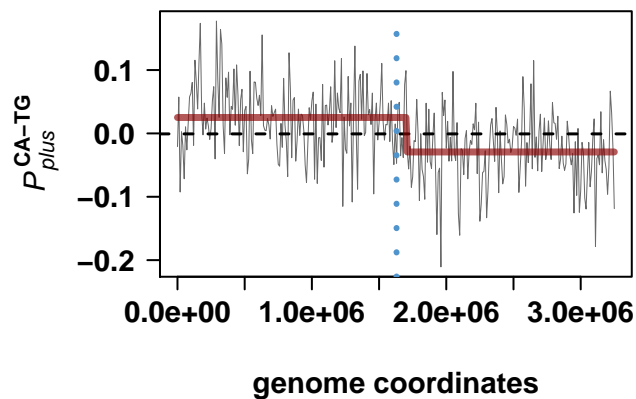
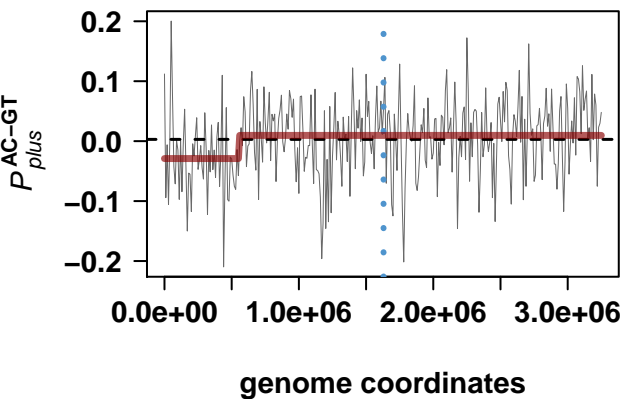
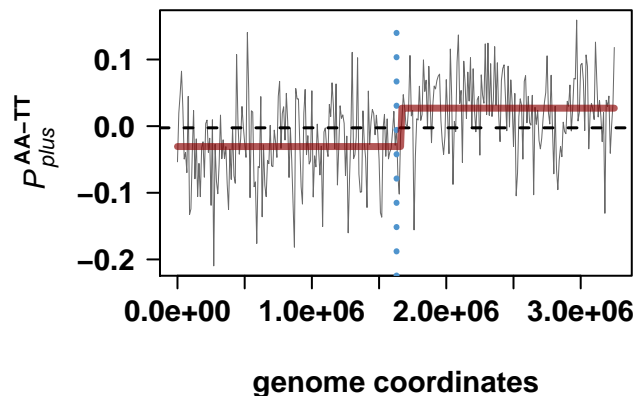
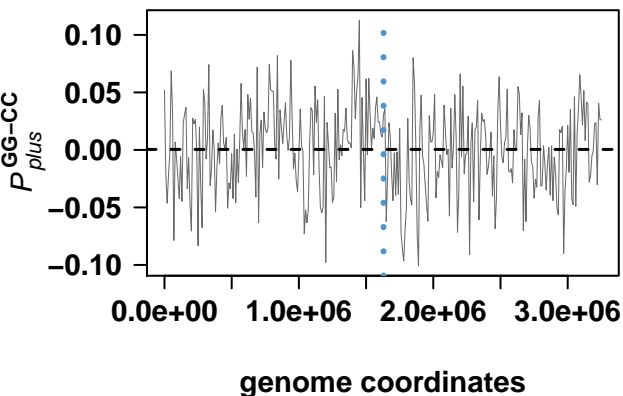
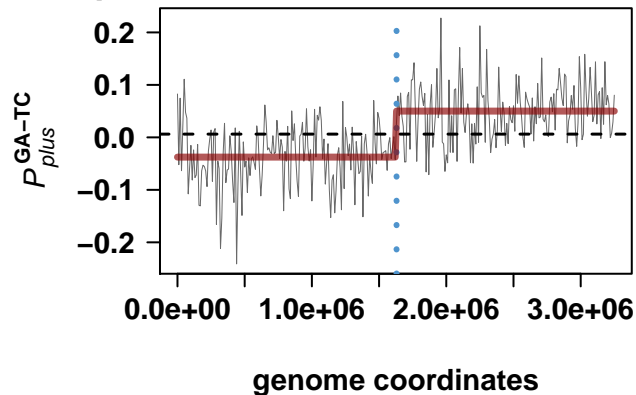
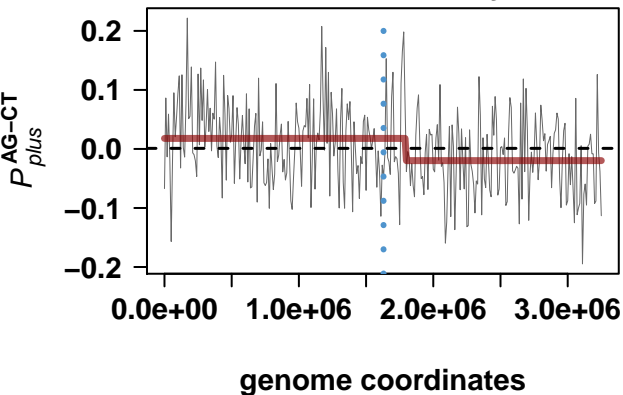
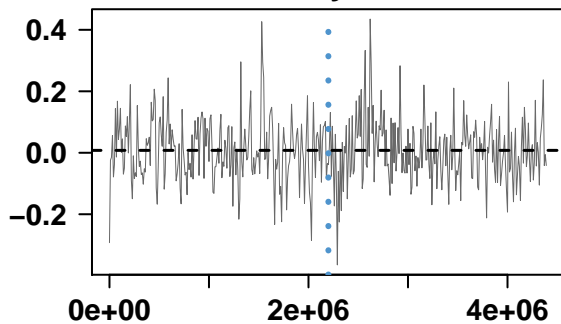


Diagrams (gray curve) and fitted linear models (red thick line) for dinucleotide odds-ratio skews ($P_{\text{plus}}^{\text{AG-CT}}$, $P_{\text{plus}}^{\text{GA-TC}}$, $P_{\text{plus}}^{\text{GG-CC}}$, $P_{\text{plus}}^{\text{AA-TT}}$, $P_{\text{plus}}^{\text{AC-GT}}$ and $P_{\text{plus}}^{\text{CA-TG}}$) along the plus (published) strand of all bacteria chromosomes in our collection. Each step-like breakpoint of the red thick line corresponds to a statistically significant structural change of the skew pattern. In cases where no significant structural changes are detected, the red line is omitted. The vertical dotted blue line indicates the origin of replication (*ori*). There are three distinct types of skew patterns; “sharp”: at least one step-like breakpoint is located close to the *ori*, “vague”: at least one step-like breakpoint is detected, but all breakpoints are far from the *ori*, and “flat”: no step-like breakpoints are detected. The horizontal dashed black line is drawn at the mean value of the skew.

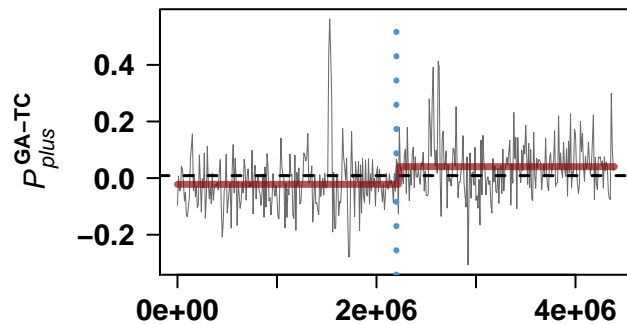
Mycobacterium leprae TN



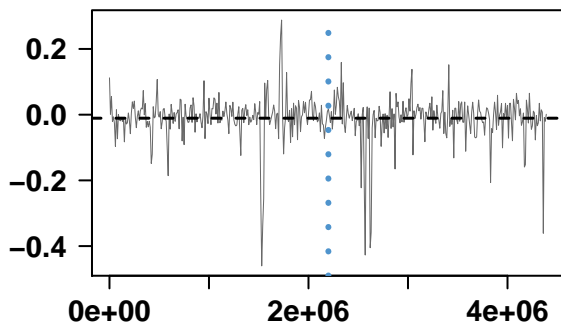
Mycobacterium tuberculosis CDC1551



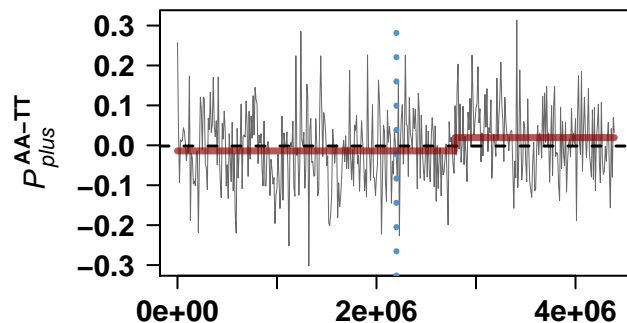
genome coordinates



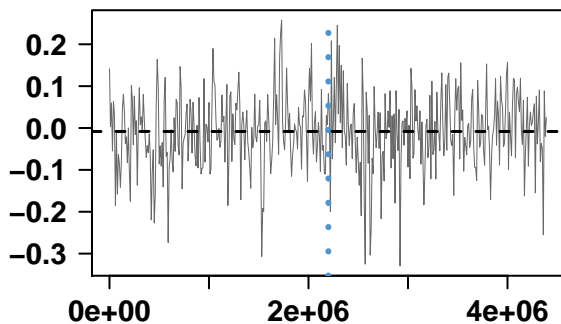
genome coordinates



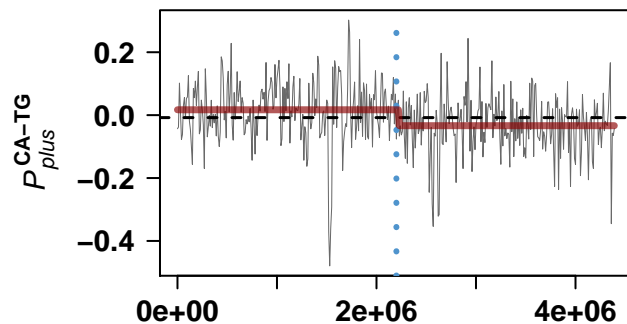
genome coordinates



genome coordinates

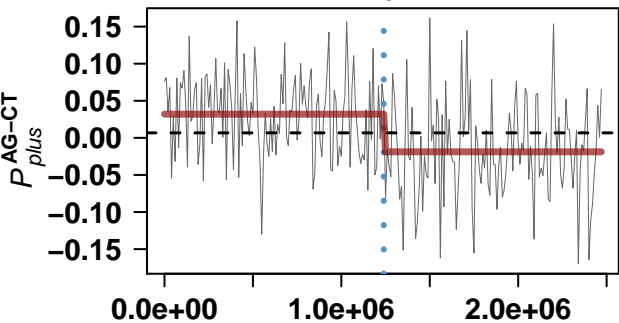


genome coordinates

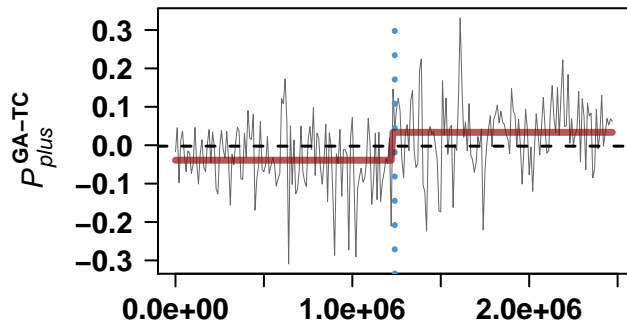


genome coordinates

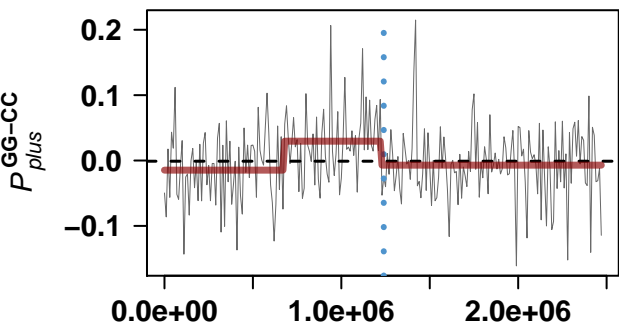
Corynebacterium diphtheriae NCTC 13129



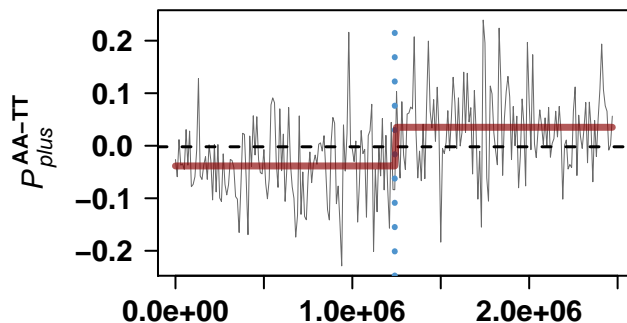
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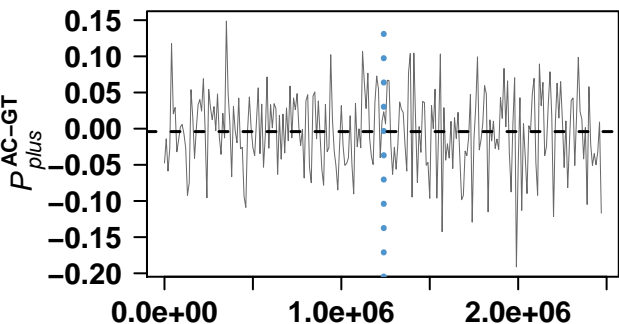
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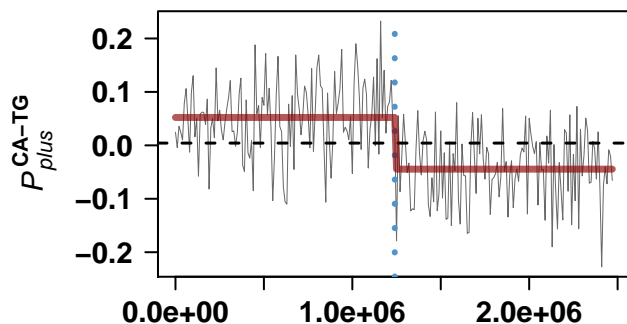
genome coordinates



genome coordinates

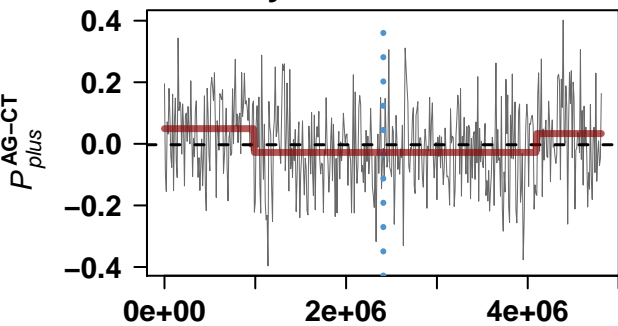


genome coordinates

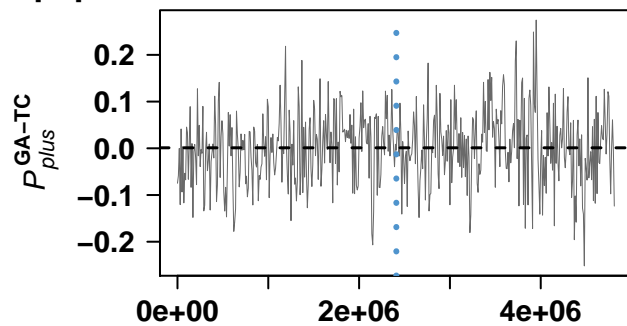


genome coordinates

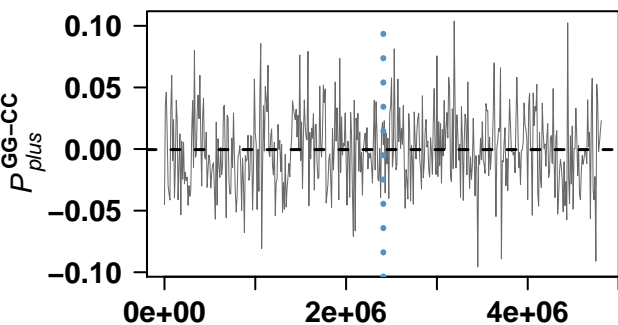
Mycobacterium avium subsp. paratuberculosis K-10



