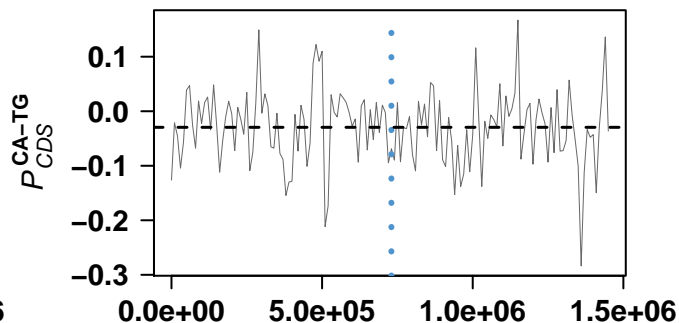
genome coordinates



genome coordinates

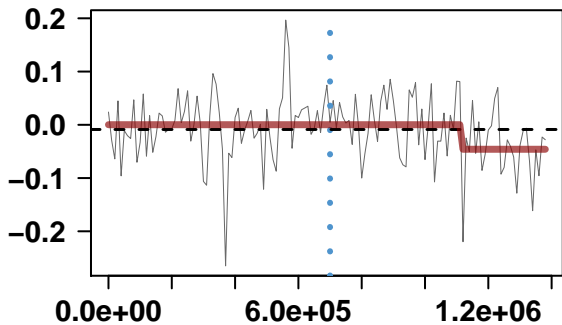


genome coordinates

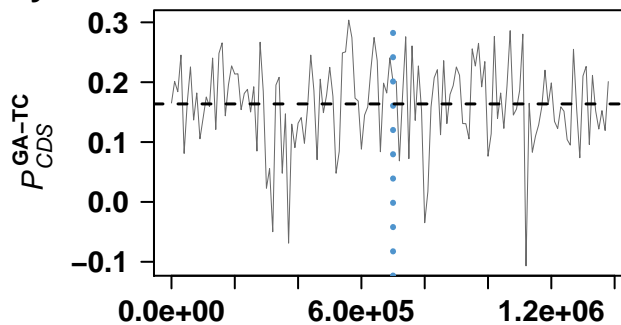


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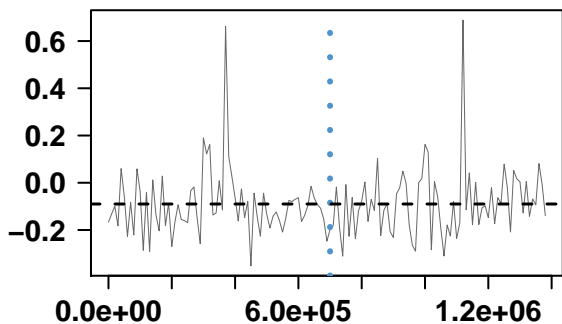
Helicobacter acinonychis str. Sheeba



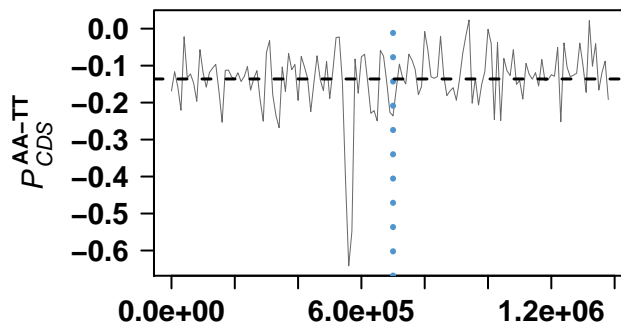
genome coordinates



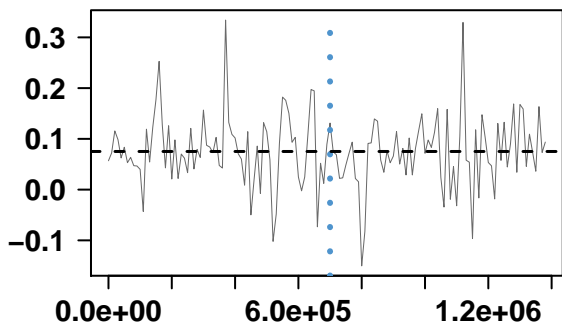
genome coordinates



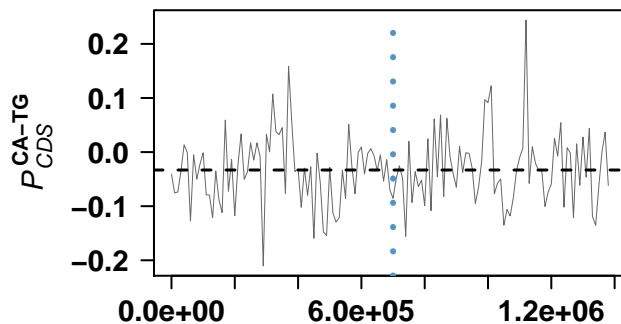
genome coordinates



genome coordinates

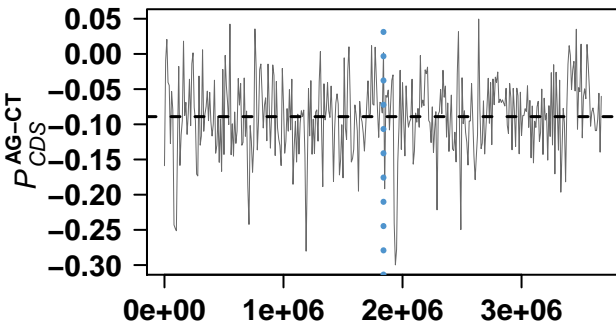


genome coordinates

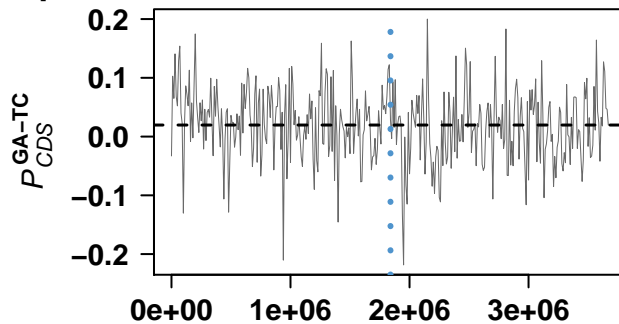


genome coordinates

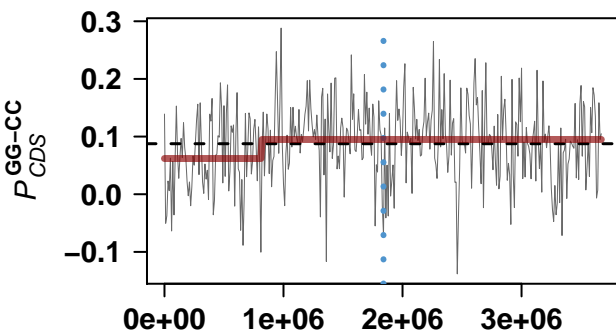
Bacillus subtilis subsp. subtilis str. 168



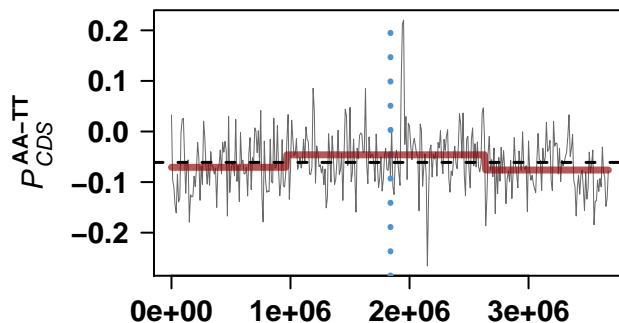
genome coordinates



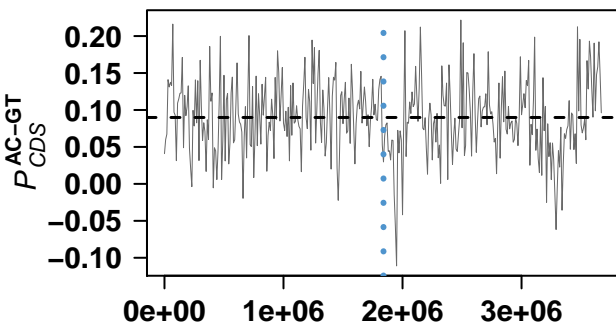
genome coordinates



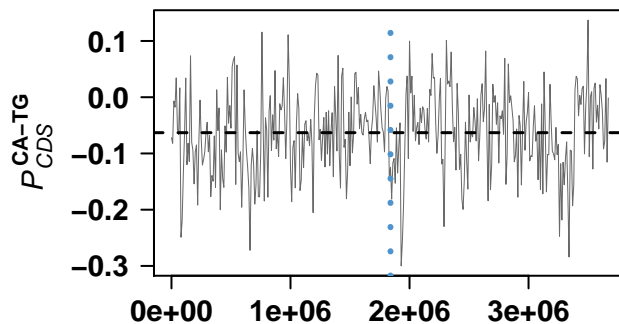
genome coordinates



genome coordinates

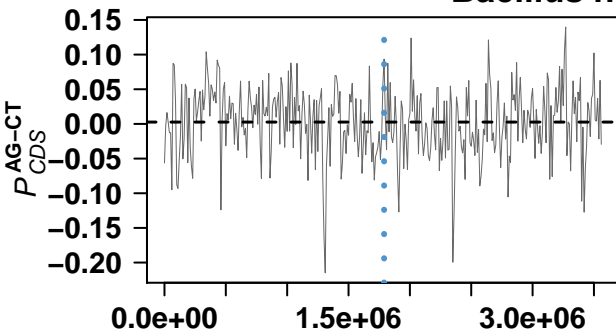


genome coordinates

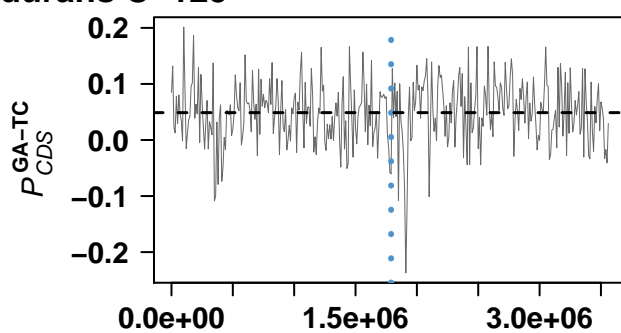


genome coordinates

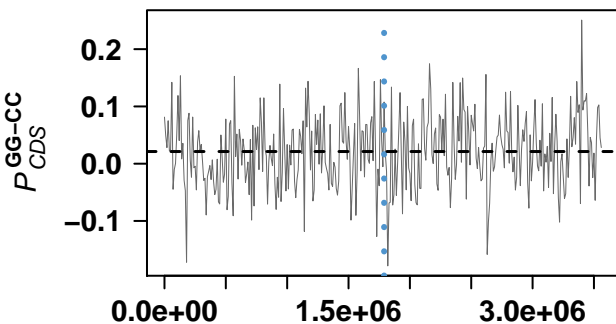
Bacillus halodurans C-125



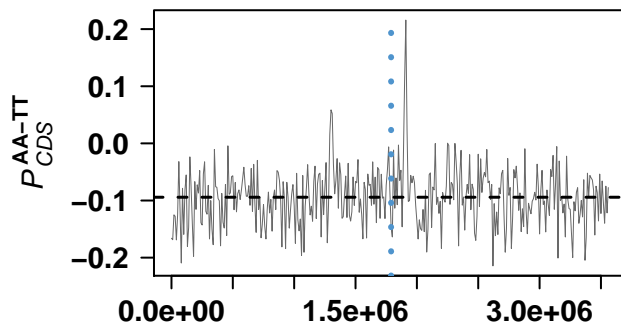
genome coordinates



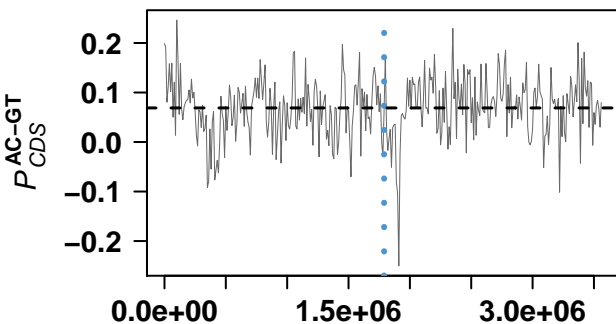
genome coordinates



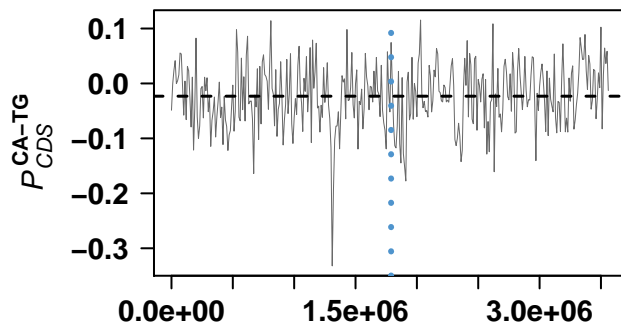
genome coordinates



genome coordinates

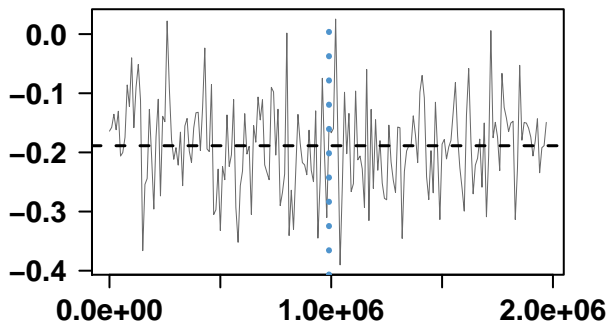


genome coordinates

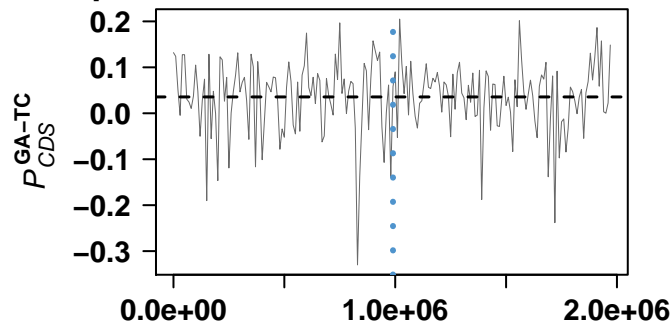


genome coordinates

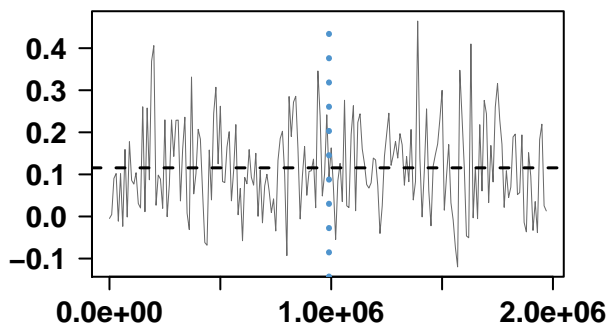
Lactococcus lactis subsp. lactis II1403



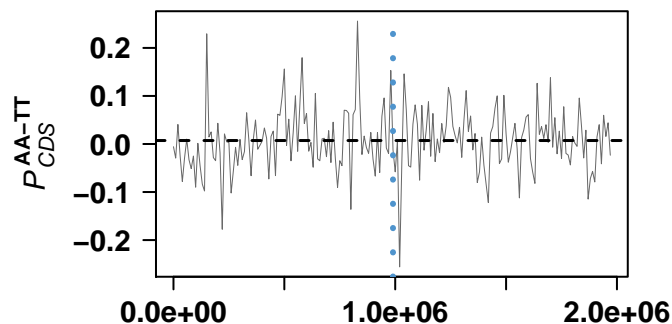
genome coordinates



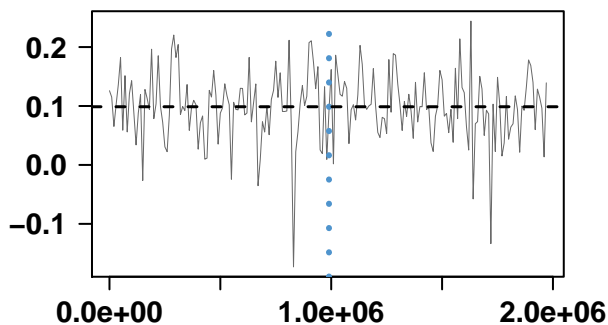
genome coordinates



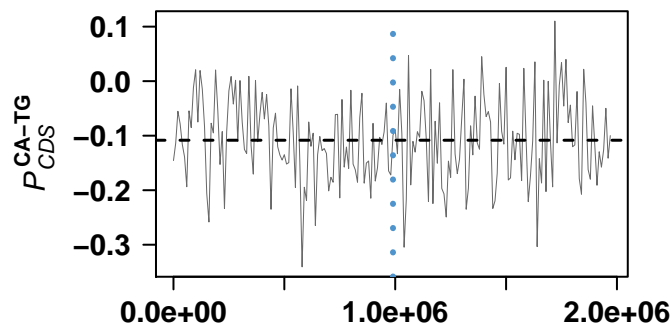
genome coordinates



genome coordinates

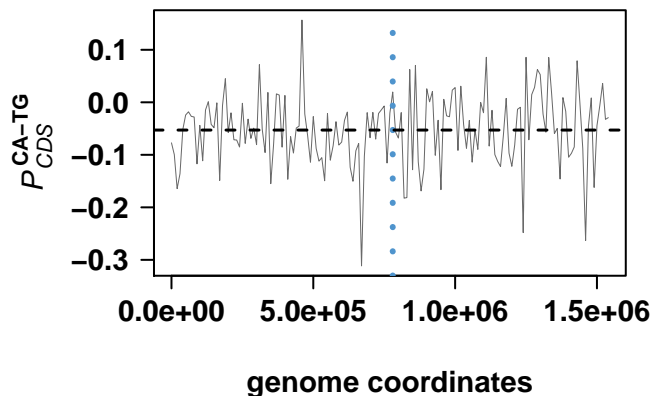
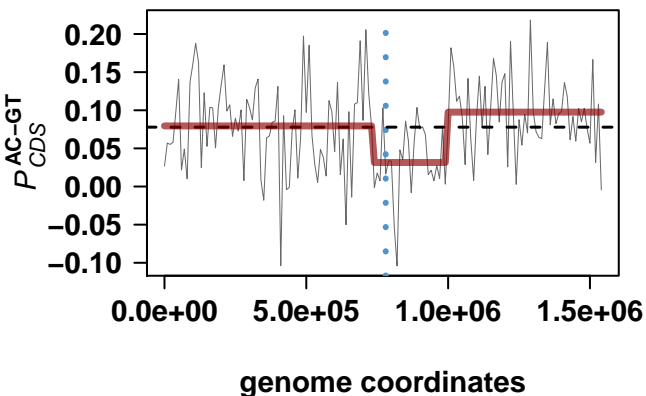
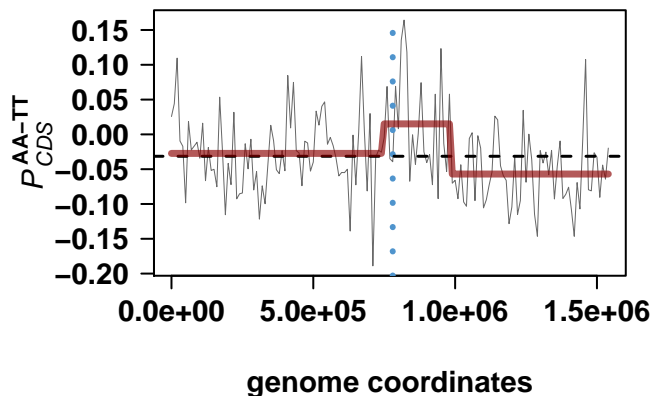
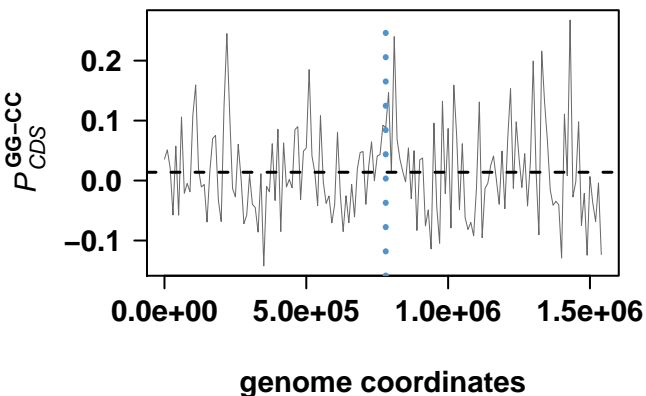
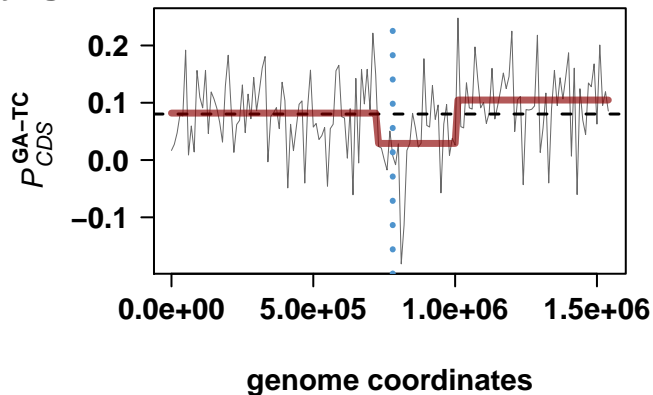
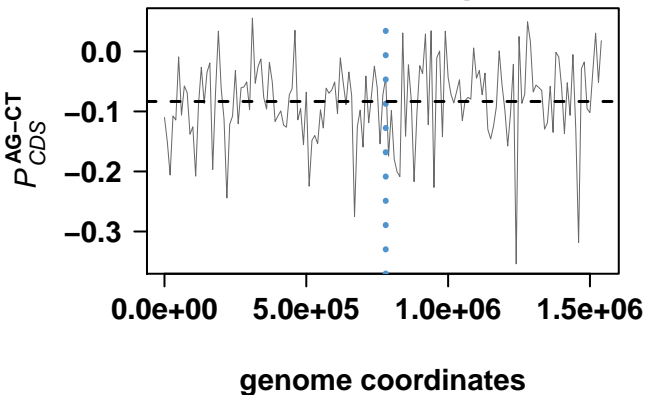


genome coordinates

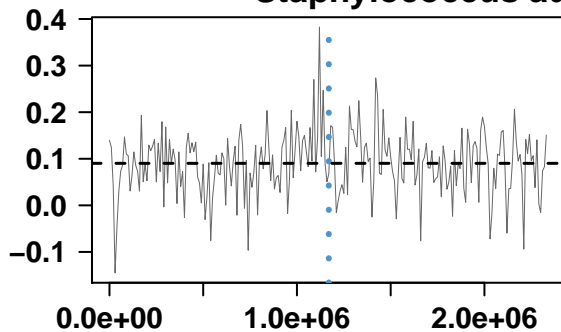


genome coordinates

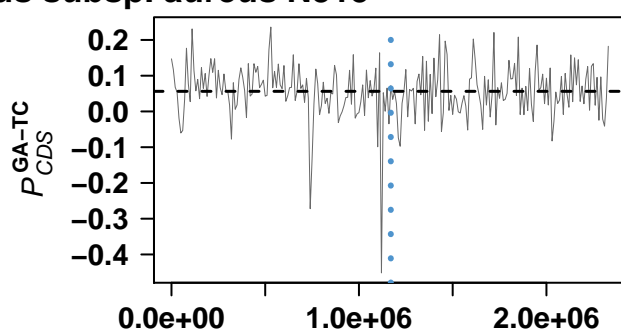
Streptococcus pyogenes M1 GAS



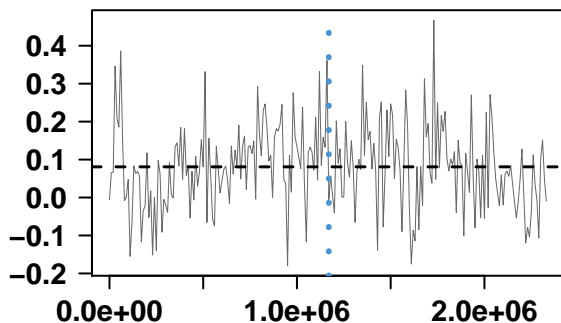
Staphylococcus aureus subsp. aureus N315



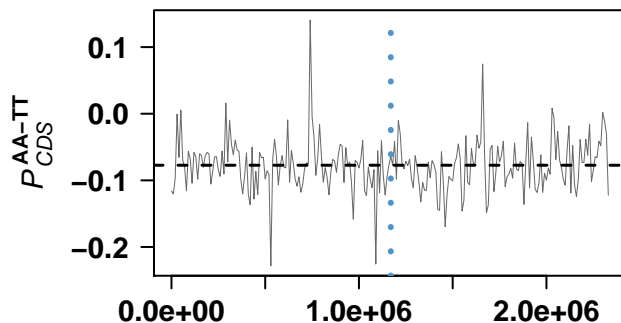
genome coordinates



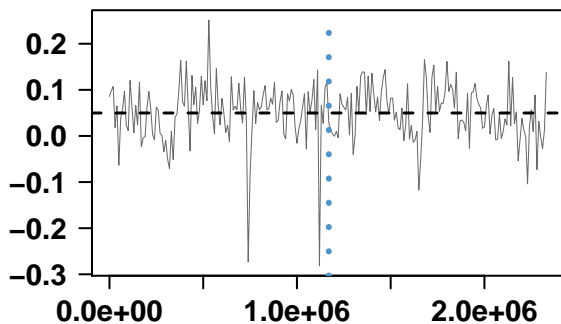
genome coordinates



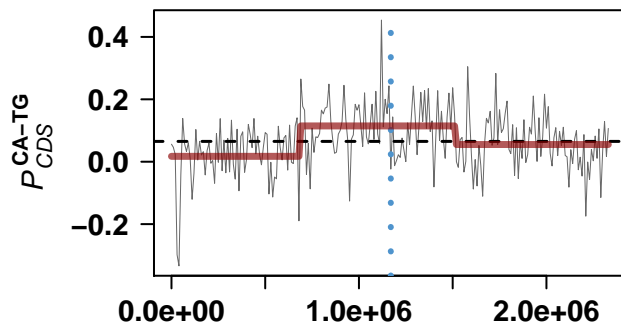
genome coordinates



genome coordinates

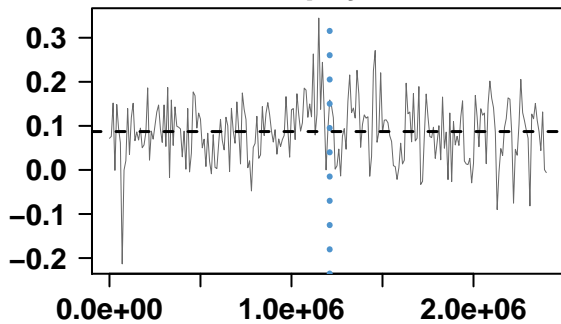


genome coordinates

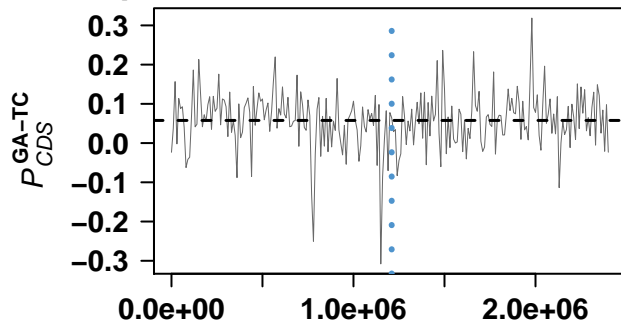


genome coordinates

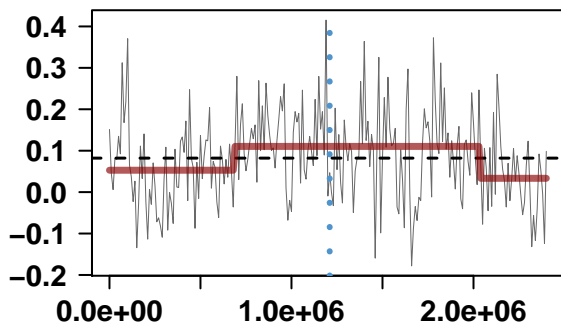
Staphylococcus aureus subsp. aureus Mu50



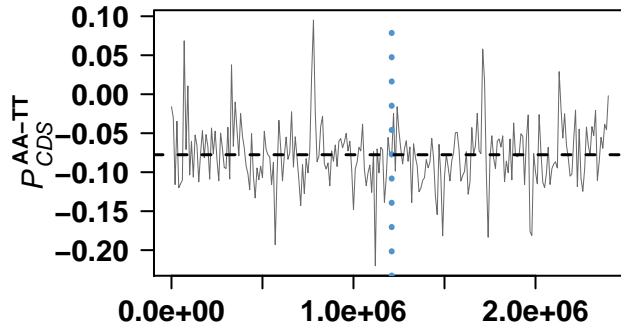
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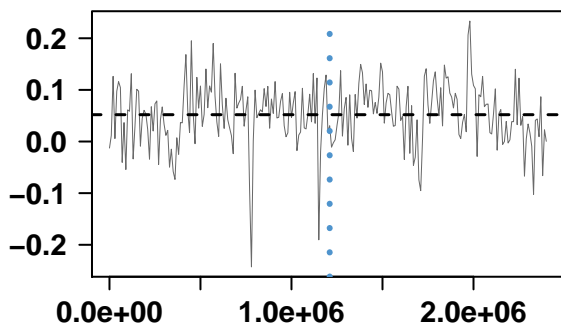
genome coordinates



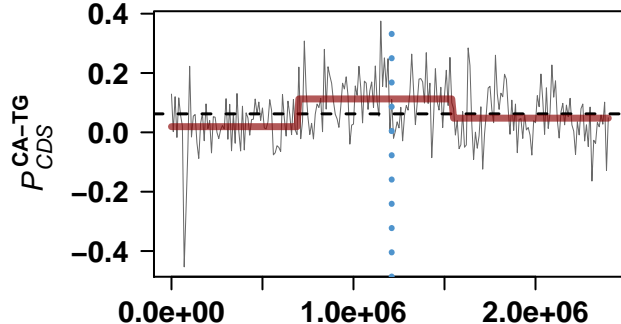
genome coordinates



genome coordinates

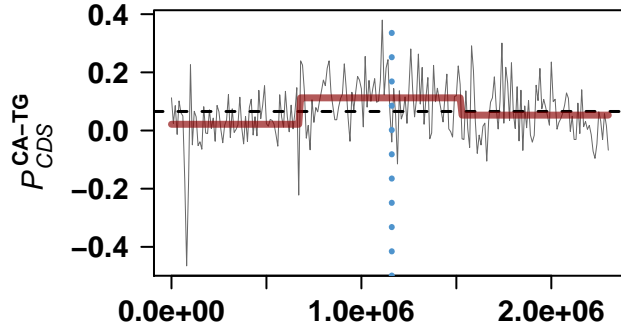
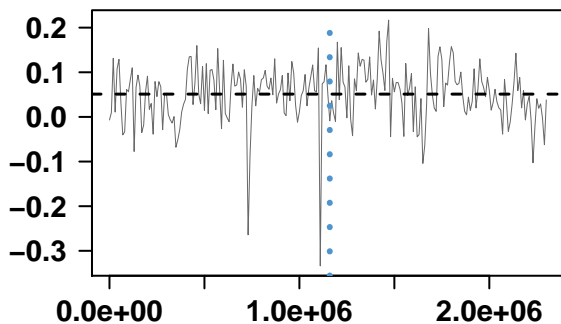
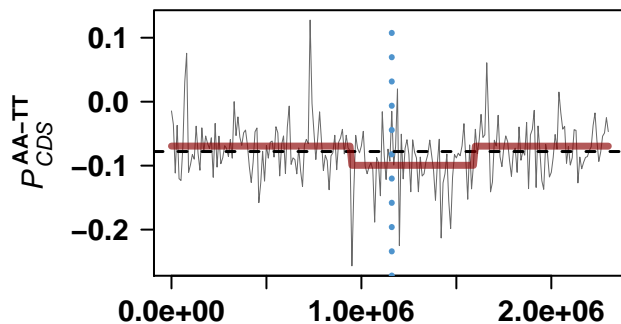
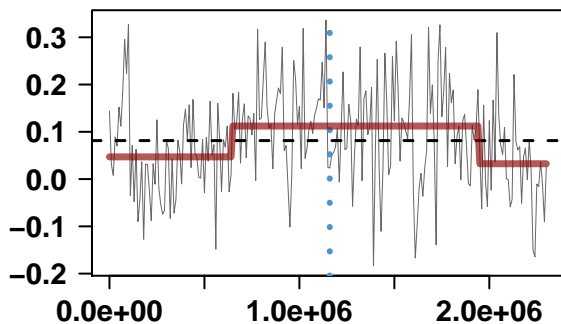
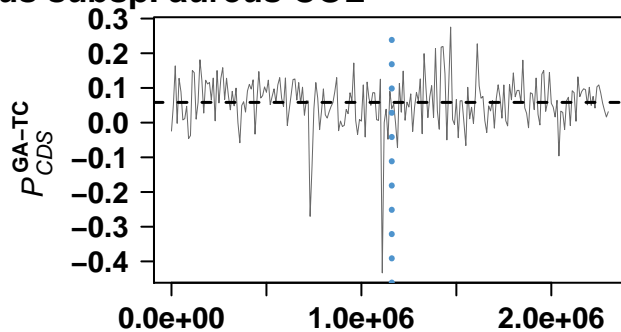
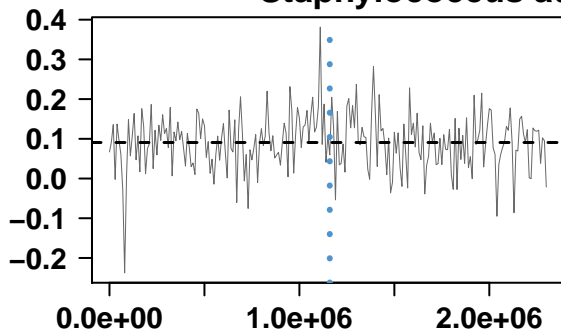


genome coordinates

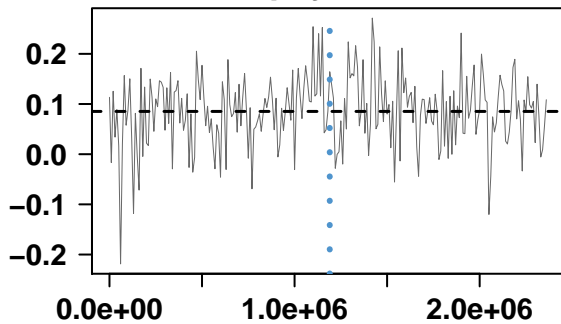


genome coordinates

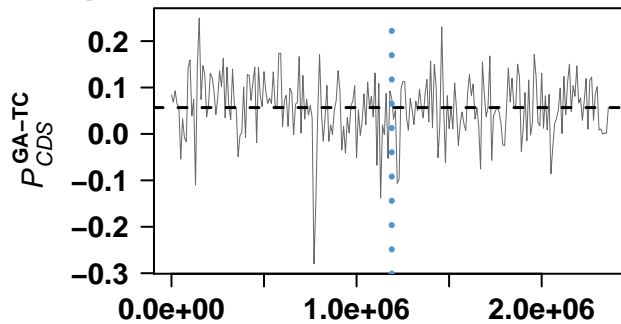
Staphylococcus aureus subsp. aureus COL



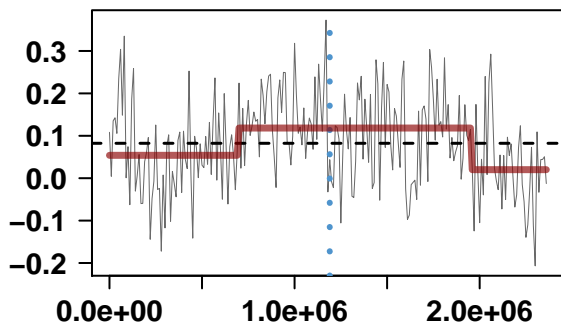
Staphylococcus aureus subsp. aureus MRSA252



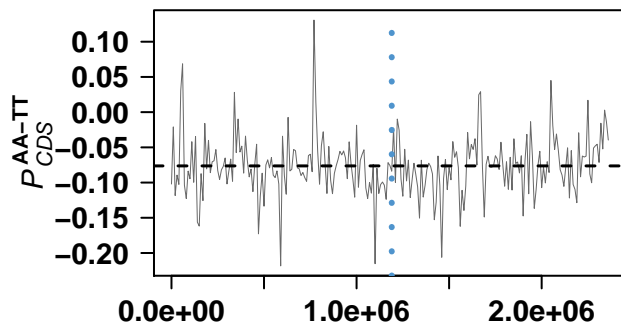
genome coordinates



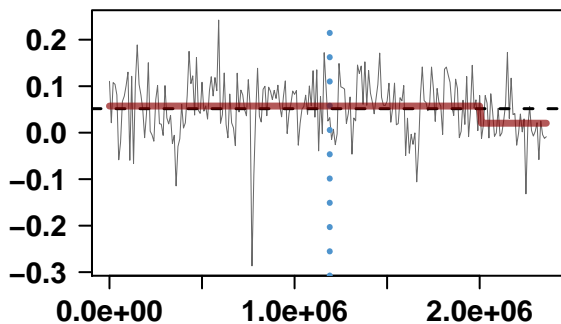
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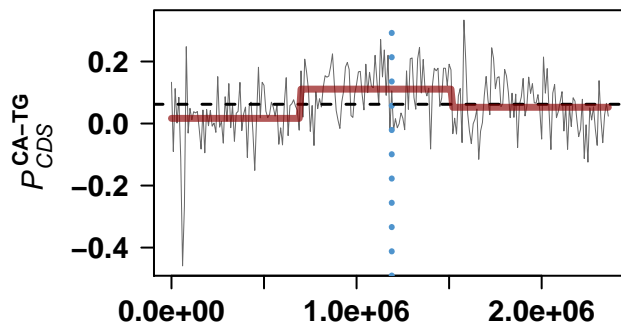
genome coordinates



genome coordinates

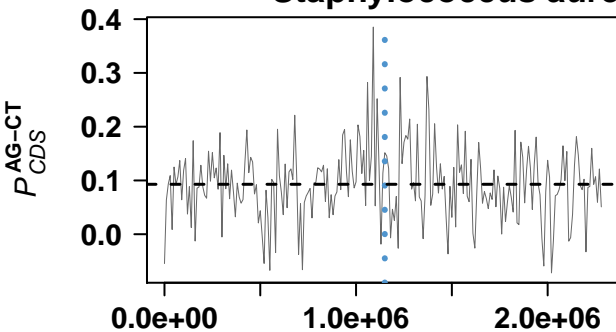


genome coordinates

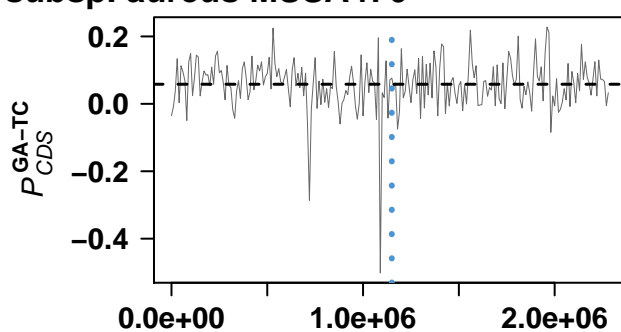


genome coordinates

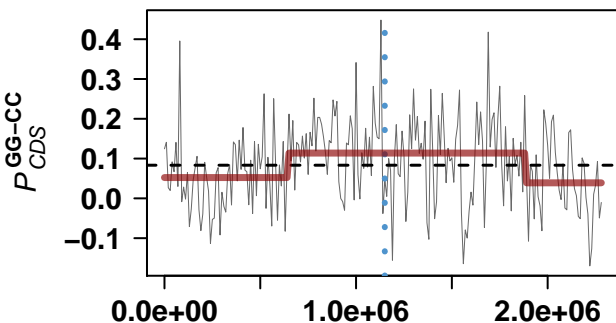
Staphylococcus aureus subsp. aureus MSSA476



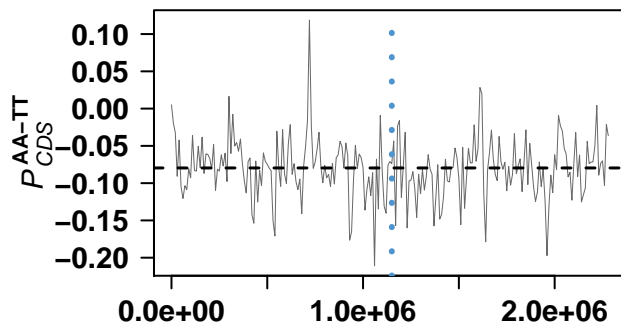
genome coordinates



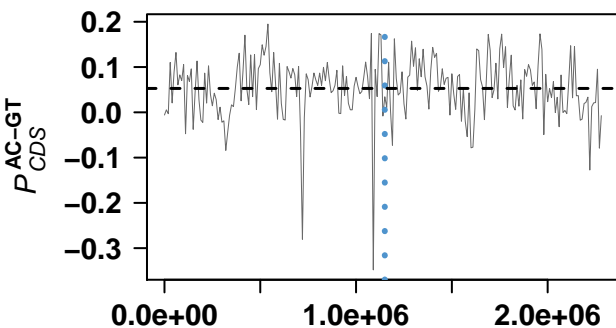
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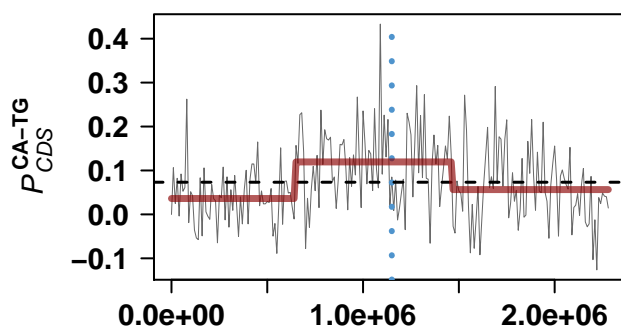
genome coordinates



genome coordinates

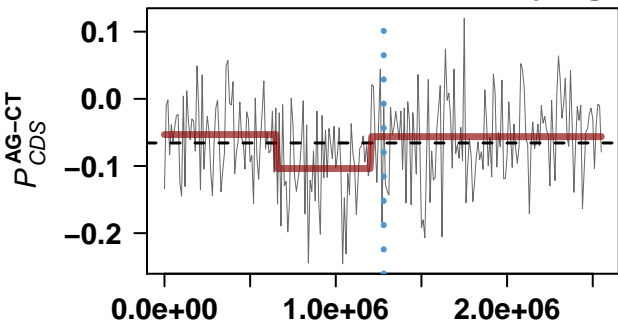


genome coordinates

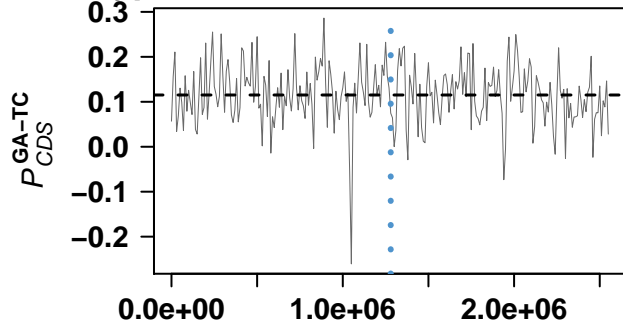


genome coordinates

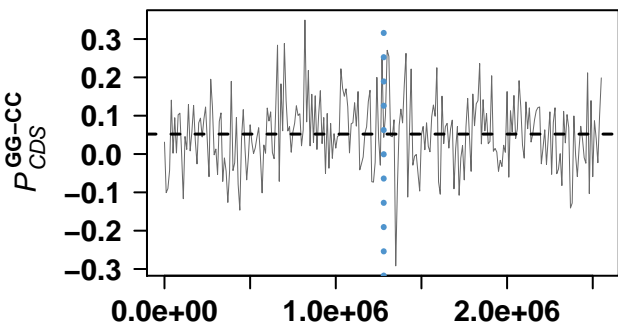
Listeria monocytogenes serotype 4b str. F2365



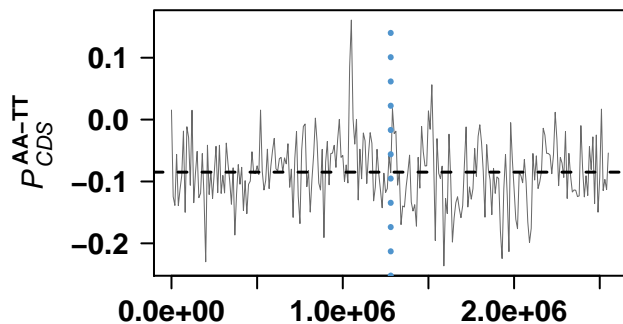
genome coordinates



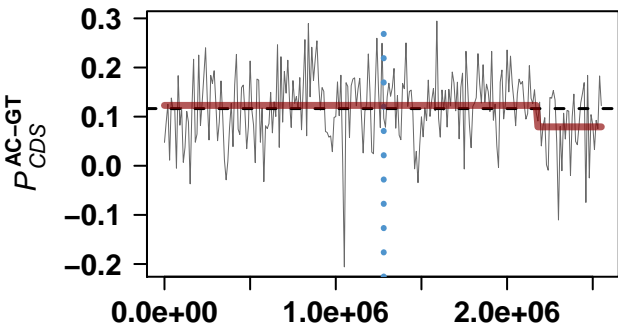
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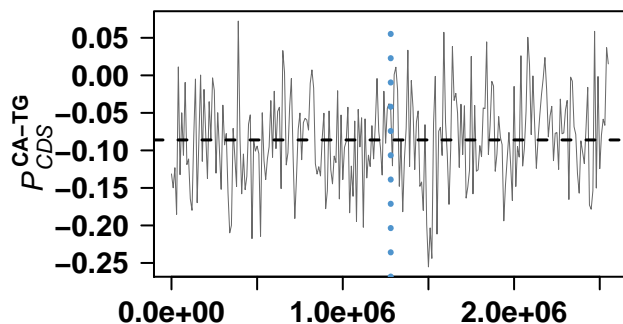
genome coordinates



genome coordinates

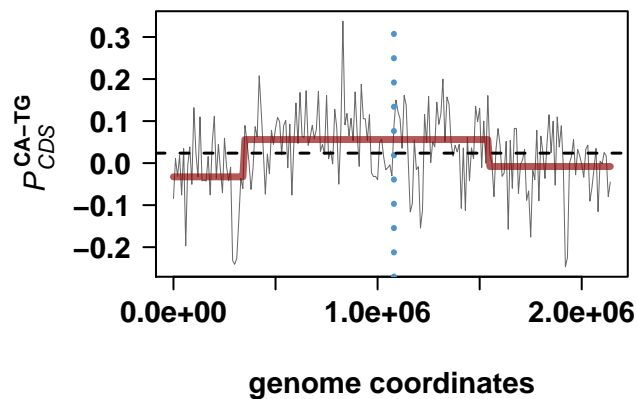
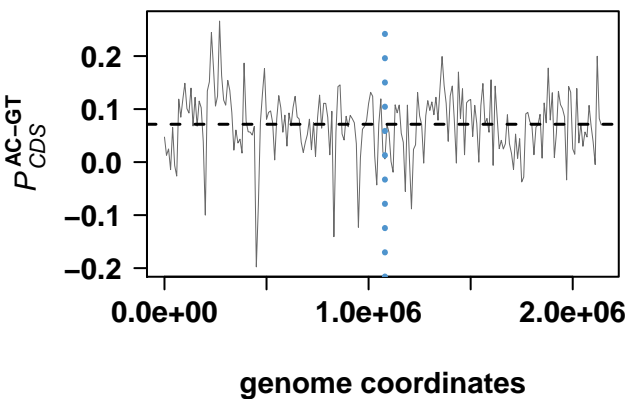
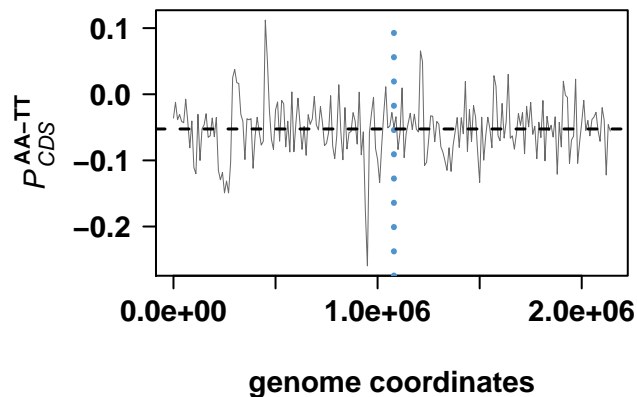
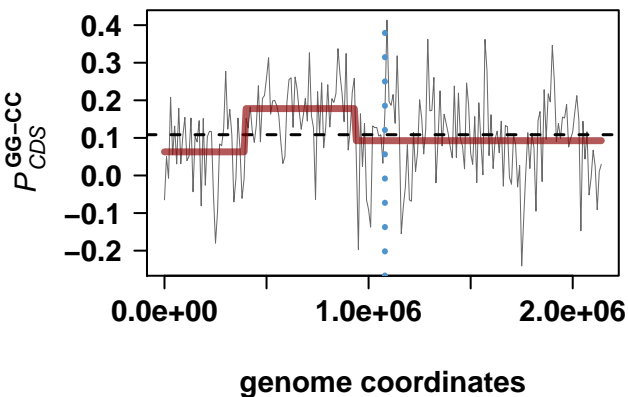
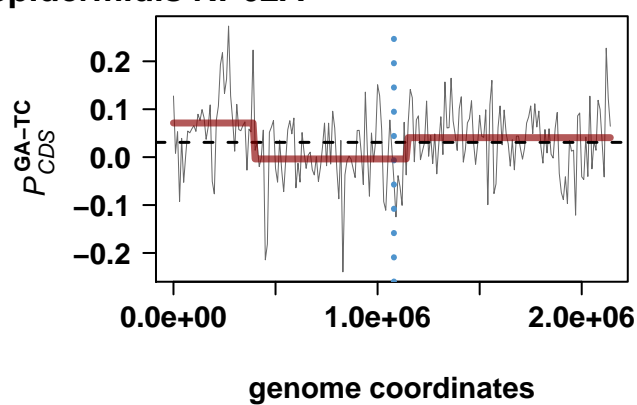
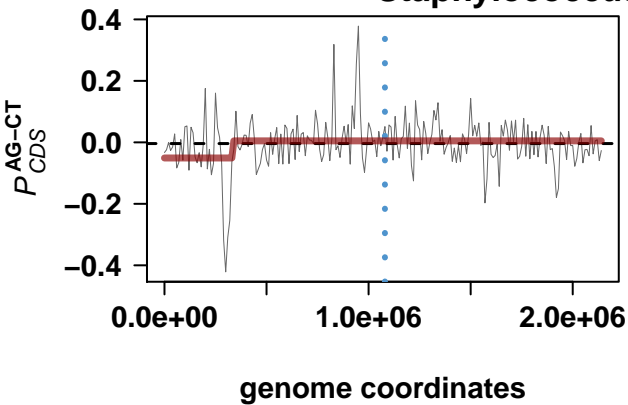


genome coordinates

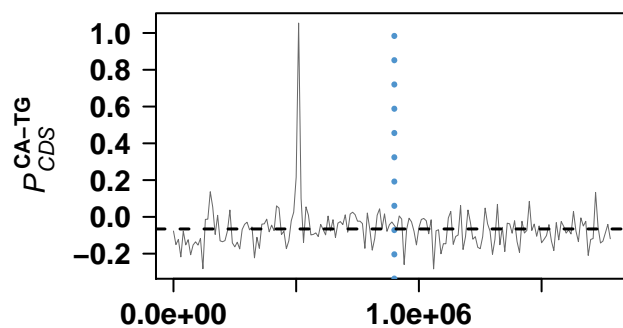
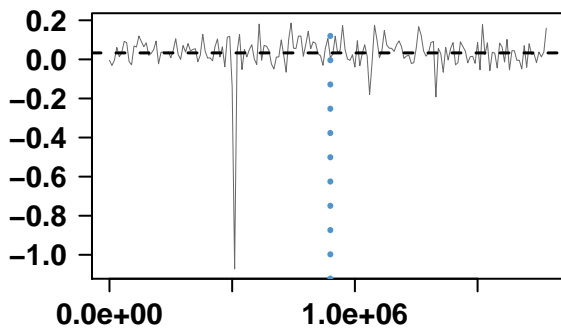
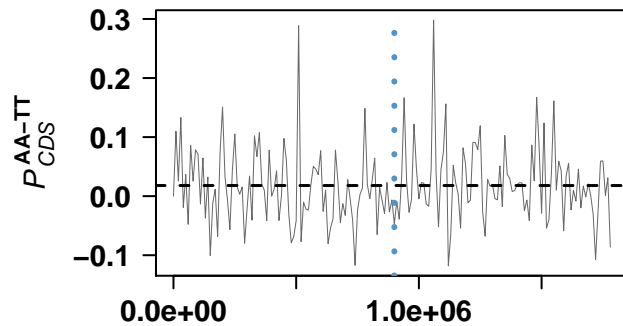
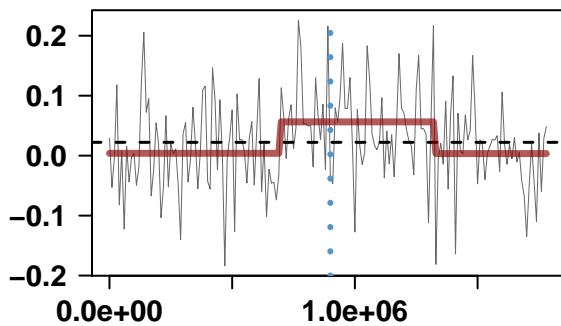
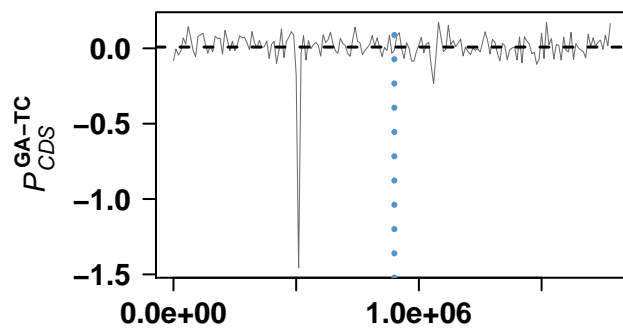
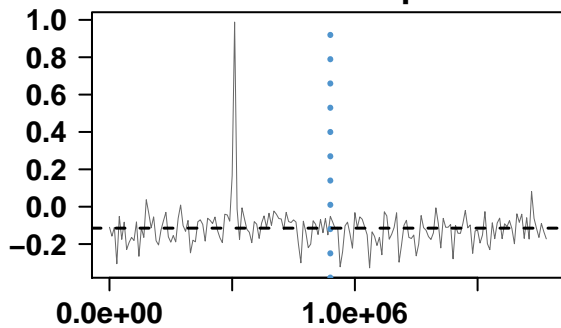


genome coordinates

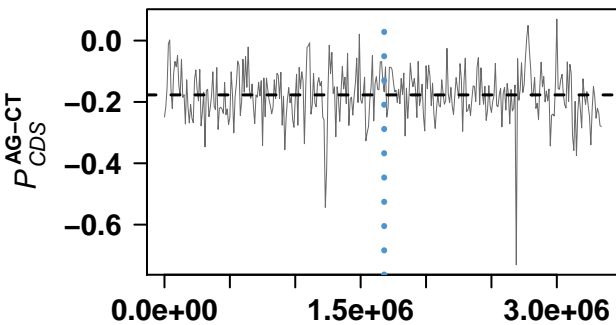
Staphylococcus epidermidis RP62A



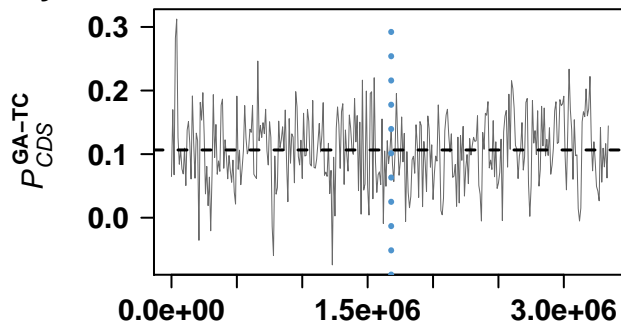
Streptococcus pneumoniae TIGR4



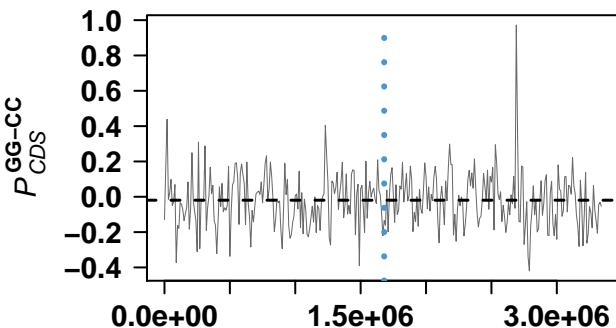
Clostridium acetobutylicum ATCC 824



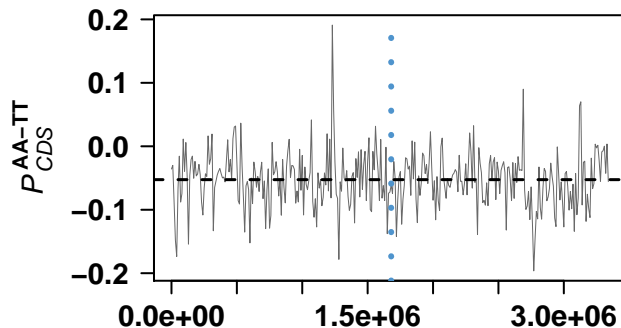
genome coordinates



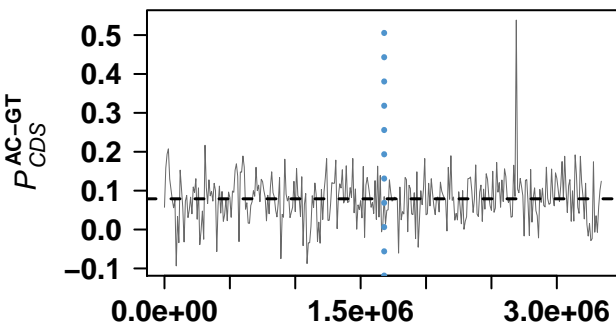
genome coordinates



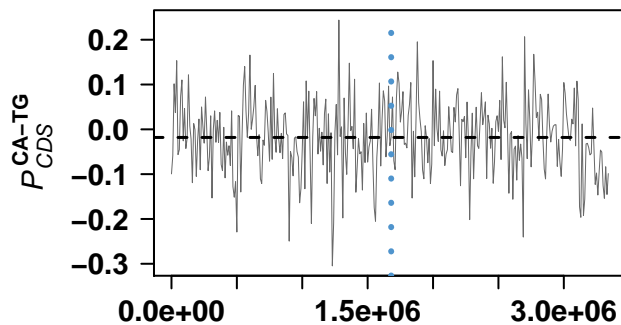
genome coordinates



genome coordinates

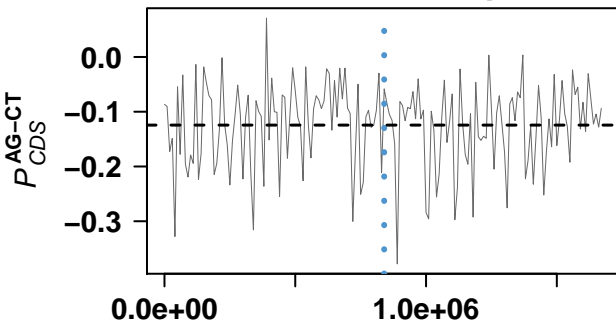


genome coordinates

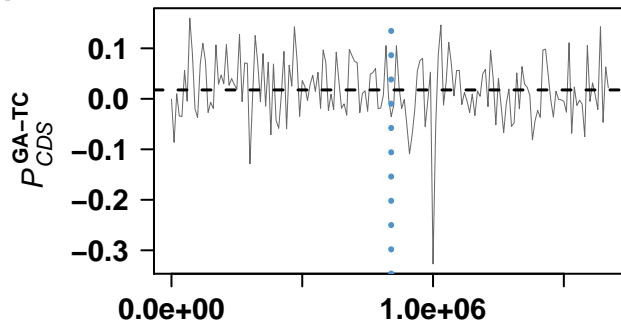


genome coordinates

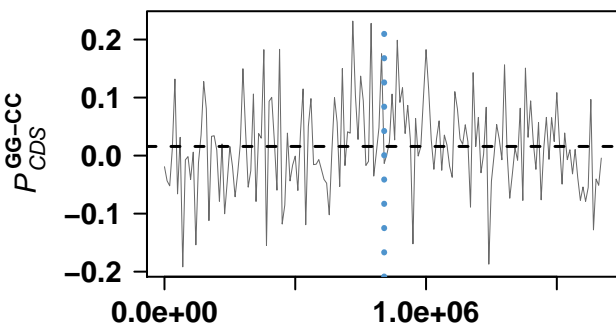
Streptococcus pneumoniae R6



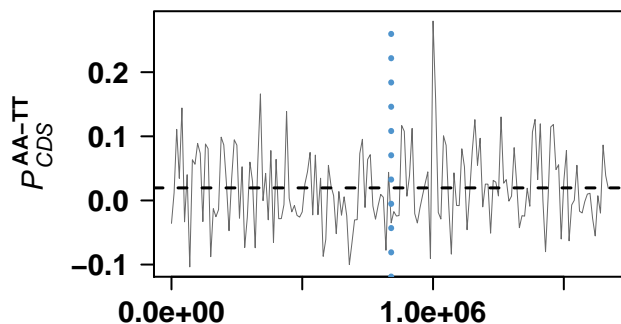
genome coordinates



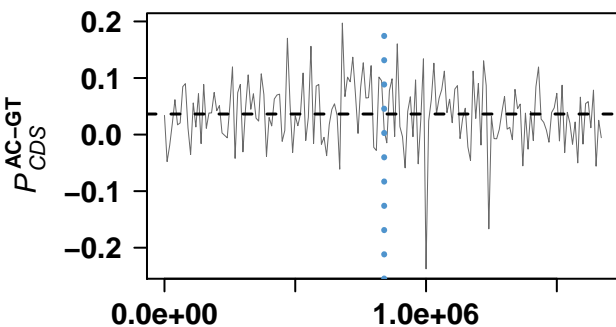
genome coordinates



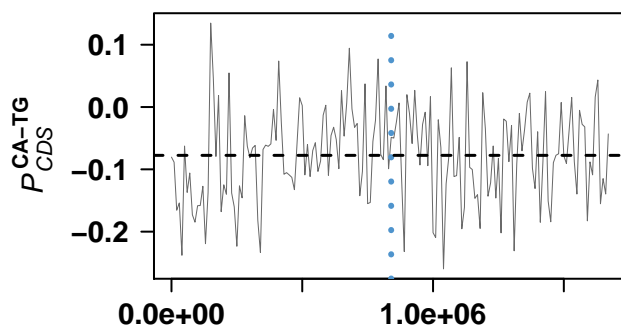
genome coordinates



genome coordinates

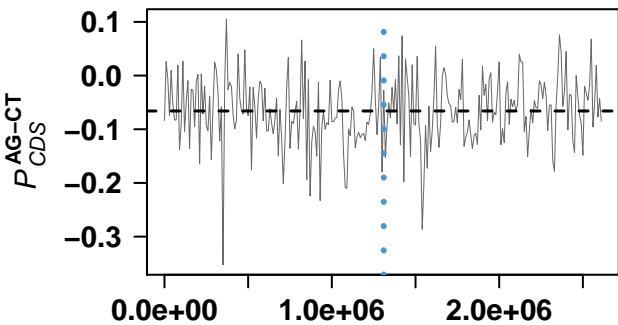


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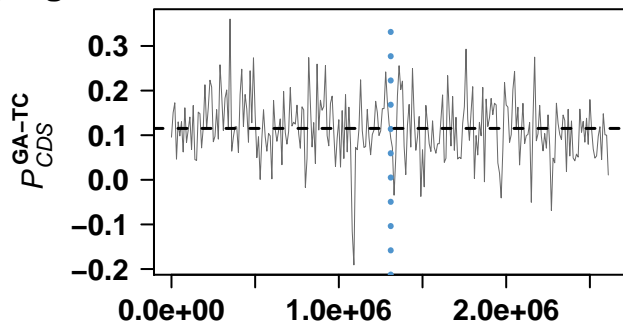


genome coordinates

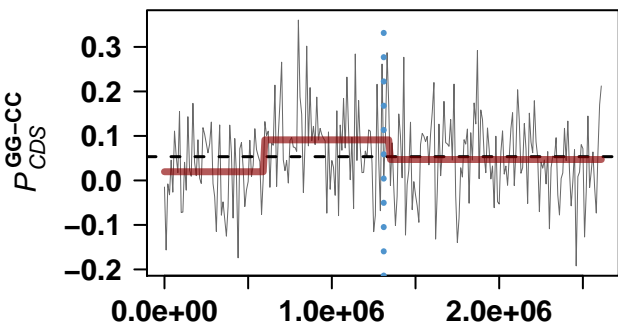
Listeria monocytogenes EGD-e



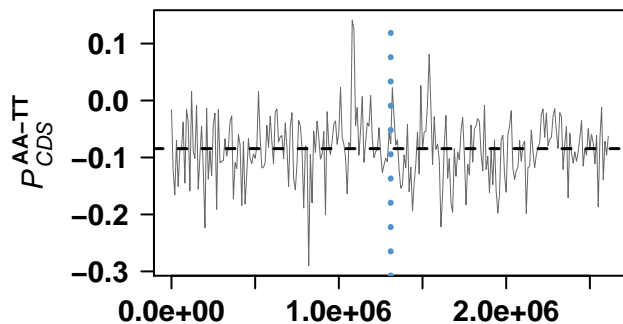
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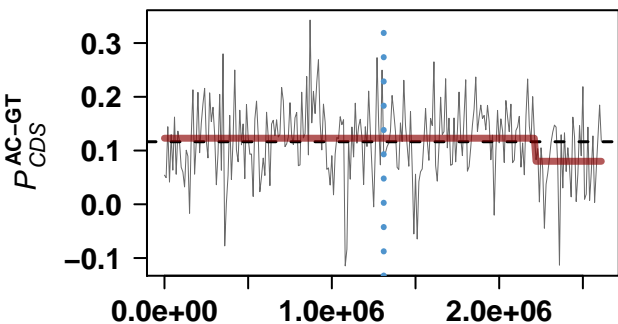
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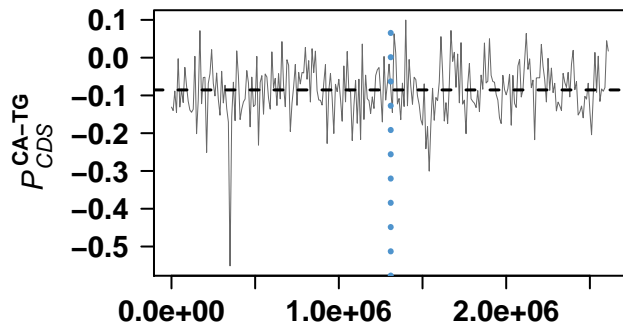
genome coordinates



genome coordinates

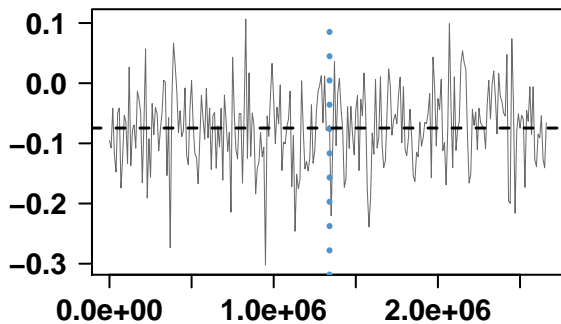


genome coordinates

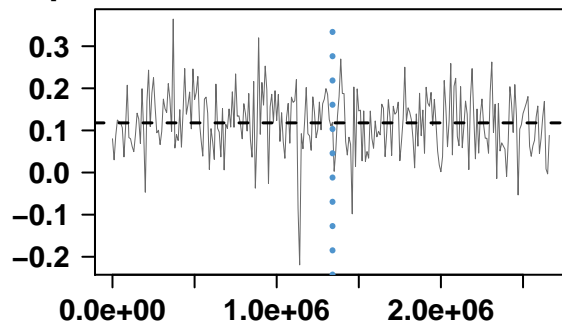


genome coordinates

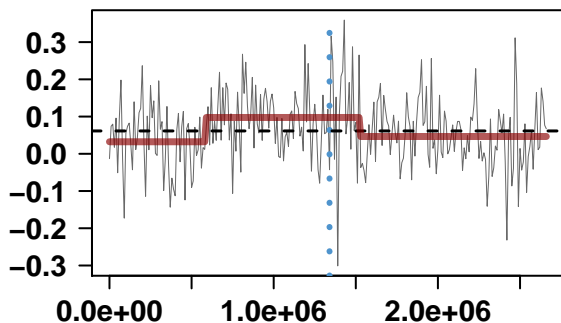
Listeria innocua Clip11262



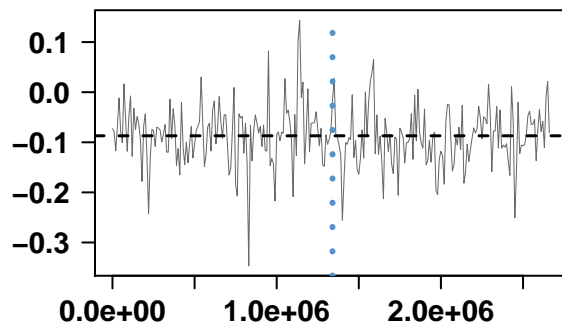
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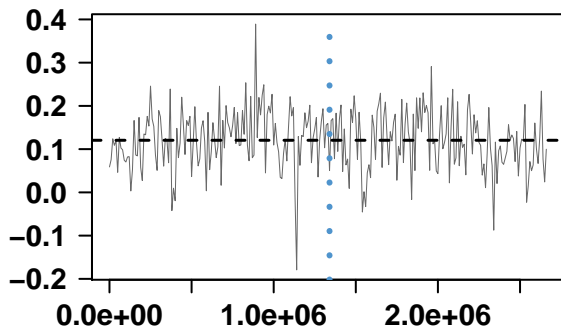
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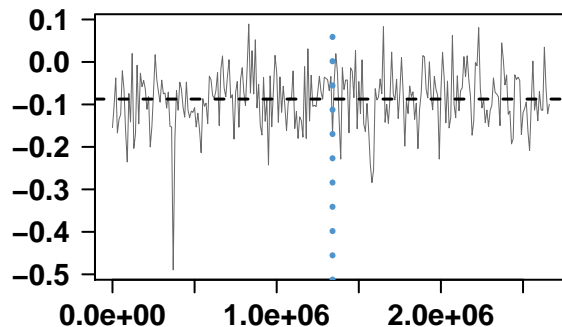
genome coordinates



genome coordinates

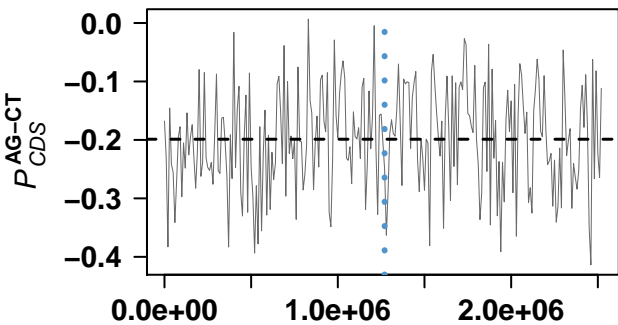


genome coordinates

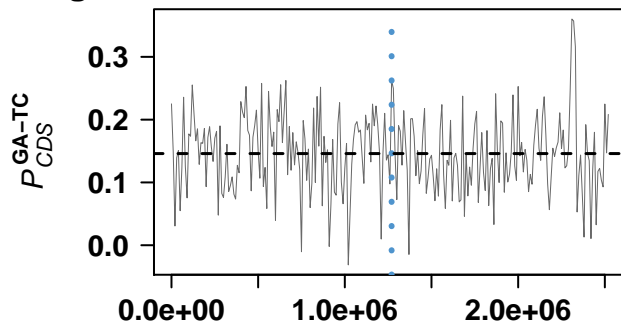


genome coordinates

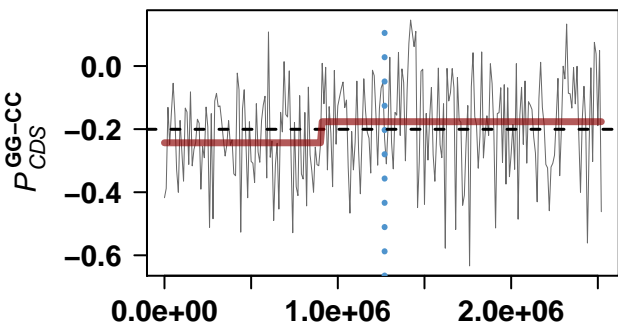
Clostridium perfringens str. 13



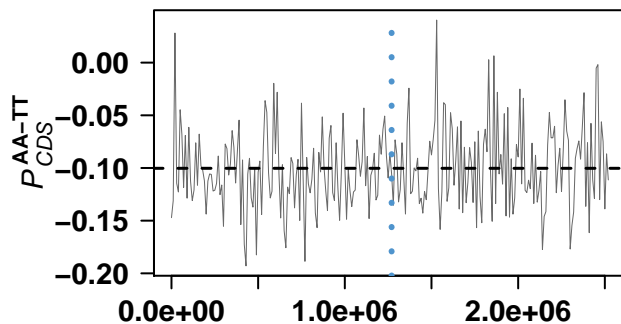
genome coordinates



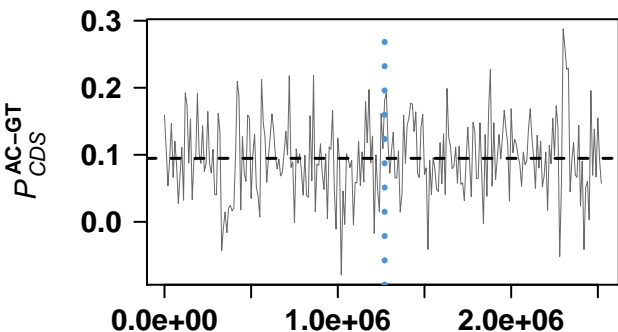
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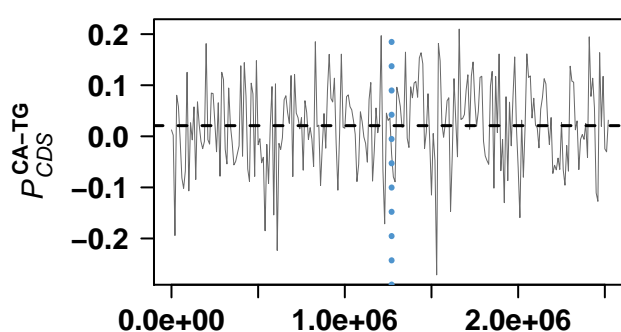
genome coordinates



genome coordinates

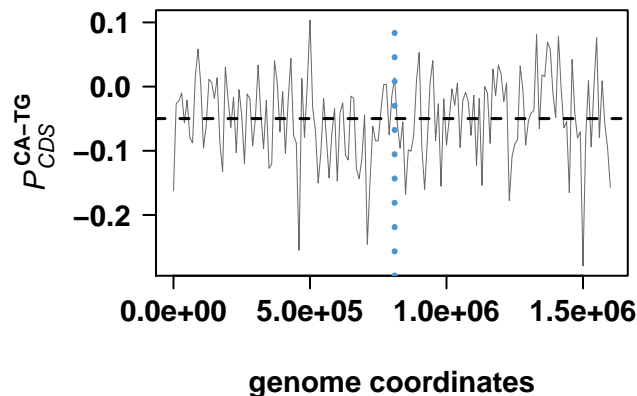
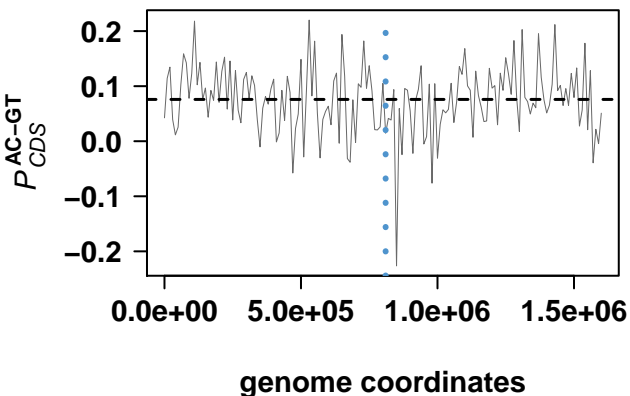
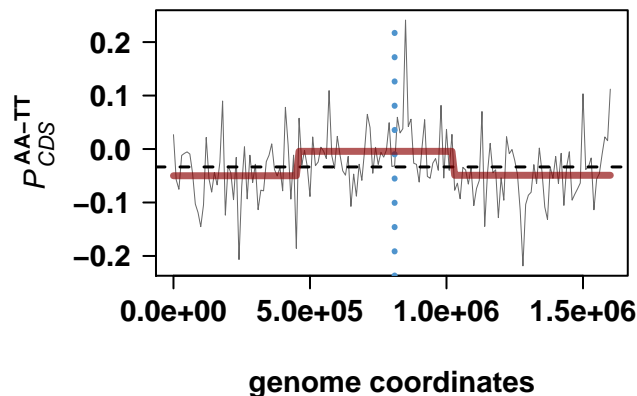
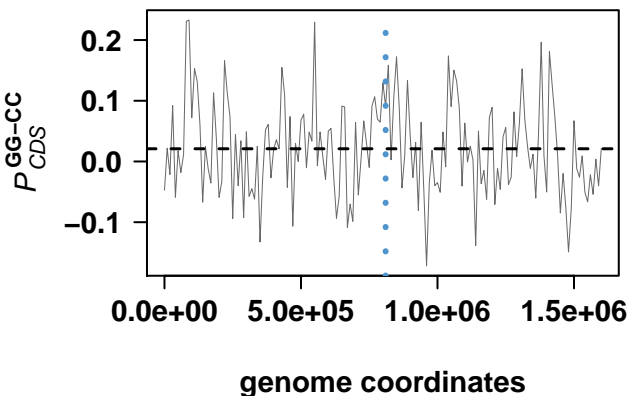
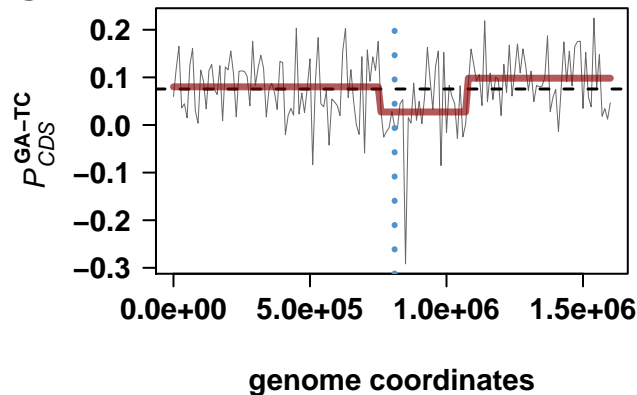
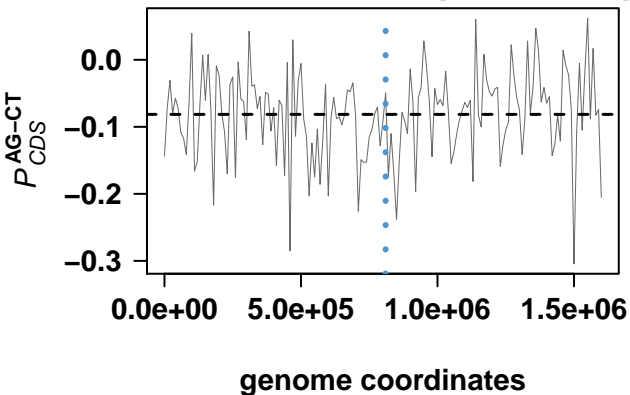


genome coordinates

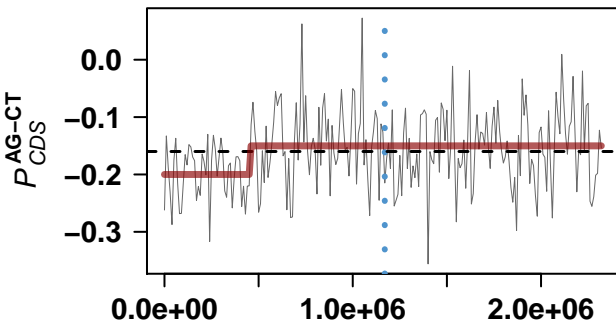


genome coordinates

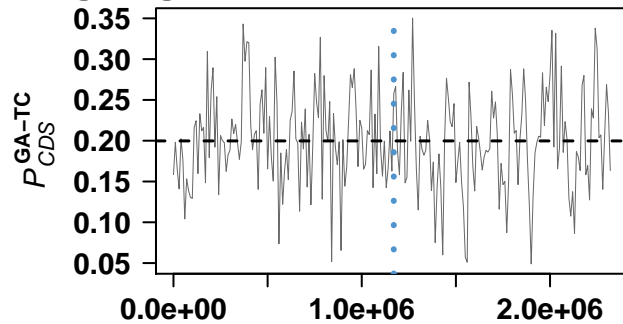
Streptococcus pyogenes MGAS8232



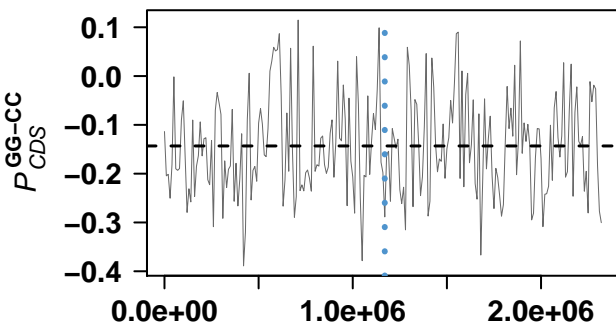
Thermoanaerobacter tengcongensis MB4



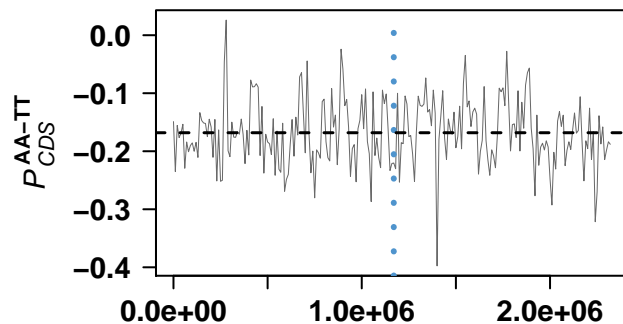
genome coordinates



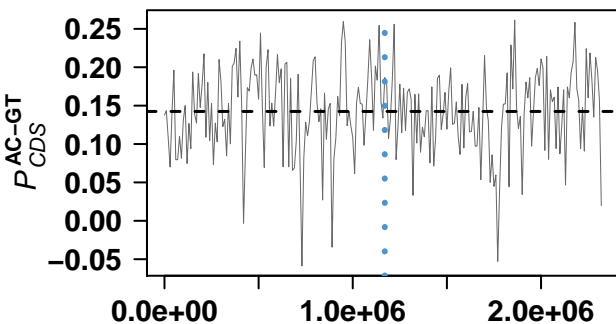
genome coordinates



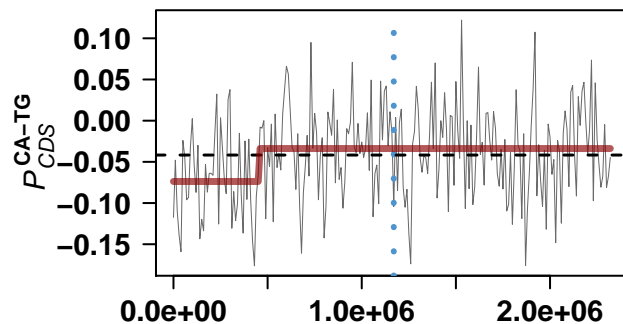
genome coordinates



genome coordinates

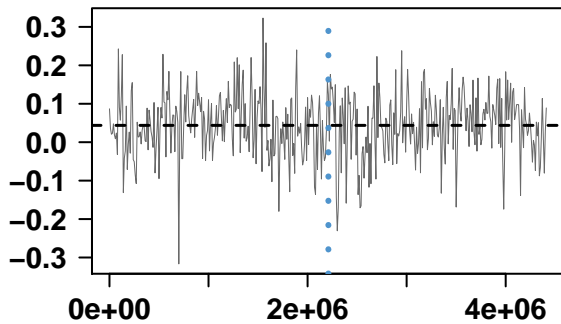


genome coordinates

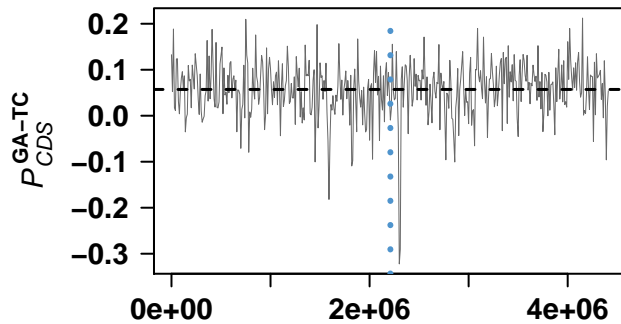


genome coordinates

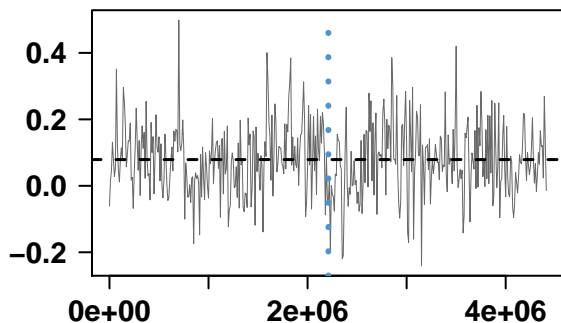
Bacillus cereus ATCC 10987



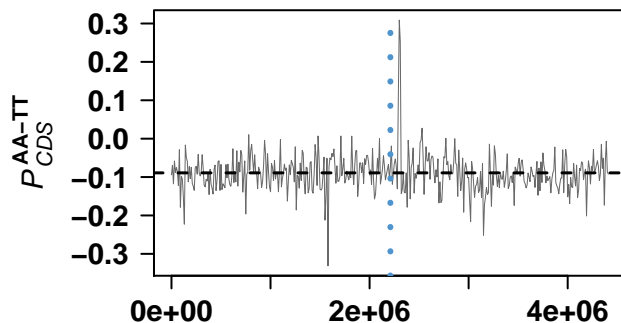
genome coordinates



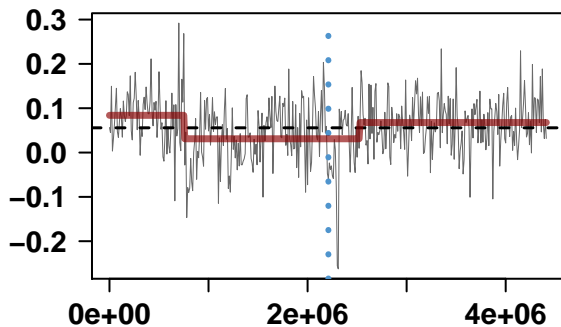
genome coordinates



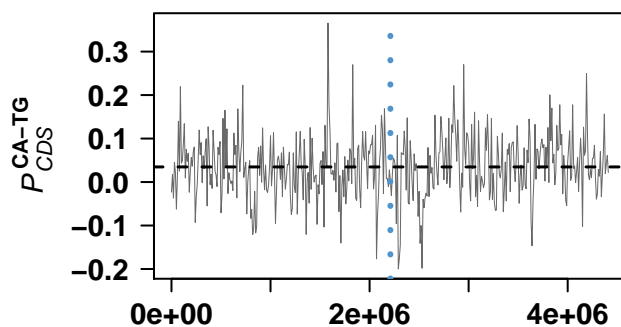
genome coordinates



genome coordinates

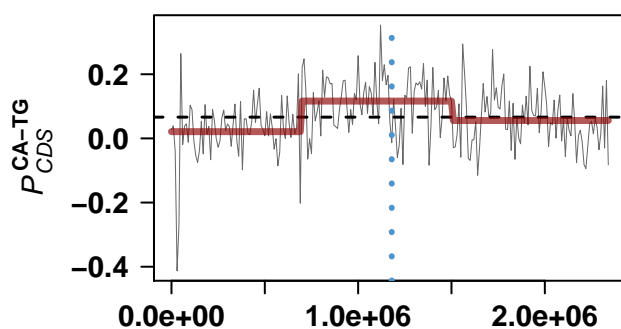
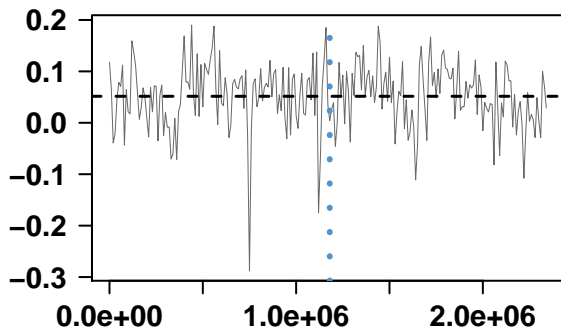
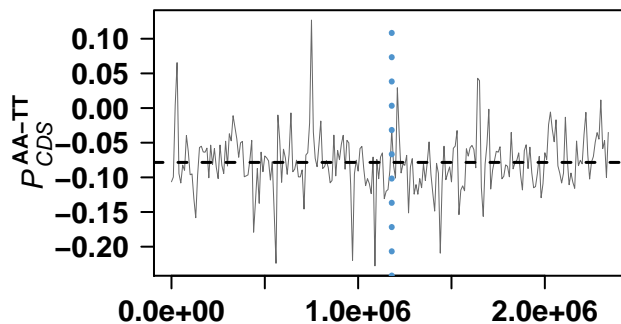
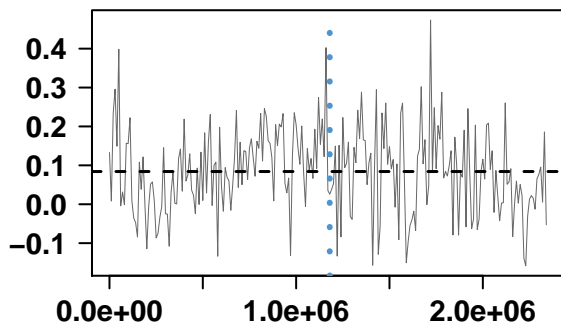
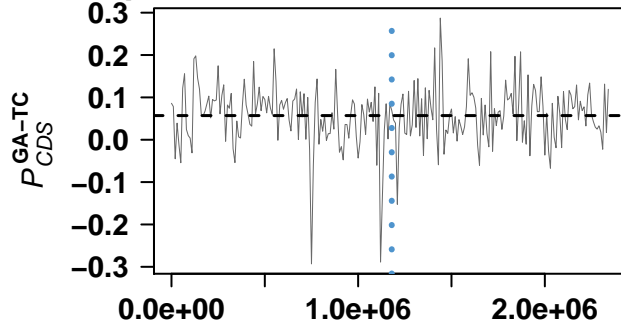
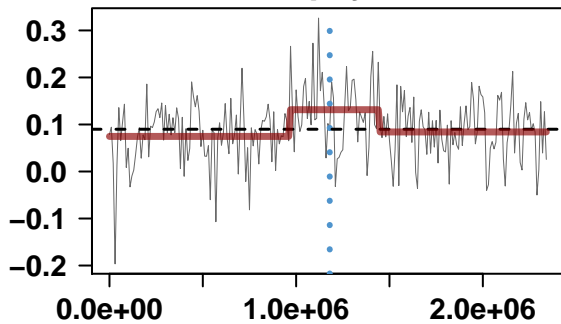