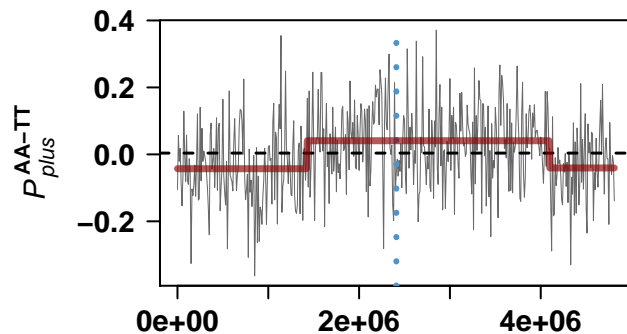
genome coordinates



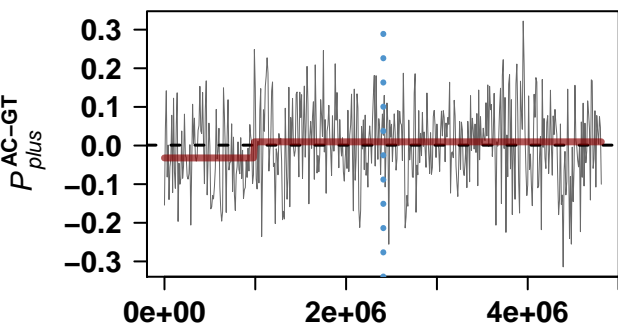
genome coordinates



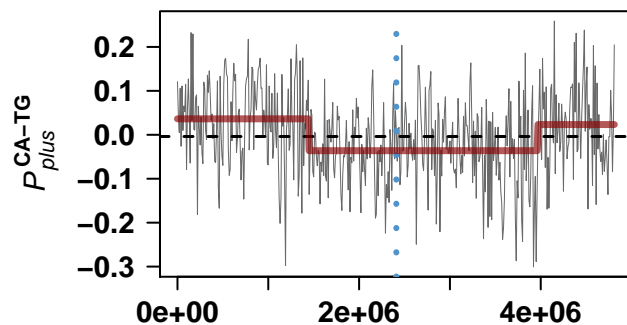
genome coordinates



genome coordinates

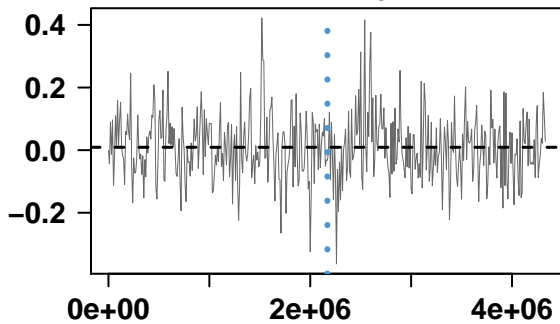


genome coordinates

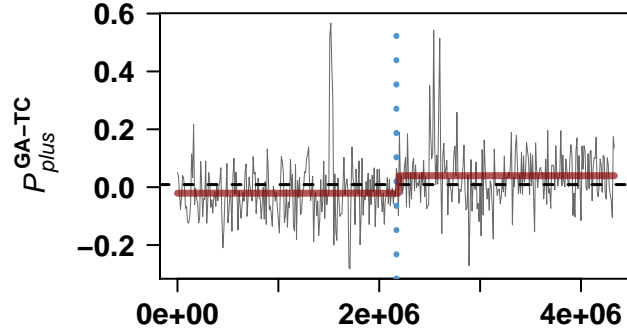


genome coordinates

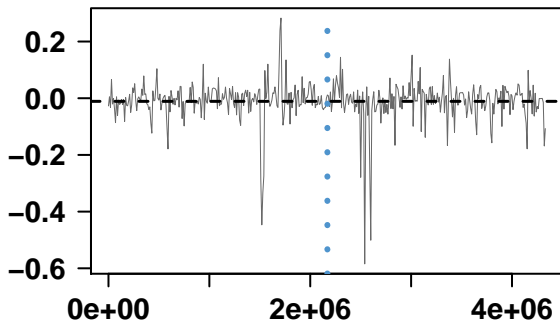
Mycobacterium bovis AF2122/97



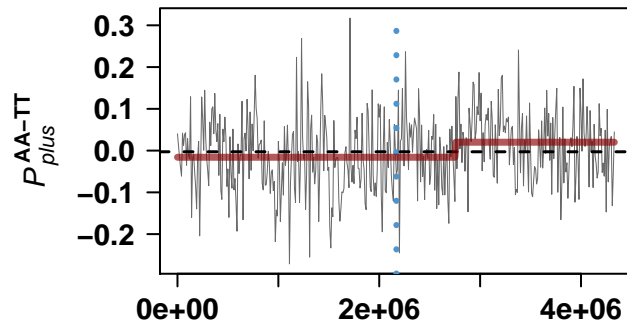
genome coordinates



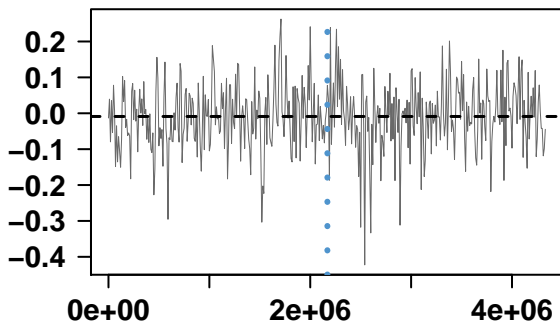
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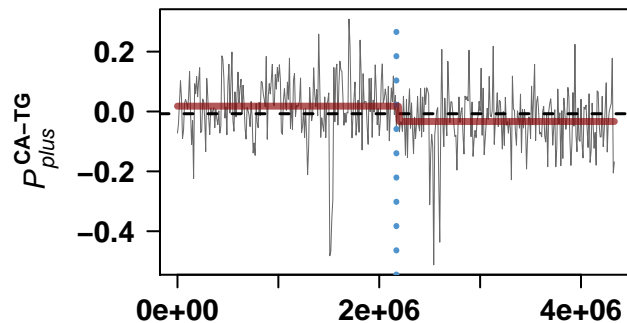
genome coordinates



genome coordinates

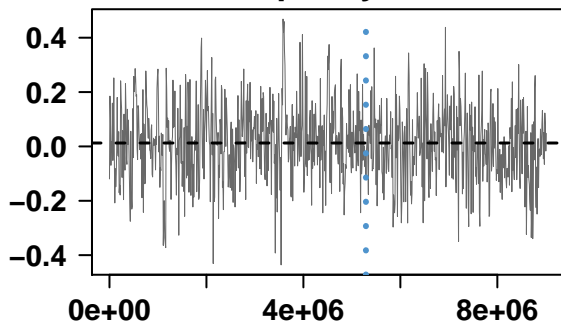


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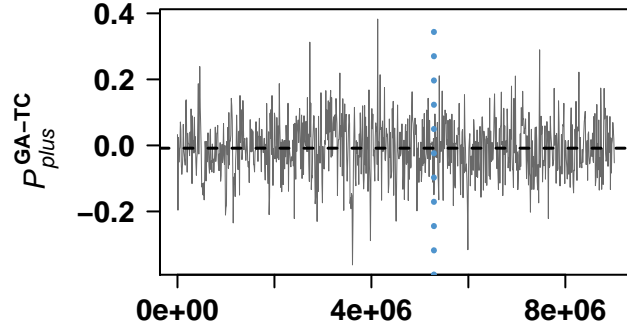


genome coordinates

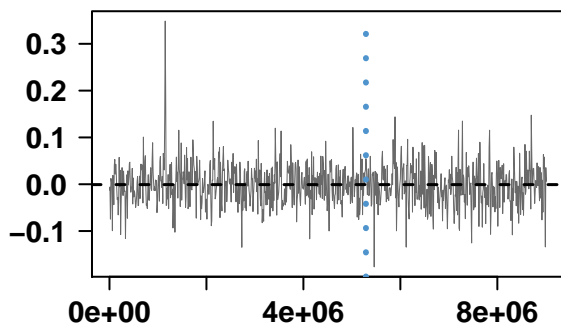
Streptomyces avermitilis MA-4680 = NBRC 14893



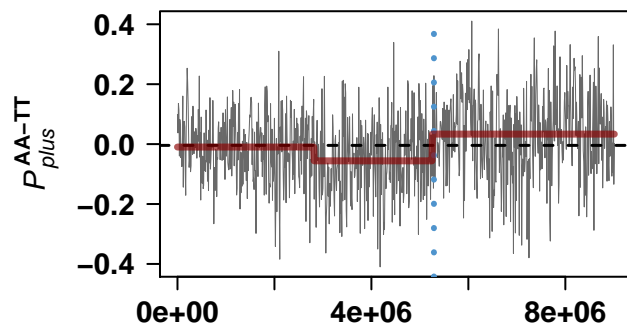
genome coordinates



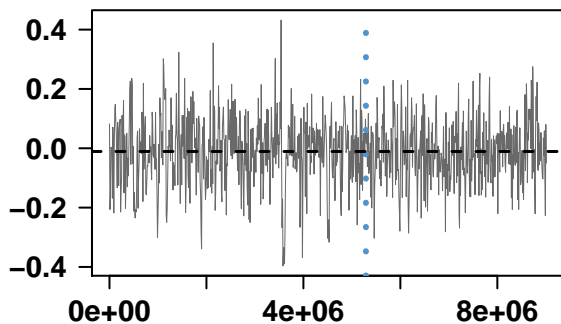
genome coordinates



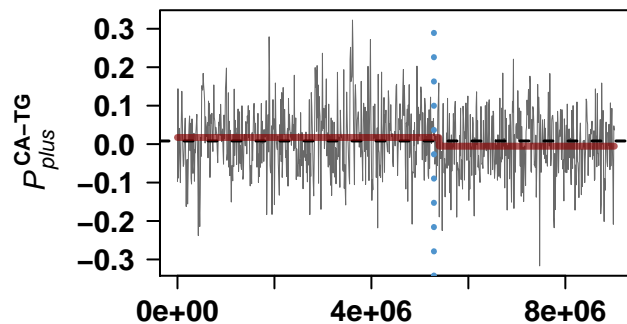
genome coordinates



genome coordinates

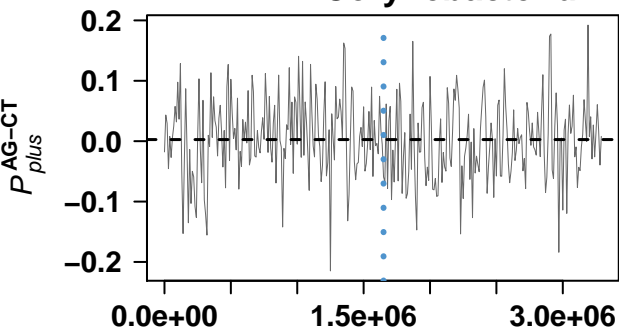


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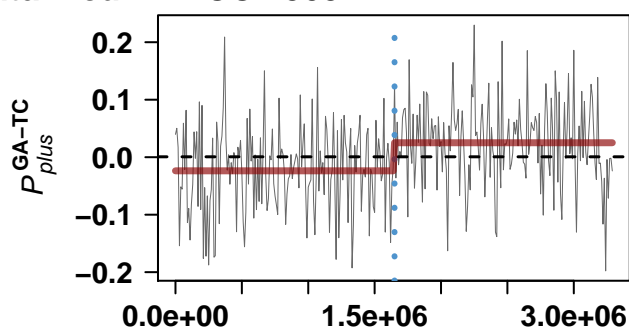


genome coordinates

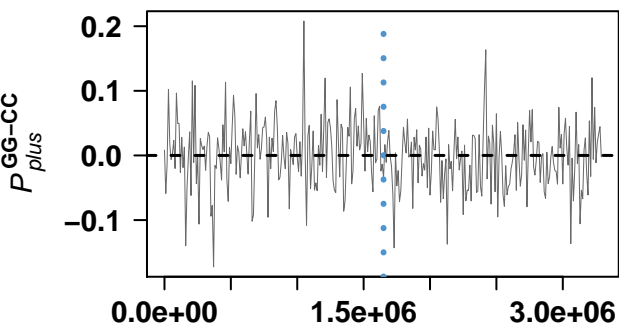
Corynebacterium glutamicum ATCC 13032



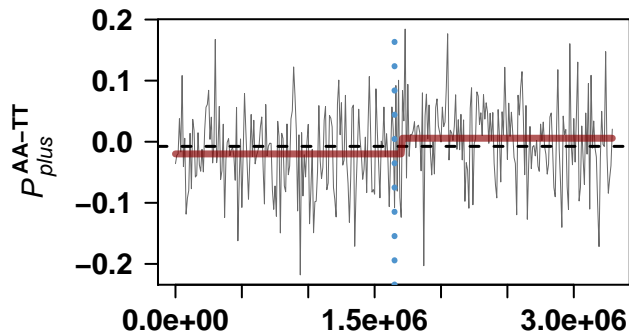
genome coordinates



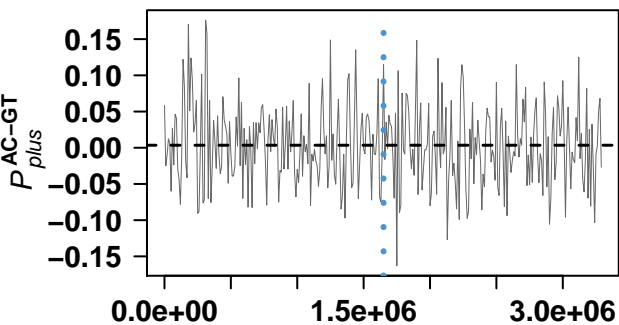
genome coordinates



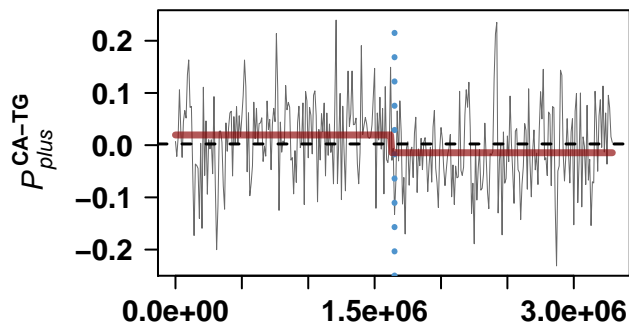
genome coordinates



genome coordinates

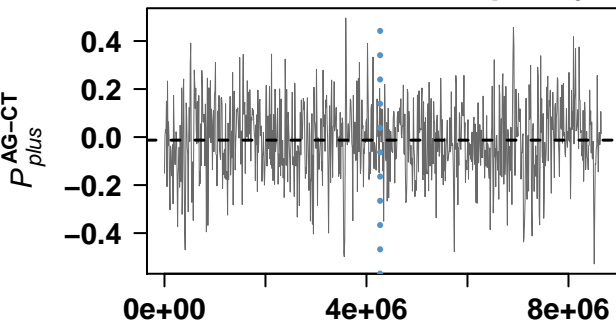


genome coordinates

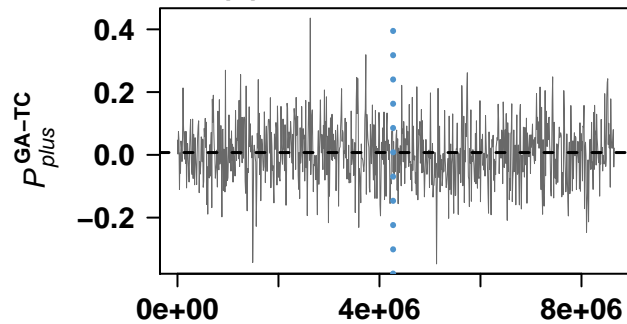


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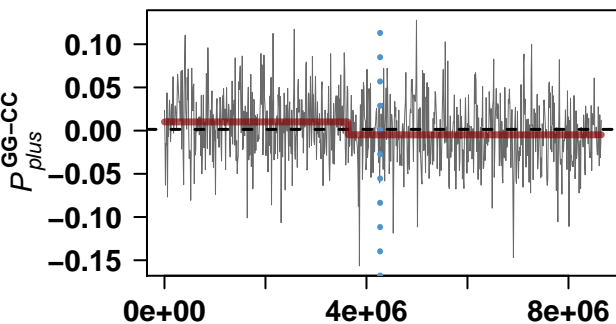
Streptomyces coelicolor A3(2)



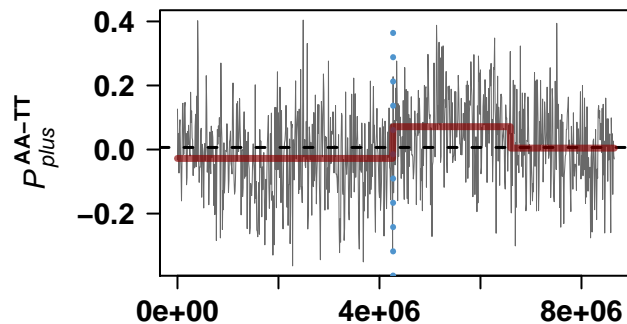
genome coordinates



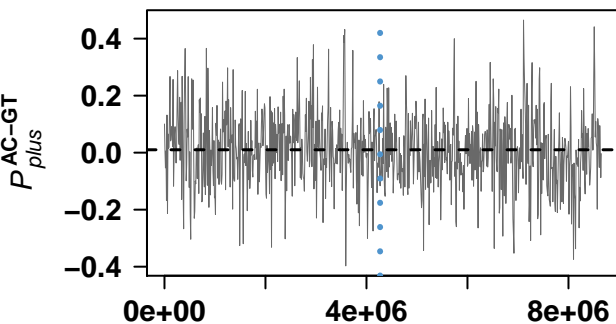
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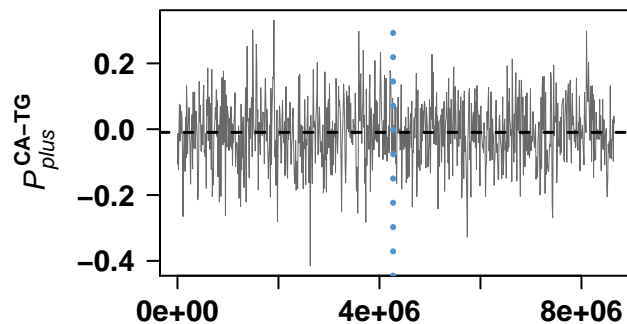
genome coordinates



genome coordinates

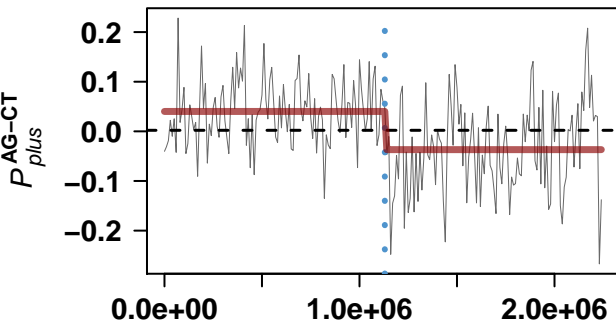


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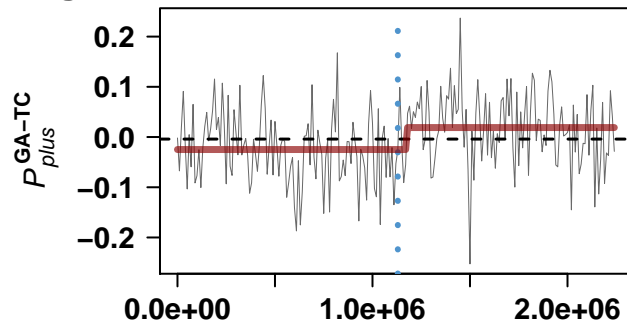


genome coordinates

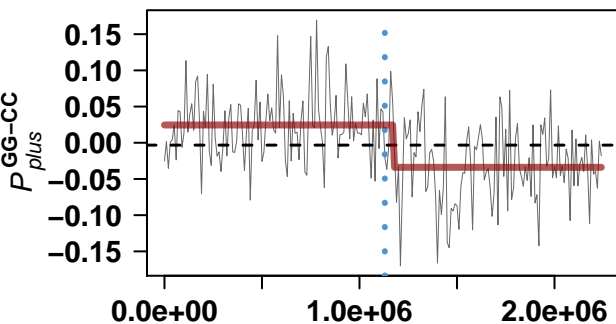
Bifidobacterium longum NCC2705



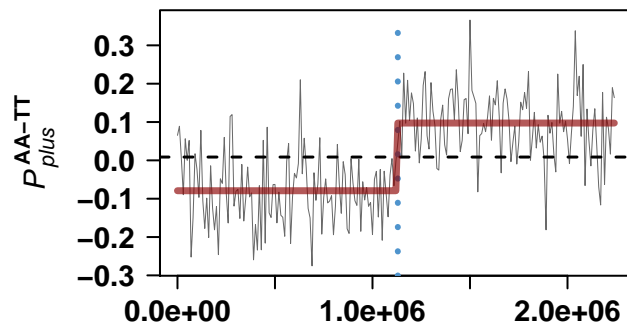
genome coordinates



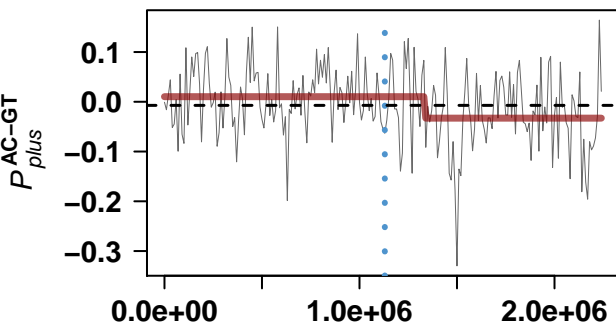
genome coordinates



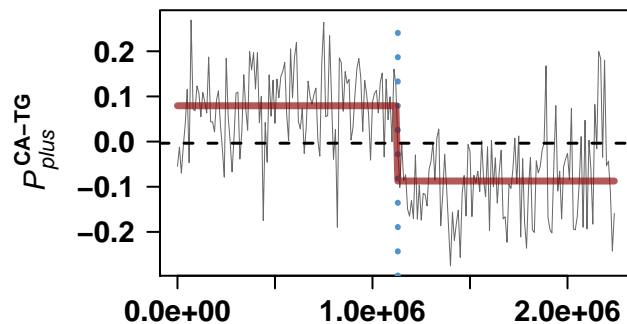
genome coordinates



genome coordinates

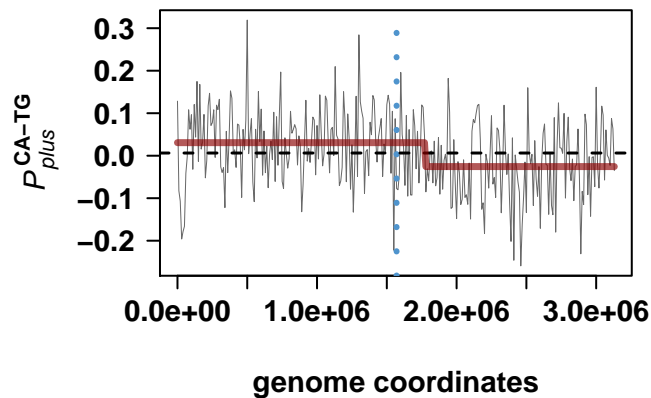
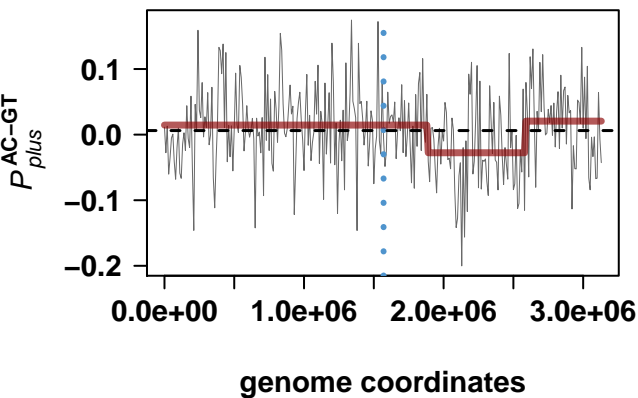
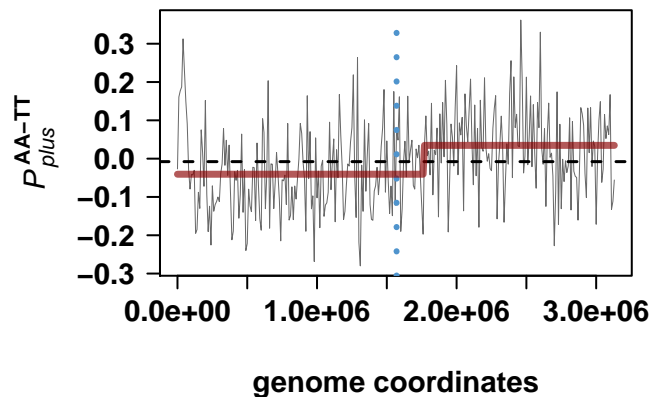
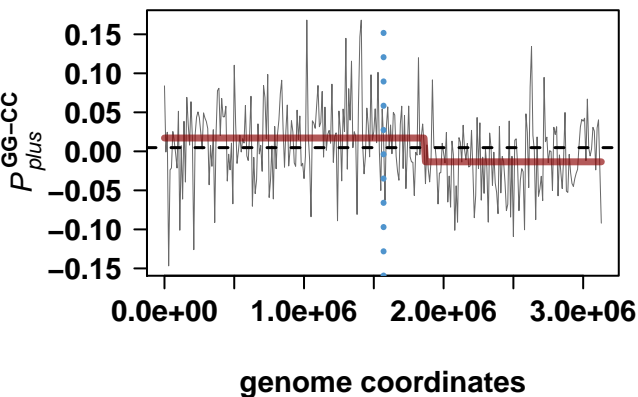
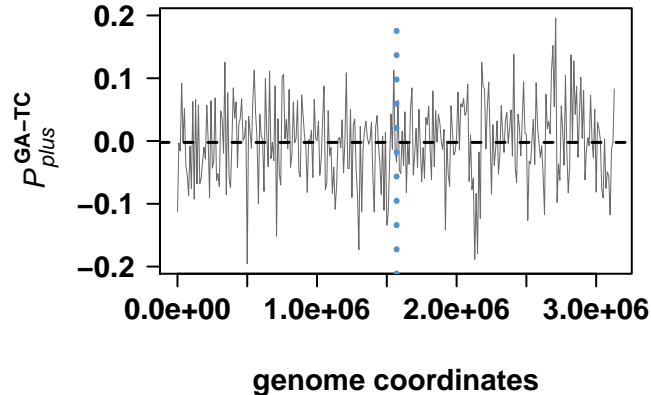
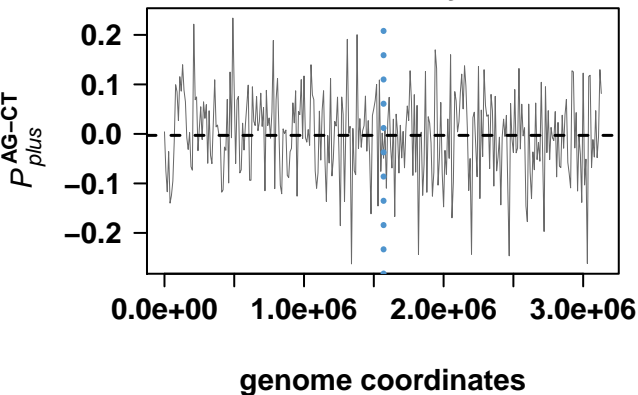


genome coordinates

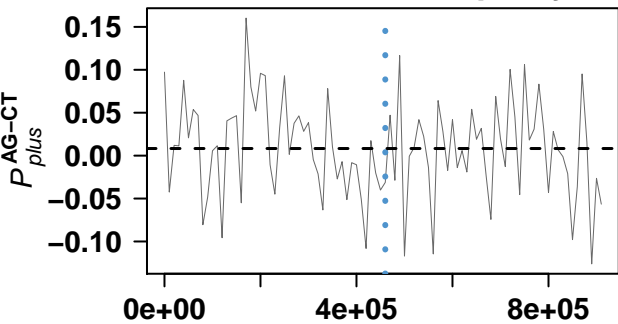


genome coordinates

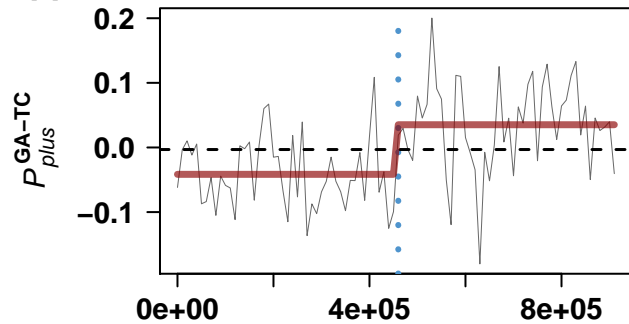
Corynebacterium efficiens YS-314



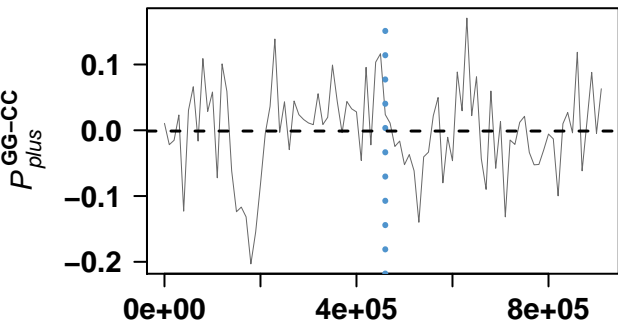
Tropheryma whipplei TW08/27



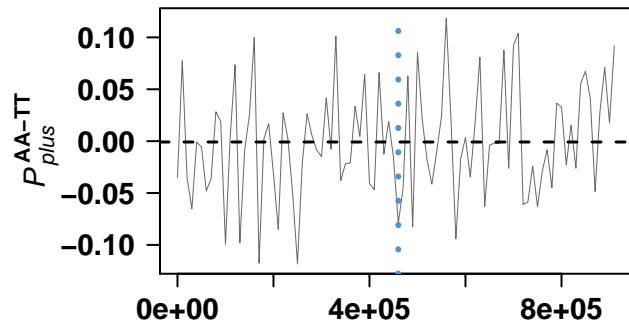
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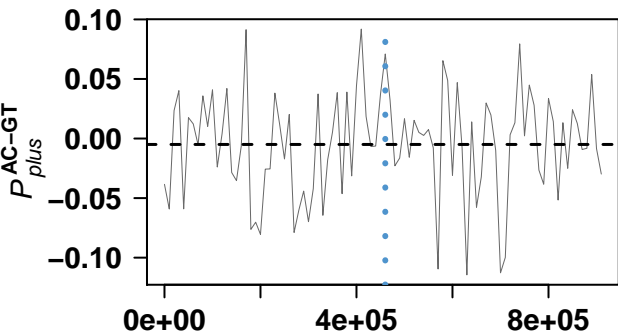
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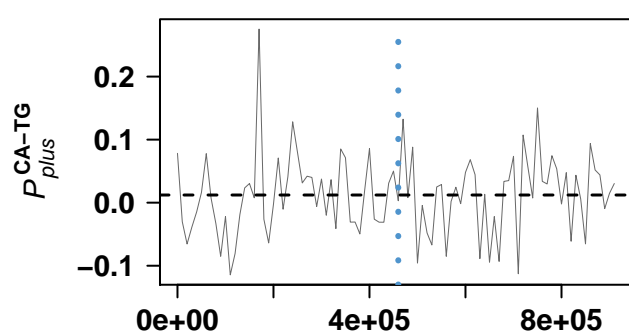
genome coordinates



genome coordinates

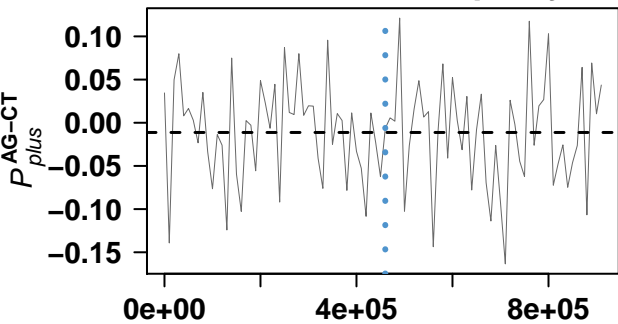


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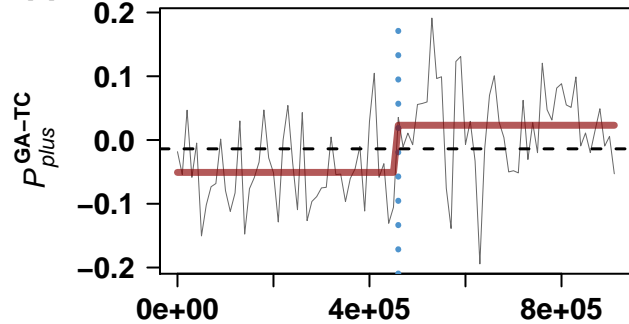