genome coordinates

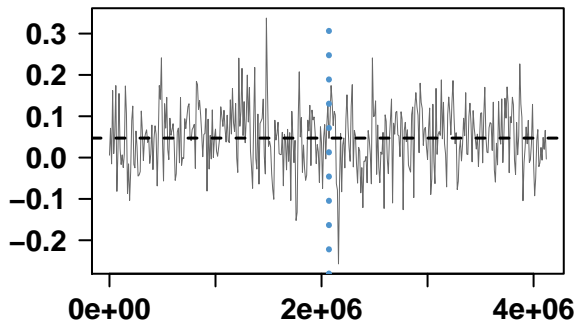


genome coordinates

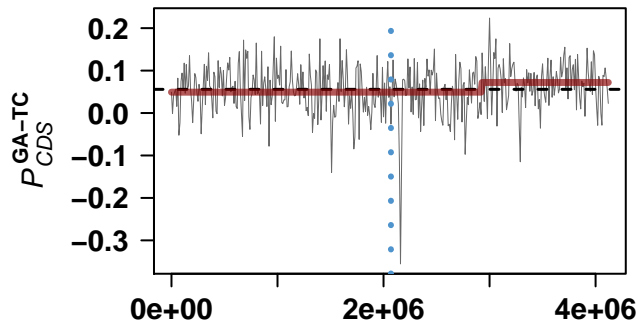
Staphylococcus aureus subsp. aureus MW2



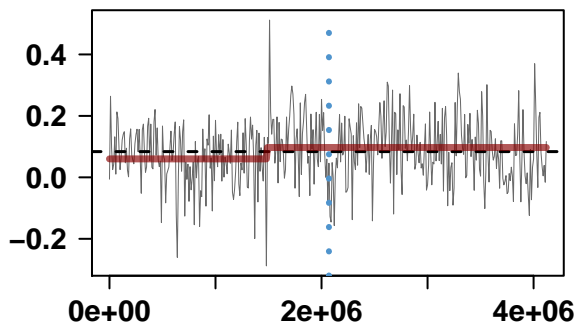
Bacillus anthracis str. Ames



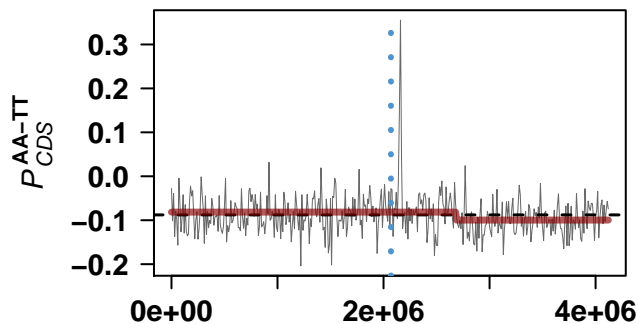
genome coordinates



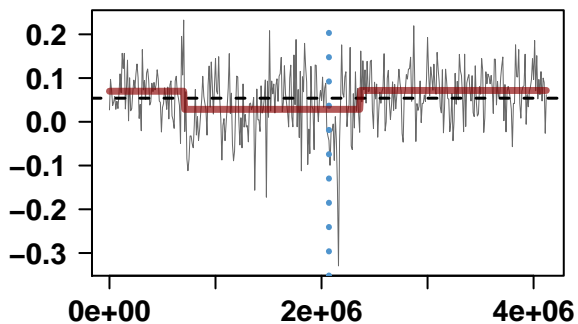
genome coordinates



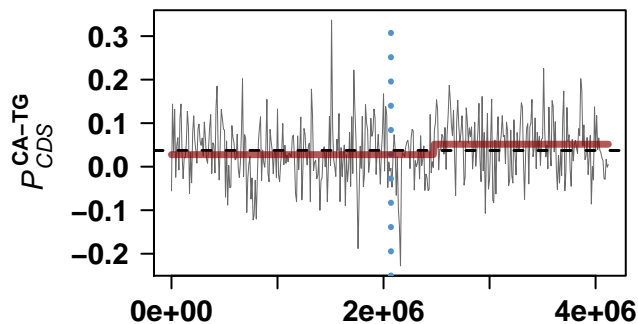
genome coordinates



genome coordinates

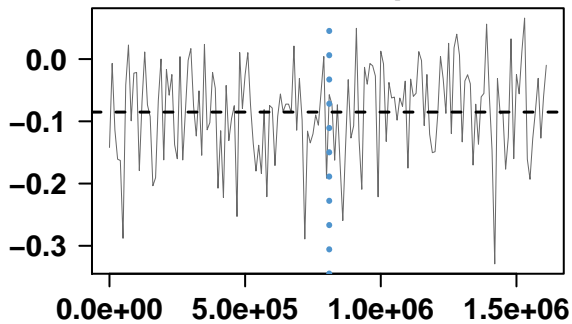


genome coordinates

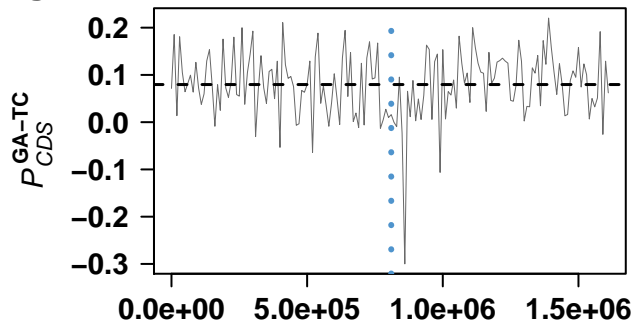


genome coordinates

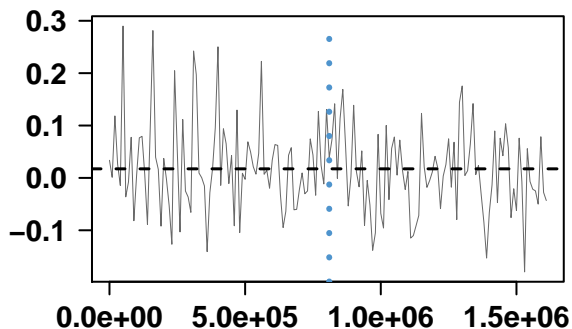
Streptococcus pyogenes MGAS315



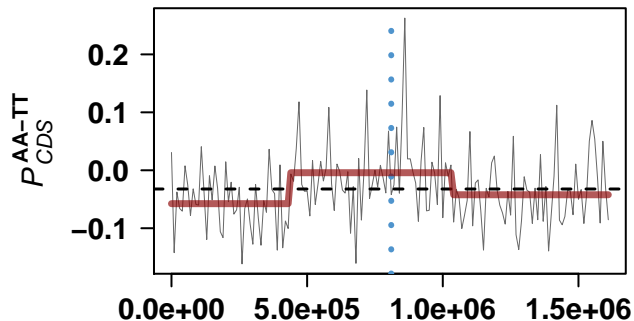
genome coordinates



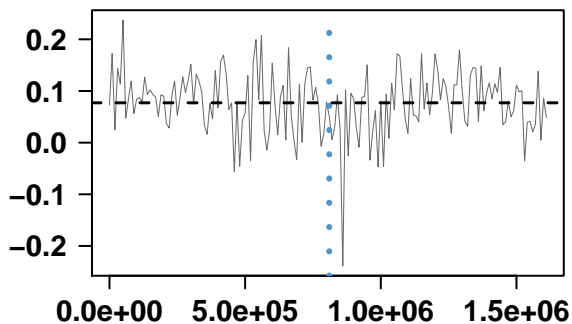
genome coordinates



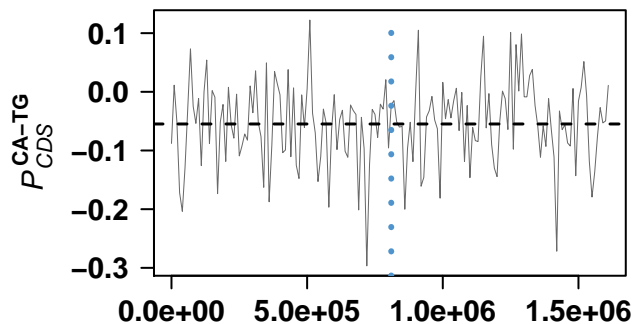
genome coordinates



genome coordinates

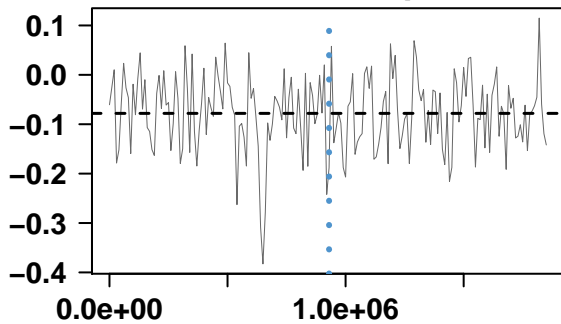


genome coordinates

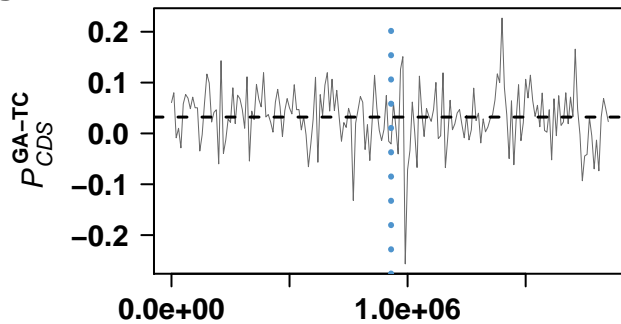


genome coordinates

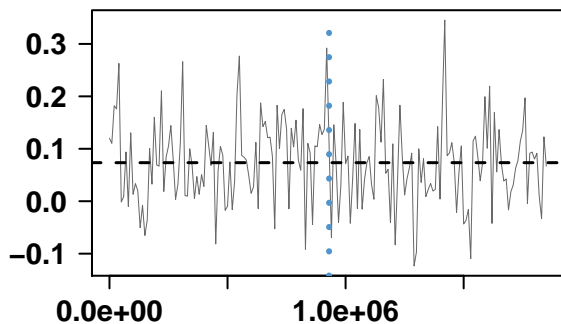
Streptococcus agalactiae 2603V/R



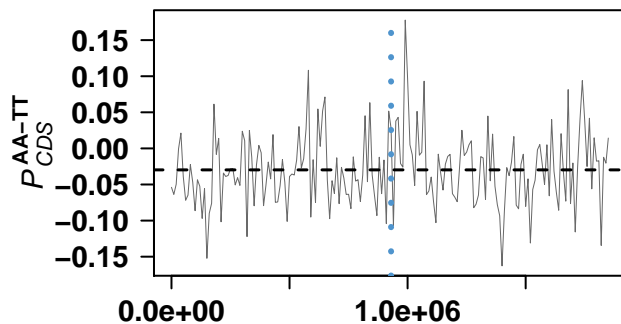
genome coordinates



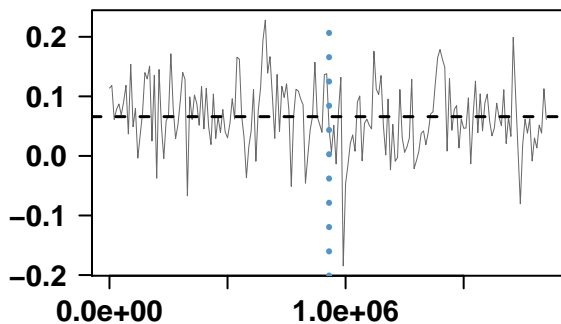
genome coordinates



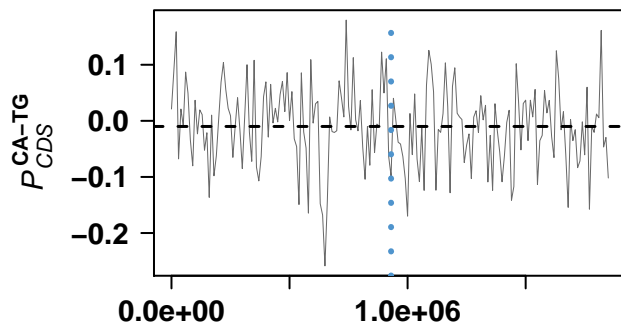
genome coordinates



genome coordinates

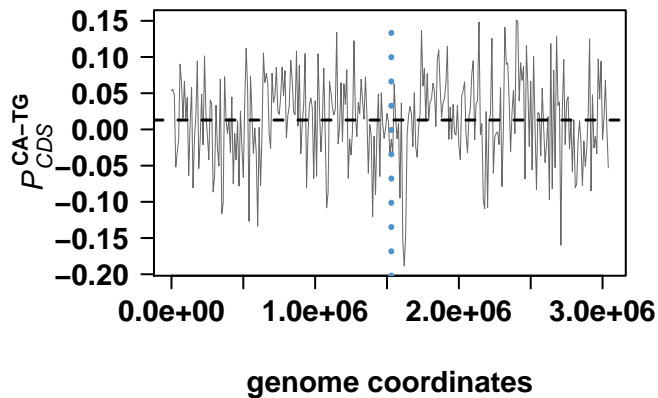
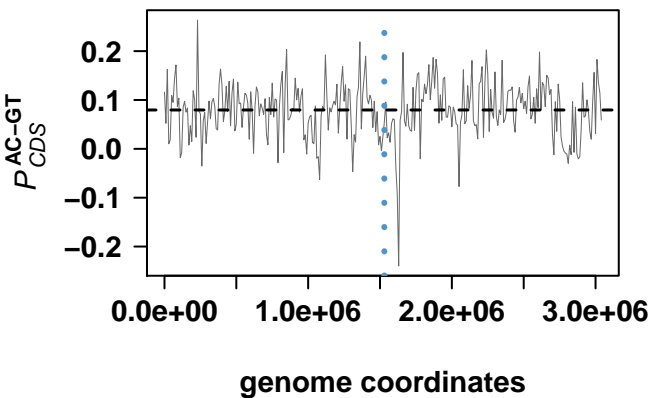
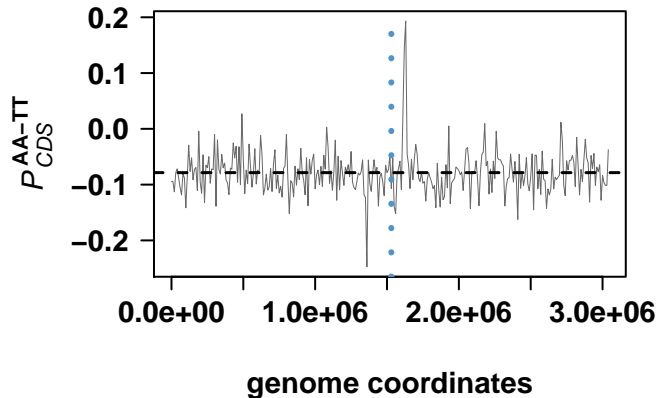
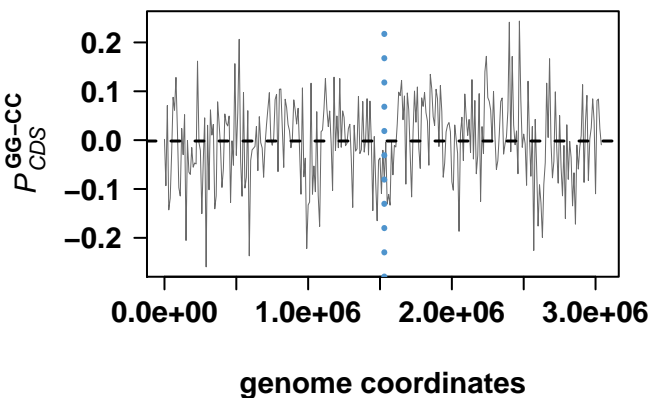
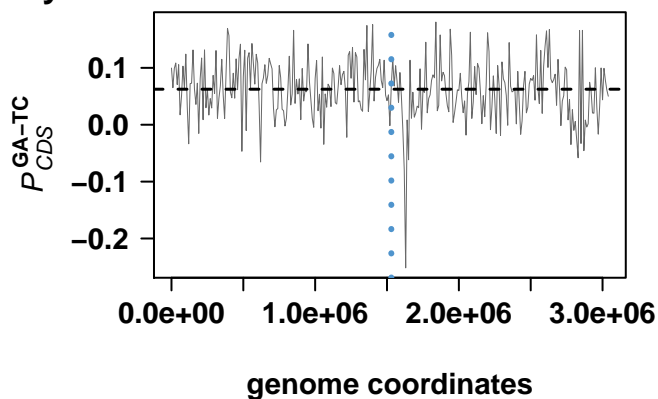
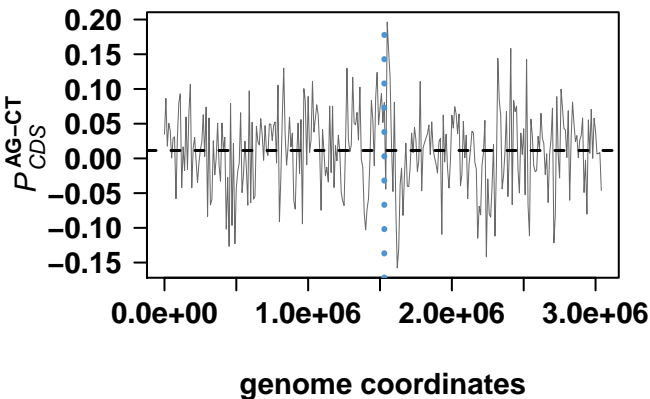


genome coordinates

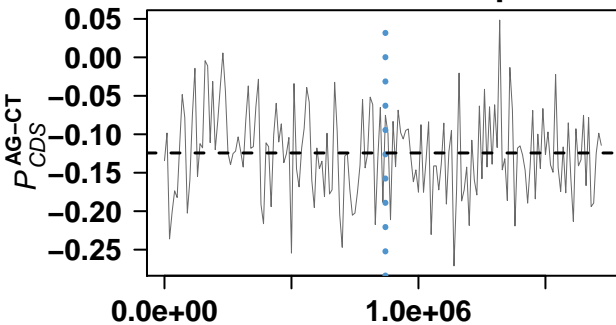


genome coordinates

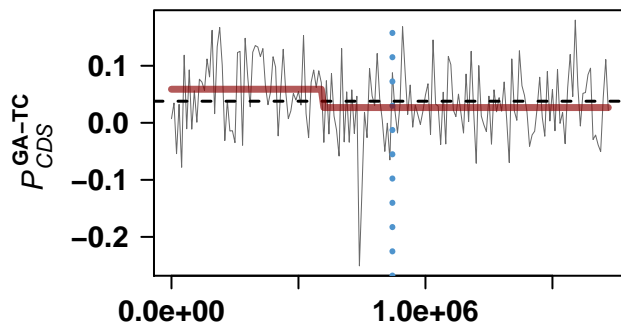
Oceanobacillus hieyensis HTE831



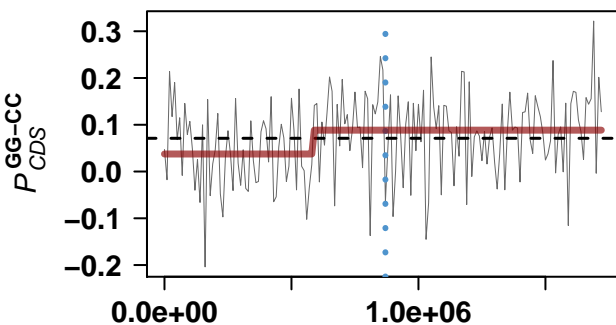
Streptococcus mutans UA159



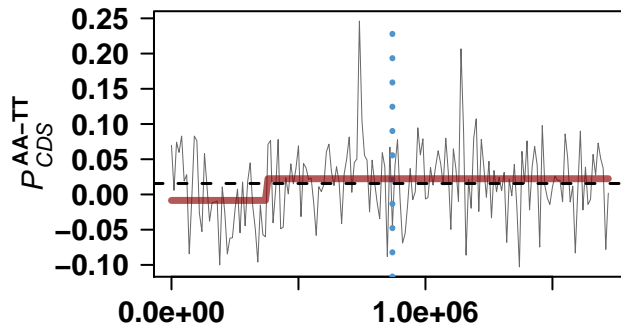
genome coordinates



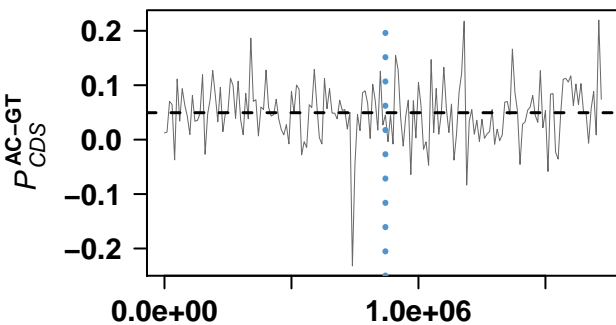
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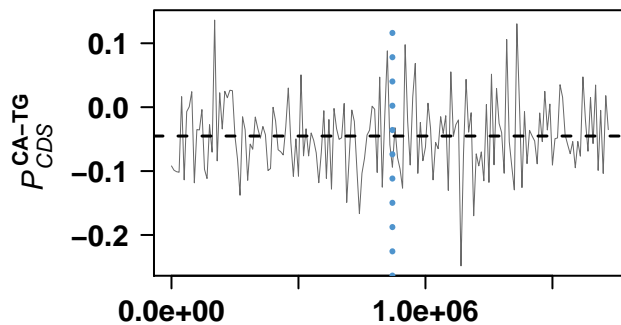
genome coordinates



genome coordinates

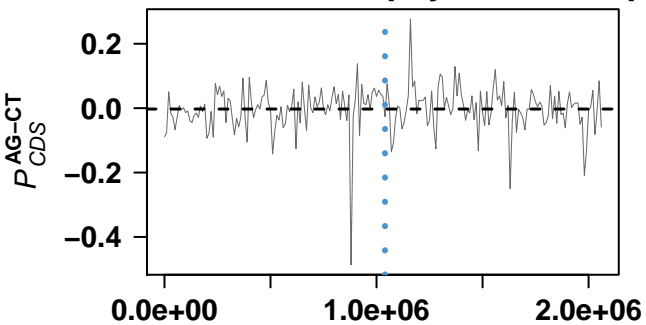


genome coordinates

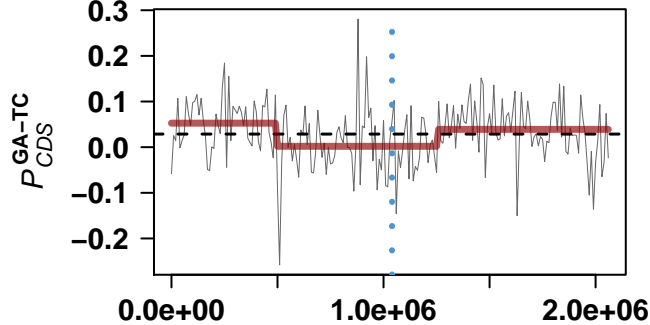


genome coordinates

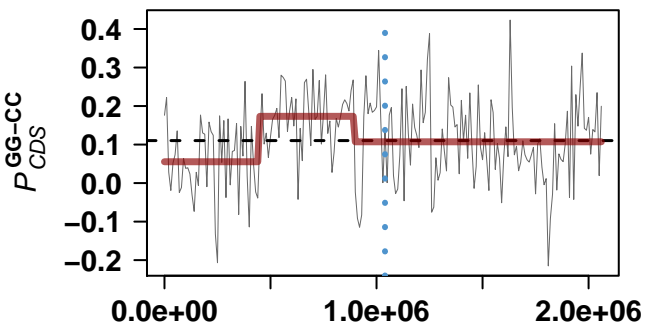
Staphylococcus epidermidis ATCC 12228



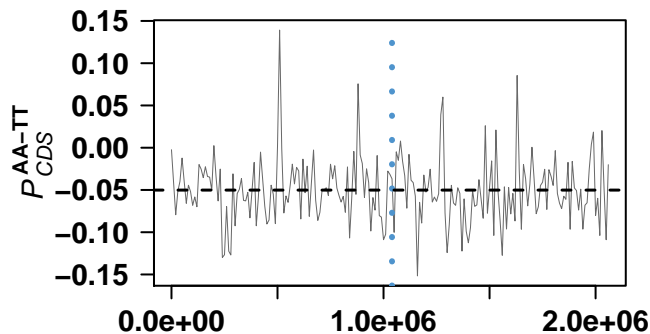
genome coordinates



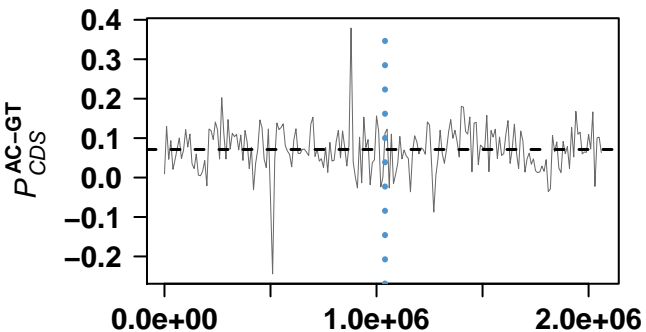
genome coordinates



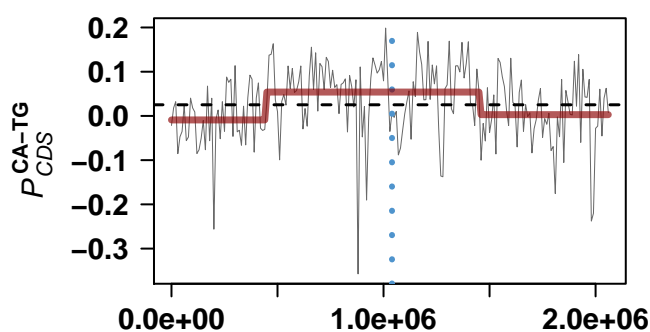
genome coordinates



genome coordinates

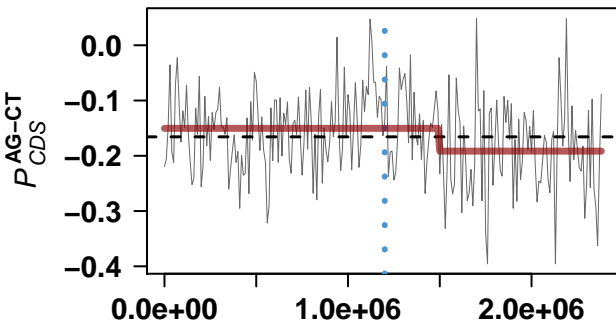


genome coordinates

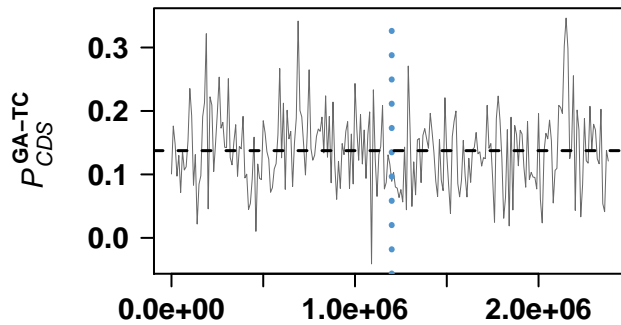


genome coordinates

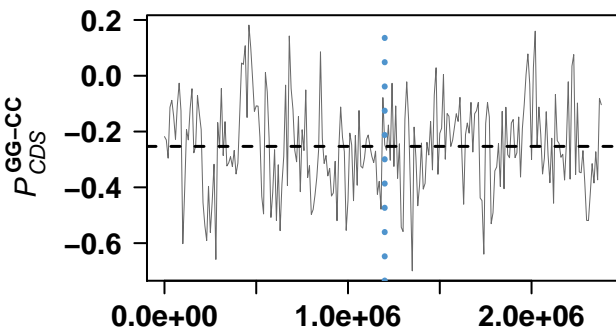
Clostridium tetani E88



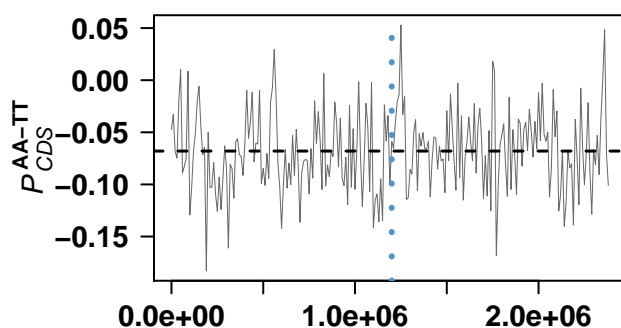
genome coordinates



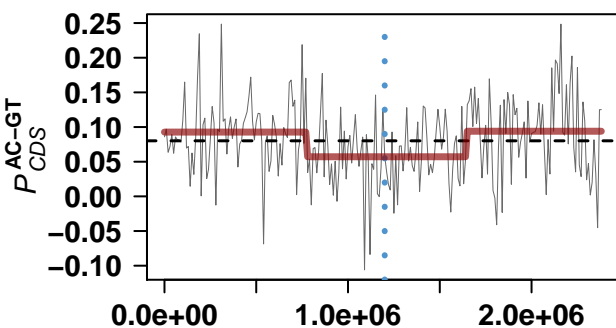
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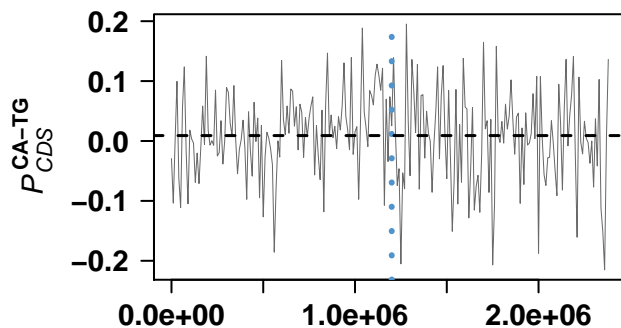
genome coordinates



genome coordinates

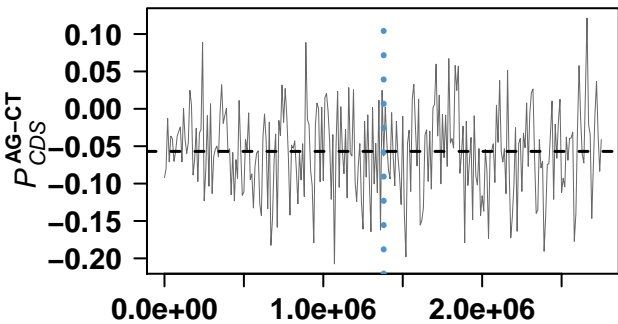


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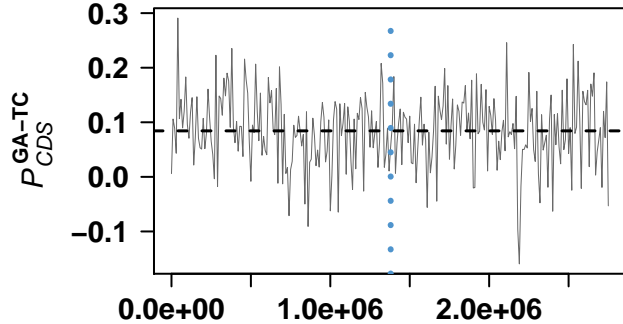


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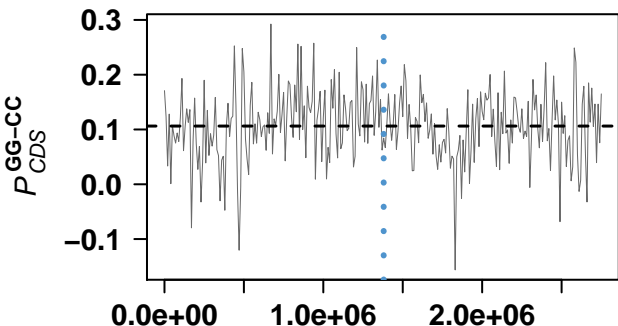
Lactobacillus plantarum WCFS1



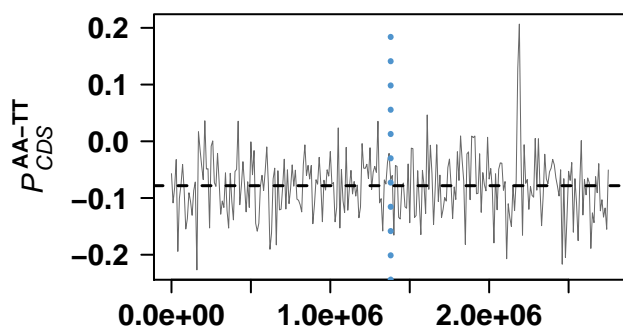
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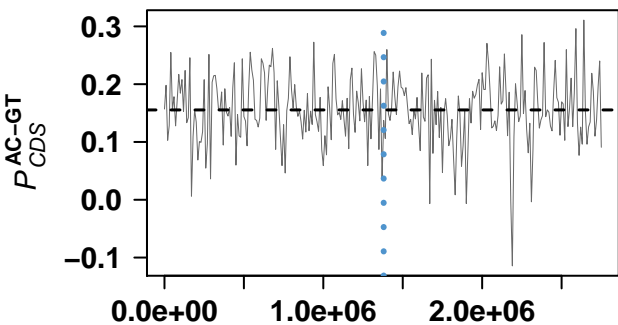
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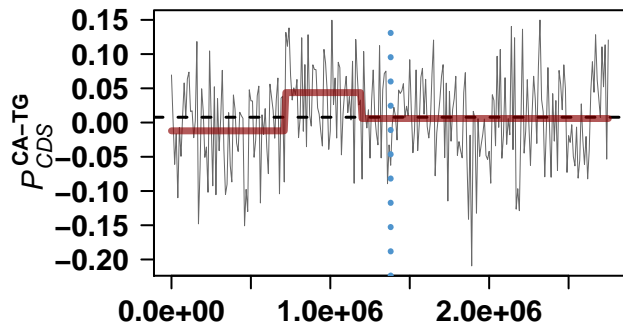
genome coordinates



genome coordinates

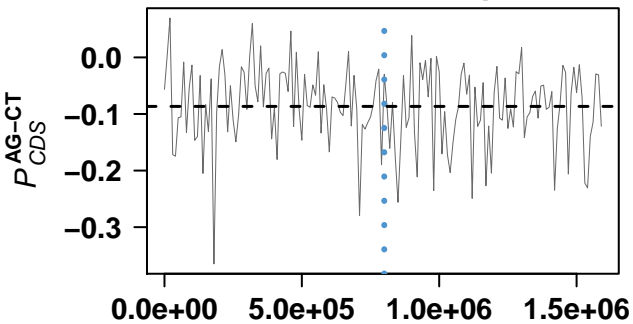


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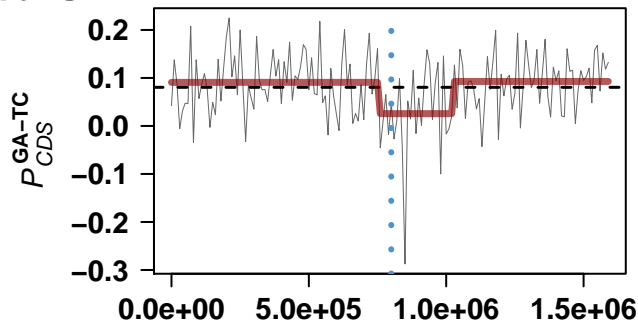


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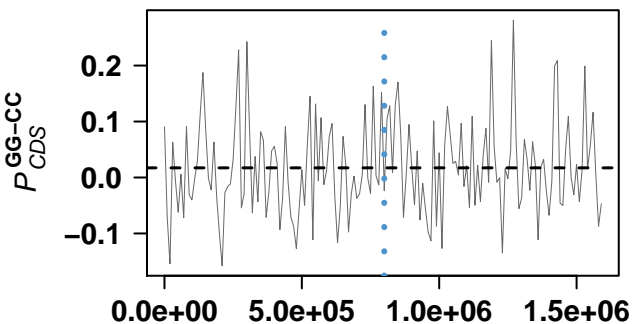
Streptococcus pyogenes SSI-1



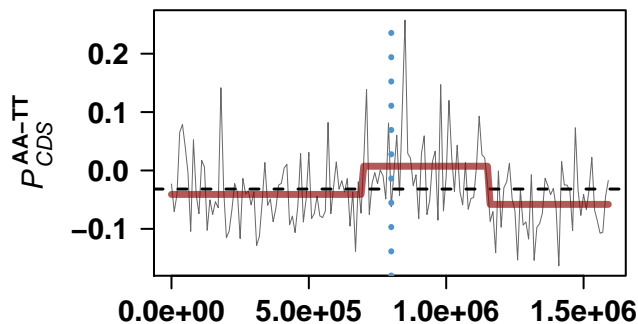
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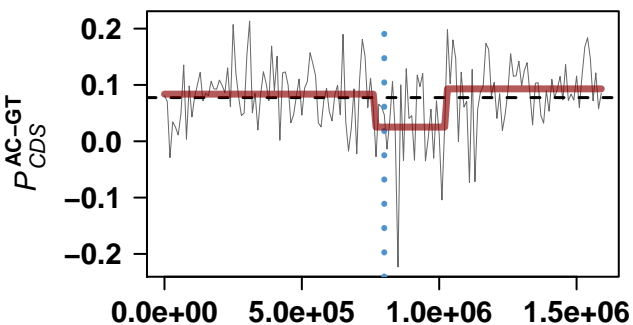
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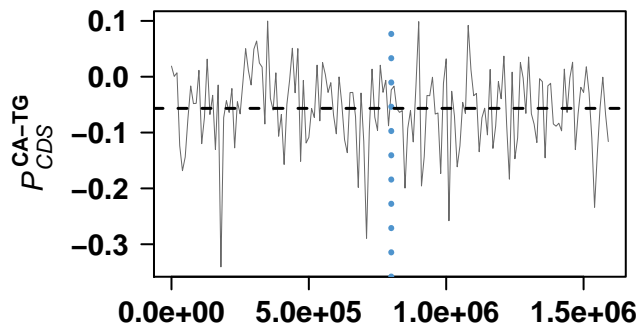
genome coordinates



genome coordinates

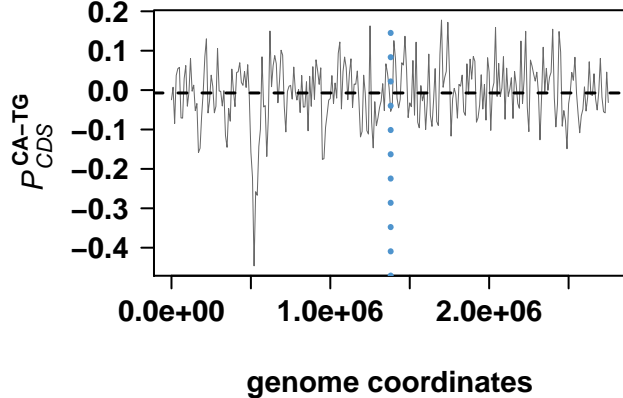
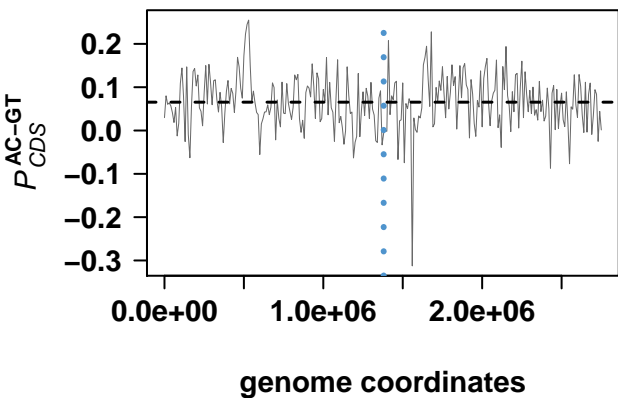
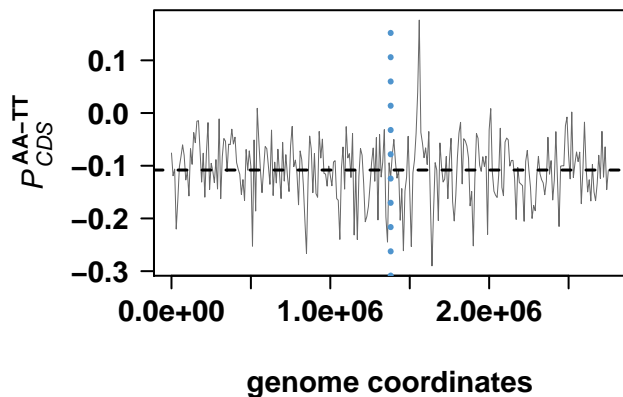
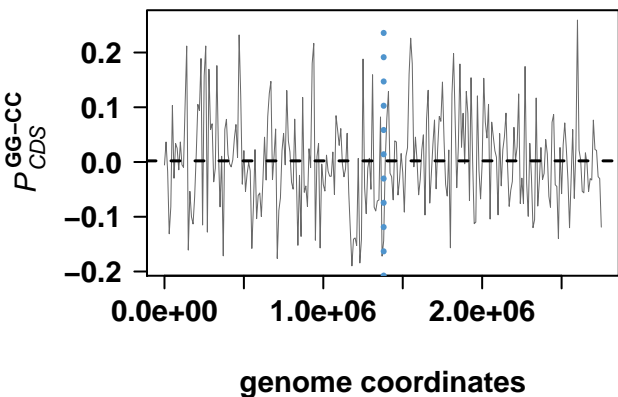
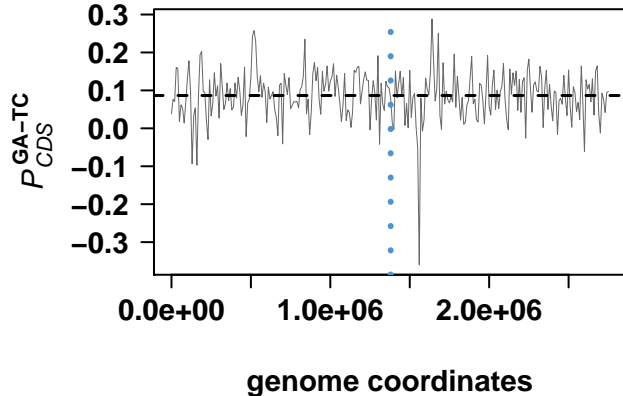
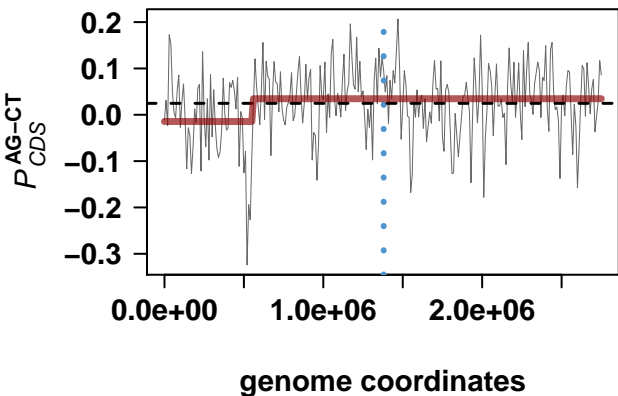


genome coordinates

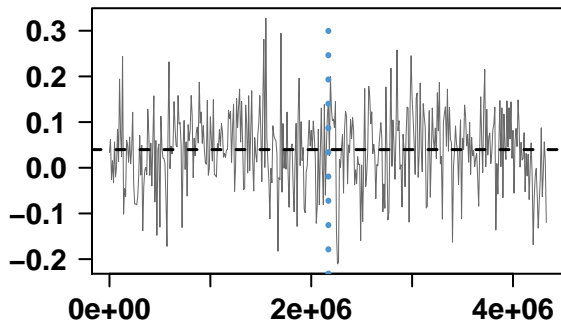


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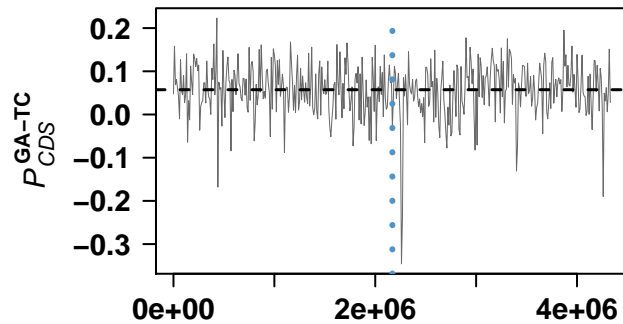
Enterococcus faecalis V583



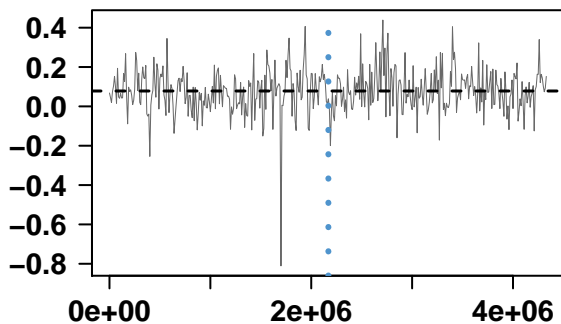
Bacillus cereus ATCC 14579



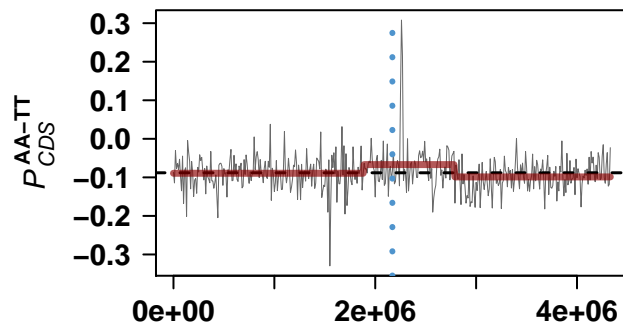
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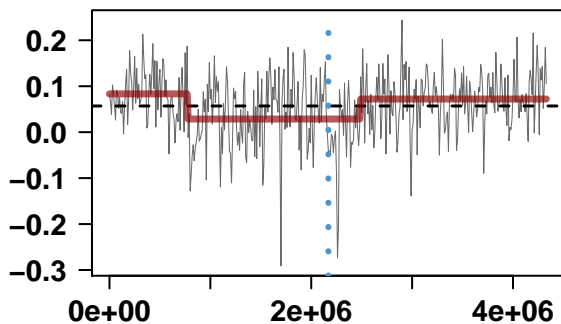
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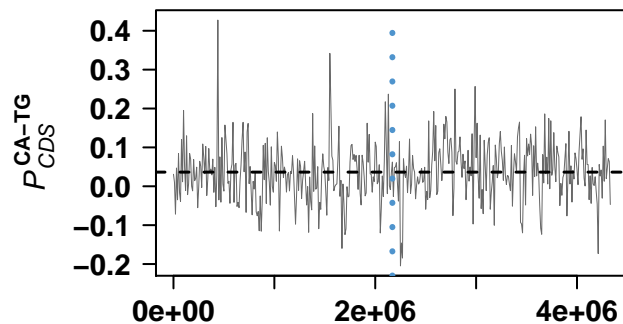
genome coordinates



genome coordinates

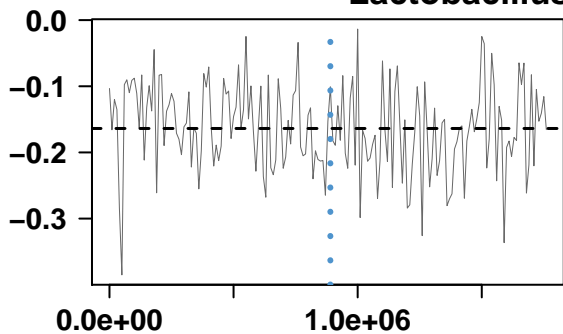


genome coordinates

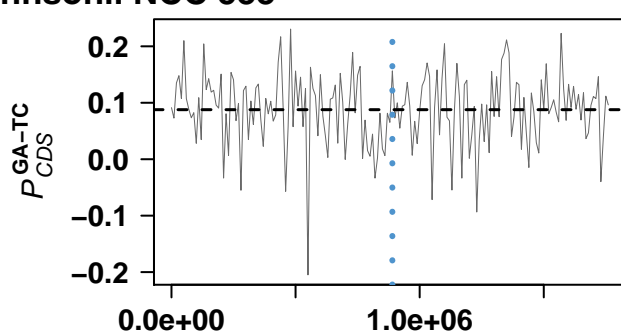


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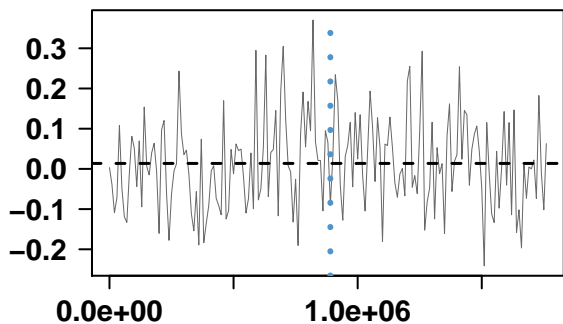
Lactobacillus johnsonii NCC 533



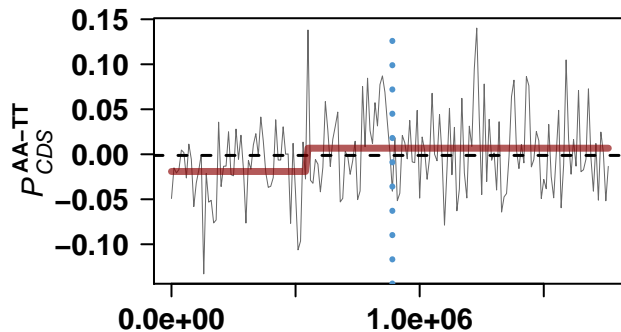
genome coordinates



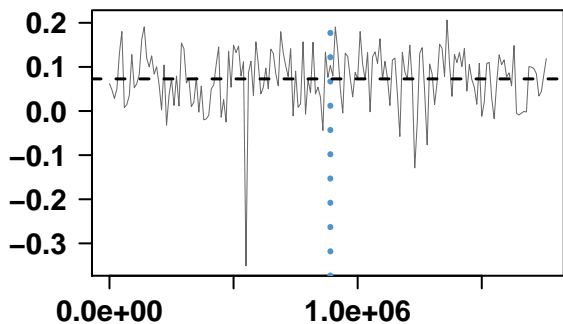
genome coordinates



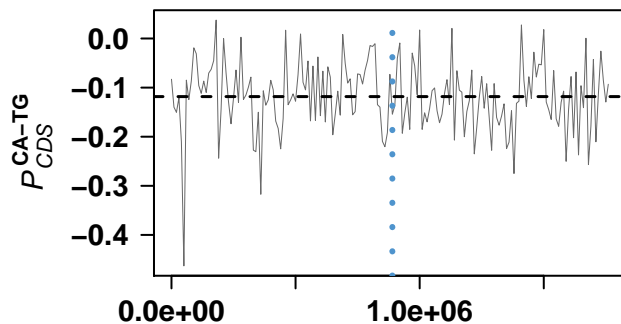
genome coordinates



genome coordinates

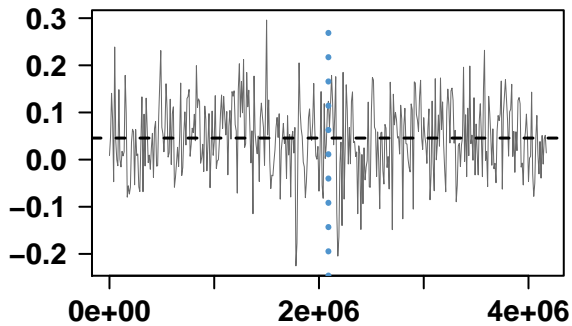


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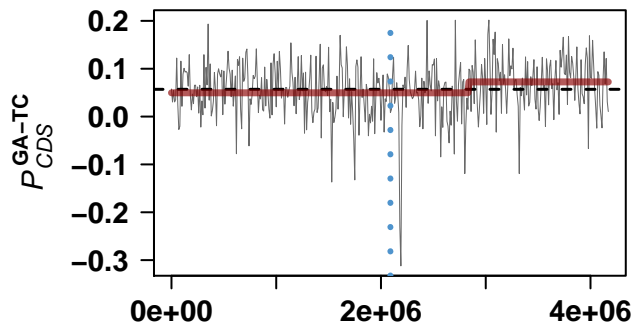


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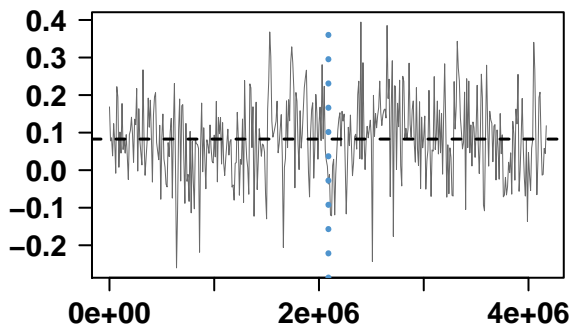
Bacillus anthracis str. Sterne



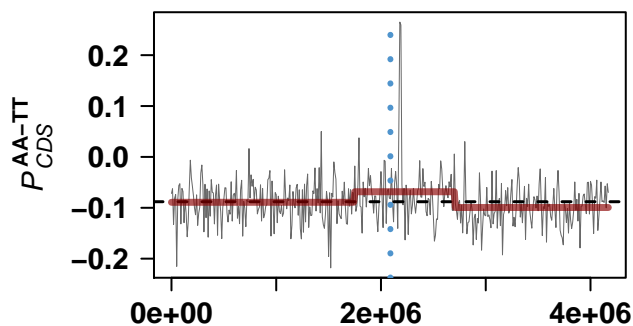
genome coordinates



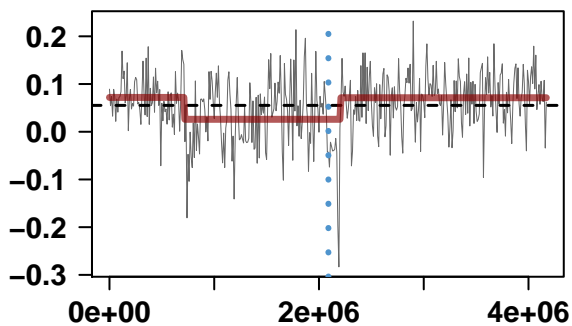
genome coordinates



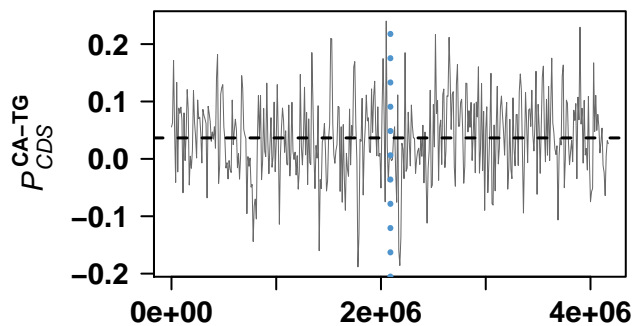
genome coordinates



genome coordinates

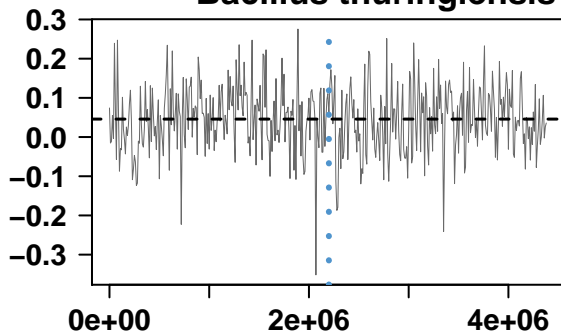


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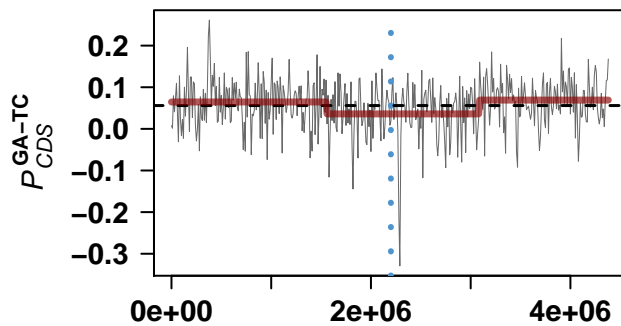


genome coordinates

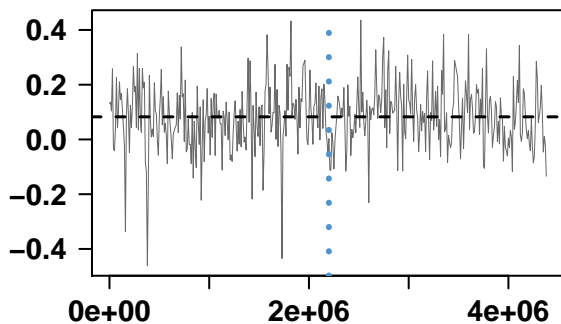
Bacillus thuringiensis serovar konkukian str. 97-27



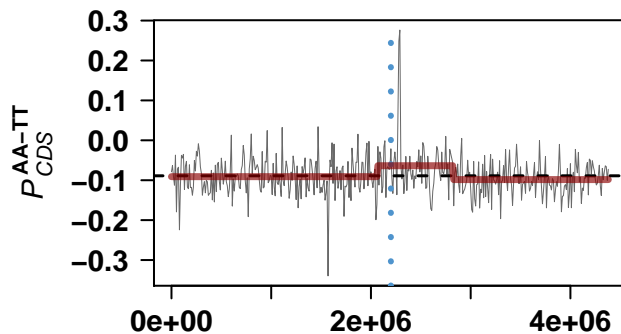
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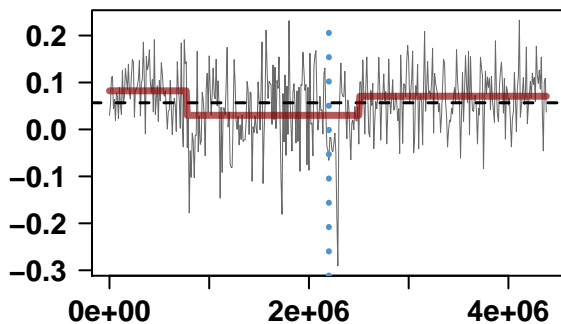
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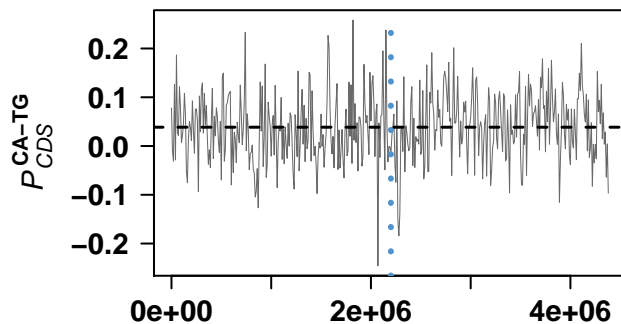
genome coordinates



genome coordinates

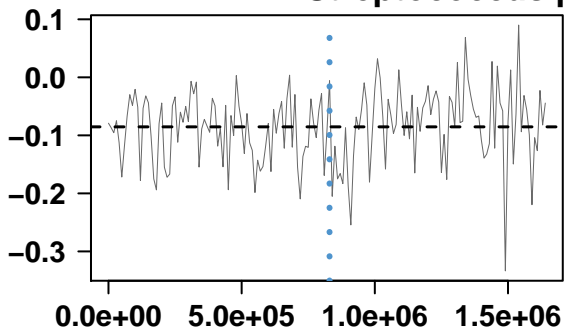


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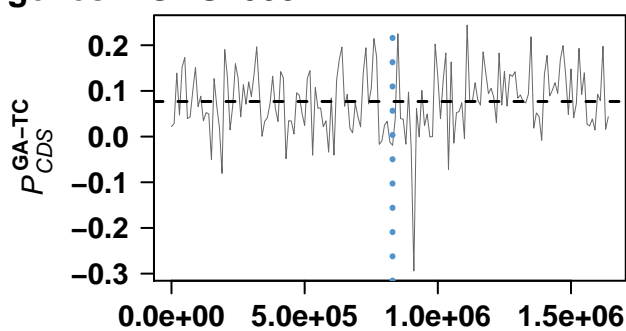


genome coordinates

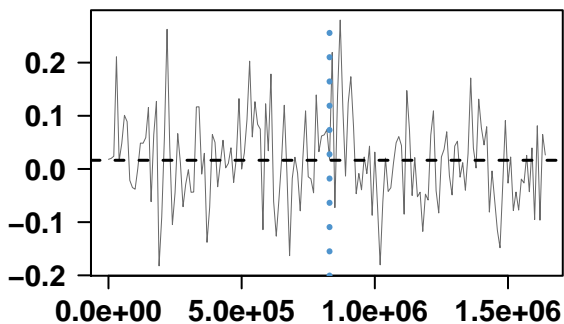
Streptococcus pyogenes MGAS10394



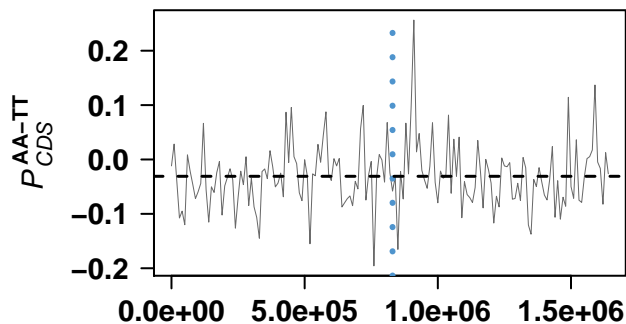
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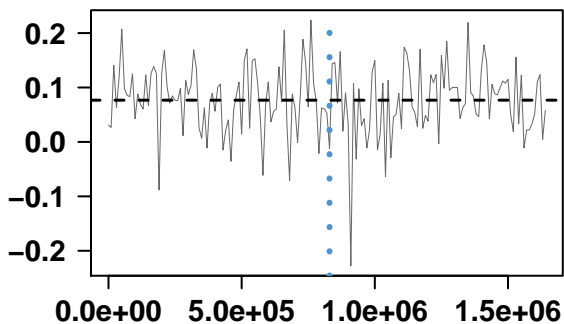
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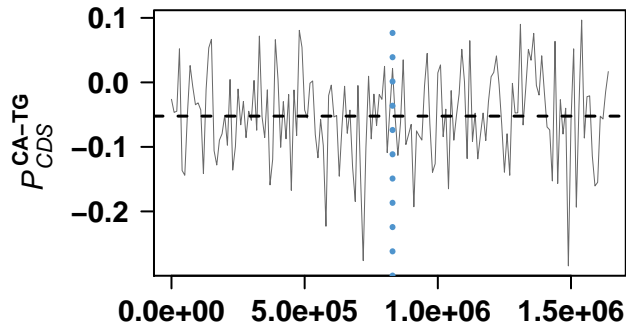
genome coordinates



genome coordinates

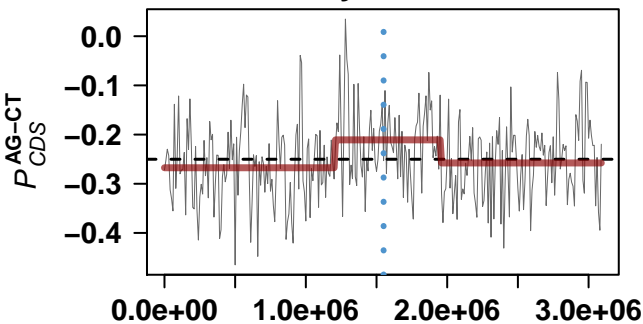


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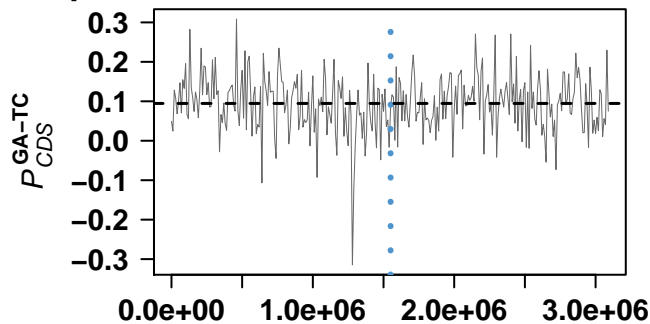


genome coordinates

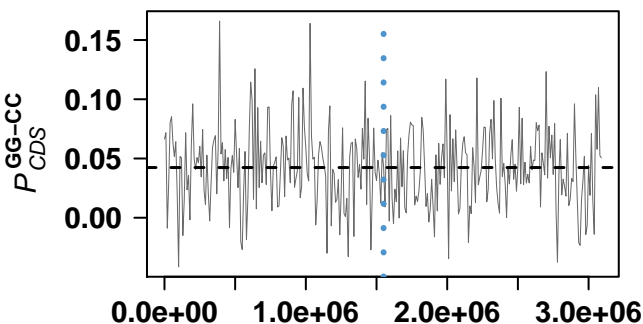
Symbiobacterium thermophilum IAM 14863



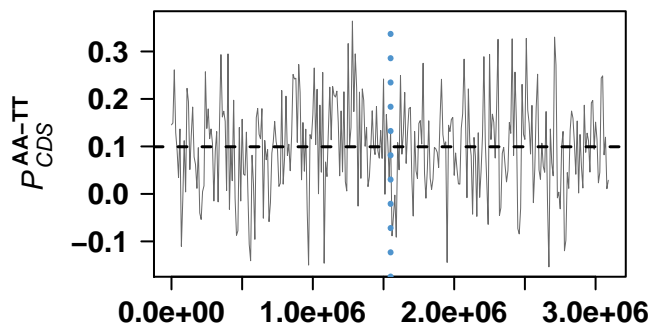
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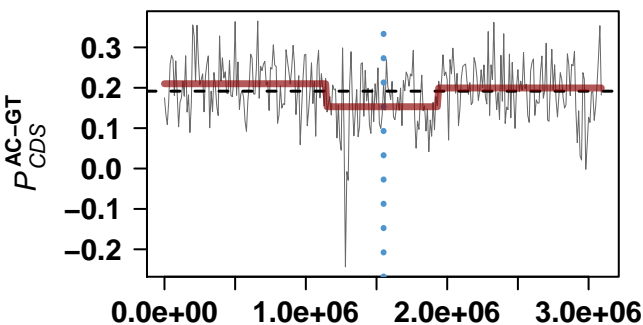
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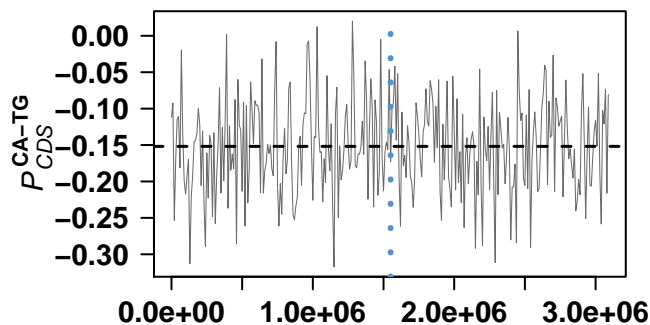
genome coordinates



genome coordinates

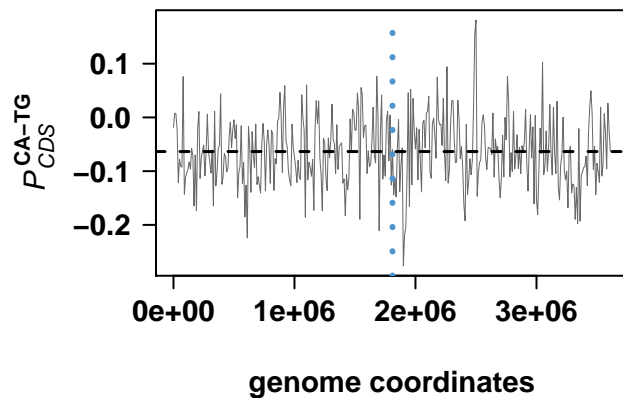
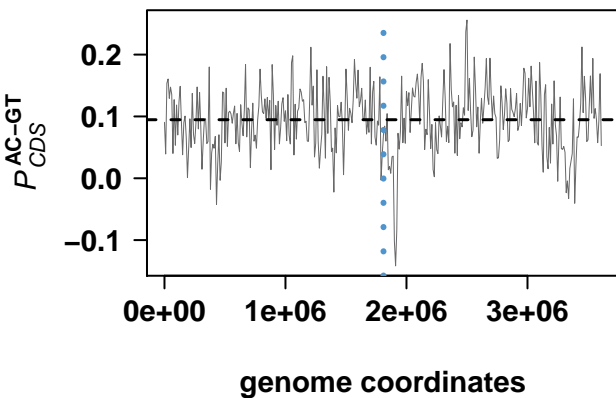
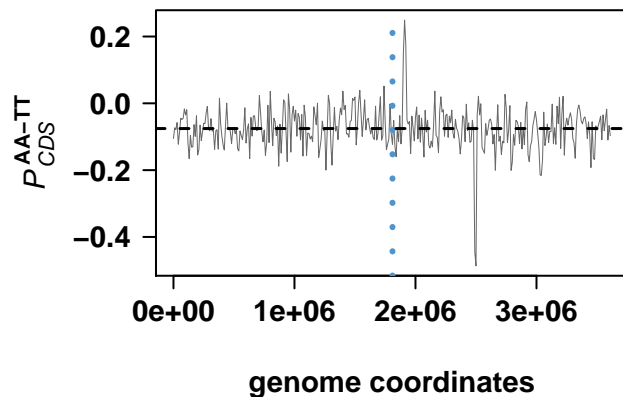
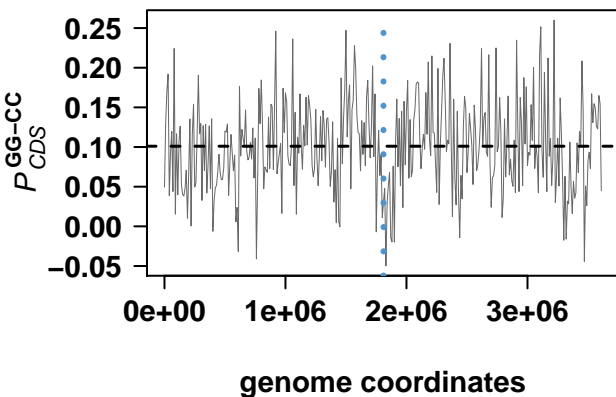
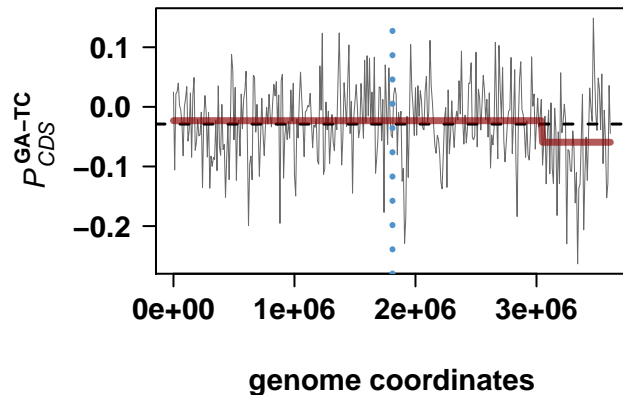
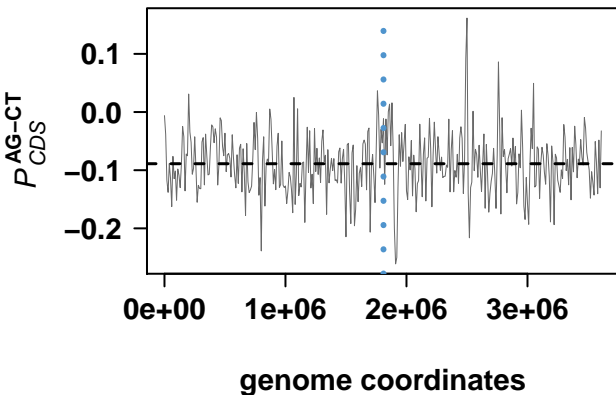


genome coordinates

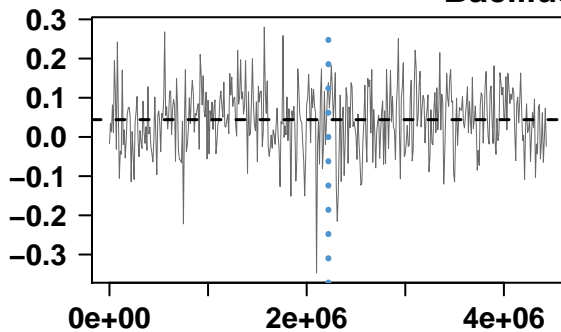


genome coordinates

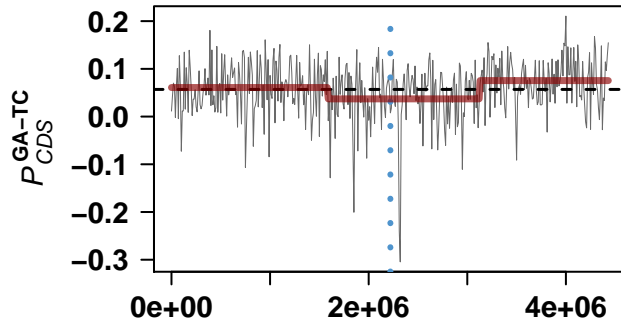
Bacillus licheniformis DSM 13 = ATCC 14580



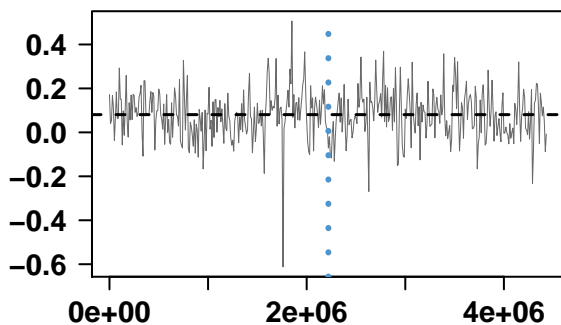
Bacillus cereus E33L



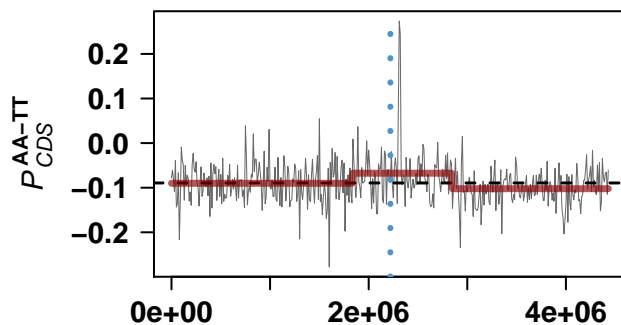
genome coordinates



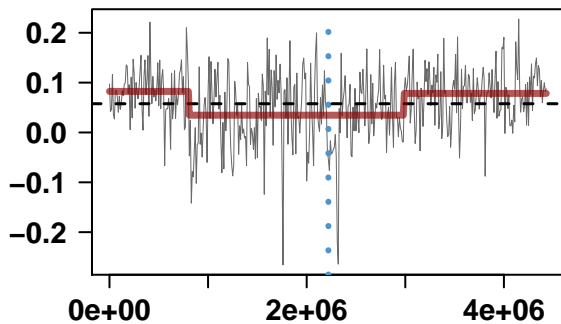
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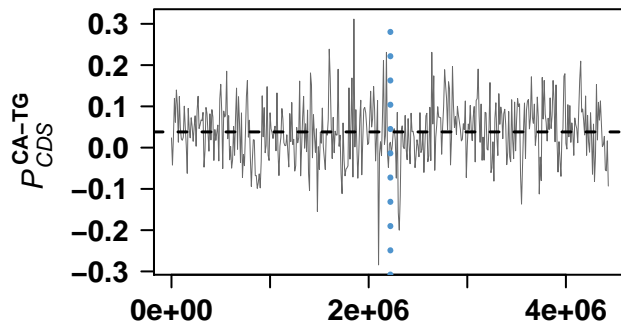
genome coordinates



genome coordinates

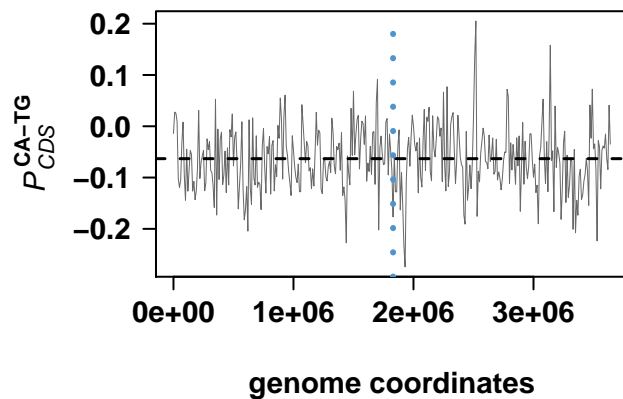
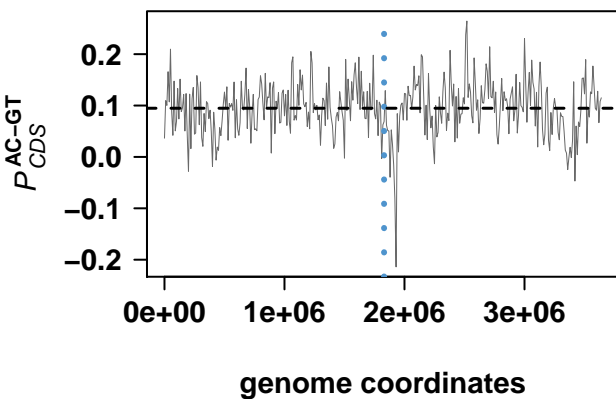
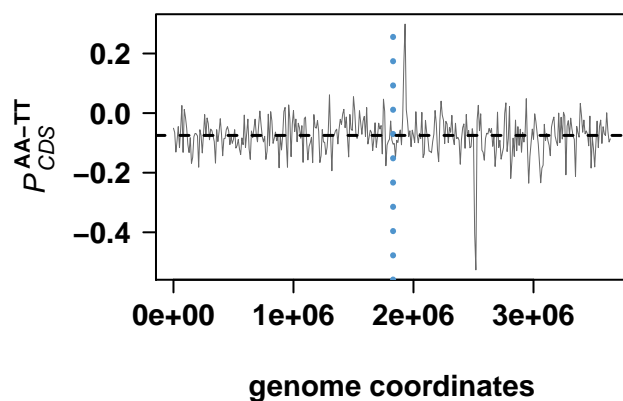
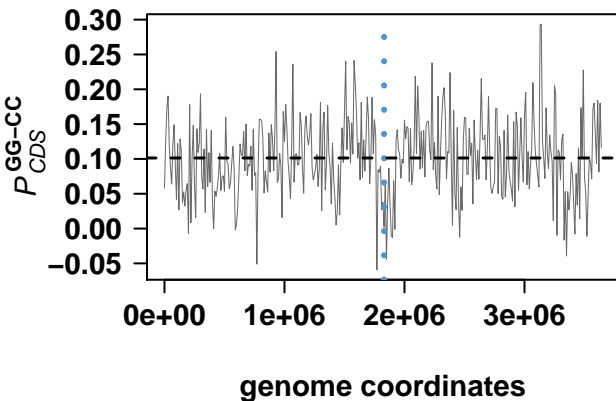
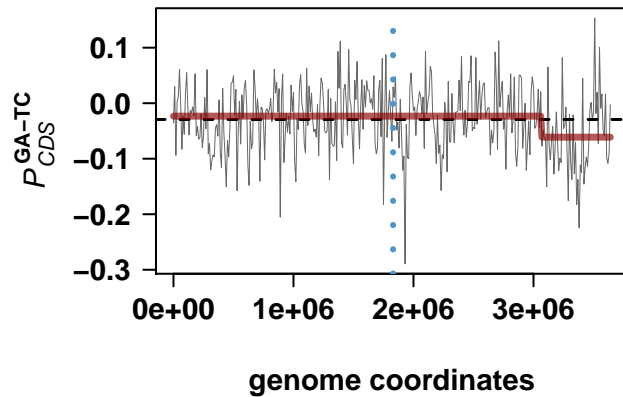
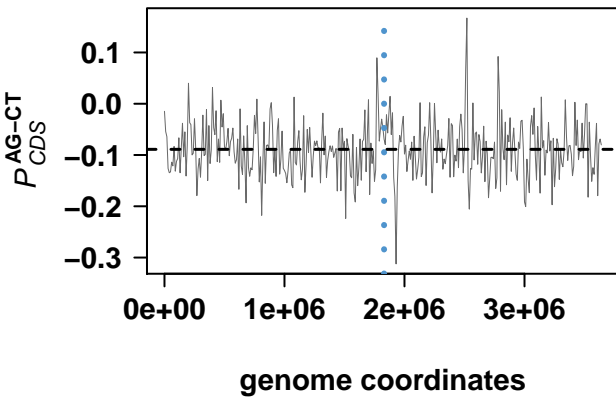


genome coordinates

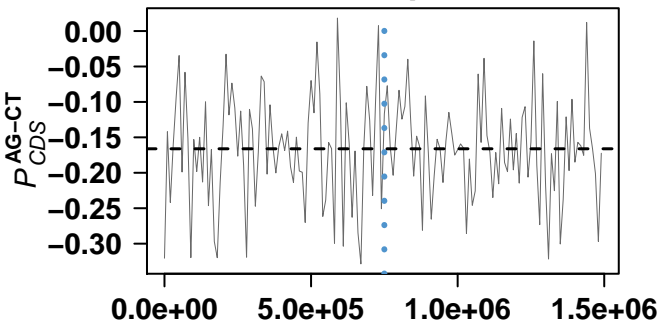


genome coordinates

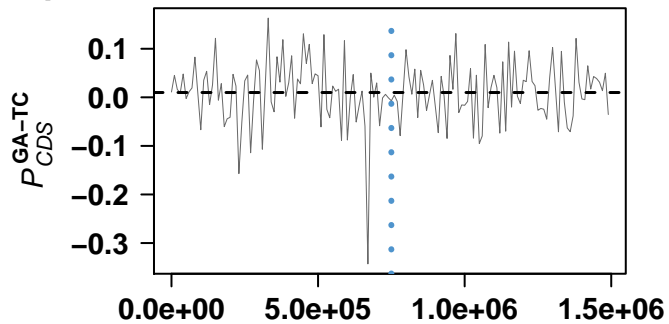
Bacillus licheniformis DSM 13 = ATCC 14580



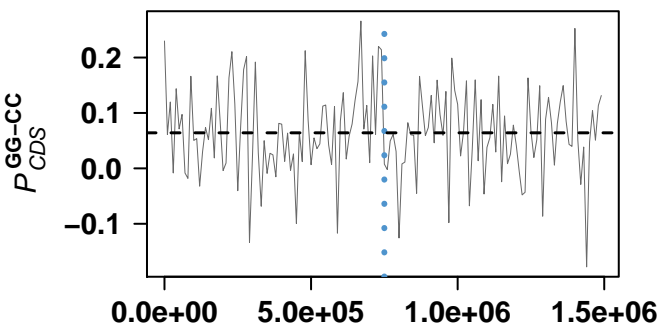
Streptococcus thermophilus LMG 18311



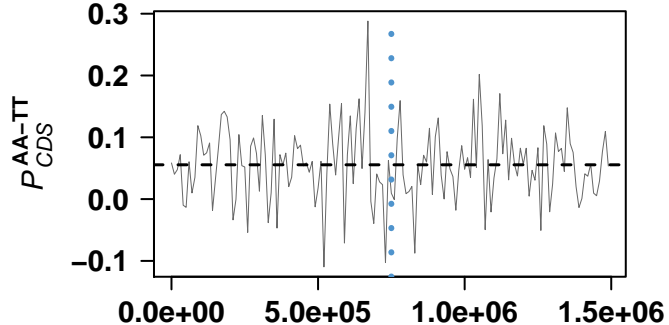
genome coordinates



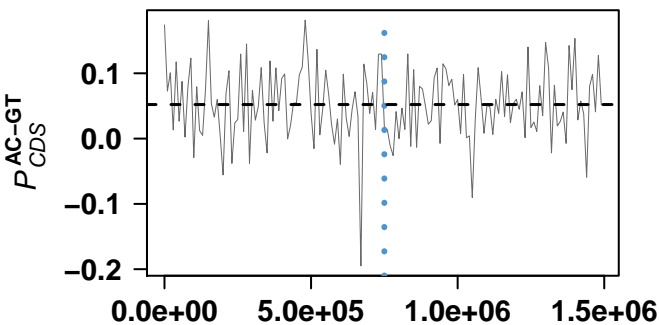
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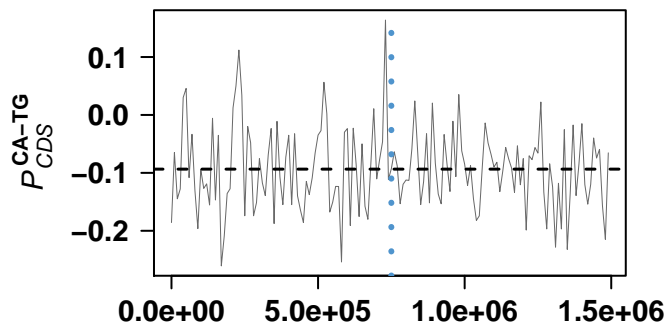
genome coordinates



genome coordinates

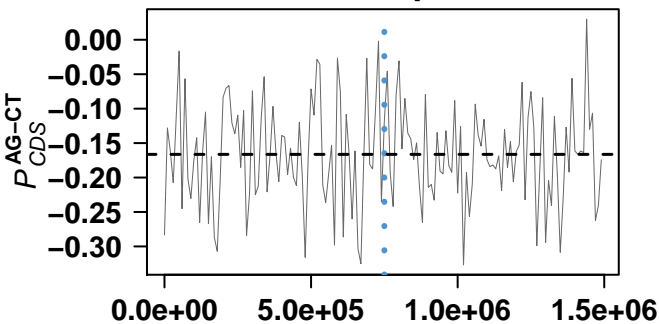


genome coordinates

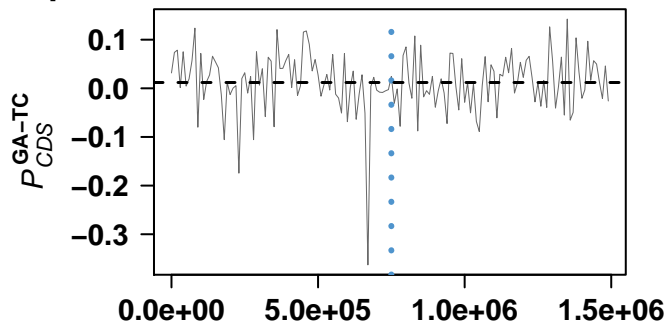


genome coordinates

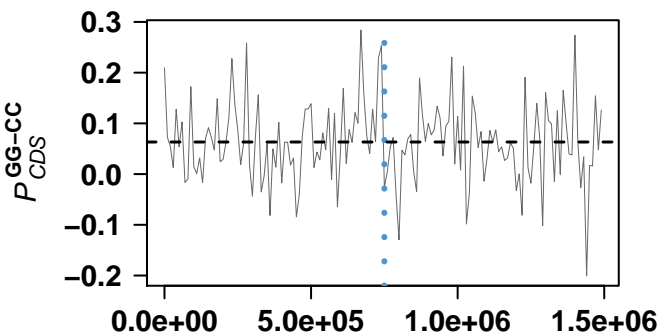
Streptococcus thermophilus CNRZ1066



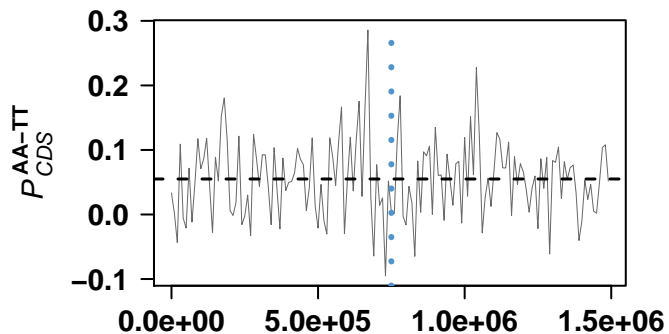
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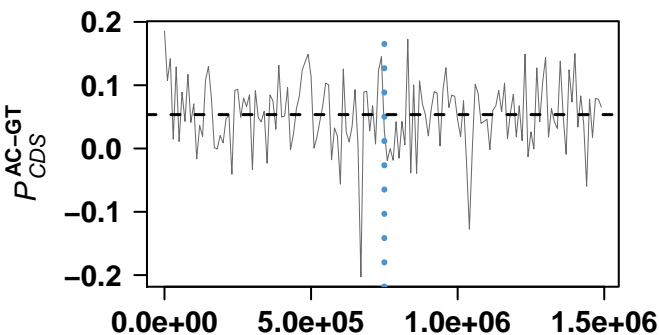
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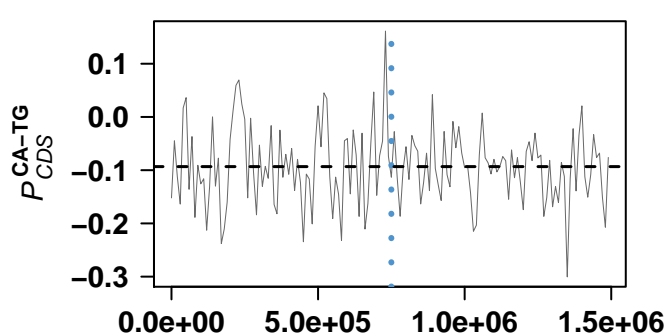
genome coordinates



genome coordinates

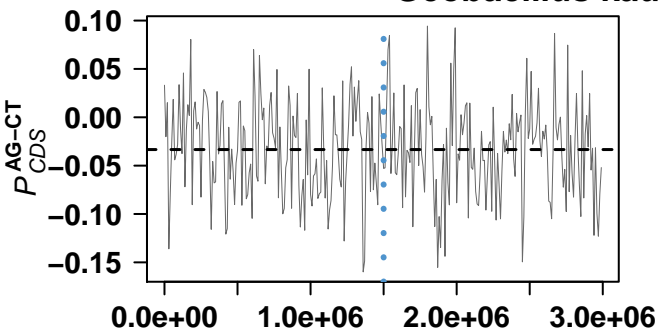


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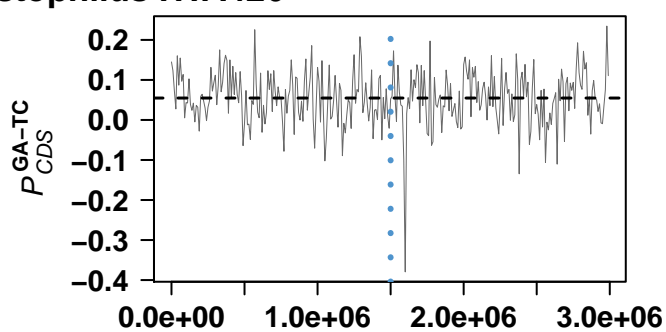


genome coordinates

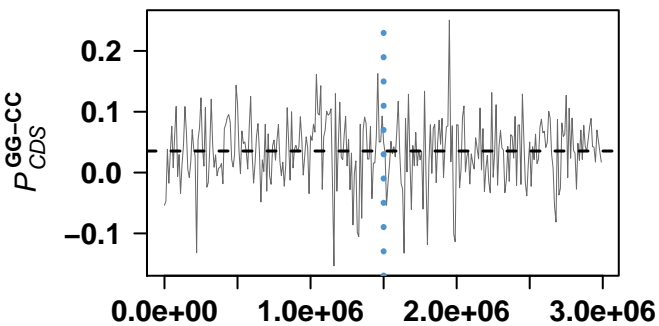
Geobacillus kaustophilus HTA426



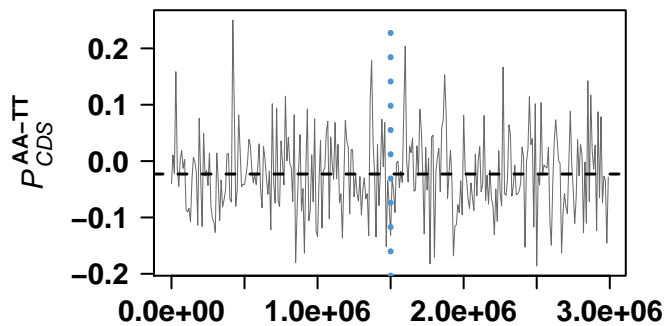
genome coordinates



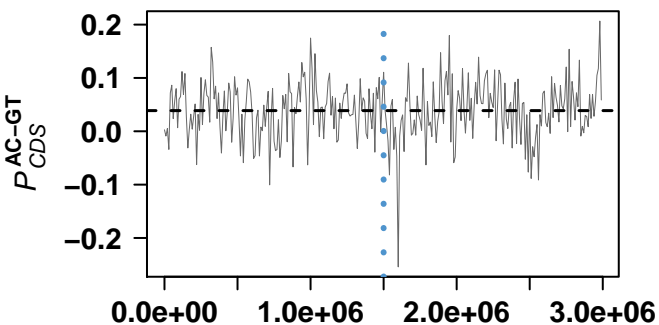
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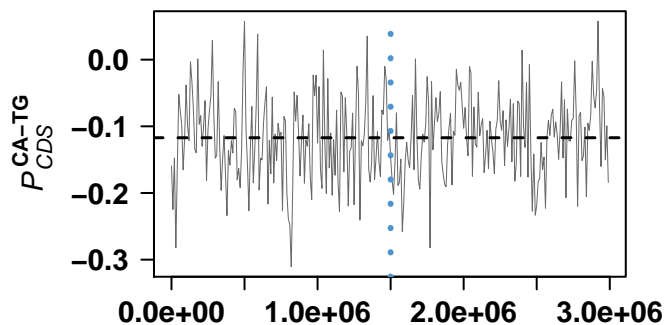
genome coordinates



genome coordinates

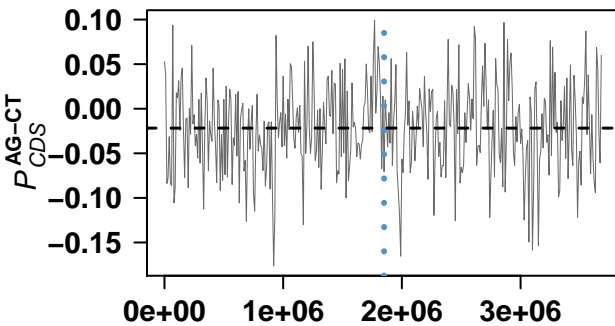


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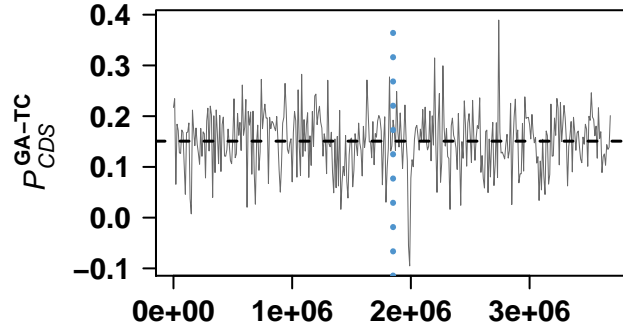


genome coordinates

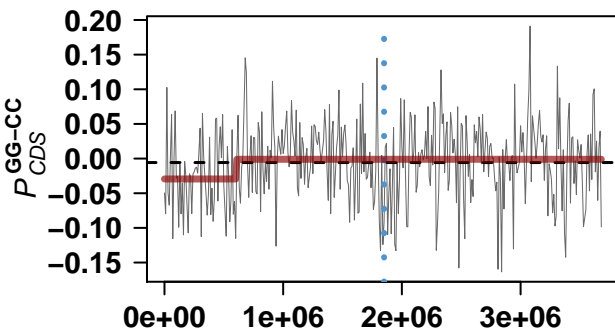
Bacillus clausii KSM-K16



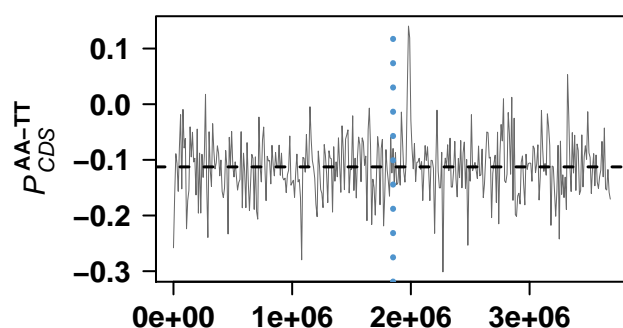
genome coordinates



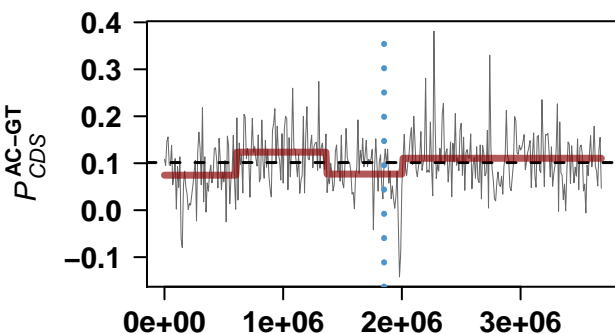
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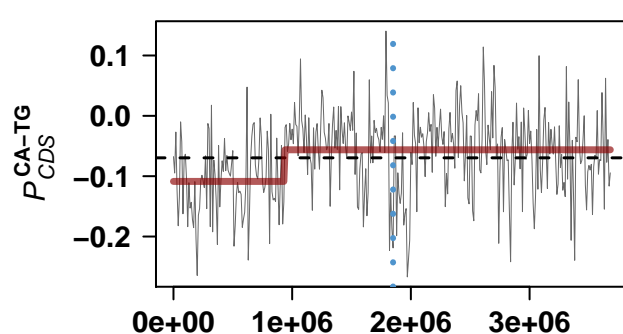
genome coordinates



genome coordinates

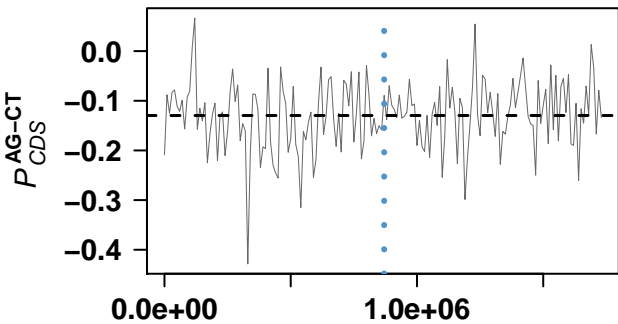


genome coordinates

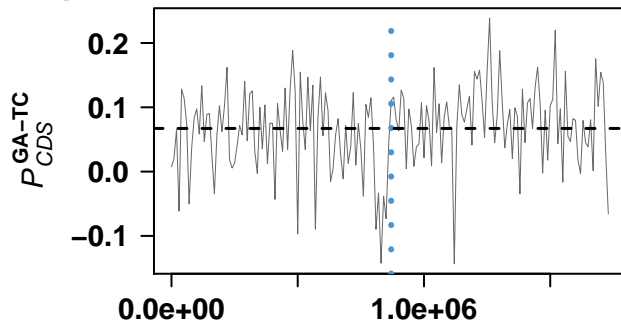


genome coordinates

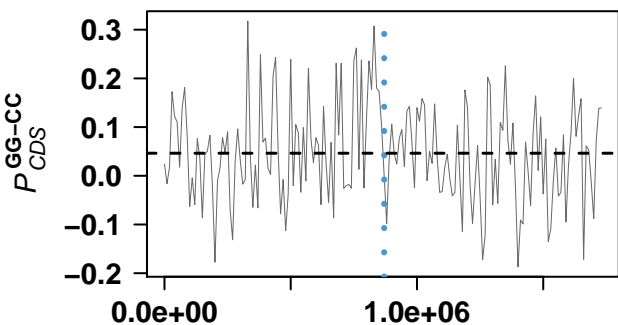
Lactobacillus acidophilus NCFM



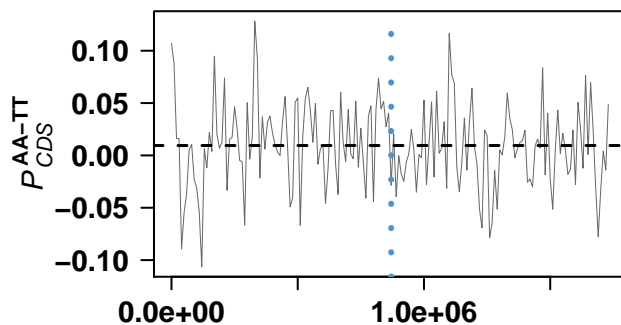
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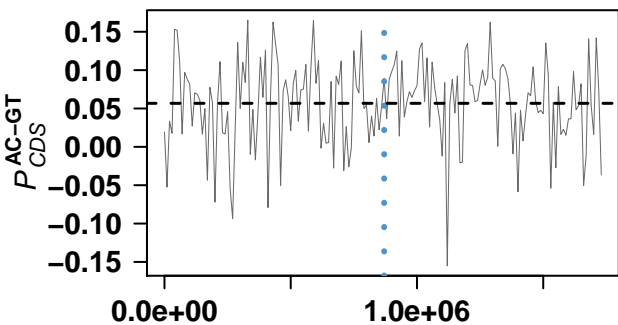
genome coordinates



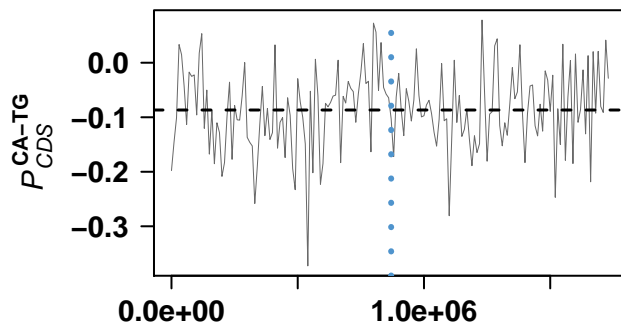
genome coordinates



genome coordinates

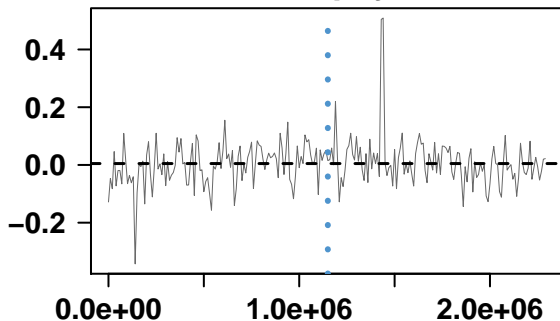


genome coordinates

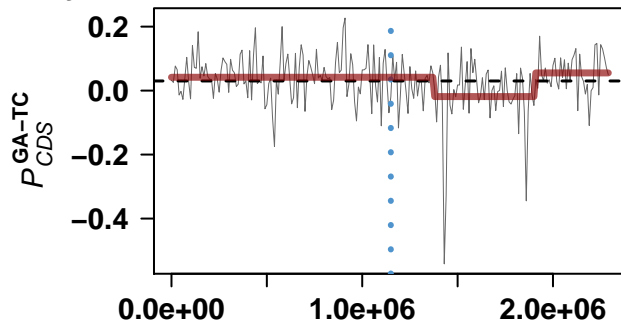


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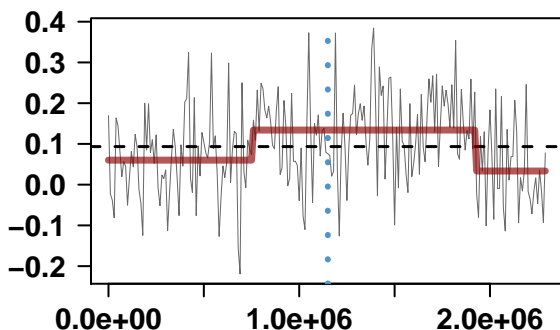
Staphylococcus haemolyticus JCSC1435



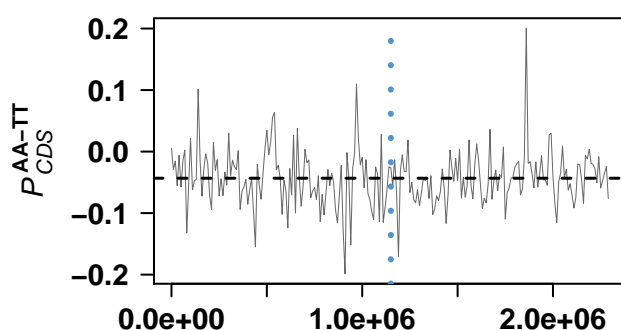
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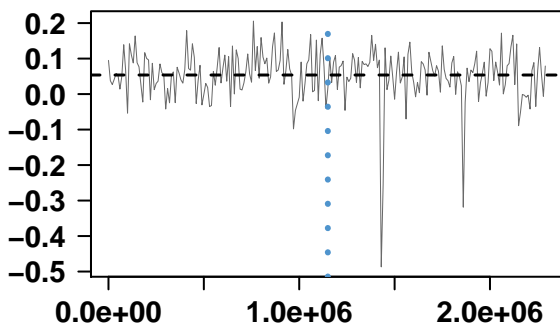
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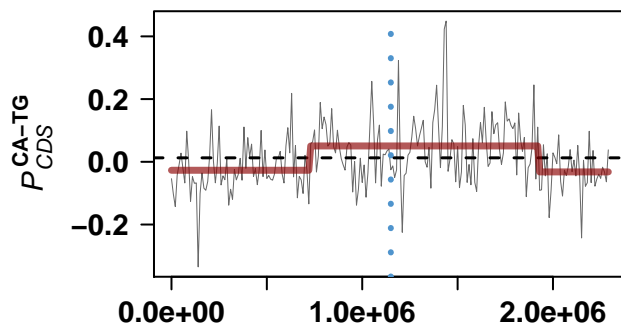
genome coordinates



genome coordinates

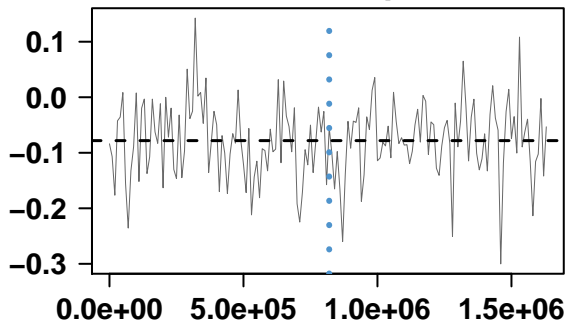


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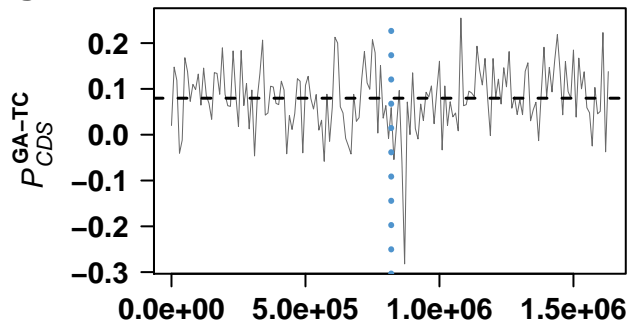


genome coordinates

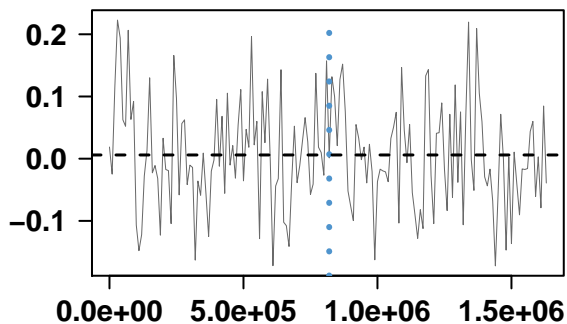
Streptococcus pyogenes MGAS6180



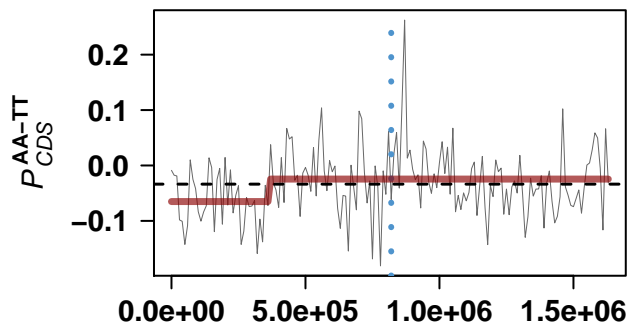
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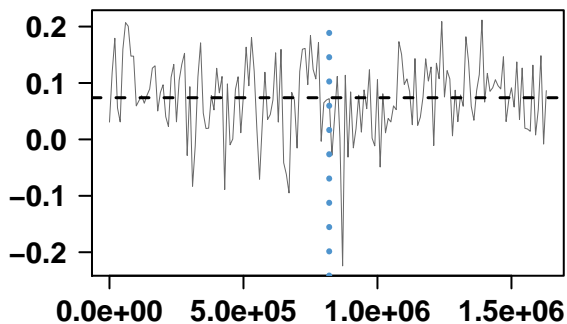
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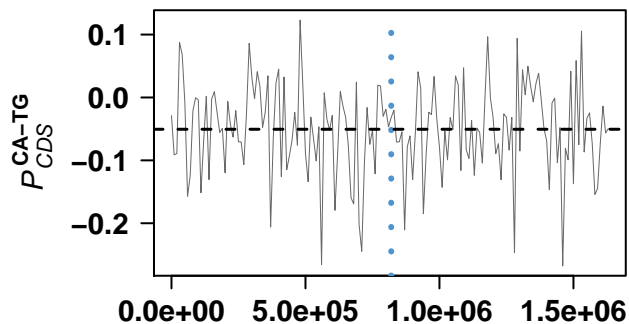
genome coordinates



genome coordinates

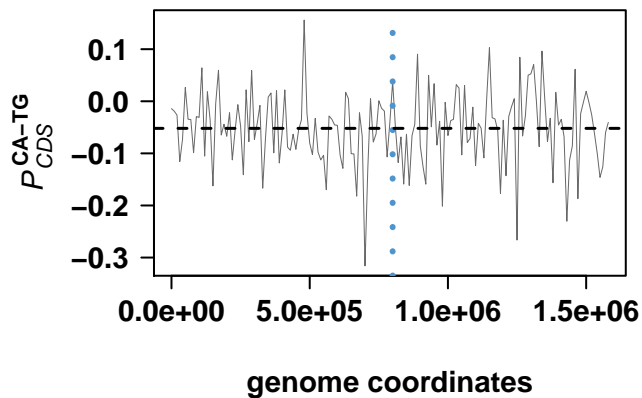
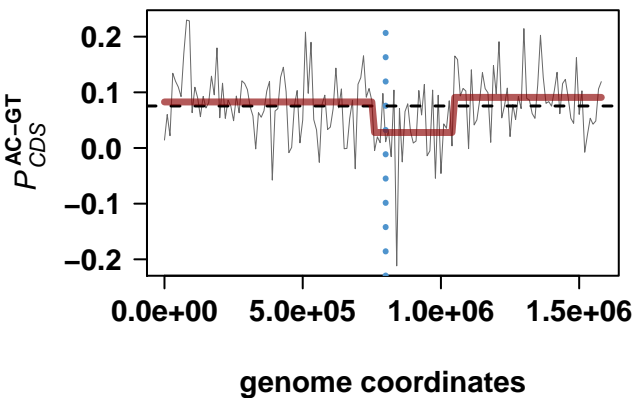
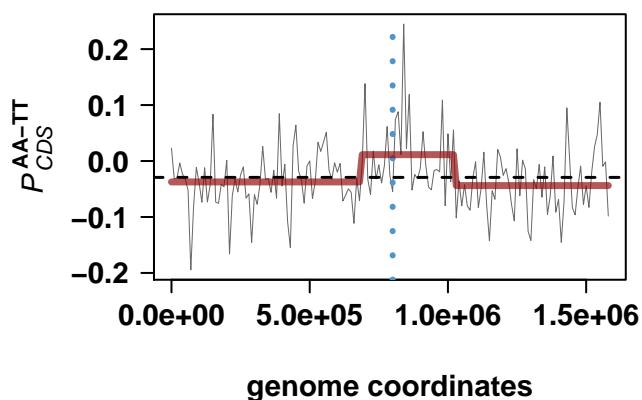
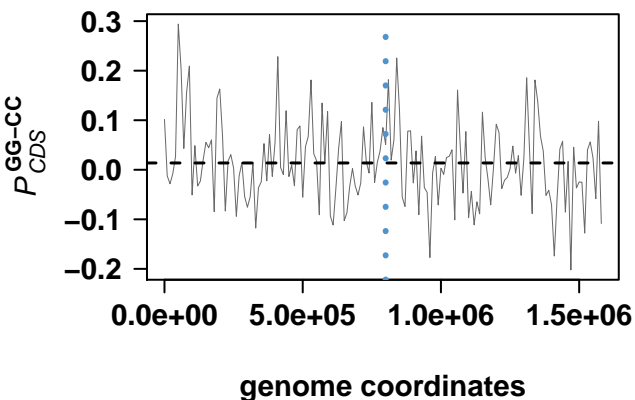
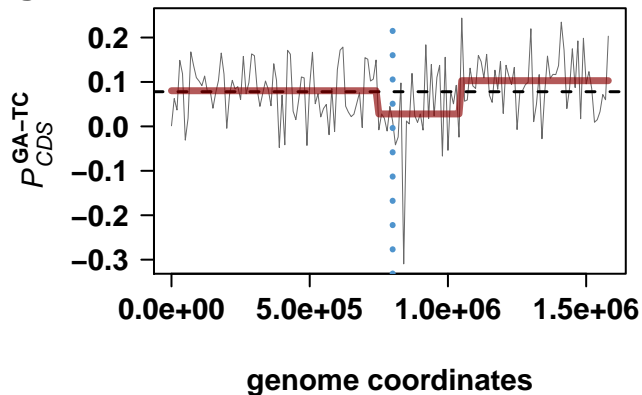
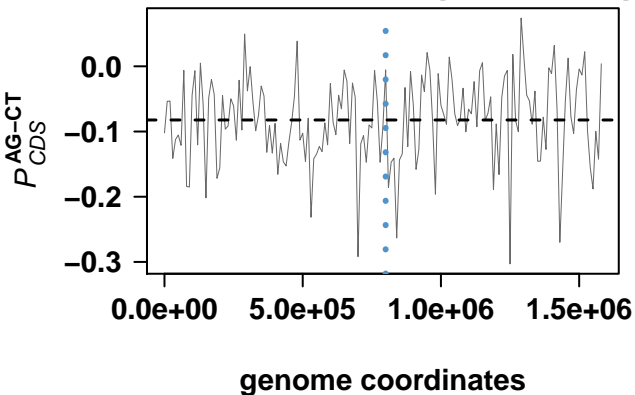


genome coordinates

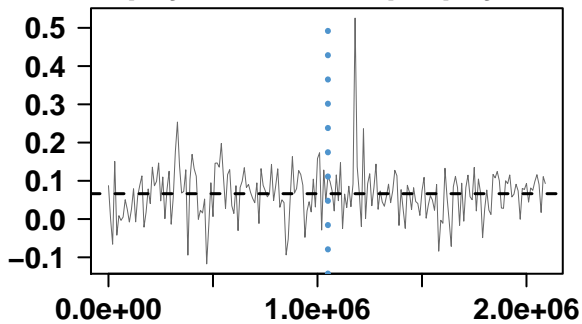


genome coordinates

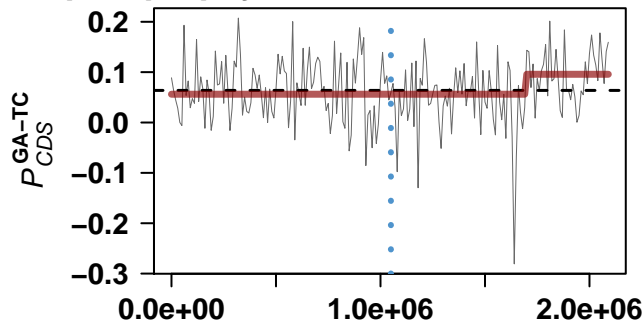
Streptococcus pyogenes MGAS5005



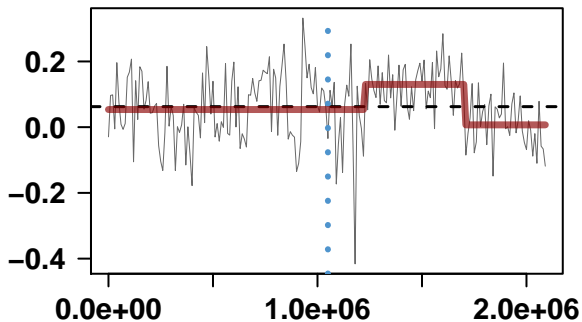
Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305



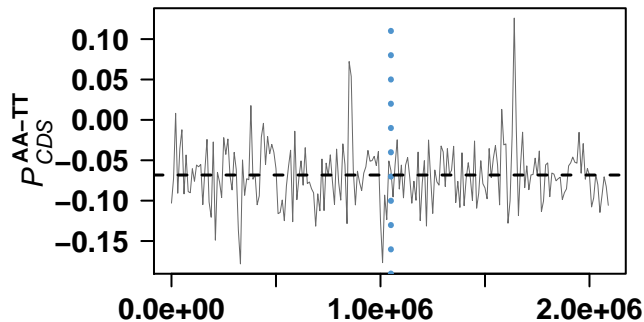
genome coordinates



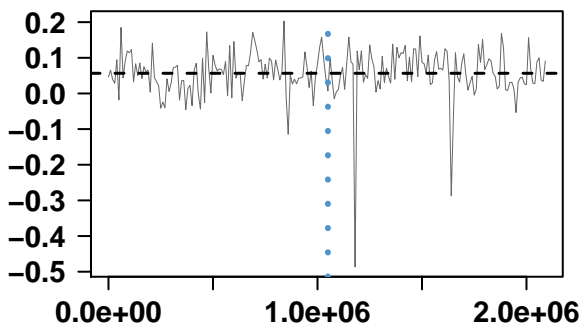
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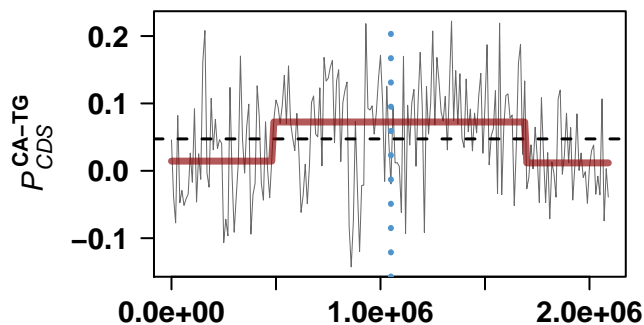
genome coordinates



genome coordinates

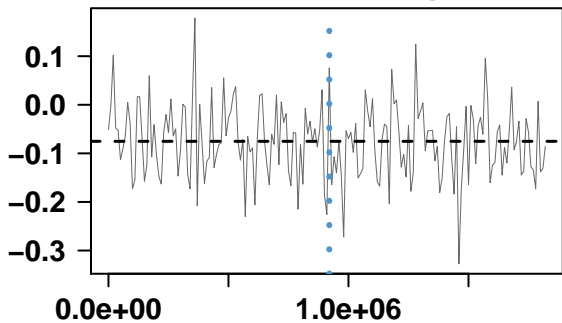


genome coordinates

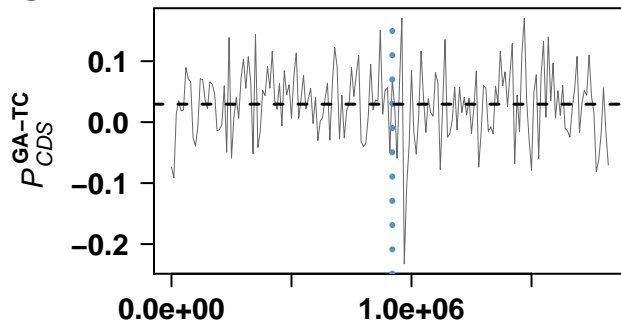


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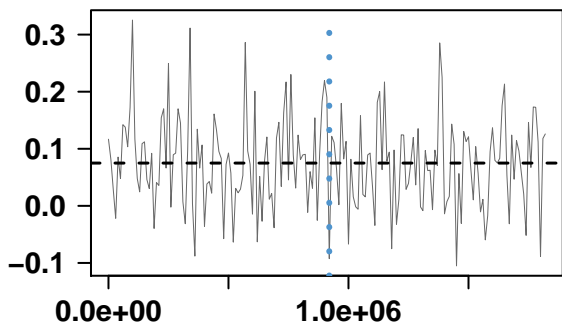
Streptococcus agalactiae A909



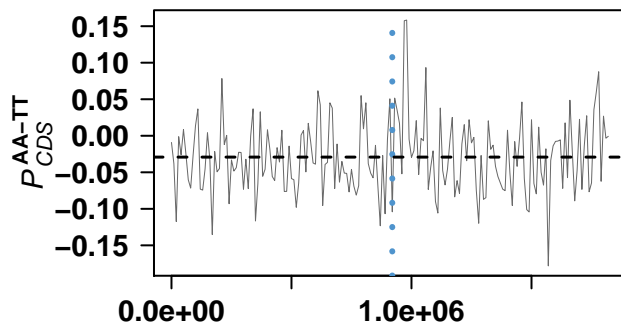
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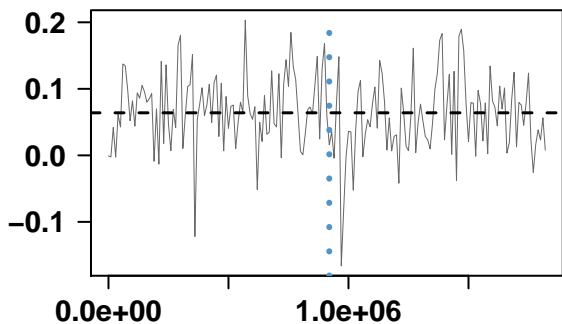
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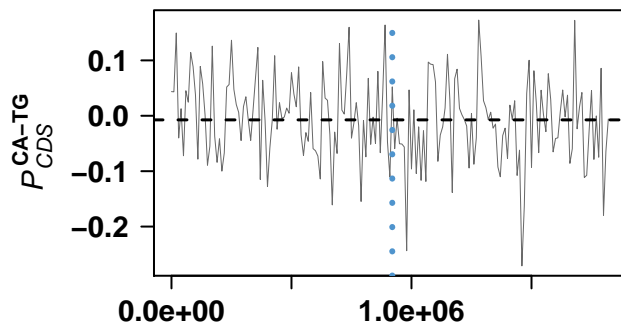
genome coordinates



genome coordinates

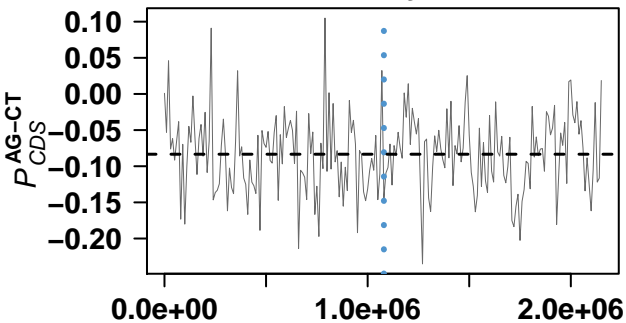


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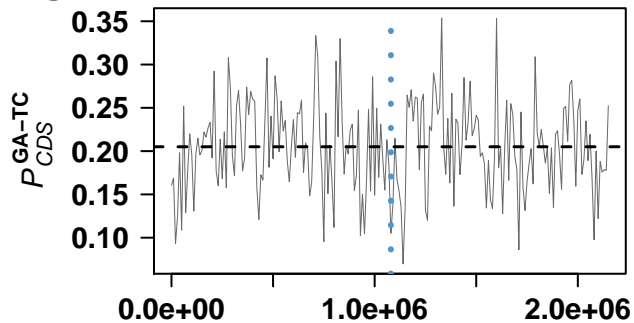


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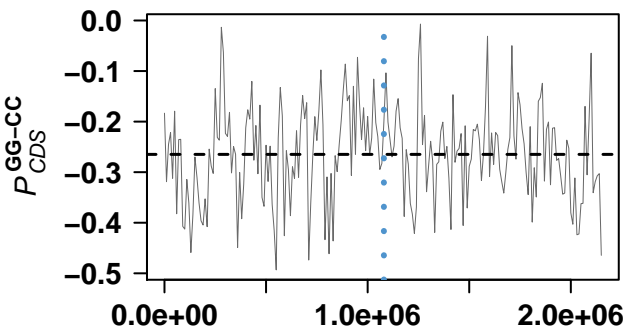
Carboxydothemus hydrogenoformans Z-2901



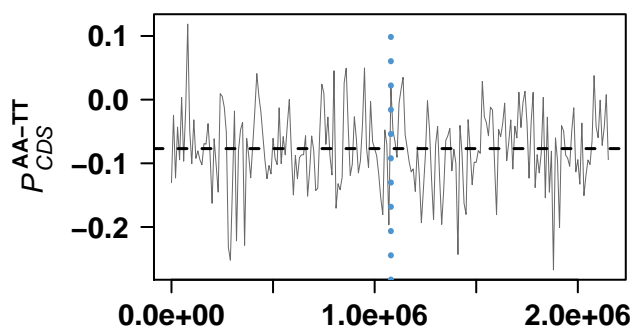
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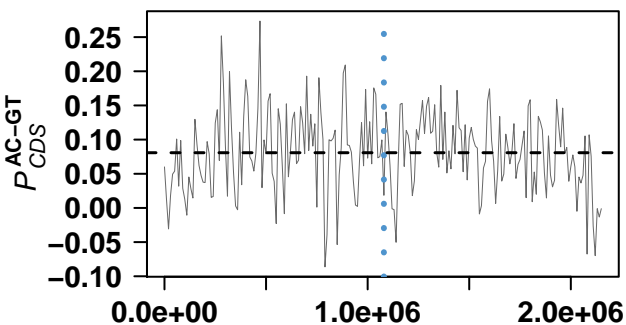
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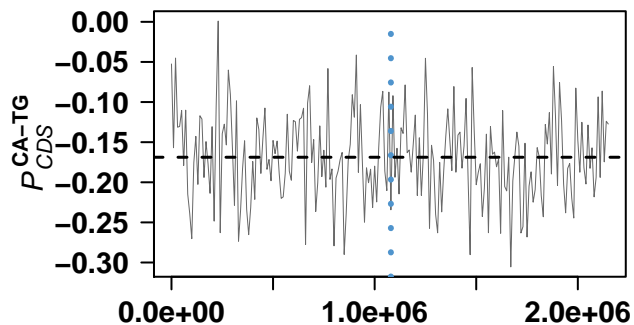
genome coordinates



genome coordinates

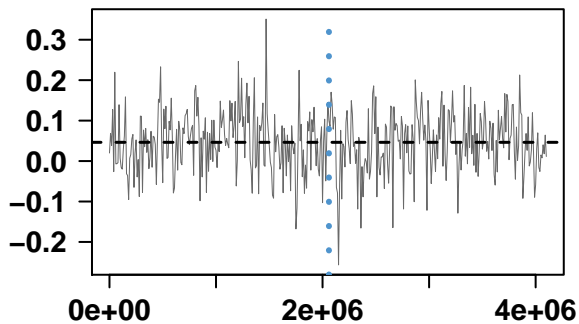


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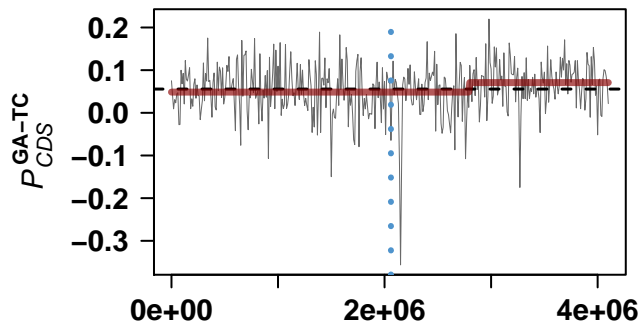


genome coordinates

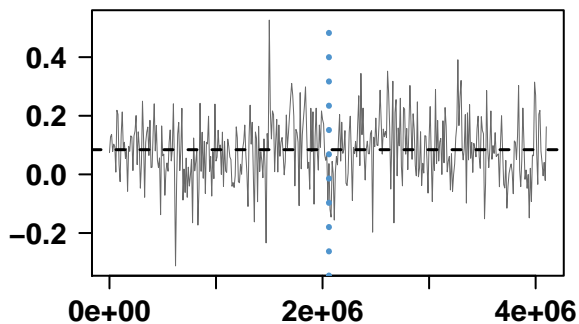
Bacillus anthracis str. 'Ames Ancestor'



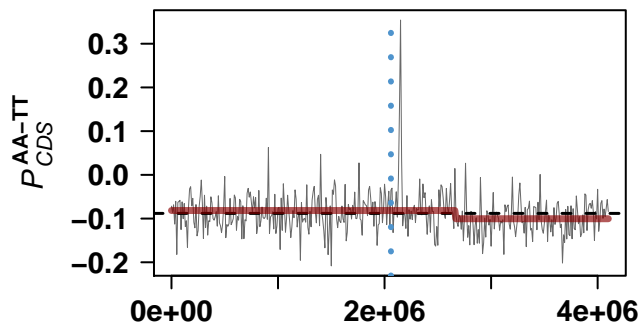
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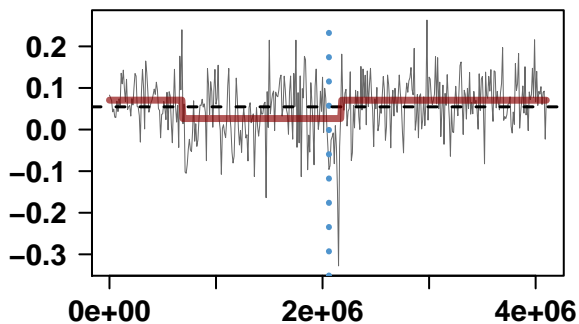
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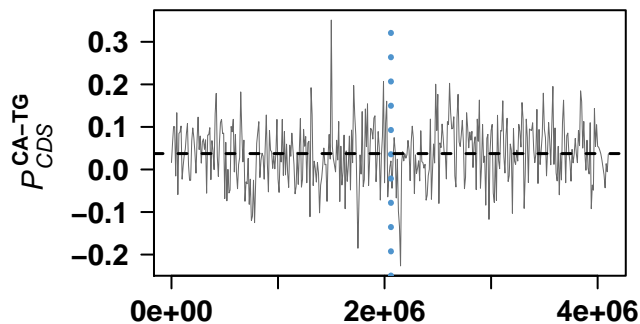
genome coordinates



genome coordinates

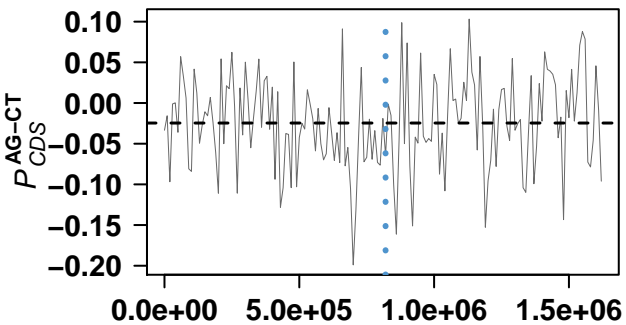


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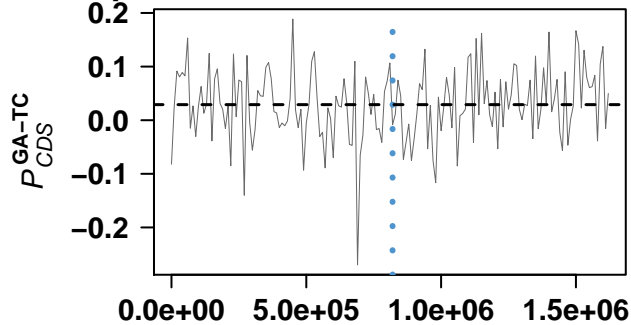


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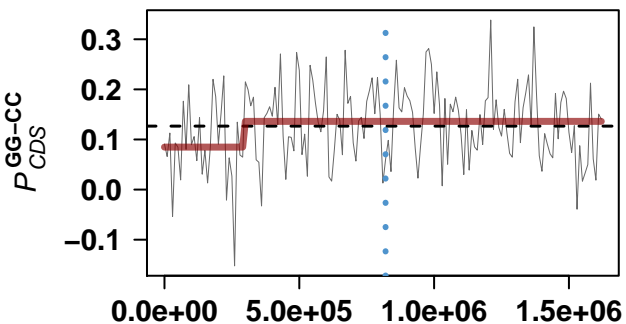
Lactobacillus sakei subsp. sakei 23K



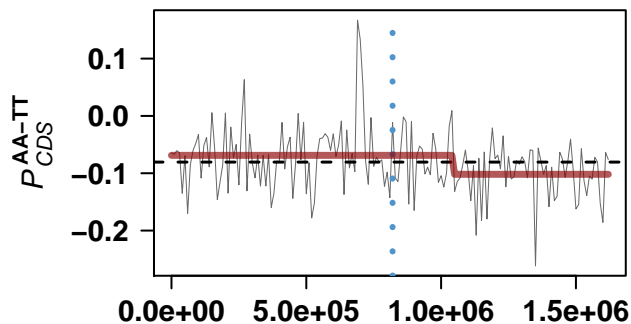
genome coordinates



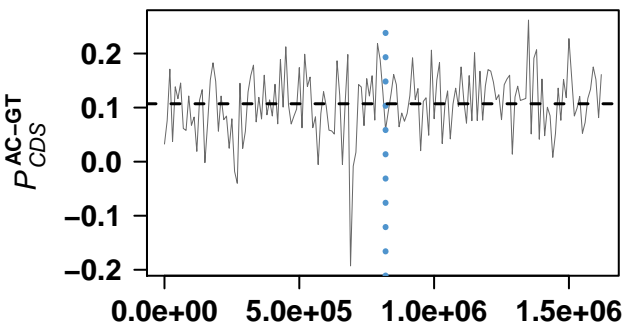
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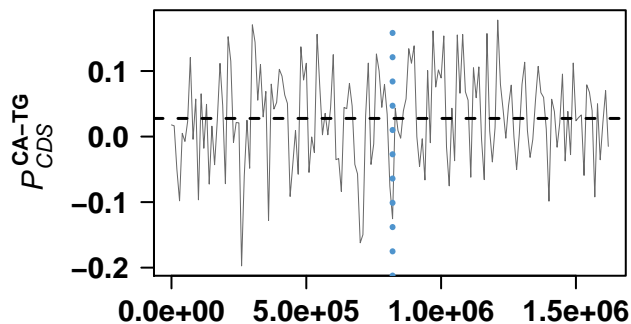
genome coordinates



genome coordinates

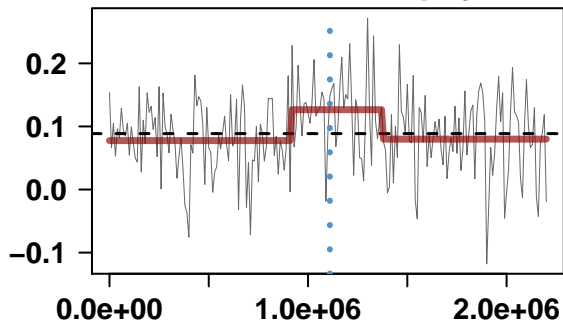


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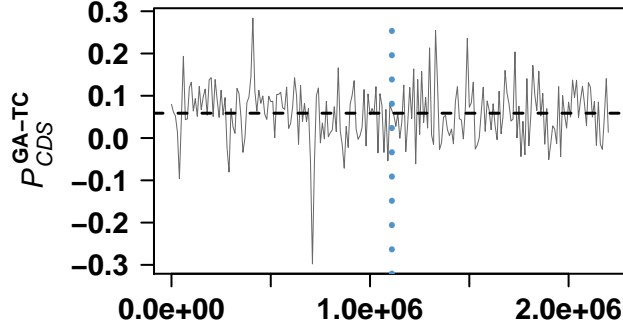


genome coordinates

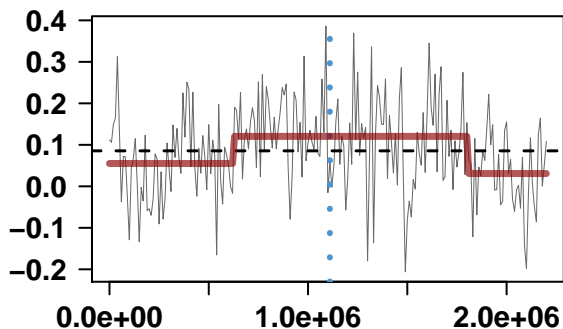
Staphylococcus aureus RF122



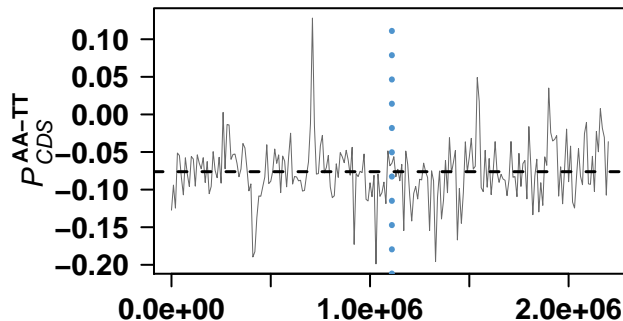
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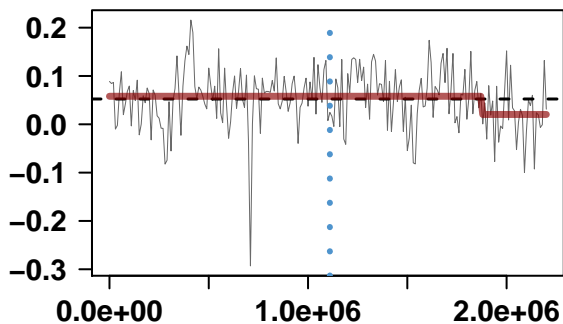
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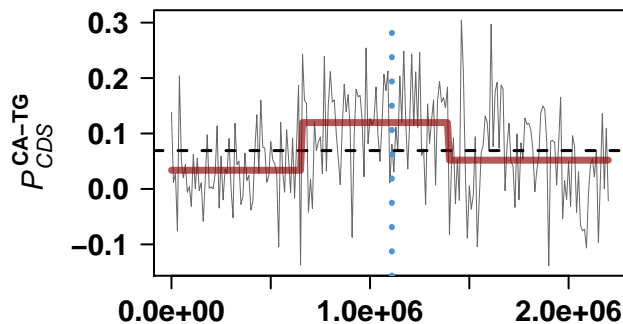
genome coordinates



genome coordinates

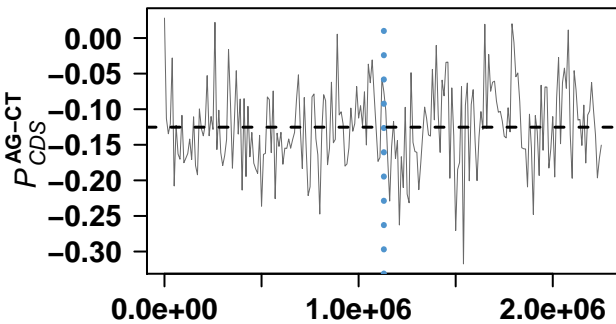


genome coordinates

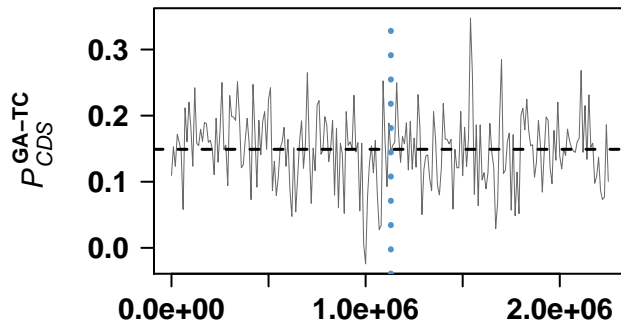


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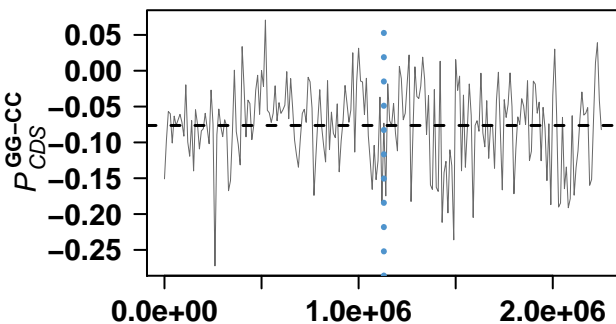
Moorella thermoacetica ATCC 39073



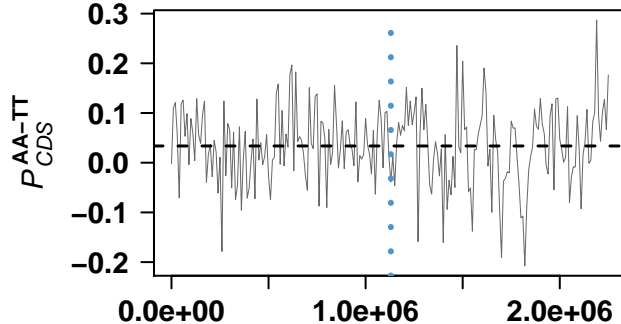
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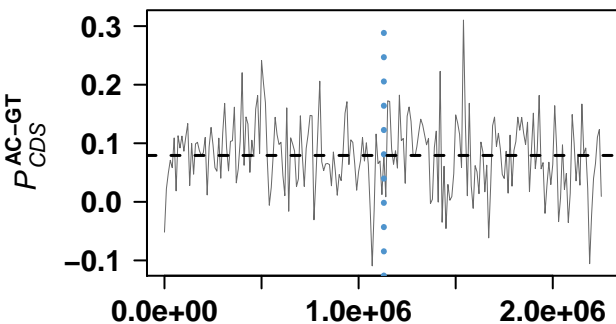
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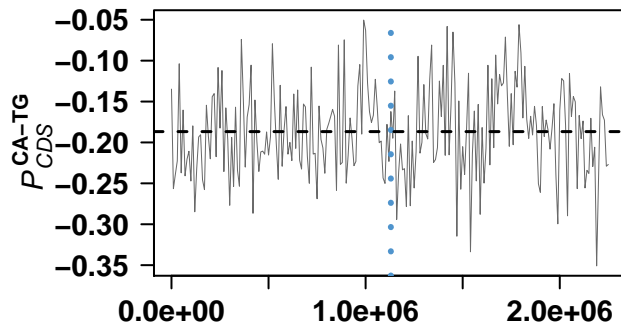
genome coordinates



genome coordinates

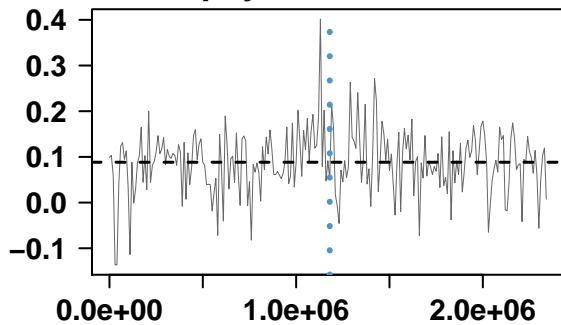


genome coordinates

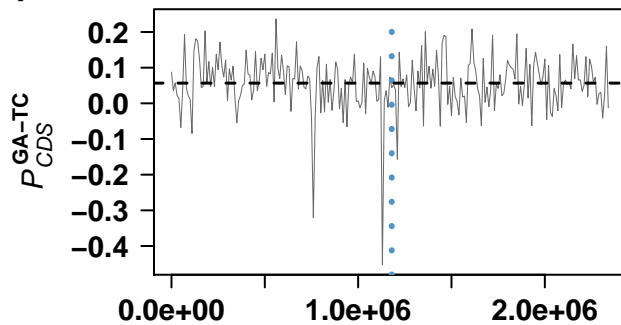


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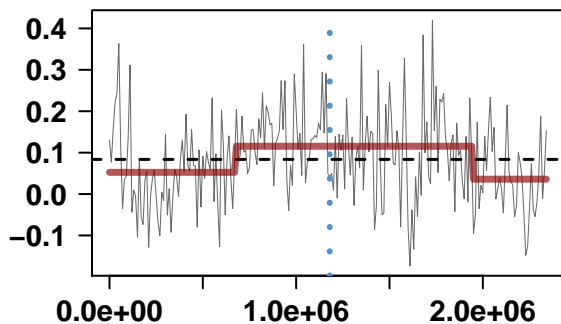
Staphylococcus aureus subsp. aureus USA300_FPR3757



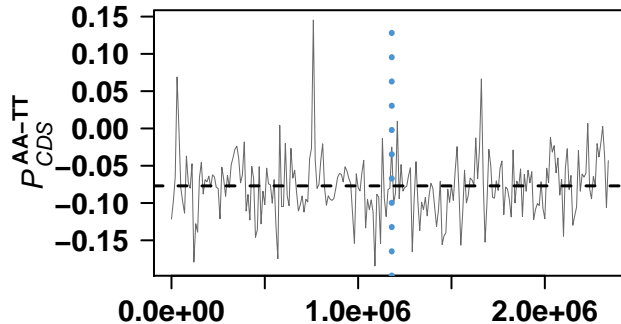
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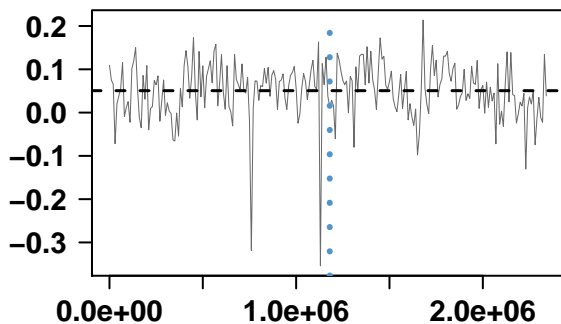
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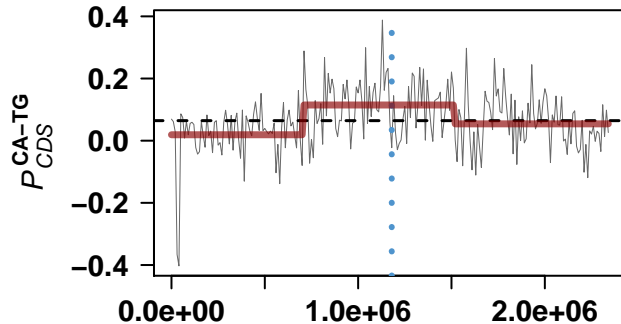
genome coordinates



genome coordinates

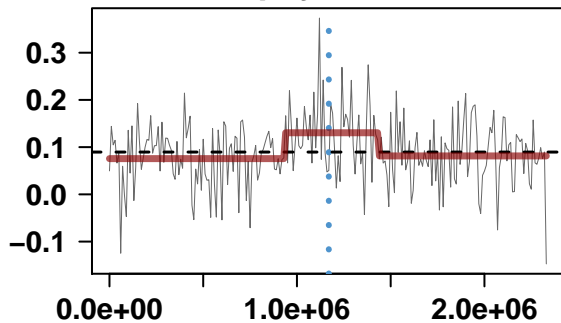


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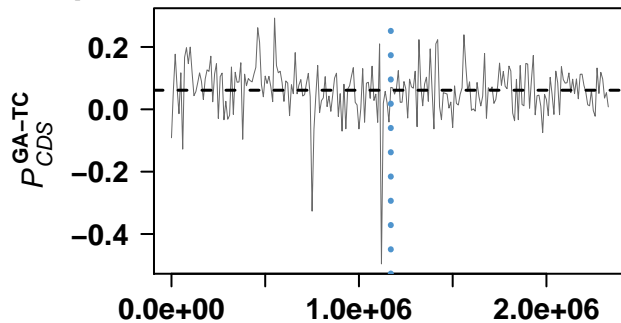


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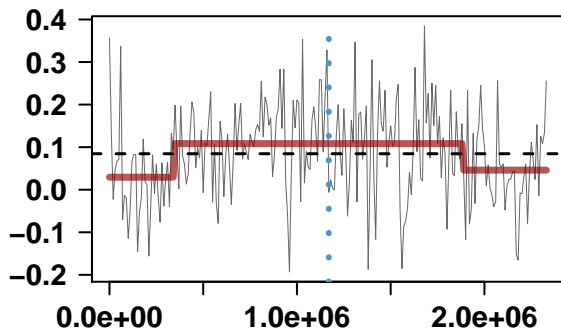
Staphylococcus aureus subsp. aureus NCTC 8325



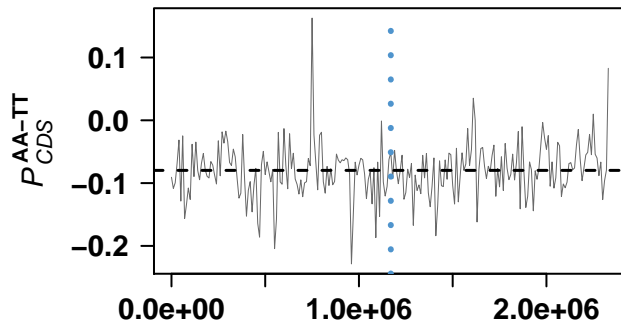
genome coordinates



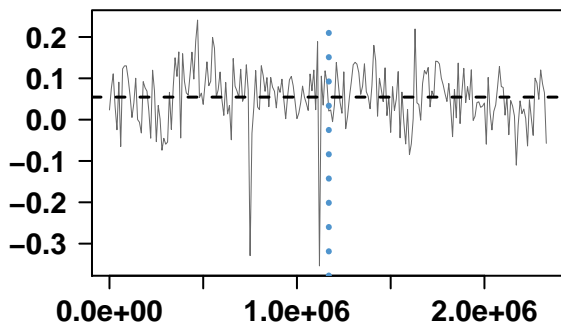
genome coordinates



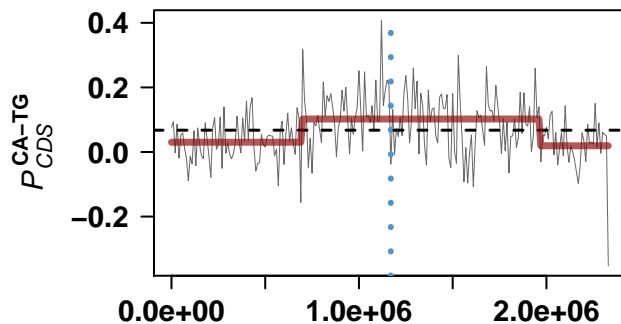
genome coordinates



genome coordinates

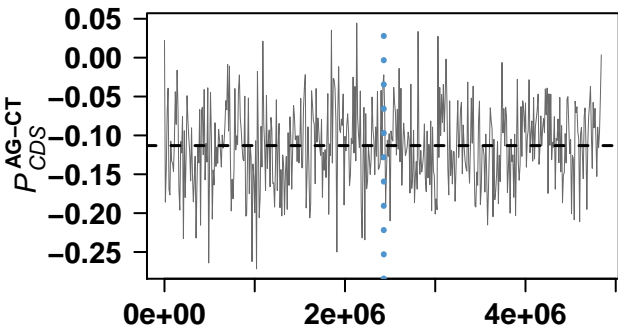


genome coordinates

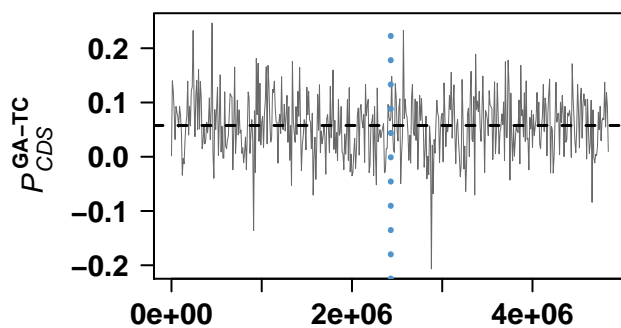


genome coordinates

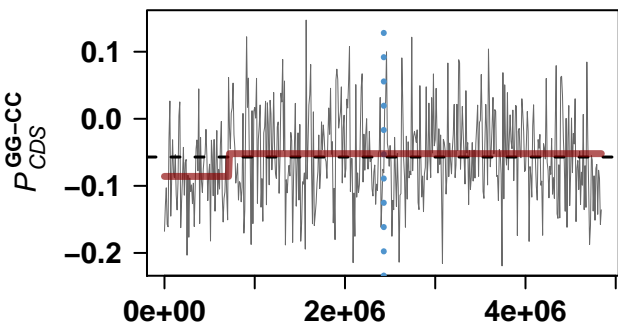
Desulfitobacterium hafniense Y51



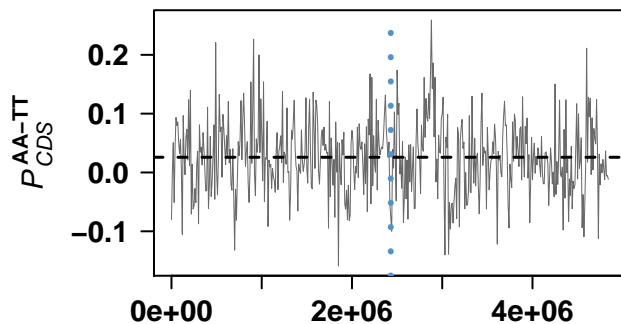
genome coordinates



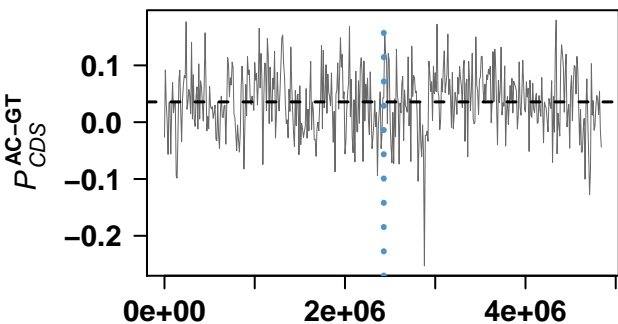
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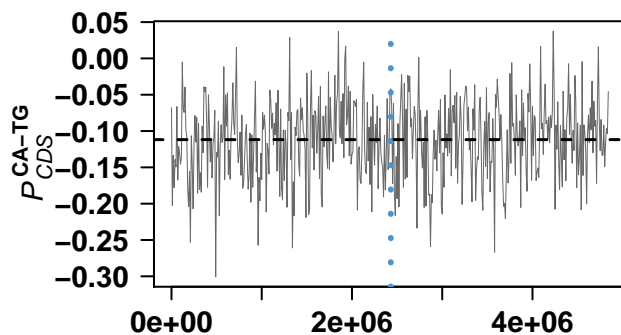
genome coordinates



genome coordinates

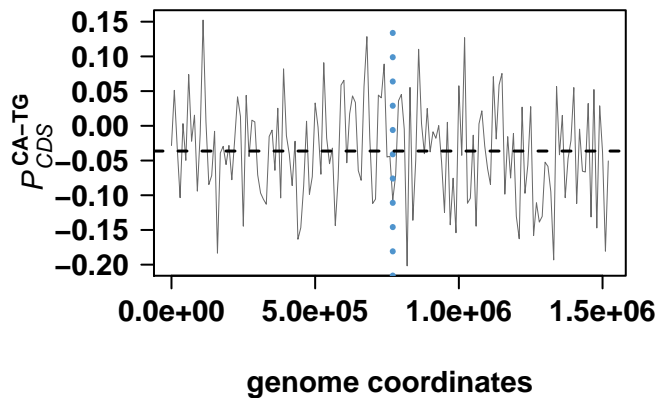
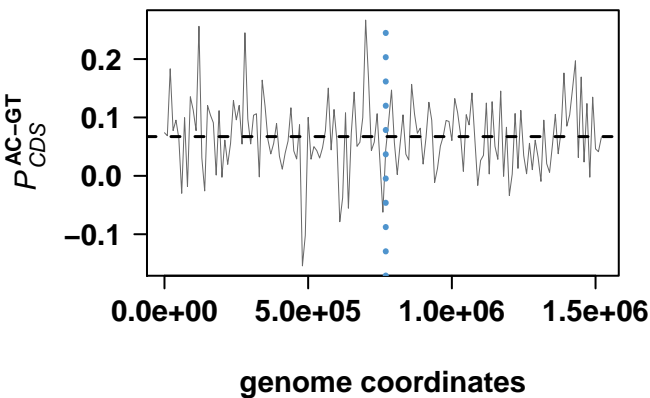
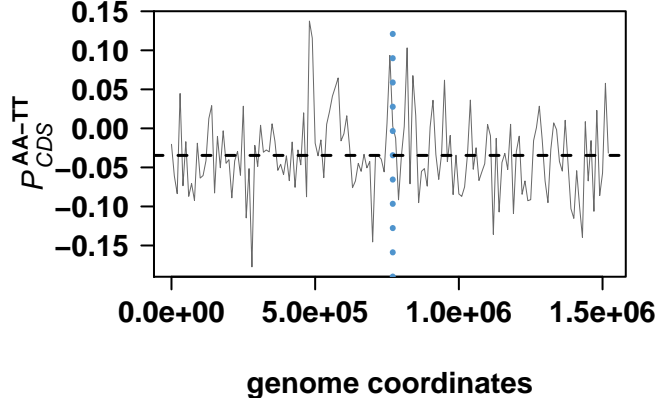
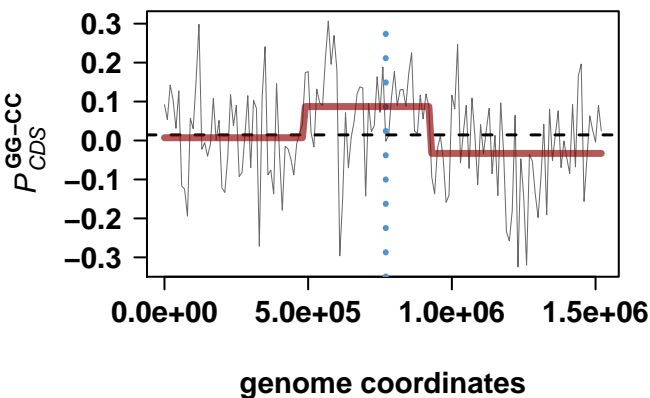
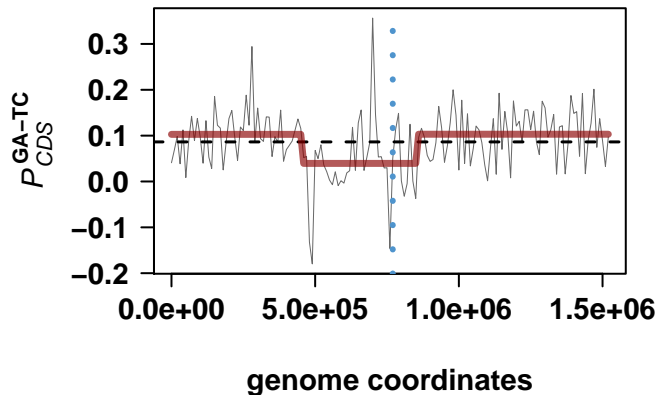
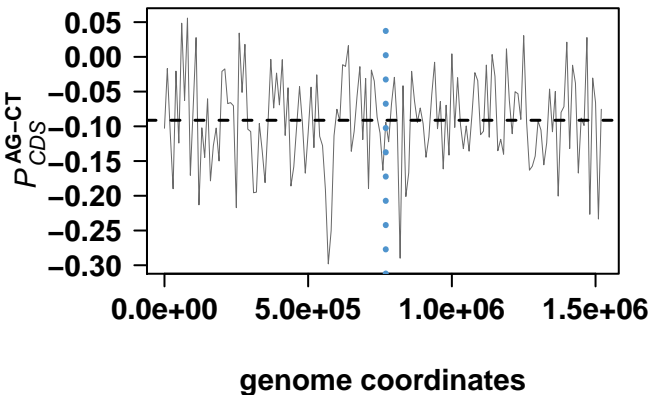


genome coordinates

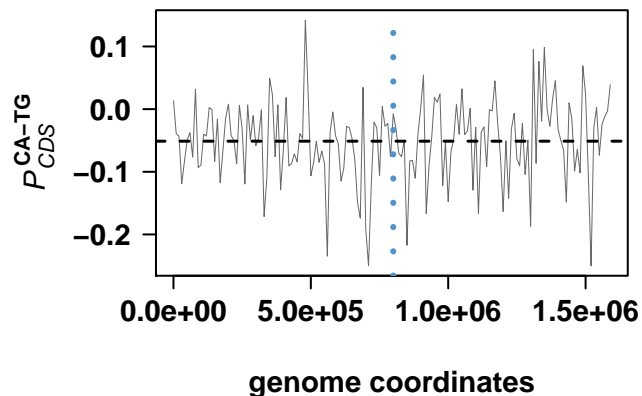
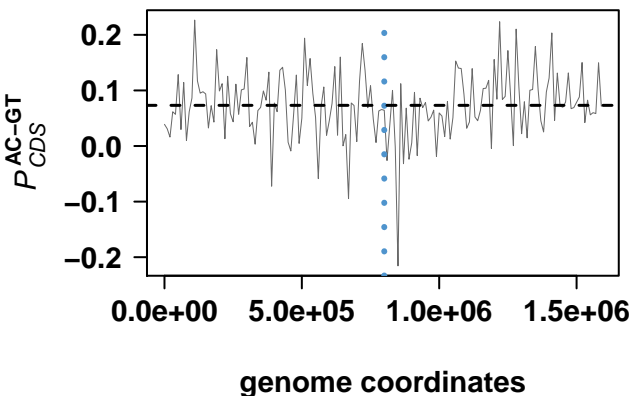
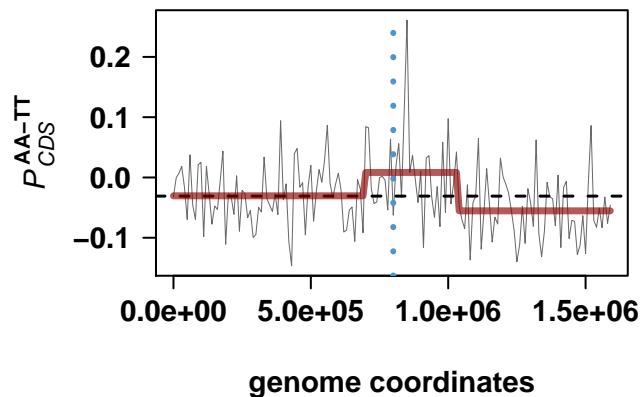
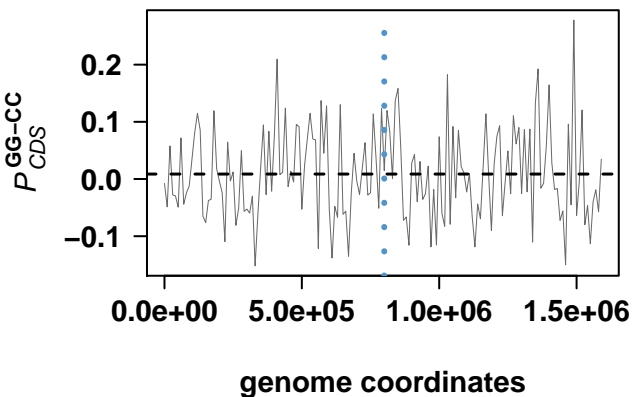
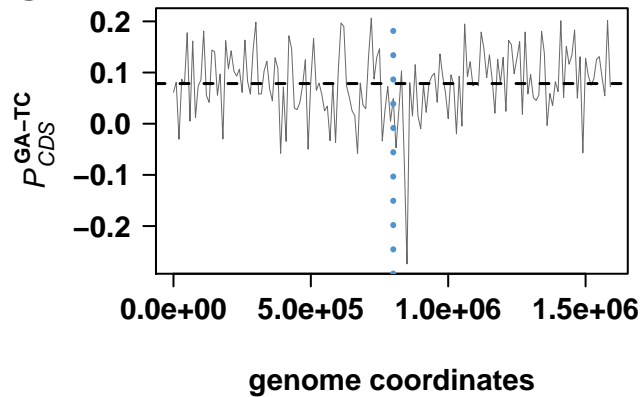
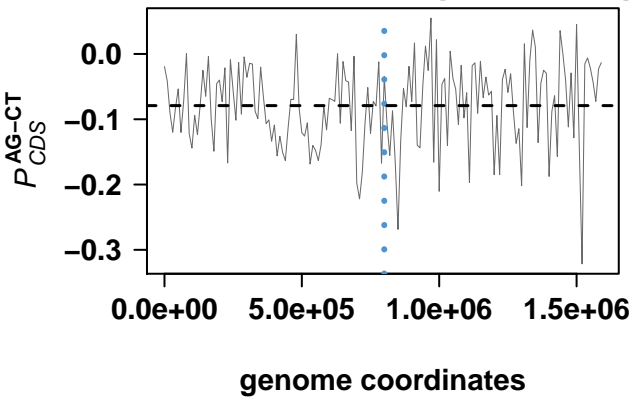


genome coordinates

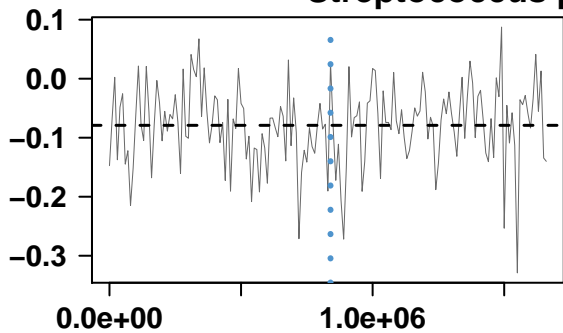
Lactobacillus salivarius UCC118



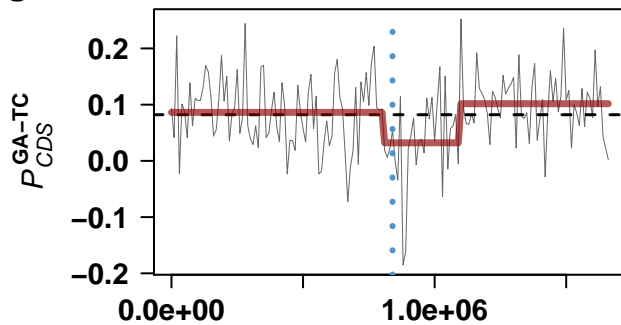
Streptococcus pyogenes MGAS9429



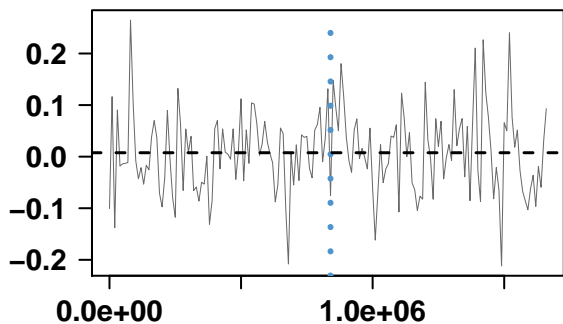
Streptococcus pyogenes MGAS10270



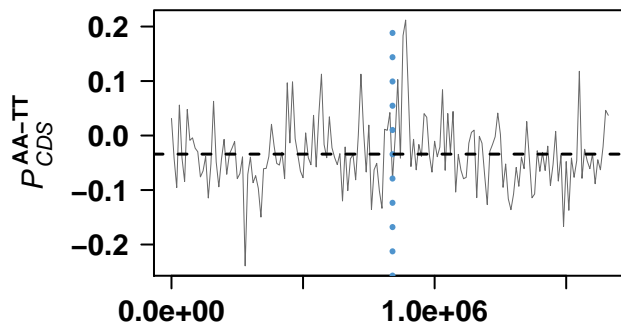
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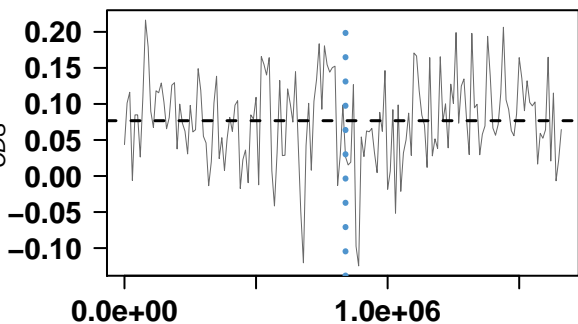
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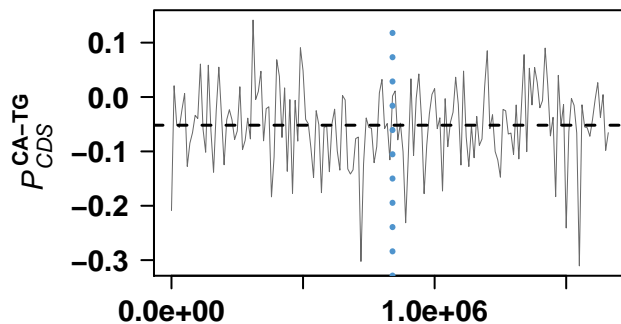
genome coordinates



genome coordinates

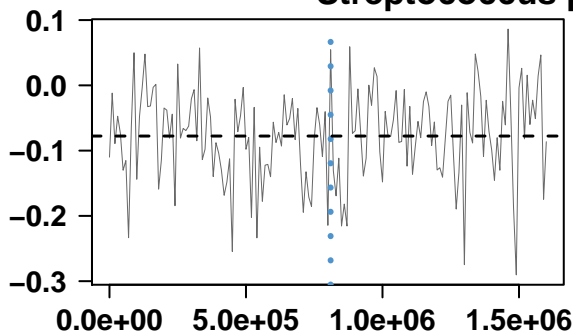


genome coordinates

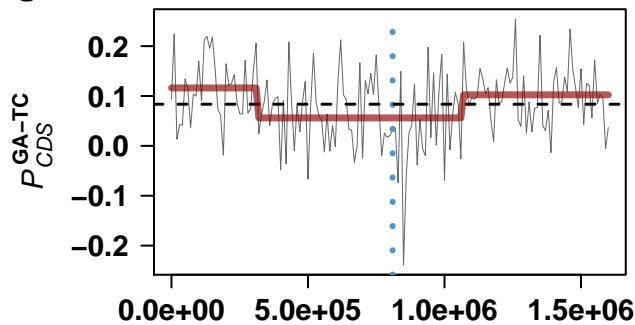


genome coordinates

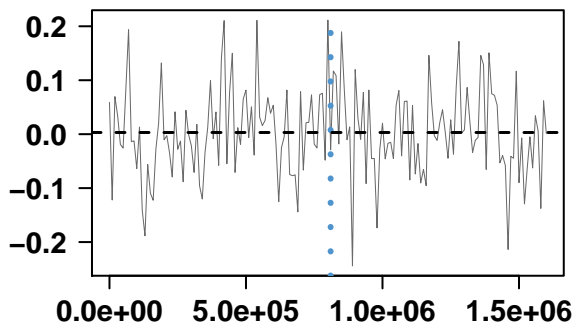
Streptococcus pyogenes MGAS2096



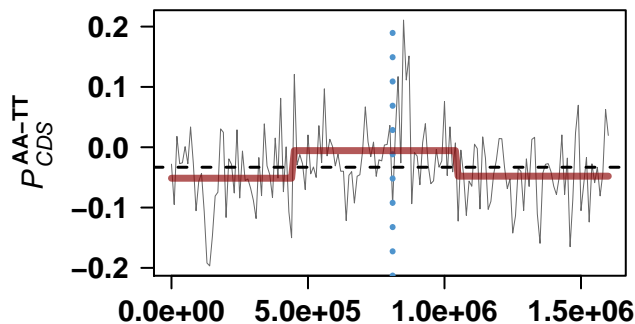
genome coordinates



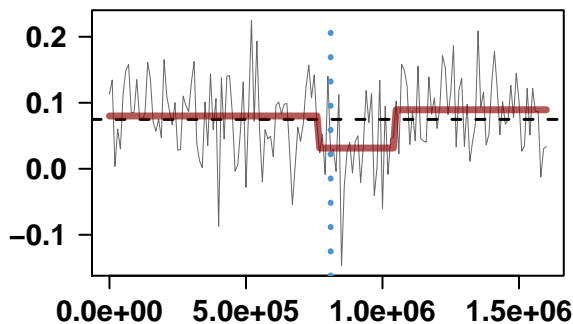
genome coordinates



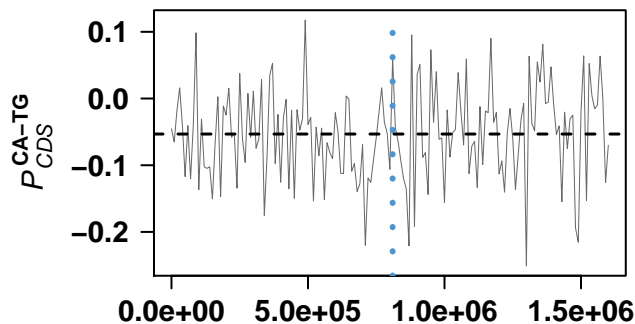
genome coordinates



genome coordinates

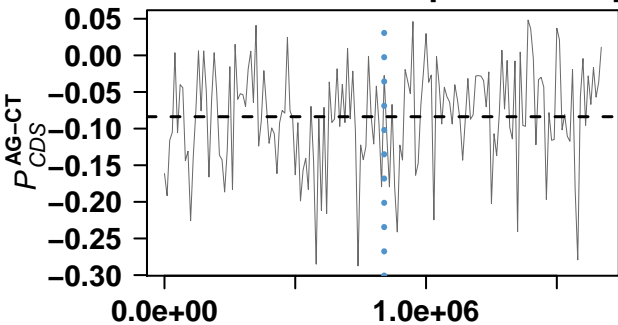


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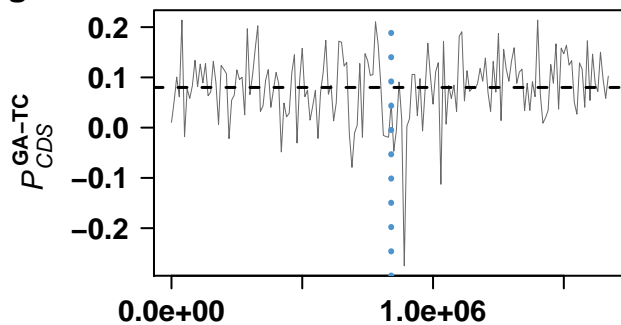


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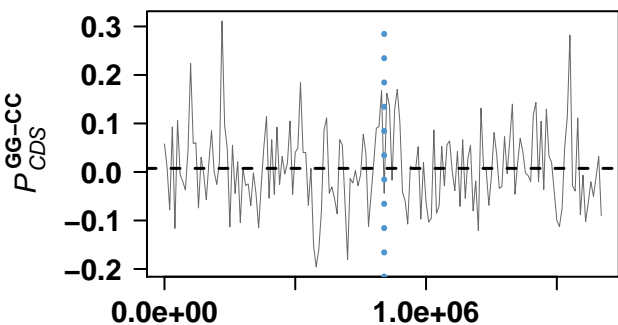
Streptococcus pyogenes MGAS10750



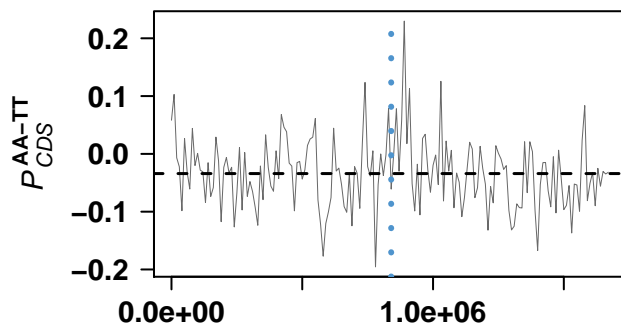
genome coordinates



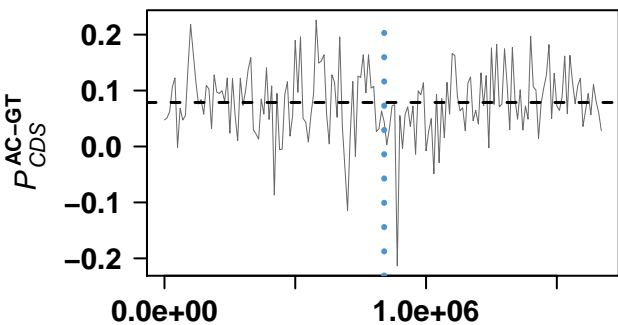
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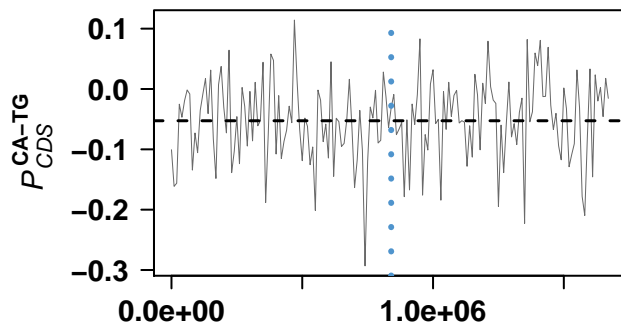
genome coordinates



genome coordinates

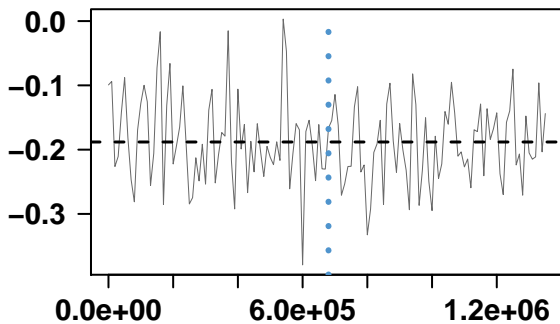


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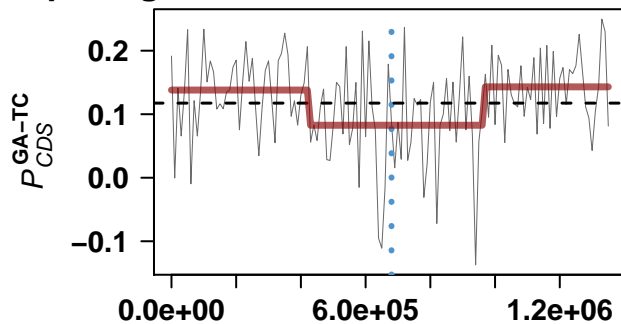


genome coordinates

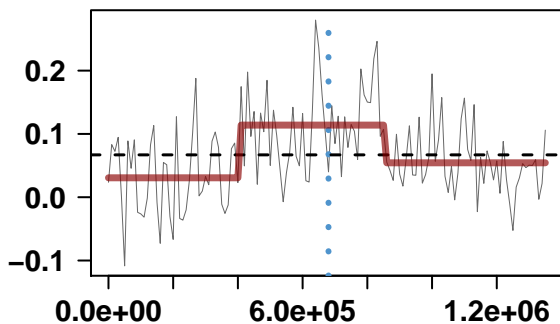
Lactobacillus delbrueckii subsp. bulgaricus ATCC 11842



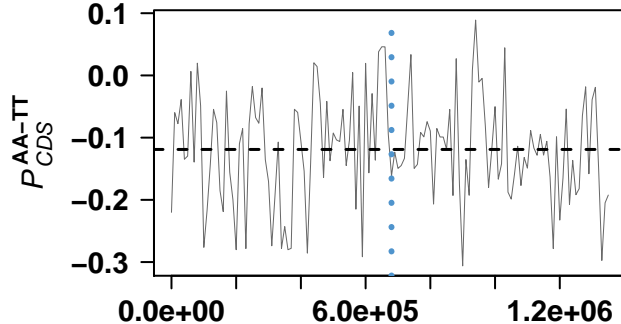
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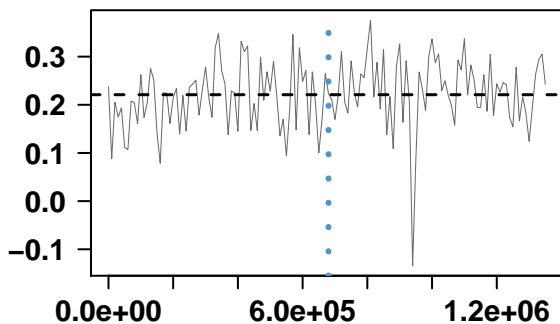
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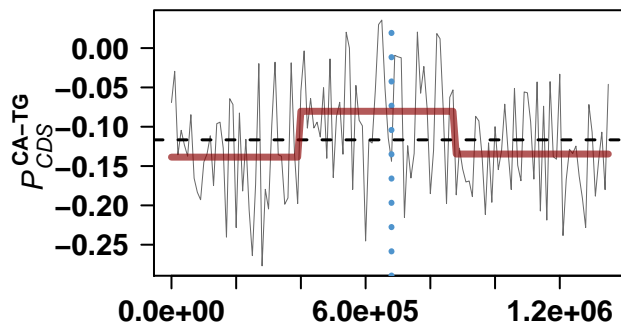
genome coordinates



genome coordinates

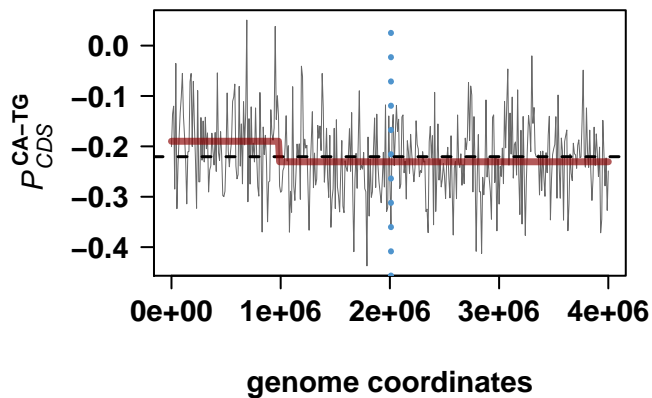
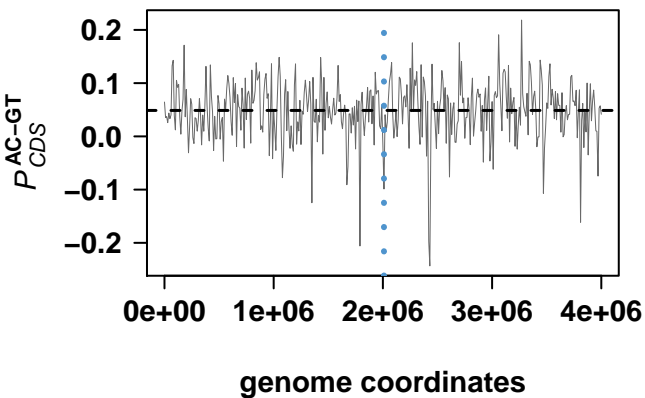
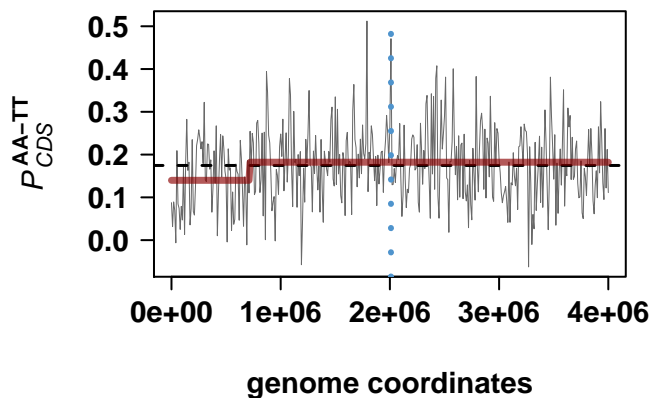
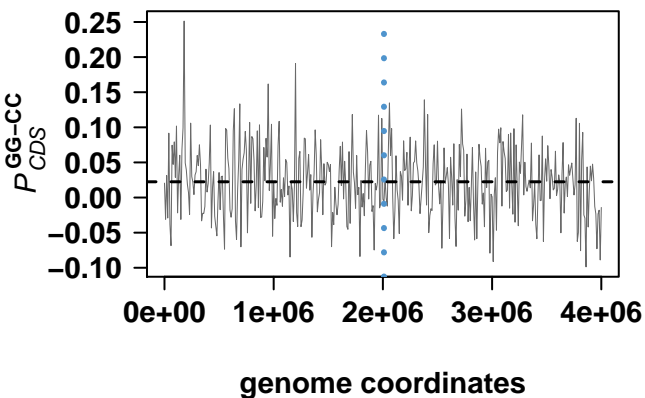
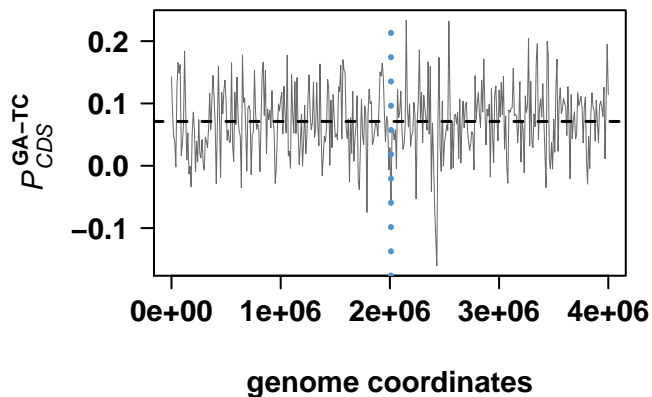
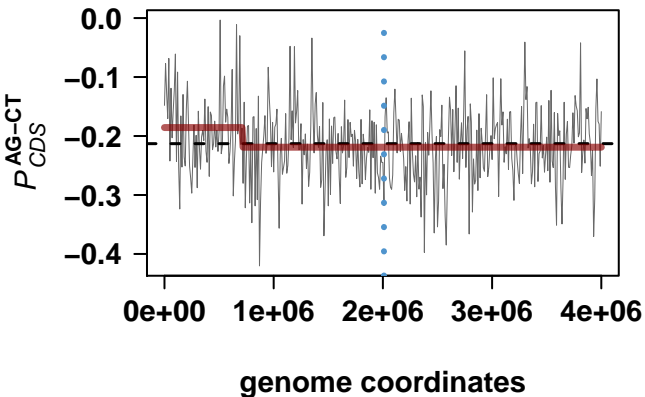


genome coordinates

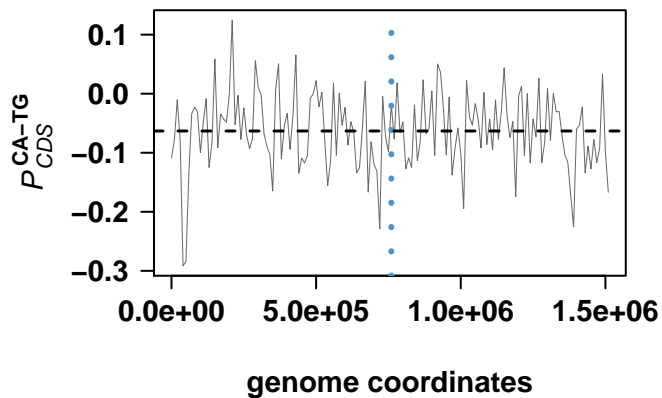
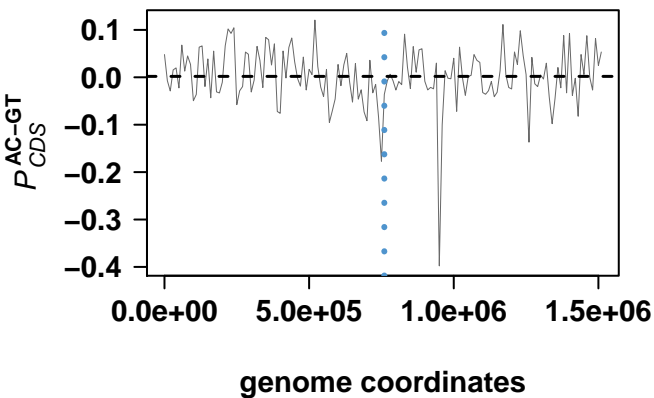
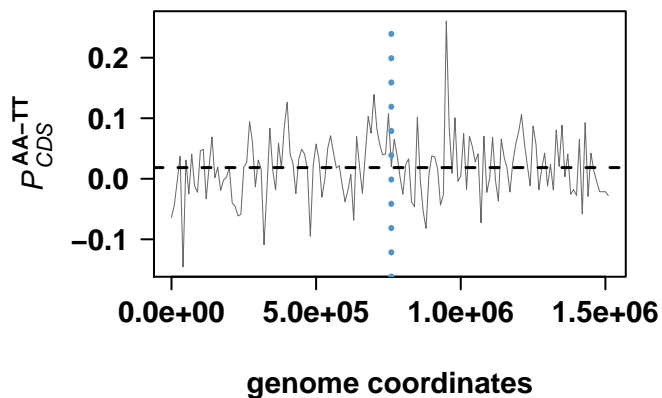
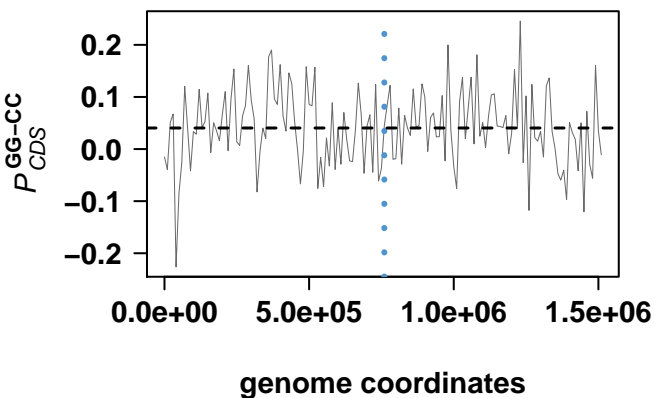
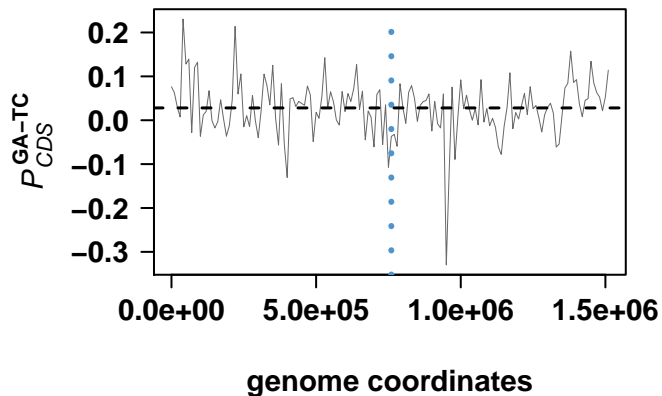
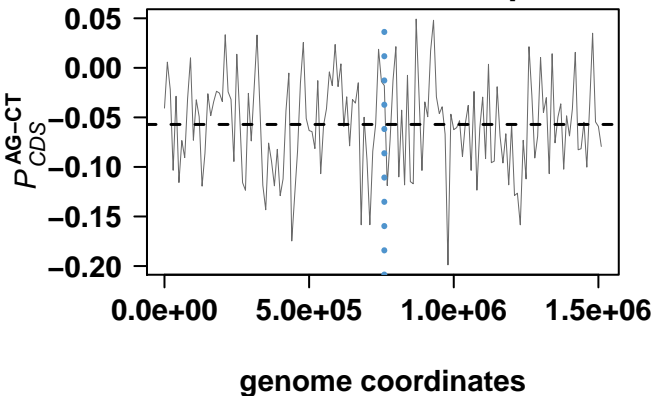


genome coordinates

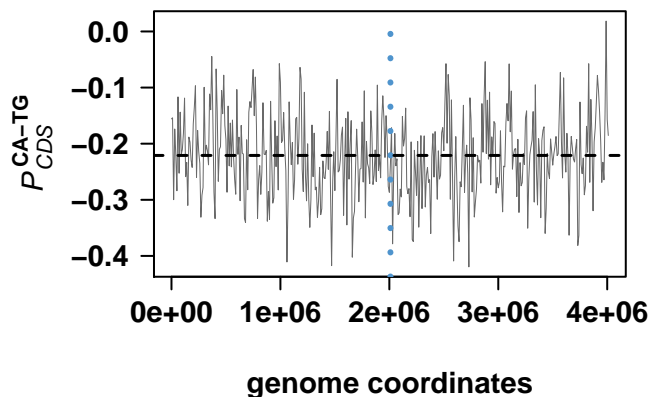
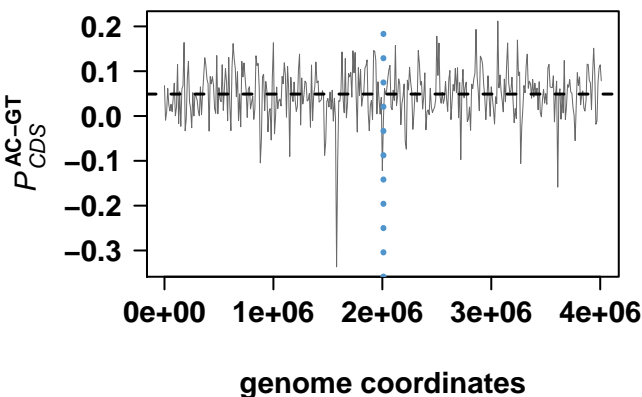
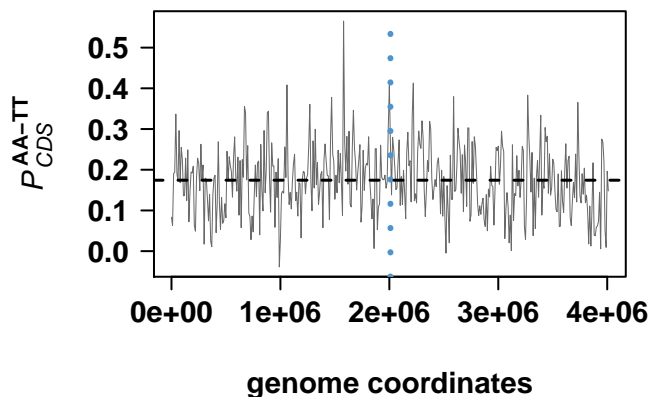
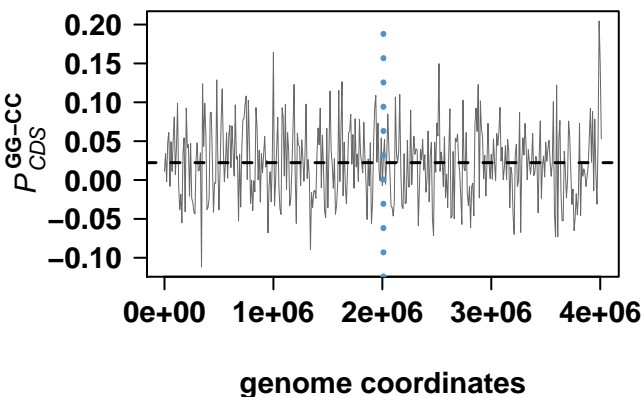
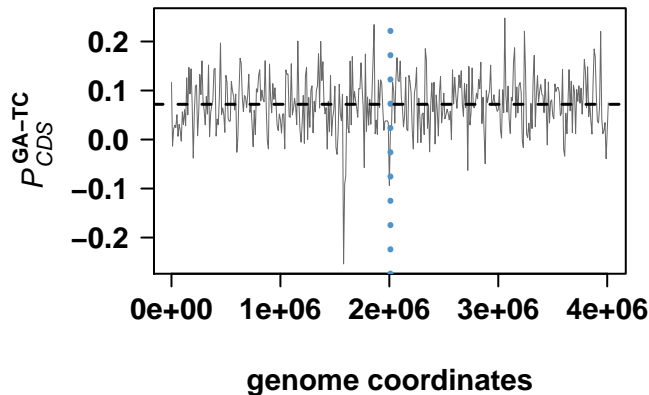
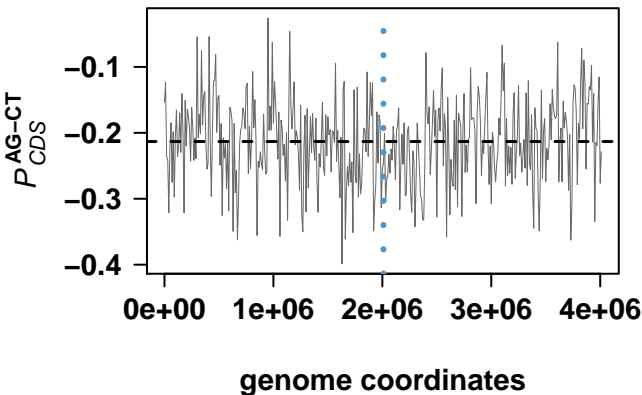
Escherichia coli str. K-12 substr. W3110