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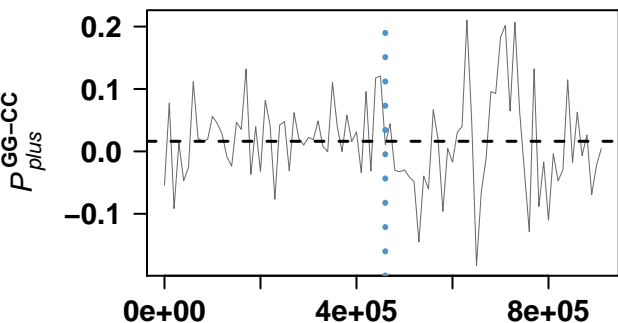
Tropheryma whipplei str. Twist



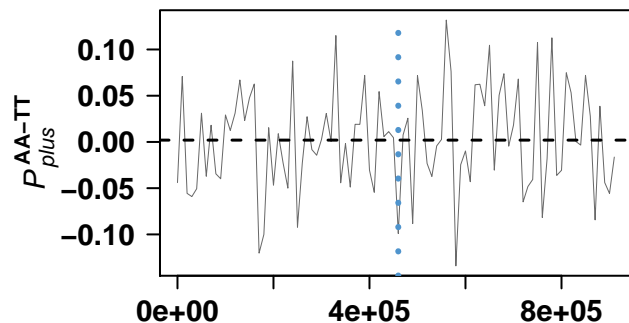
genome coordinates



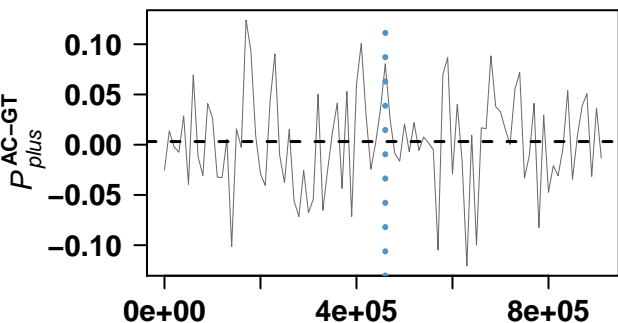
genome coordinates



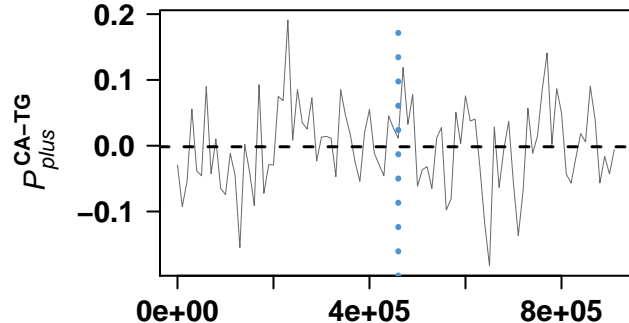
genome coordinates



genome coordinates

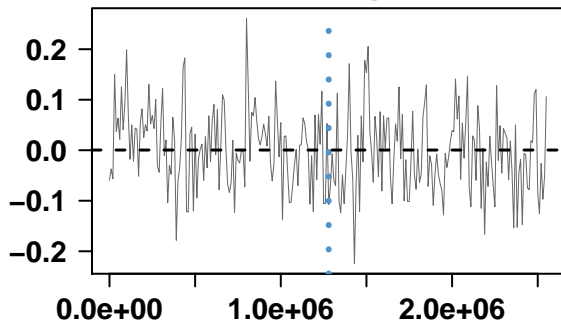


genome coordinates

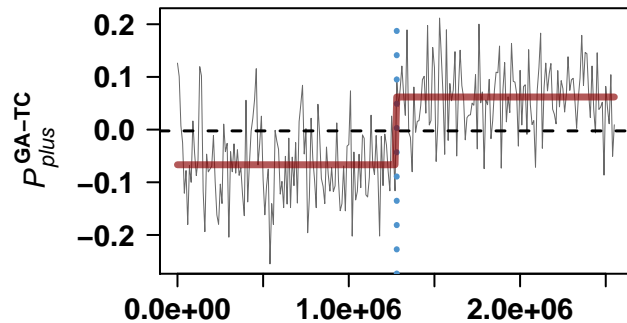


genome coordinates

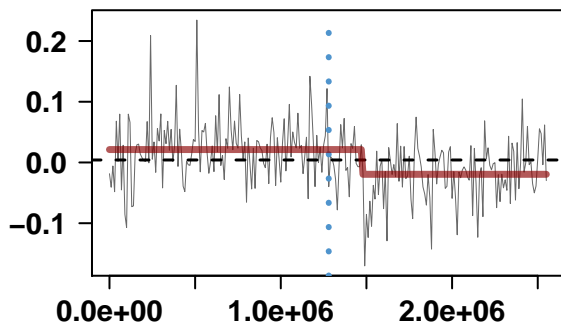
Propionibacterium acnes KPA171202



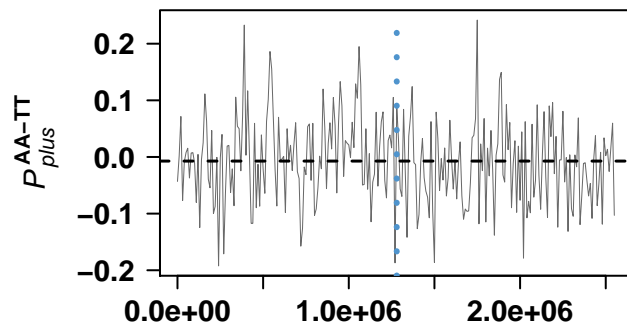
genome coordinates



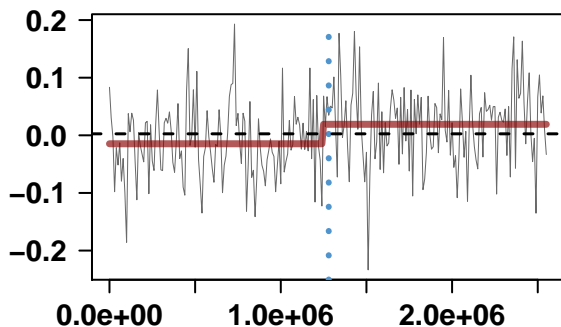
genome coordinates



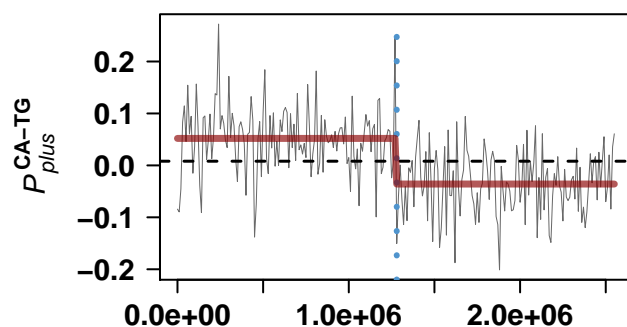
genome coordinates



genome coordinates

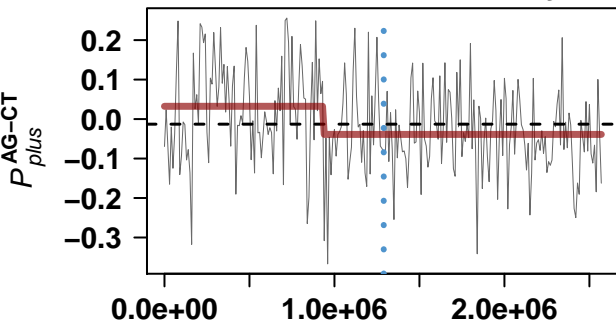


genome coordinates

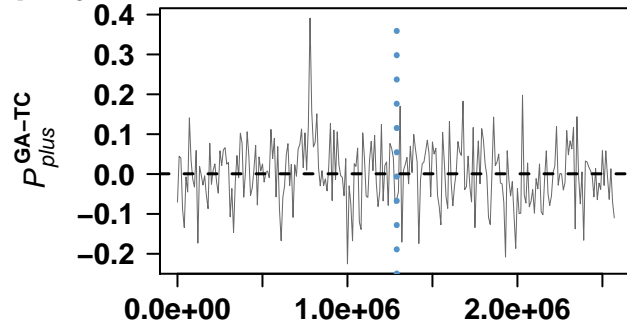


genome coordinates

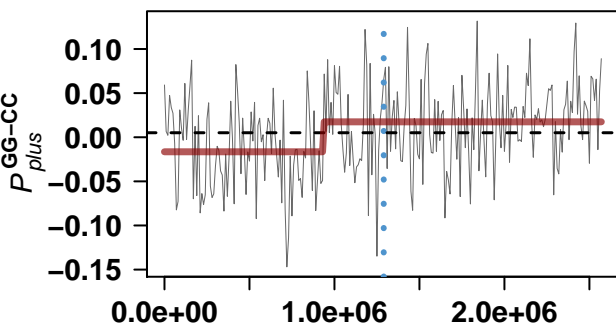
Leifsonia xyli subsp. xyli str. CTCB07



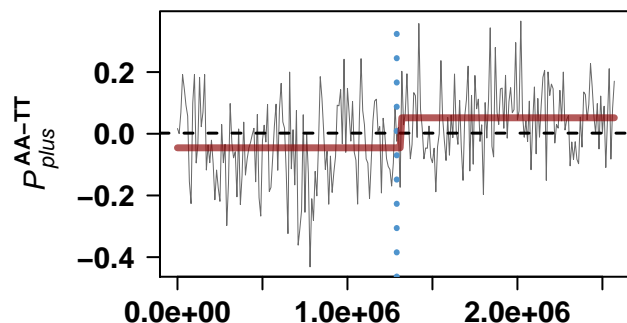
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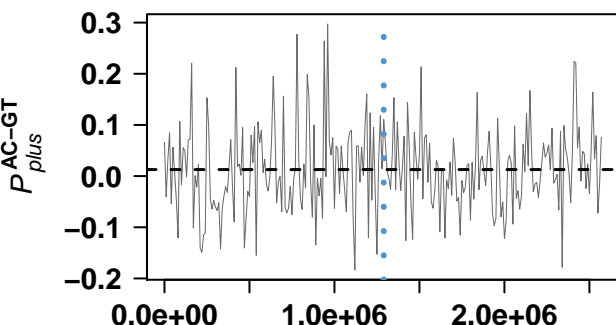
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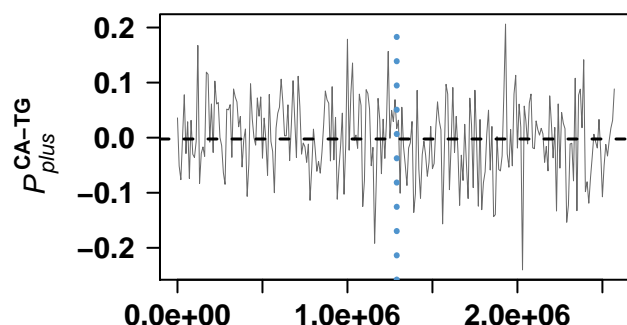
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genome coordinates

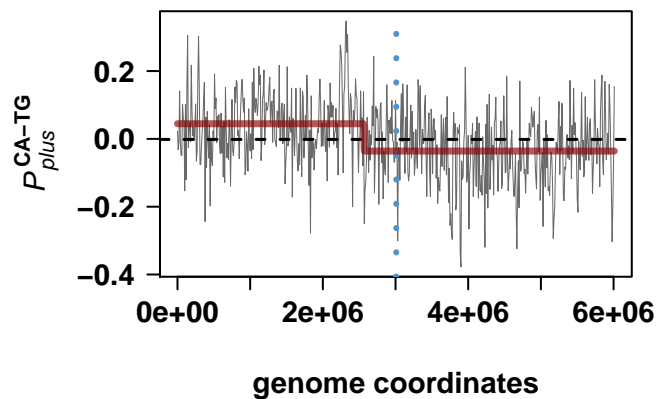
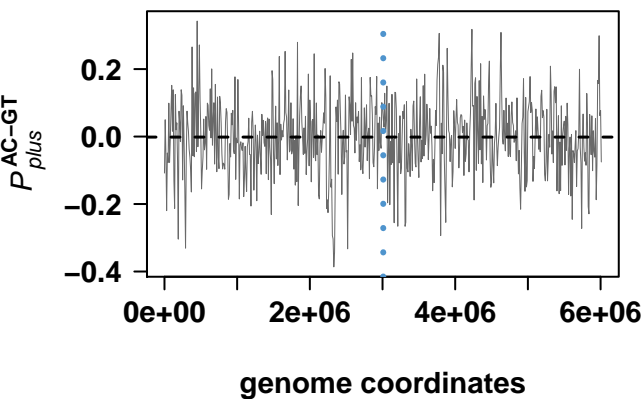
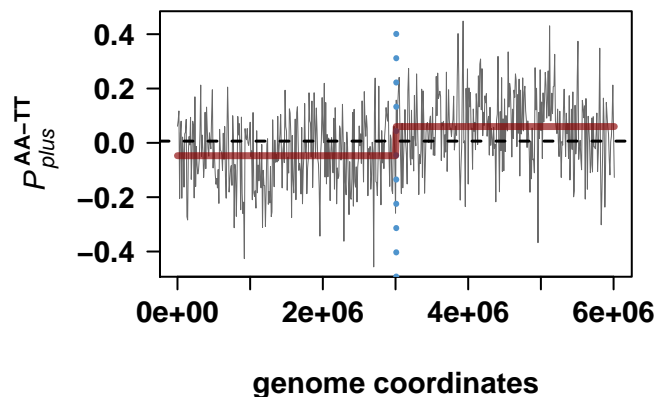
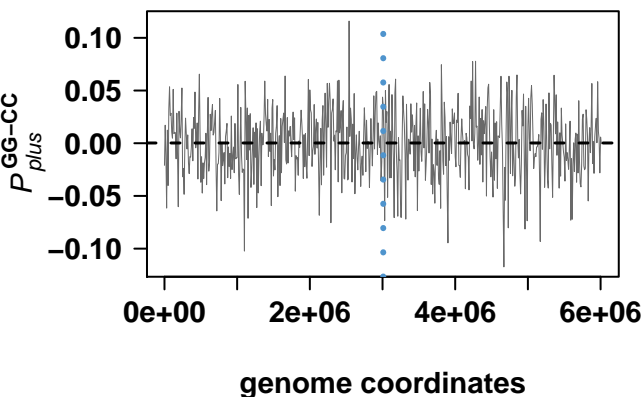
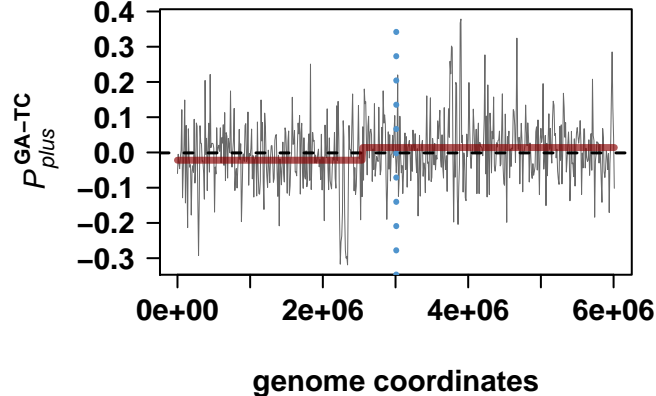
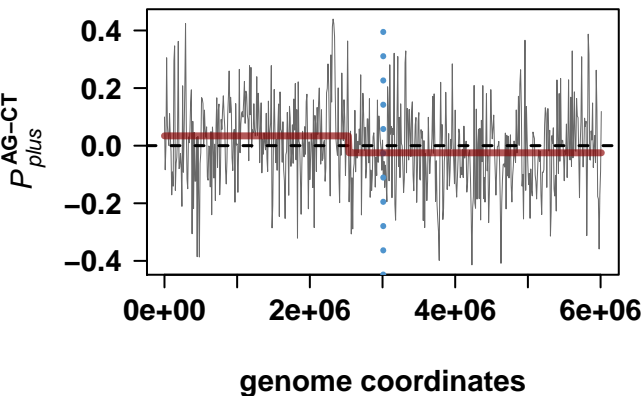