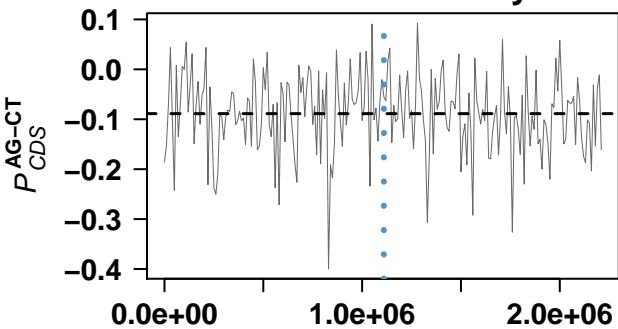
Haemophilus influenzae Rd KW20



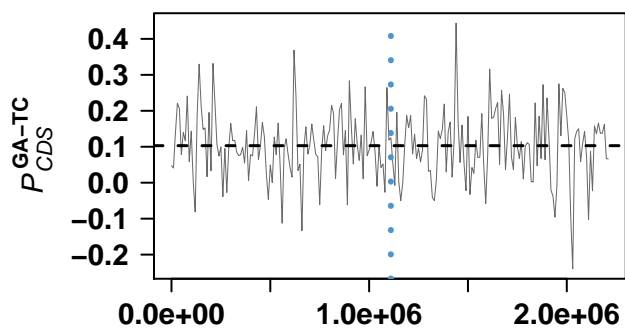
Escherichia coli str. K-12 substr. MG1655



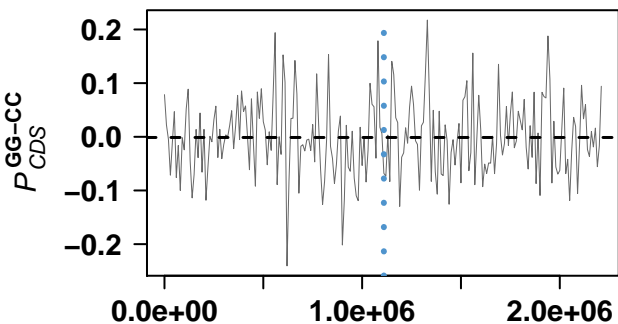
Xylella fastidiosa 9a5c



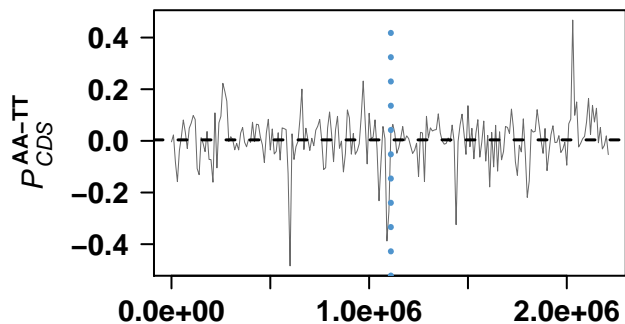
genome coordinates



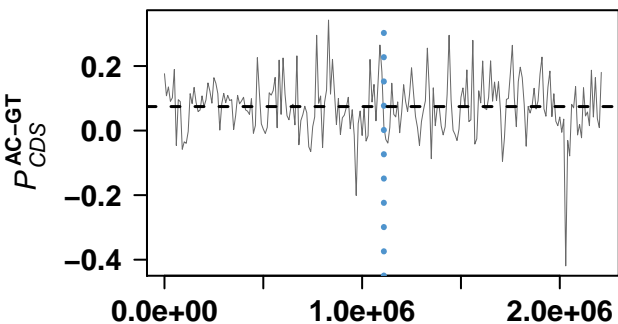
genome coordinates



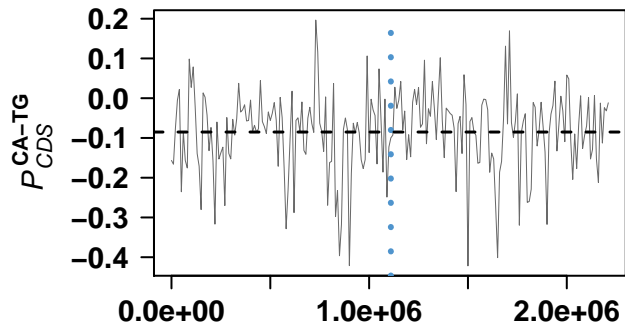
genome coordinates



genome coordinates

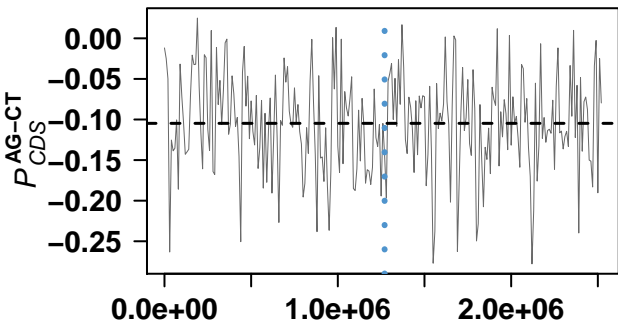


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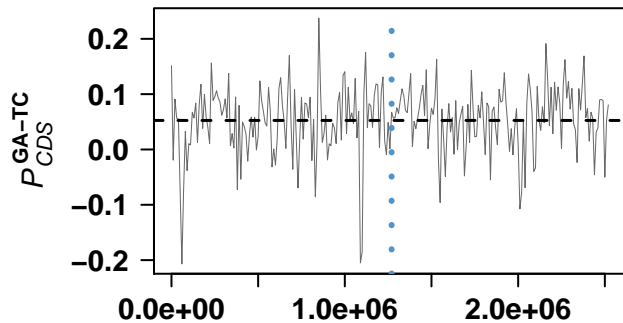


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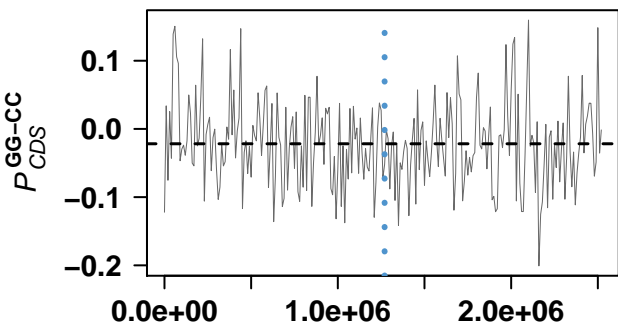
Vibrio cholerae O1 biovar El Tor str. N16961



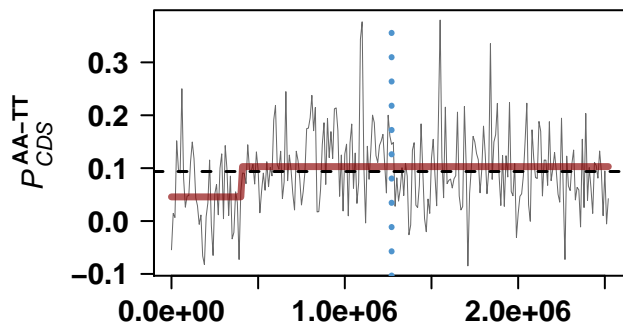
genome coordinates



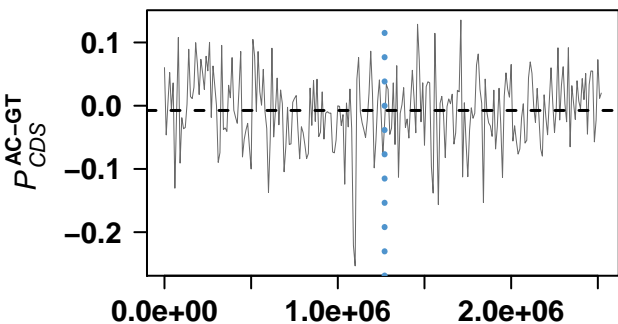
genome coordinates



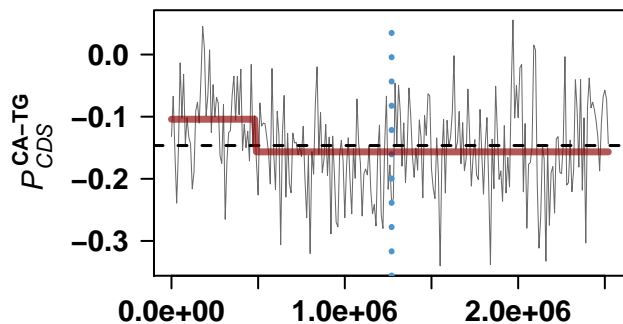
genome coordinates



genome coordinates

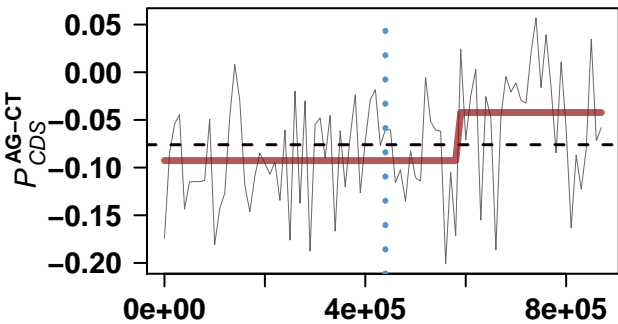


genome coordinates

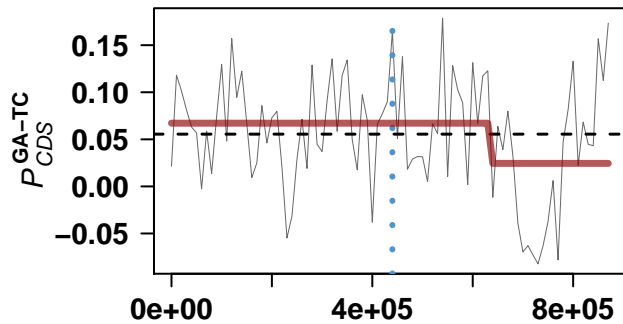


genome coordinates

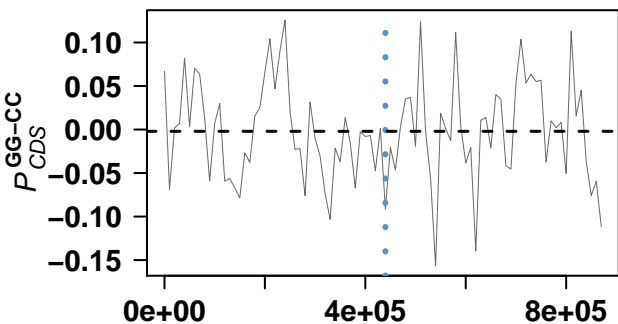
Vibrio cholerae O1 biovar El Tor str. N16961



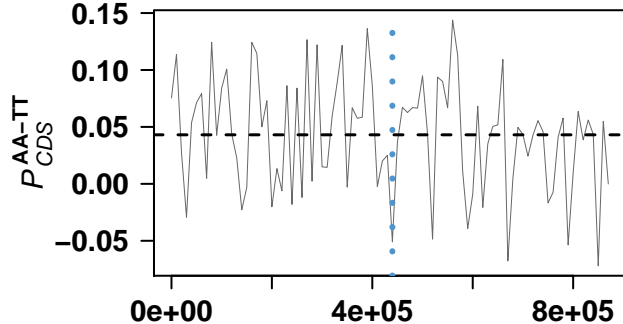
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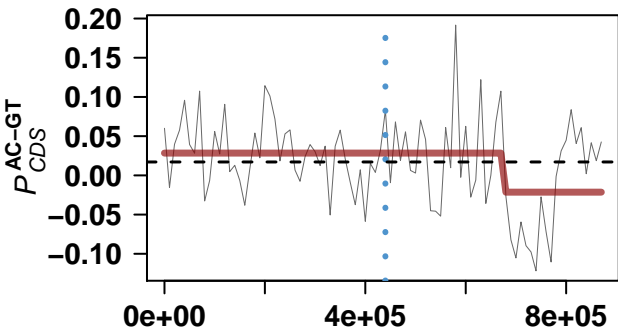
genome coordinates



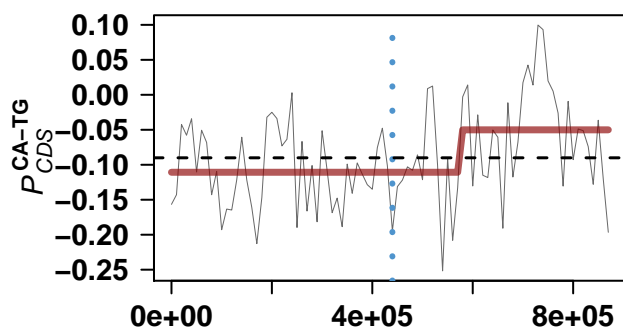
genome coordinates



genome coordinates

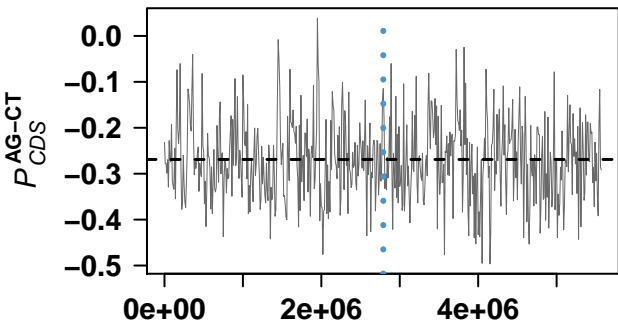


genome coordinates

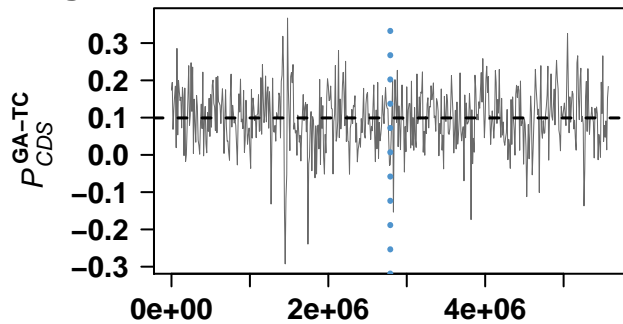


genome coordinates

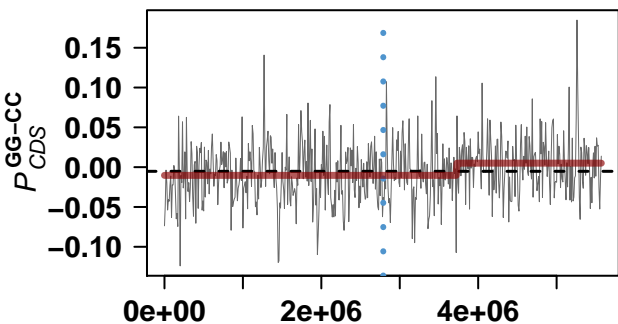
Pseudomonas aeruginosa PAO1



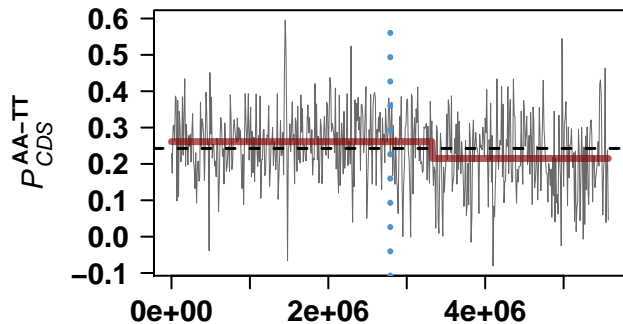
genome coordinates



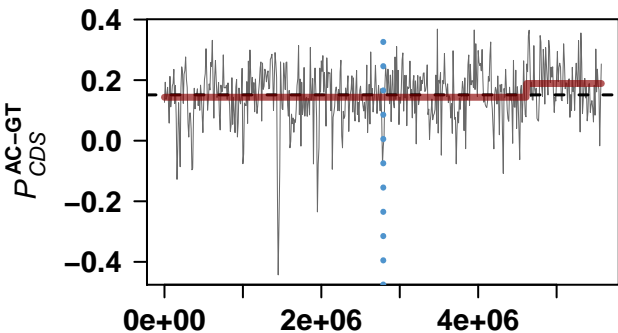
genome coordinates



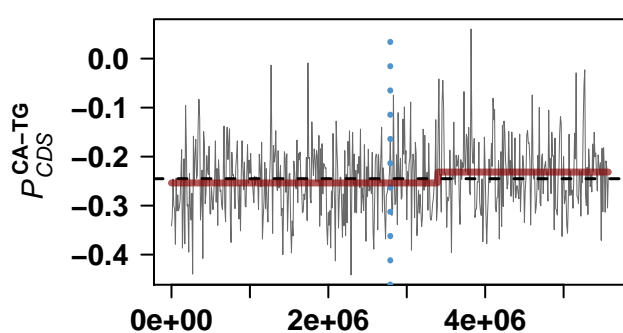
genome coordinates



genome coordinates

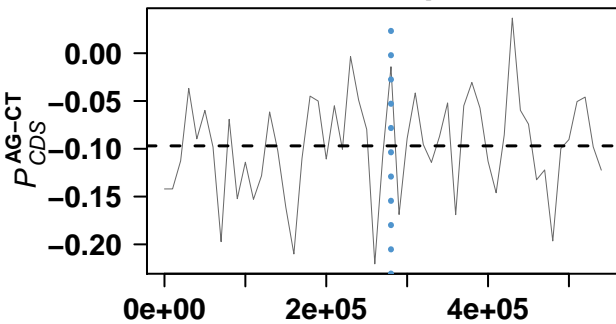


genome coordinates

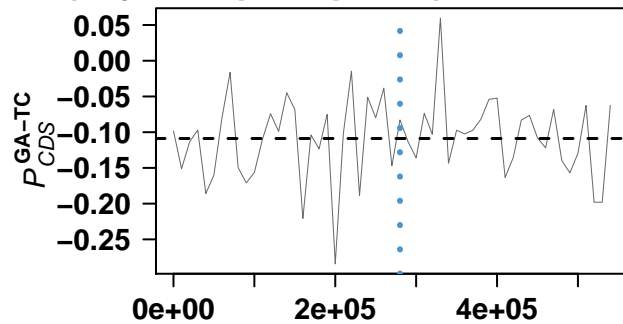


genome coordinates

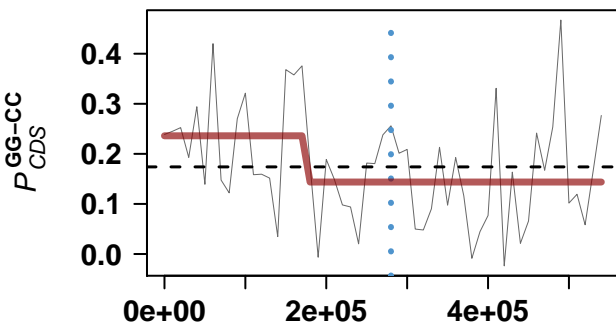
Buchnera aphidicola str. APS (Acyrthosiphon pisum)



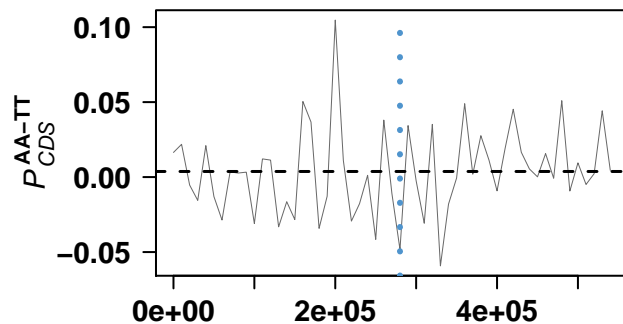
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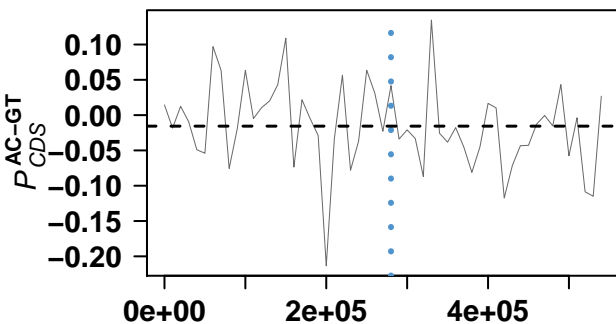
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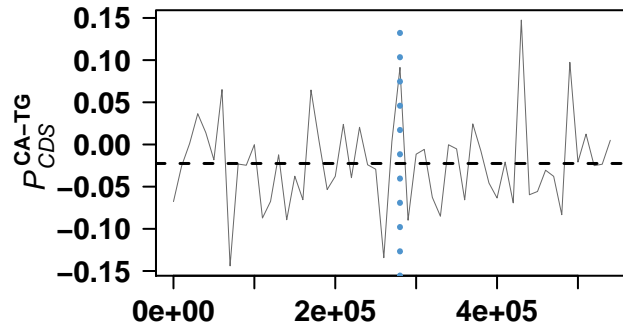
genome coordinates



genome coordinates

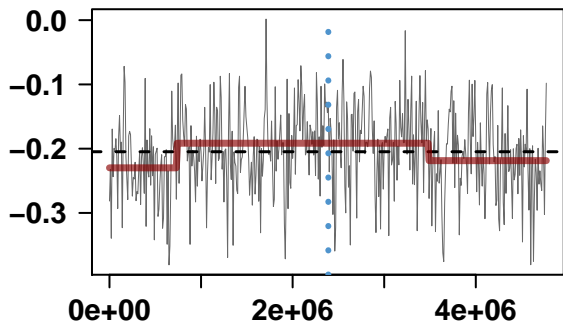


genome coordinates

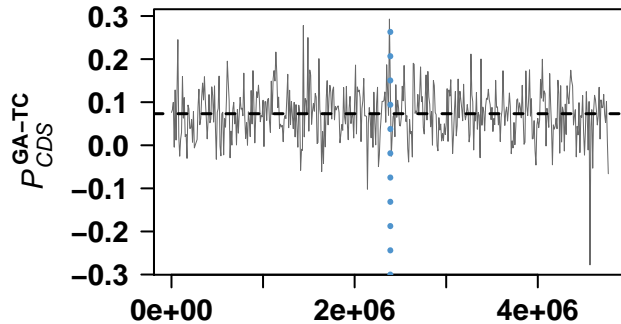


genome coordinates

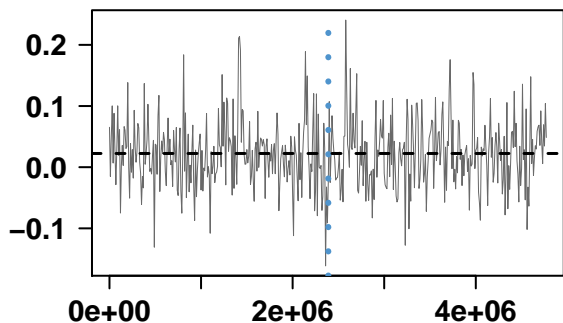
Escherichia coli O157:H7 str. EDL933



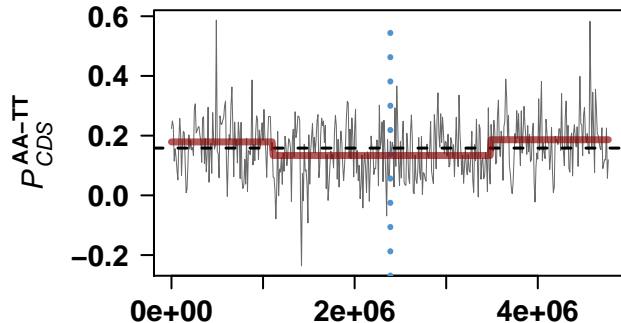
genome coordinates



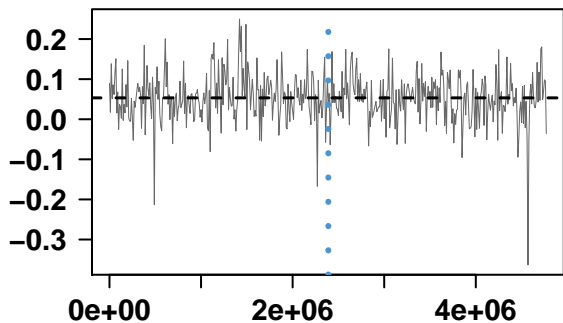
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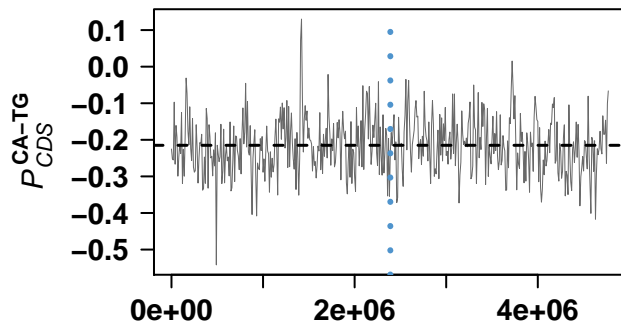
genome coordinates



genome coordinates

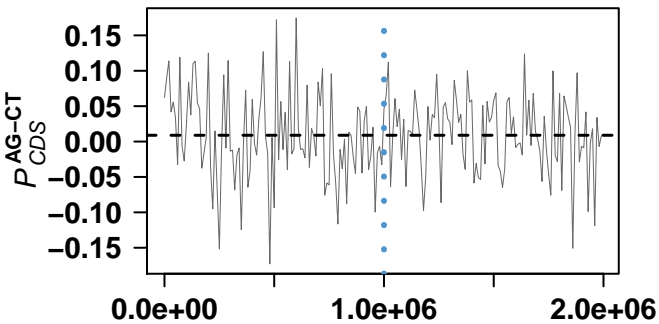


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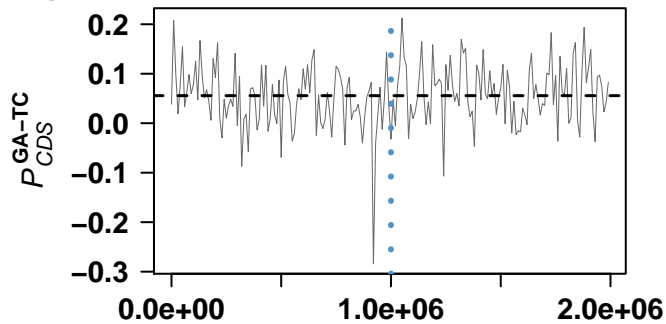


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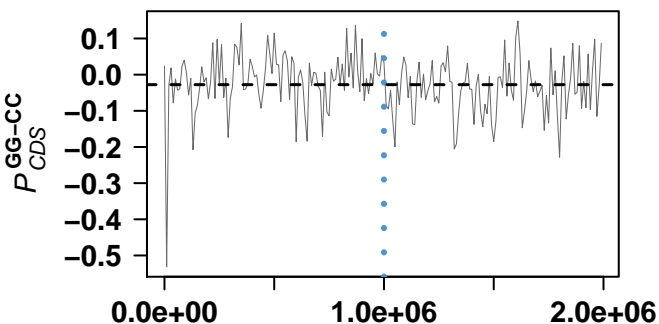
Pasteurella multocida subsp. *multocida* str. Pm70



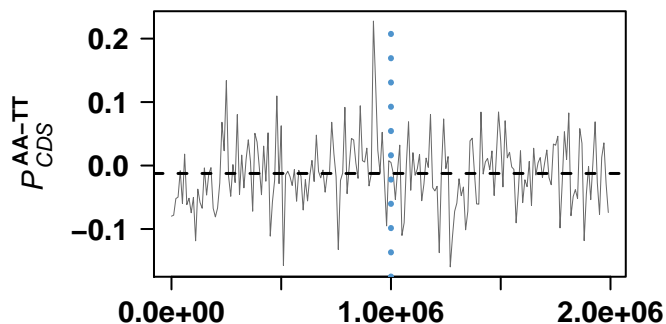
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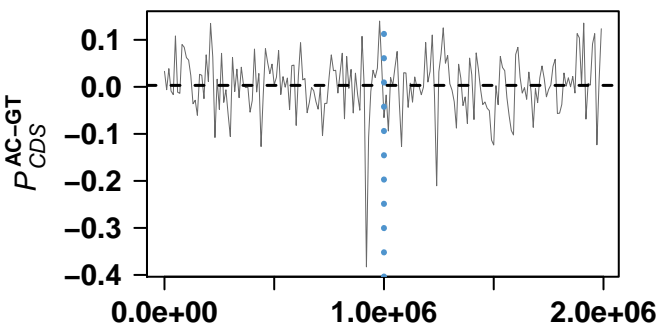
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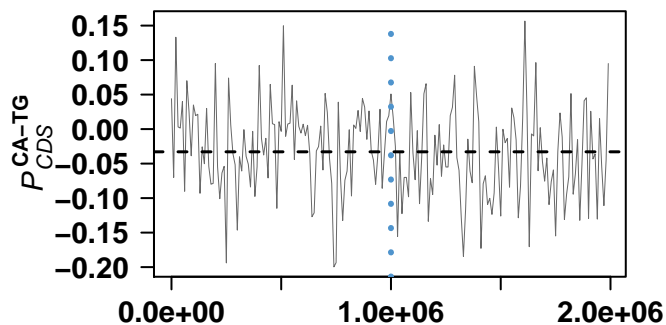
genome coordinates



genome coordinates

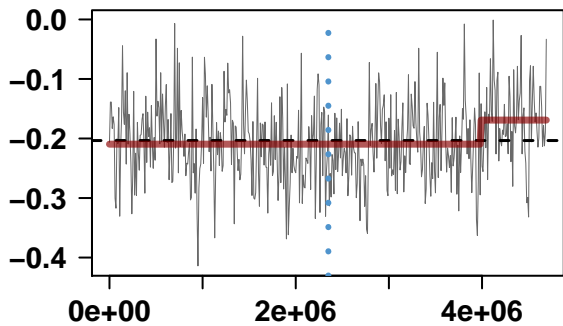


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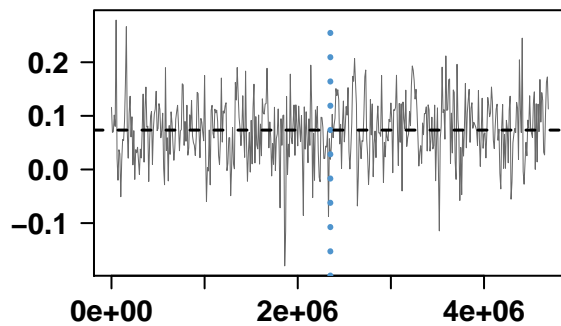


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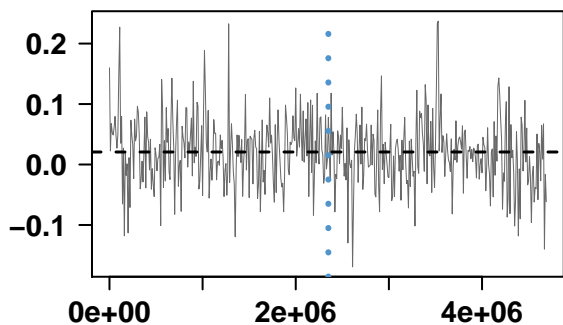
Escherichia coli O157:H7 str. Sakai



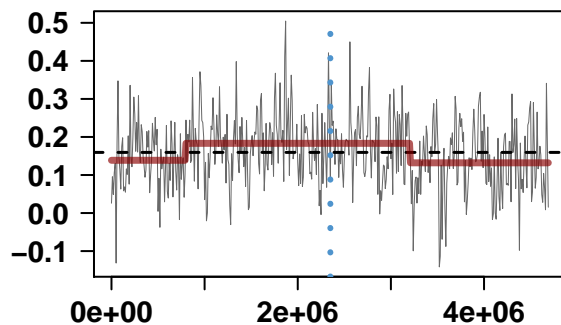
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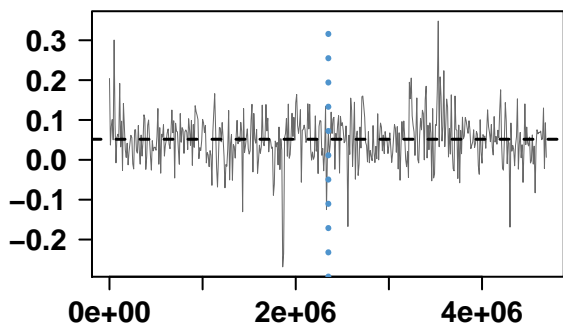
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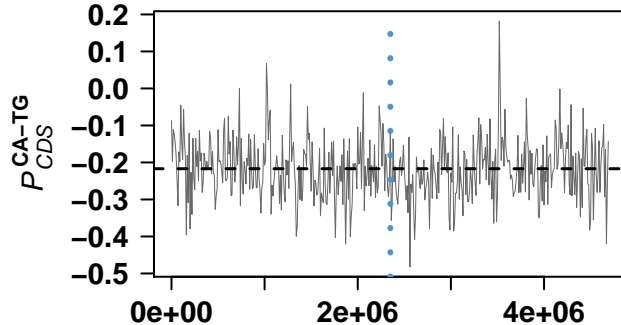
genome coordinates



genome coordinates

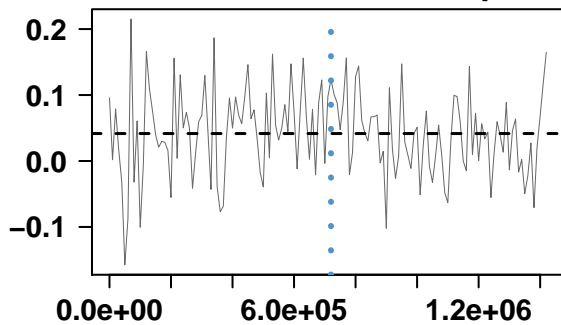


genome coordinates

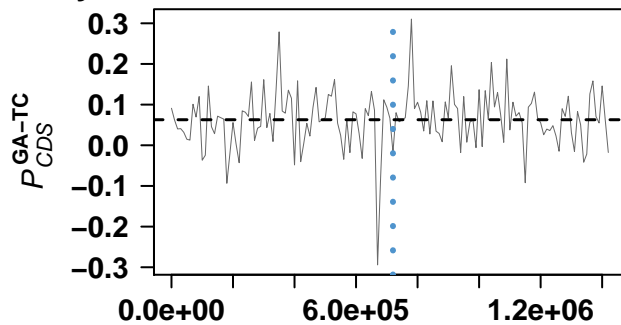


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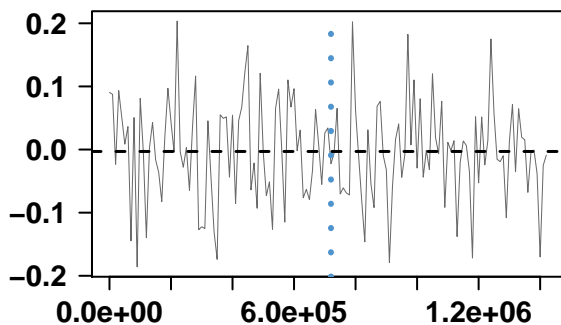
Haemophilus ducreyi 35000HP



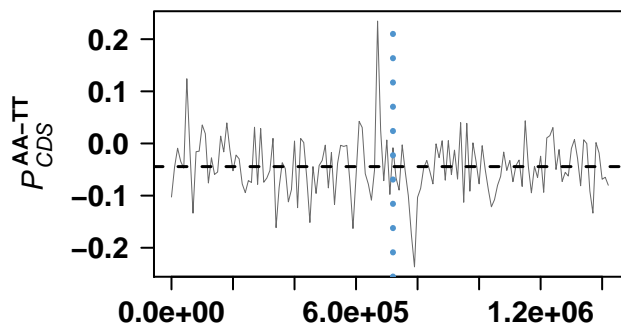
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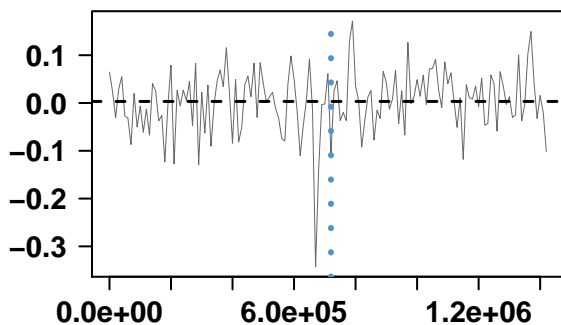
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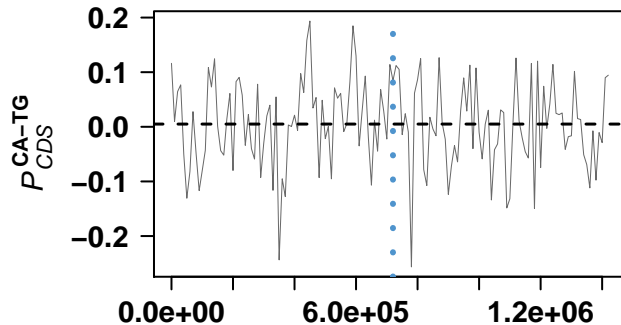
genome coordinates



genome coordinates

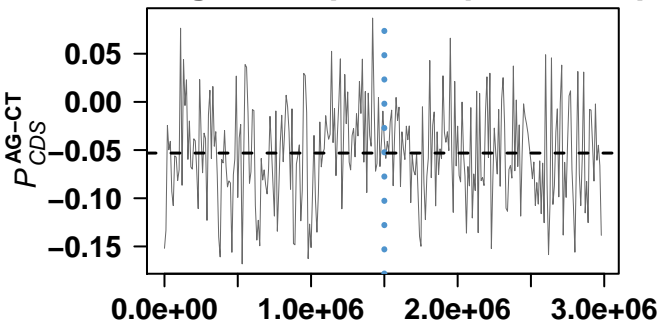


genome coordinates

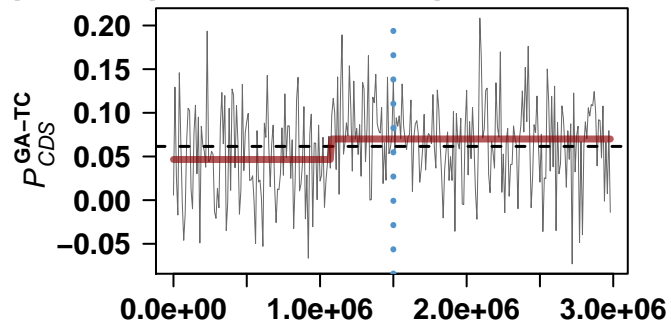


genome coordinates

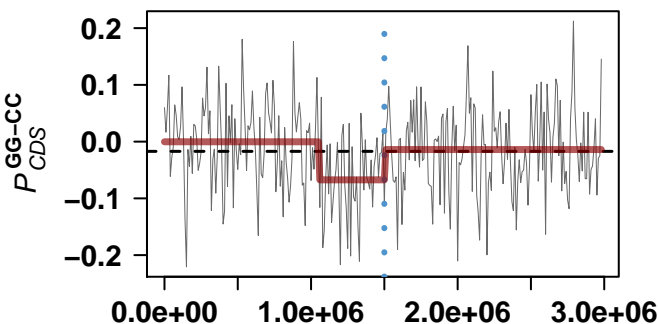
Legionella pneumophila subsp. pneumophila str. Philadelphia 1



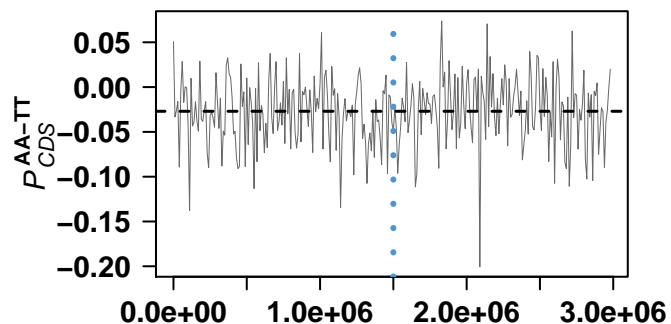
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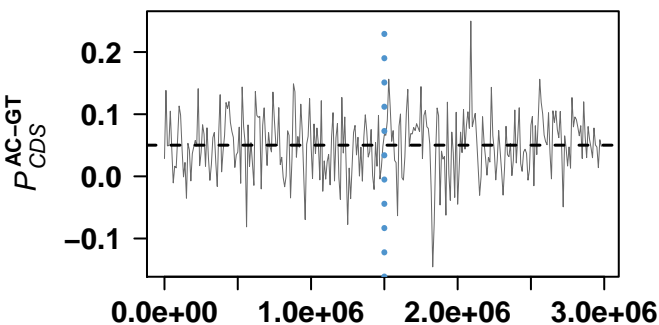
genome coordinates



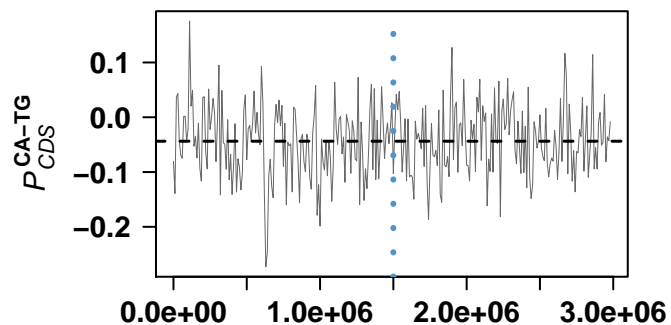
genome coordinates



genome coordinates

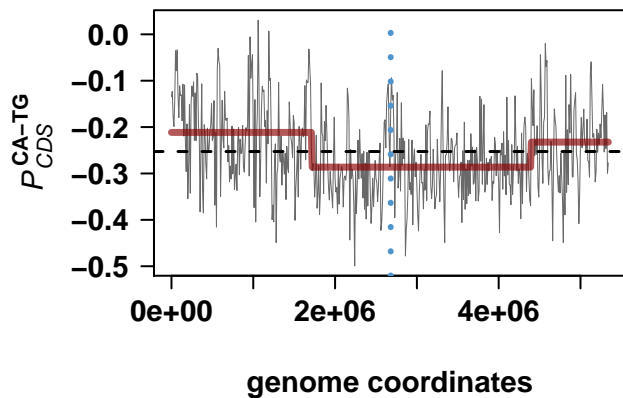
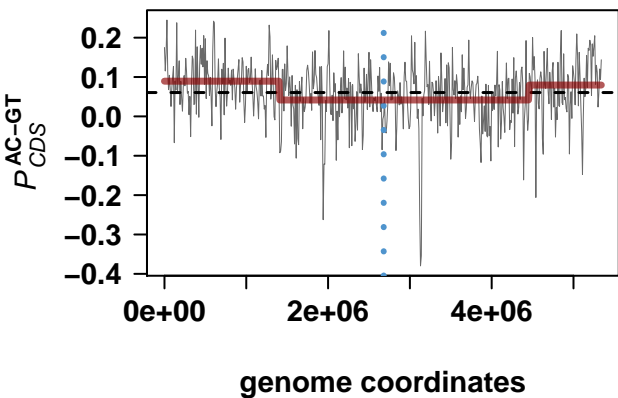
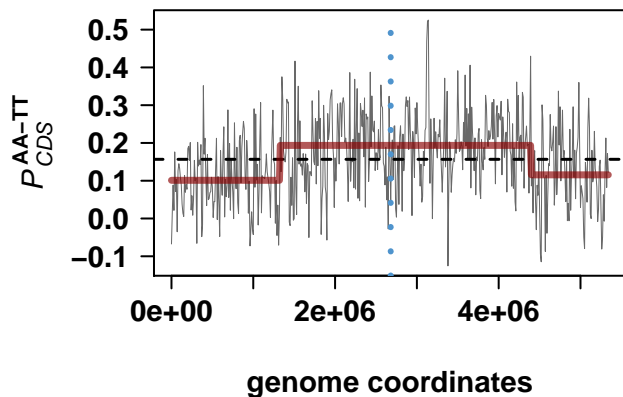
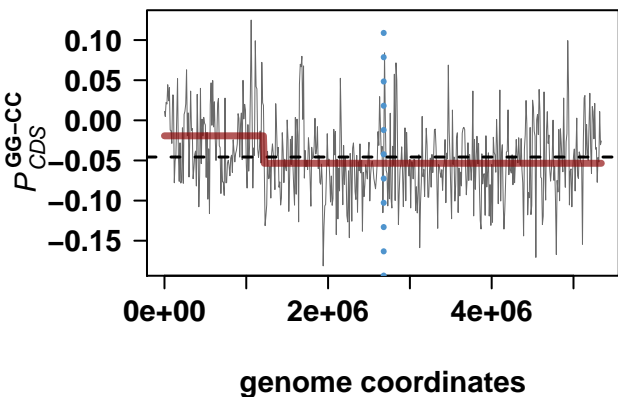
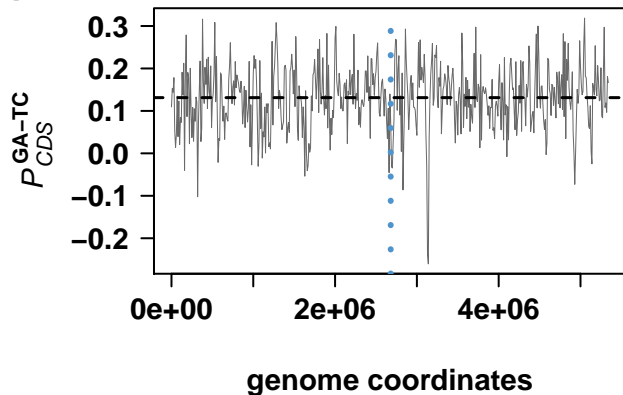
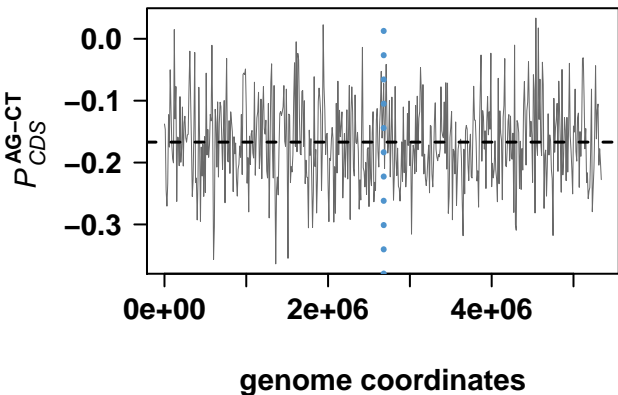


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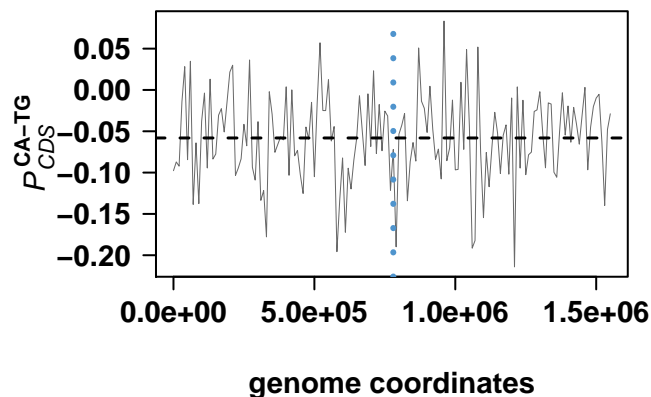
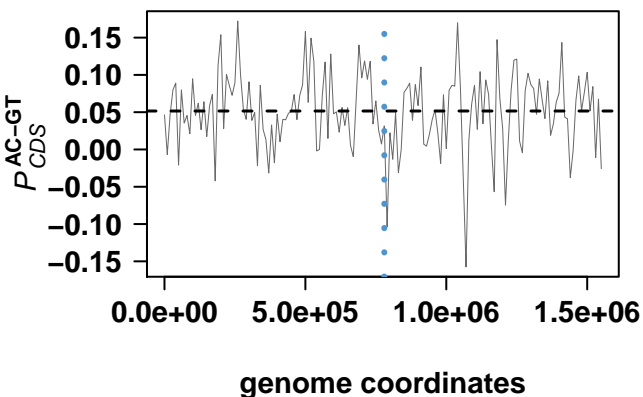
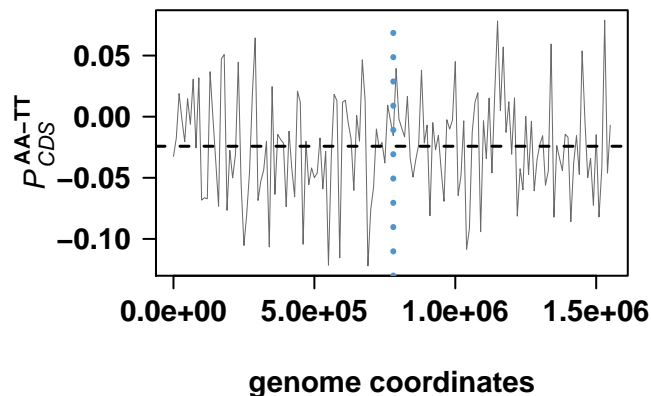
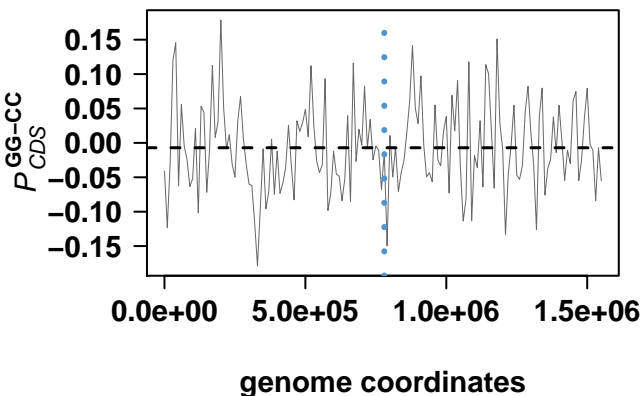
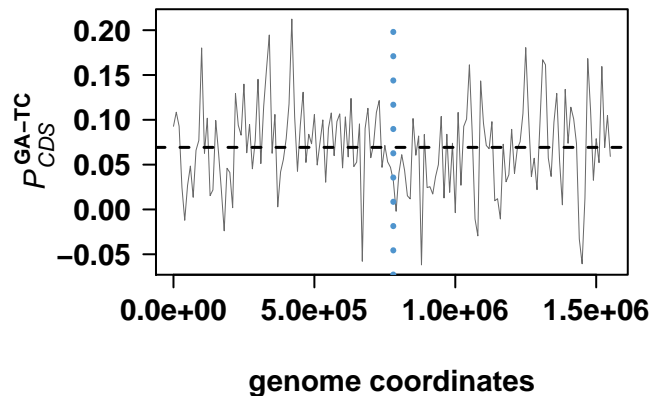
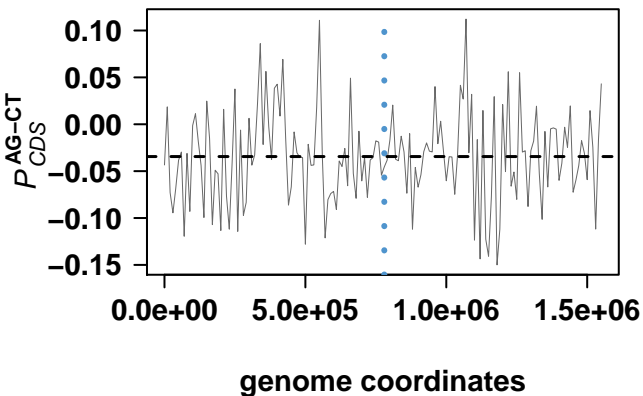


genome coordinates

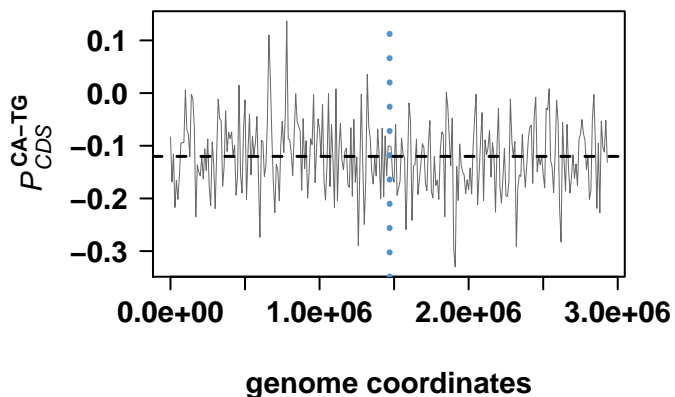
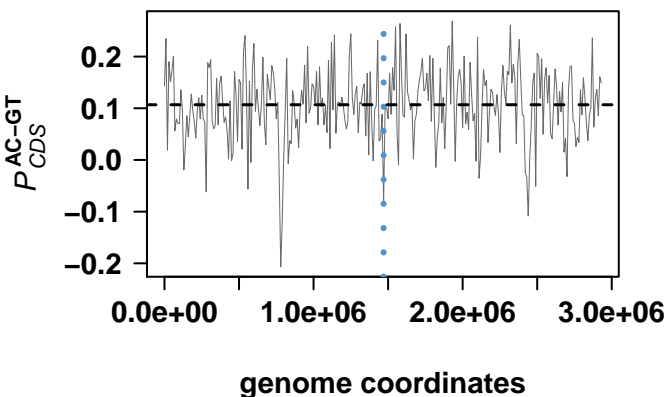
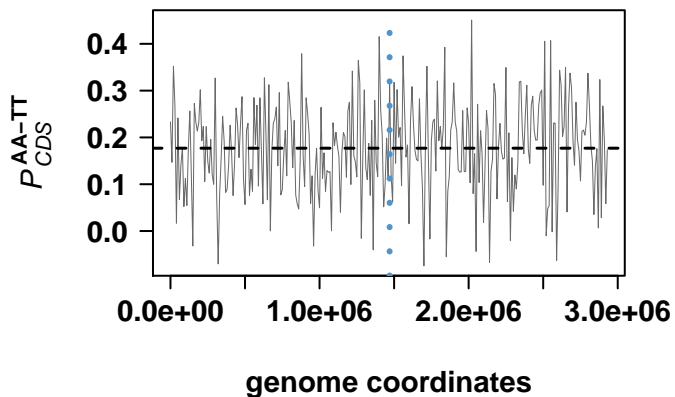
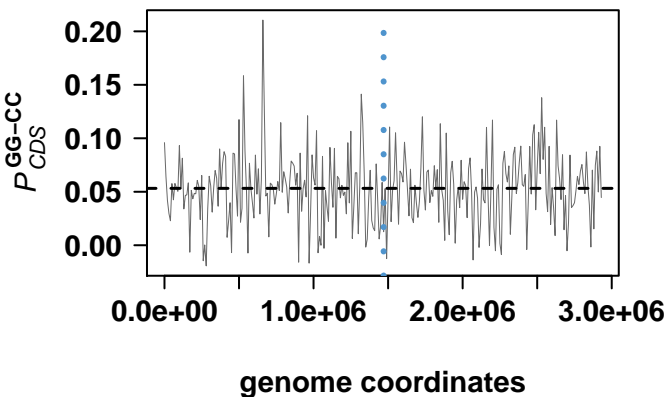
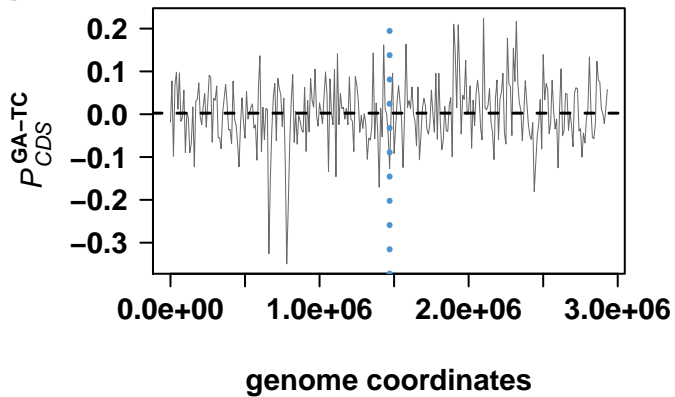
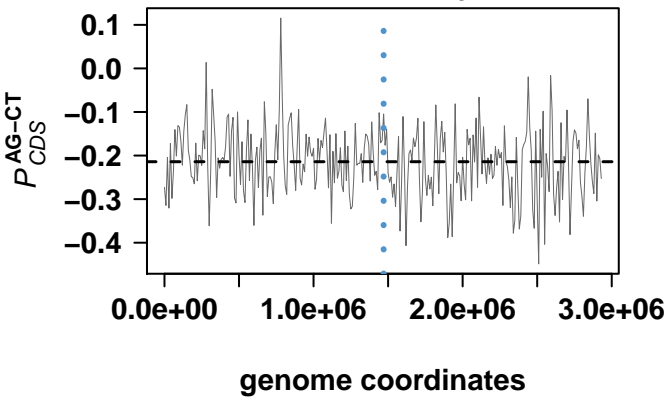
Pseudomonas putida KT2440



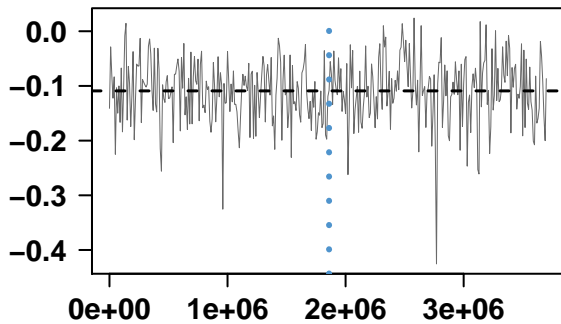
Coxiella burnetii RSA 493



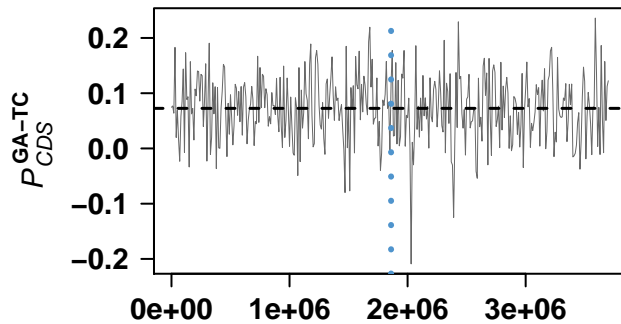
Methylococcus capsulatus str. Bath



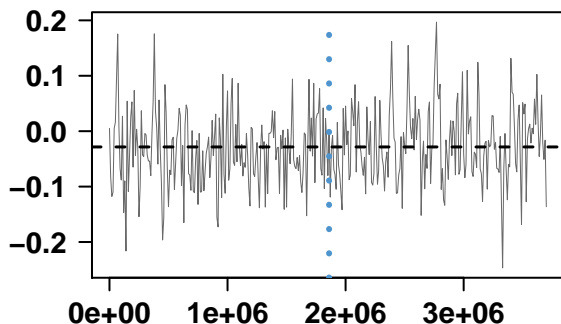
Yersinia pestis CO92



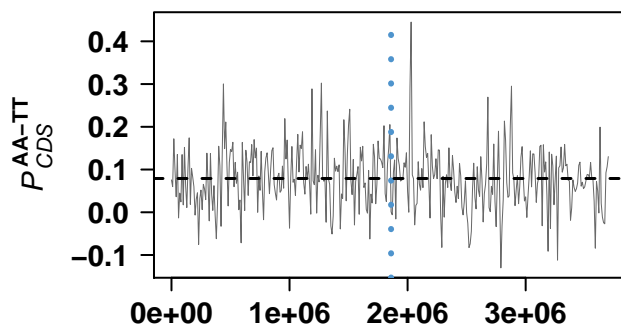
genome coordinates



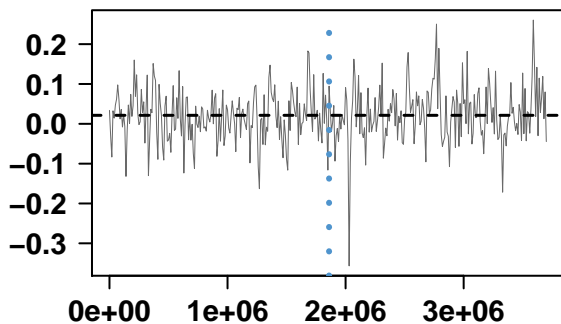
genome coordinates



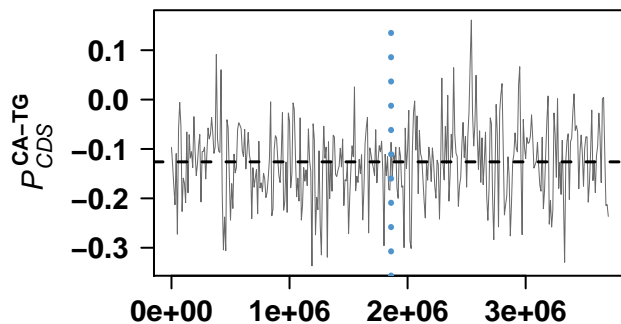
genome coordinates



genome coordinates

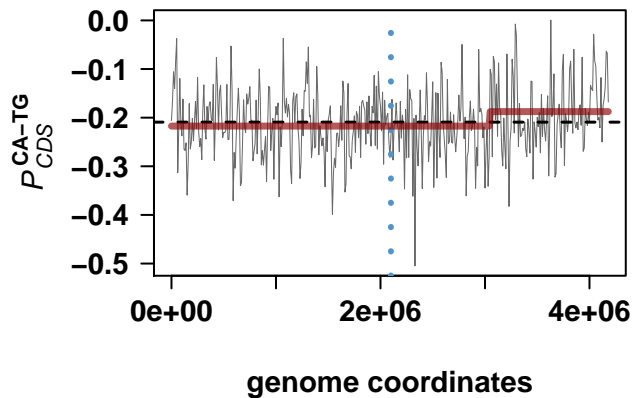
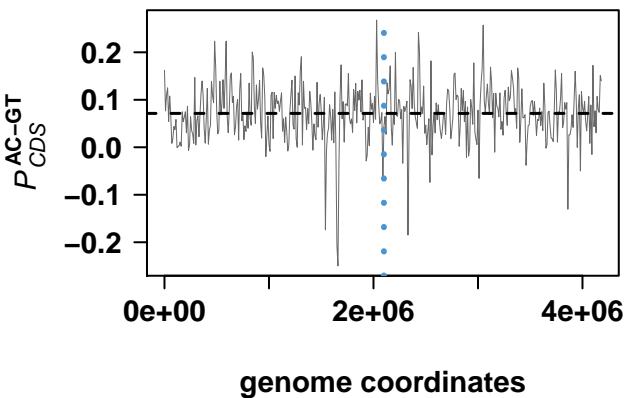
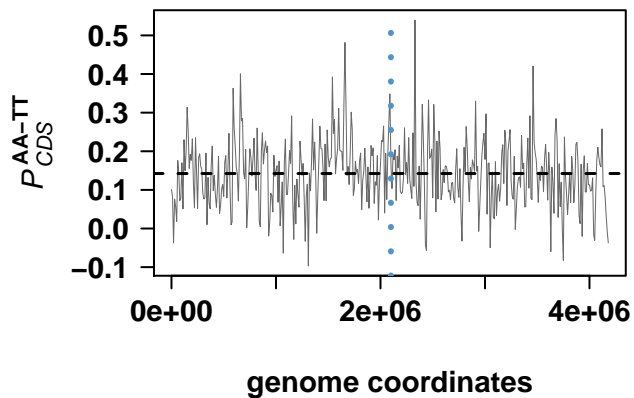
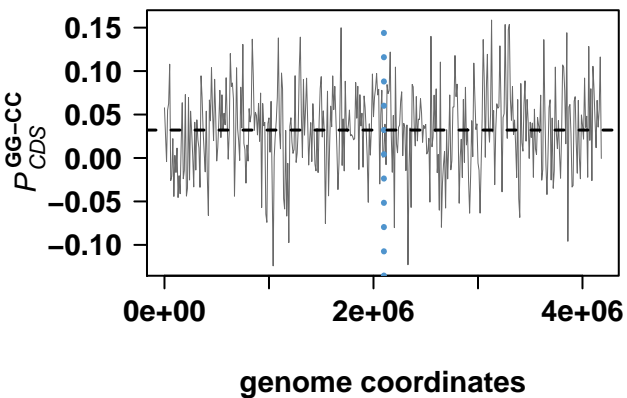
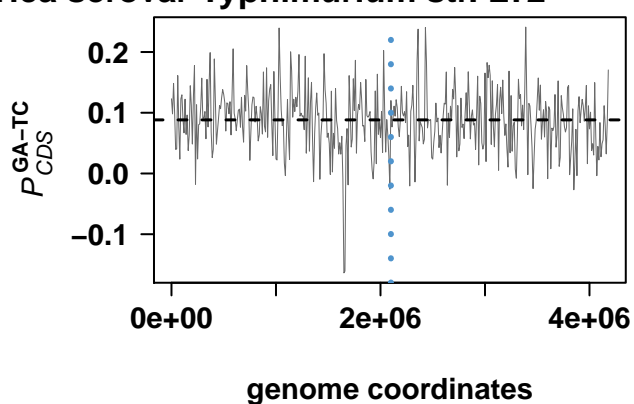
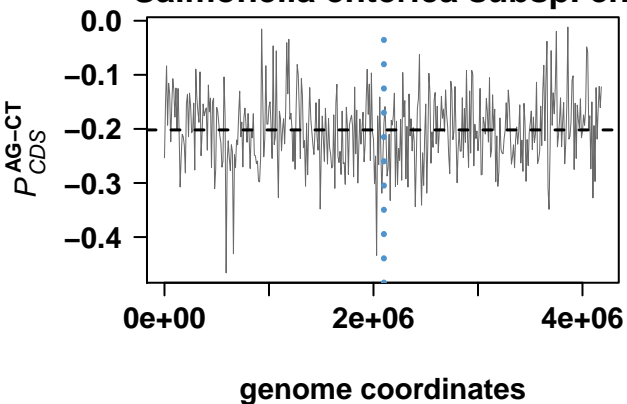


genome coordinates

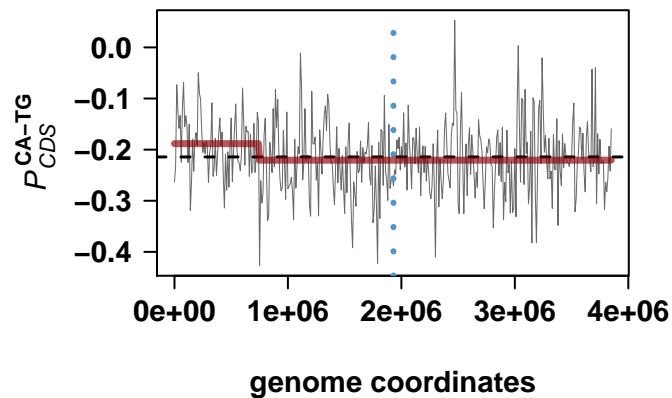
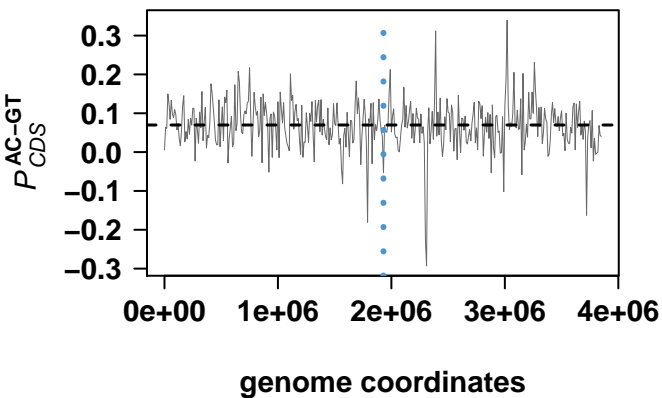
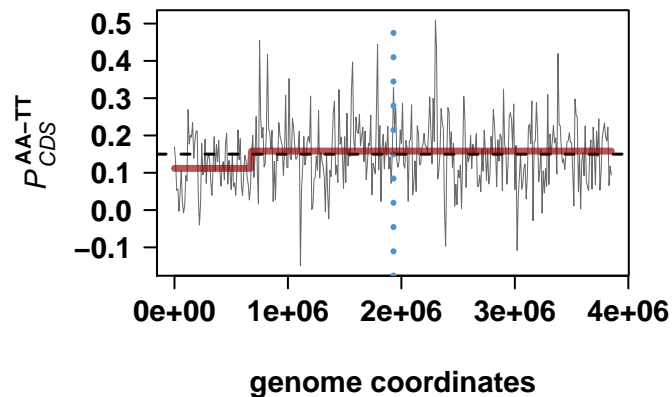
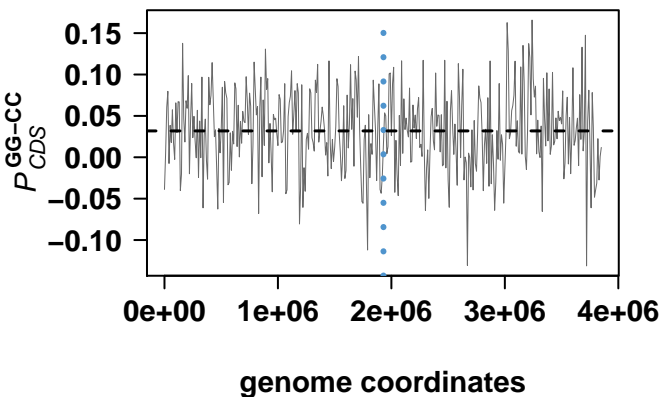
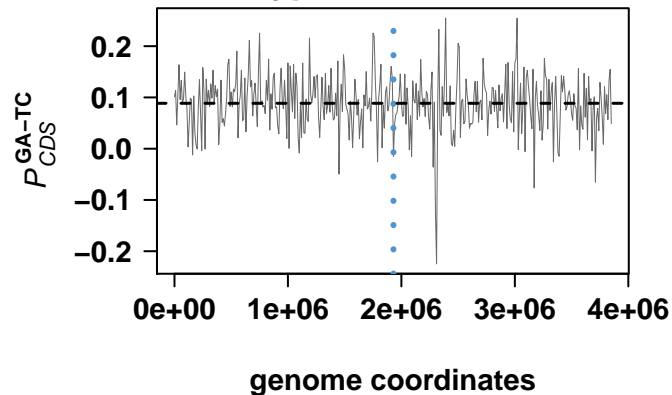
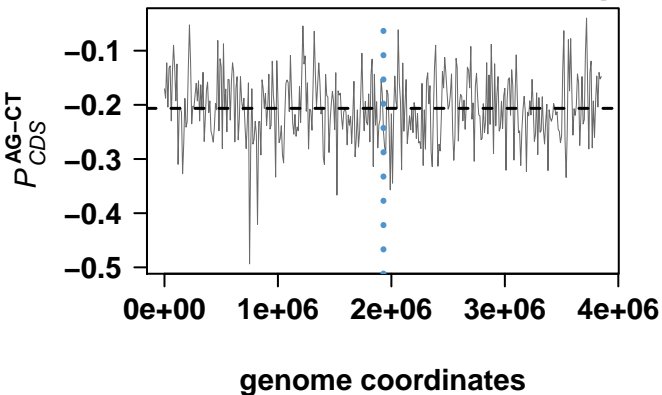


genome coordinates

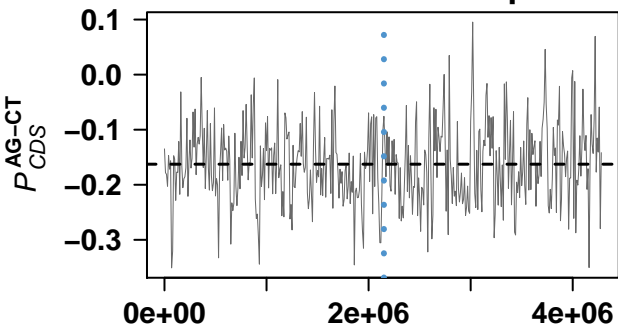
Salmonella enterica subsp. enterica serovar Typhimurium str. LT2



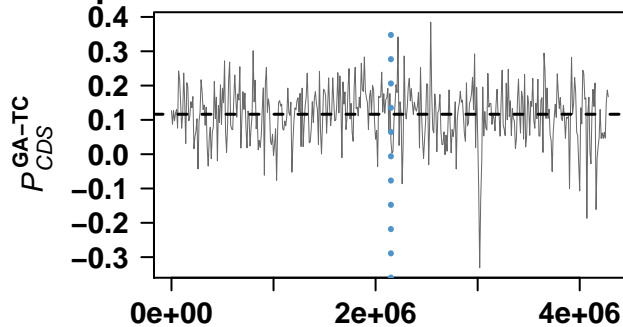
Salmonella enterica subsp. enterica serovar Typhi str. CT18



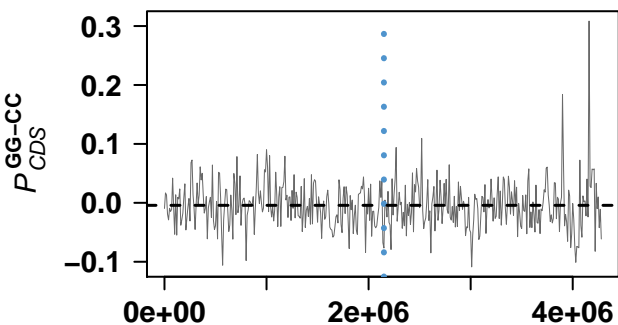
Xanthomonas campestris pv. *campestris* str. ATCC 33913



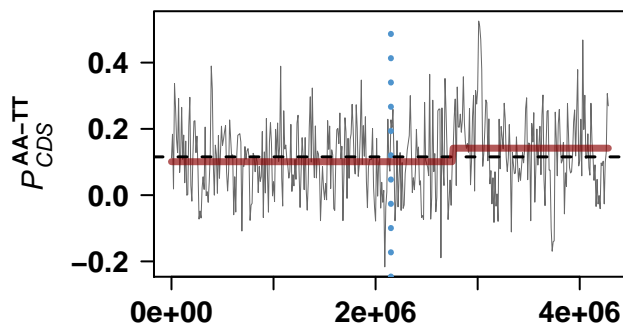
genome coordinates



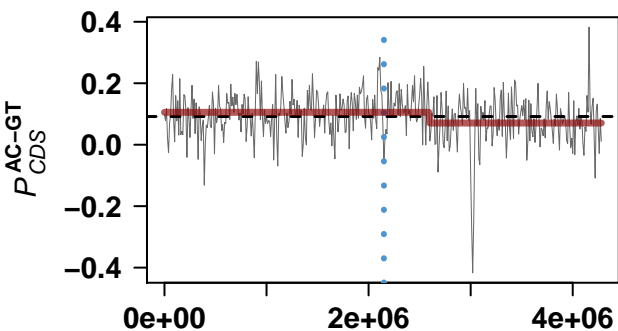
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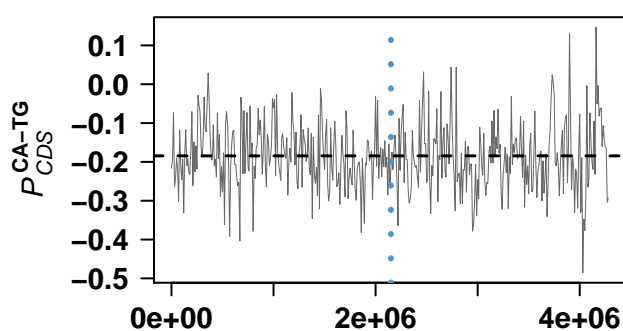
genome coordinates



genome coordinates

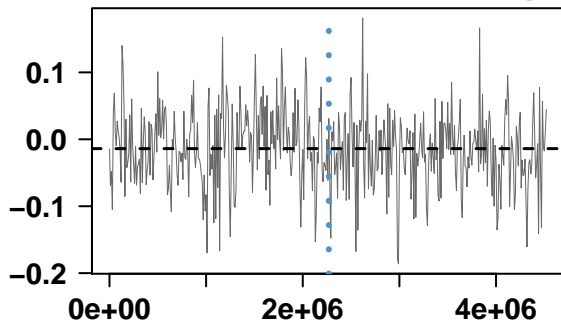


genome coordinates

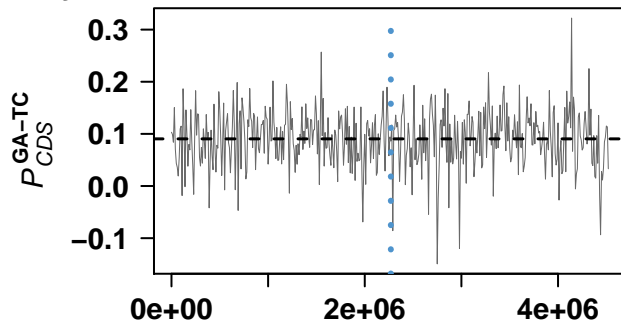


genome coordinates

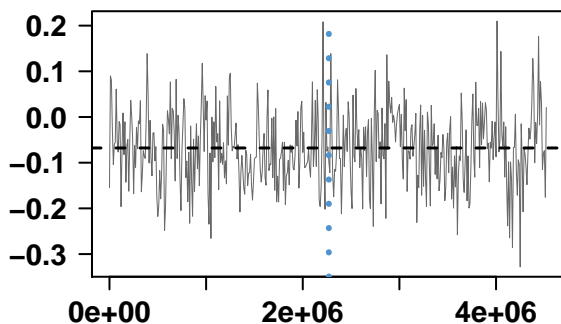
Colwellia psychrerythraea 34H



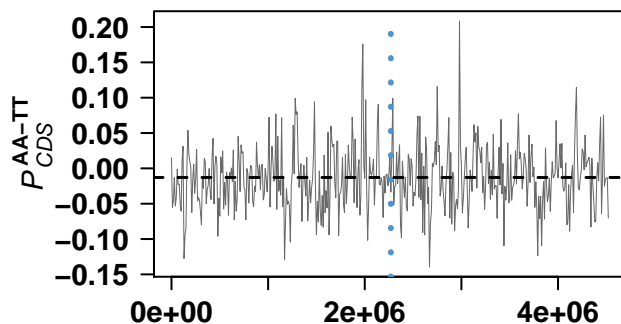
genome coordinates



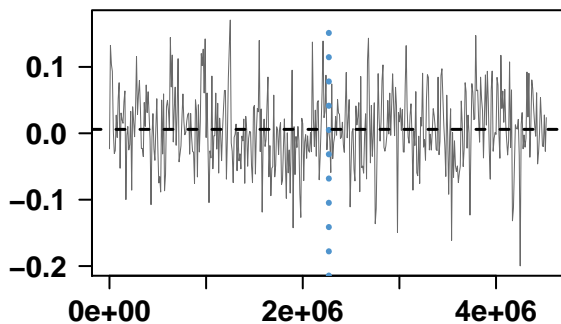
genome coordinates



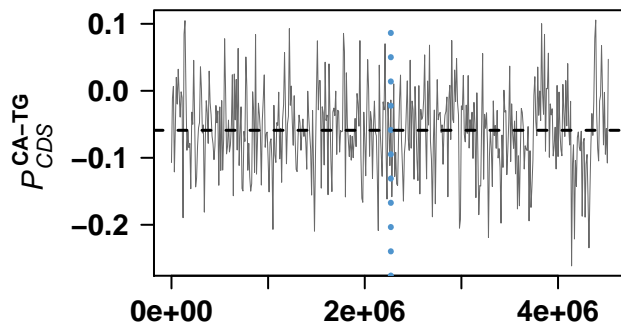
genome coordinates



genome coordinates

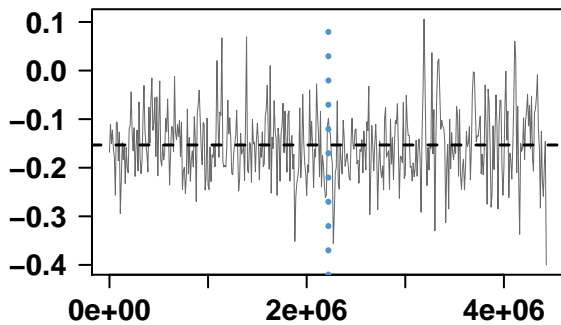


genome coordinates

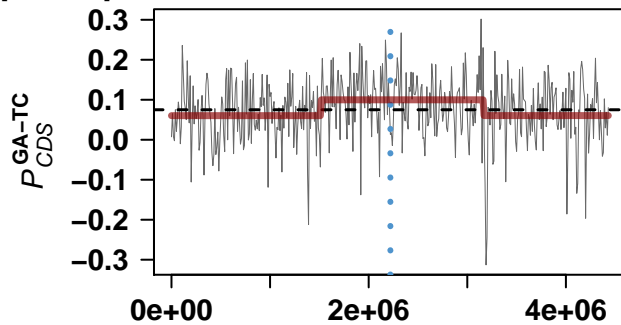


genome coordinates

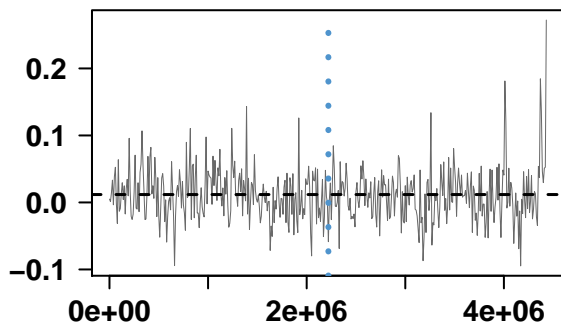
Xanthomonas axonopodis pv. citri str. 306



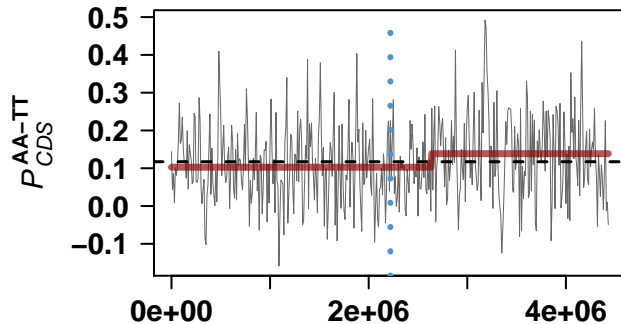
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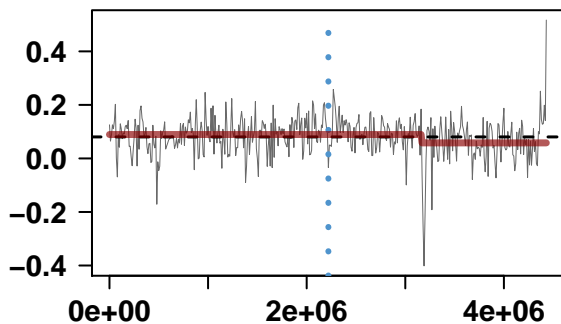
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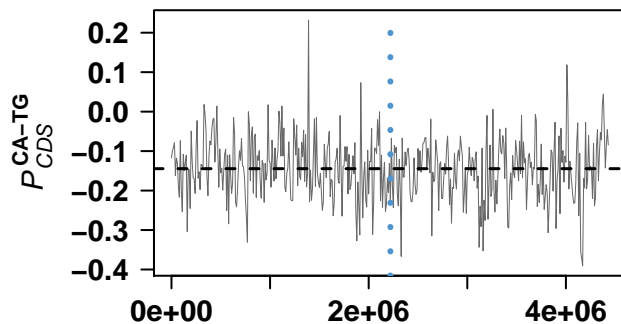
genome coordinates



genome coordinates

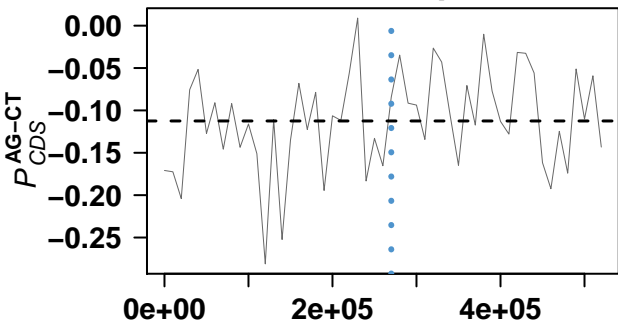


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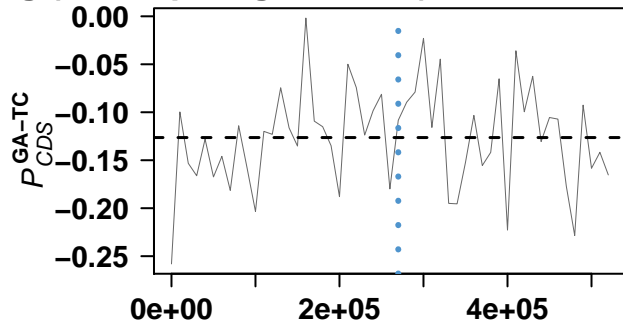


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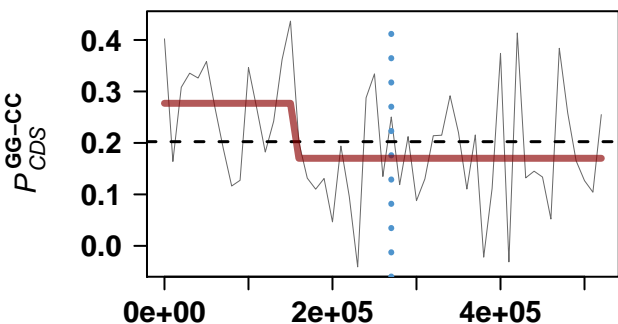
Buchnera aphidicola str. Sg (Schizaphis graminum)



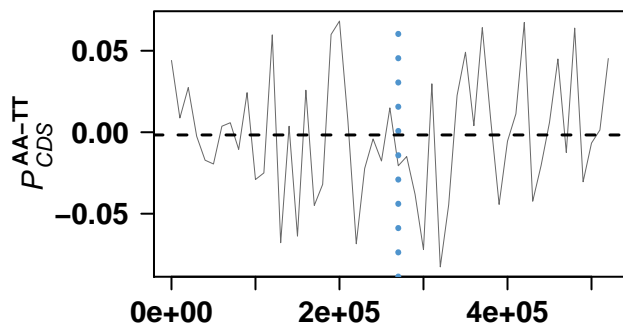
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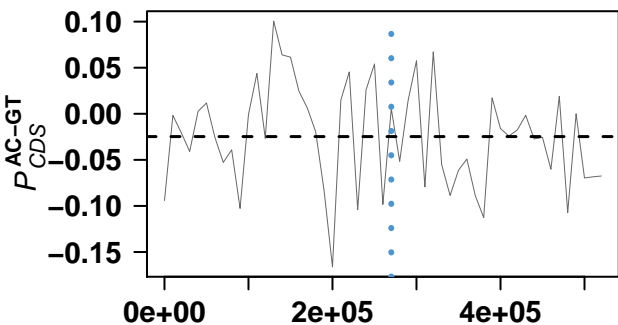
genome coordinates



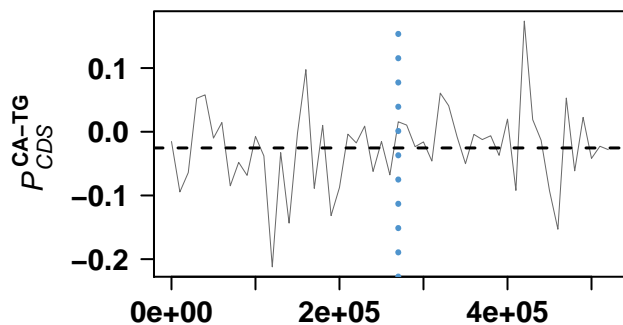
genome coordinates



genome coordinates

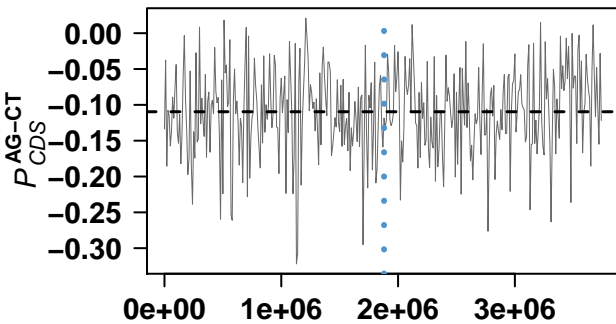


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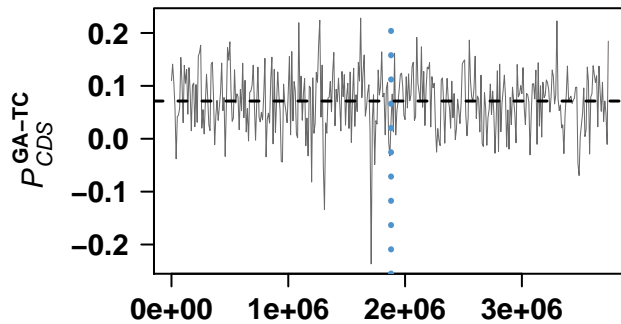


genome coordinates

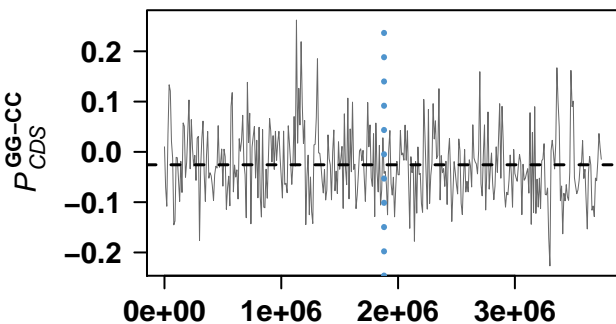
Yersinia pestis KIM10+



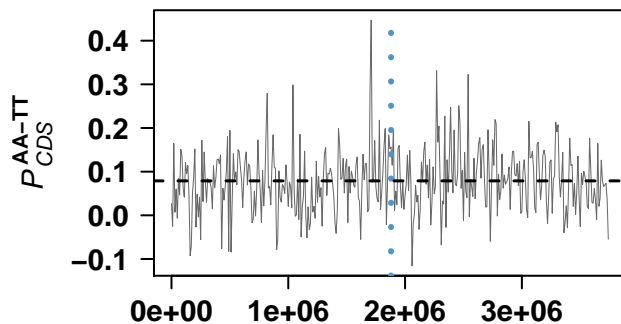
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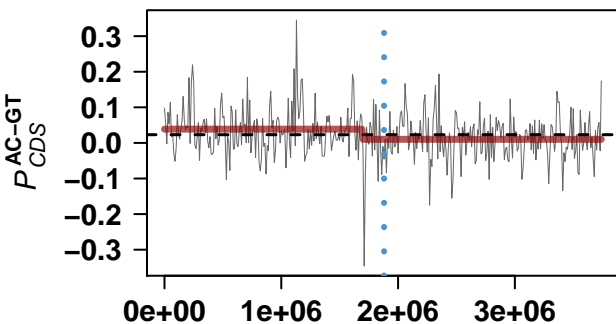
genome coordinates



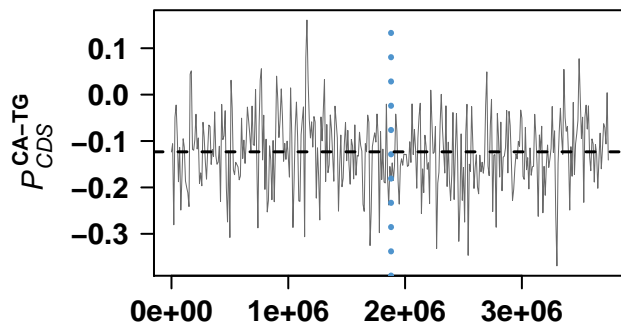
genome coordinates



genome coordinates

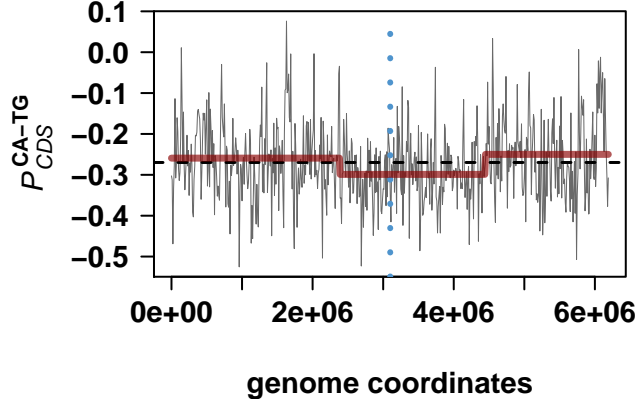
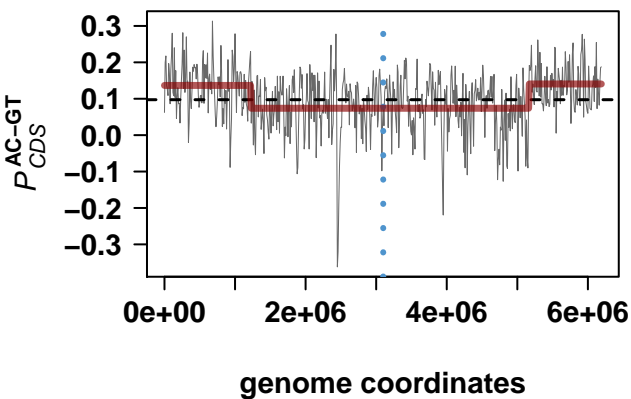
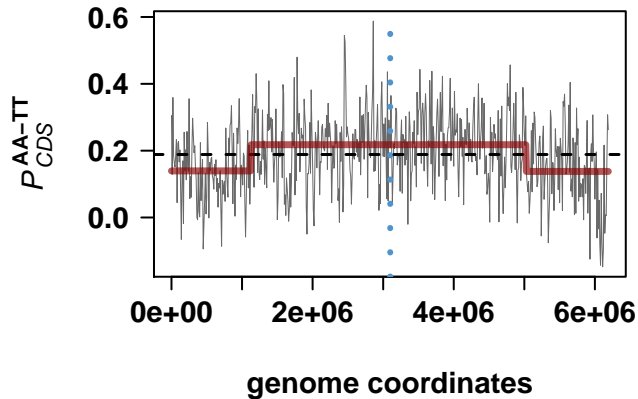
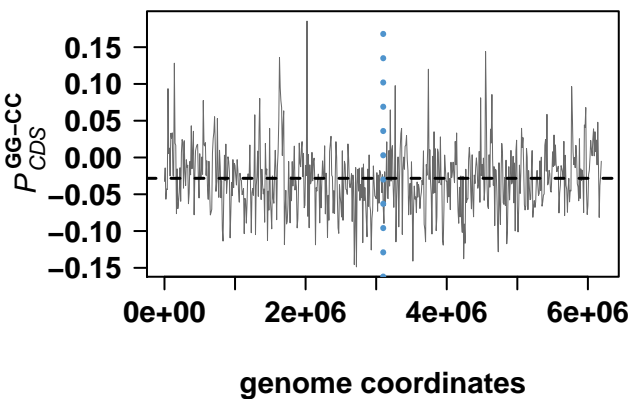
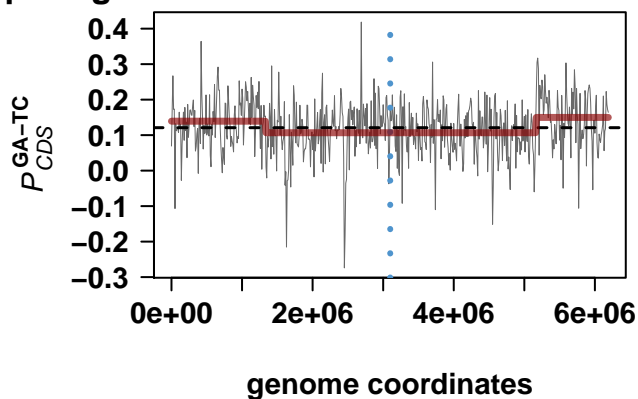
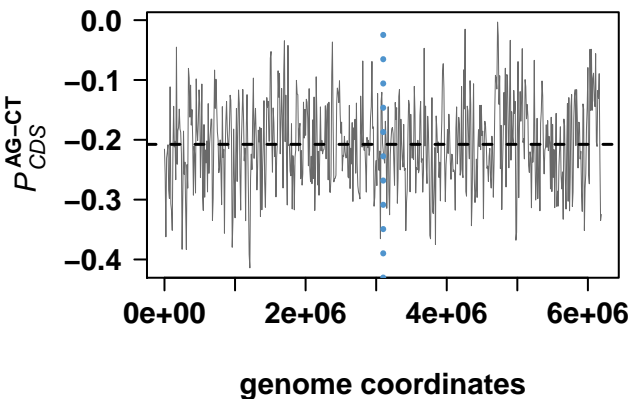


genome coordinates

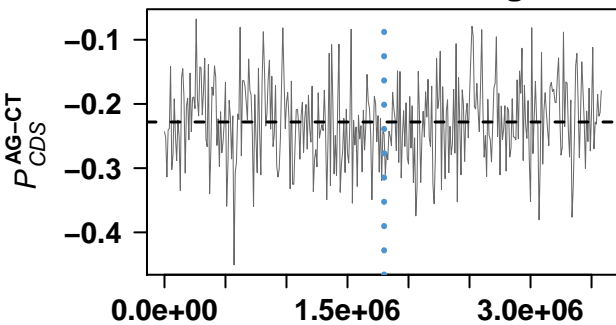


genome coordinates

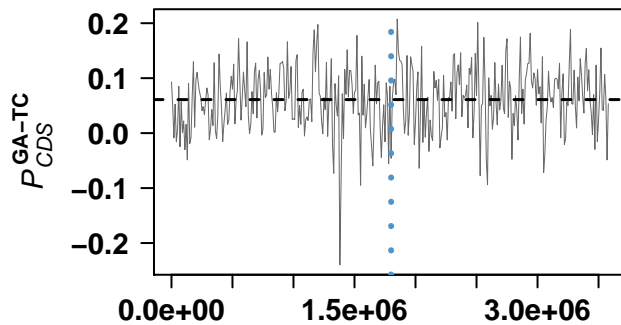
Pseudomonas protegens Pf-5



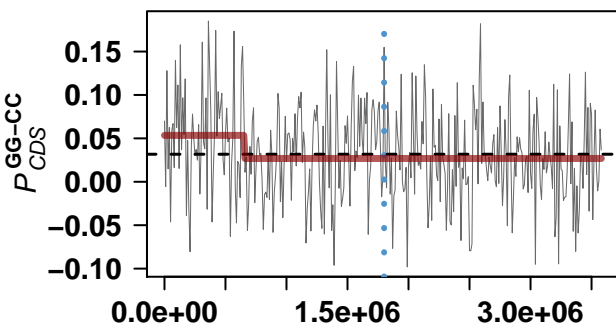
Shigella flexneri 2a str. 301



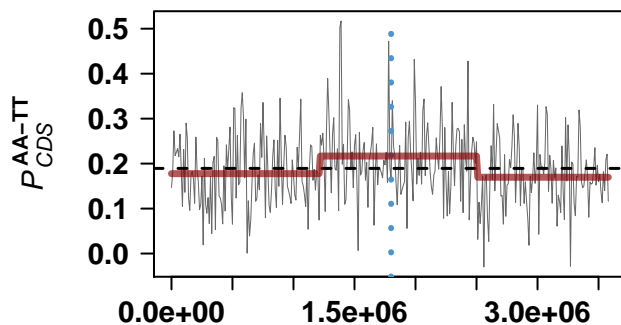
genome coordinates



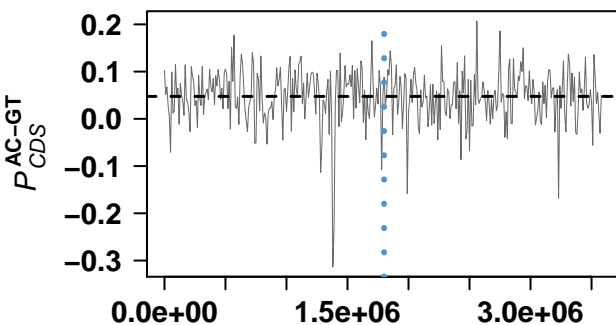
genome coordinates



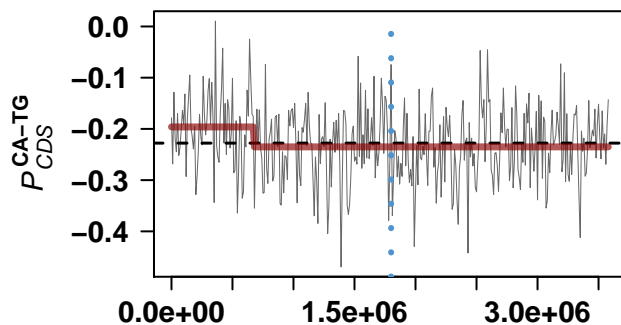
genome coordinates



genome coordinates

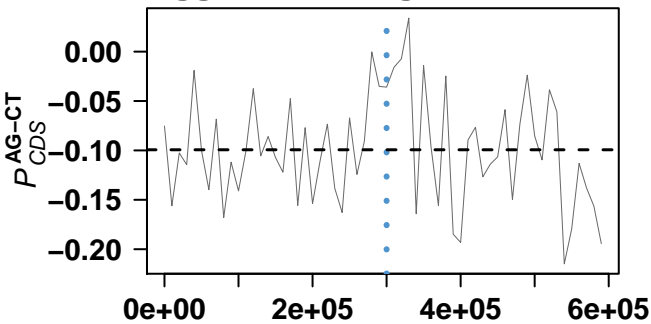


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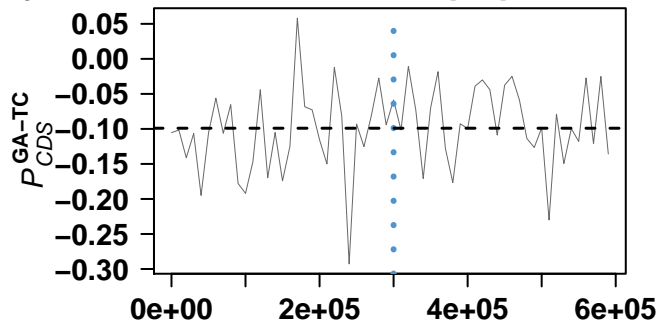


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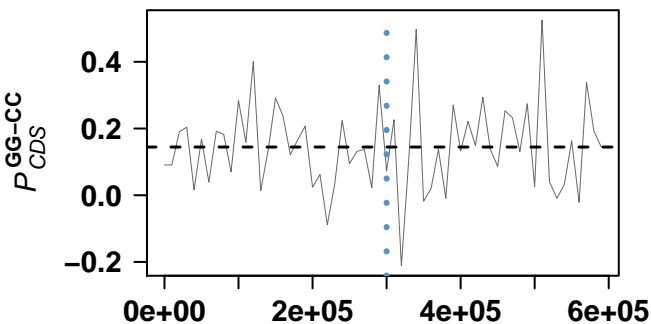
Wigglesworthia glossinidia endosymbiont of Glossina brevipalpis



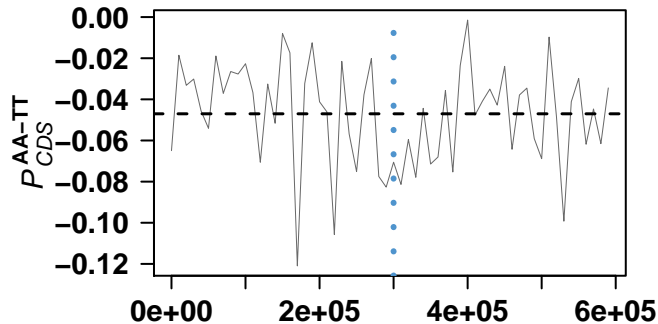
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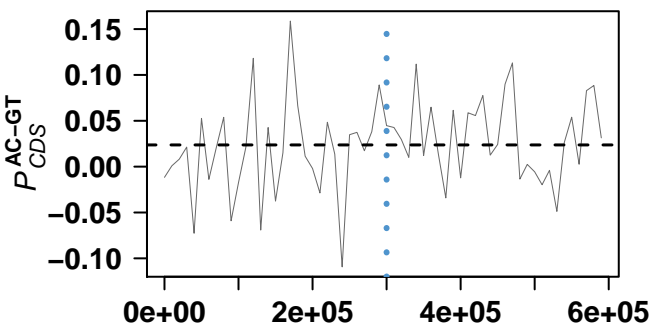
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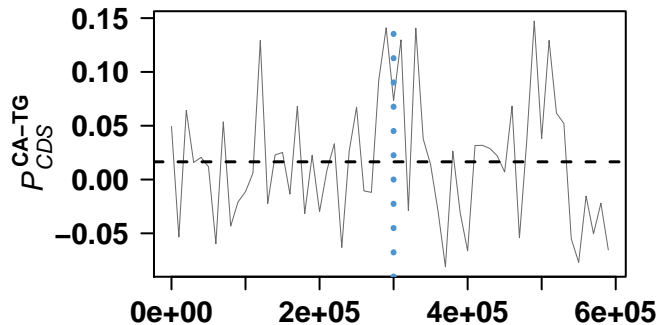
genome coordinates



genome coordinates

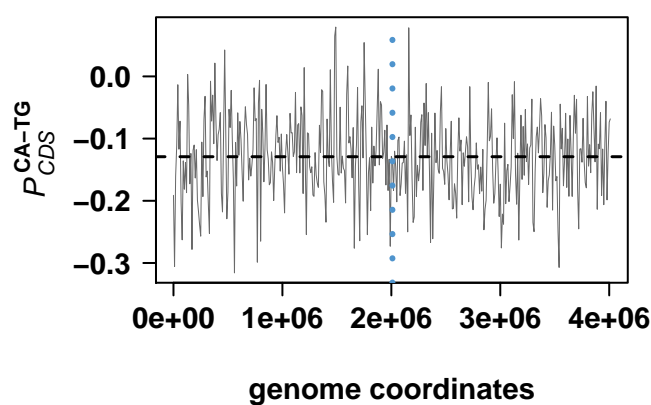
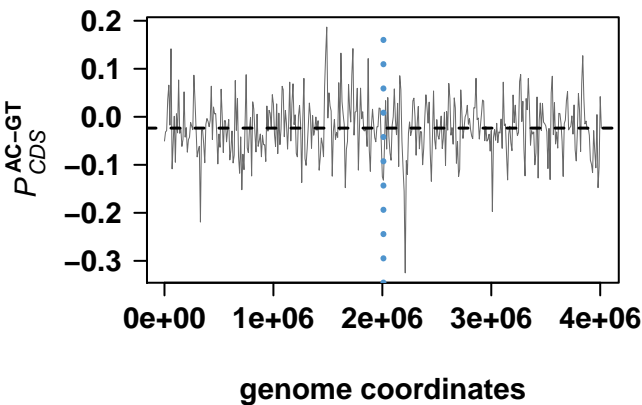
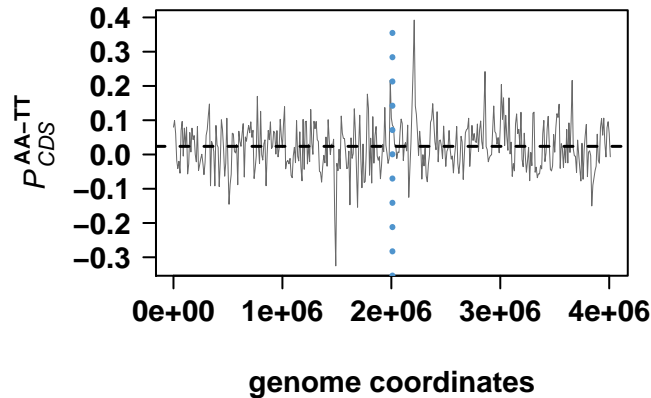
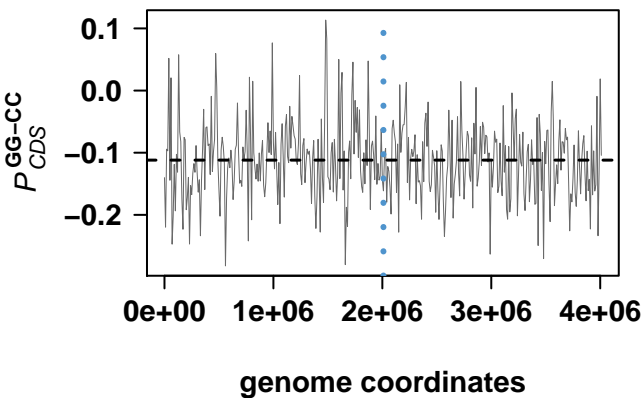
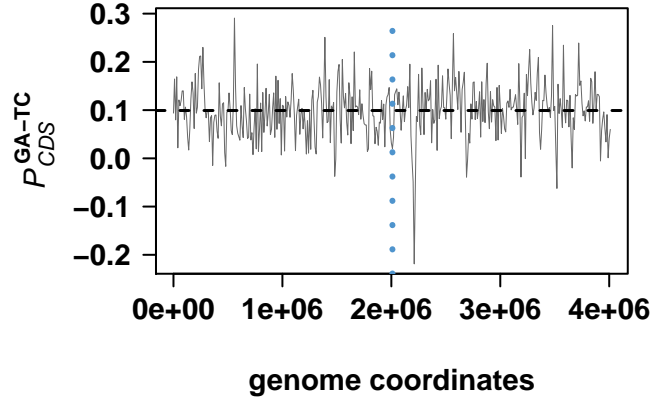
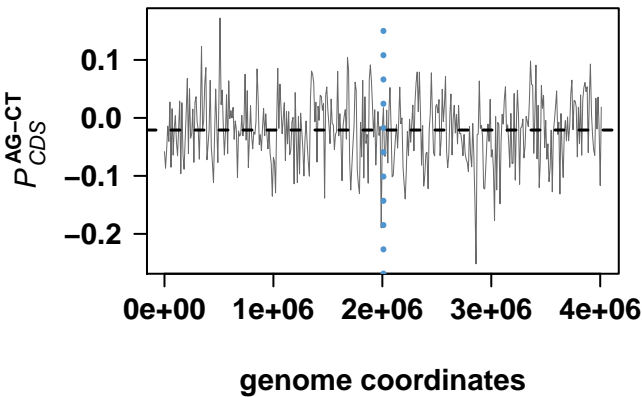


genome coordinates

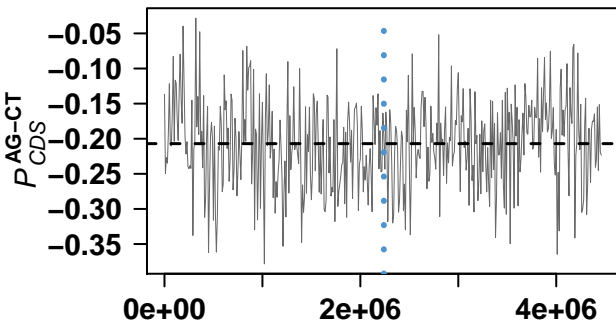


genome coordinates

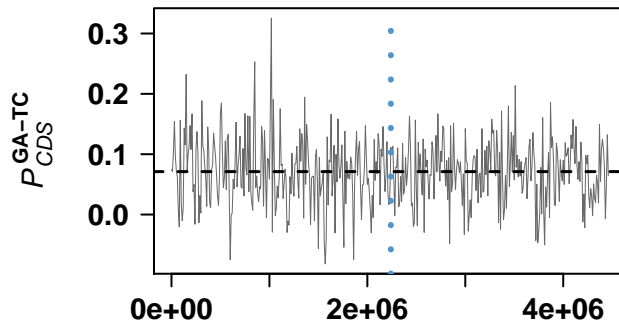
Shewanella oneidensis MR-1



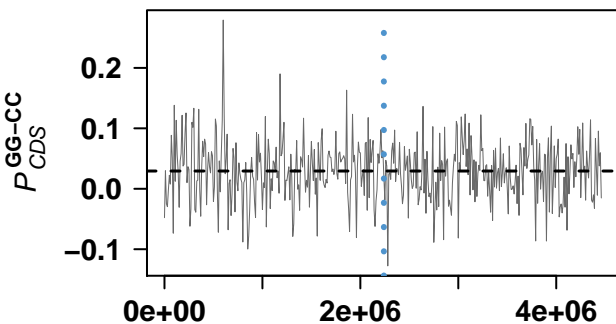
Escherichia coli CFT073



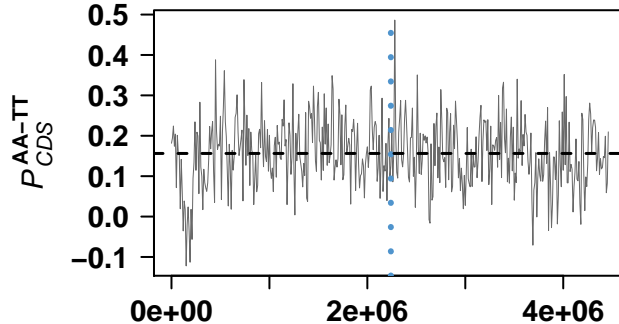
genome coordinates



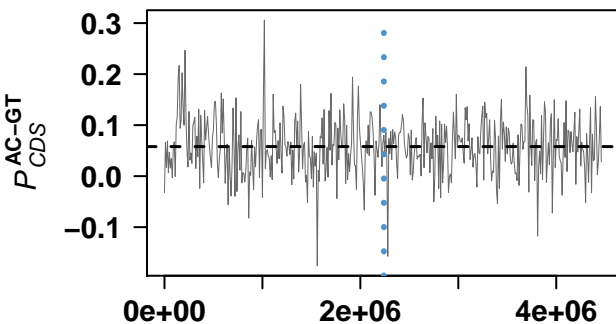
genome coordinates



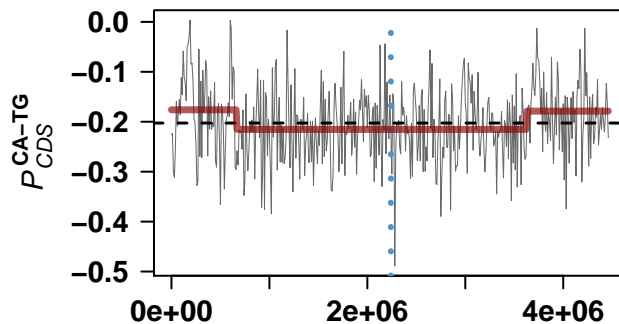
genome coordinates



genome coordinates

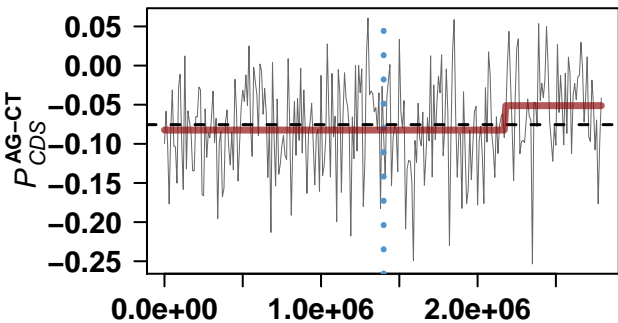


genome coordinates

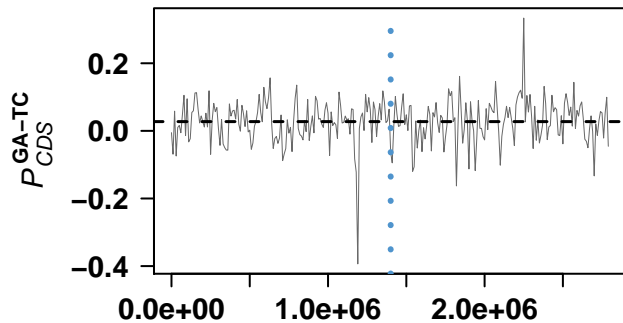


genome coordinates

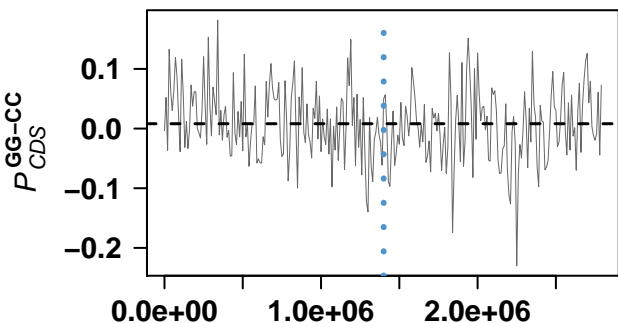
Vibrio vulnificus CMCP6



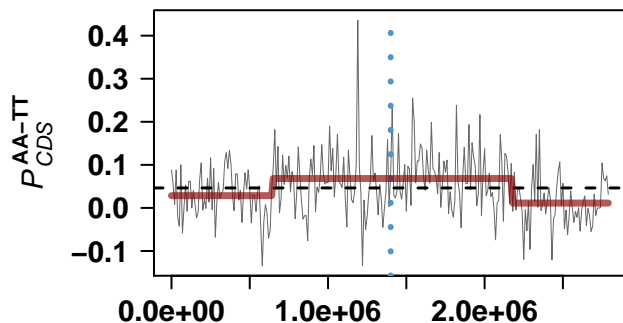
genome coordinates



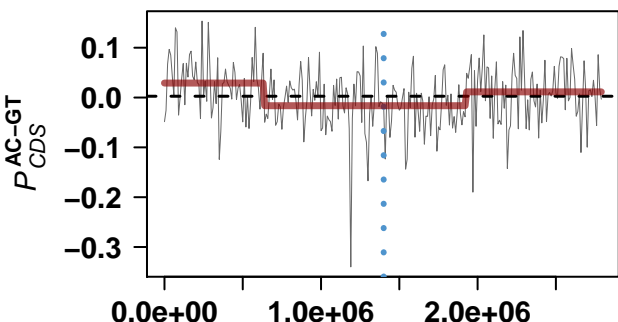
genome coordinates



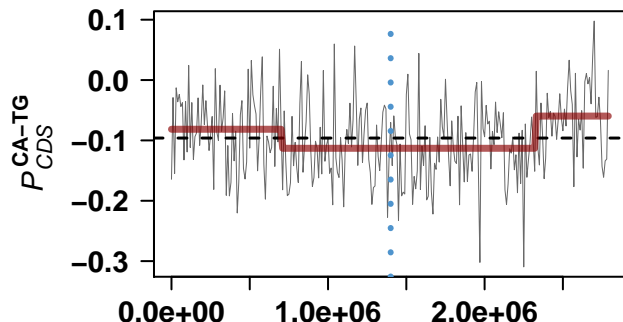
genome coordinates



genome coordinates

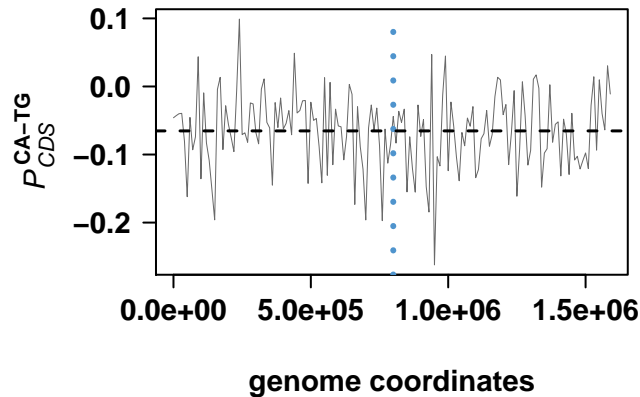
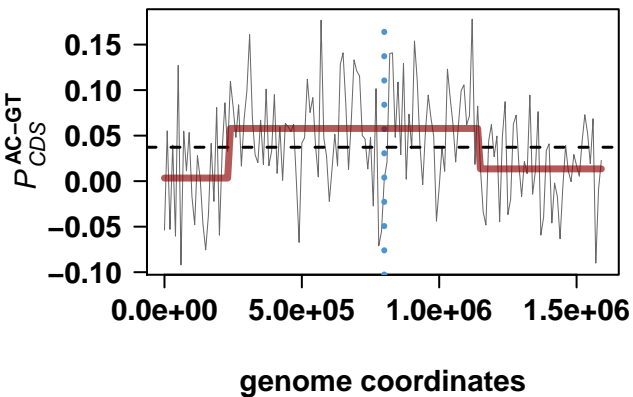
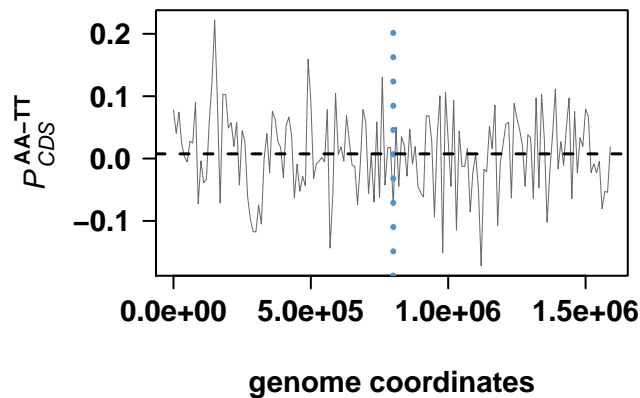
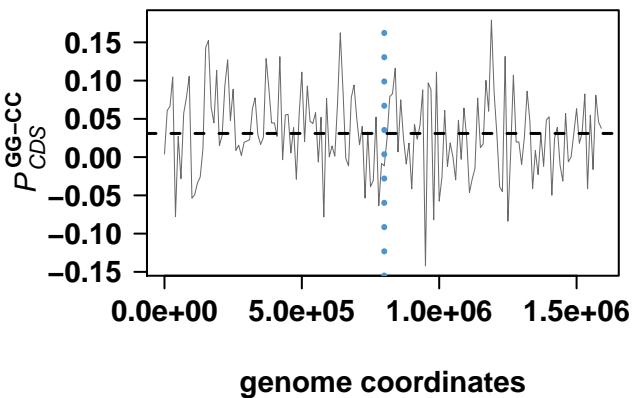
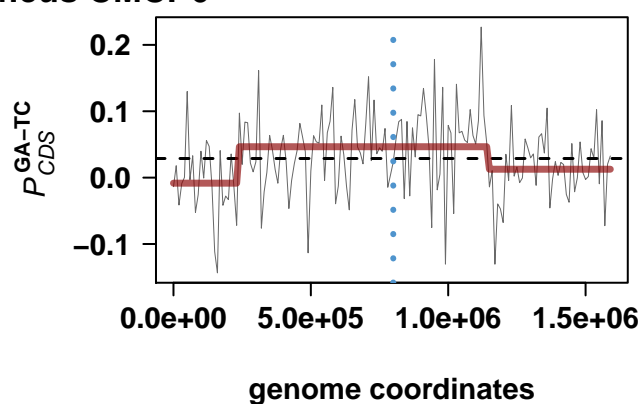
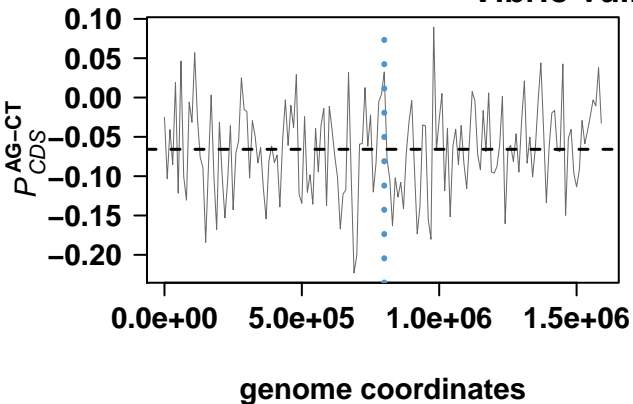


genome coordinates

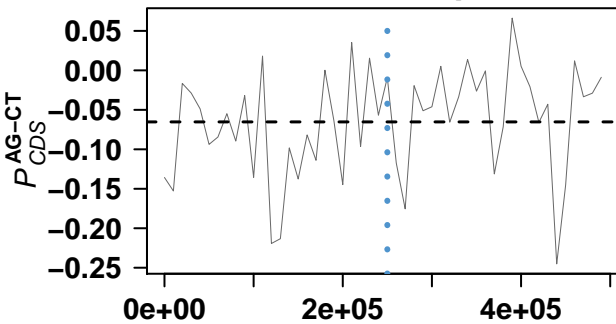


genome coordinates

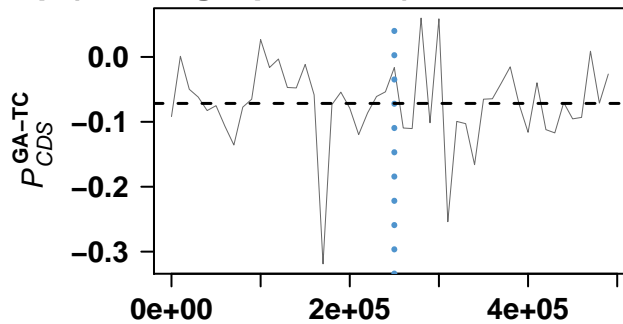
Vibrio vulnificus CMCP6



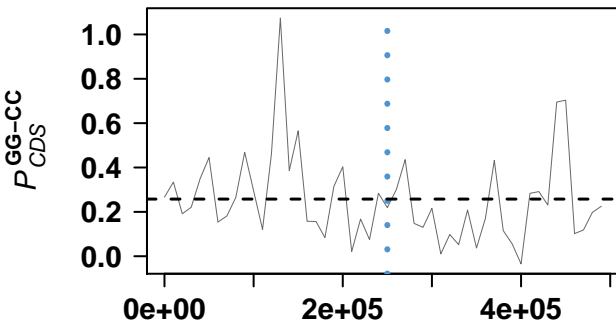
Buchnera aphidicola str. Bp (Baizongia pistaciae)



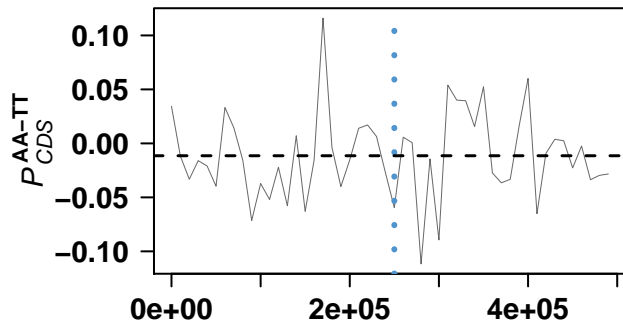
genome coordinates



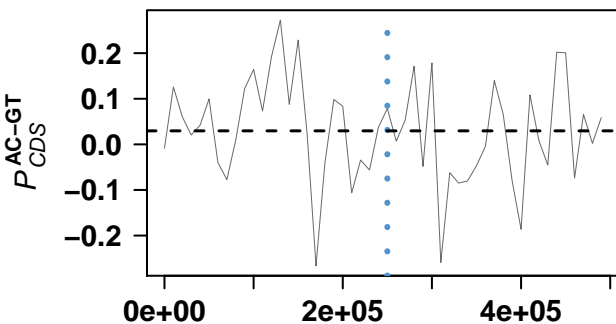
genome coordinates



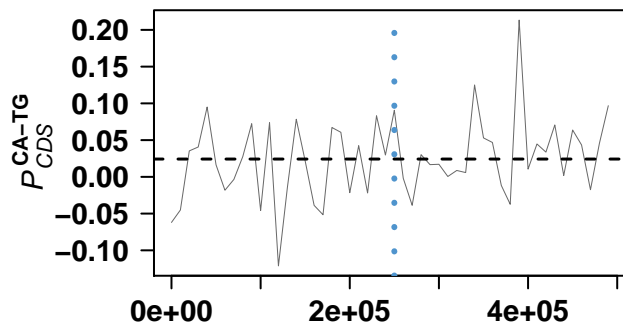
genome coordinates



genome coordinates

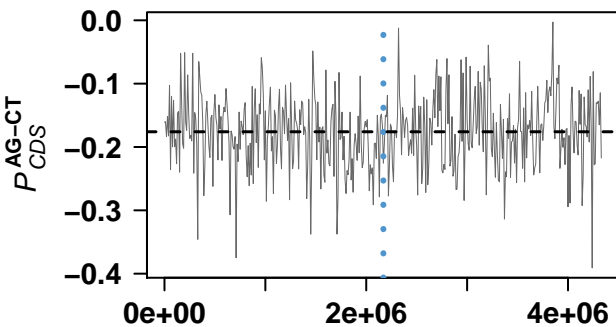


genome coordinates

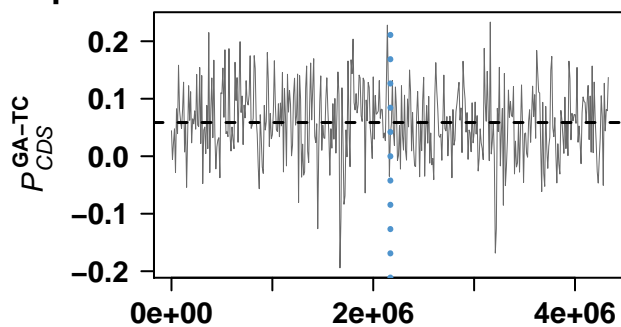


genome coordinates

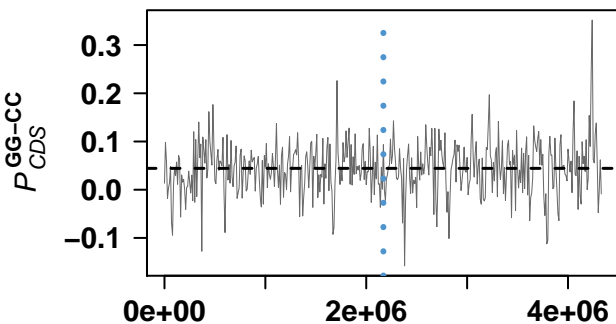
Pectobacterium atrosepticum SCRI1043



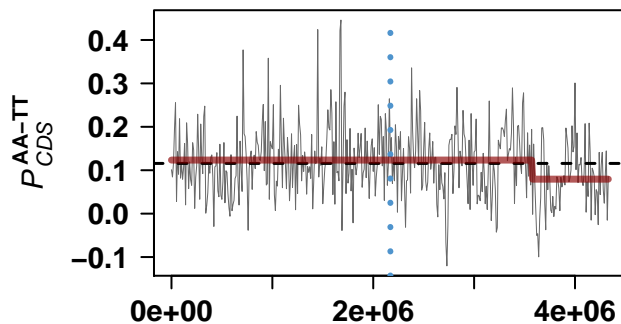
genome coordinates



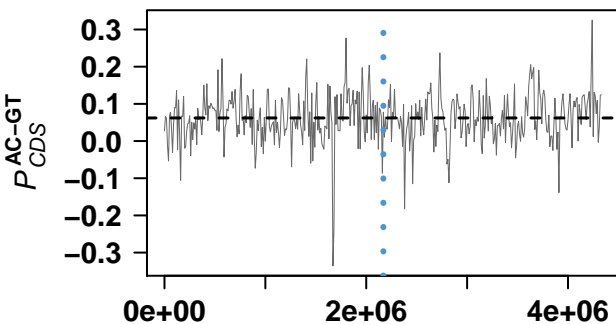
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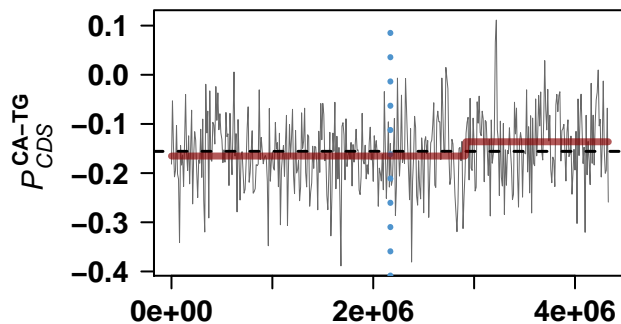
genome coordinates



genome coordinates

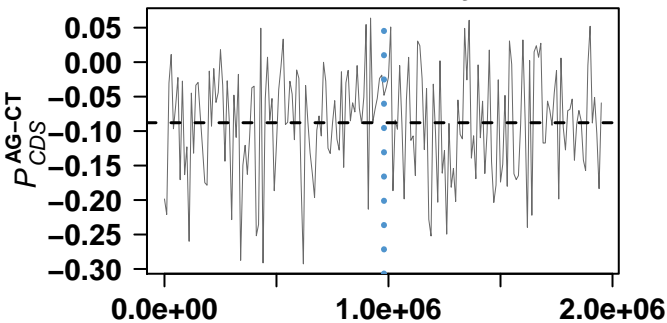


genome coordinates

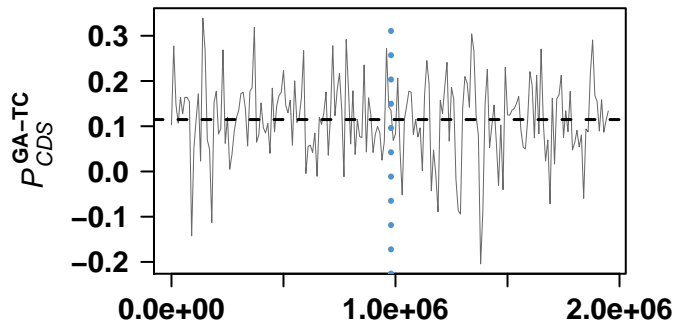


genome coordinates

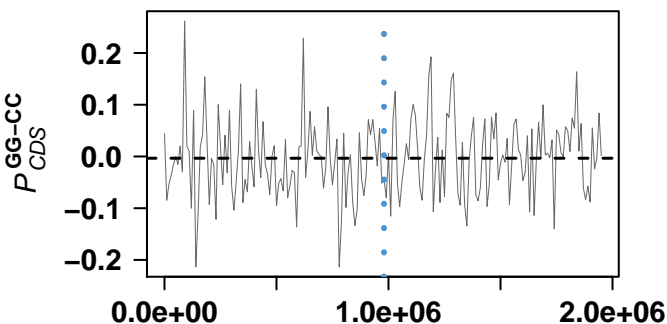
Xylella fastidiosa Temecula1



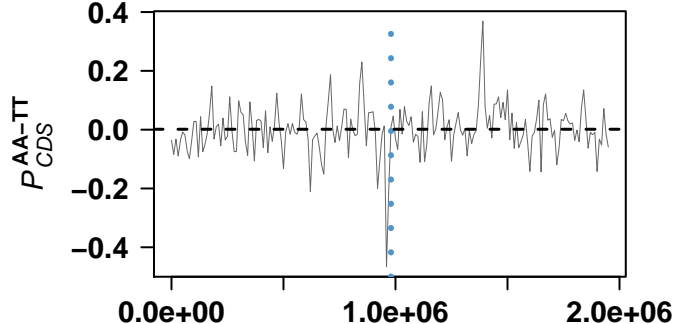
genome coordinates



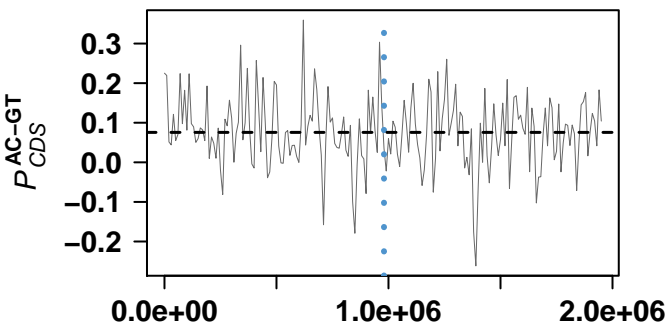
genome coordinates



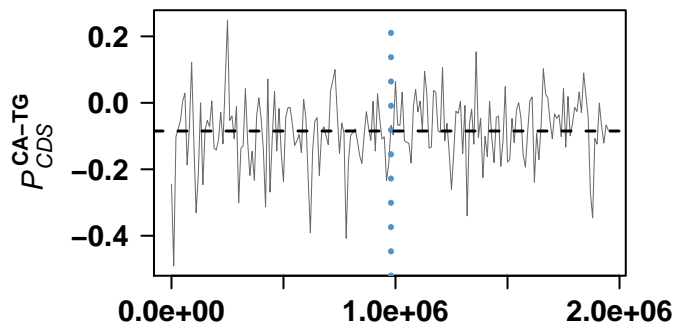
genome coordinates



genome coordinates

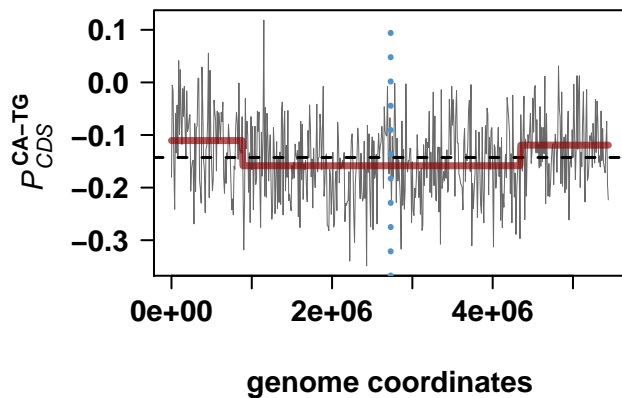
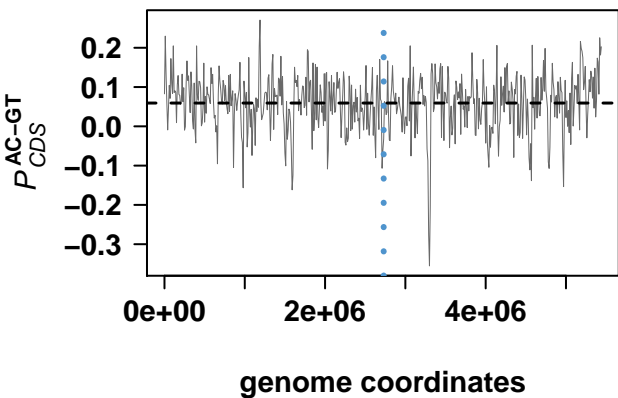
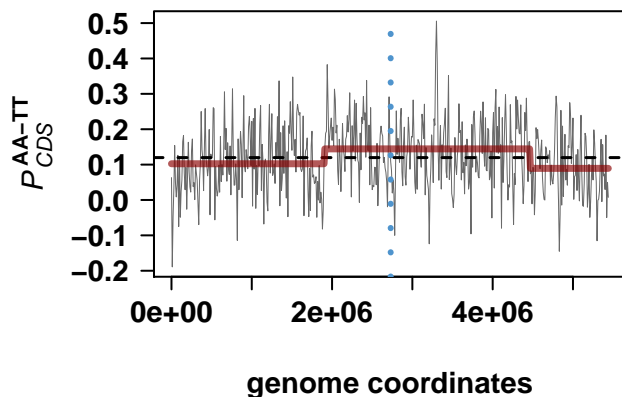
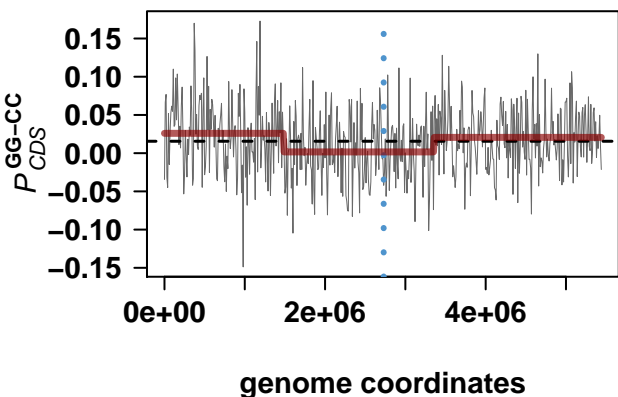
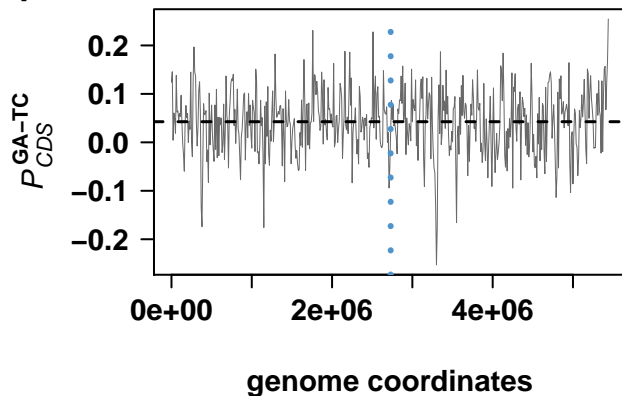
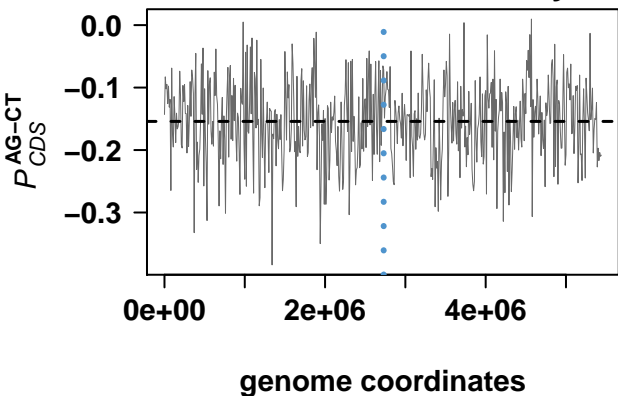


genome coordinates

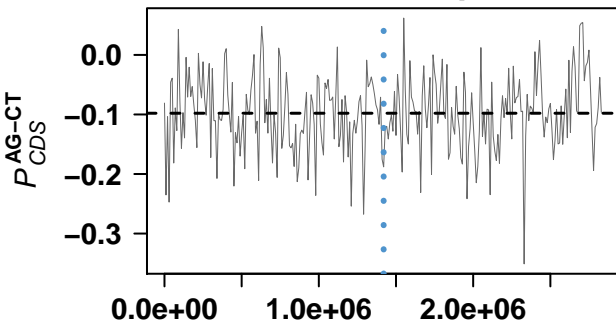


genome coordinates

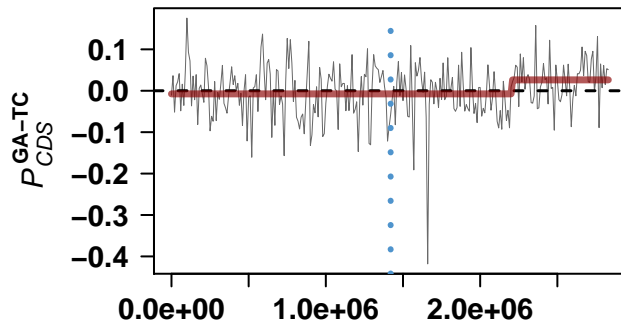
Pseudomonas syringae pv. *tomato* str. DC3000



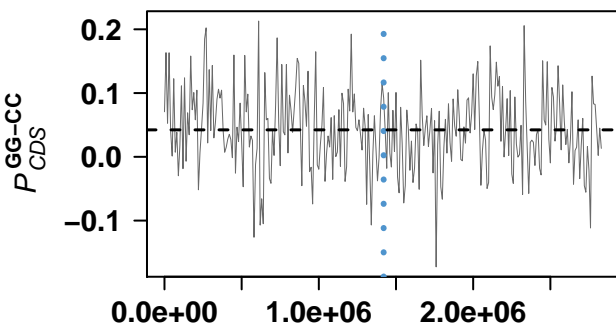
Vibrio parahaemolyticus RIMD 2210633



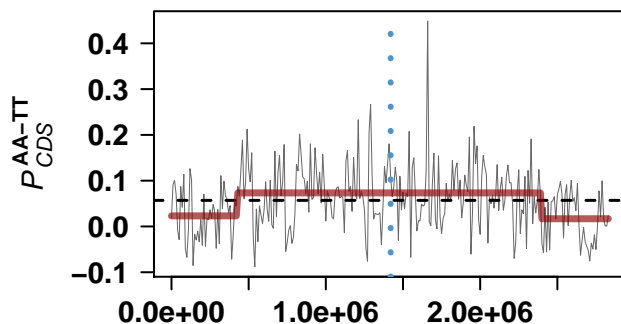
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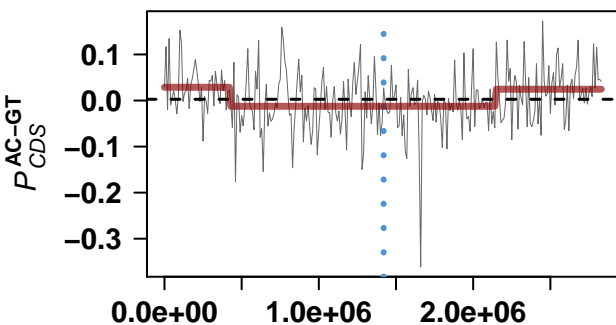
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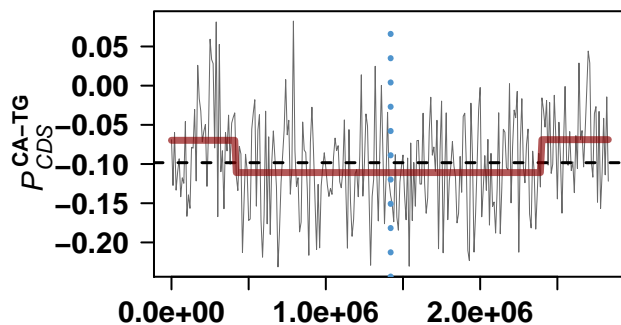
genome coordinates



genome coordinates

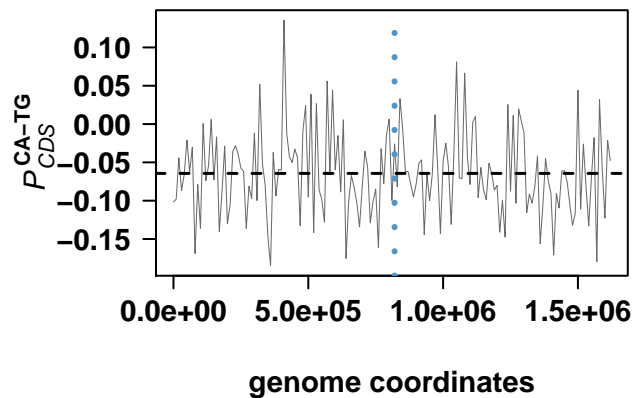
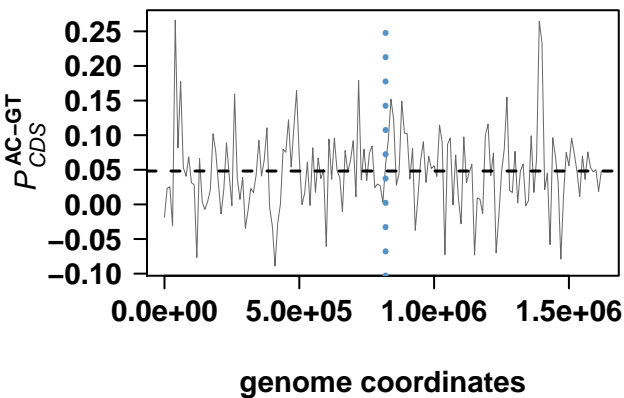
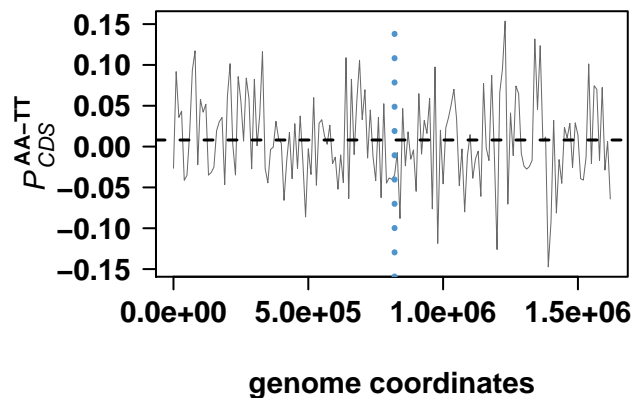
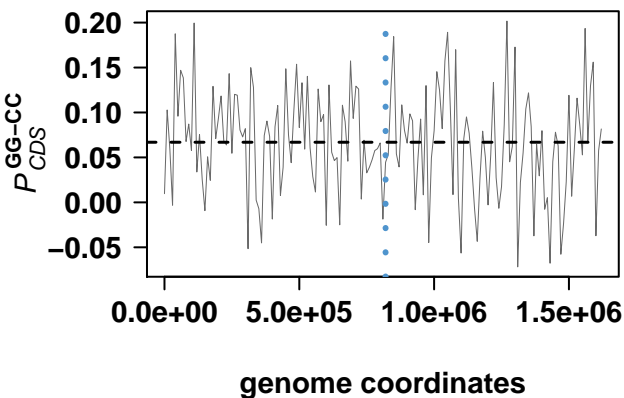
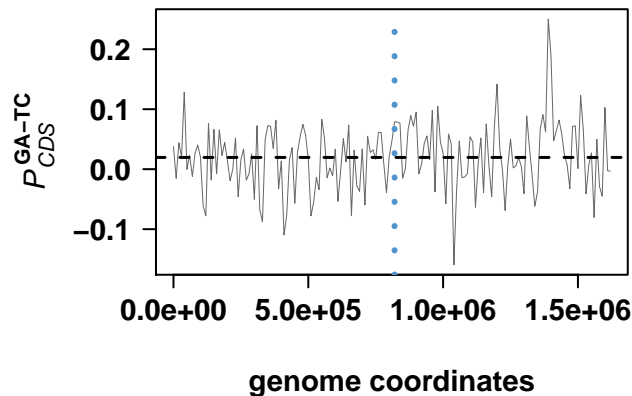
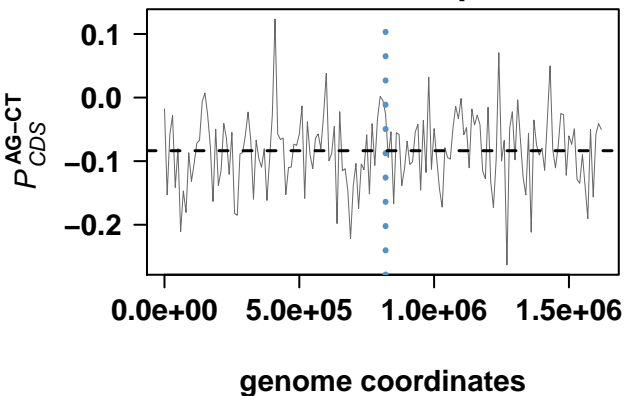


genome coordinates

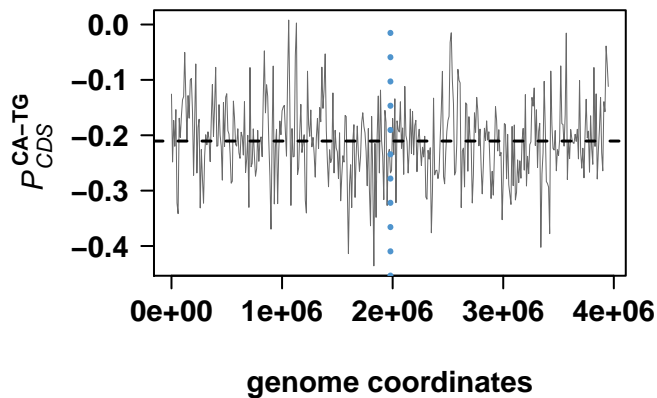
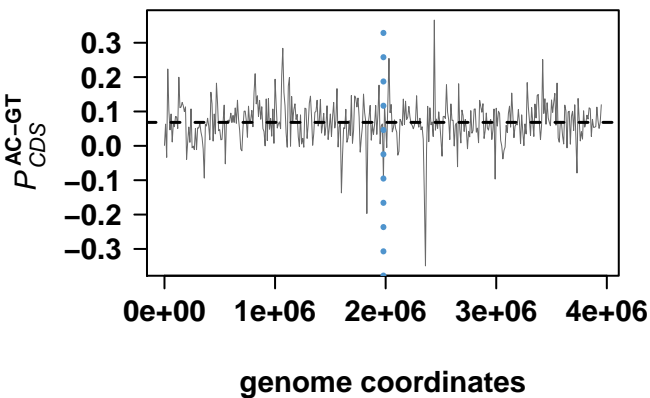
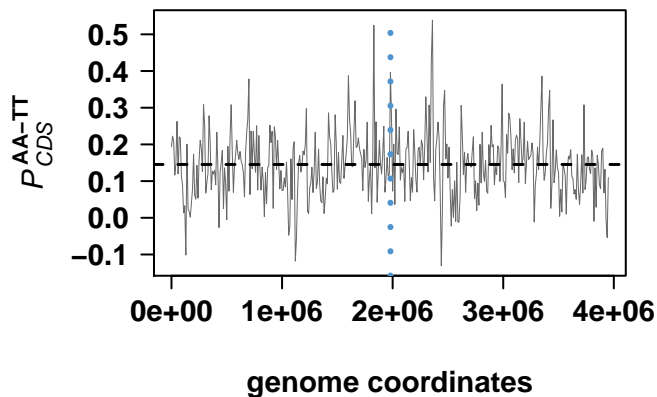
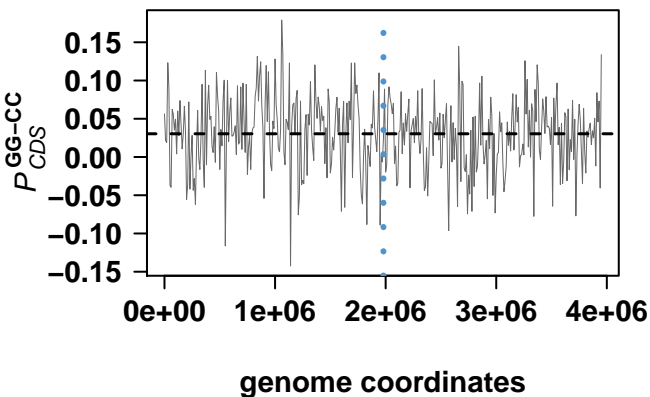
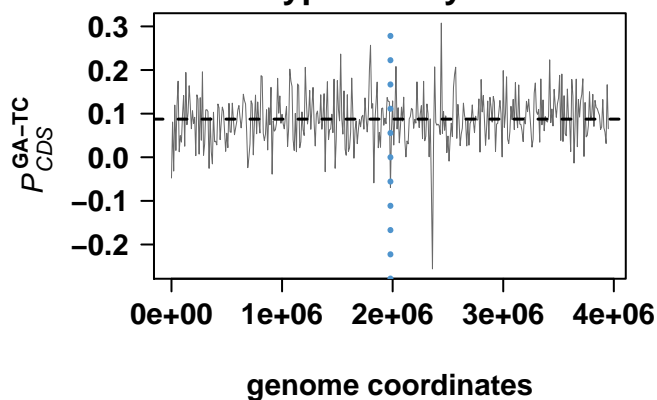
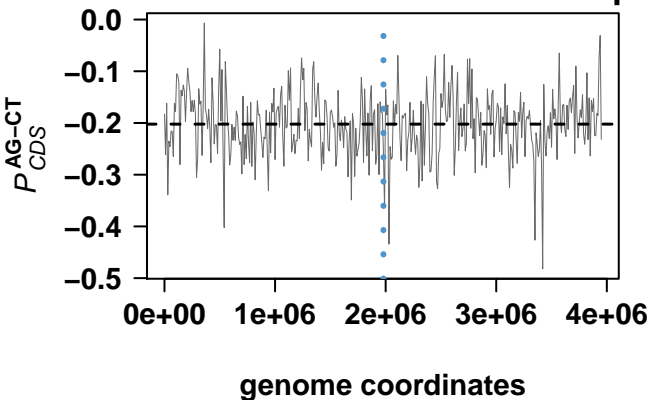


genome coordinates

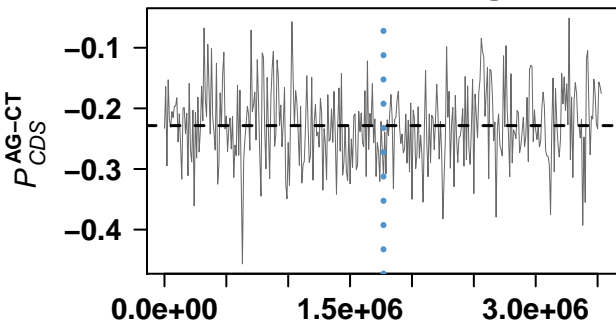
Vibrio parahaemolyticus RIMD 2210633



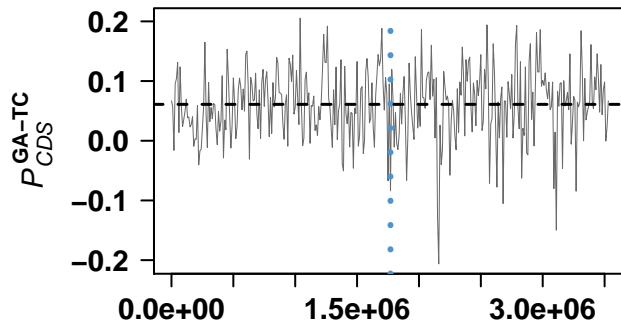
Salmonella enterica subsp. enterica serovar Typhi str. Ty2



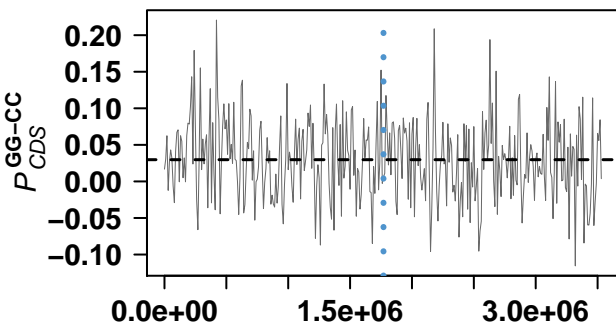
Shigella flexneri 2a str. 2457T



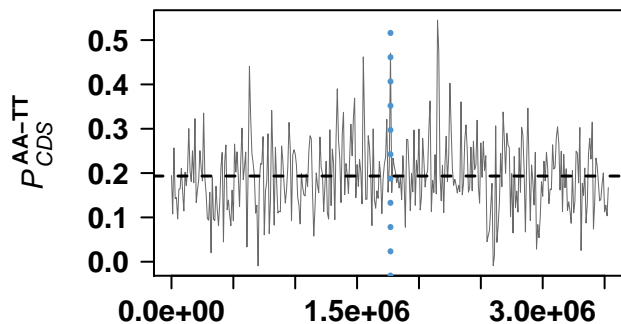
genome coordinates



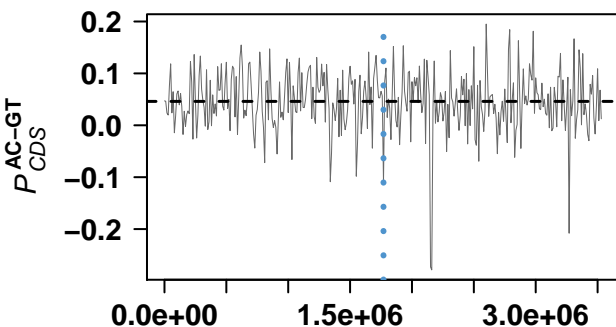
genome coordinates



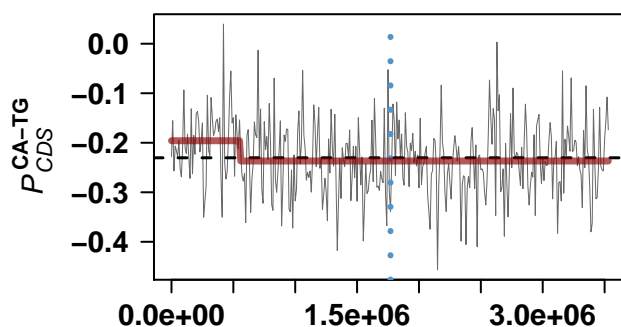
genome coordinates



genome coordinates

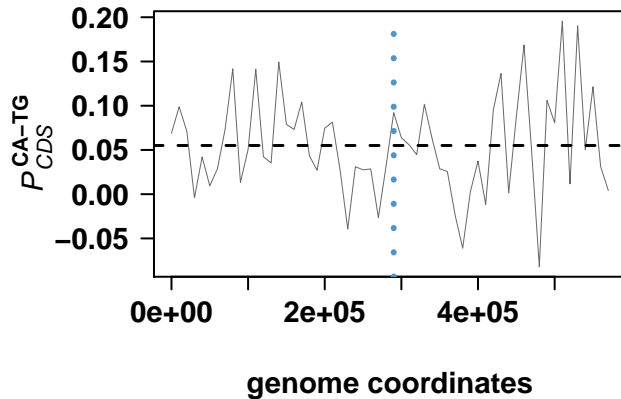
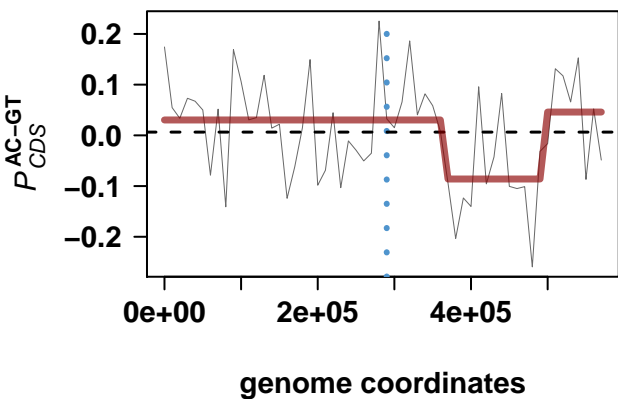
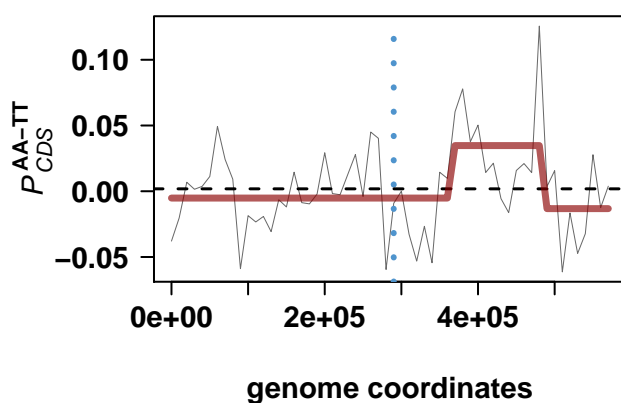
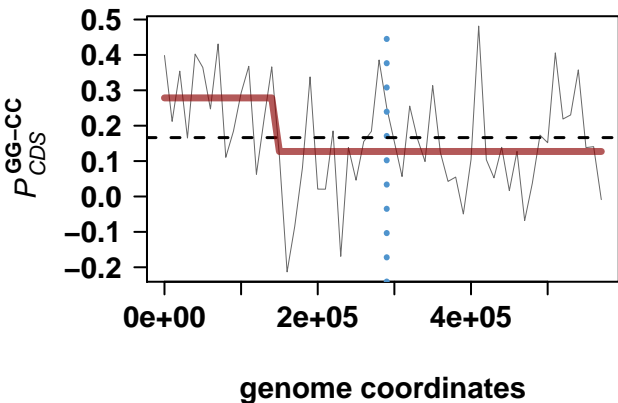
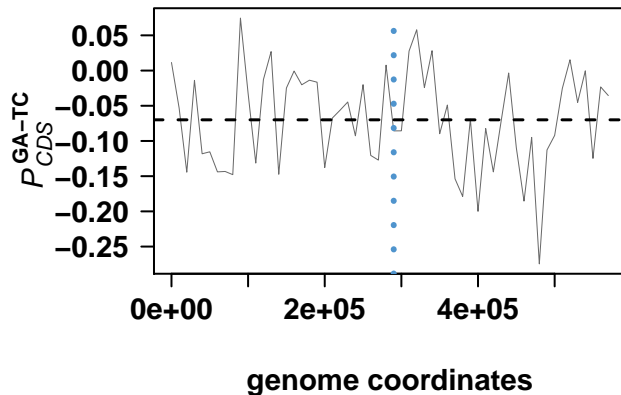
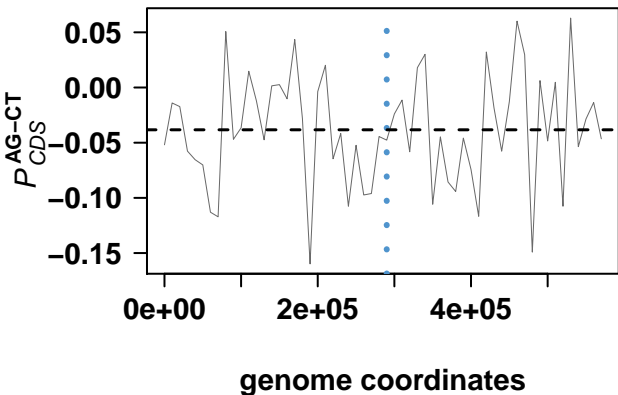


genome coordinates

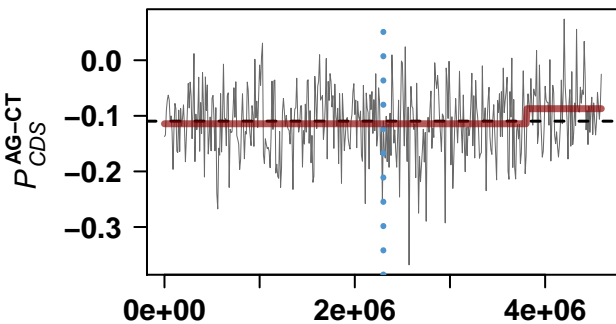


genome coordinates

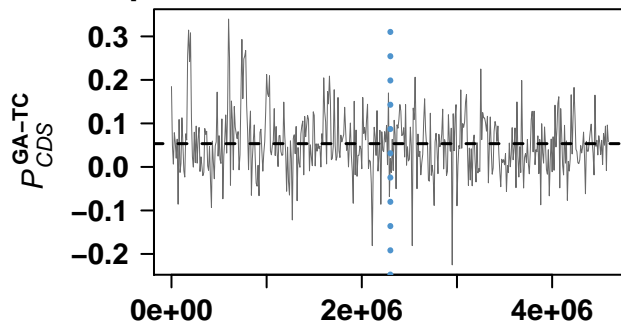
Candidatus Blochmannia floridanus



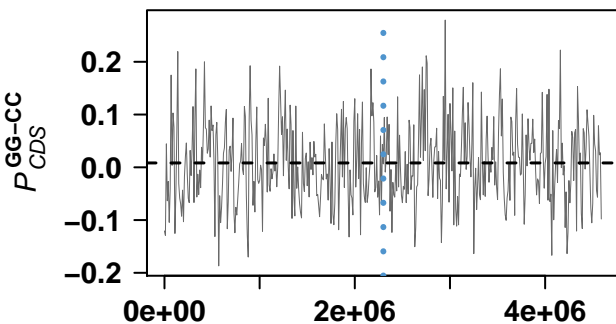
Photorhabdus luminescens subsp. laumondii TTO1



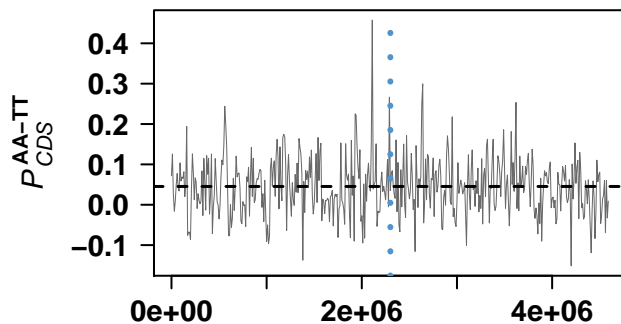
genome coordinates



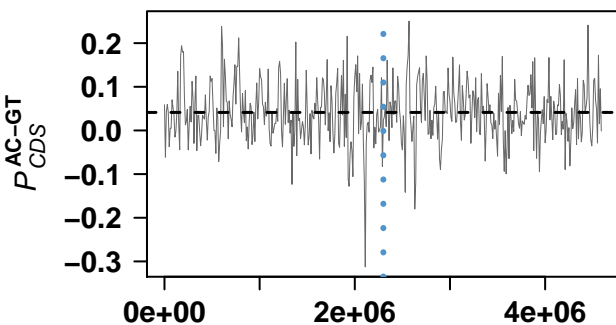
genome coordinates



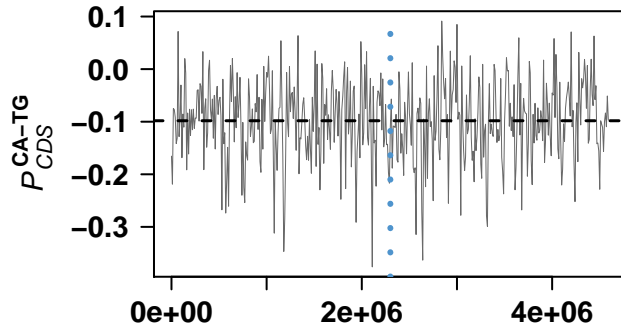
genome coordinates



genome coordinates

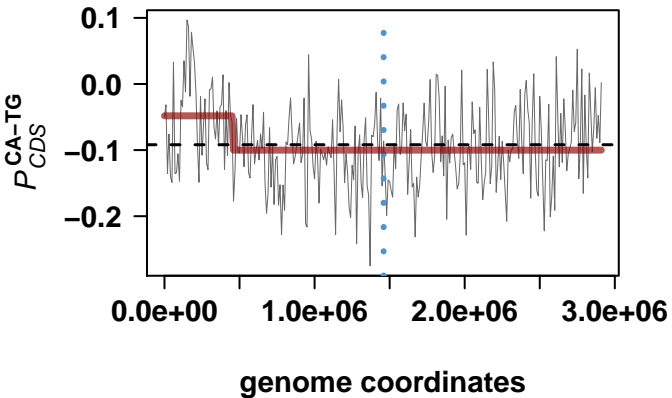
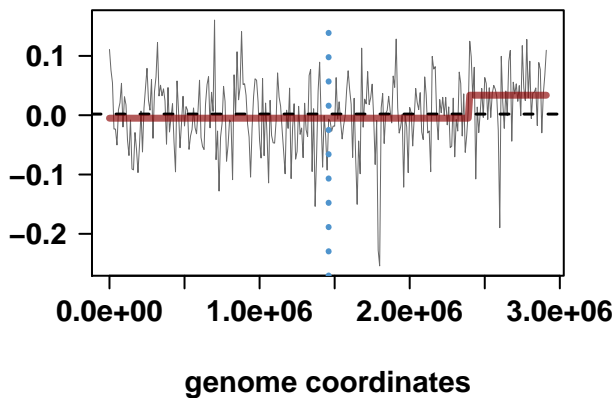
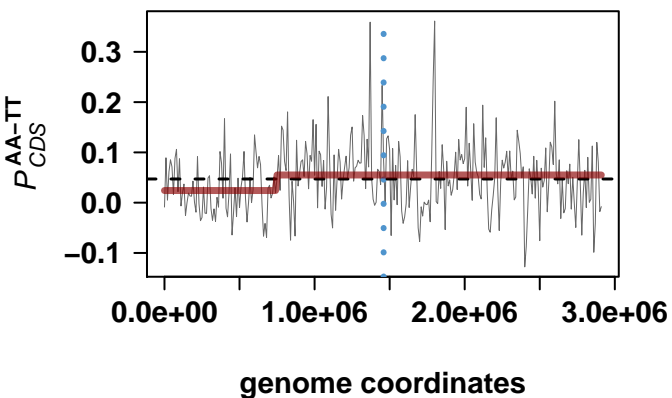
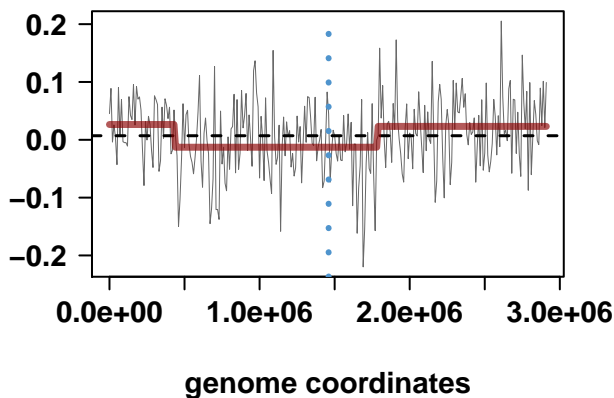
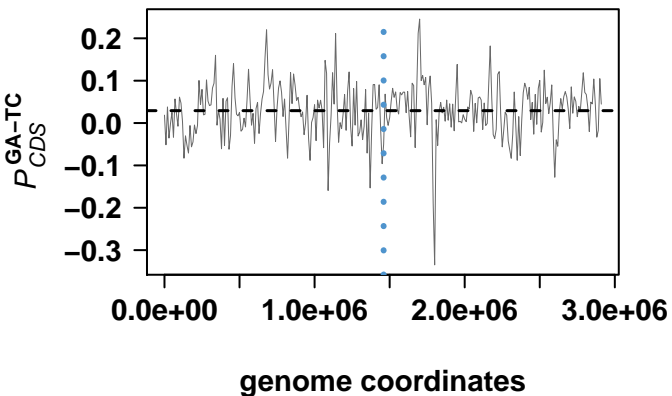
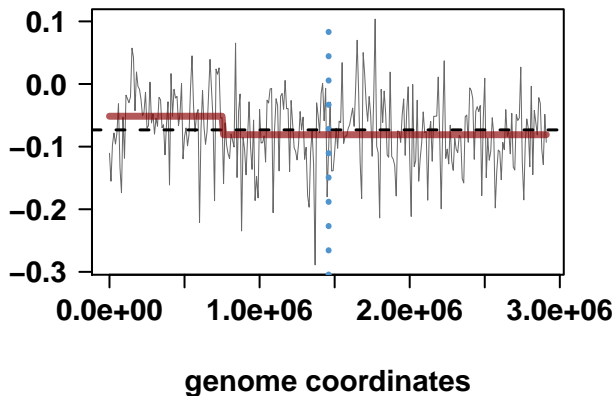


genome coordinates

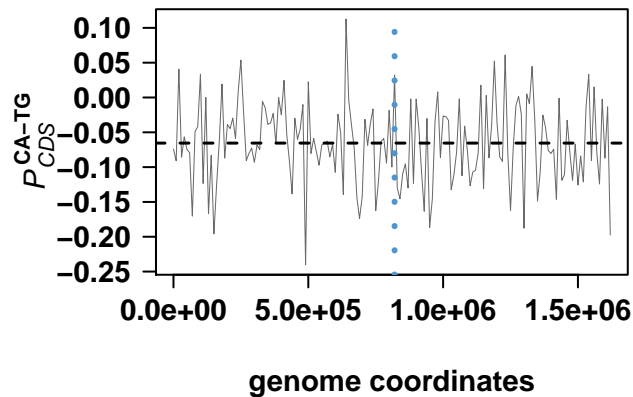
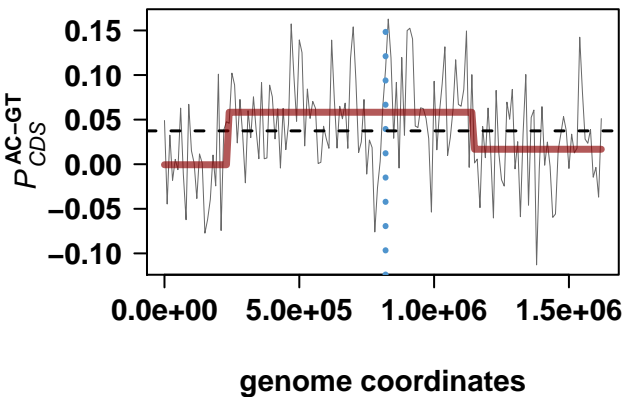
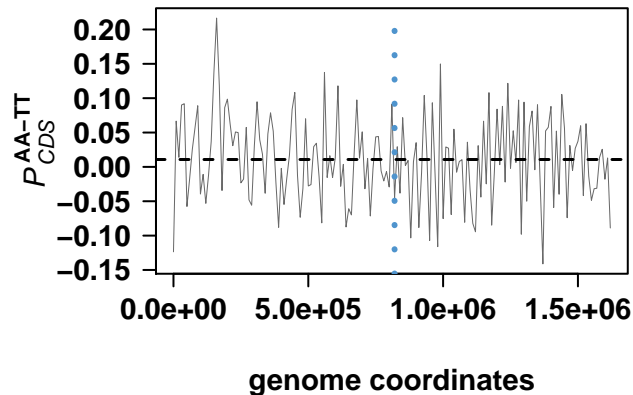
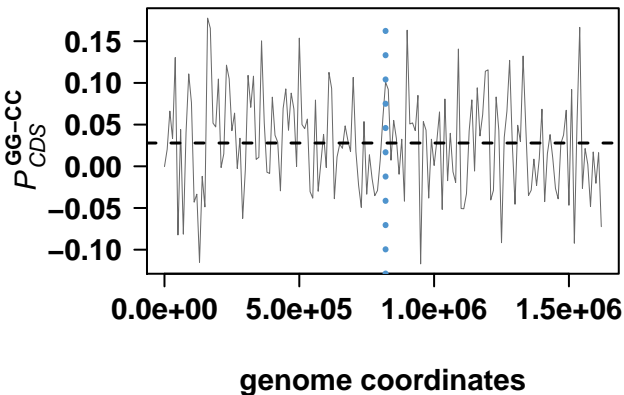
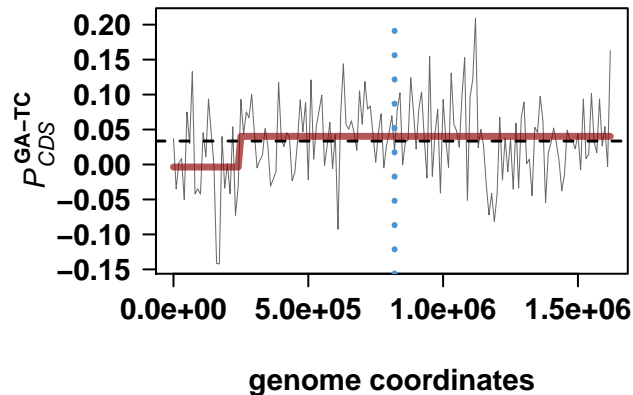
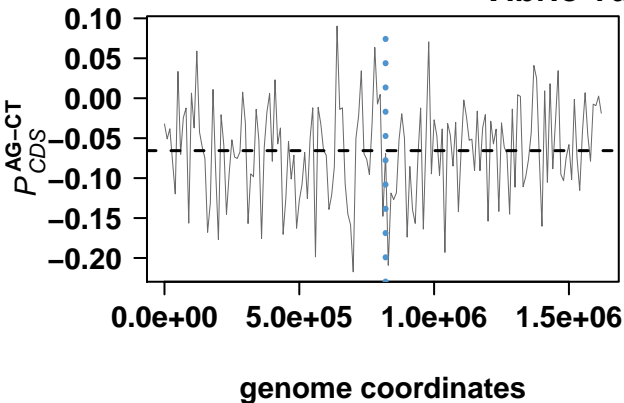


genome coordinates

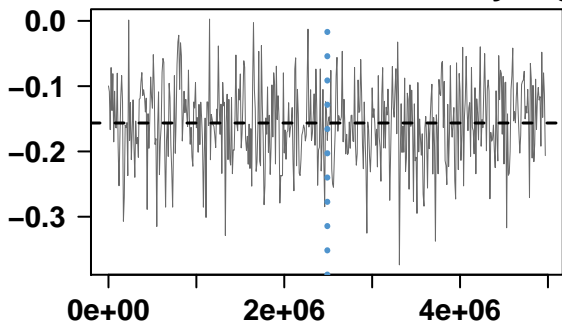
Vibrio vulnificus YJ016



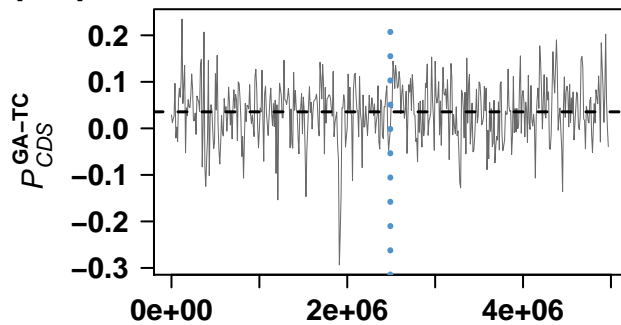
Vibrio vulnificus YJ016



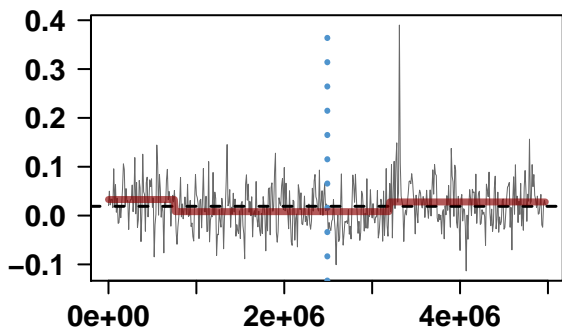
Pseudomonas syringae pv. *phaseolicola* 1448A



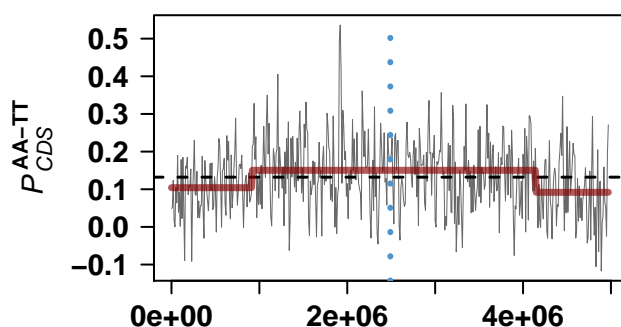
genome coordinates



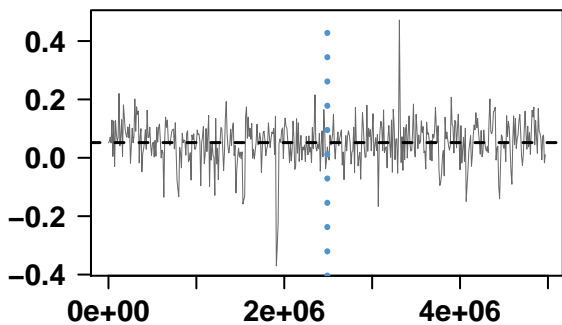
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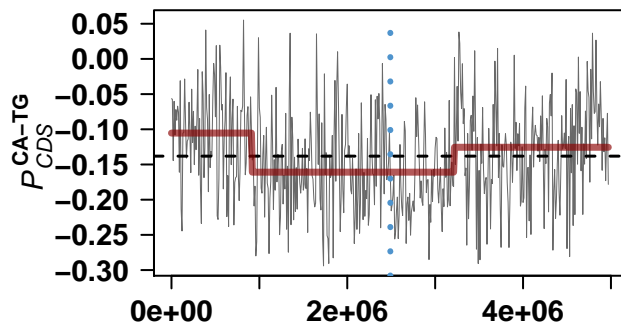
genome coordinates



genome coordinates

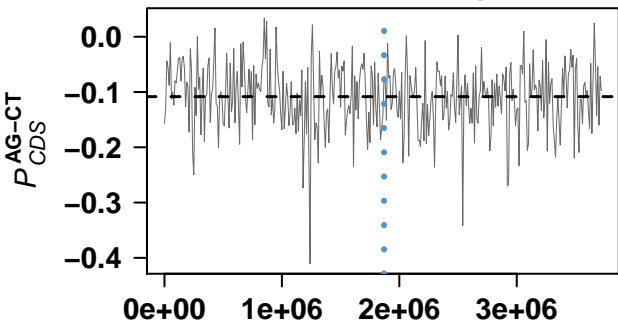


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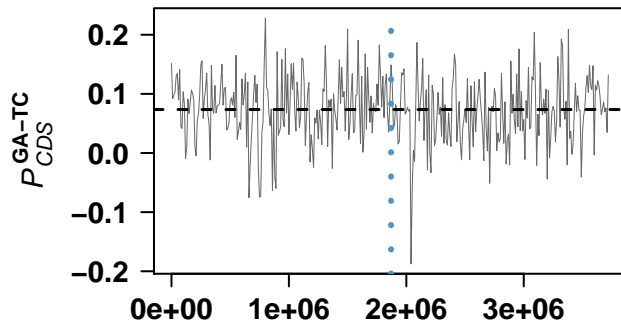


genome coordinates

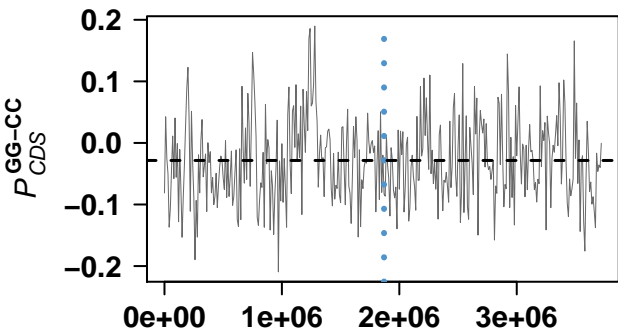
Yersinia pestis biovar *Microtus* str. 91001



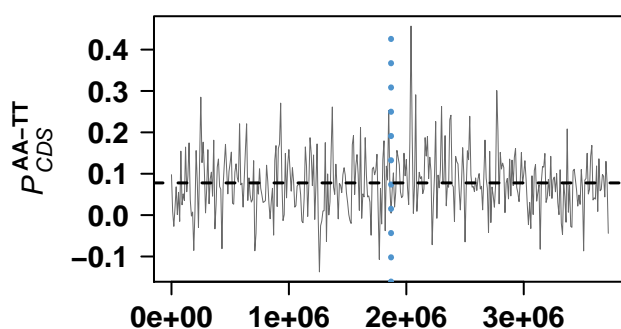
genome coordinates



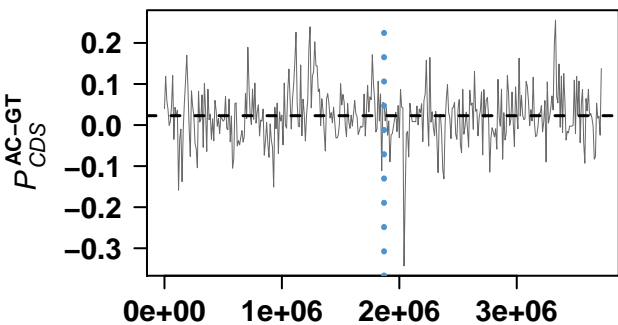
genome coordinates



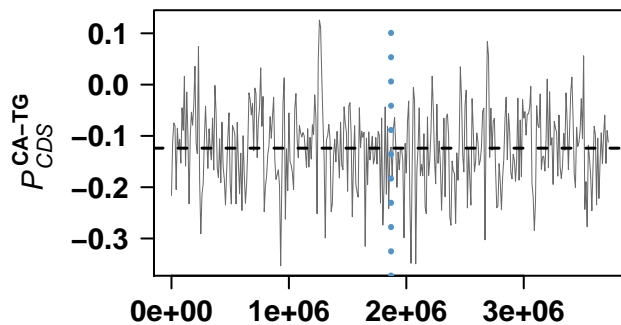
genome coordinates



genome coordinates

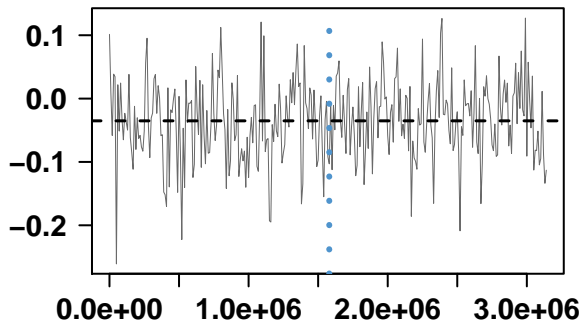


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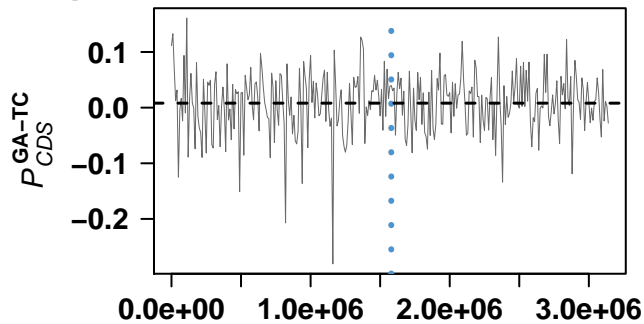


genome coordinates

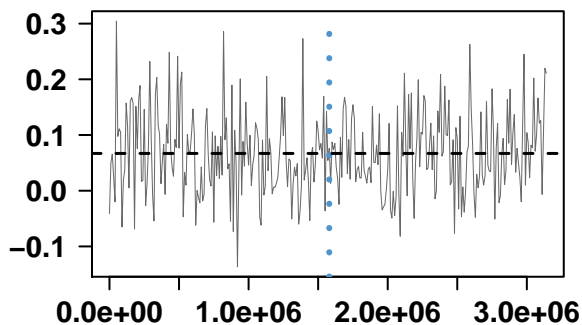
Acinetobacter sp. ADP1



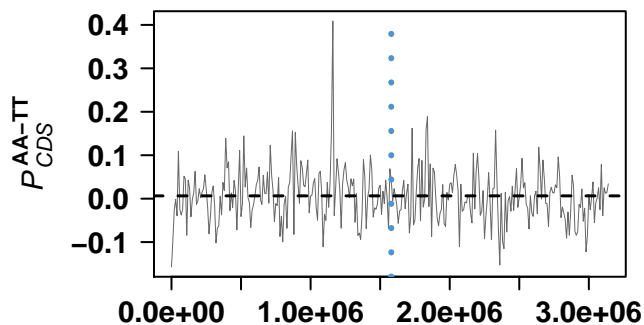
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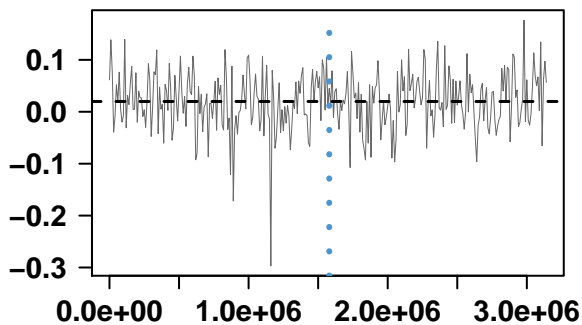
genome coordinates