genome coordinates

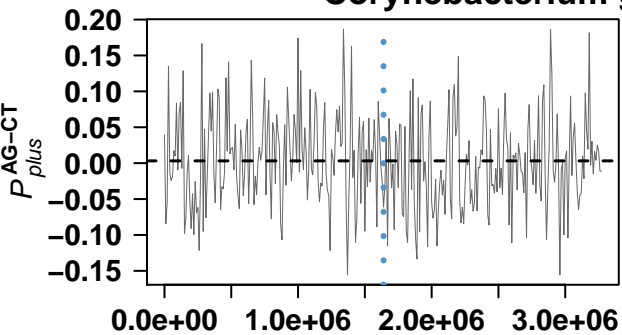


genome coordinates

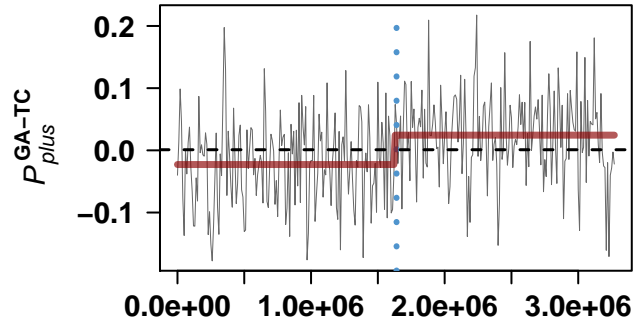
Nocardia farcinica IFM 10152



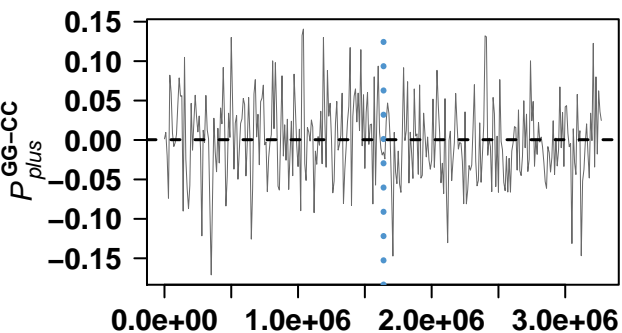
Corynebacterium glutamicum ATCC 13032



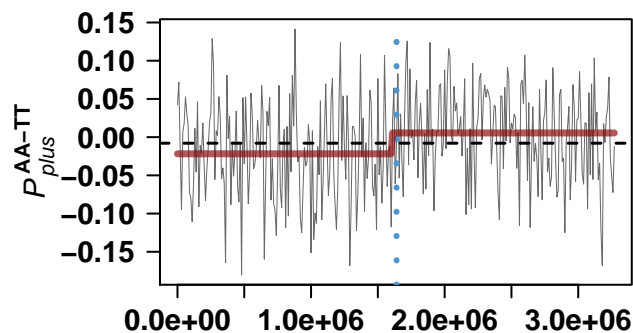
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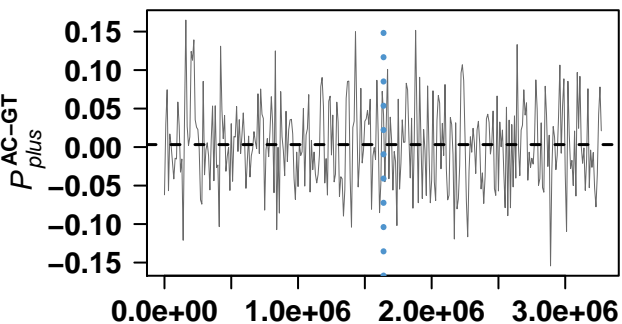
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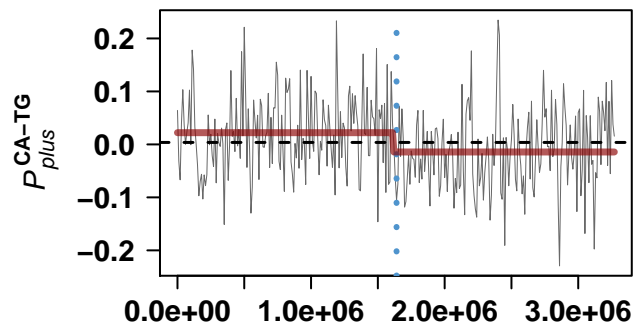
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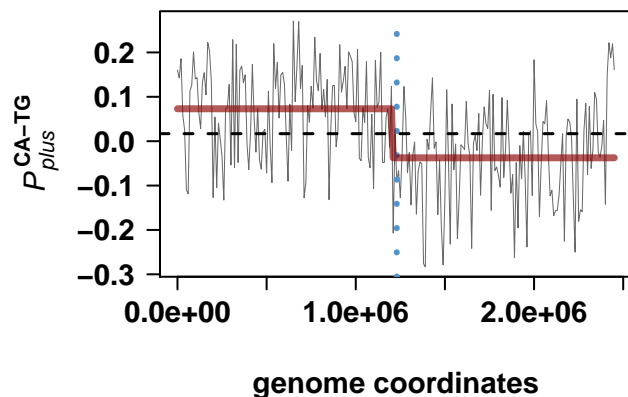
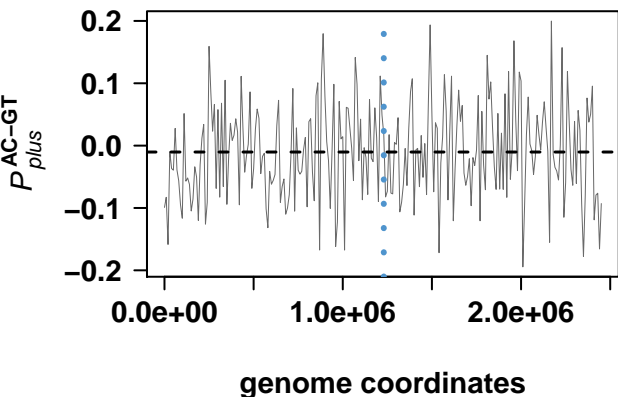
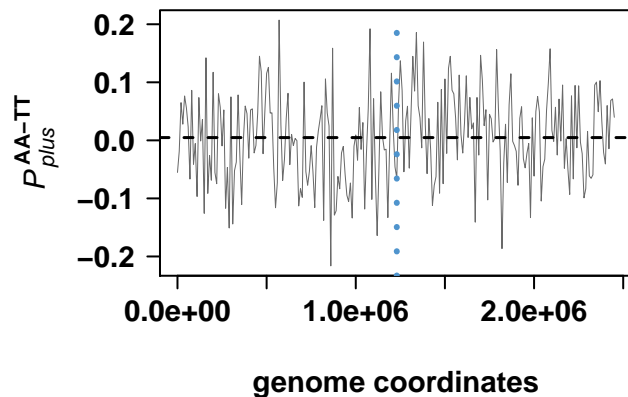
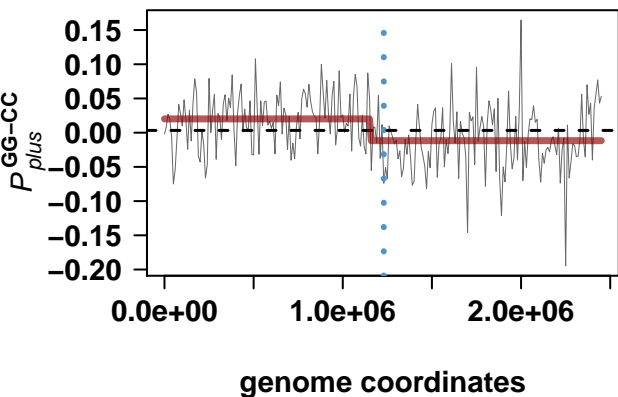
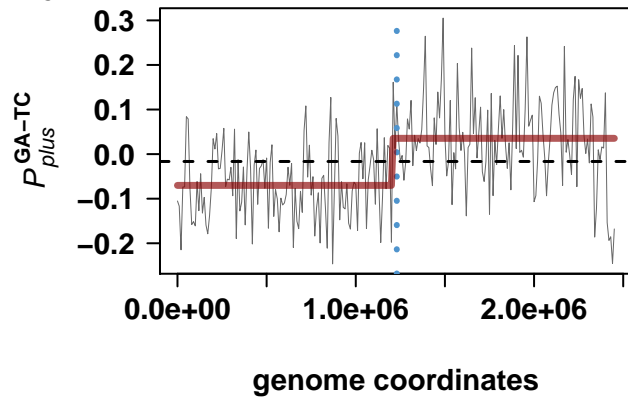
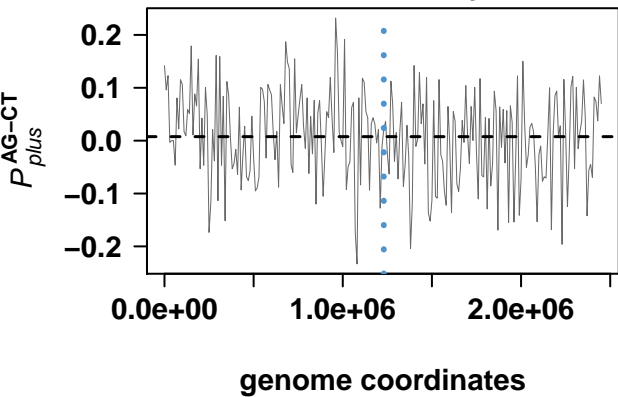


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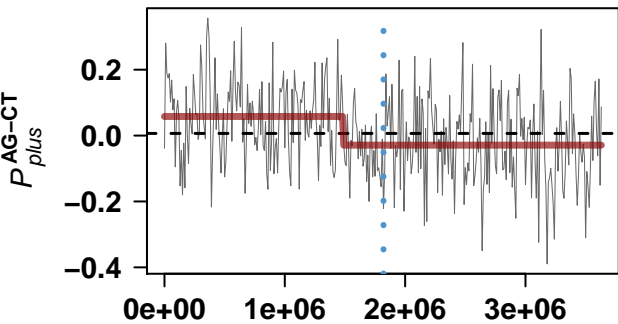


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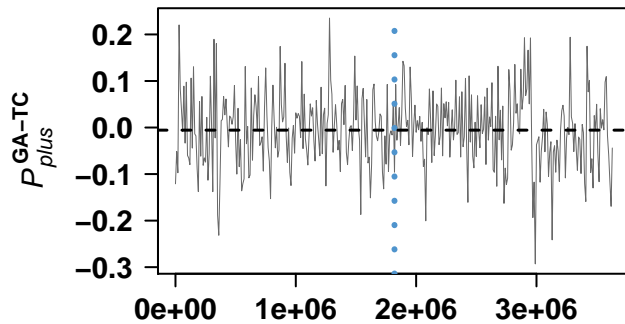
Corynebacterium jeikeium K411



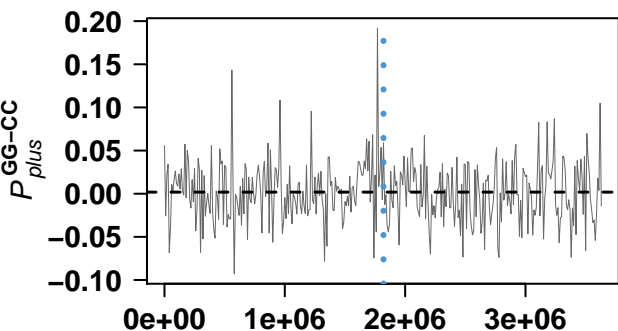
Thermobifida fusca YX



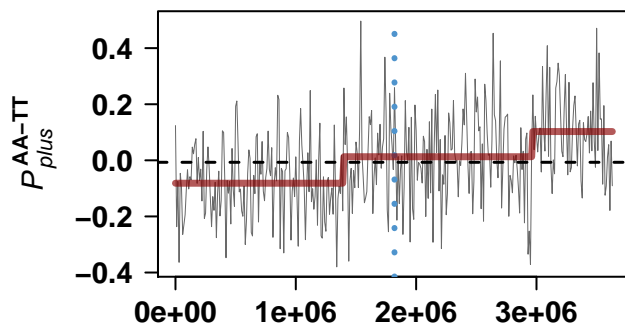
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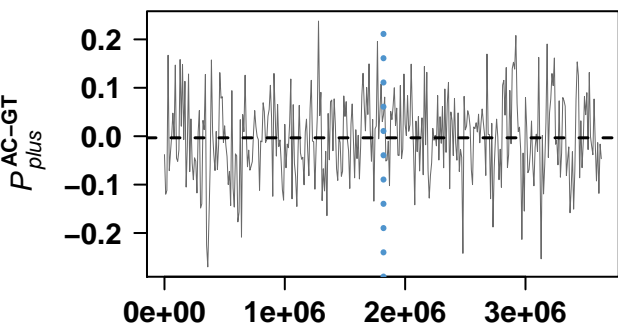
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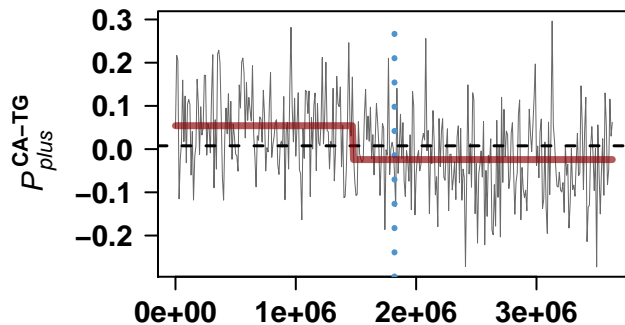
genome coordinates



genome coordinates

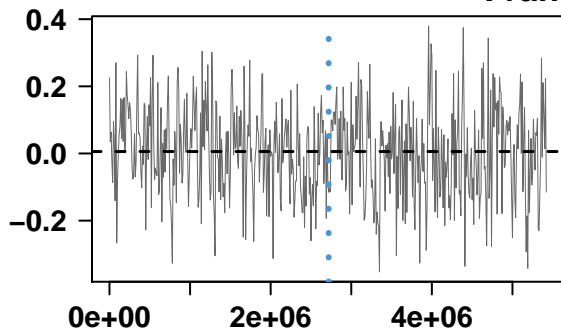


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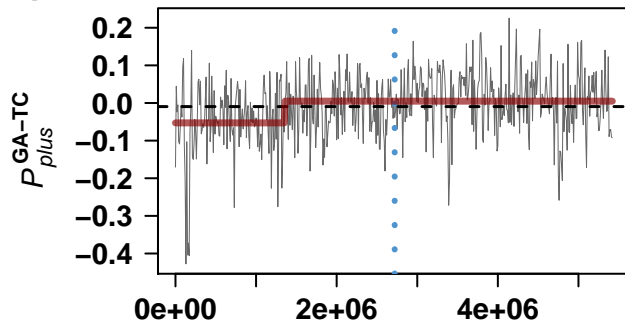


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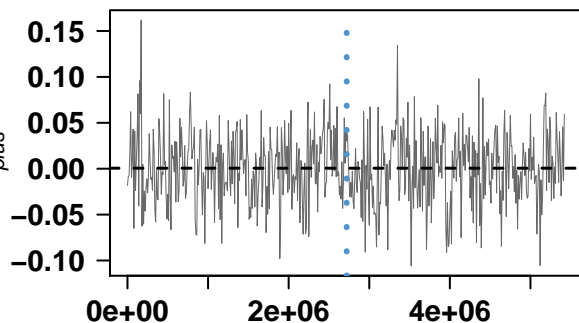
Frankia sp. Ccl3



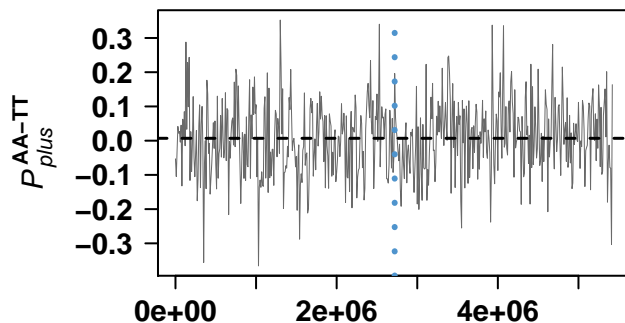
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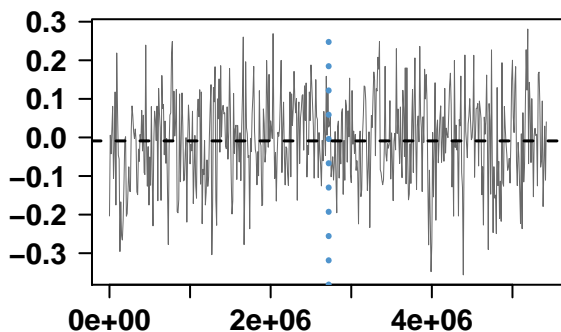
genome coordinates