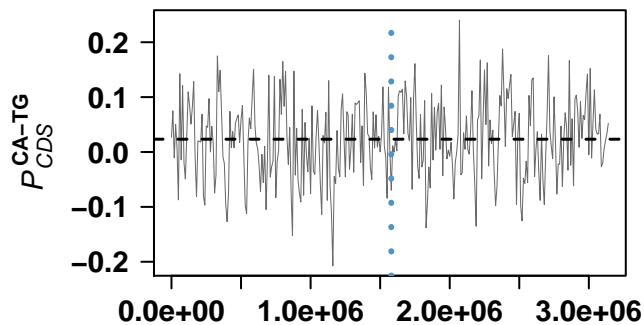
genome coordinates



genome coordinates

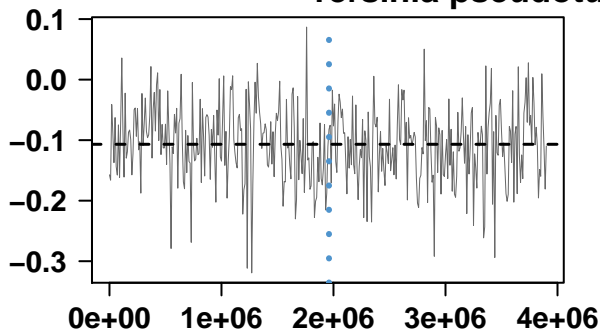


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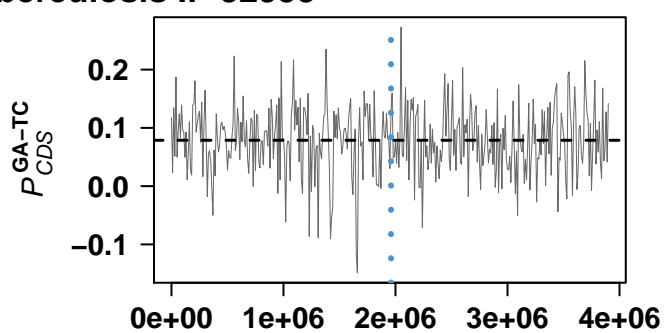


genome coordinates

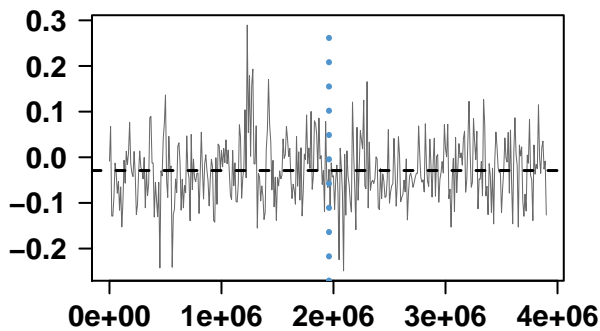
Yersinia pseudotuberculosis IP 32953



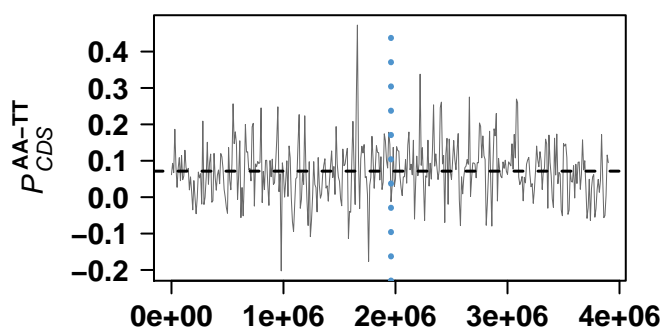
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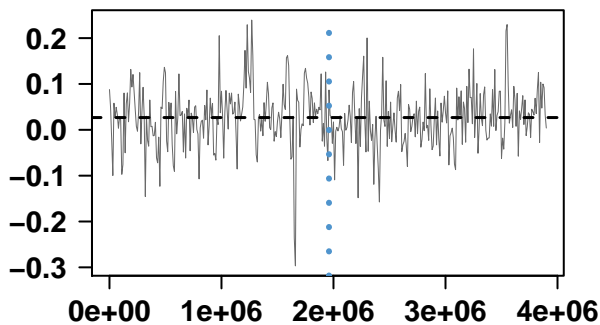
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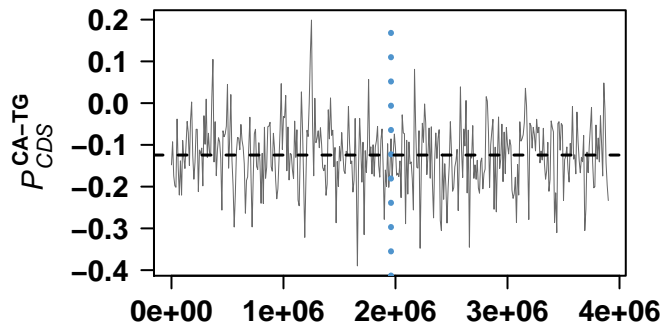
genome coordinates



genome coordinates

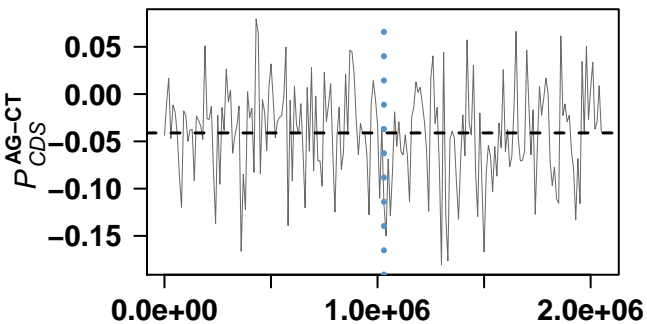


genome coordinates

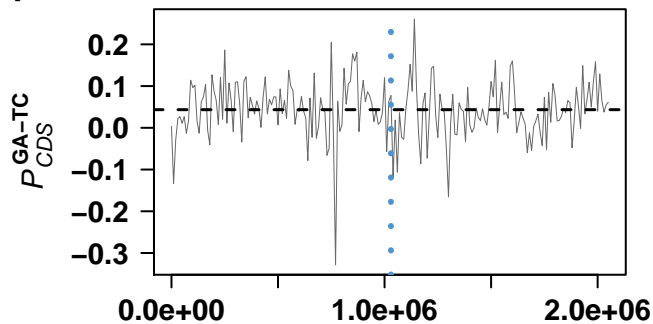


genome coordinates

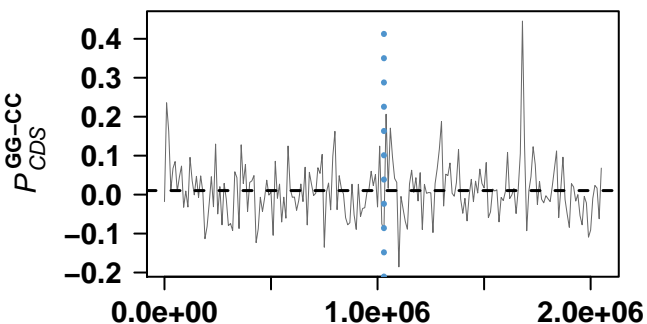
Mannheimia succiniciproducens MBEL55E



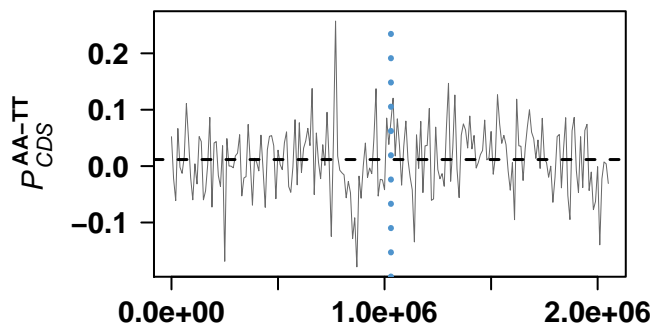
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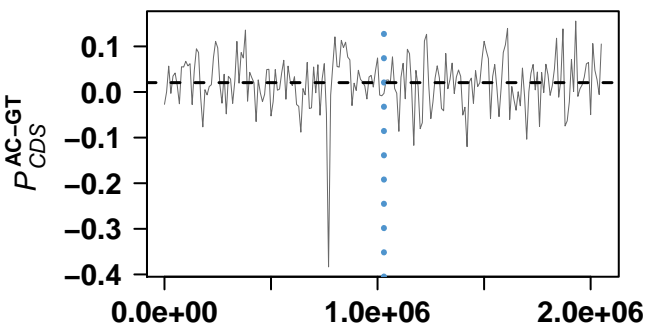
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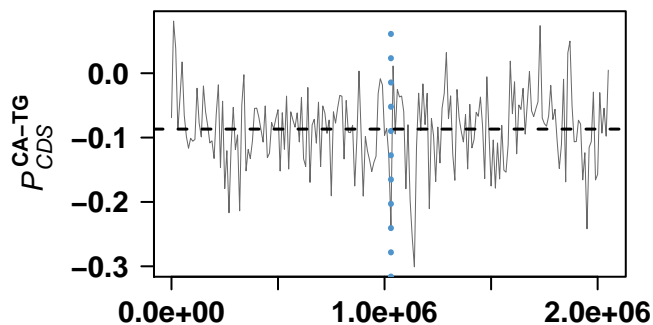
genome coordinates



genome coordinates

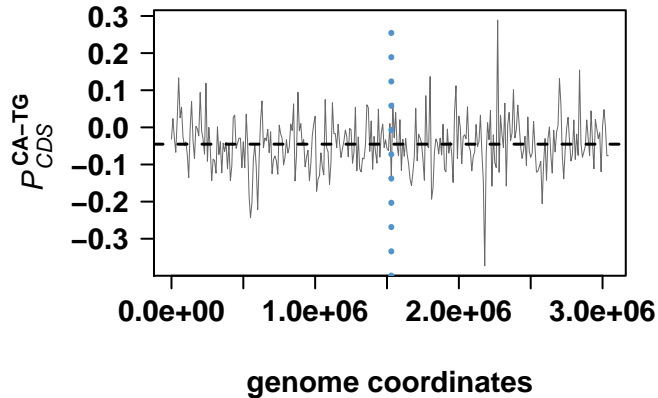
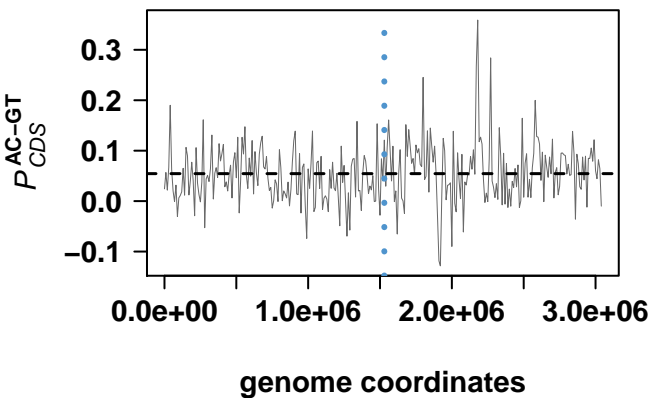
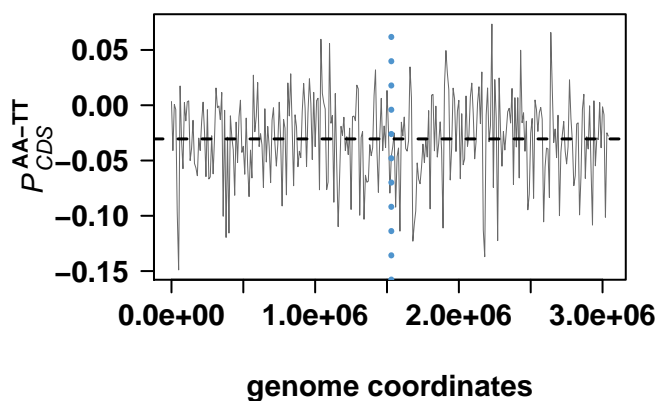
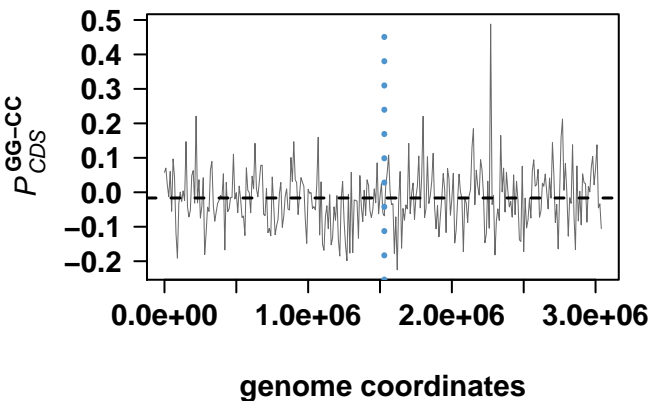
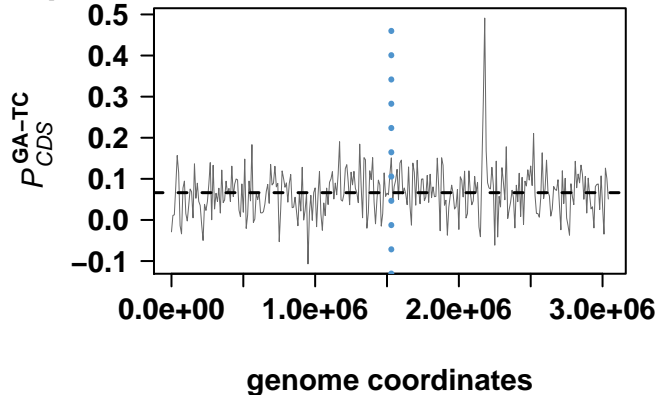
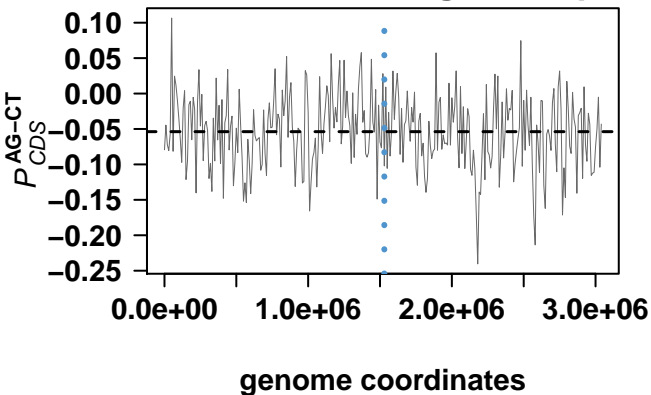


genome coordinates

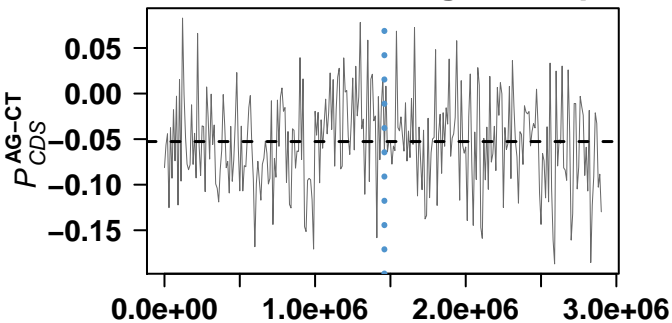


genome coordinates

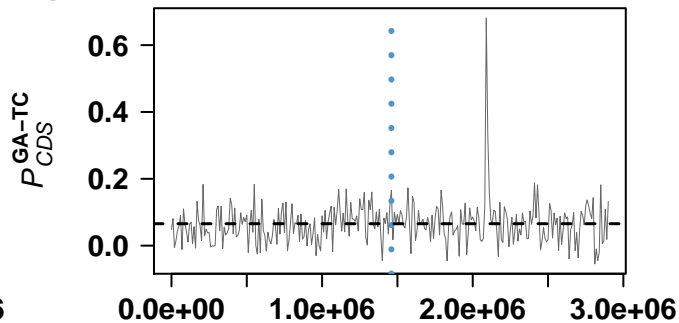
Legionella pneumophila str. Paris



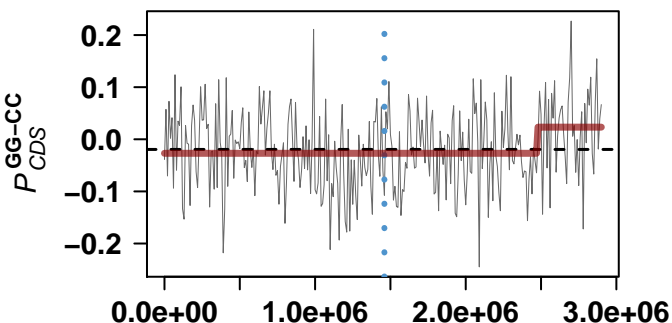
Legionella pneumophila str. Lens



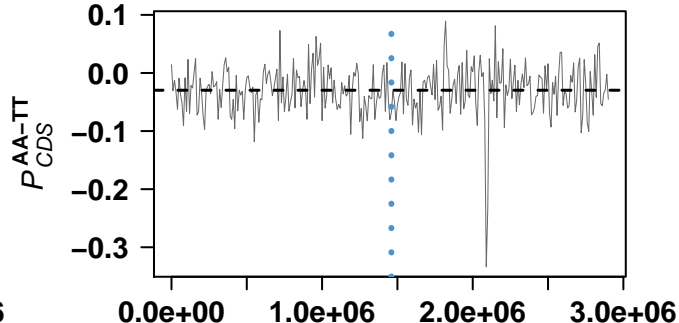
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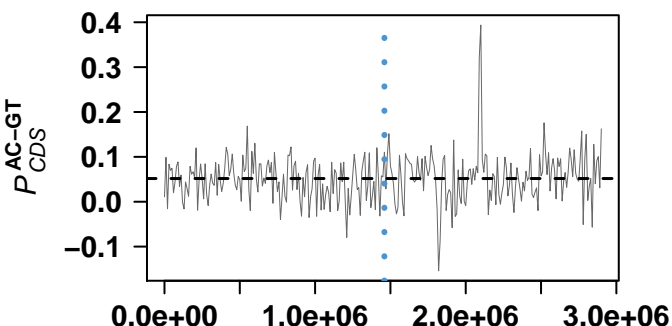
genome coordinates



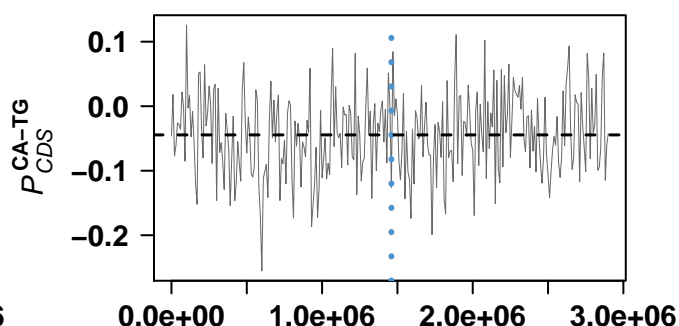
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genome coordinates

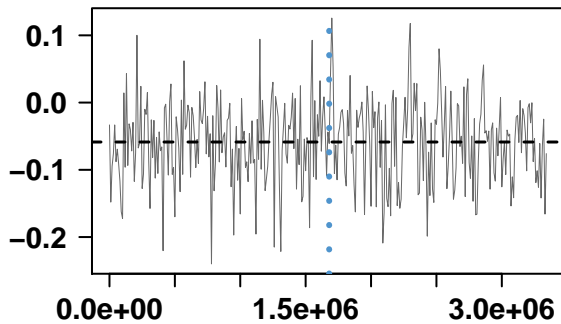


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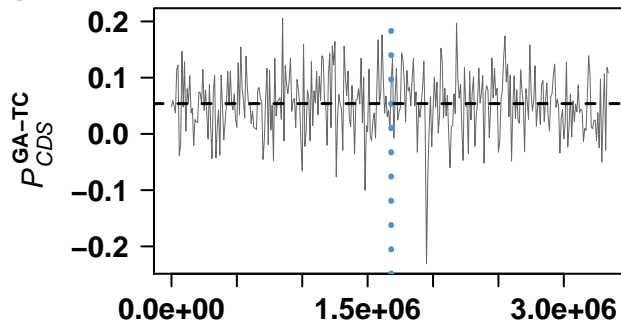


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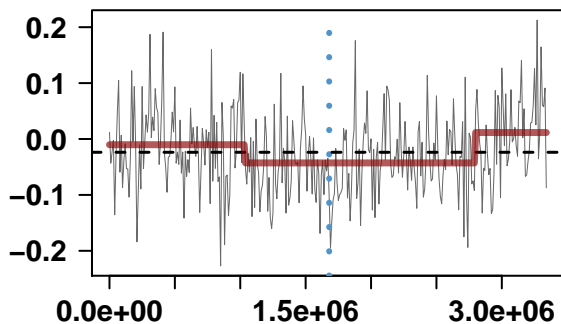
Photobacterium profundum SS9



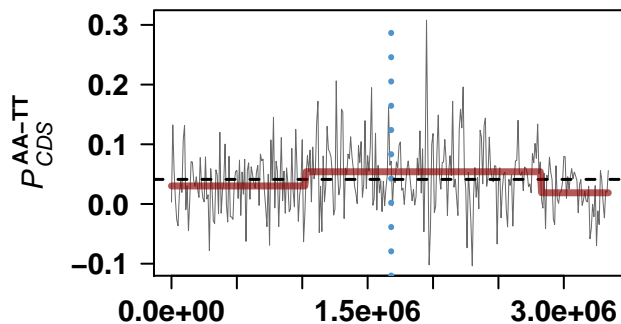
genome coordinates



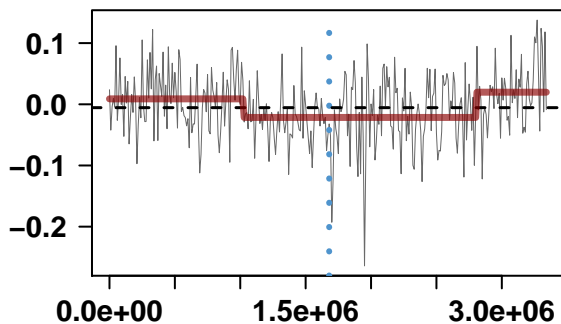
genome coordinates



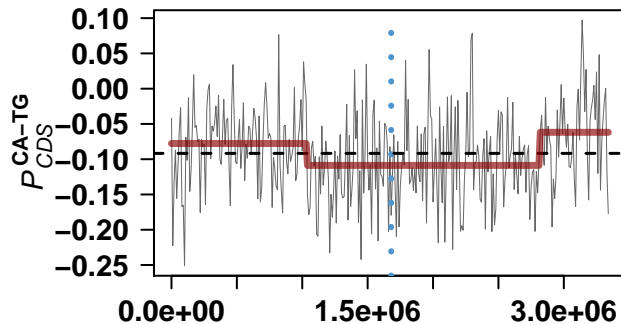
genome coordinates



genome coordinates

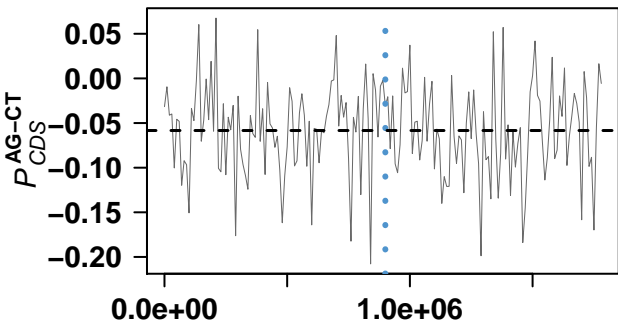


genome coordinates

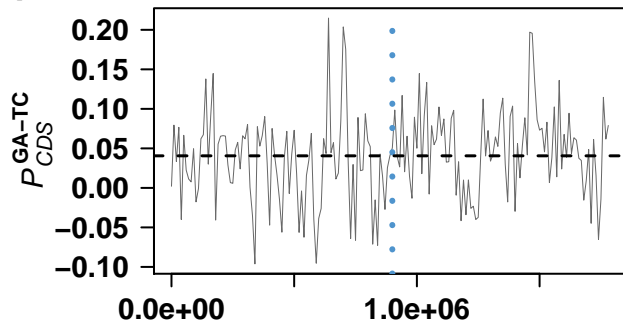


genome coordinates

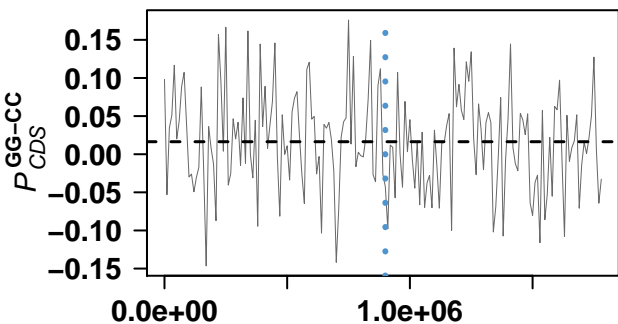
Photobacterium profundum SS9



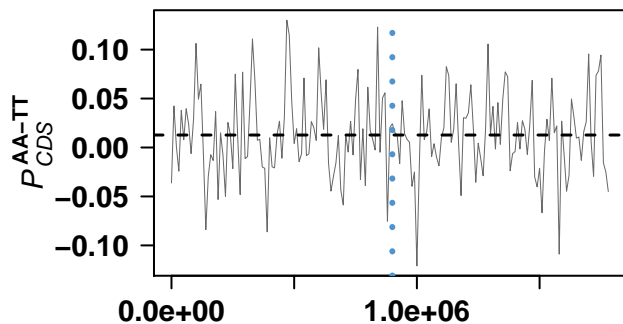
genome coordinates



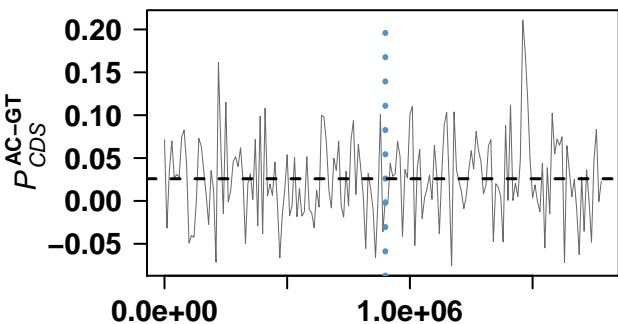
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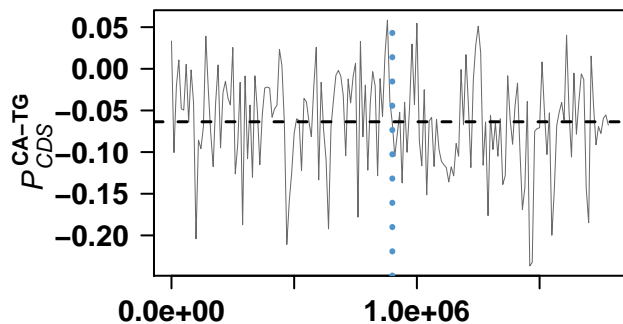
genome coordinates



genome coordinates

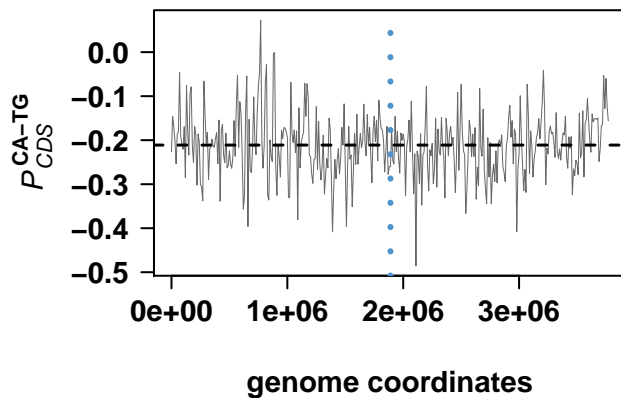
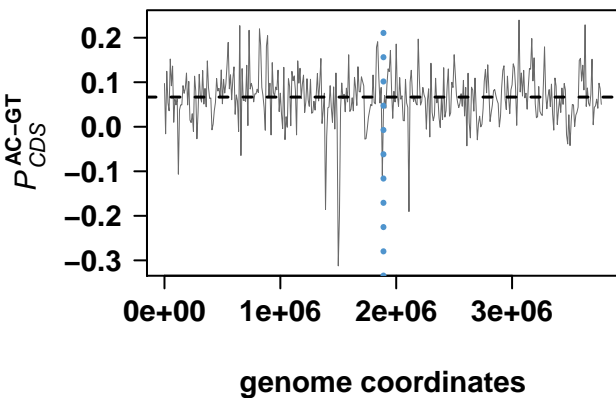
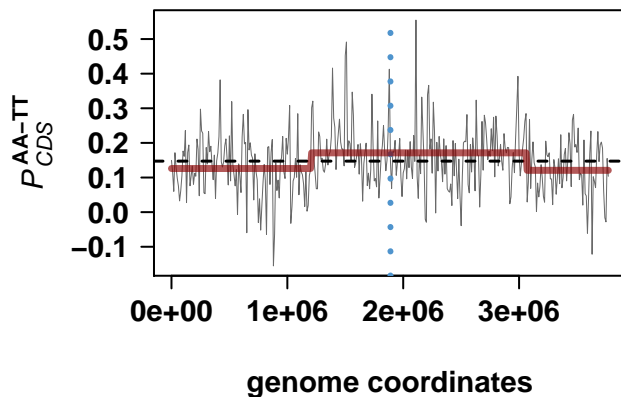
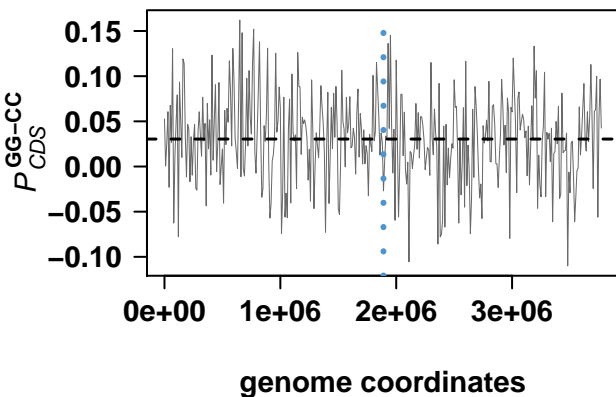
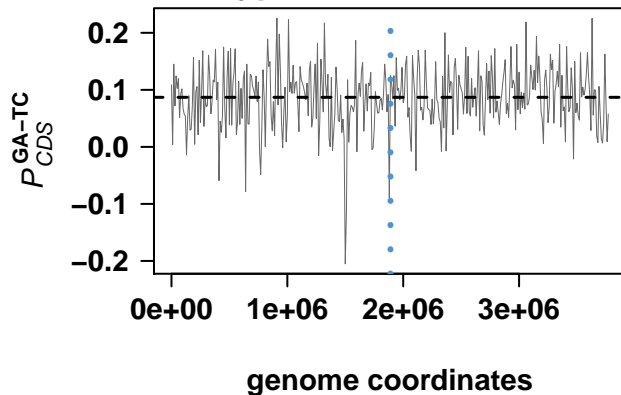
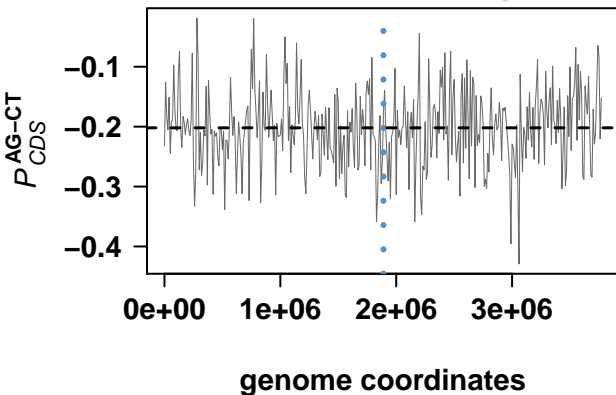


genome coordinates

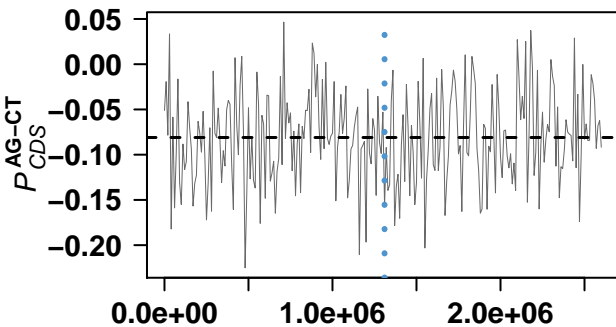


genome coordinates

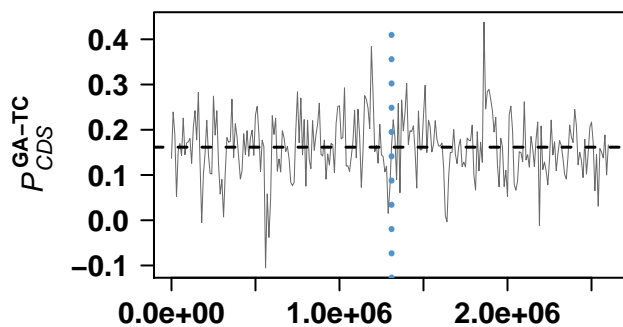
Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150



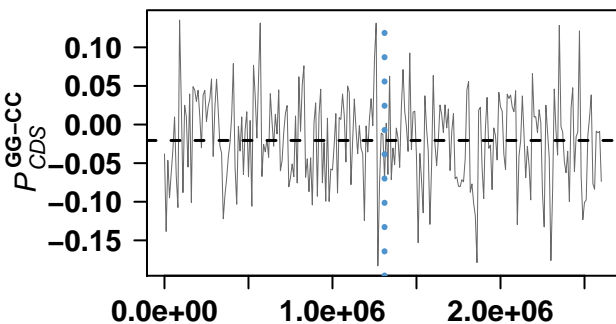
Idiomarina loihiensis L2TR



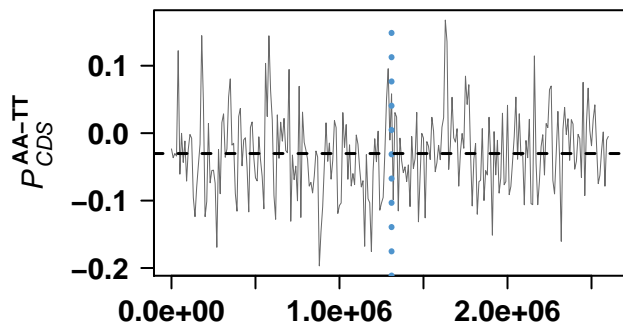
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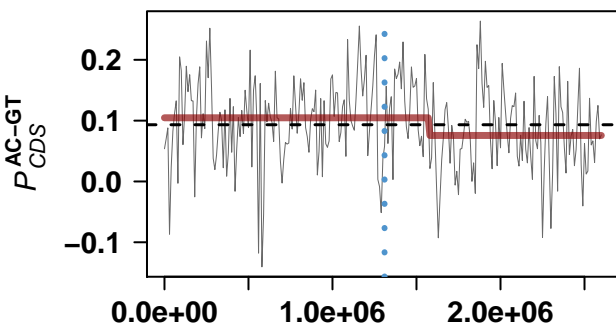
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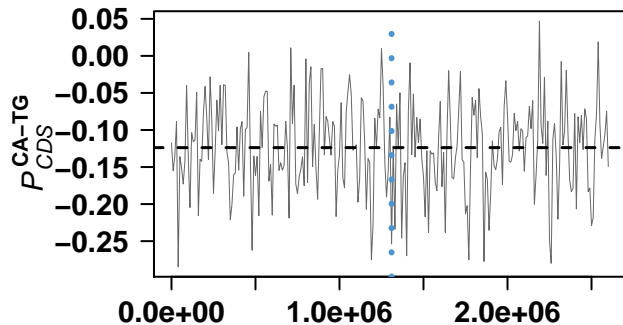
genome coordinates



genome coordinates

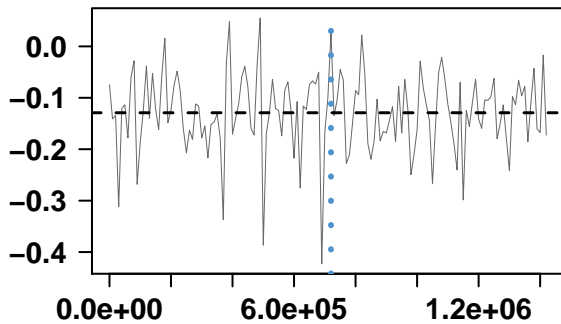


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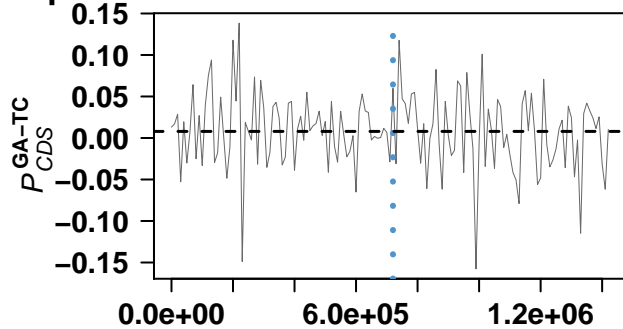


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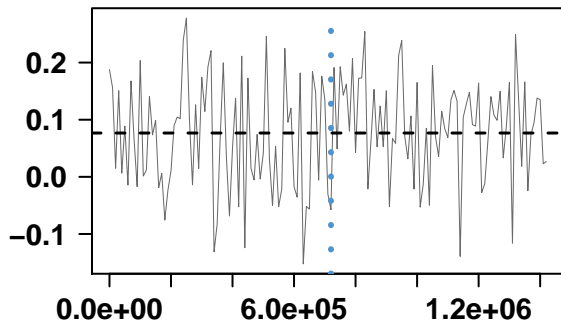
Francisella tularensis subsp. tularensis SCHU S4



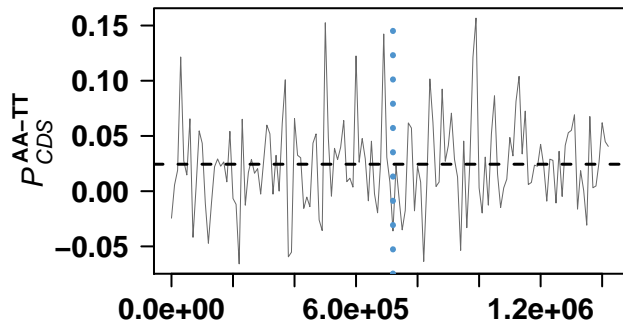
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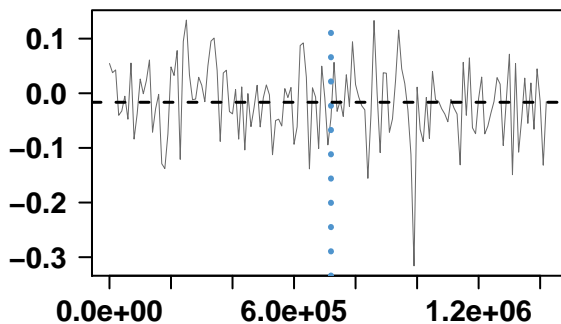
genome coordinates



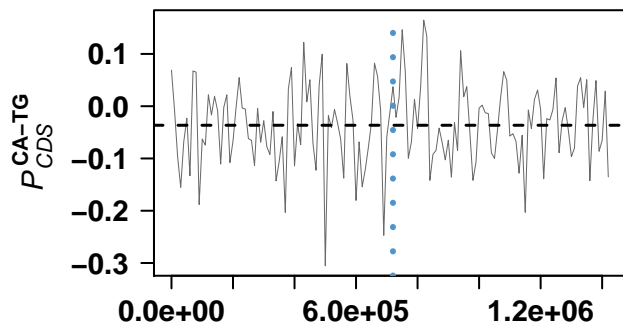
genome coordinates



genome coordinates

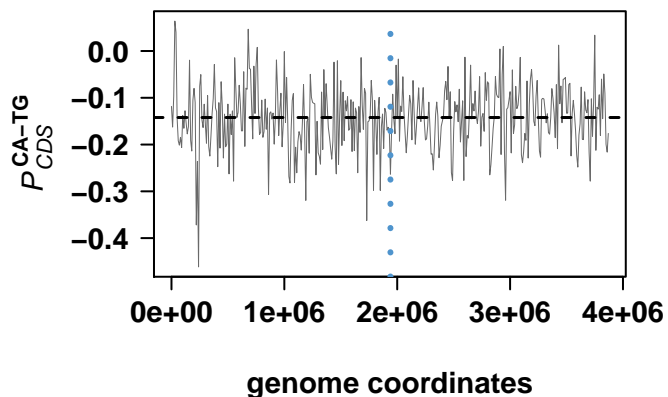
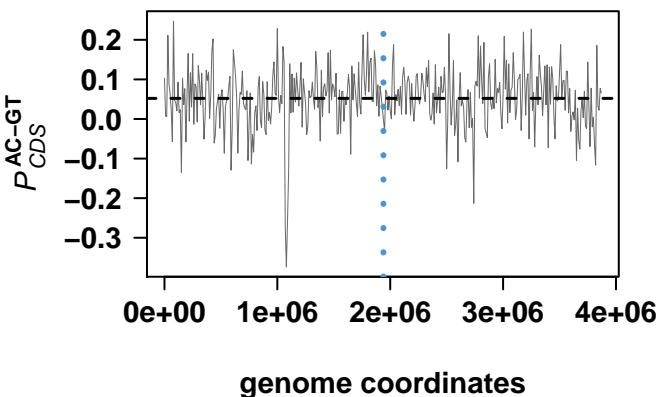
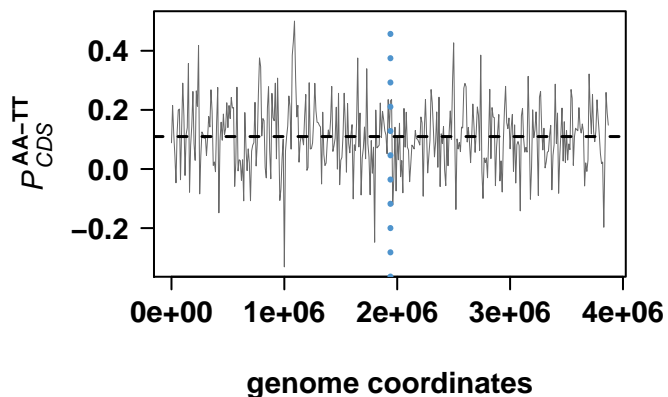
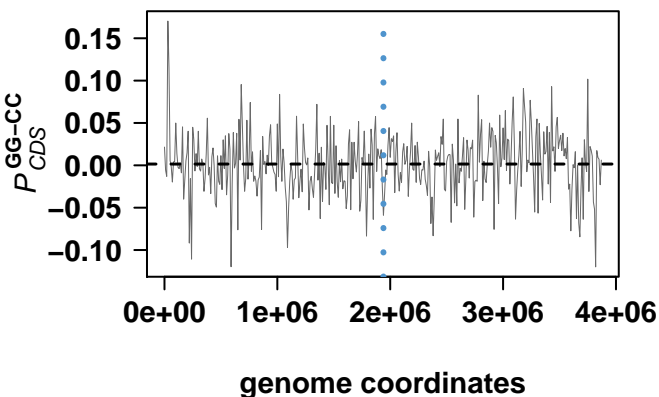
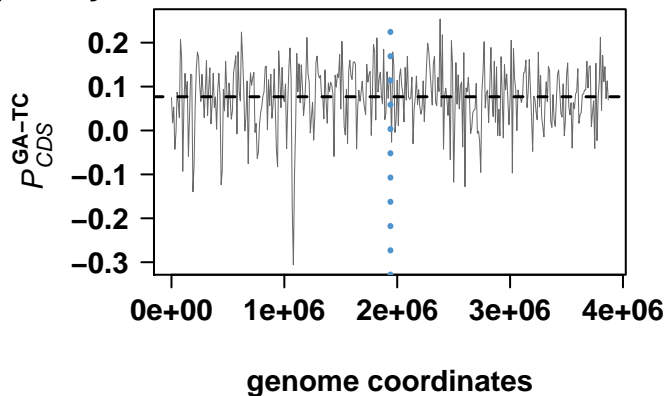
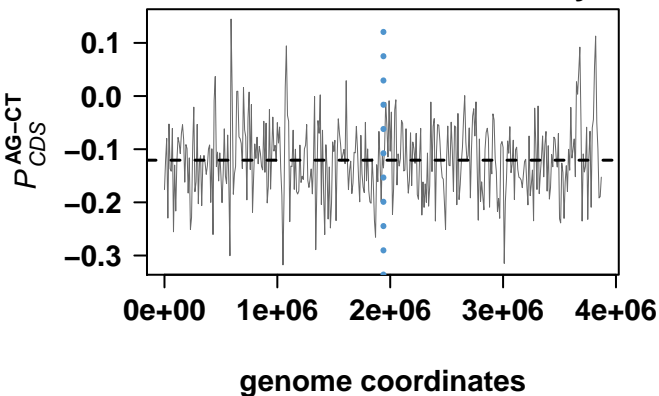


genome coordinates

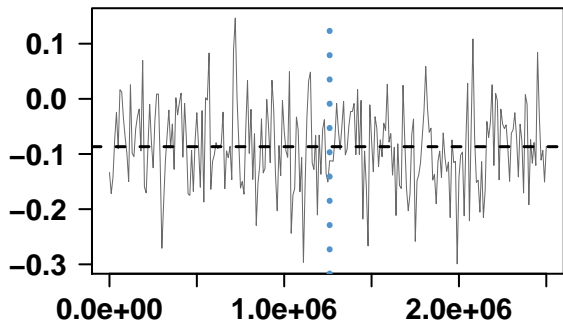


genome coordinates

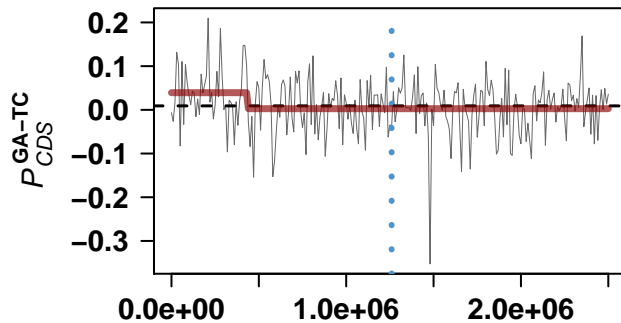
Xanthomonas oryzae pv. oryzae KACC 10331



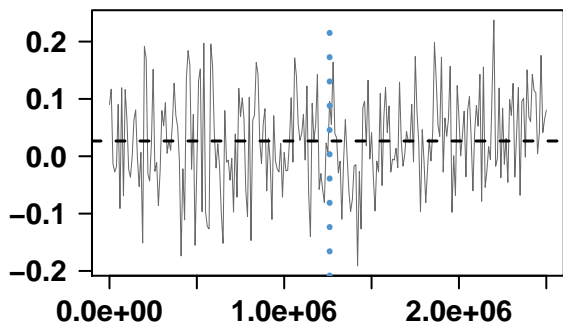
Vibrio fischeri ES114



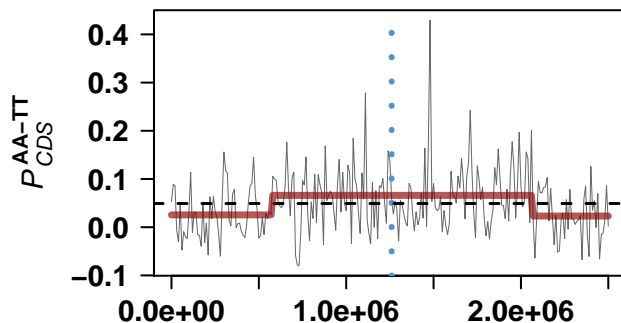
genome coordinates



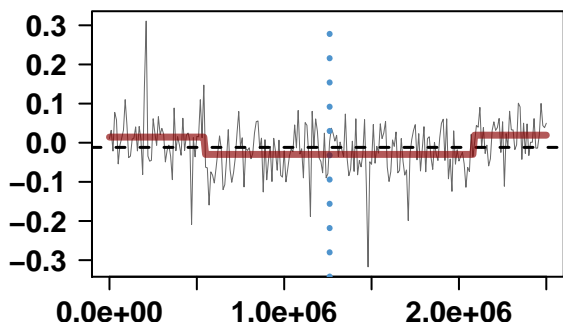
genome coordinates



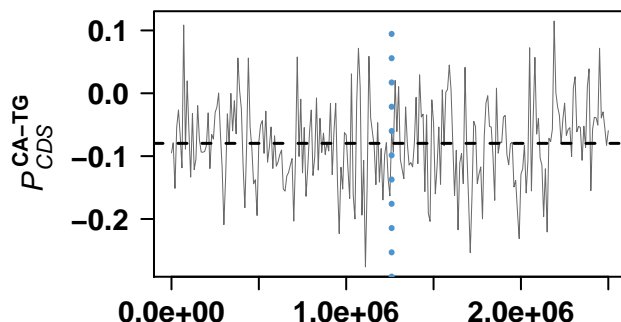
genome coordinates



genome coordinates

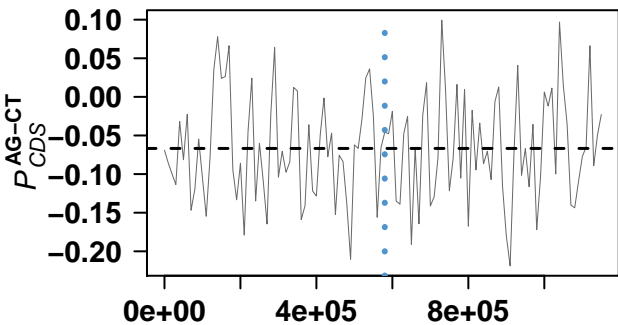


genome coordinates

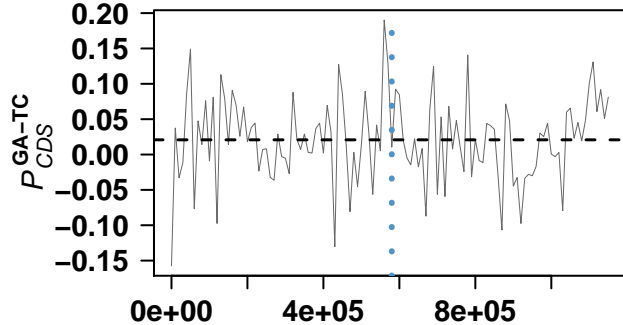


genome coordinates

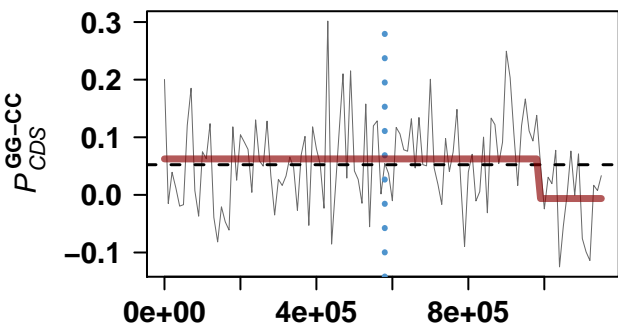
Vibrio fischeri ES114



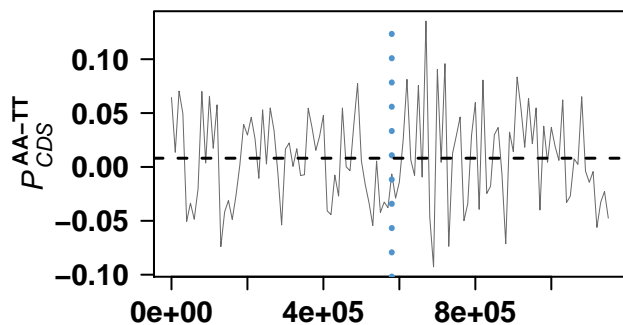
genome coordinates



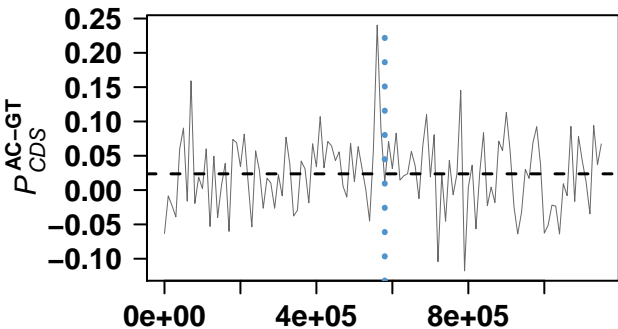
genome coordinates



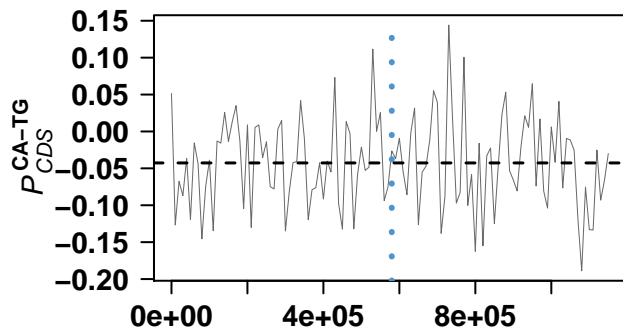
genome coordinates



genome coordinates

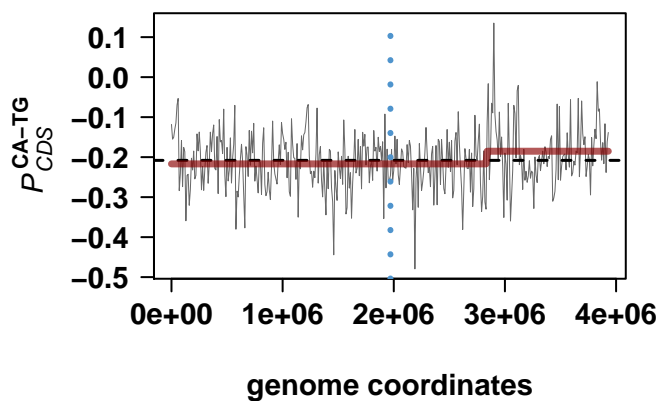
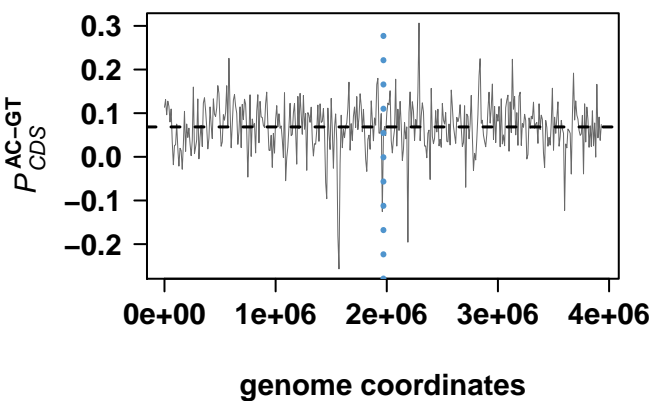
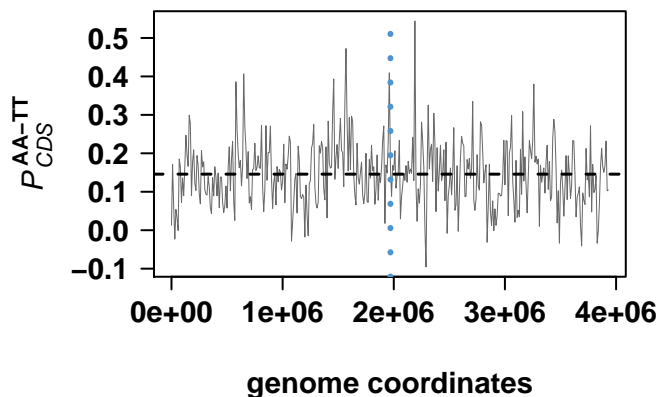
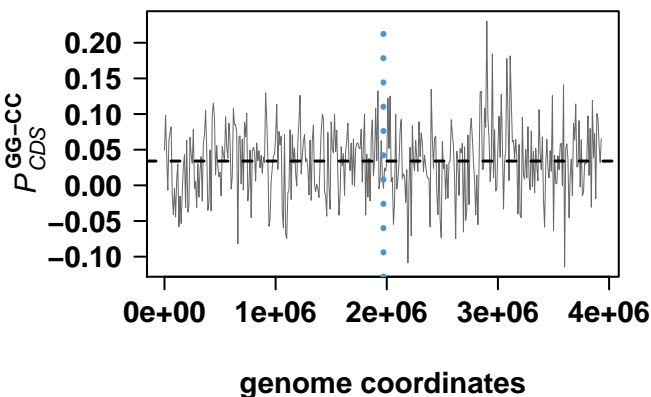
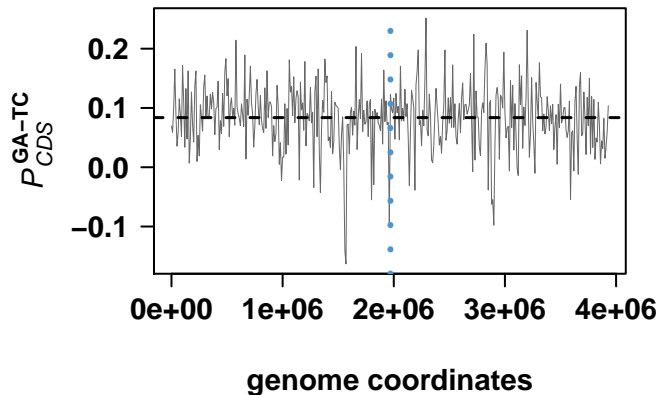
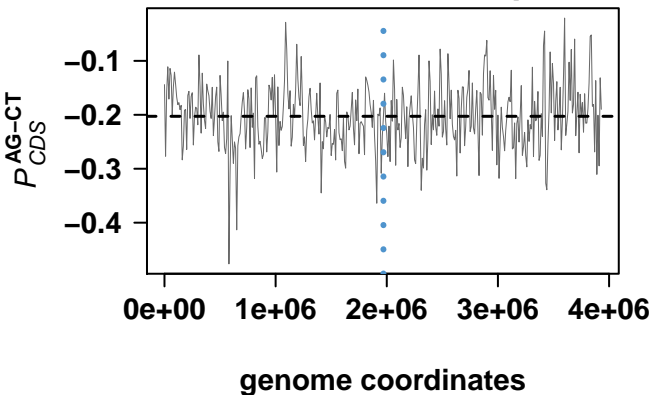


genome coordinates

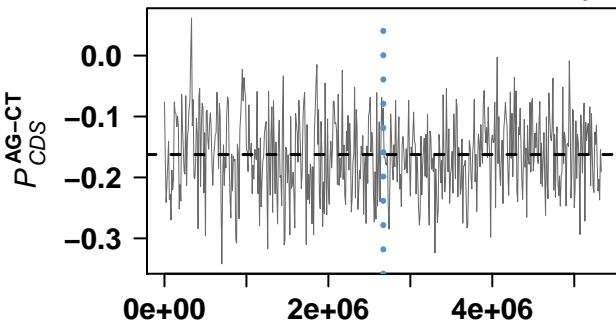


genome coordinates

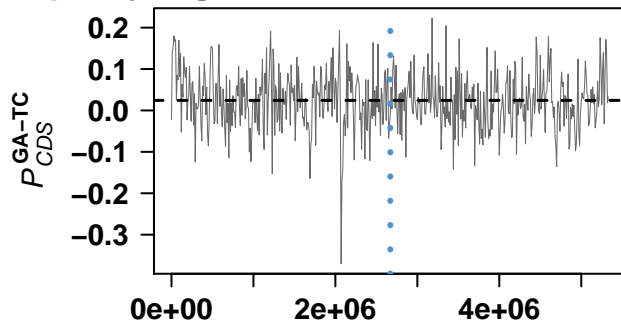
Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67



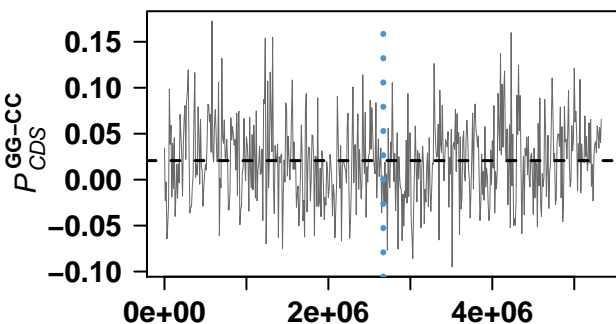
Pseudomonas syringae pv. *syringae* B728a



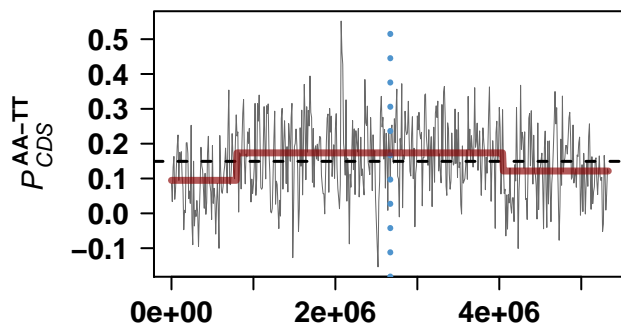
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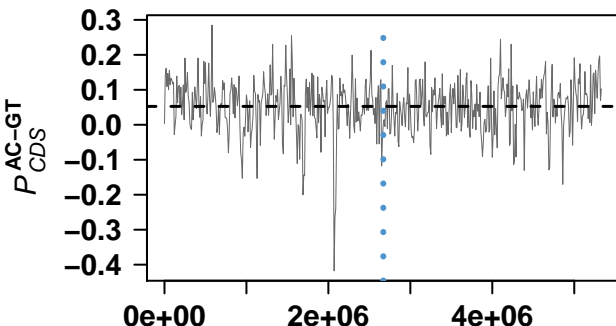
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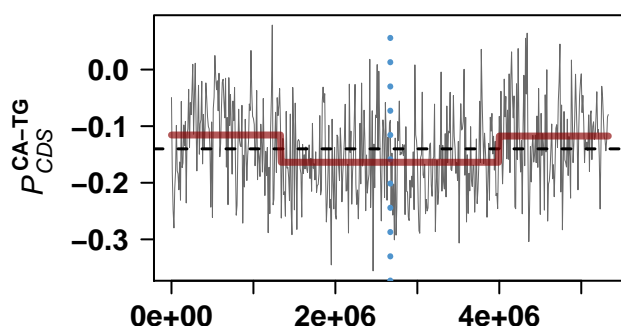
genome coordinates



genome coordinates

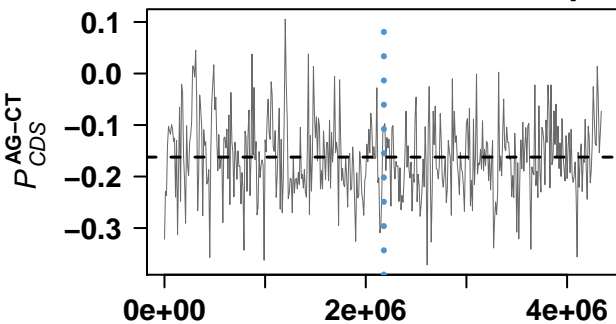


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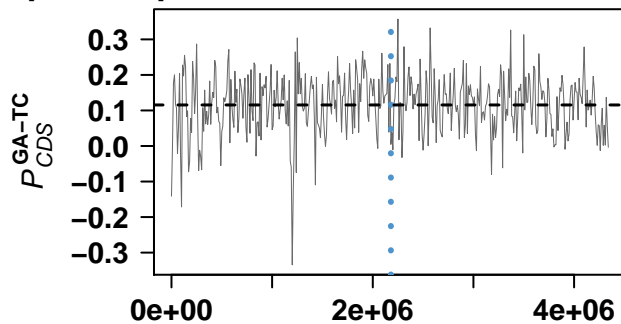


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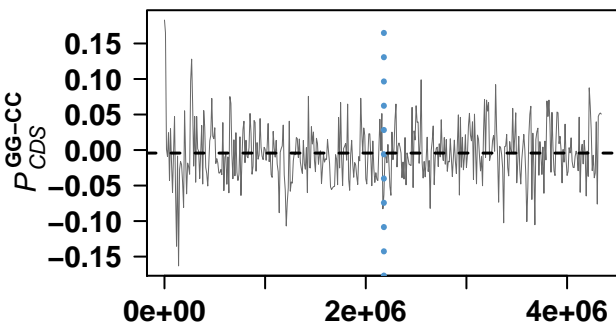
Xanthomonas campestris pv. *campestris* str. 8004



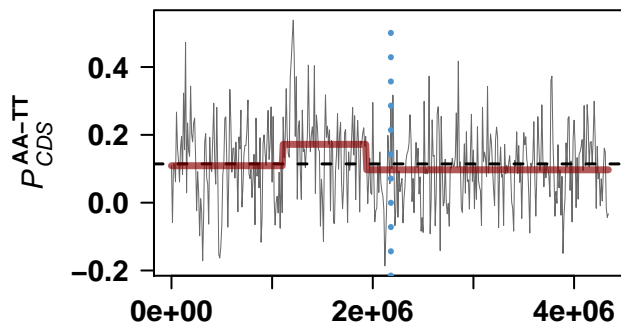
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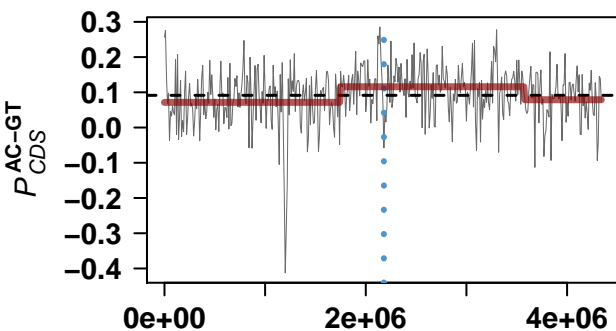
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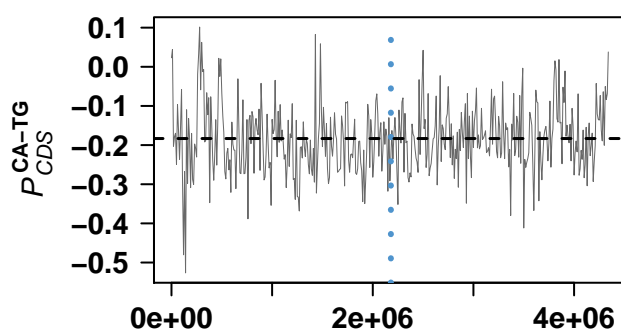
genome coordinates



genome coordinates

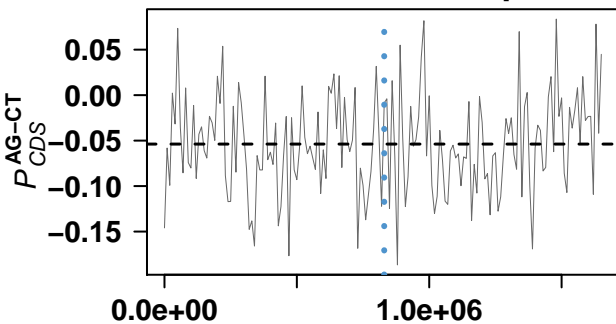


genome coordinates

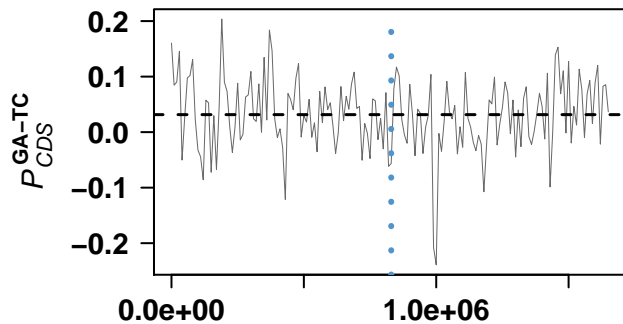


genome coordinates

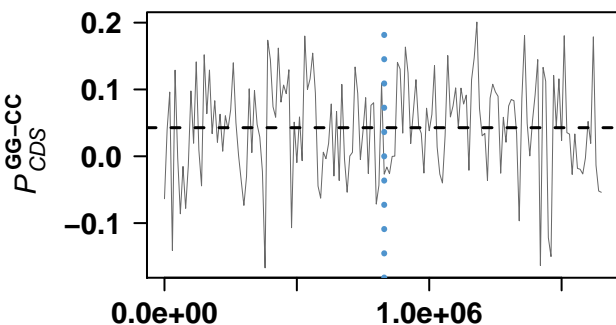
Haemophilus influenzae 86-028NP



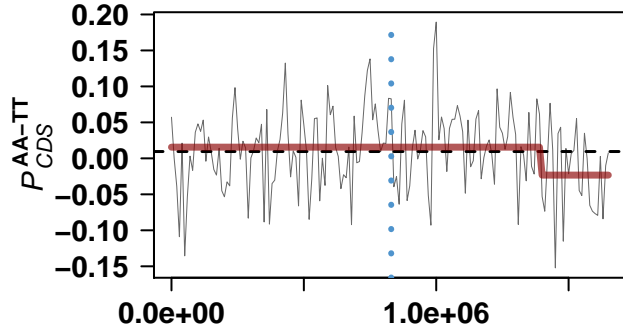
genome coordinates



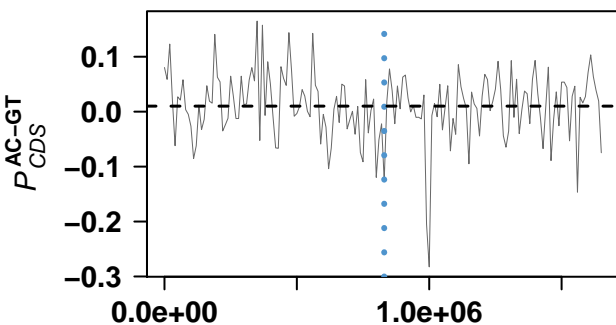
genome coordinates



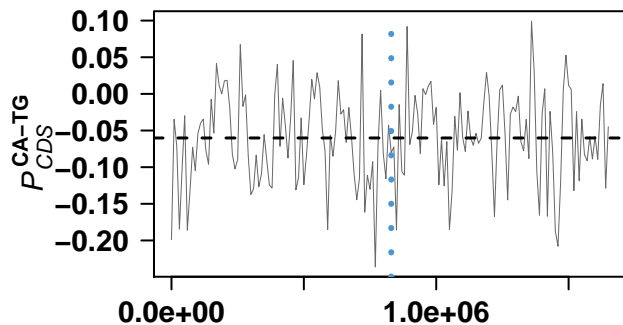
genome coordinates



genome coordinates

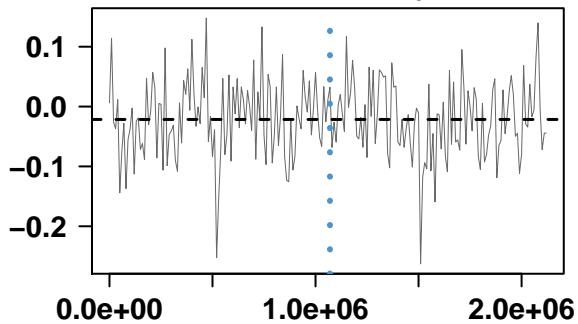


genome coordinates

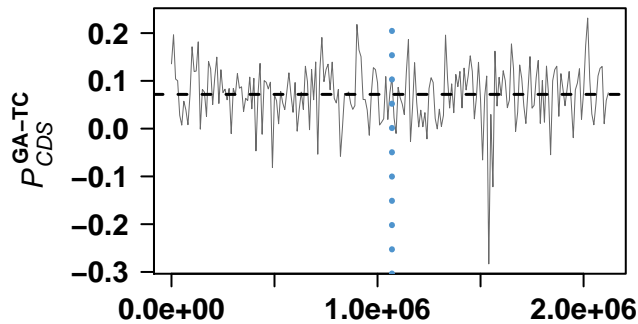


genome coordinates

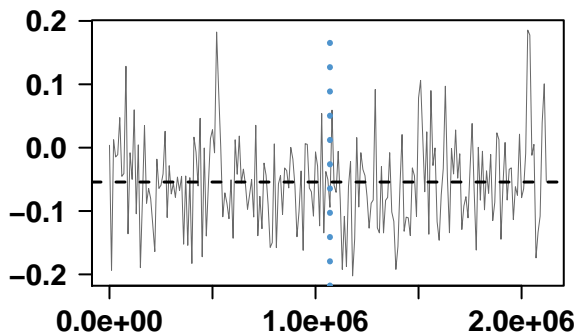
Psychrobacter arcticus 273-4



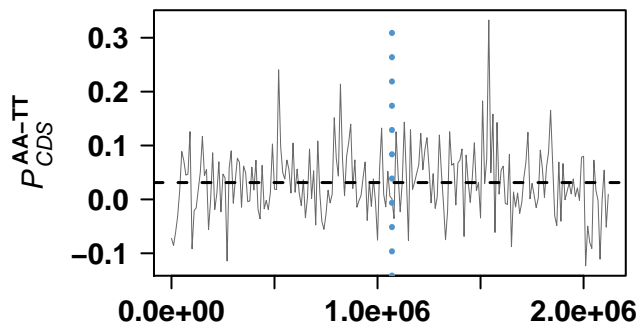
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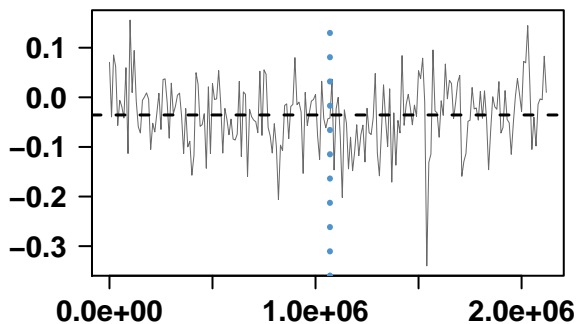
genome coordinates



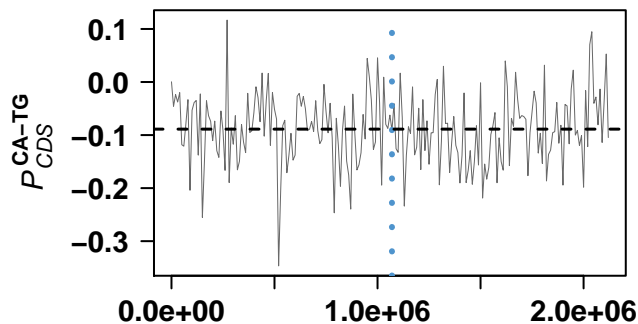
genome coordinates



genome coordinates

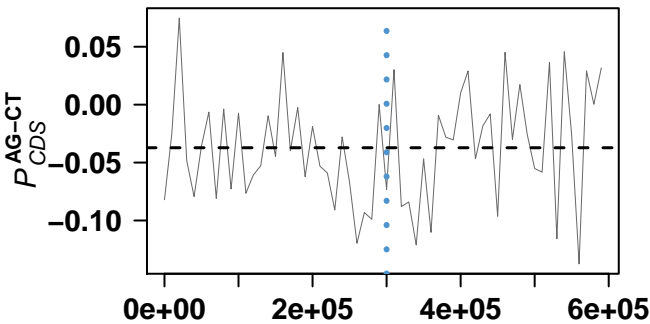


genome coordinates

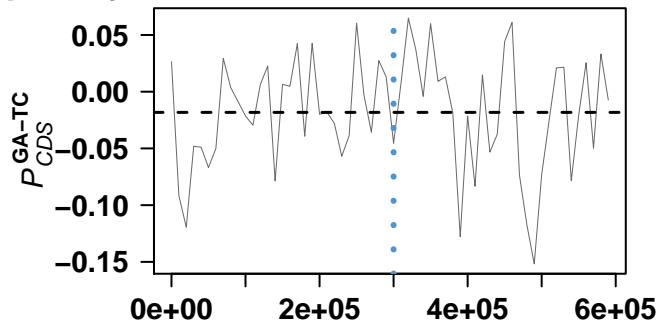


genome coordinates

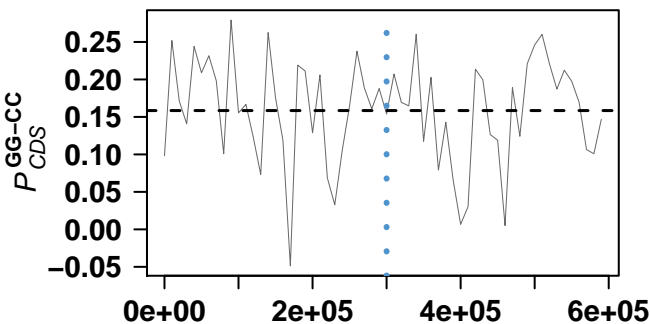
Candidatus Blochmannia pennsylvanicus str. BPEN



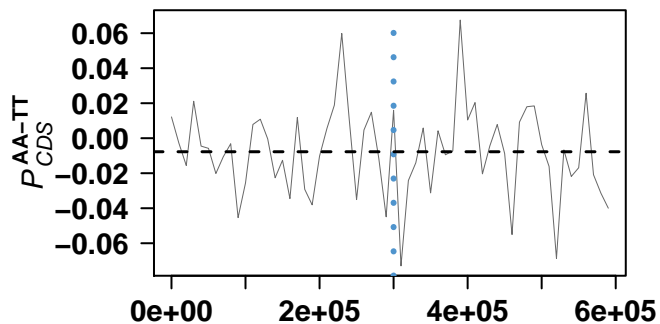
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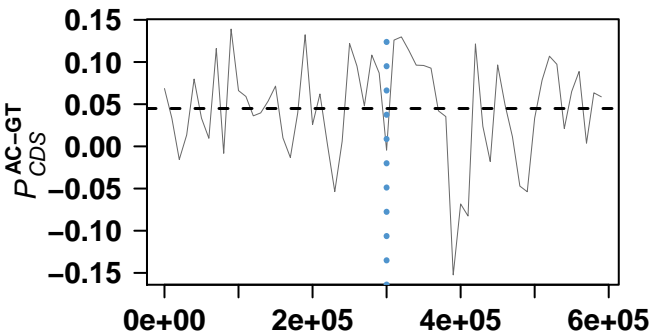
genome coordinates



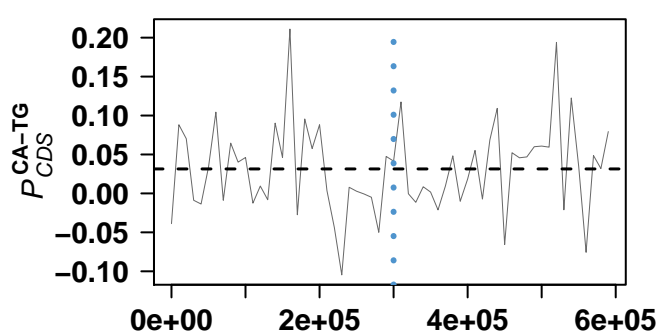
genome coordinates



genome coordinates

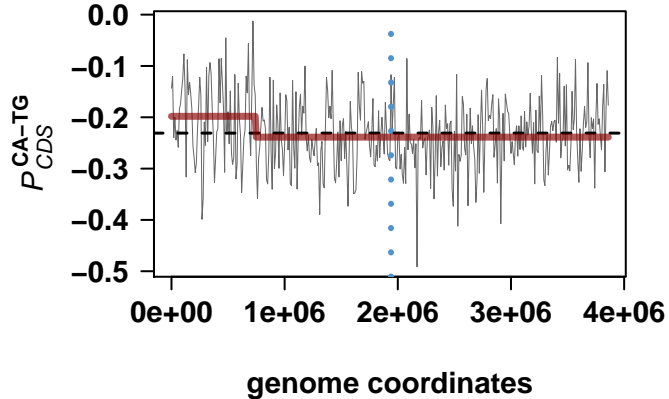
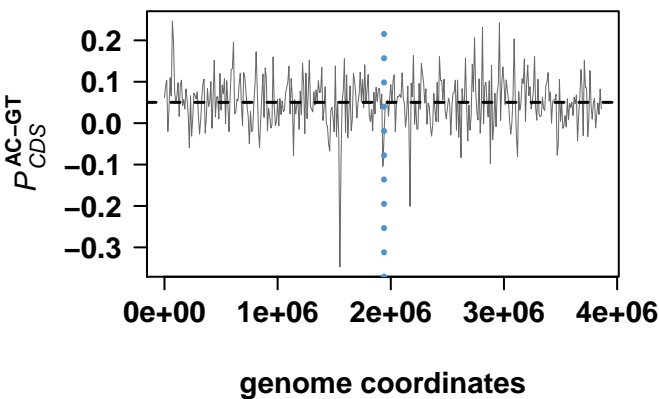
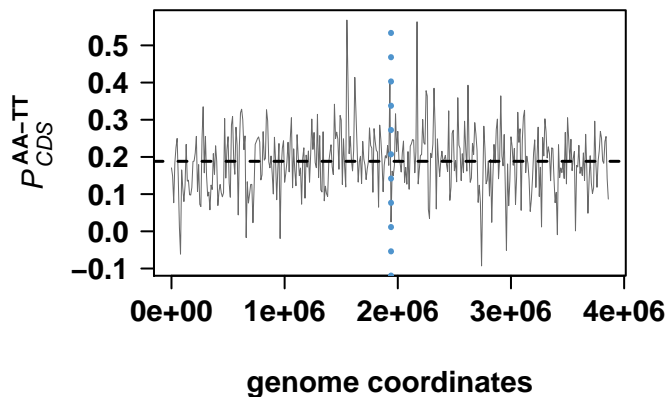
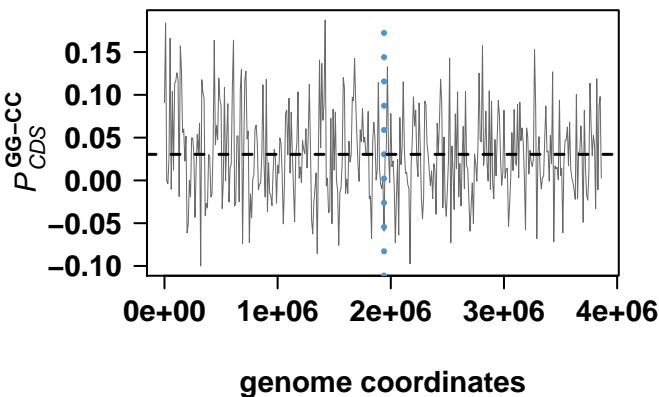
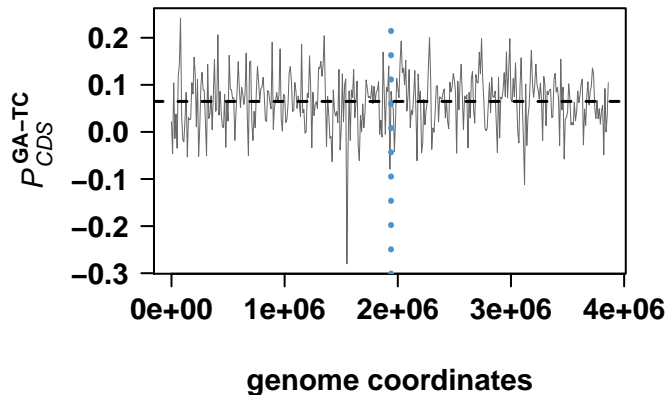
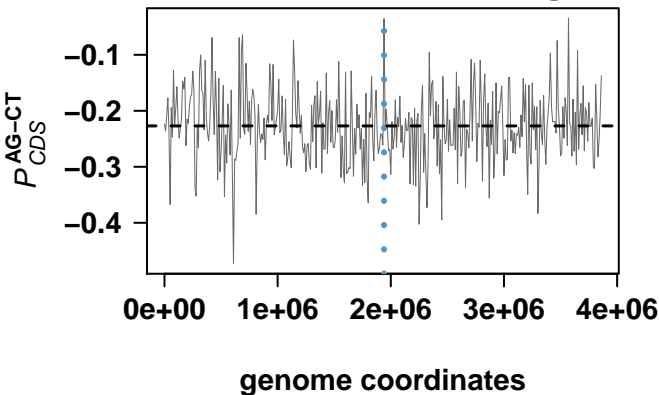


genome coordinates

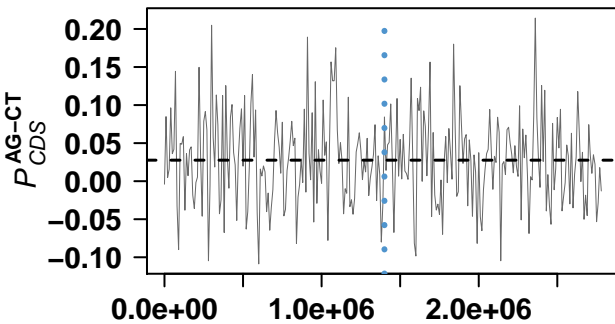


genome coordinates

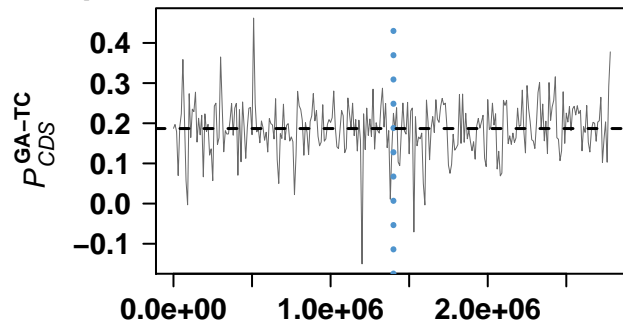
Shigella sonnei Ss046



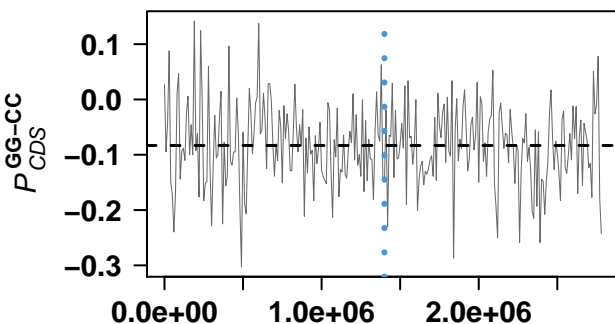
Pseudoalteromonas haloplanktis TAC125



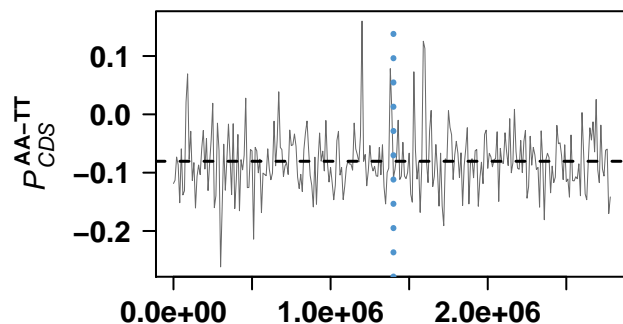
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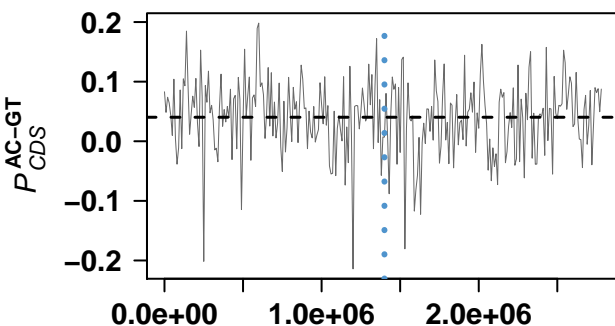
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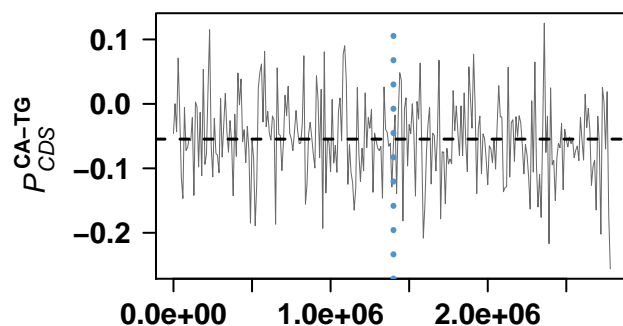
genome coordinates



genome coordinates

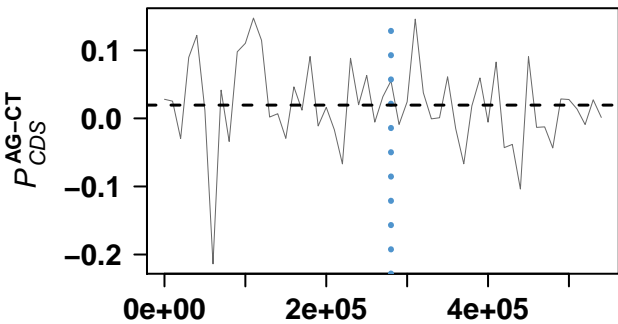


genome coordinates

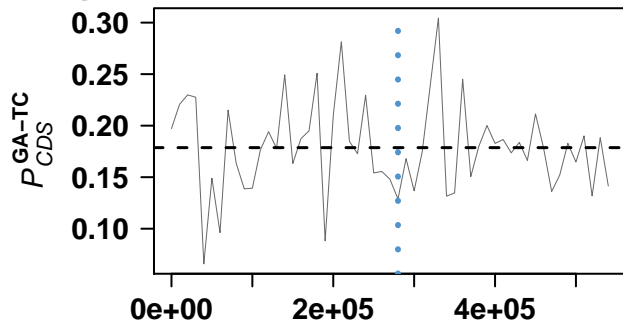


genome coordinates

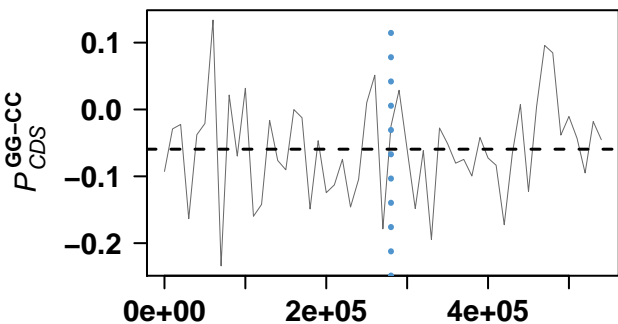
Pseudoalteromonas haloplanktis TAC125



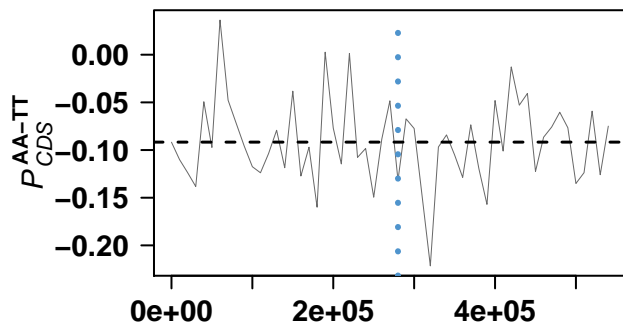
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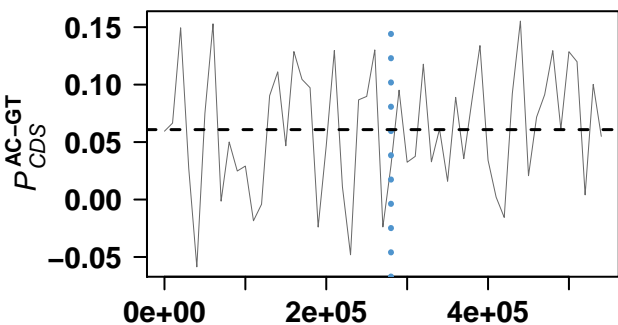
genome coordinates