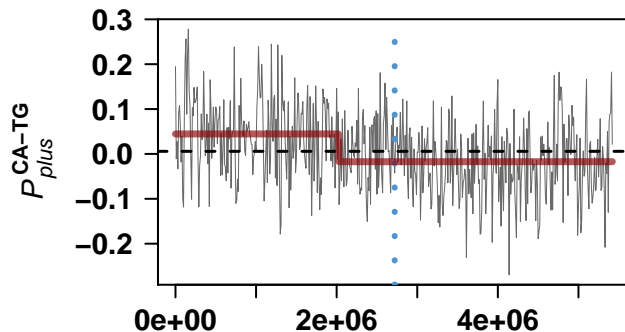
genome coordinates



genome coordinates

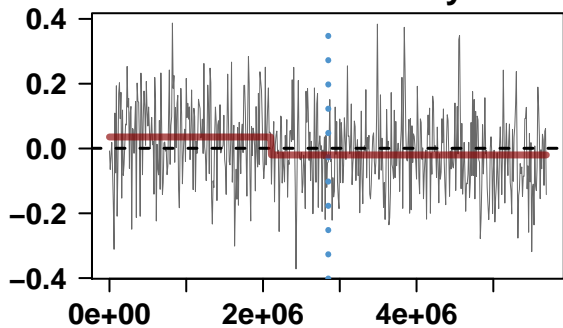


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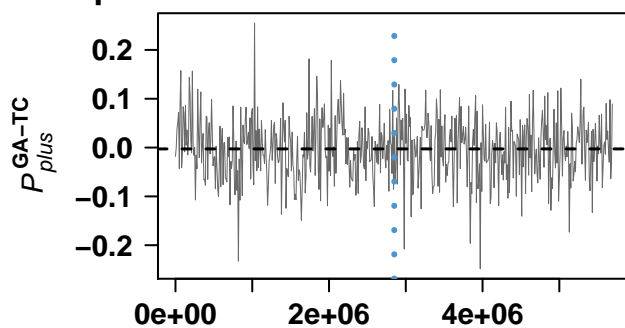


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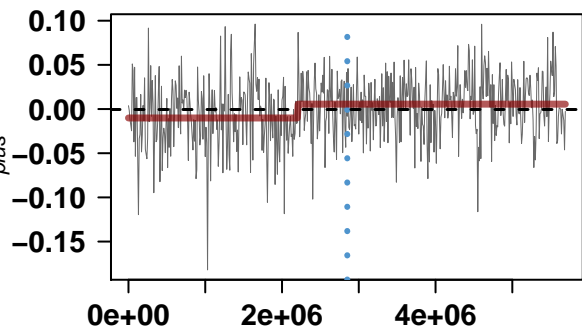
Mycobacterium sp. MCS



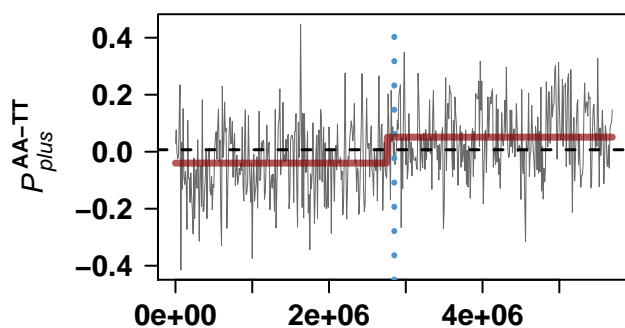
genome coordinates



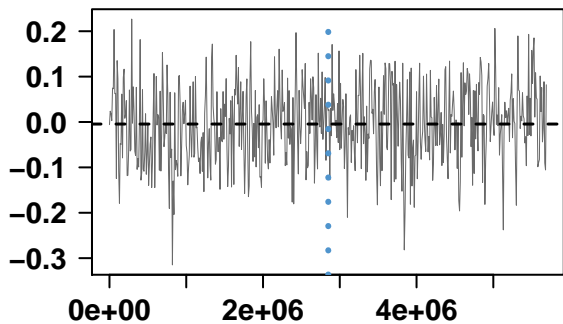
genome coordinates



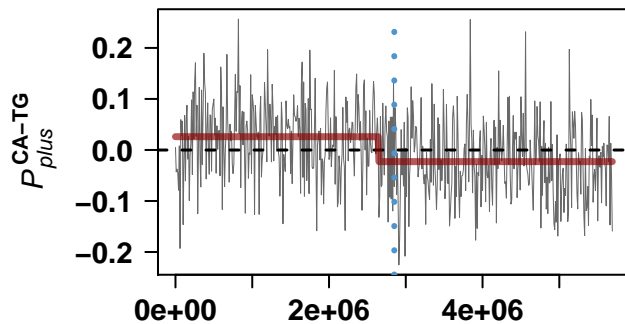
genome coordinates



genome coordinates

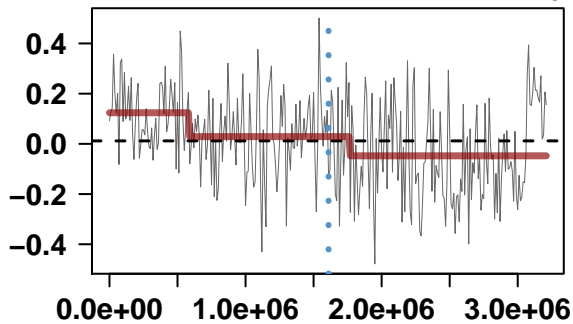


genome coordinates

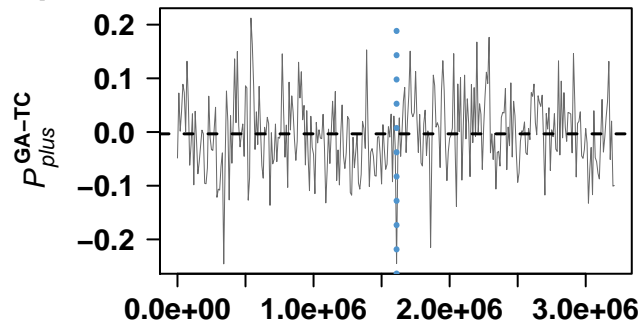


genome coordinates

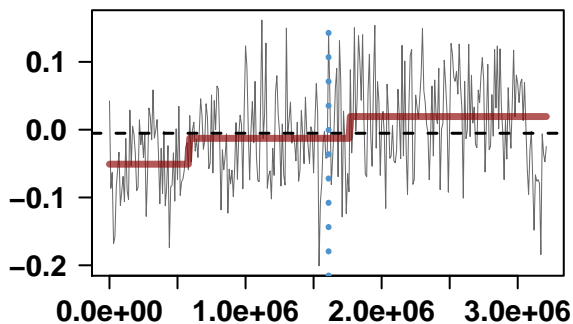
Rubrobacter xylanophilus DSM 9941



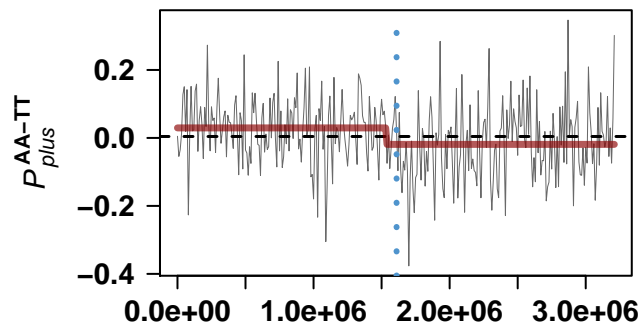
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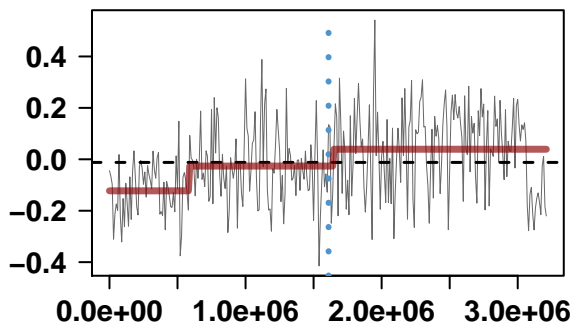
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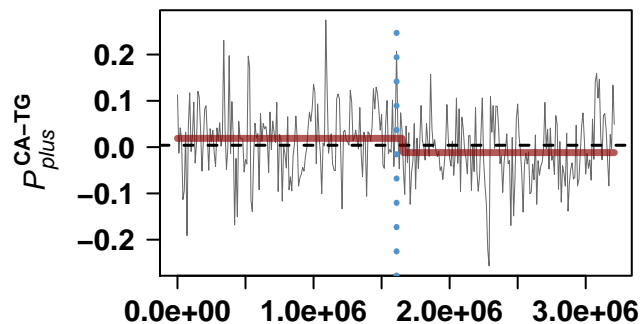
genome coordinates



genome coordinates

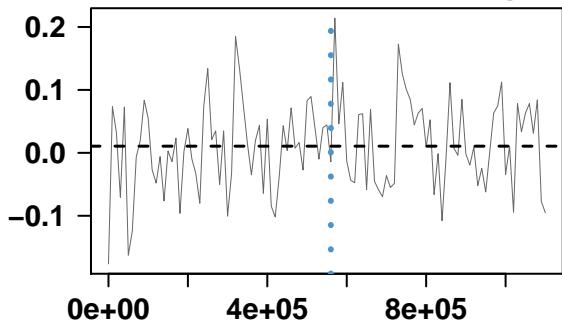


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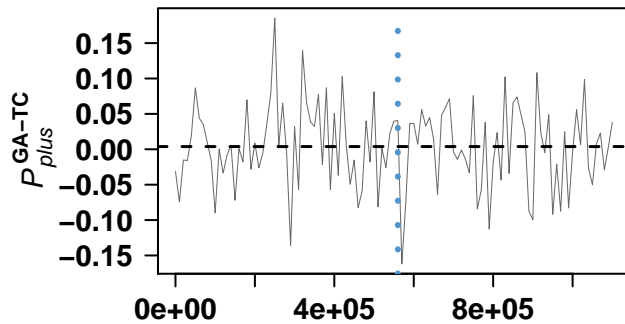


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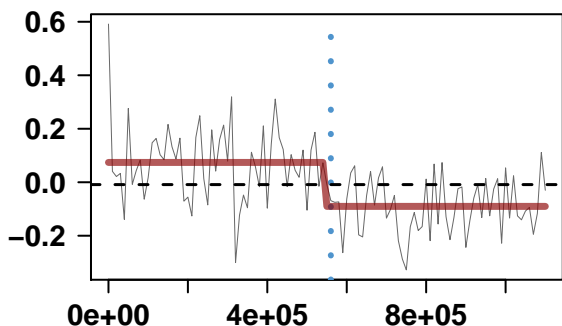
Rickettsia prowazekii str. Madrid E



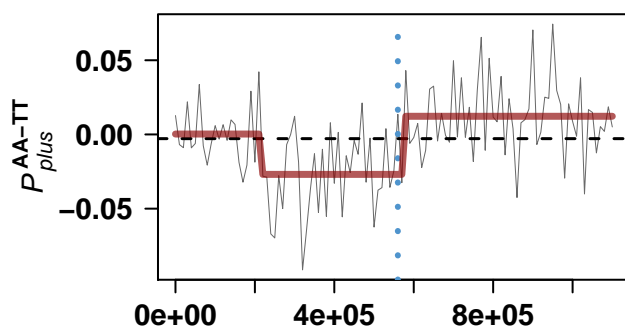
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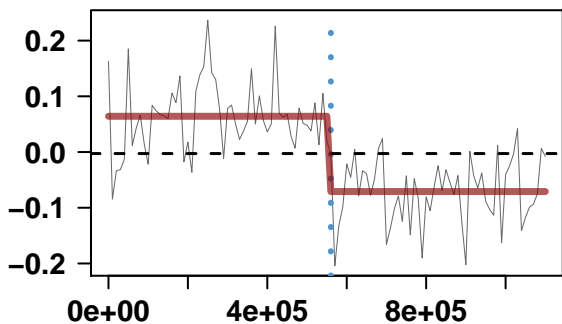
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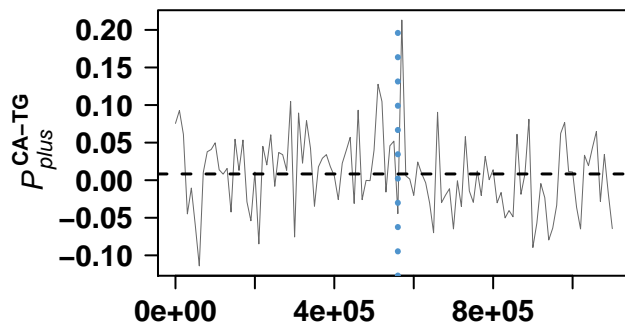
genome coordinates



genome coordinates

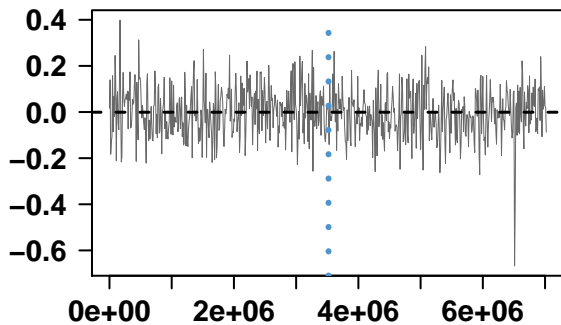


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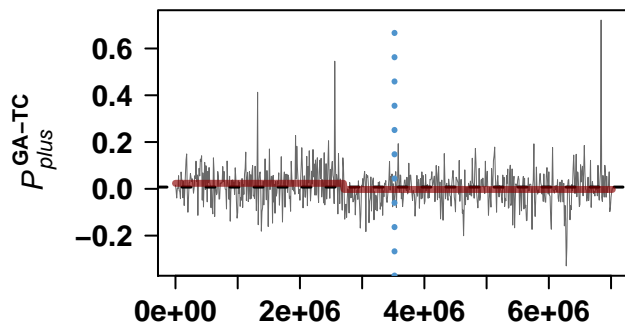


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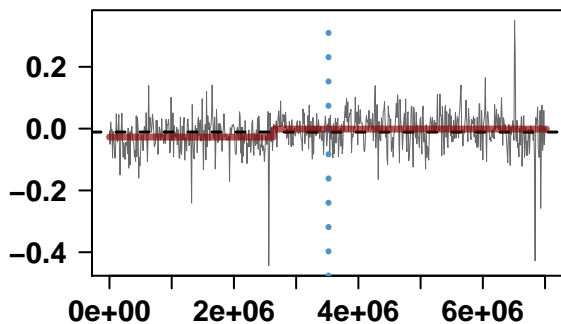
Mesorhizobium loti MAFF303099