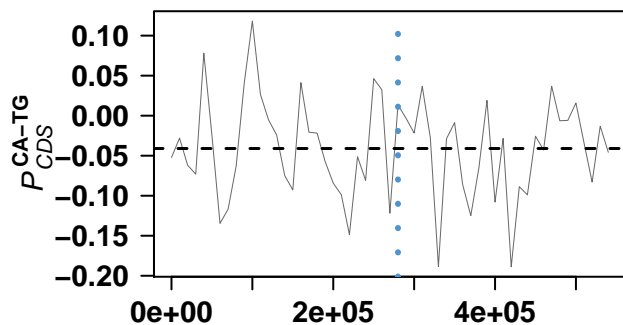
genome coordinates



genome coordinates

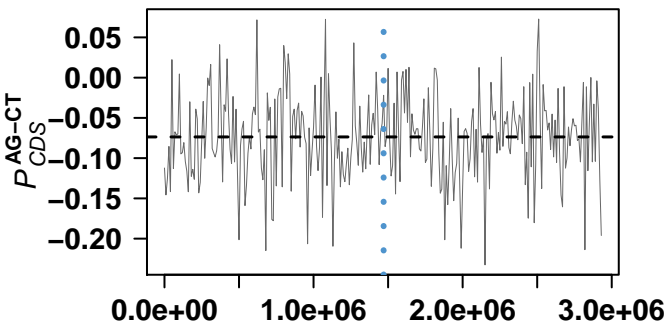


genome coordinates

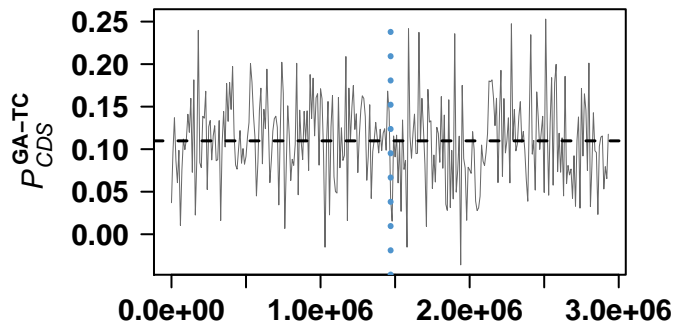


genome coordinates

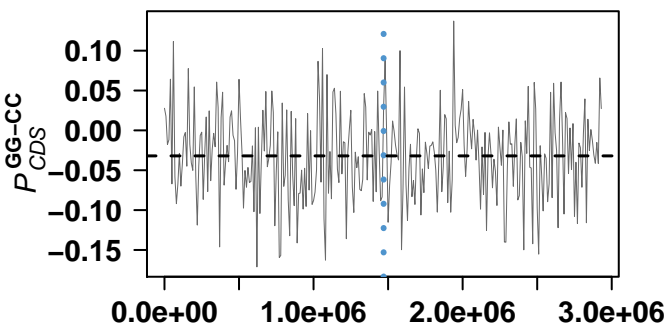
Nitrosococcus oceani ATCC 19707



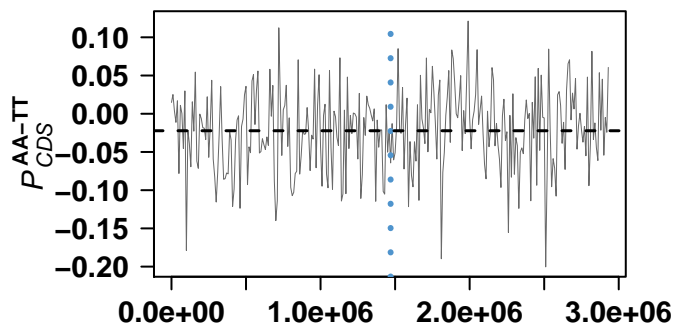
genome coordinates



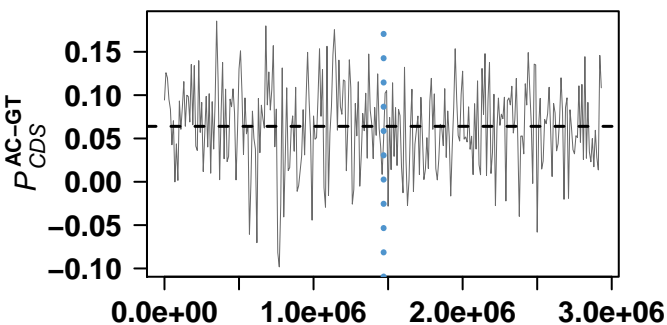
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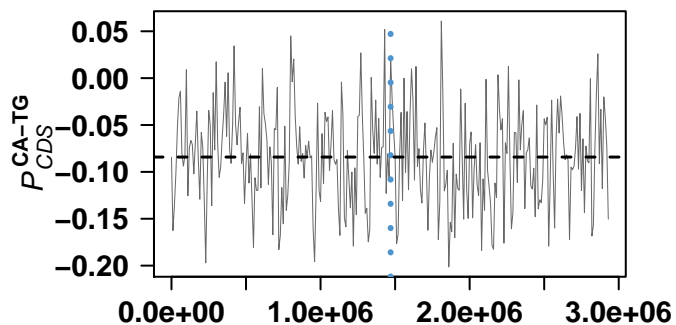
genome coordinates



genome coordinates

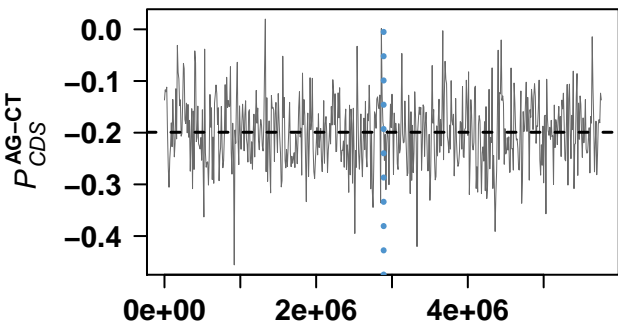


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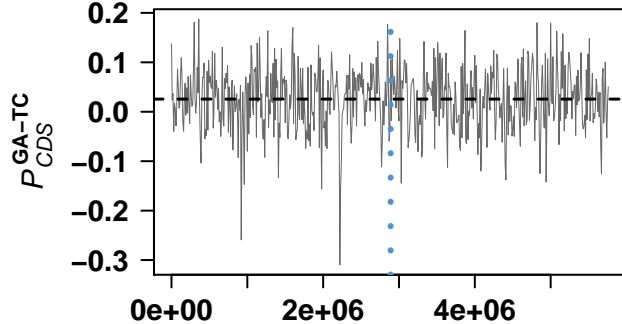


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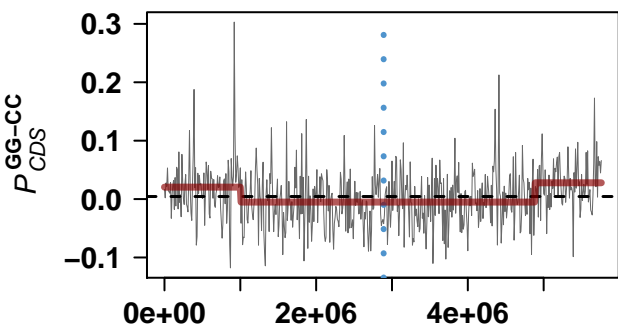
Pseudomonas fluorescens Pf0-1



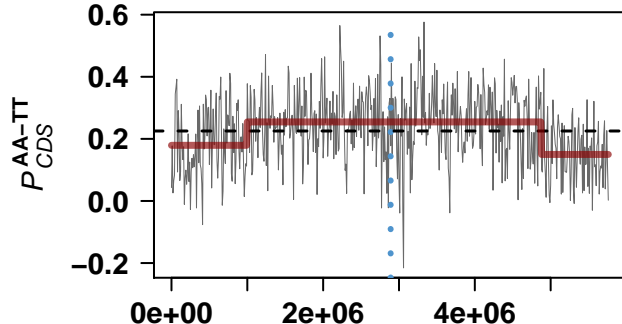
genome coordinates



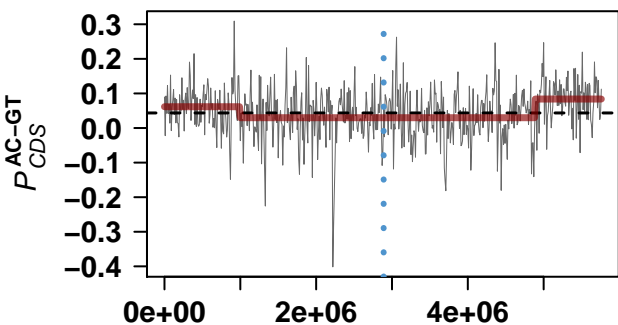
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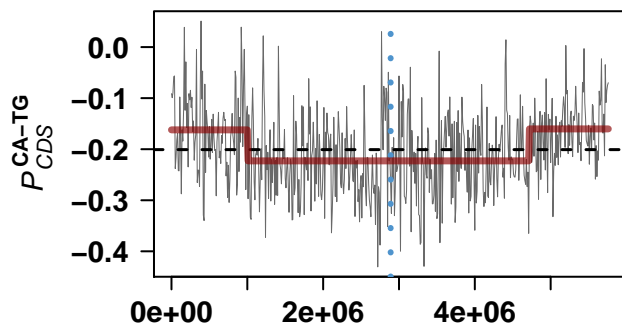
genome coordinates



genome coordinates

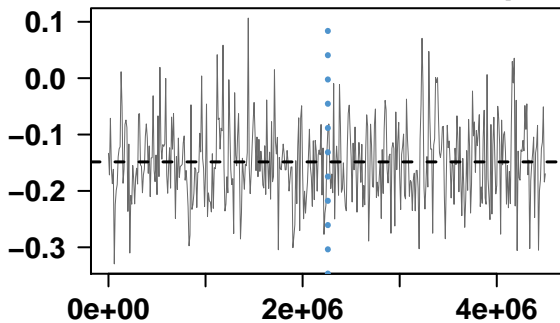


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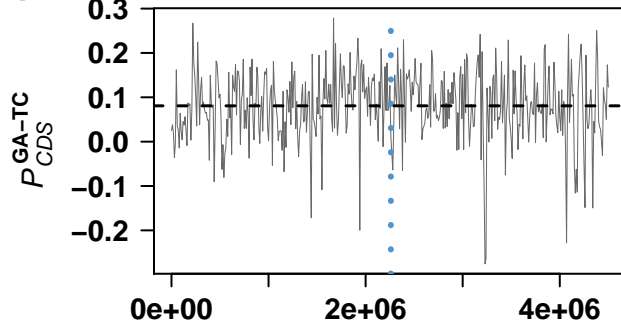


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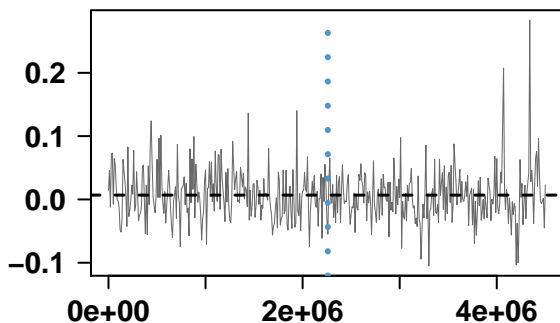
Xanthomonas campestris pv. *vesicatoria* str. 85-10



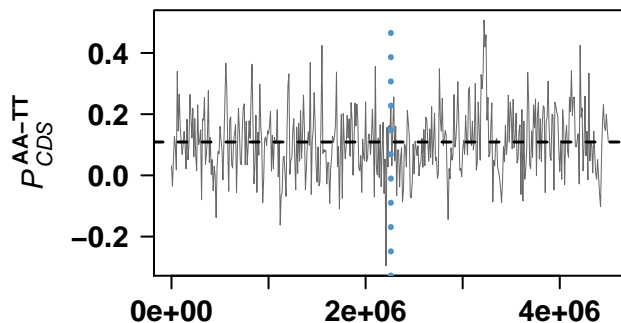
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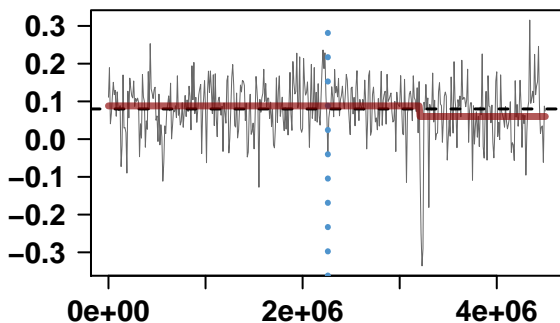
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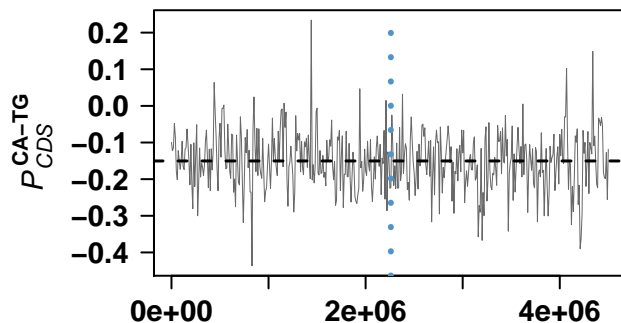
genome coordinates



genome coordinates

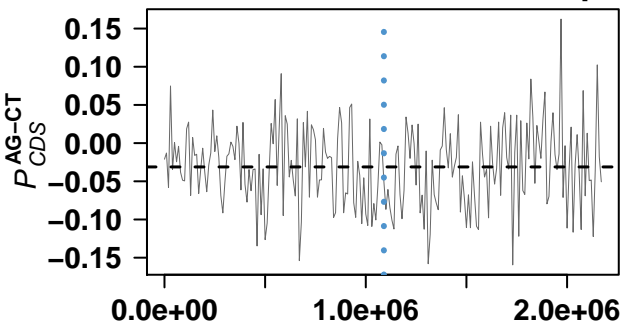


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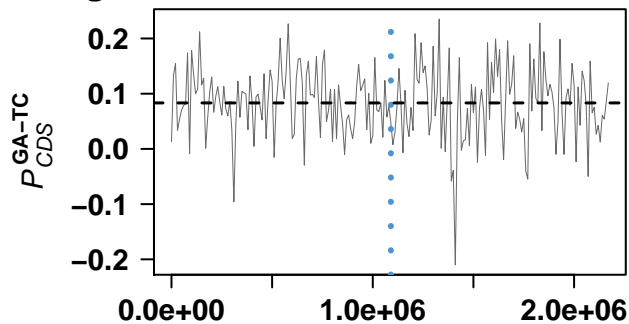


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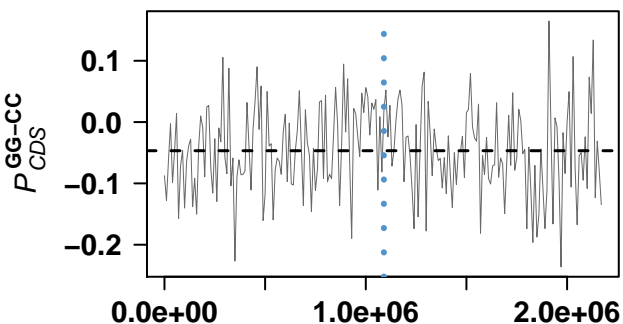
Thiomicrospira crunogena XCL-2



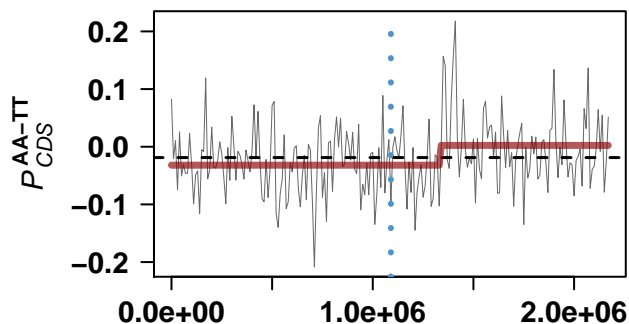
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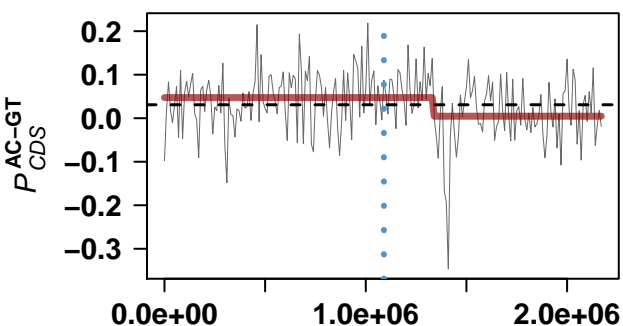
genome coordinates



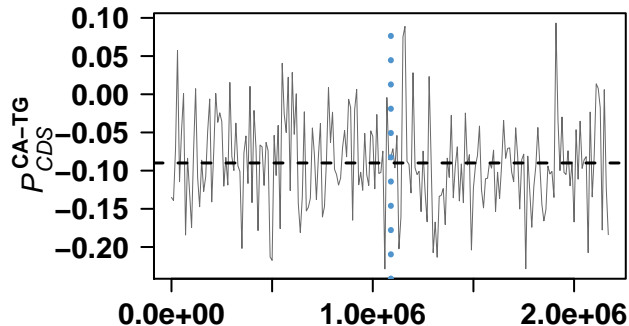
genome coordinates



genome coordinates

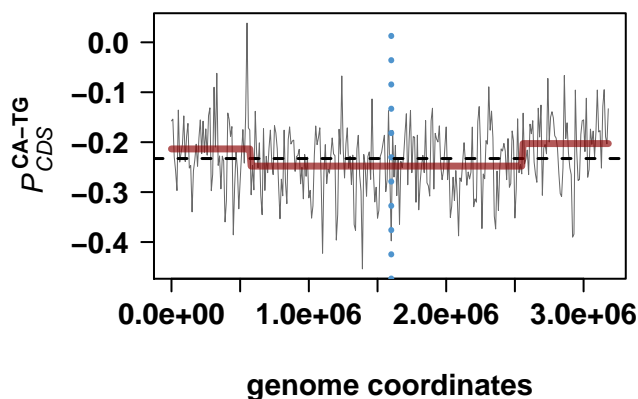
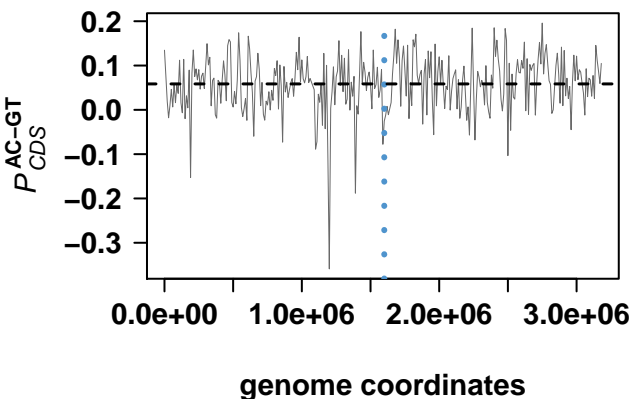
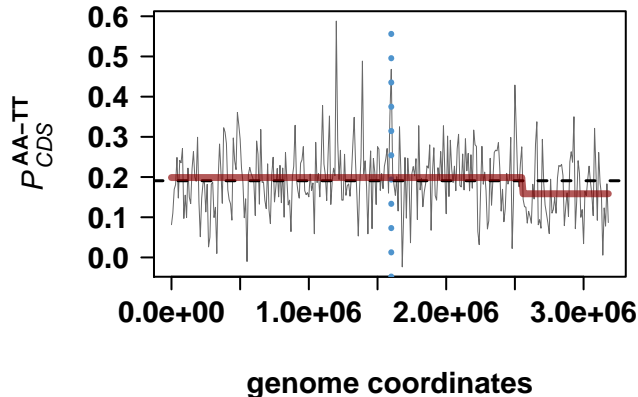
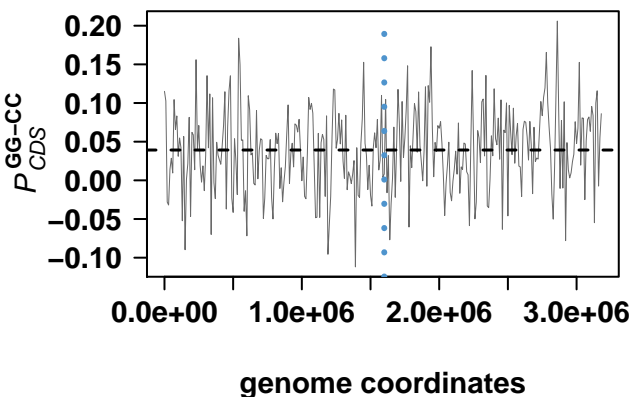
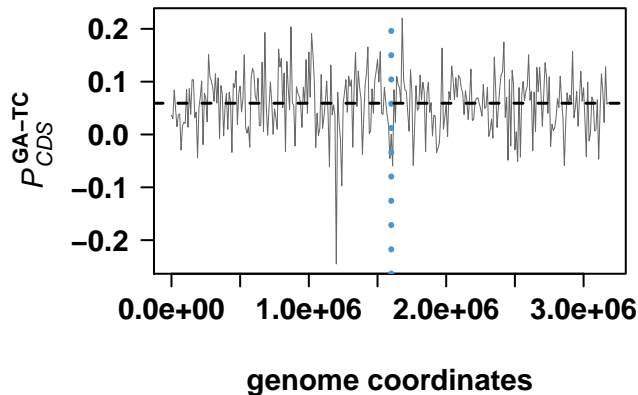
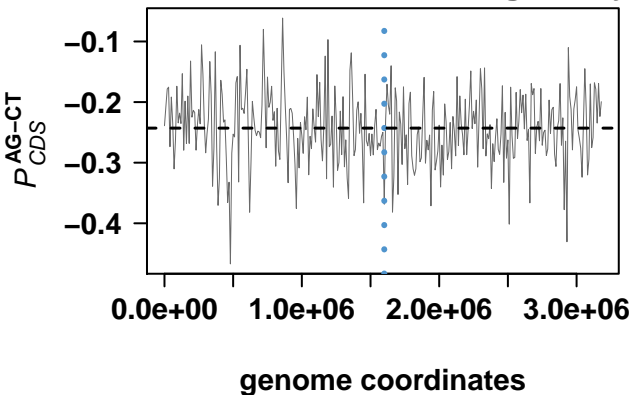


genome coordinates

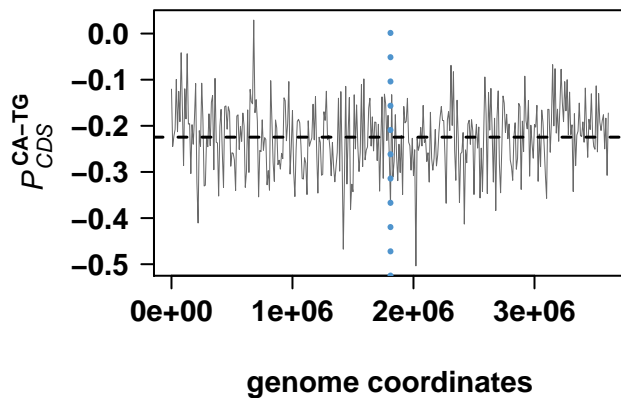
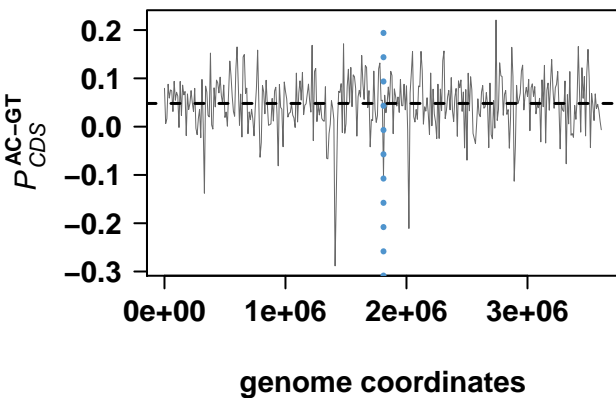
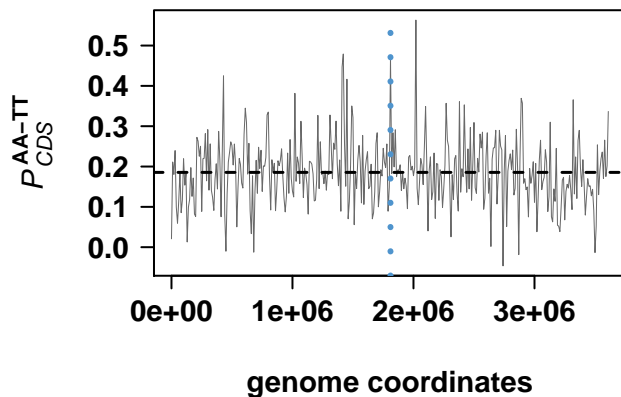
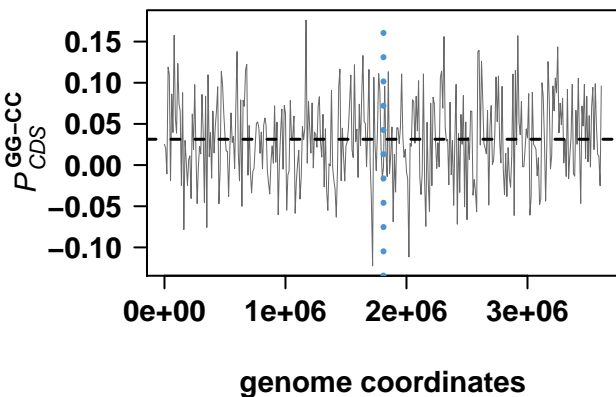
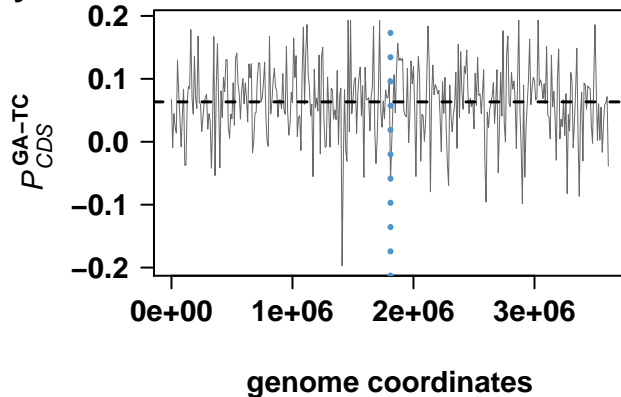
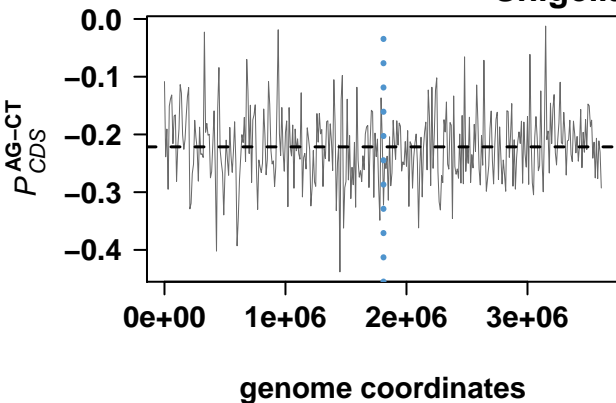


genome coordinates

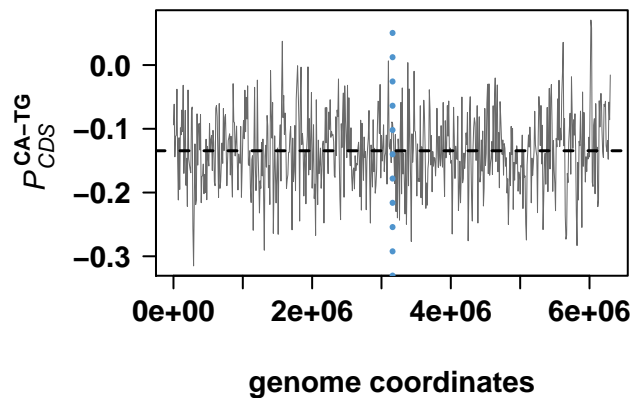
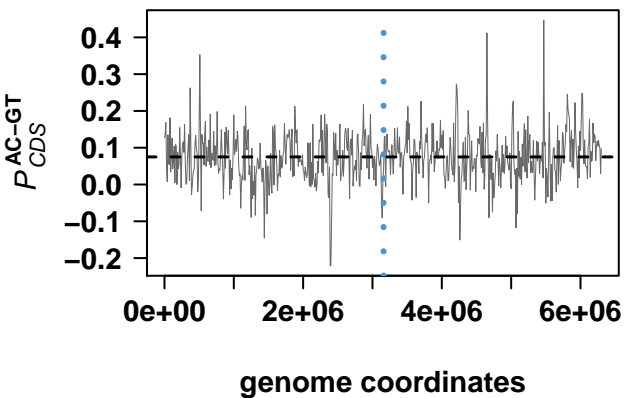
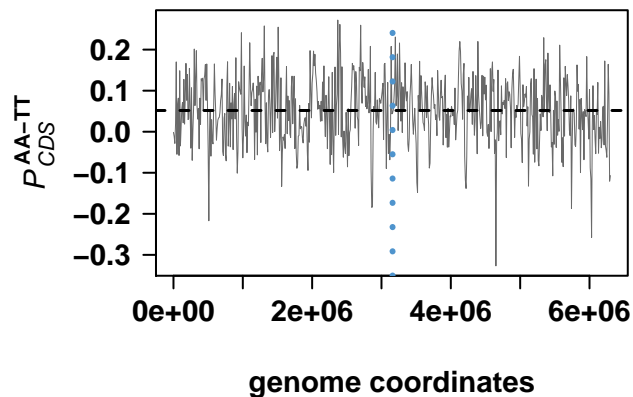
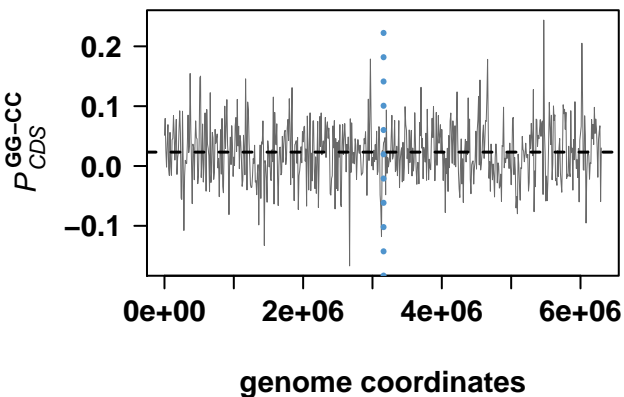
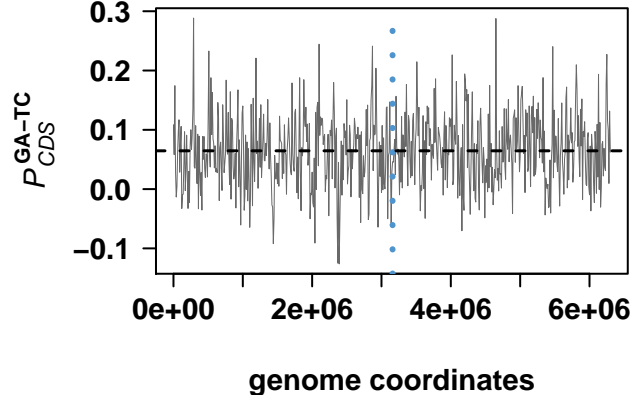
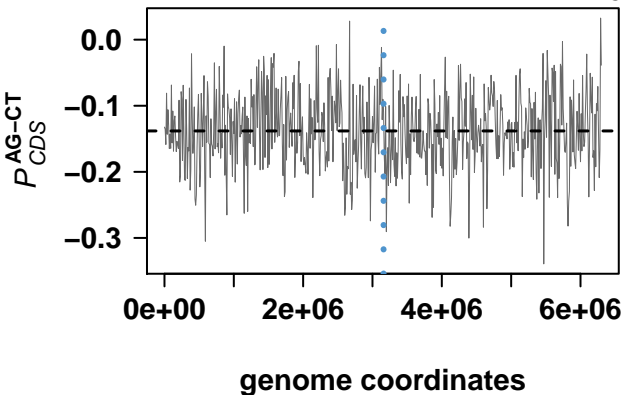
Shigella dysenteriae Sd197



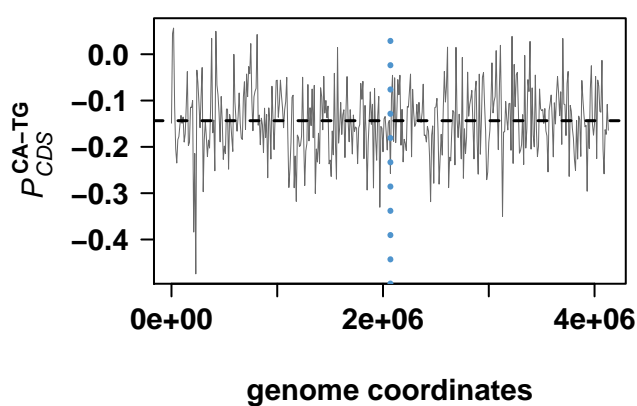
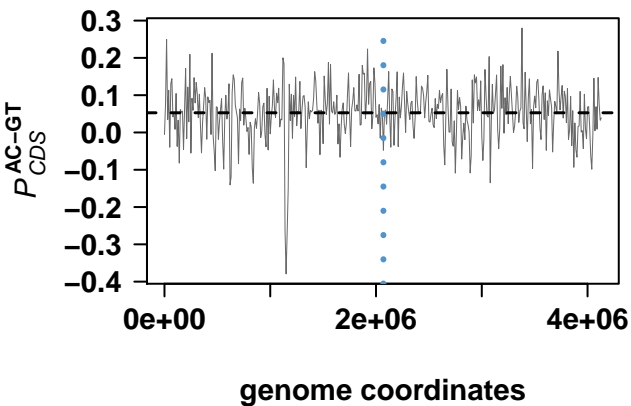
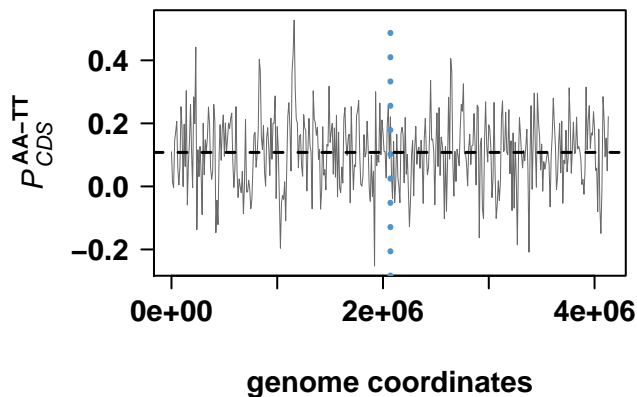
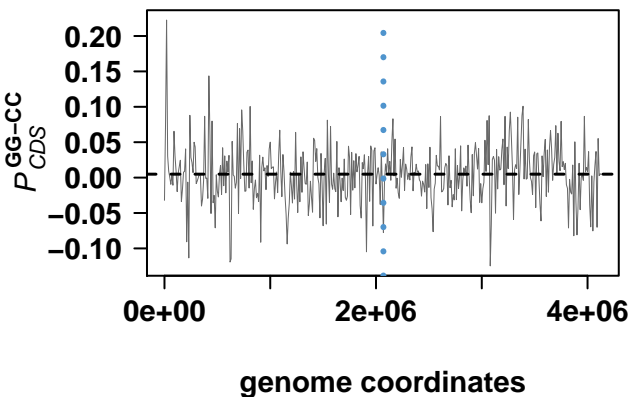
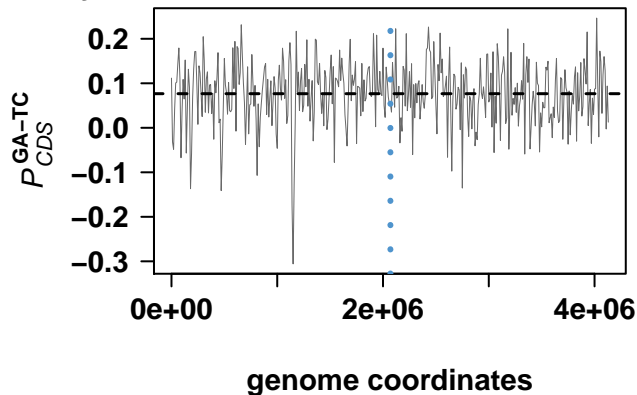
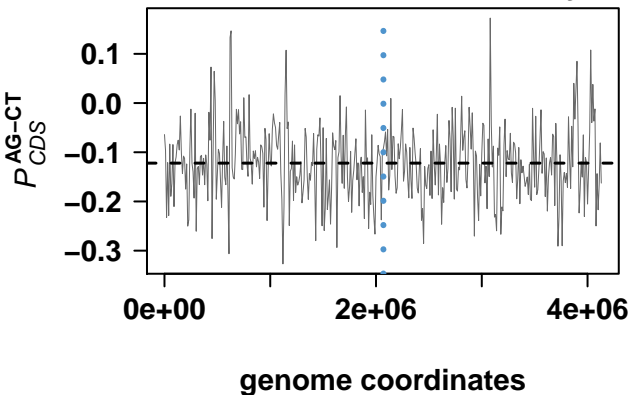
Shigella boydii Sb227



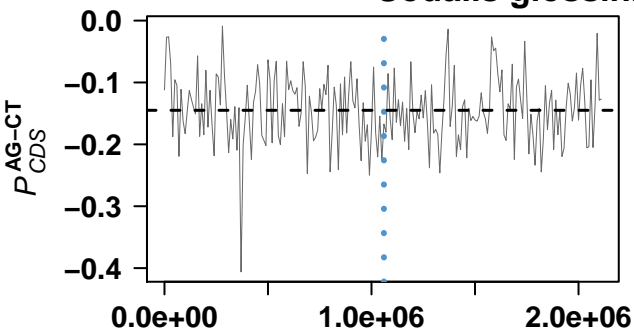
Hahella chejuensis KCTC 2396



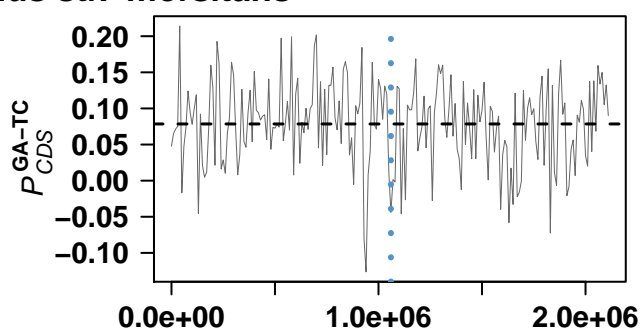
Xanthomonas oryzae pv. oryzae MAFF 311018



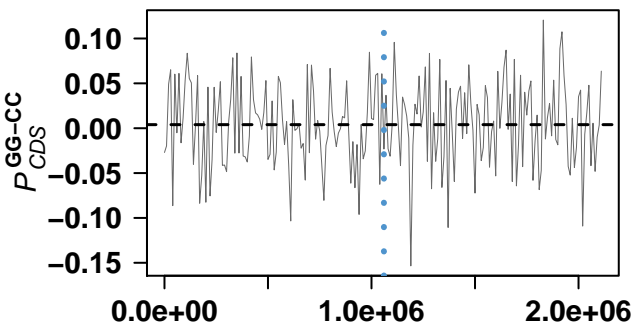
Sodalis glossinidius str. 'morsitans'



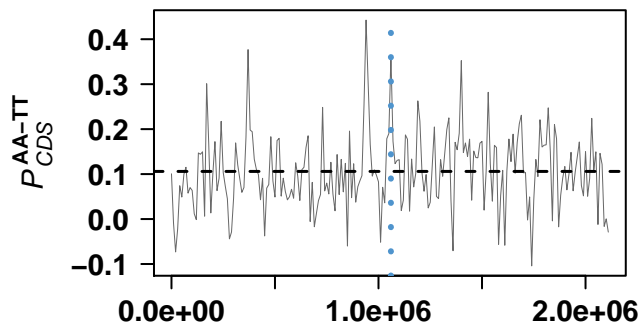
genome coordinates



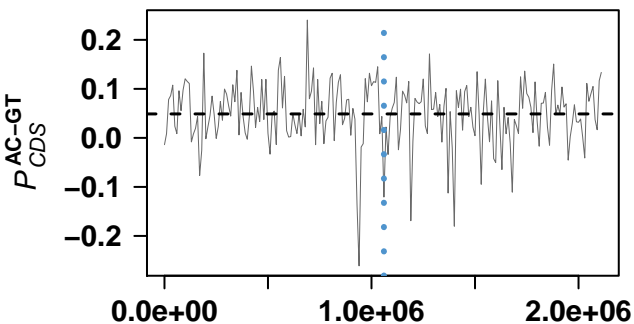
genome coordinates



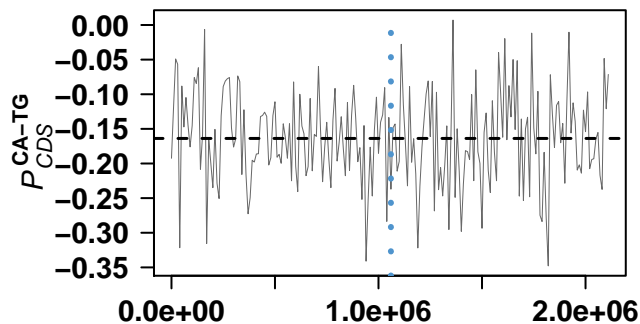
genome coordinates



genome coordinates

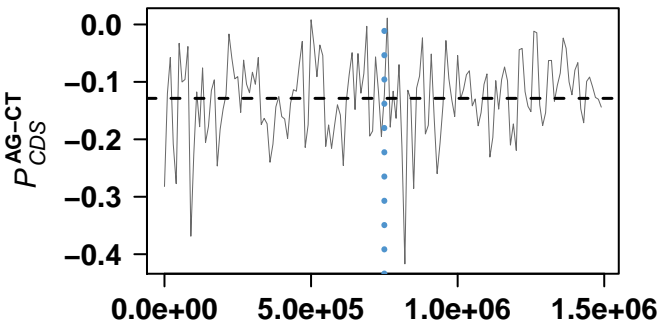


genome coordinates

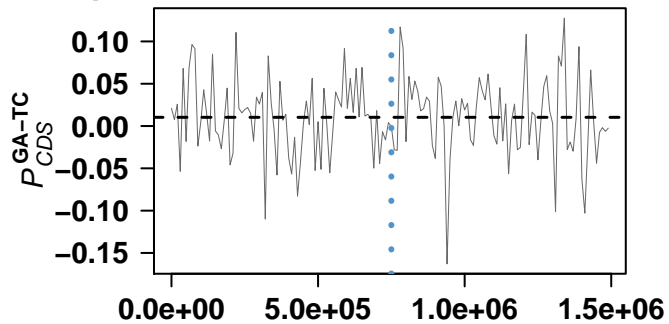


genome coordinates

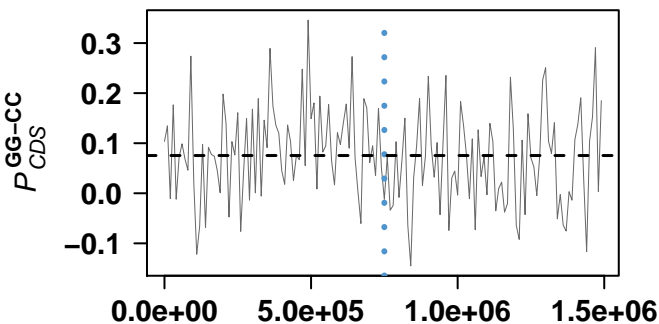
Francisella tularensis subsp. holarctica LVS



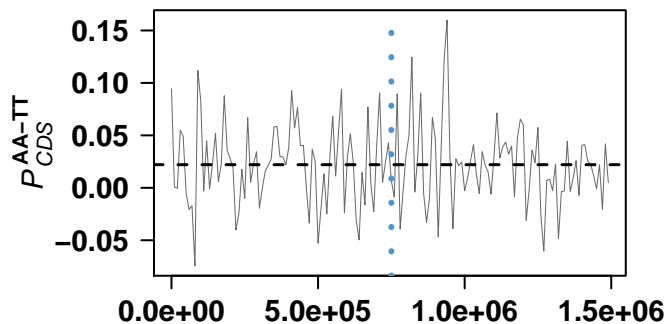
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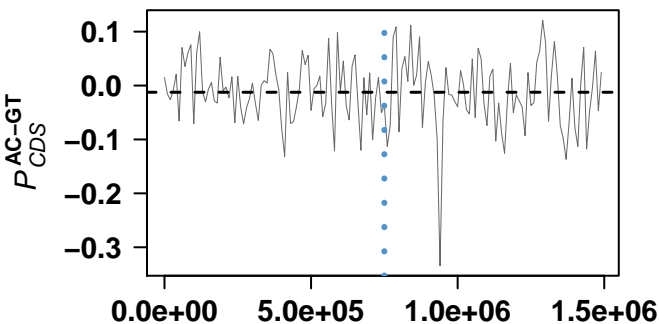
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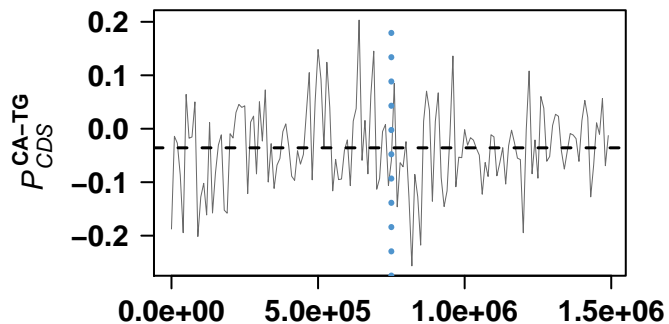
genome coordinates



genome coordinates

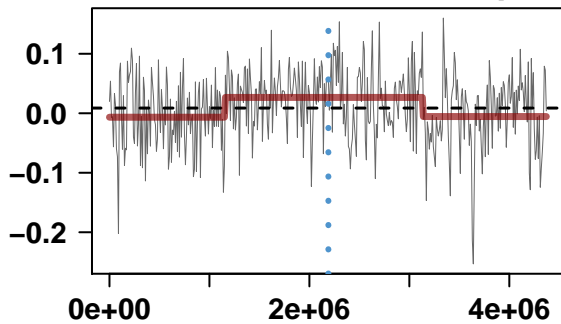


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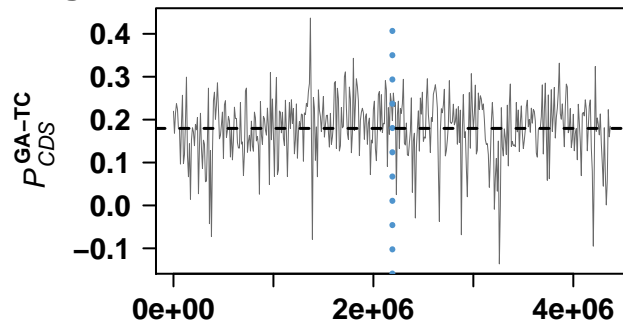


genome coordinates

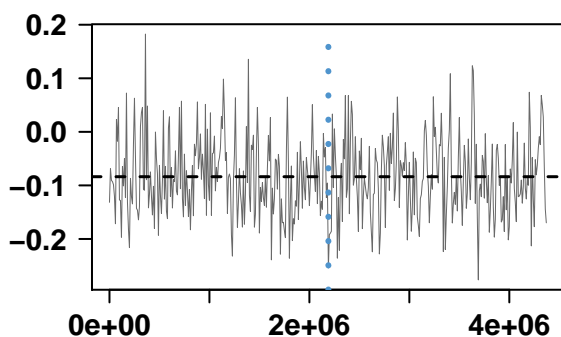
Saccharophagus degradans 2-40



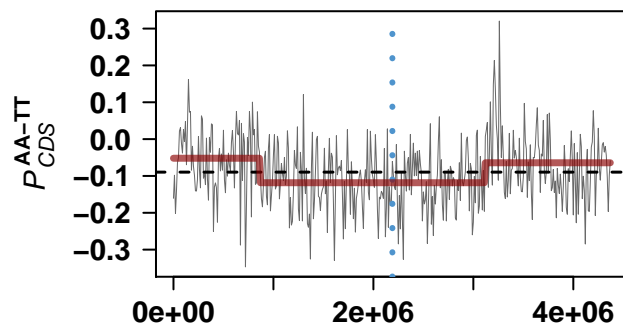
genome coordinates



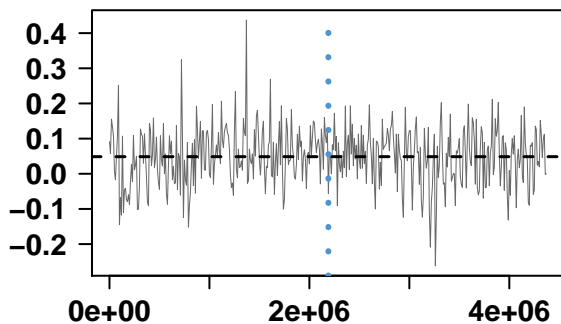
genome coordinates



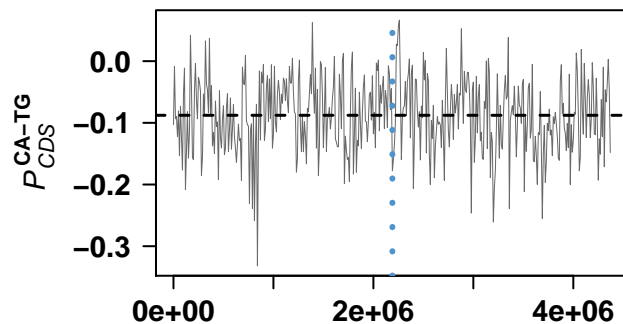
genome coordinates



genome coordinates

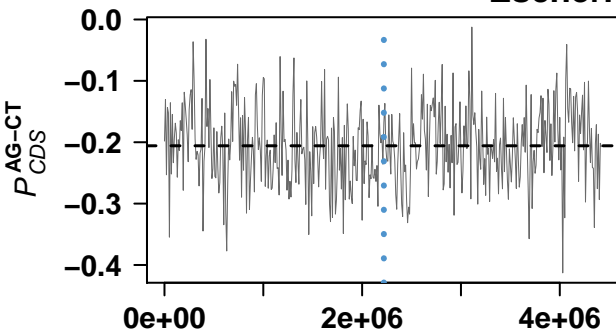


genome coordinates

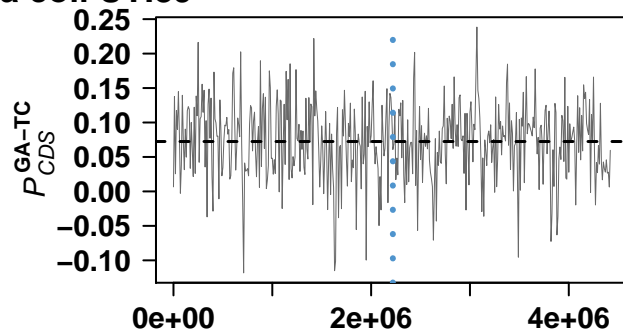


genome coordinates

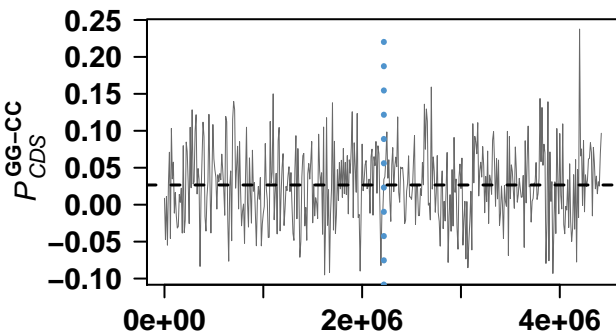
Escherichia coli UTI89



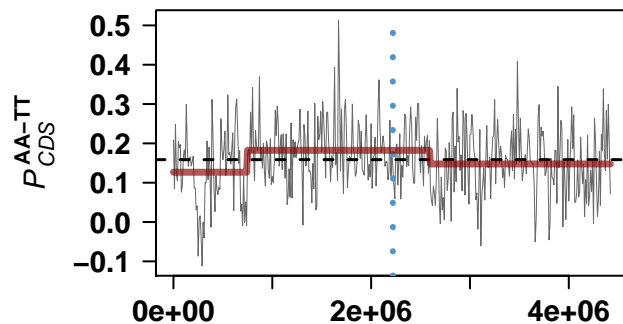
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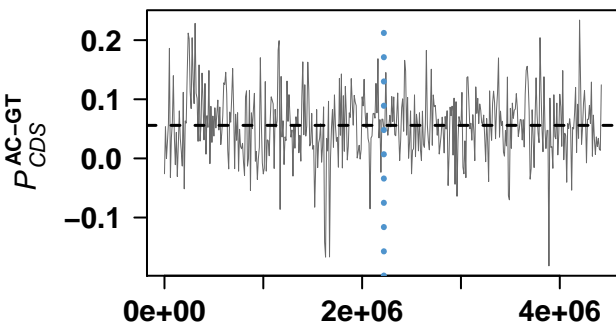
genome coordinates



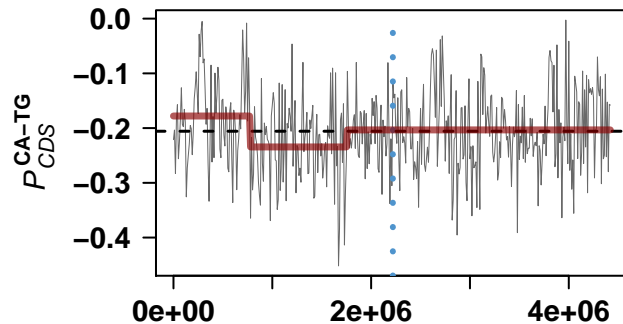
genome coordinates



genome coordinates

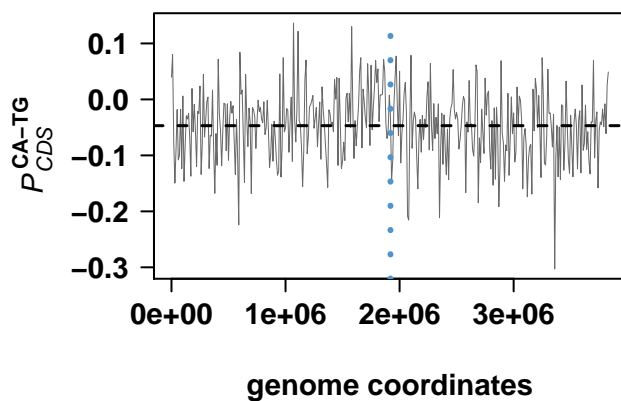
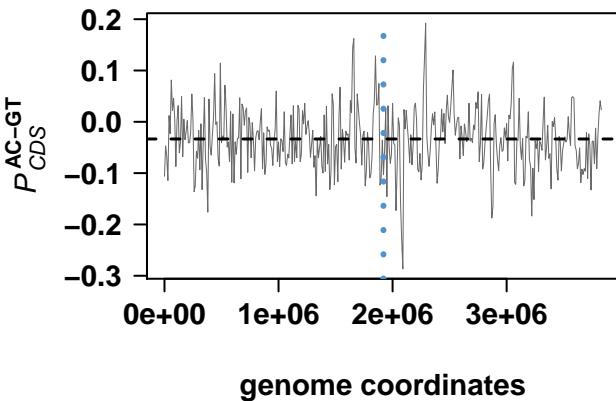
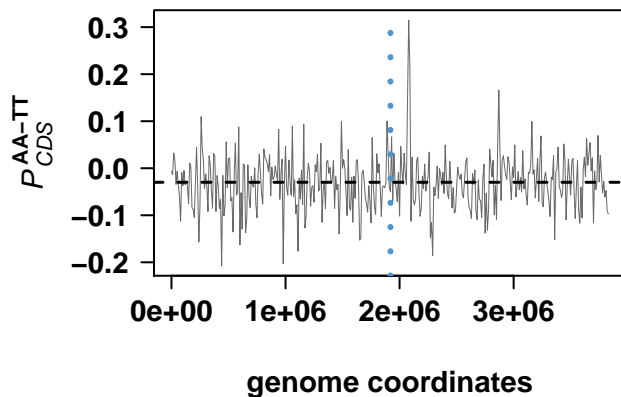
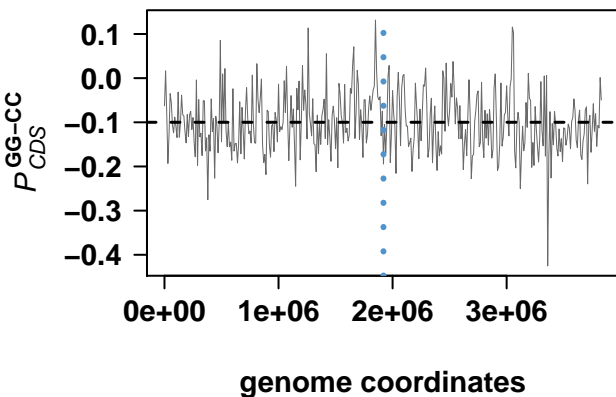
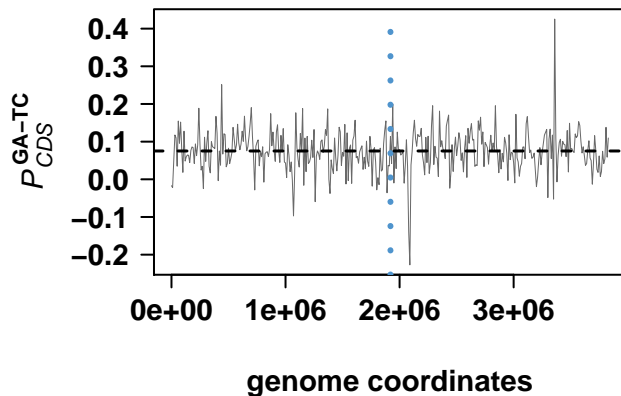
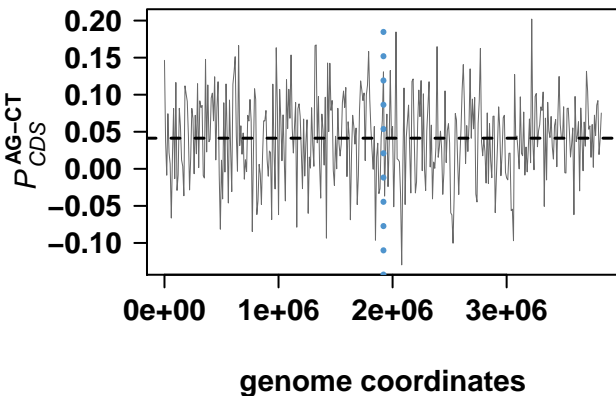


genome coordinates

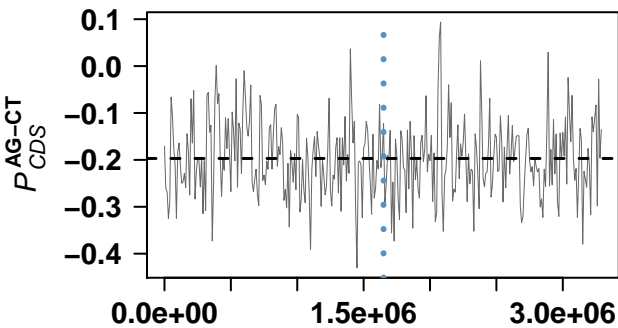


genome coordinates

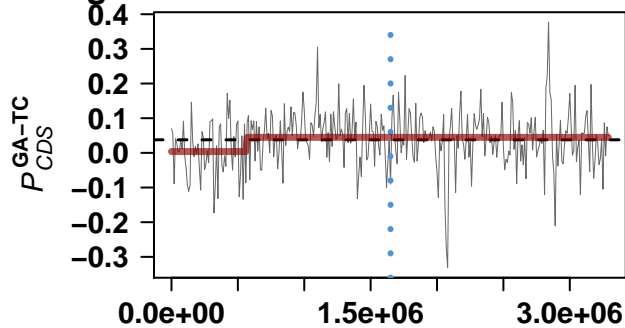
Shewanella denitrificans OS217



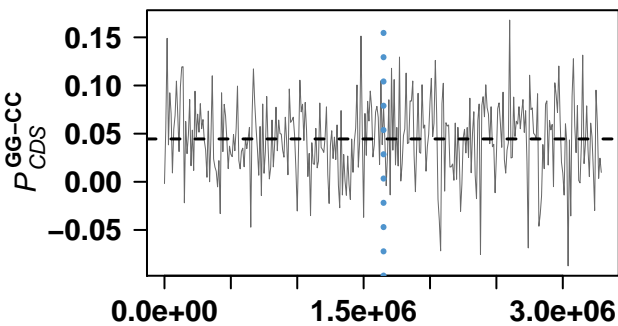
Chromohalobacter salexigens DSM 3043



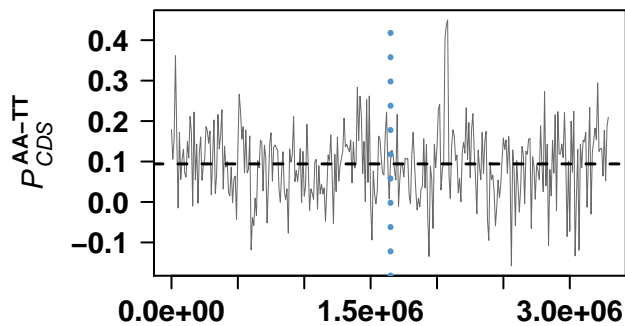
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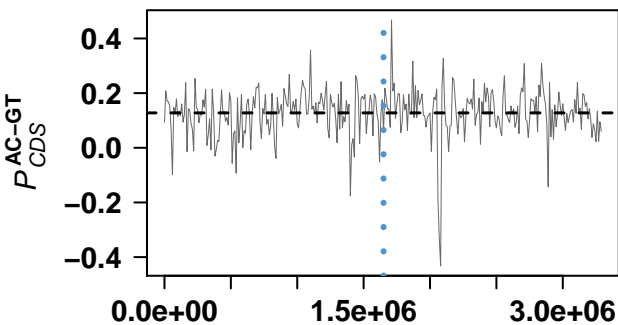
genome coordinates



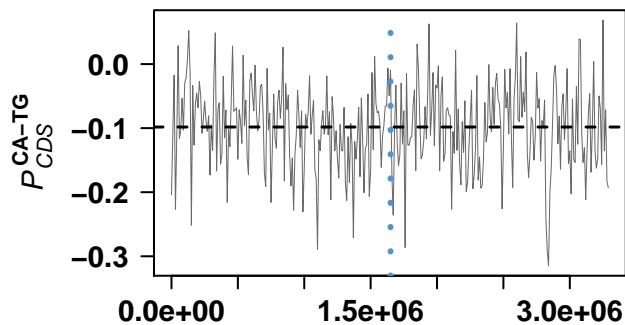
genome coordinates



genome coordinates

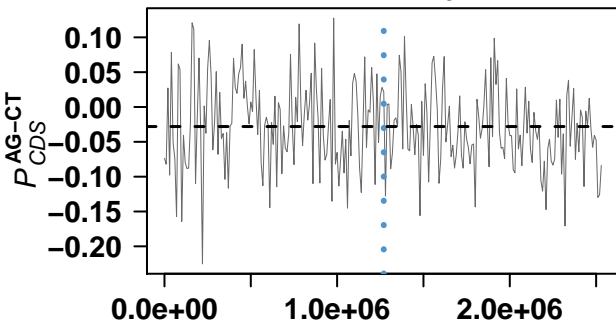


genome coordinates

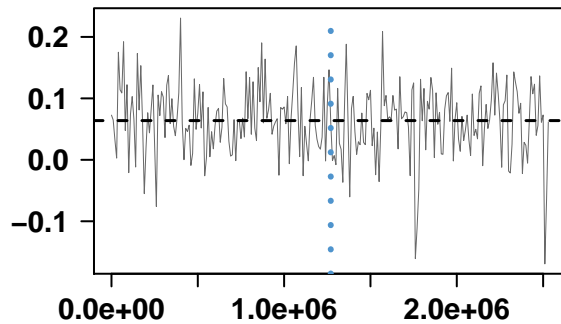


genome coordinates

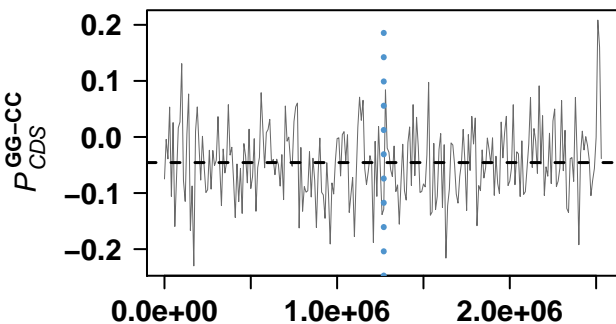
Psychrobacter cryohalientis K5



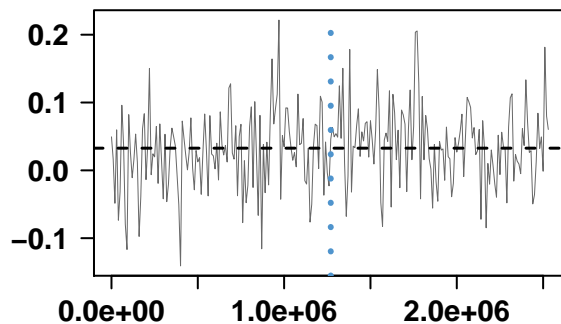
genome coordinates



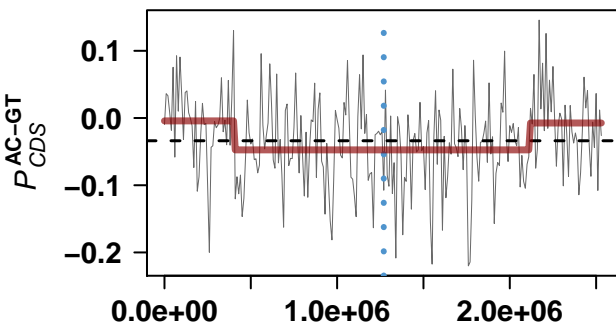
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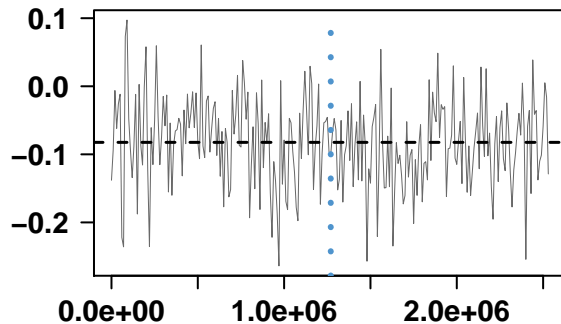
genome coordinates



genome coordinates

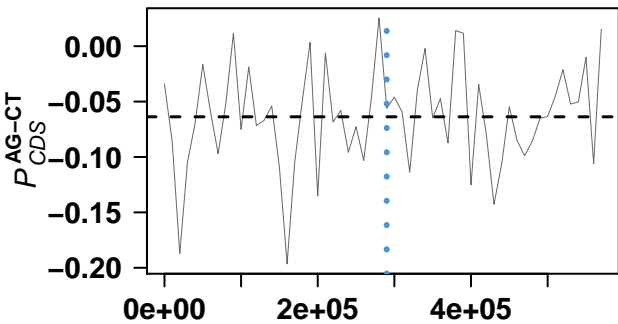


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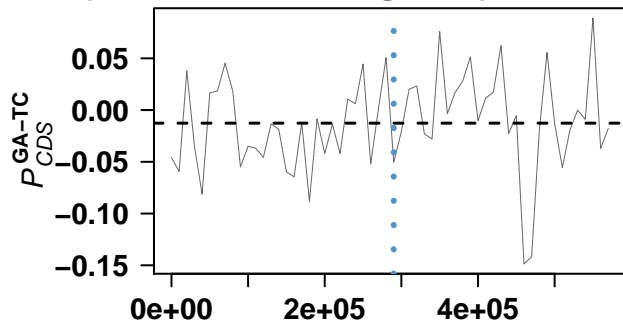


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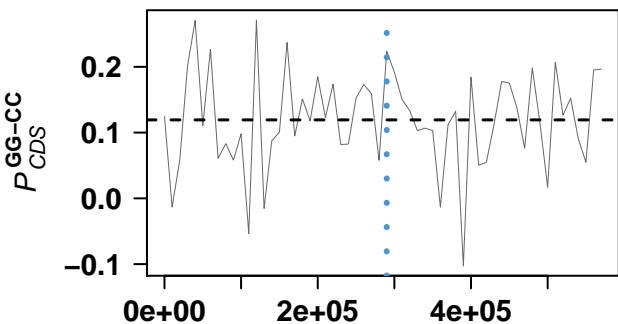
Baumannia cicadellinicola str. Hc (Homalodisca coagulata)



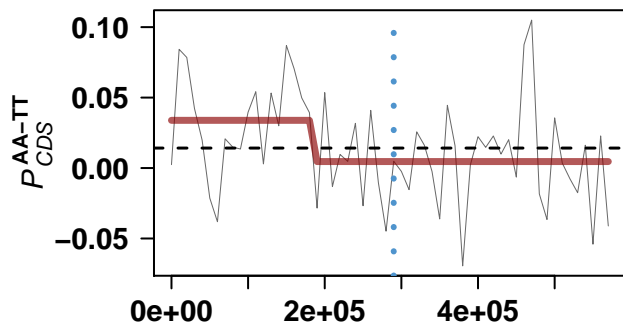
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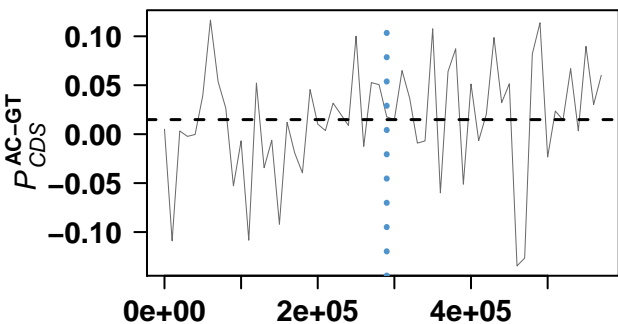
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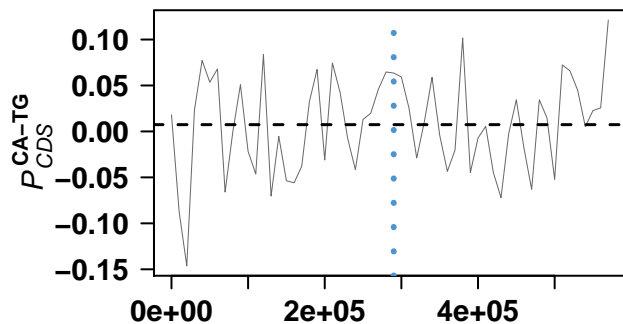
genome coordinates



genome coordinates

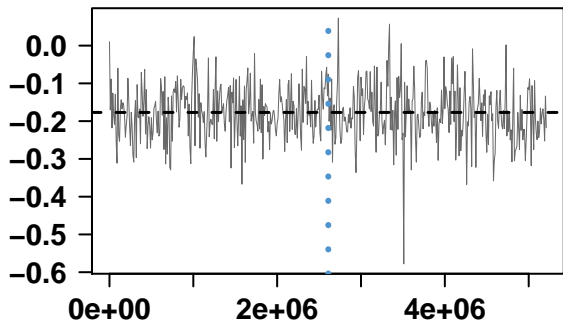


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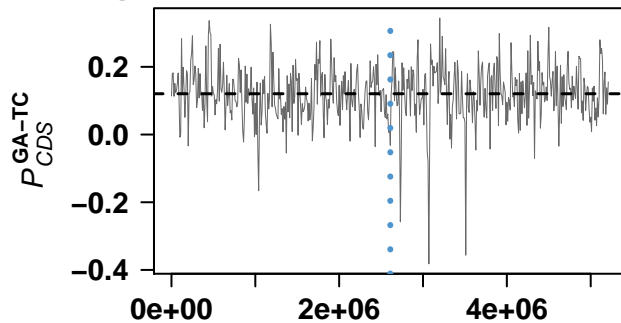


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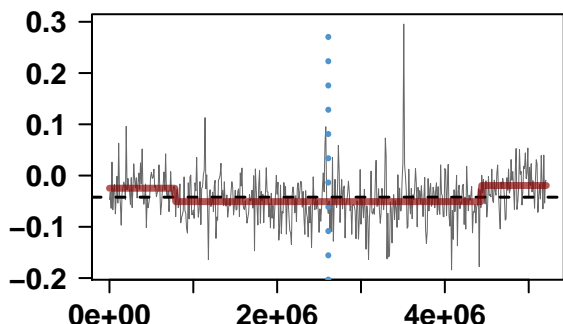
Pseudomonas entomophila L48



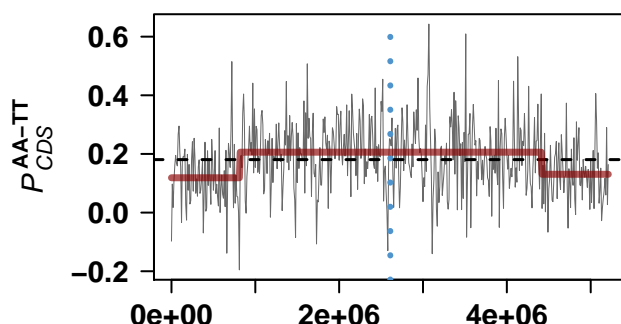
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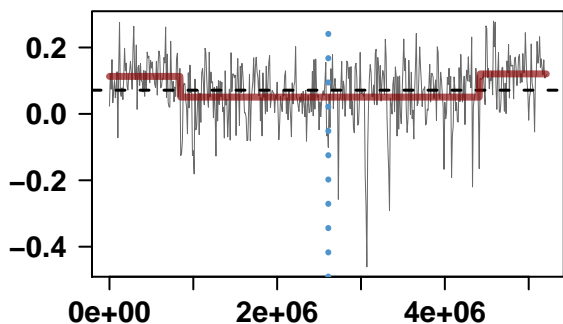
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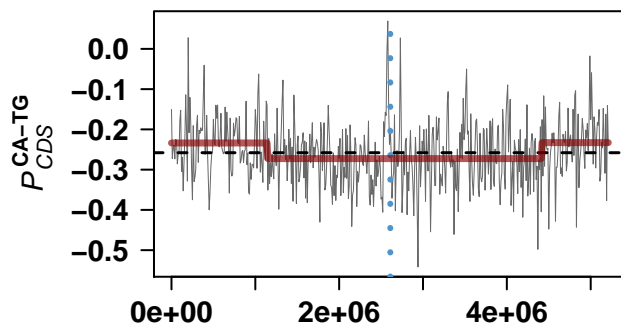
genome coordinates



genome coordinates

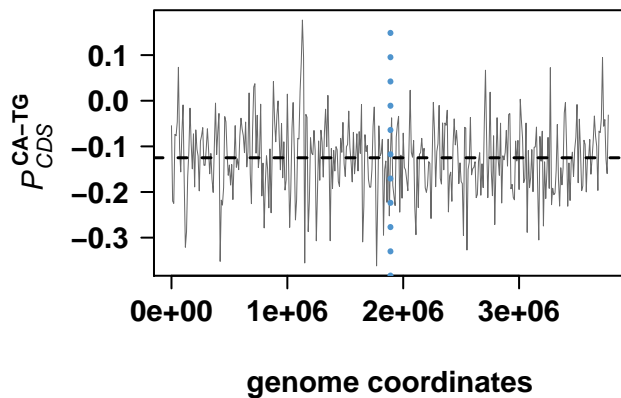
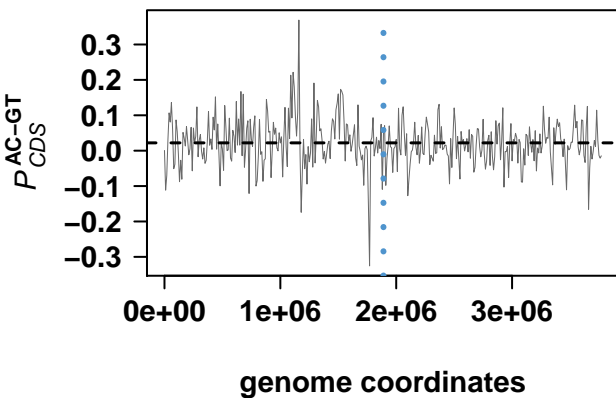
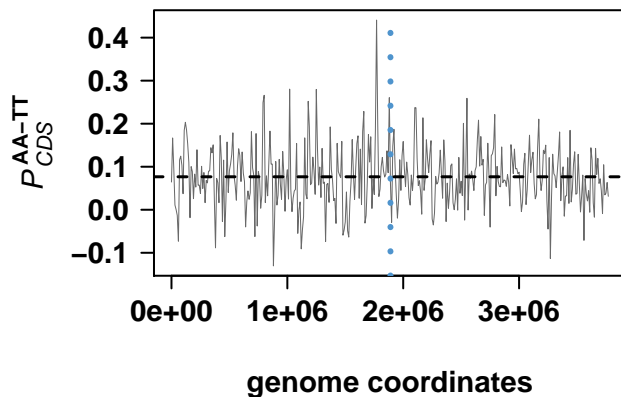
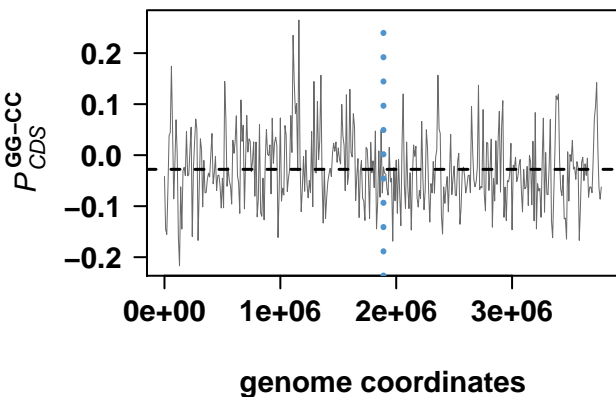
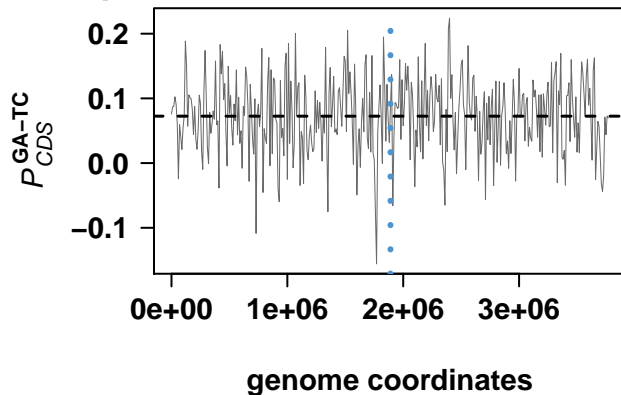
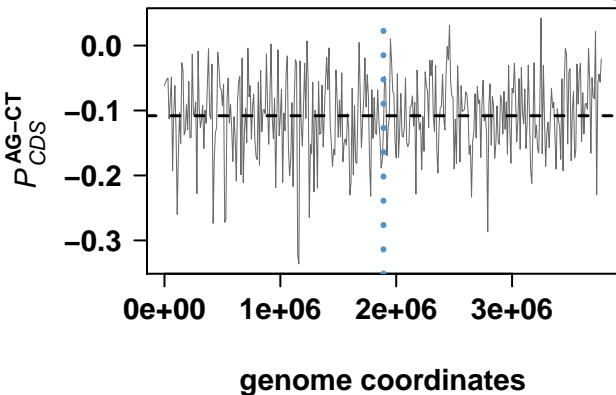


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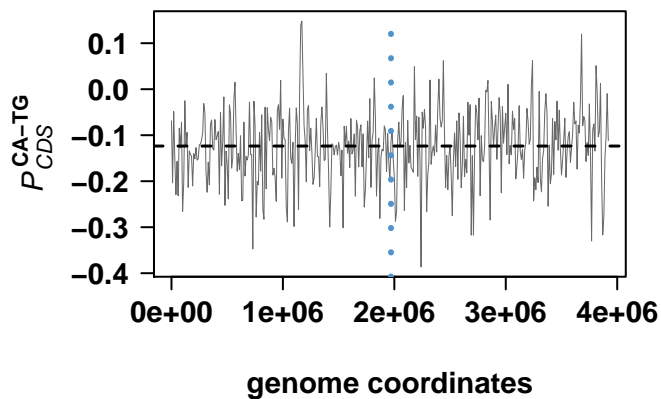
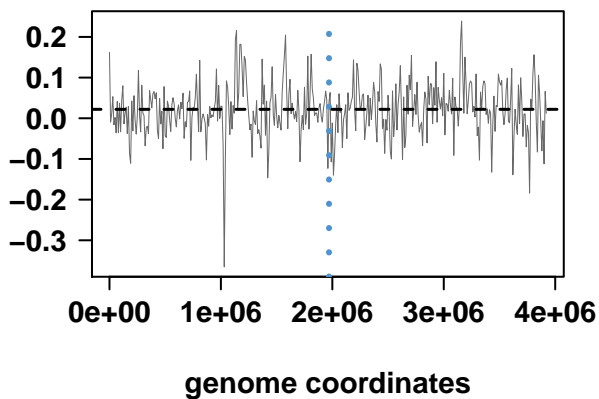
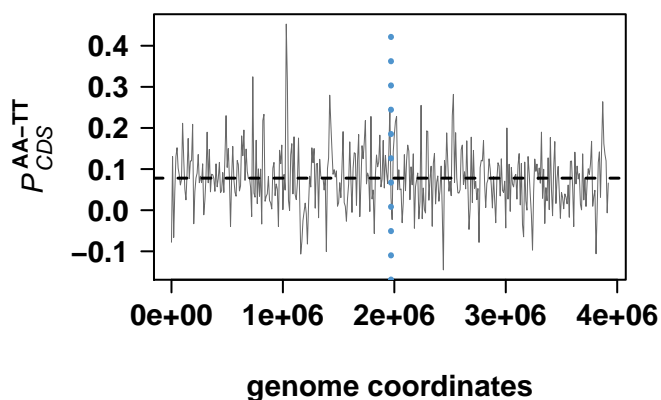
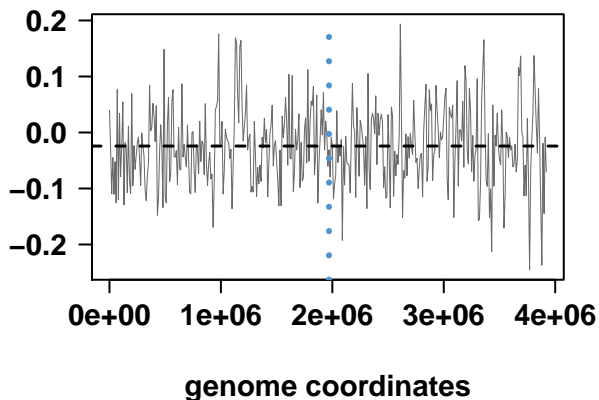
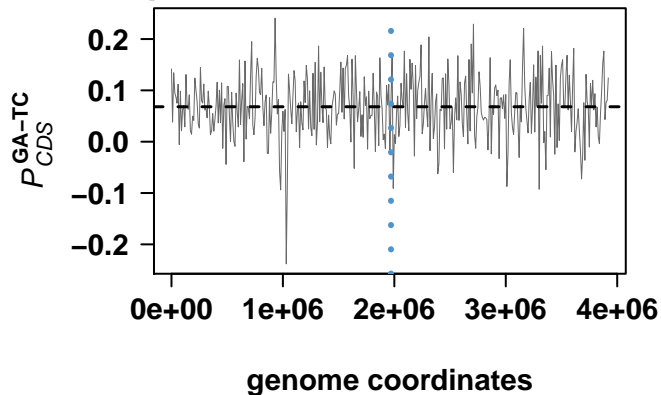
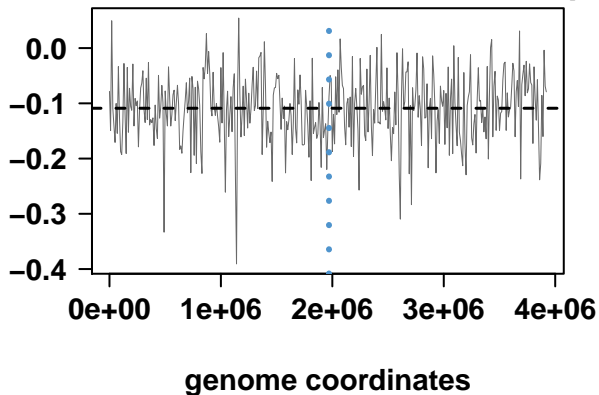


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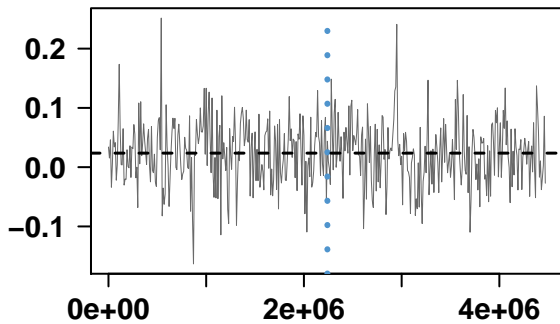
Yersinia pestis Nepal516



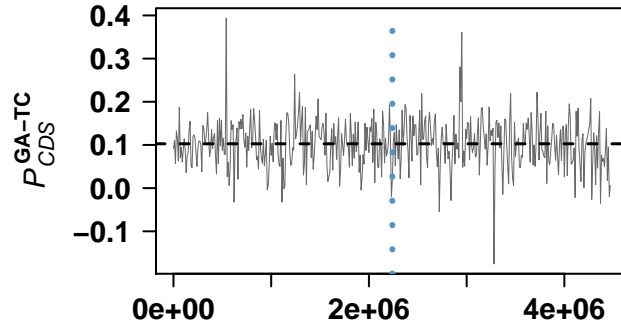
Yersinia pestis Antiqua



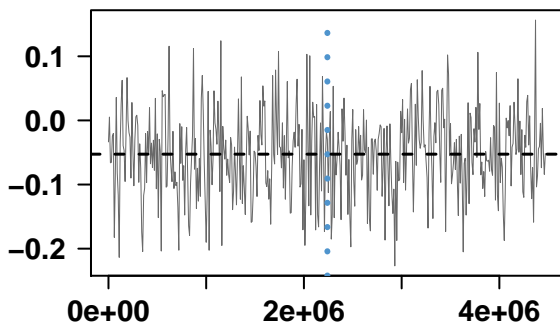
Pseudoalteromonas atlantica T6c



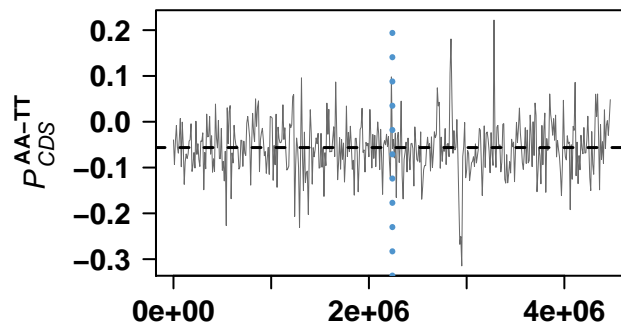
genome coordinates



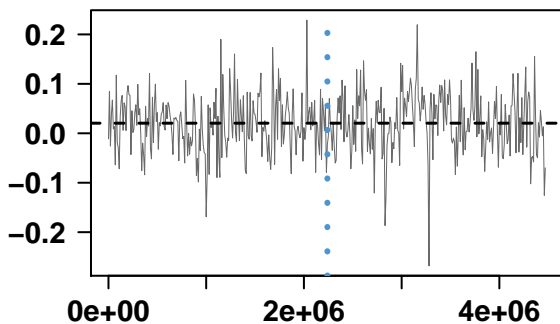
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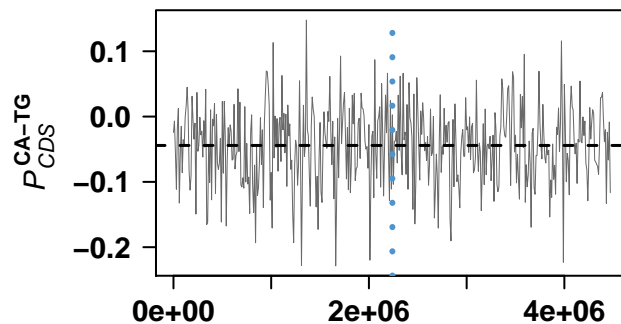
genome coordinates



genome coordinates

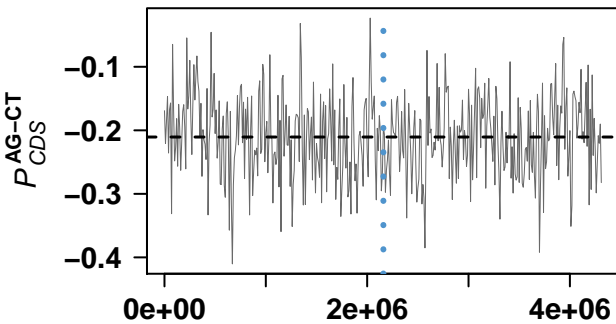


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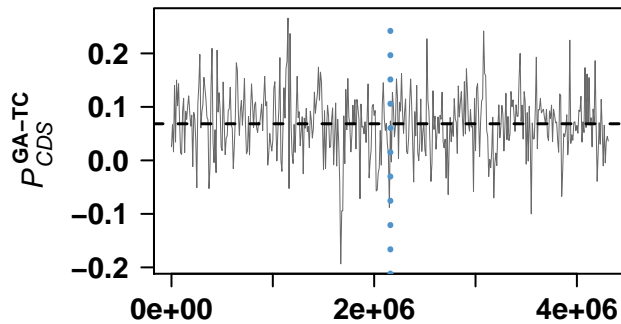


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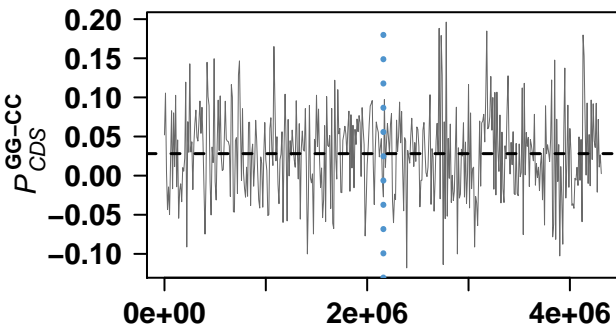
Escherichia coli 536



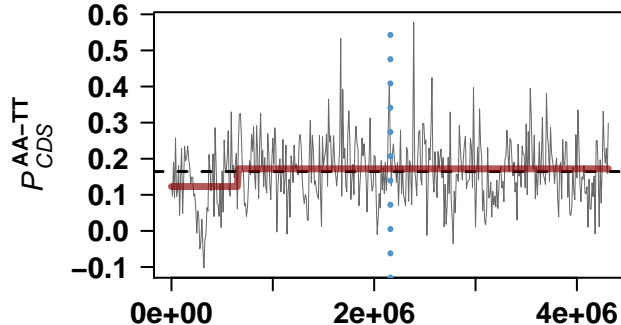
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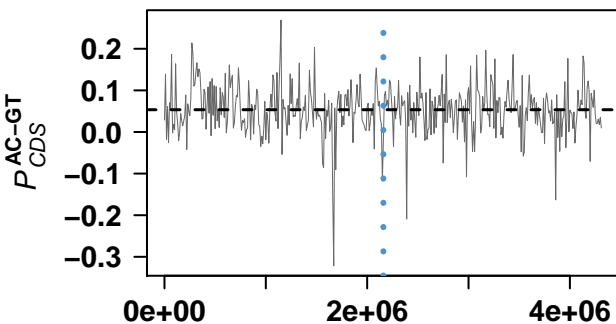
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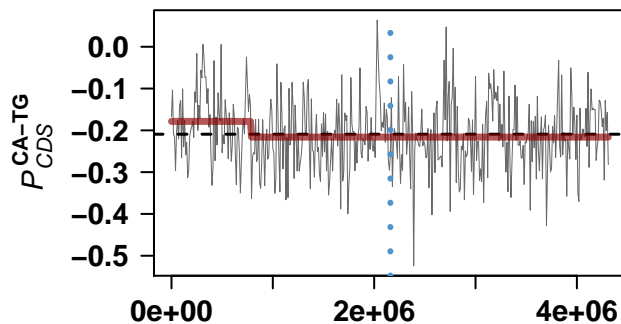
genome coordinates



genome coordinates

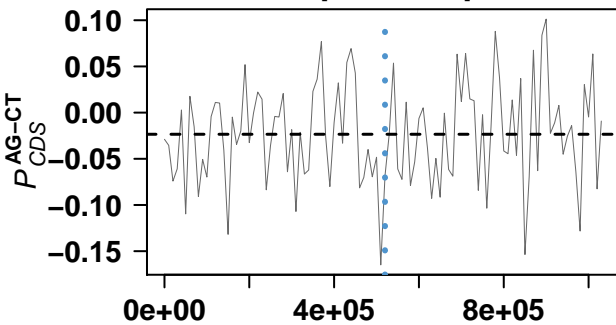


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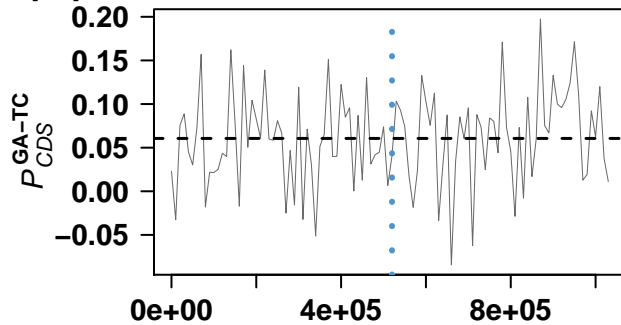


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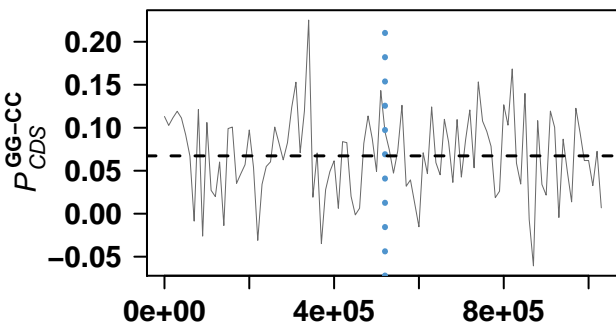
Treponema pallidum subsp. pallidum str. Nichols



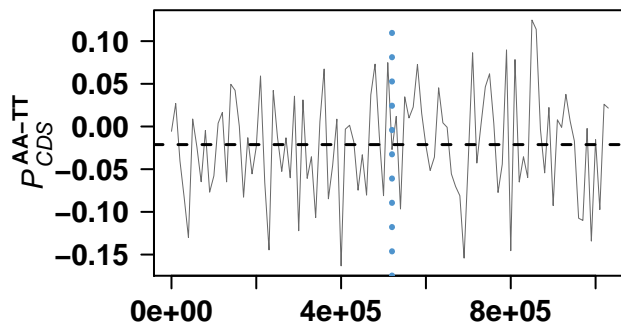
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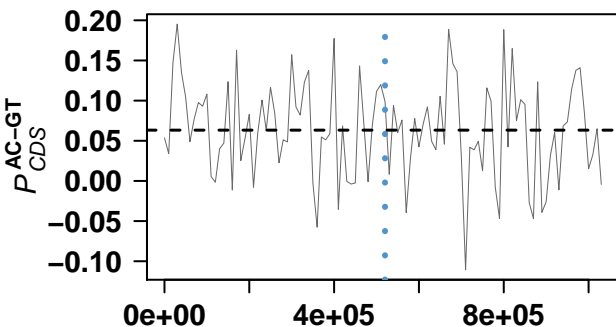
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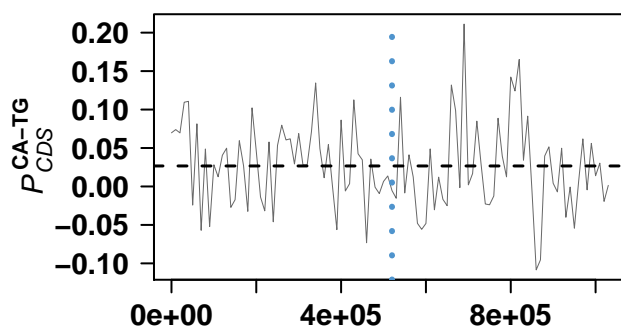
genome coordinates



genome coordinates

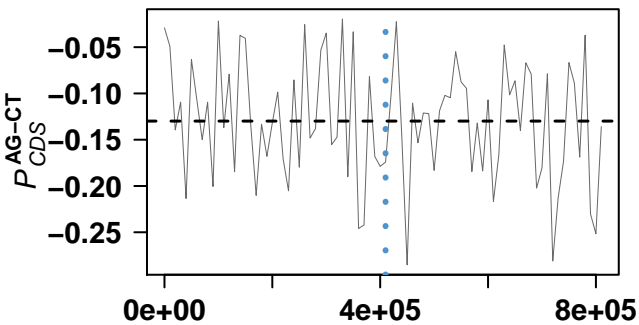


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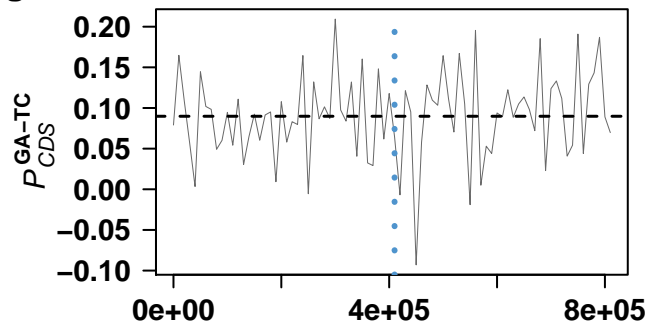