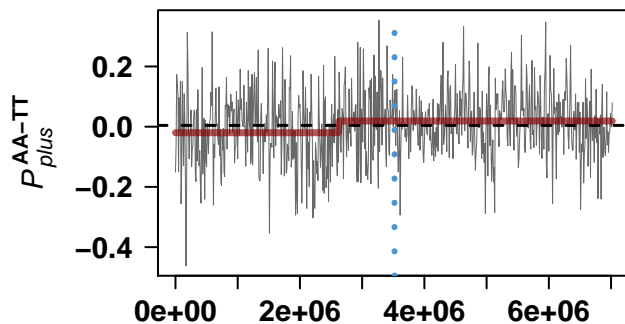
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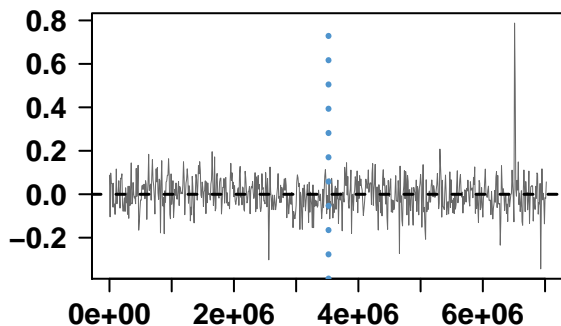
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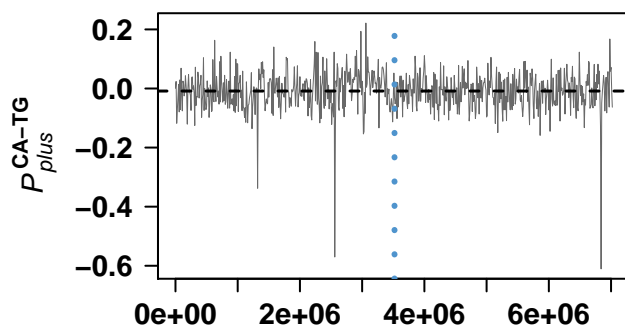
genome coordinates



genome coordinates

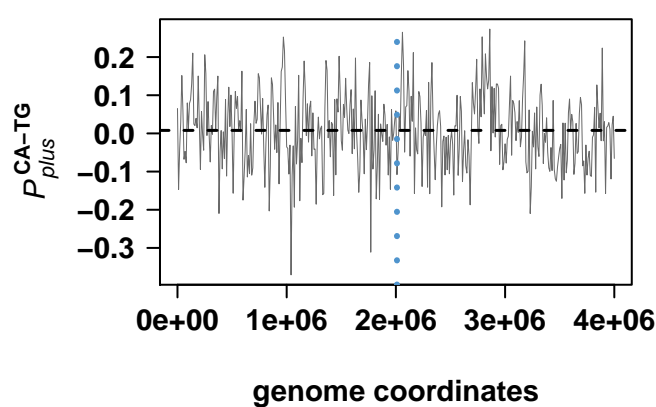
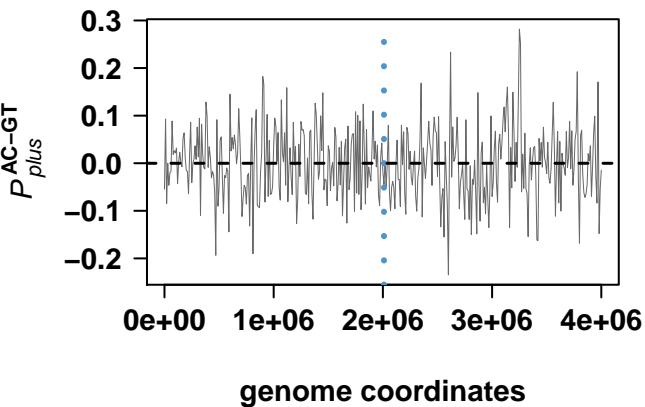
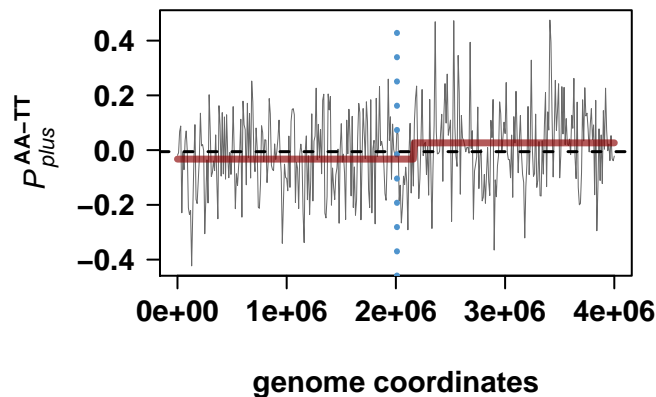
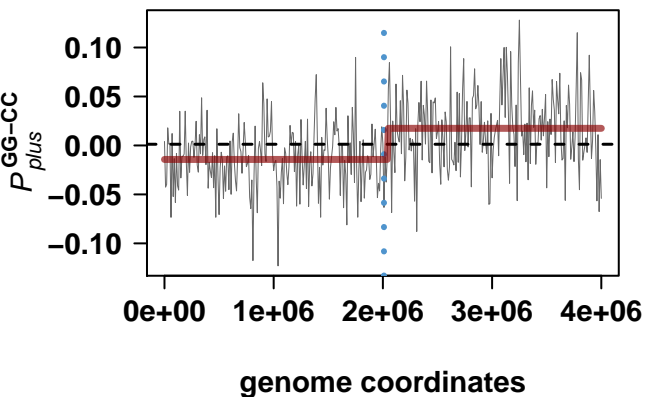
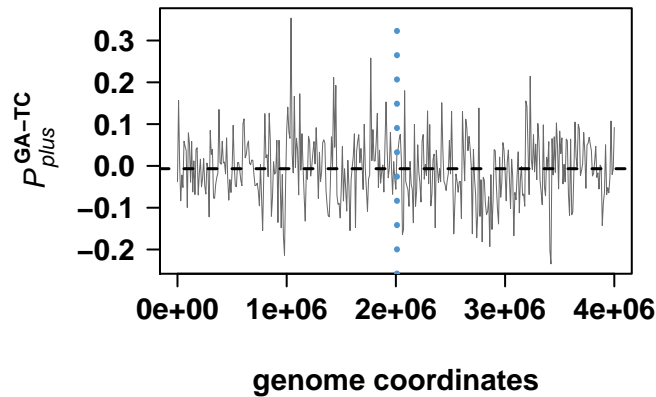
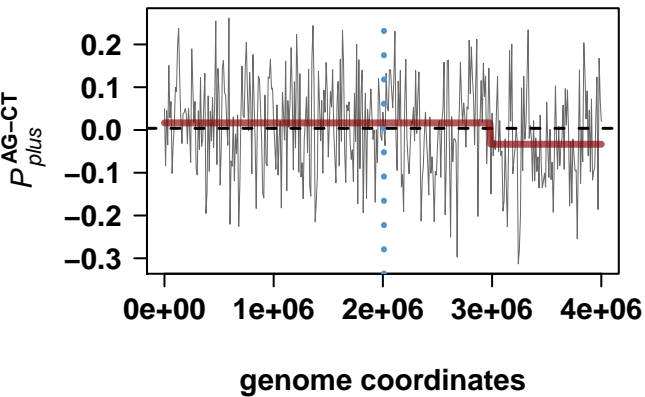


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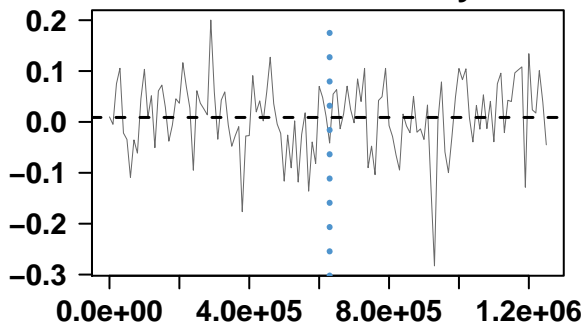


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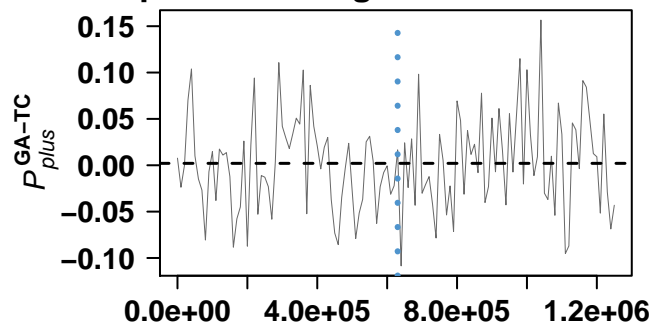
Caulobacter crescentus CB15



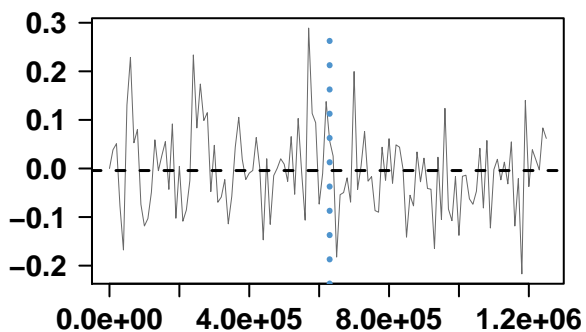
Wolbachia endosymbiont of *Drosophila melanogaster*



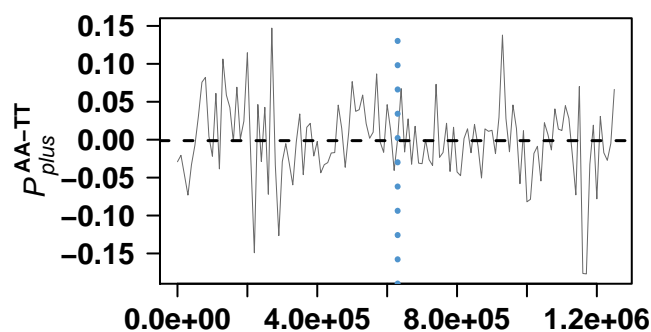
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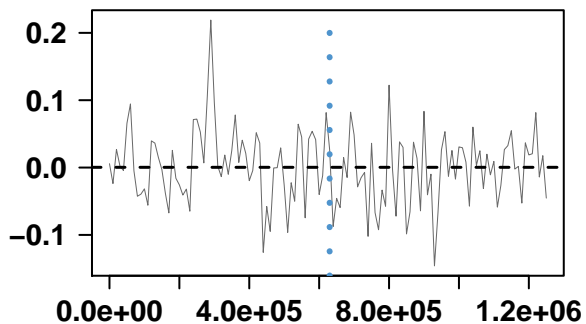
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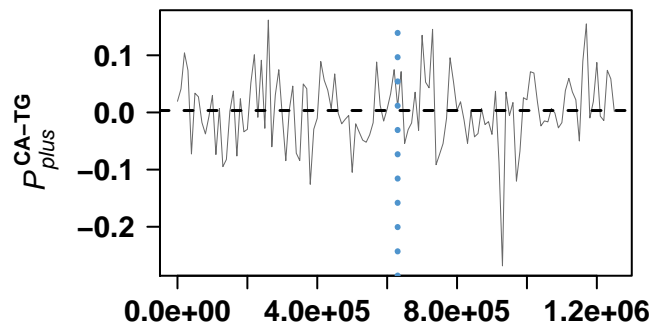
genome coordinates



genome coordinates

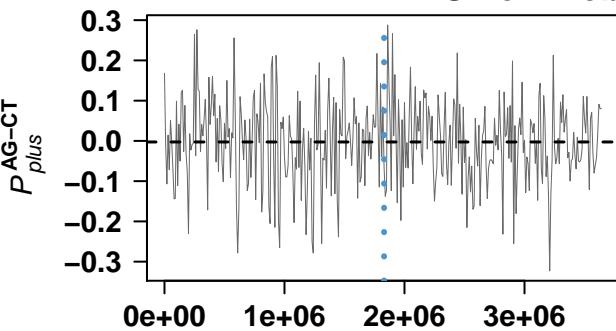


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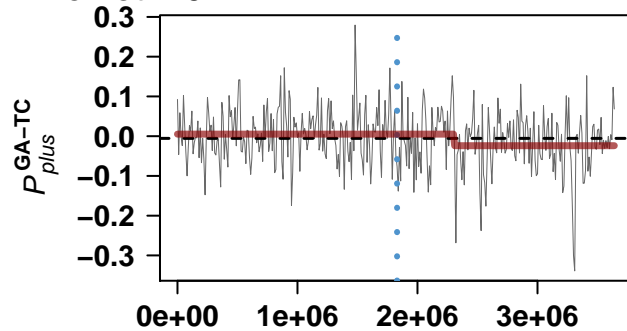


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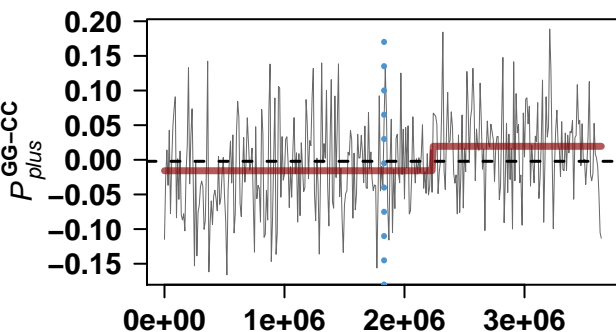
Sinorhizobium meliloti 1021



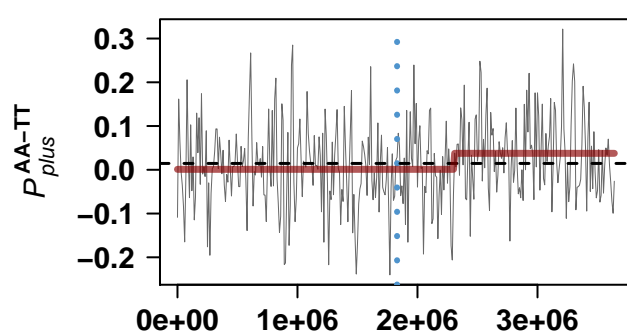
genome coordinates



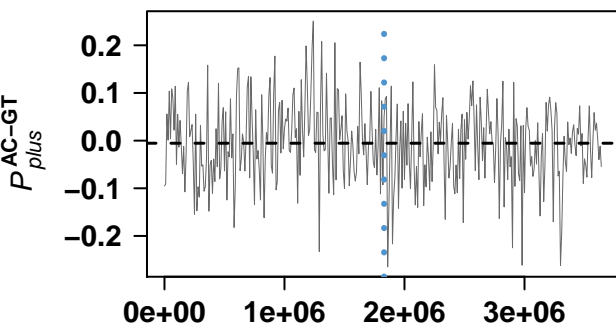
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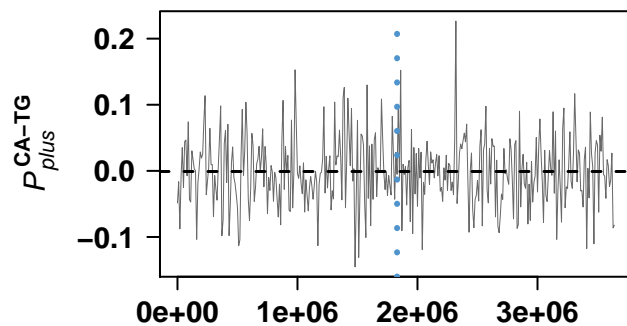
genome coordinates



genome coordinates

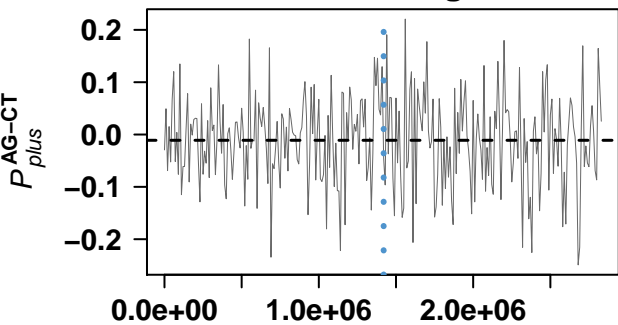


genome coordinates

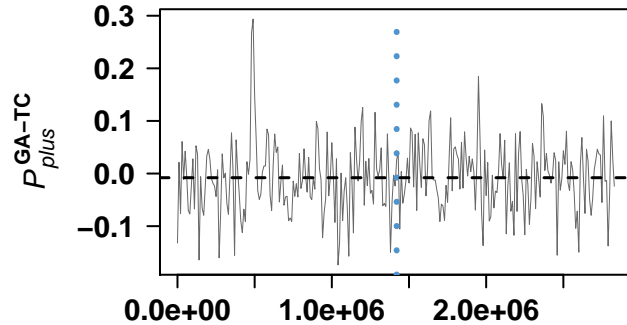


genome coordinates

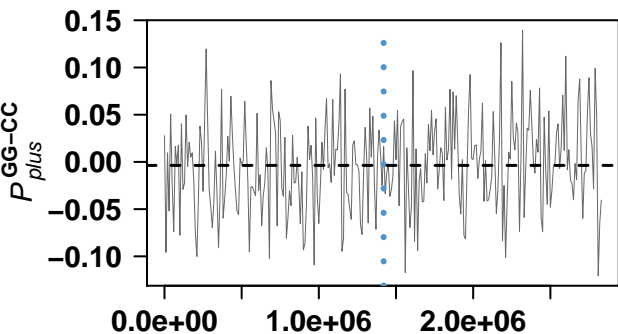
Agrobacterium fabrum str. C58



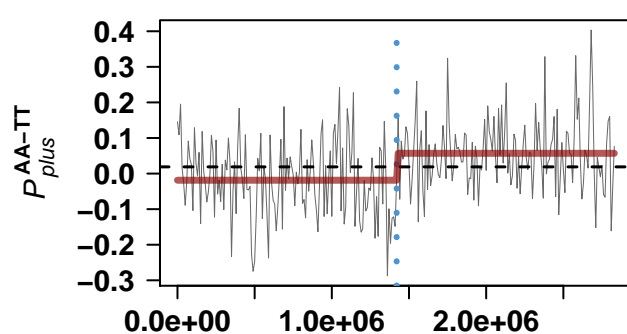
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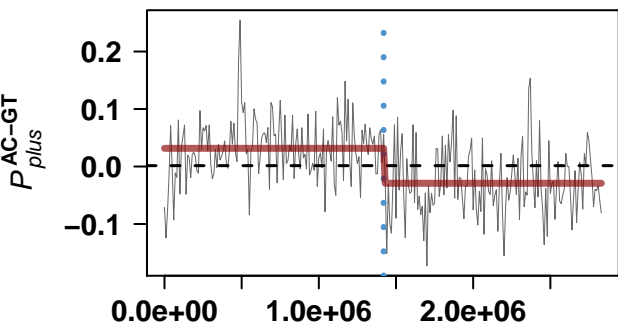
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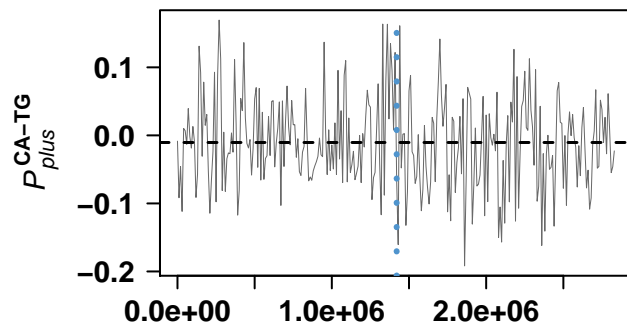
genome coordinates