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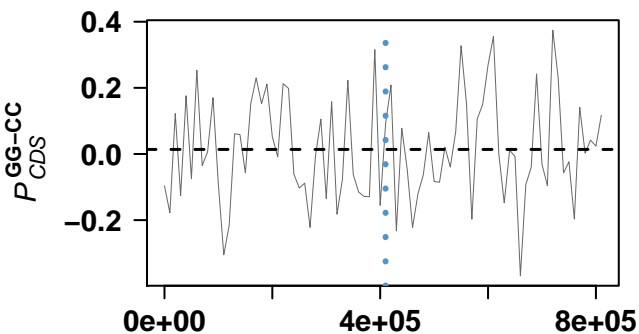
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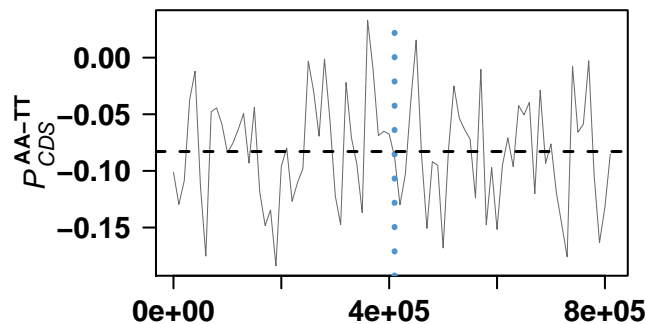
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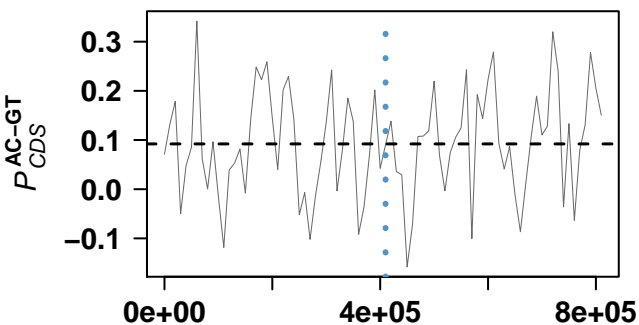
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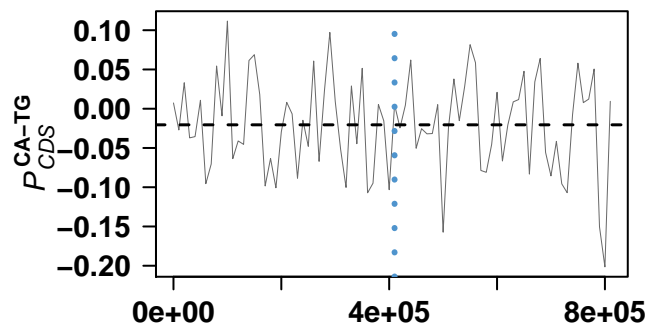
genome coordinates



genome coordinates

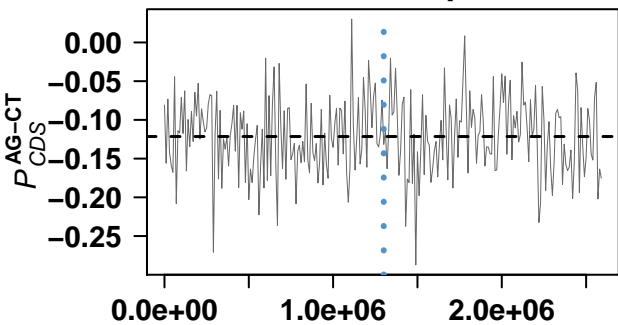


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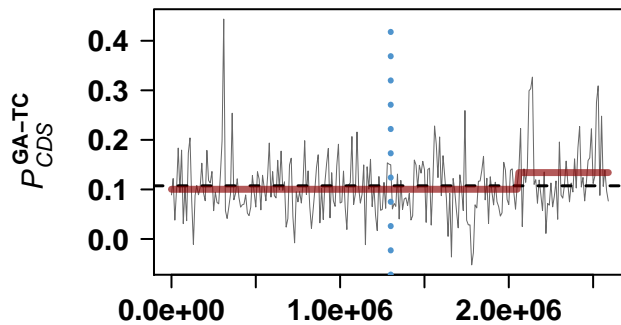


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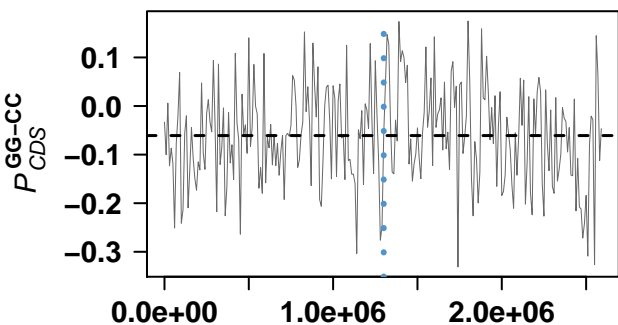
Treponema denticola ATCC 35405



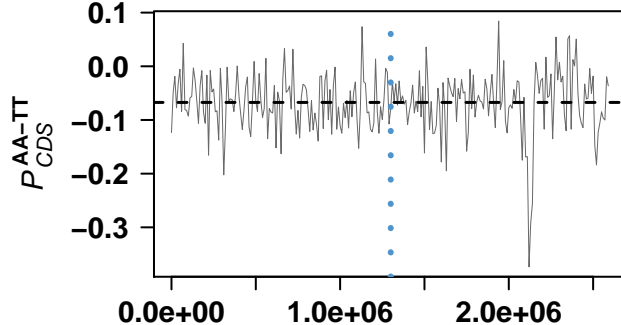
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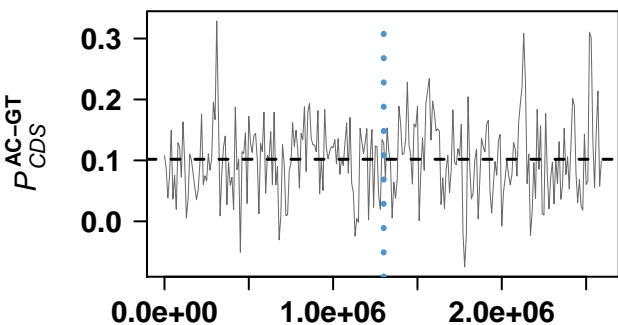
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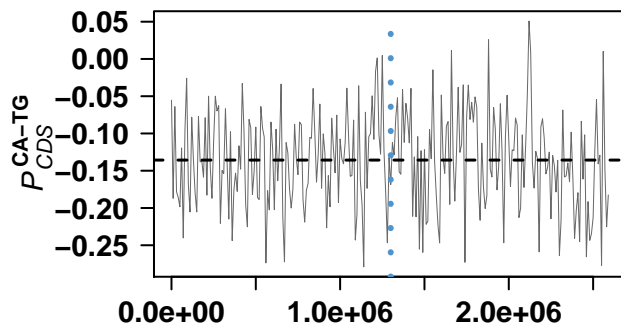
genome coordinates



genome coordinates

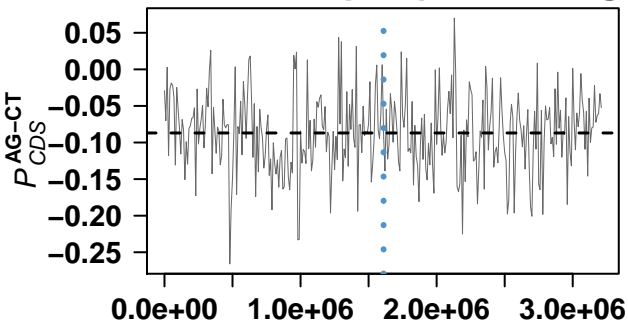


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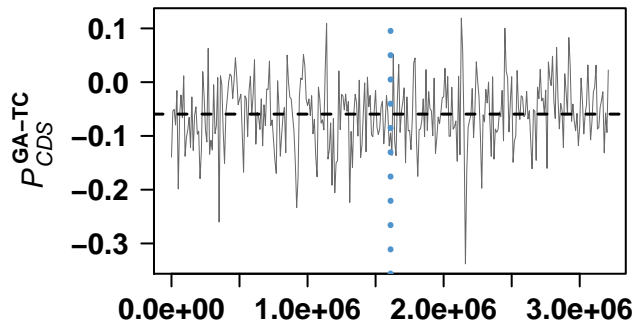


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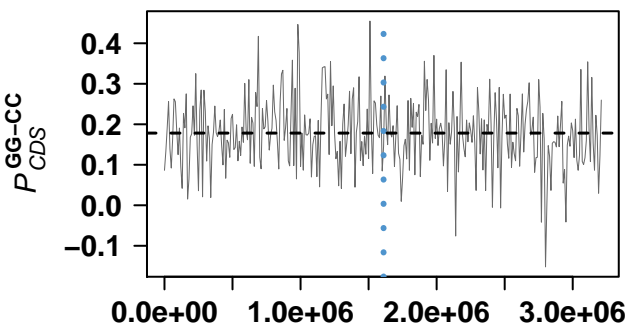
Leptospira interrogans serovar Lai str. 56601



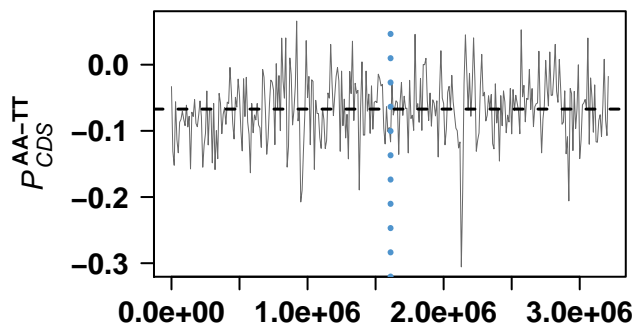
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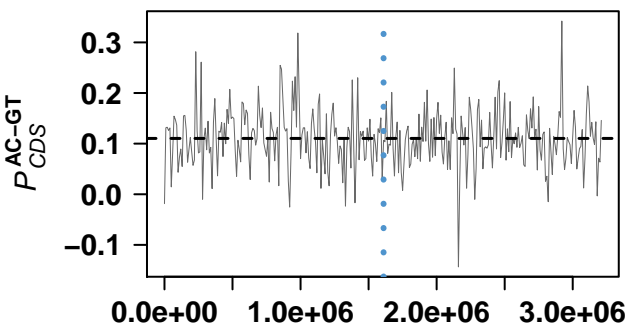
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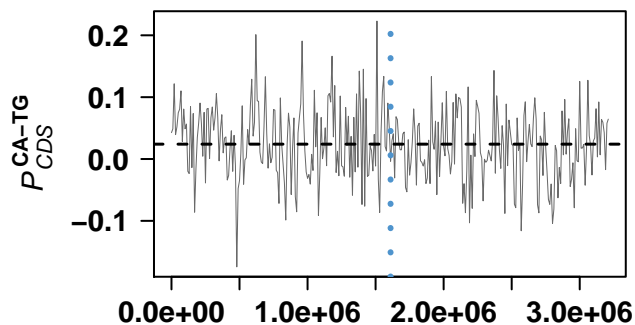
genome coordinates



genome coordinates

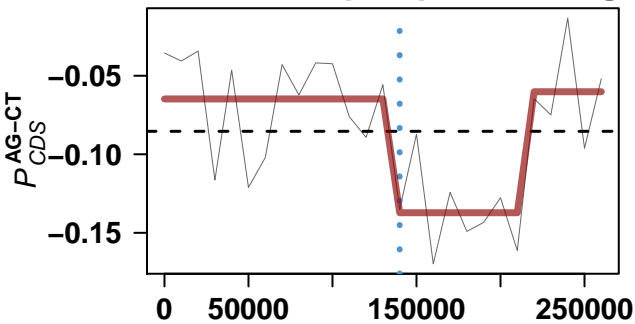


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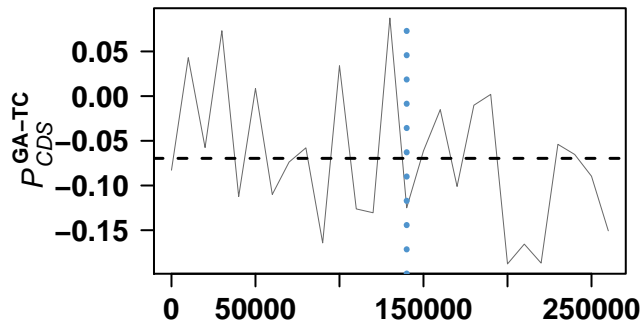


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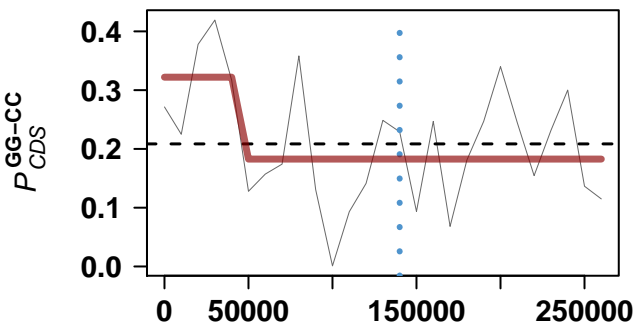
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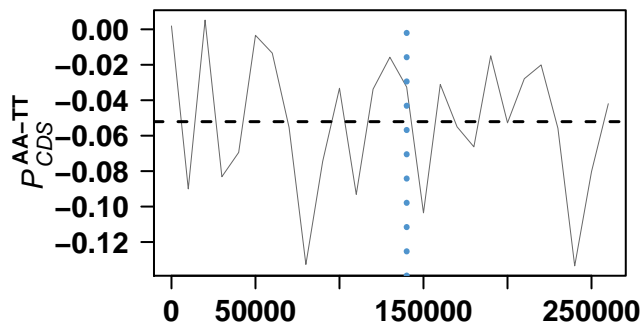
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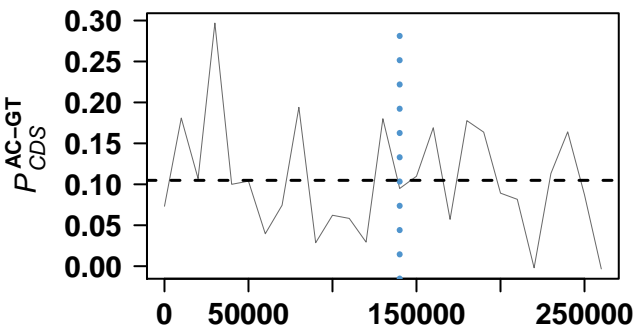
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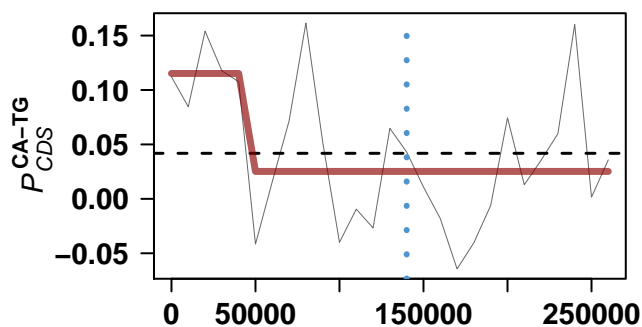
genome coordinates



genome coordinates

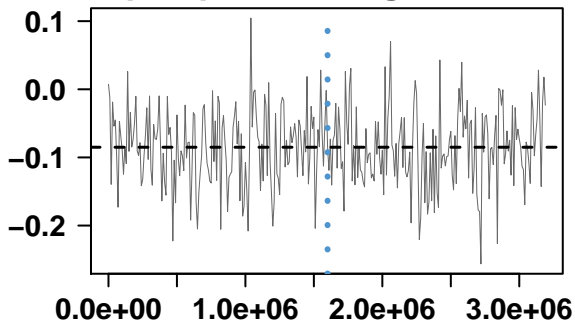


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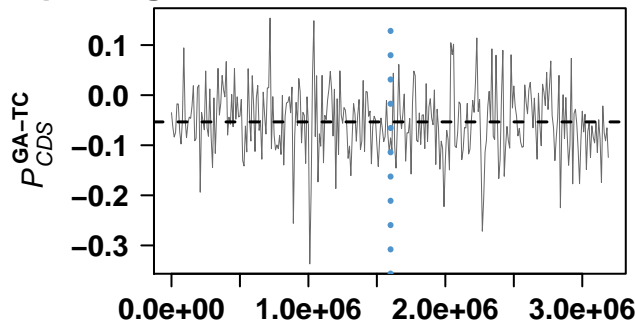


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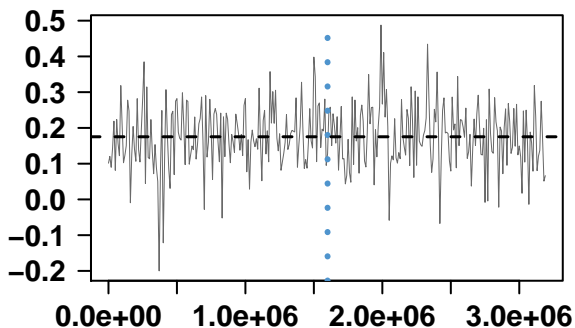
Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130



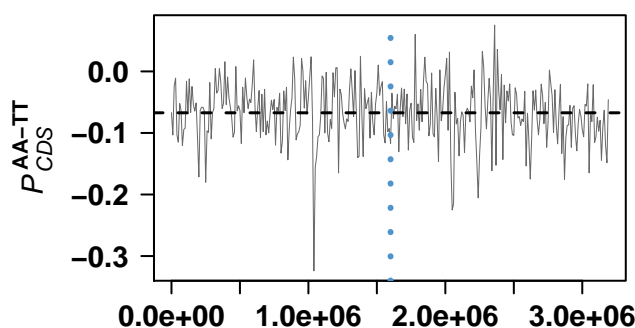
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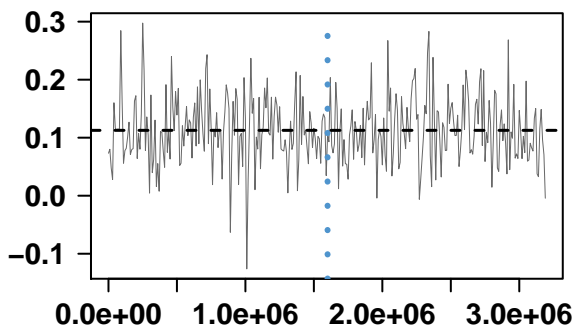
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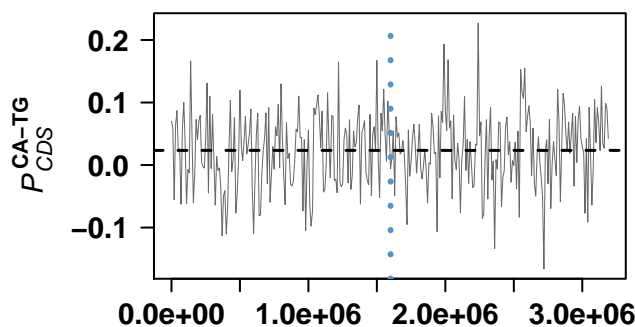
genome coordinates



genome coordinates

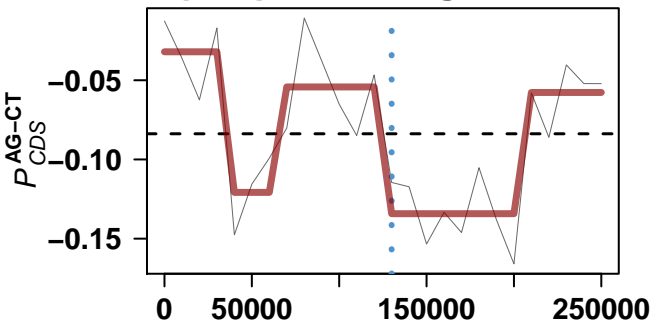


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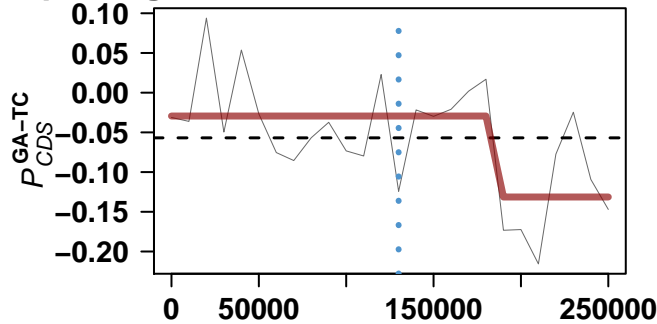


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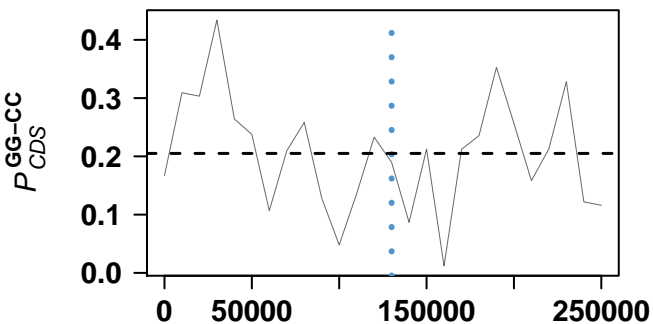
Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130



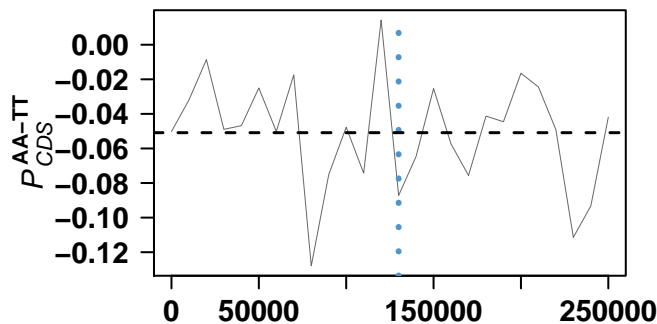
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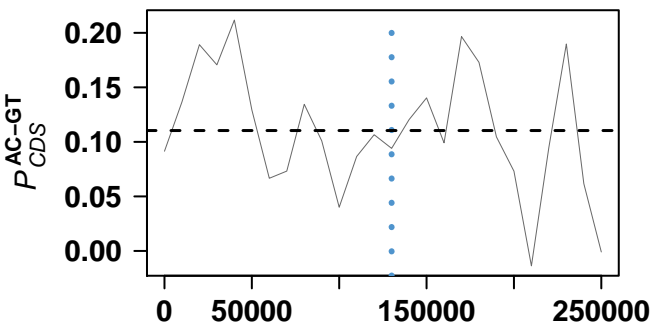
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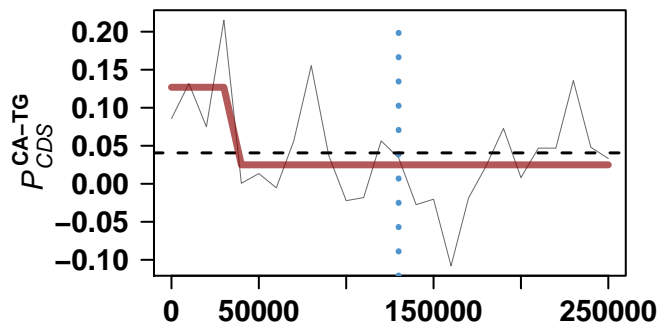
genome coordinates



genome coordinates

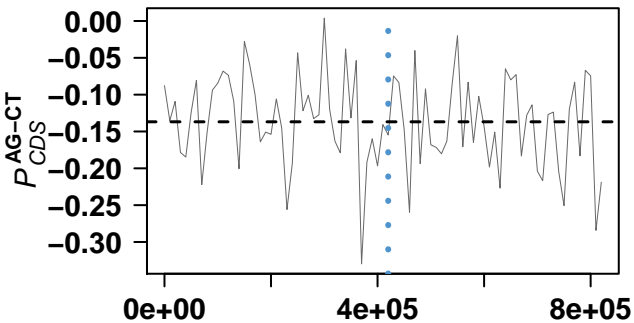


genome coordinates

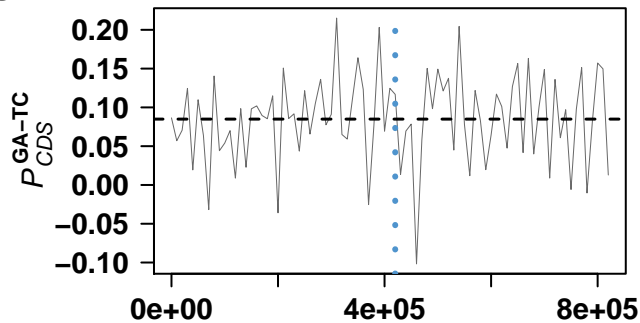


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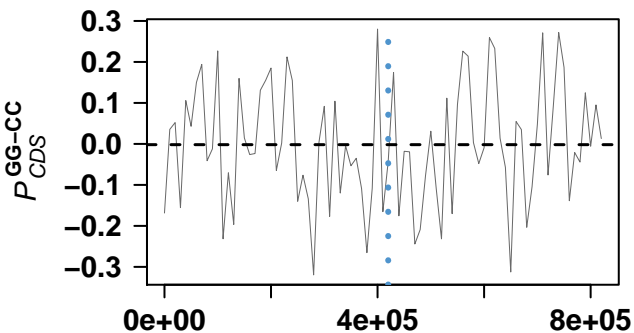
Borrelia garinii PBI



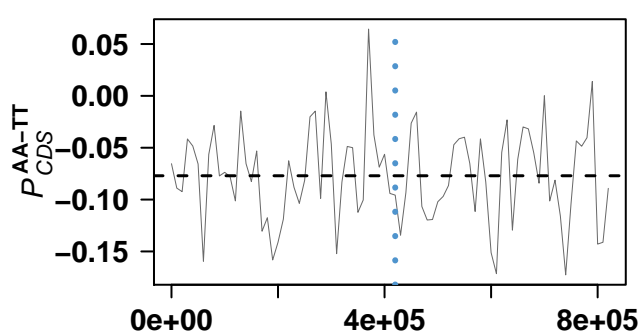
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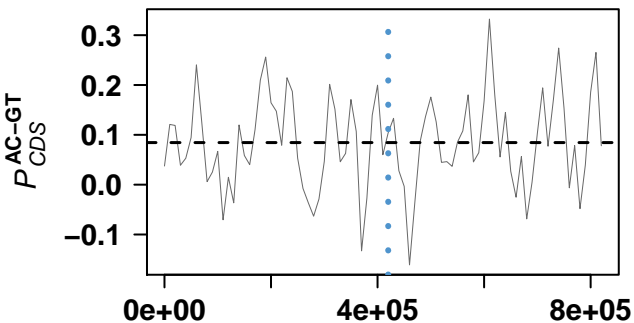
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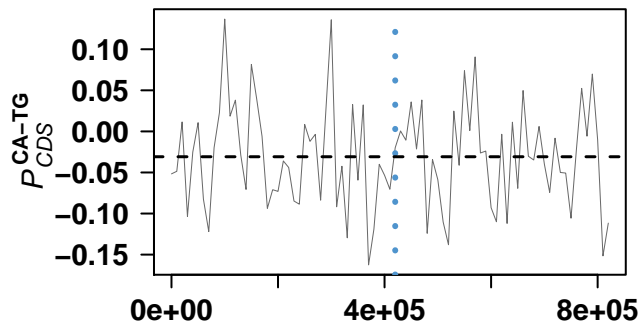
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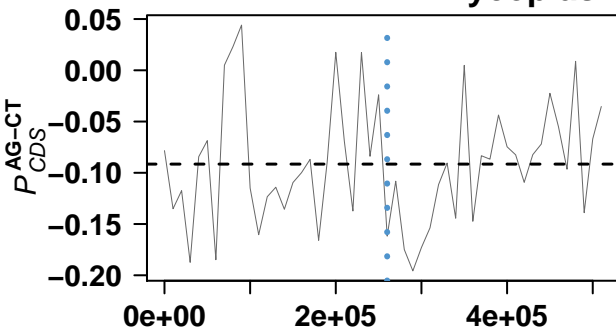


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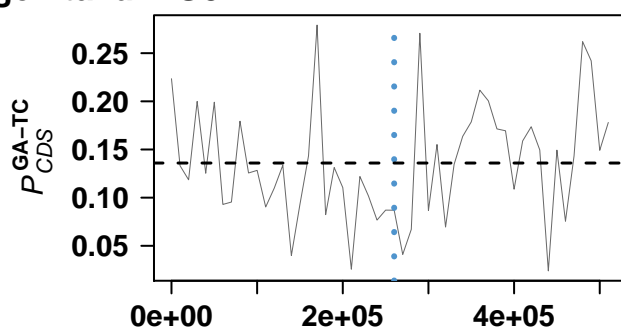


genome coordinates

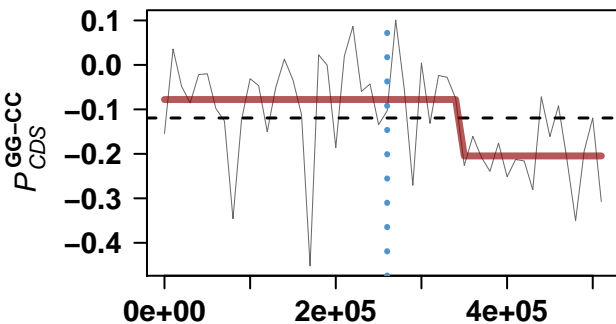
Mycoplasma genitalium G37



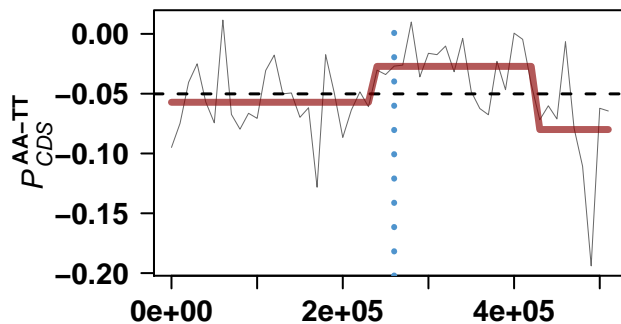
genome coordinates



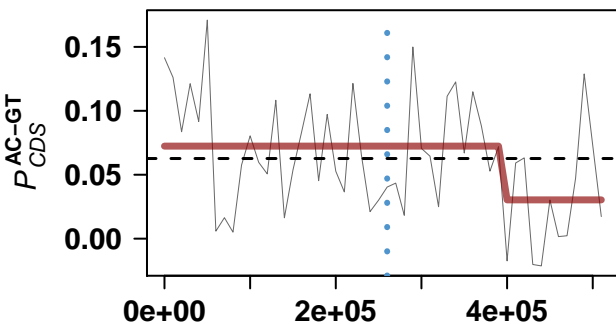
genome coordinates



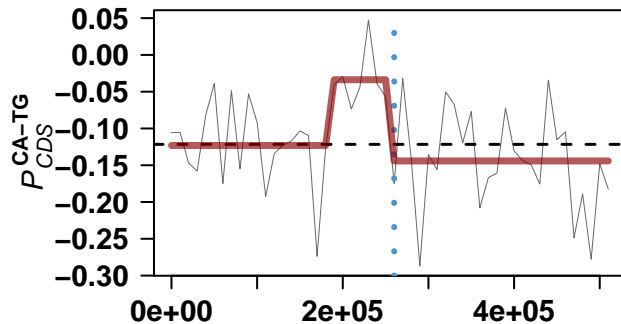
genome coordinates



genome coordinates

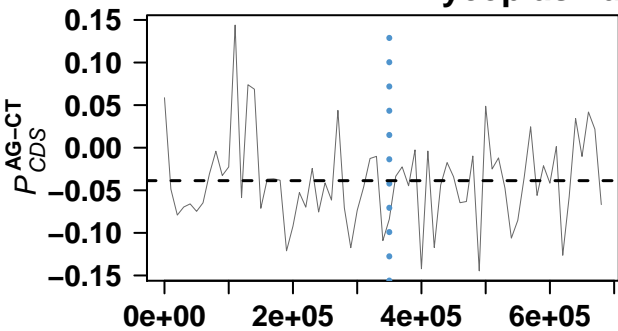


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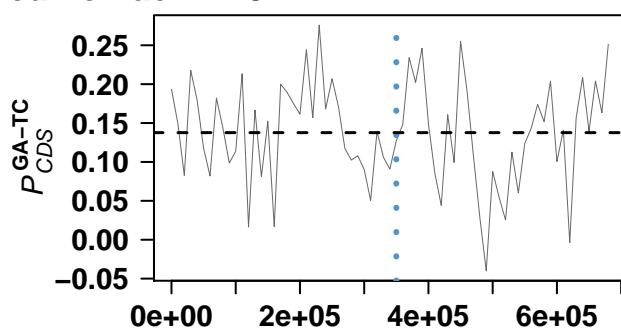


genome coordinates

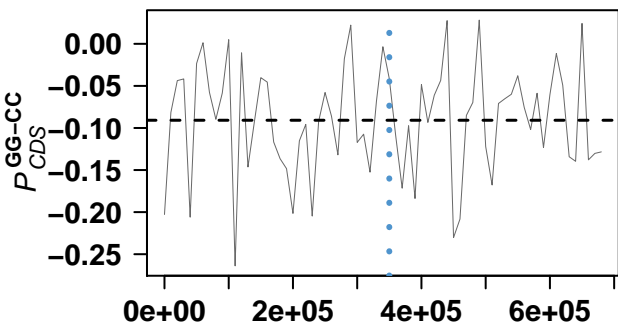
Mycoplasma pneumoniae M129



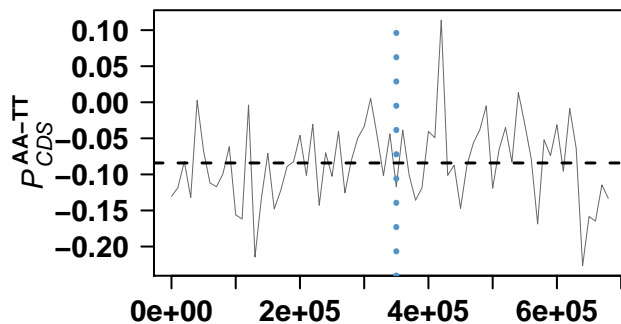
genome coordinates



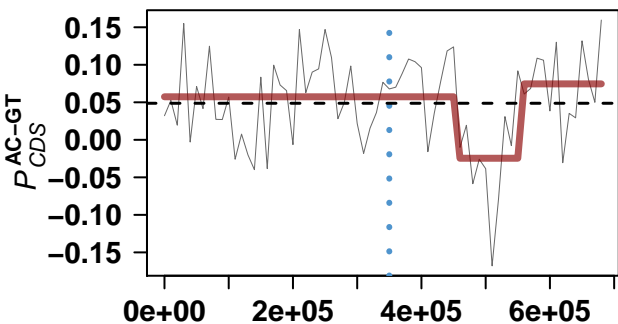
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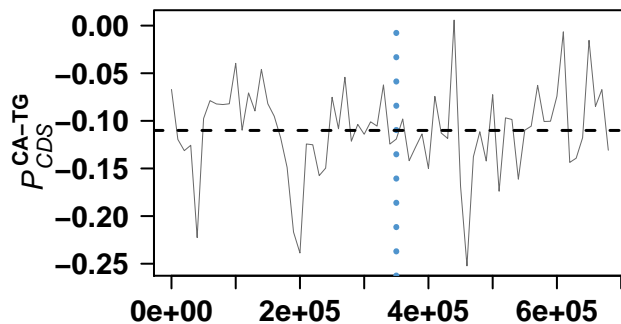
genome coordinates



genome coordinates

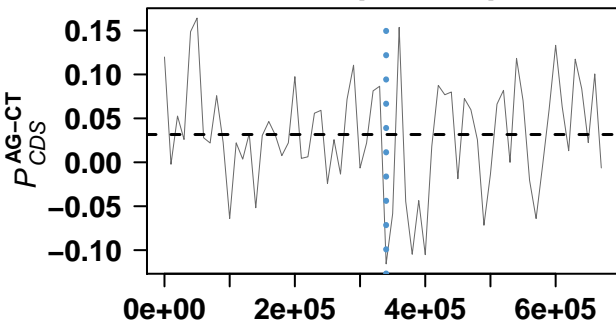


genome coordinates

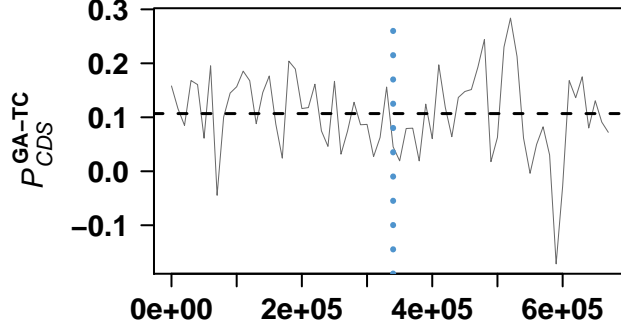


genome coordinates

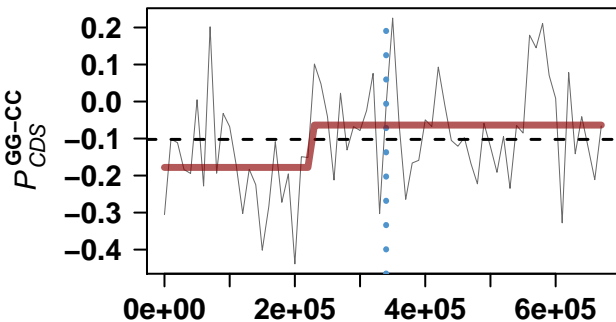
Ureaplasma parvum serovar 3 str. ATCC 700970



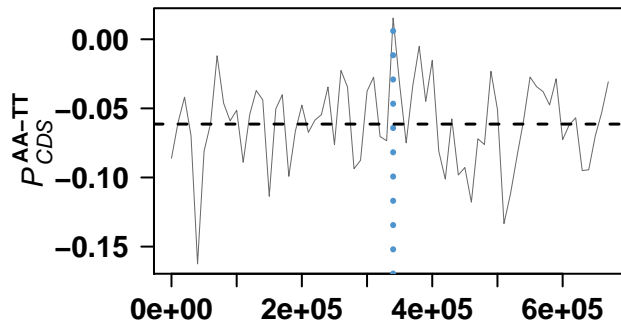
genome coordinates



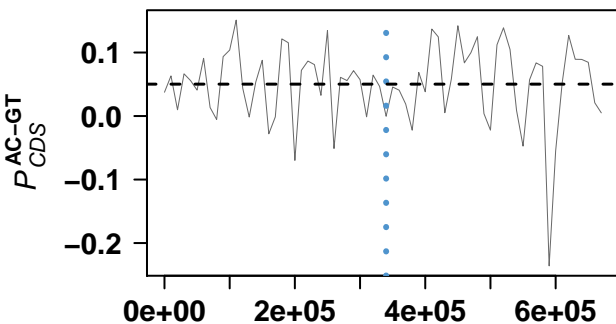
genome coordinates



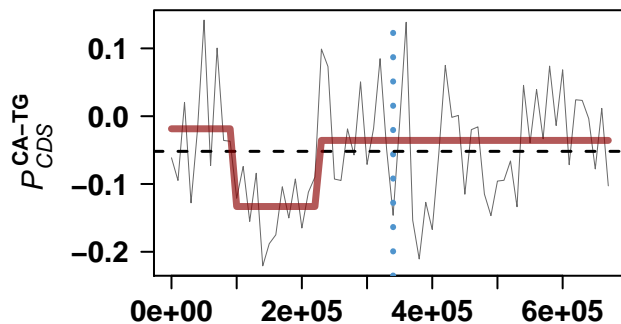
genome coordinates



genome coordinates

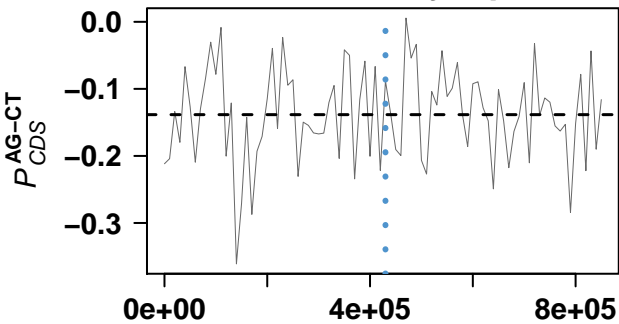


genome coordinates

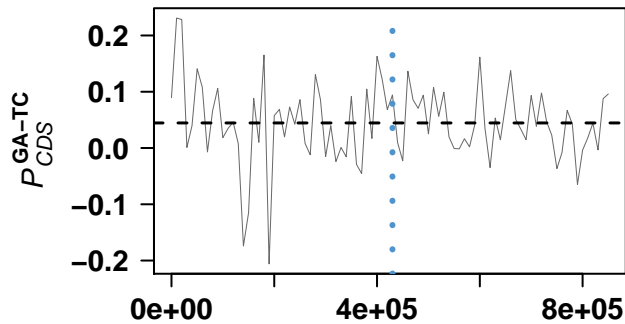


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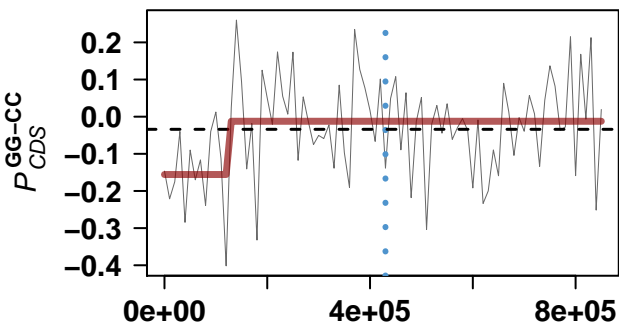
Mycoplasma pulmonis UAB CTIP



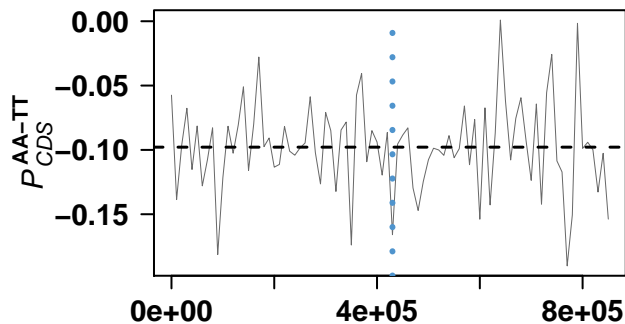
genome coordinates



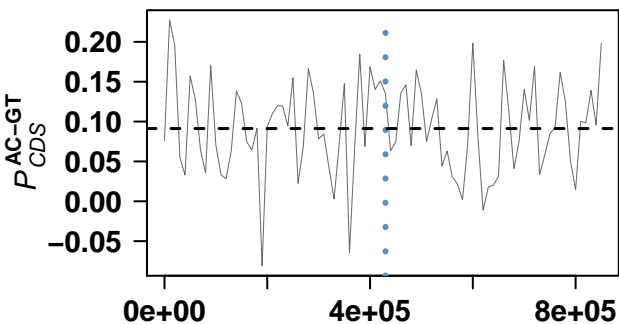
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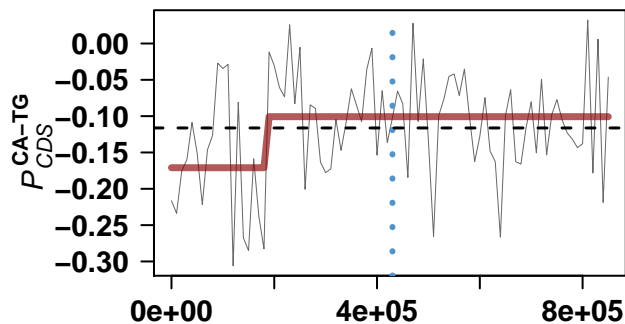
genome coordinates



genome coordinates

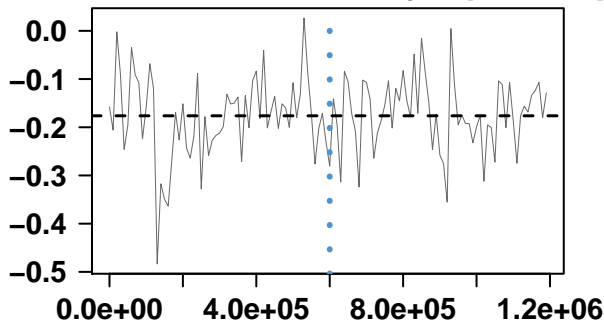


genome coordinates

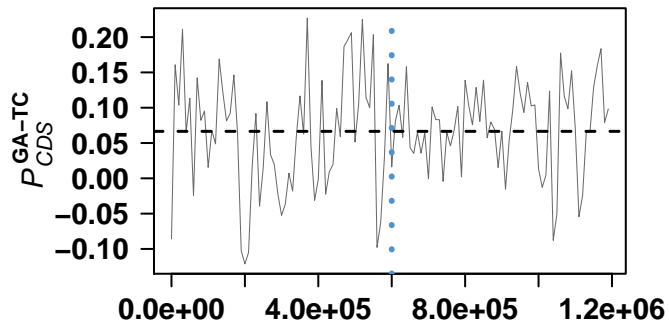


genome coordinates

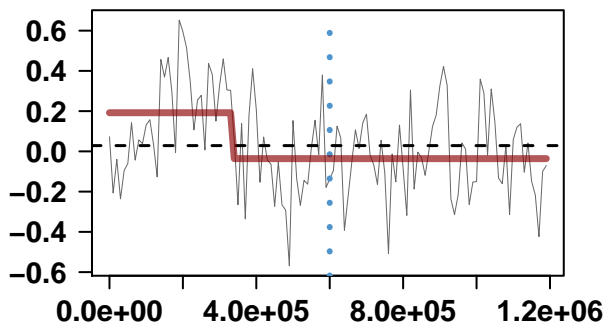
Mycoplasma penetrans HF-2



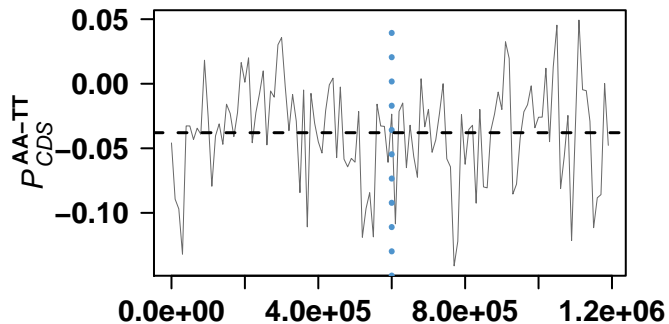
genome coordinates



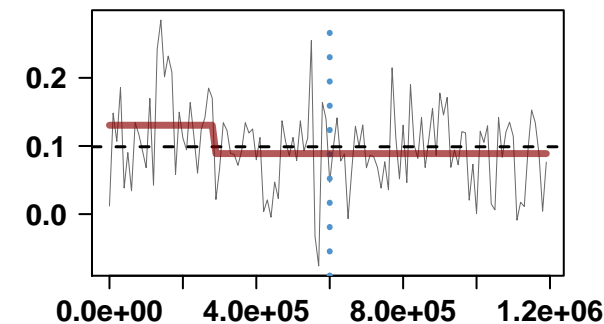
genome coordinates



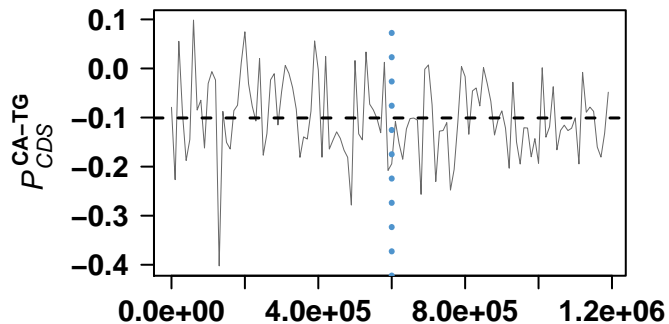
genome coordinates



genome coordinates

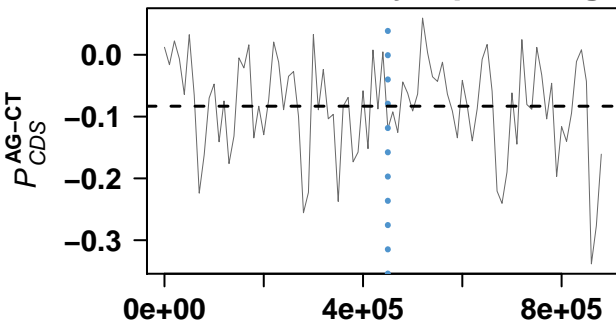


genome coordinates

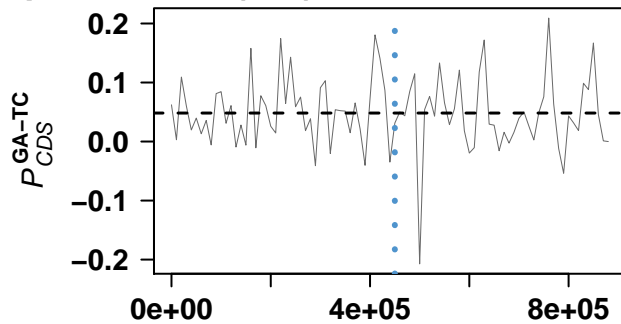


genome coordinates

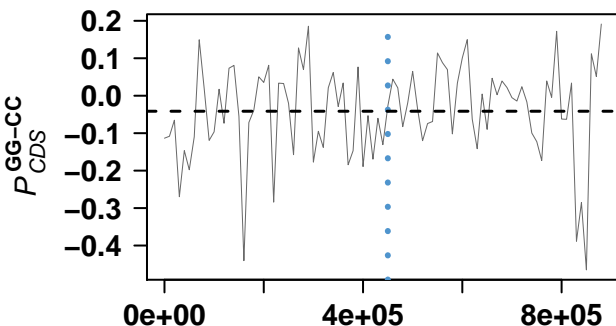
Mycoplasma gallisepticum str. R(low)



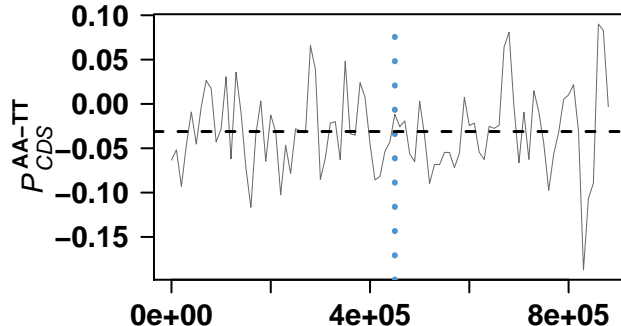
genome coordinates



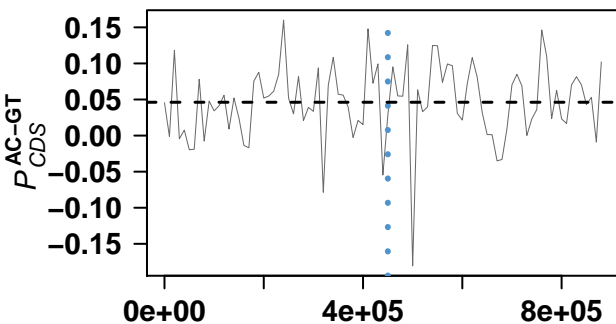
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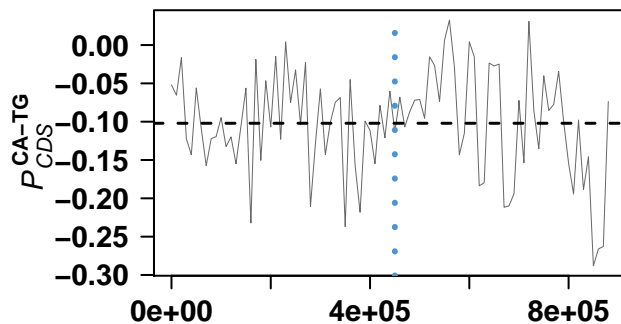
genome coordinates



genome coordinates

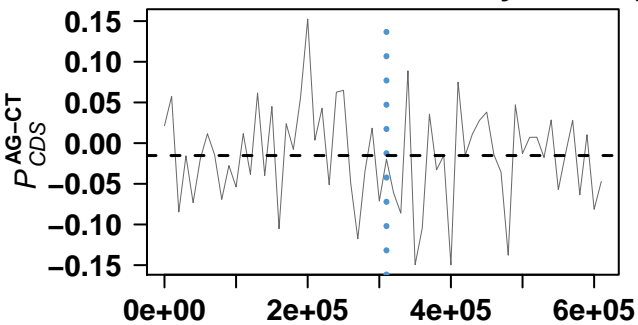


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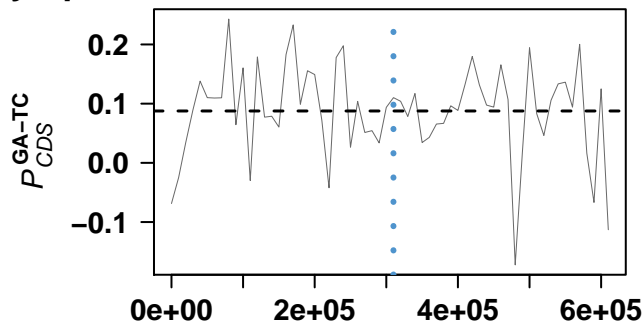


genome coordinates

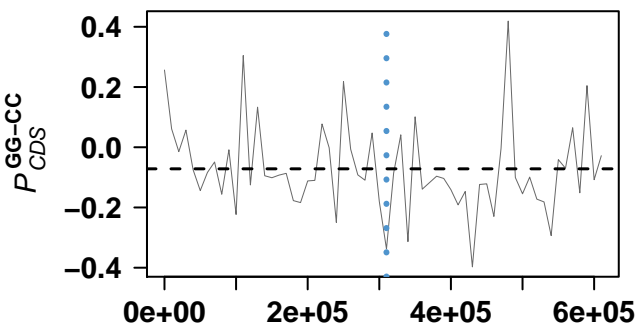
Onion yellows phytoplasma OY-M



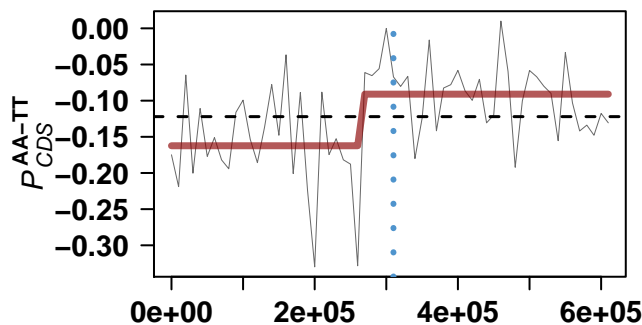
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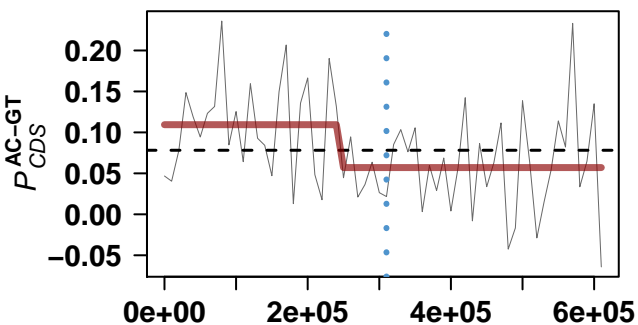
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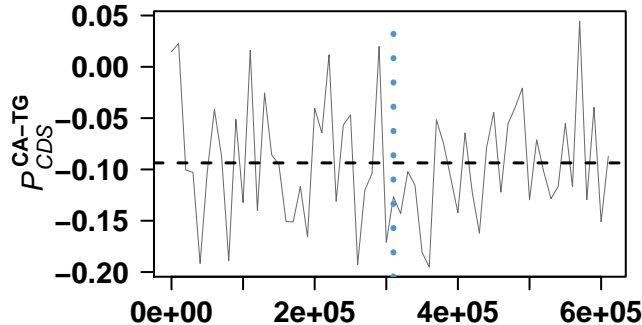
genome coordinates



genome coordinates

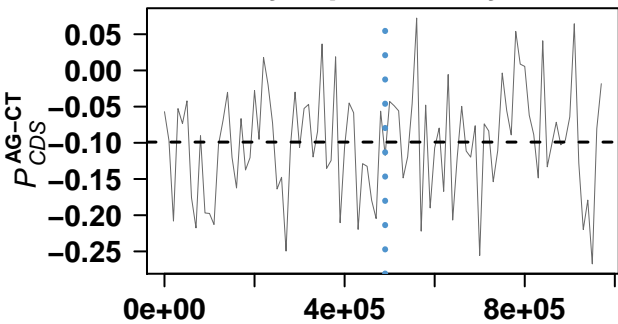


genome coordinates

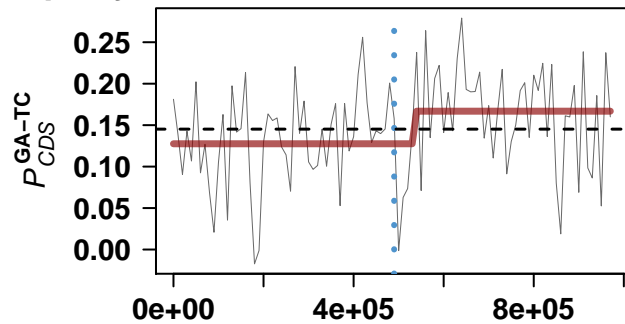


genome coordinates

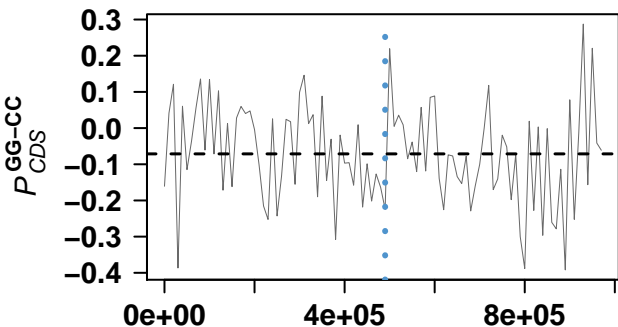
Mycoplasma mycoides subsp. *mycoides* SC str. PG1



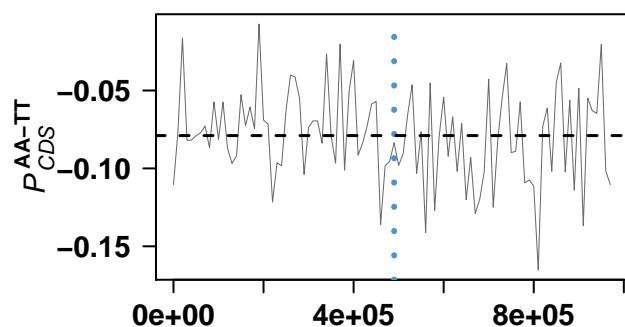
genome coordinates



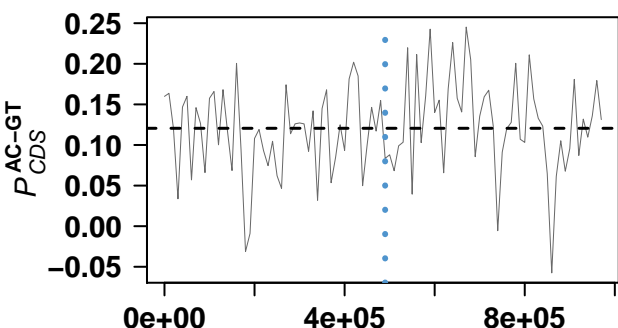
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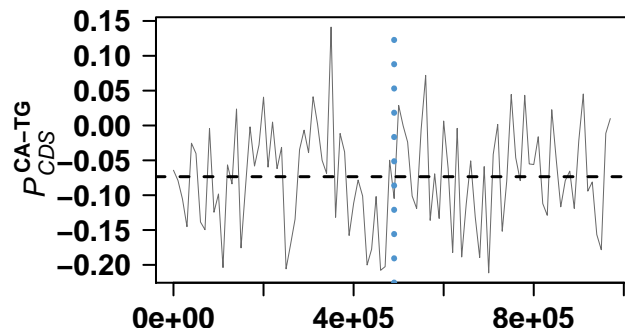
genome coordinates



genome coordinates

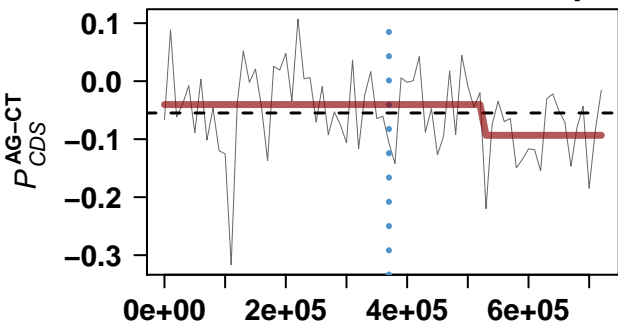


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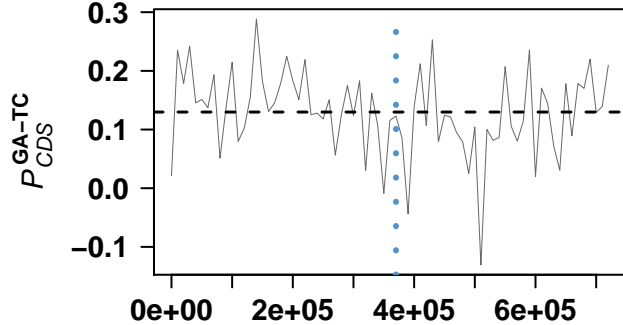


genome coordinates

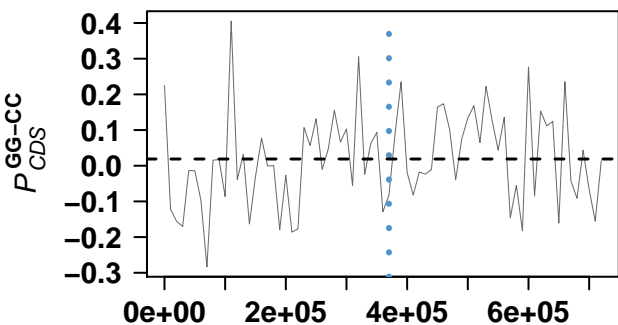
Mesoplasma florum L1



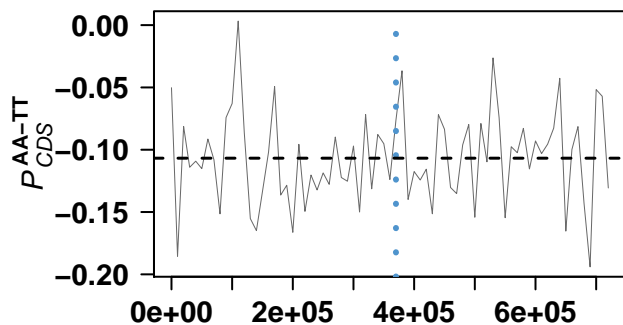
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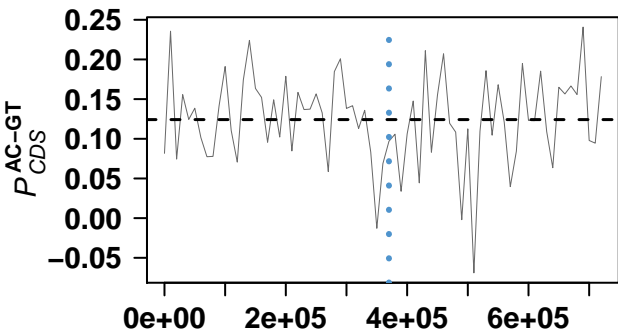
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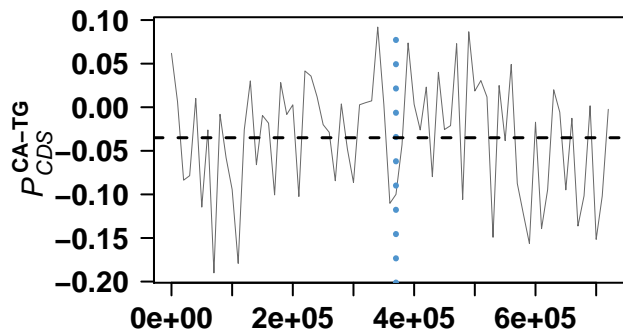
genome coordinates



genome coordinates

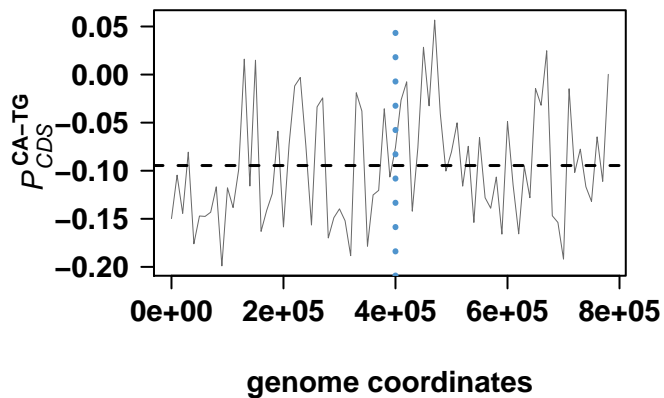
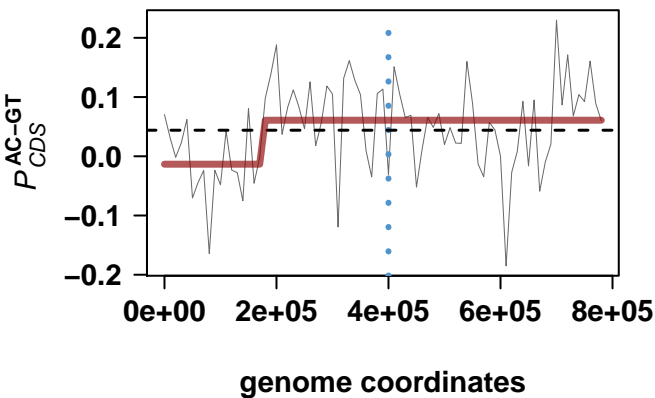
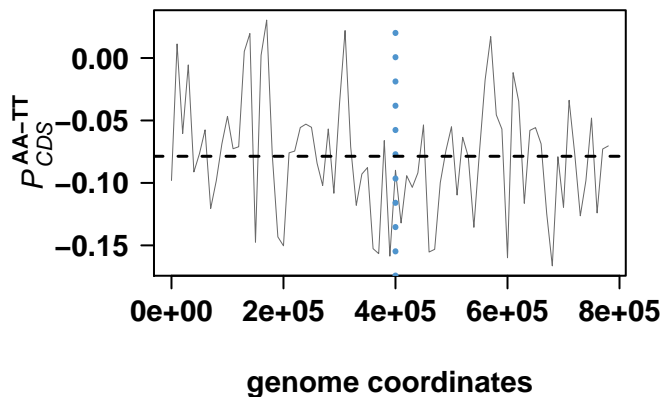
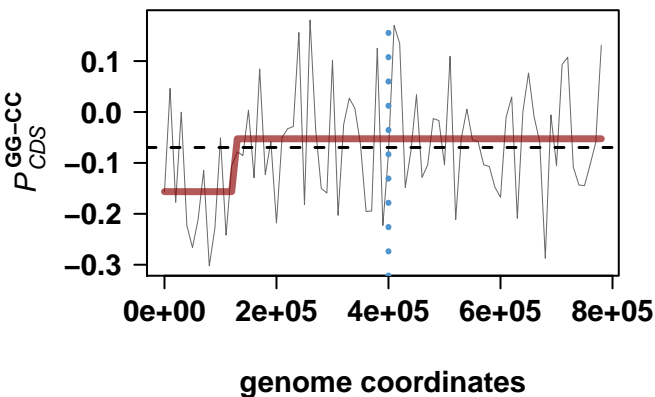
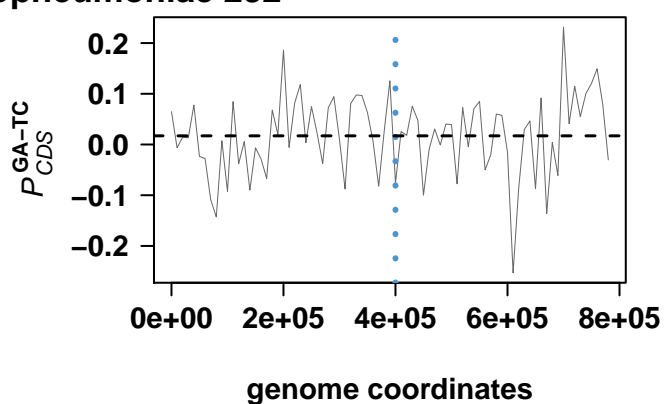
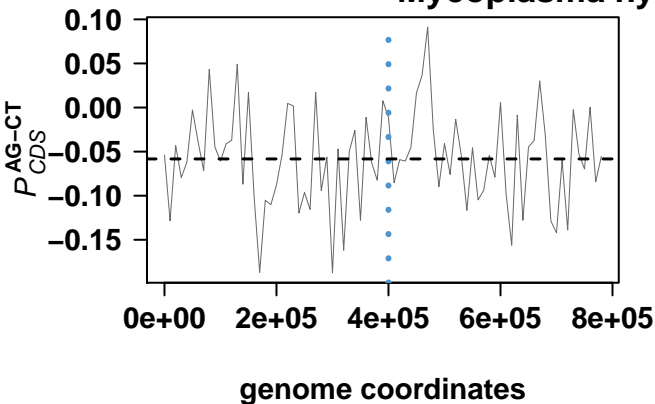


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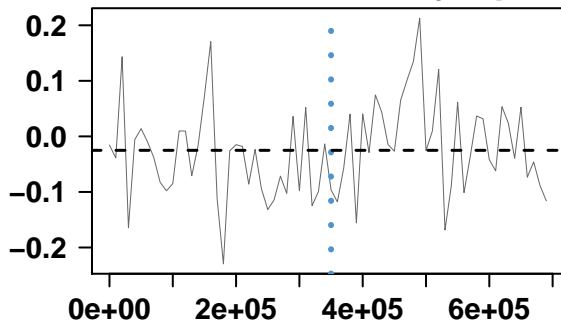


genome coordinates

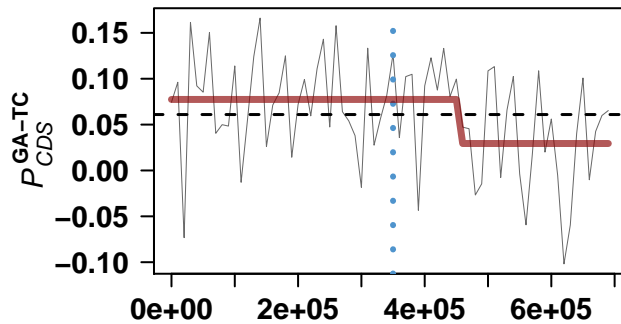
Mycoplasma hyopneumoniae 232



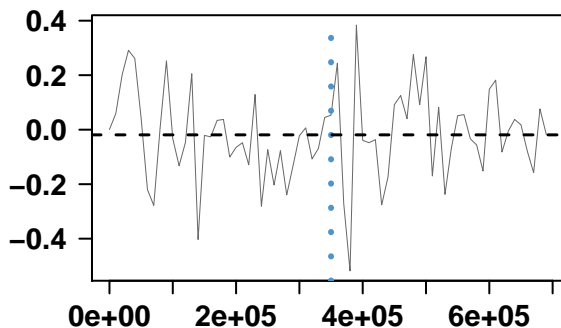
Mycoplasma mobile 163K



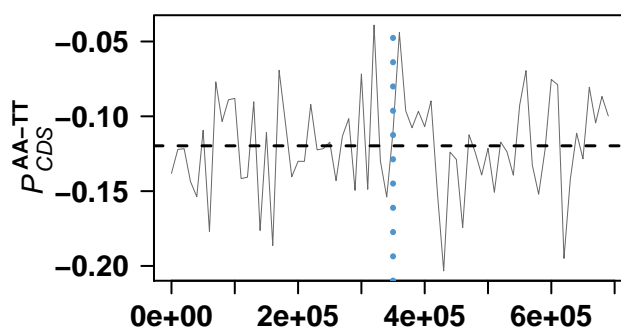
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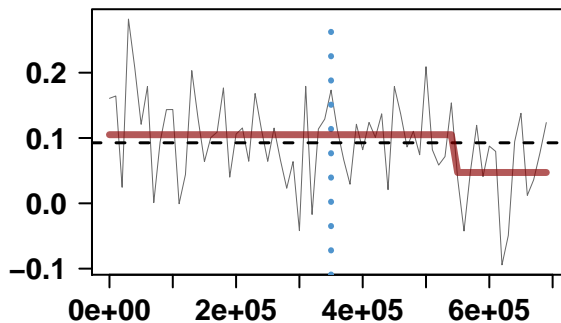
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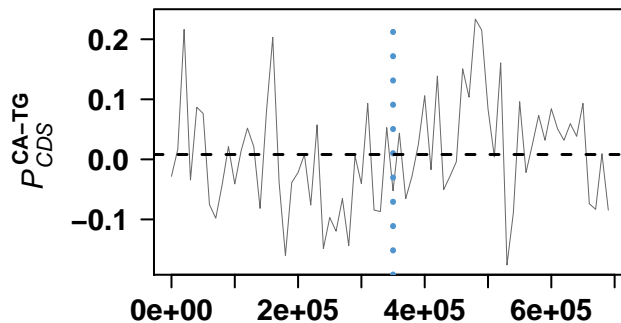
genome coordinates



genome coordinates

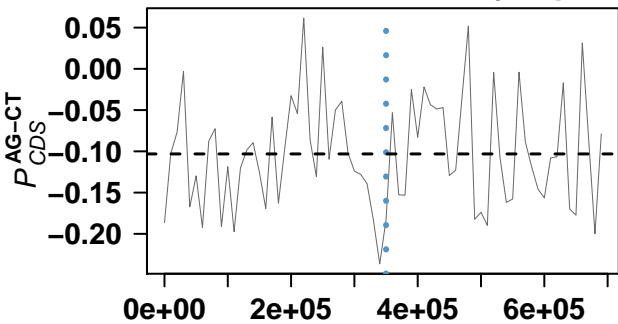


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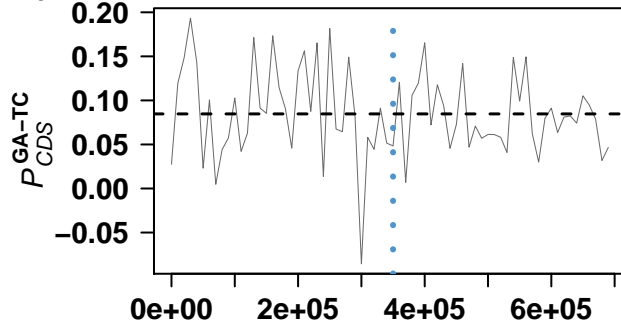


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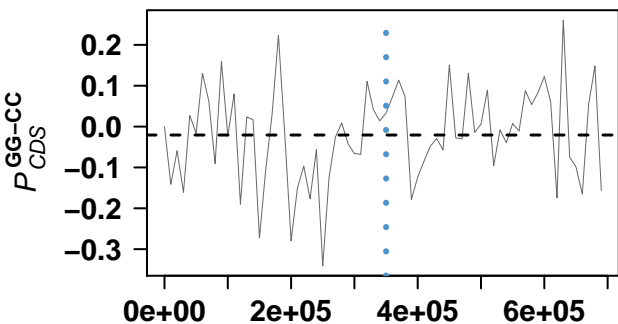
Mycoplasma synoviae 53



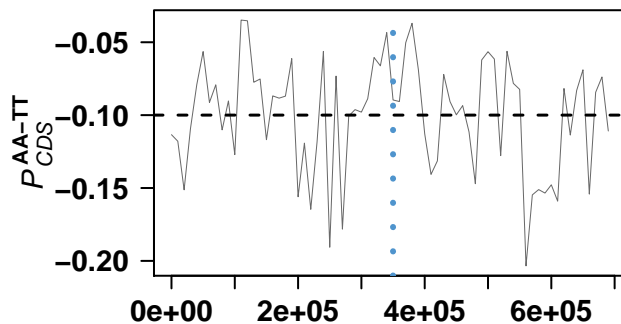
genome coordinates



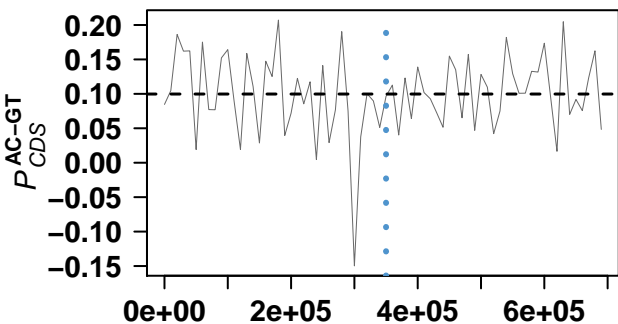
genome coordinates



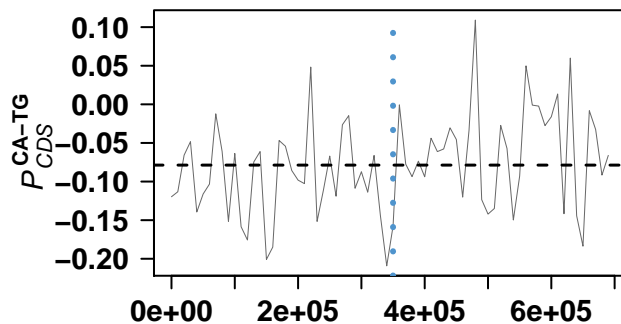
genome coordinates



genome coordinates

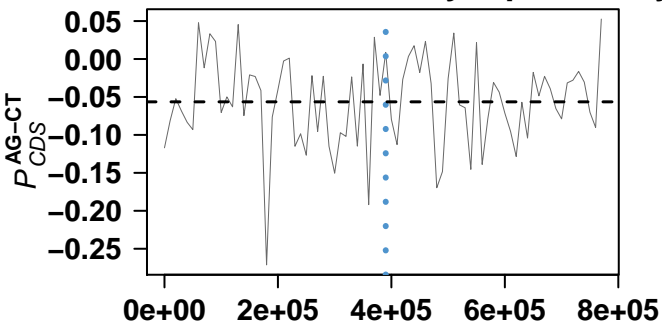


genome coordinates

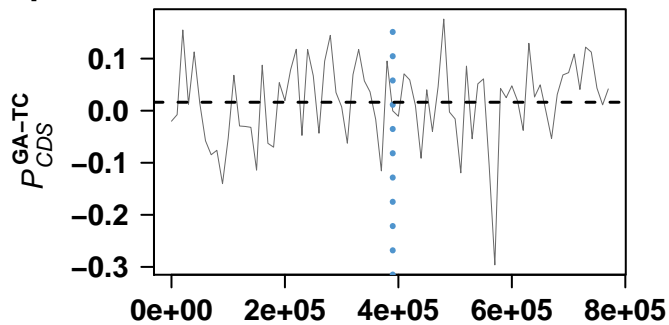


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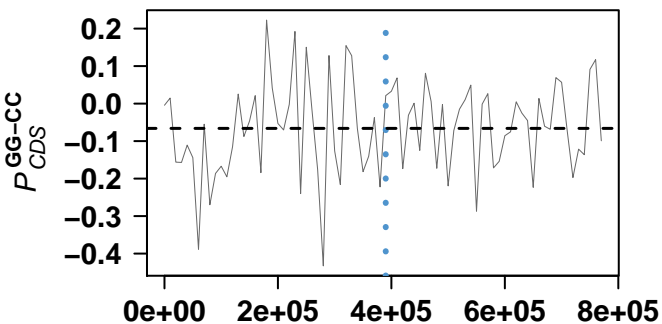
Mycoplasma hyopneumoniae J



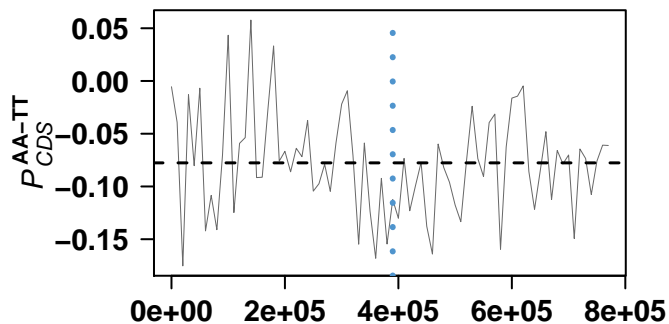
genome coordinates



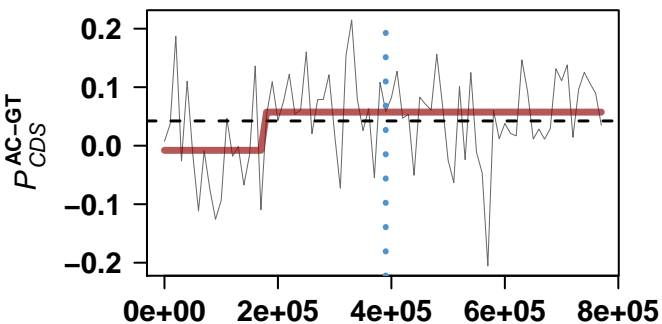
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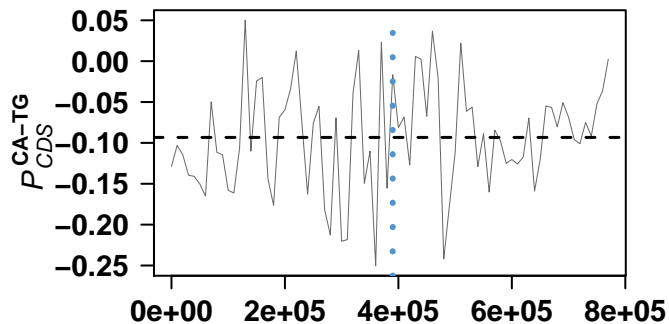
genome coordinates



genome coordinates

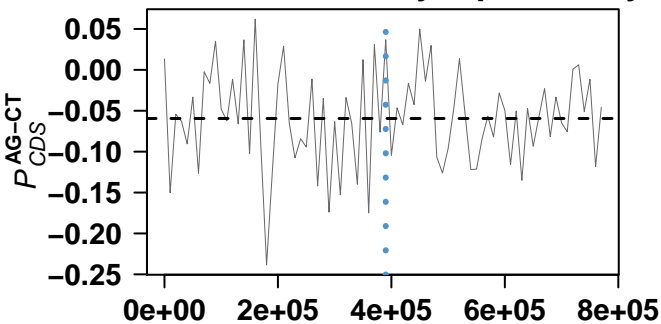


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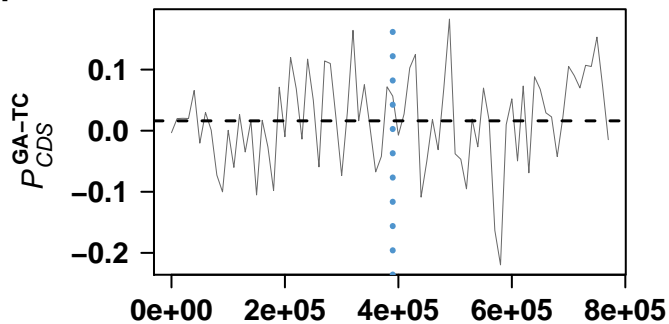


genome coordinates

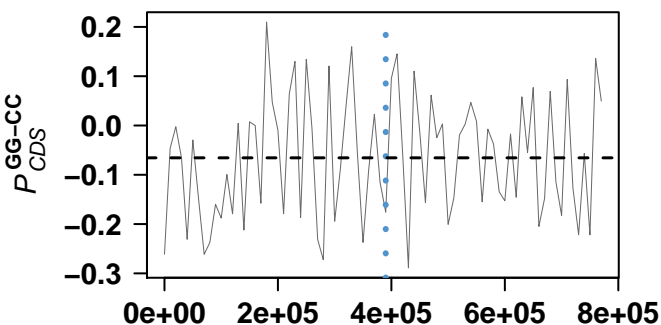
Mycoplasma hyopneumoniae 7448



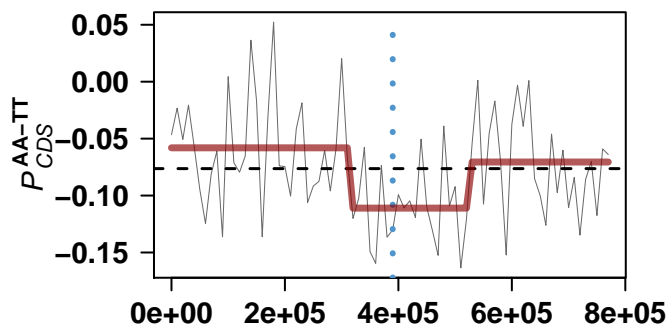
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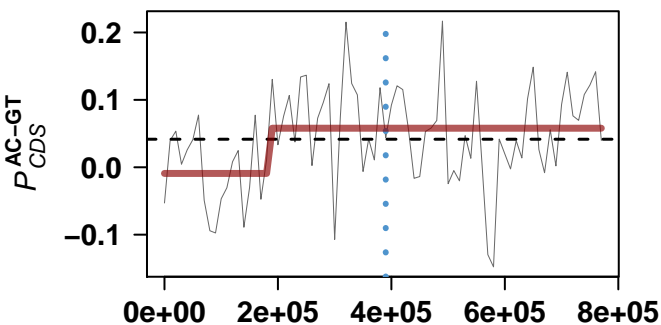
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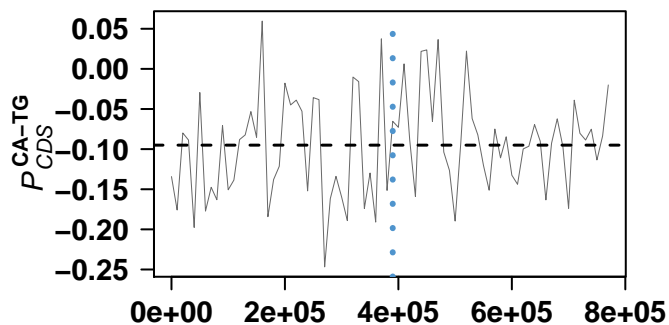
genome coordinates



genome coordinates

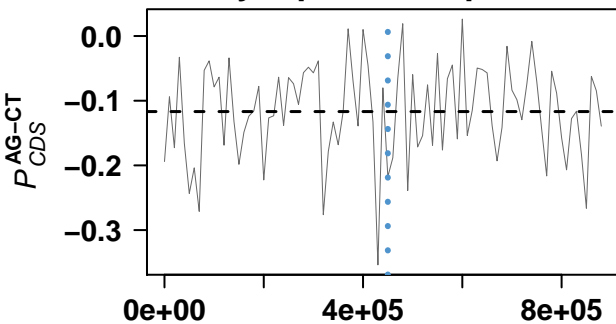


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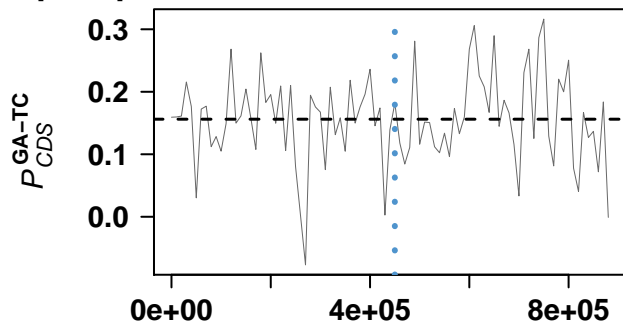


genome coordinates

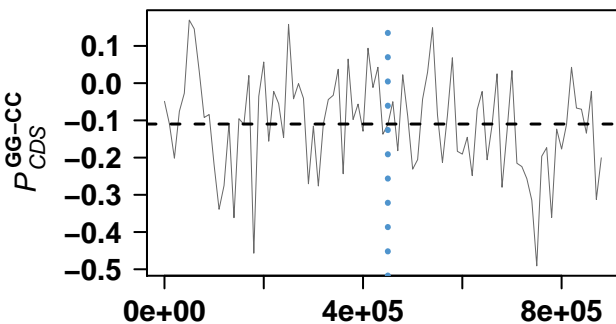
Mycoplasma capricolum subsp. *capricolum* ATCC 27343



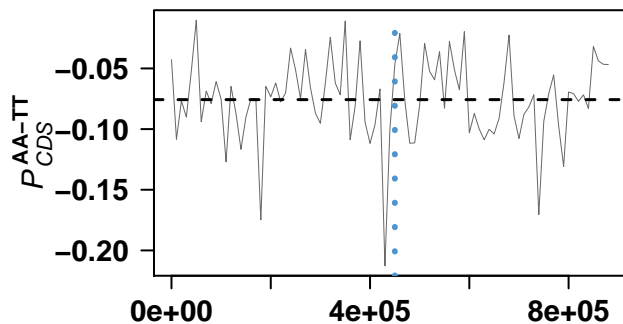
genome coordinates



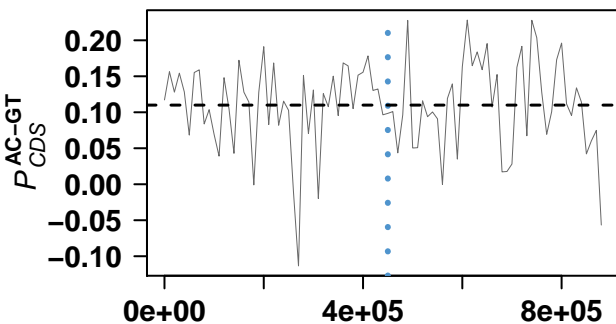
genome coordinates



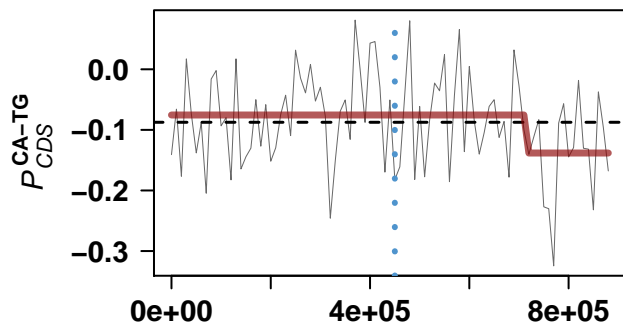
genome coordinates



genome coordinates

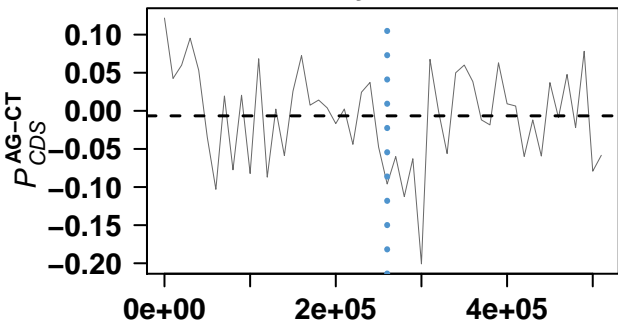


genome coordinates

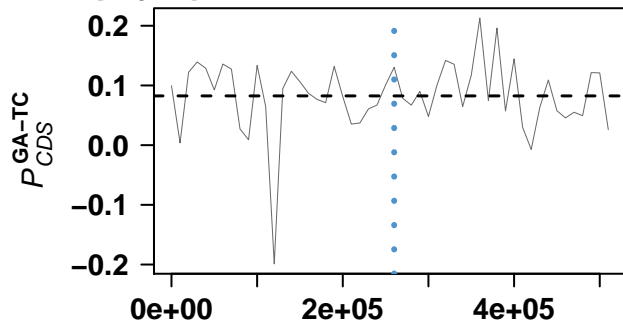


genome coordinates

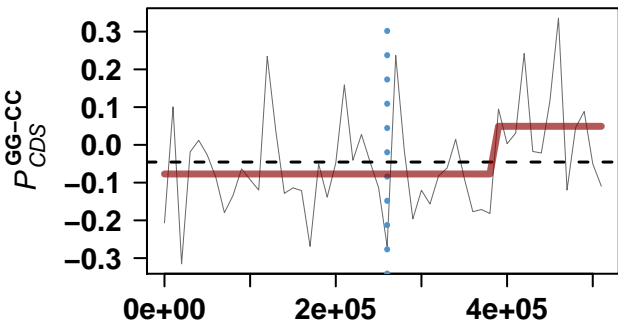
Aster yellows witches'-broom phytoplasma AYWB



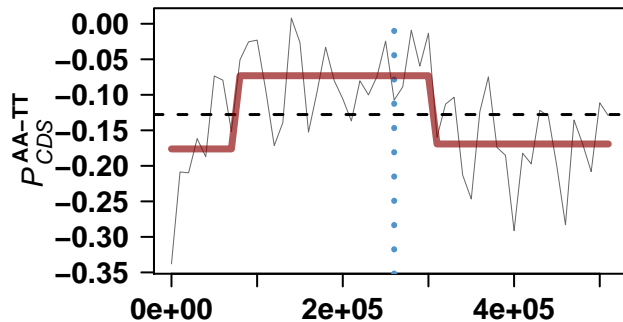
genome coordinates



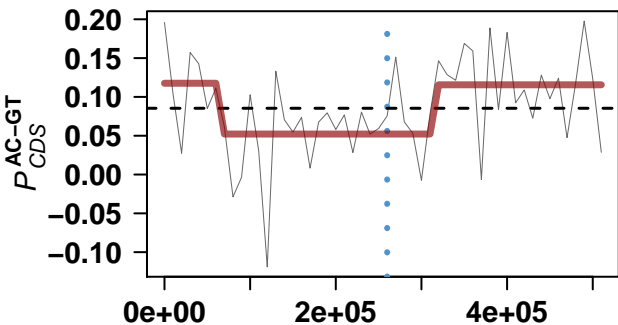
genome coordinates



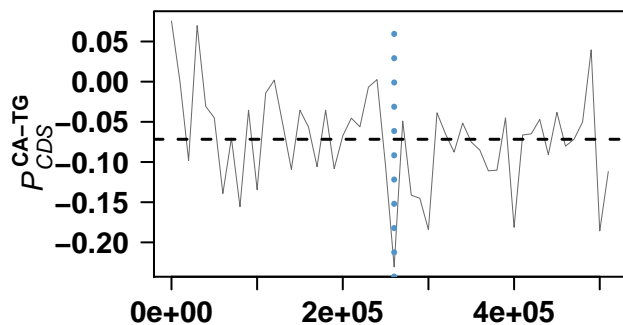
genome coordinates



genome coordinates



genome coordinates



genome coordinates