genome coordinates

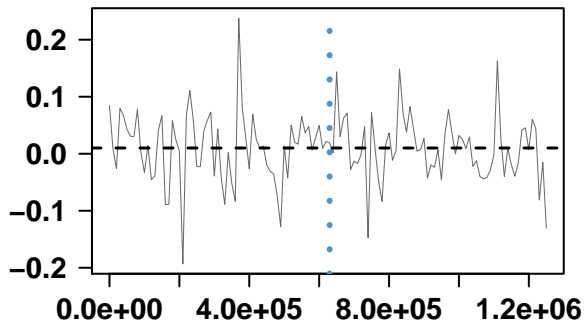


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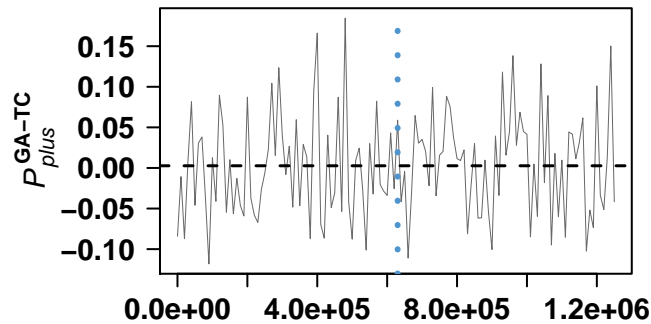


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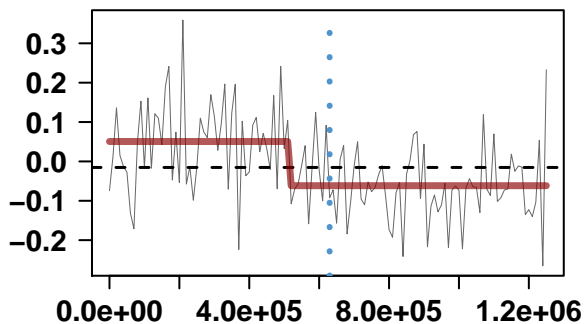
Rickettsia conorii str. Malish 7



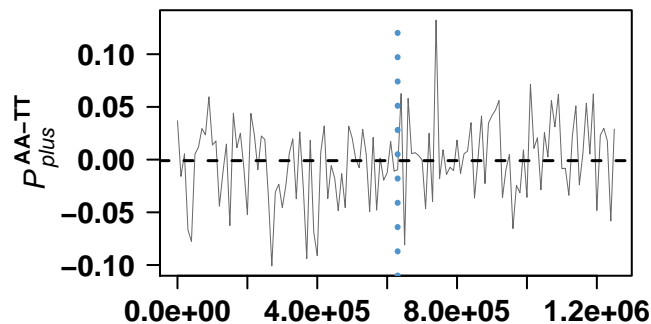
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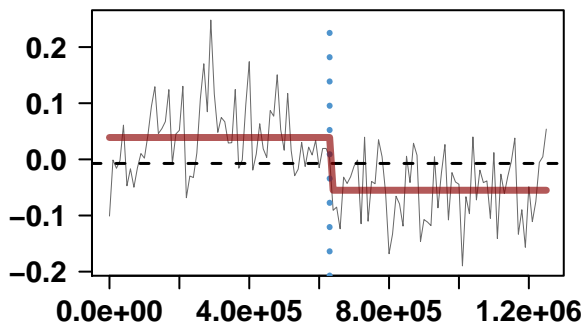
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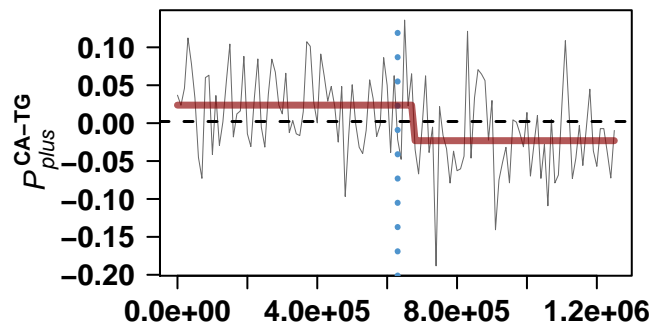
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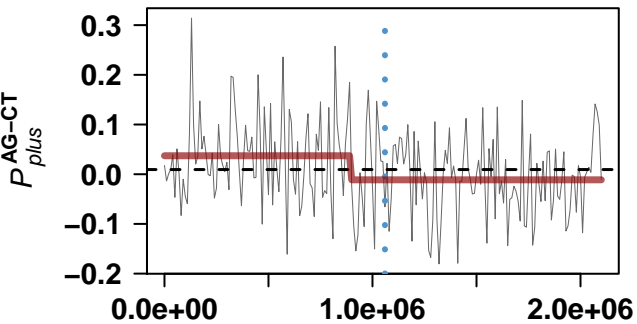


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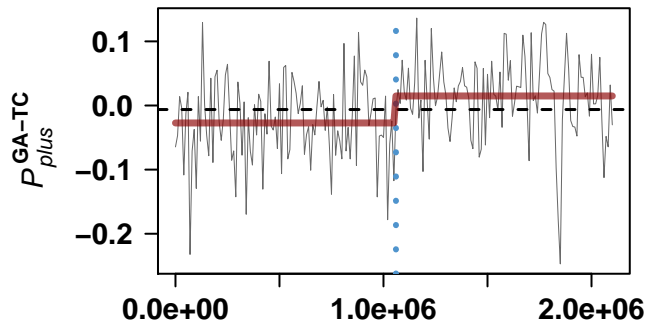


genome coordinates

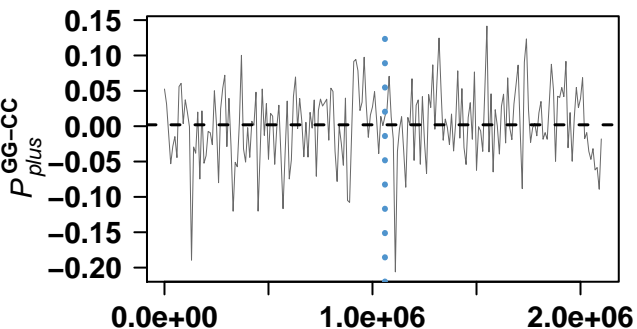
Brucella melitensis bv. 1 str. 16M



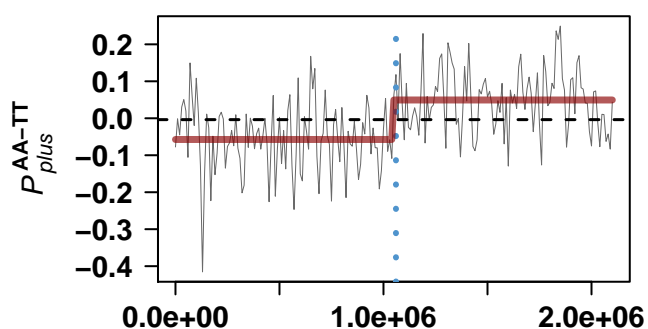
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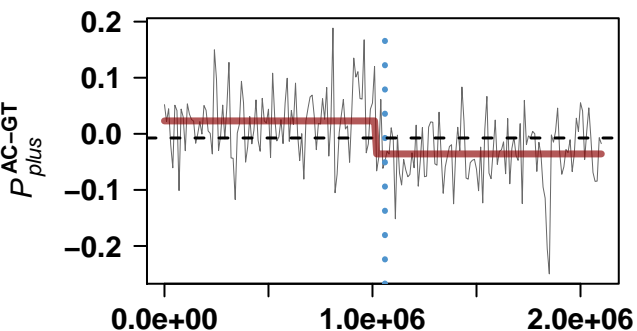
genome coordinates



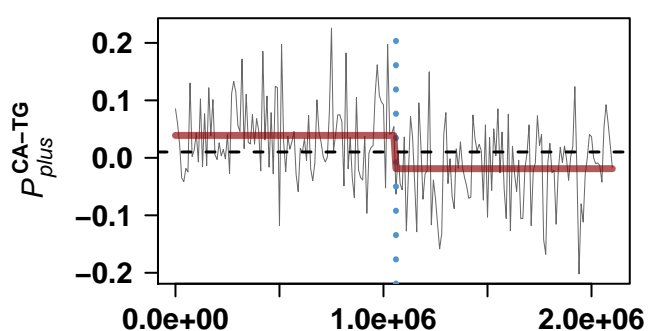
genome coordinates



genome coordinates

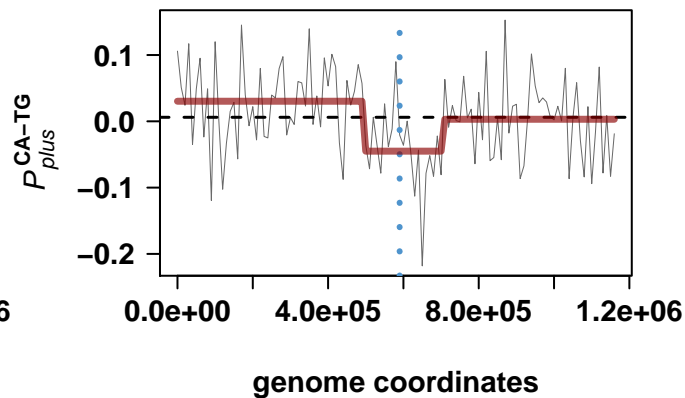
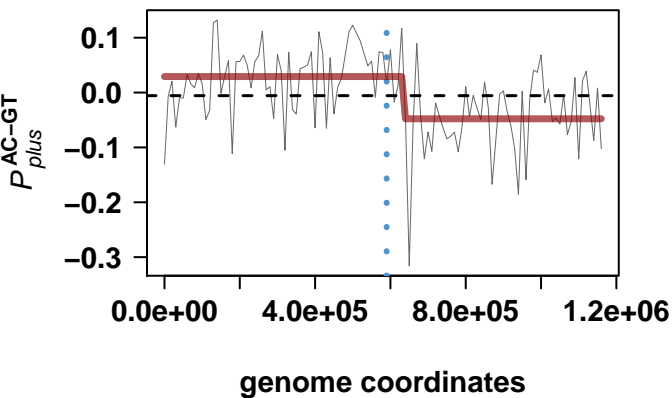
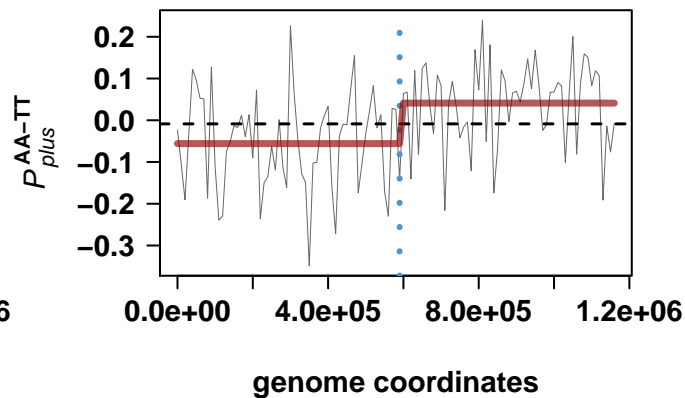
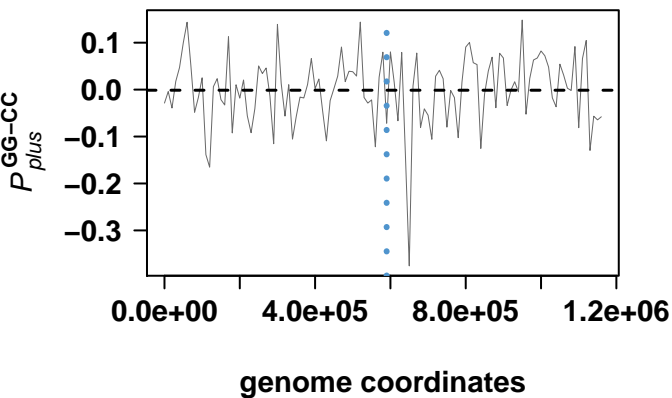
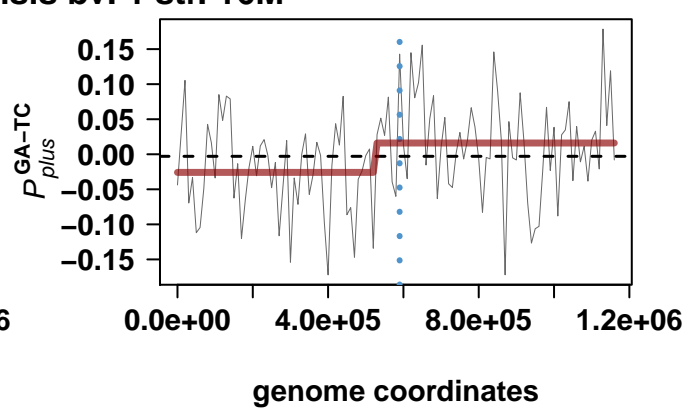
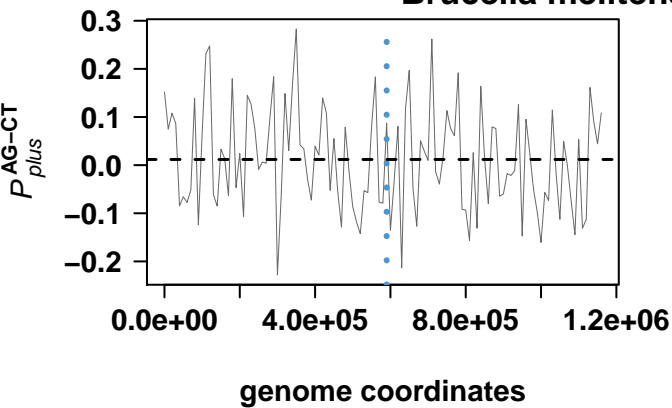


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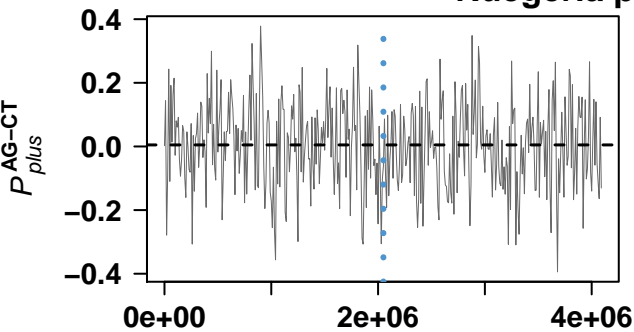


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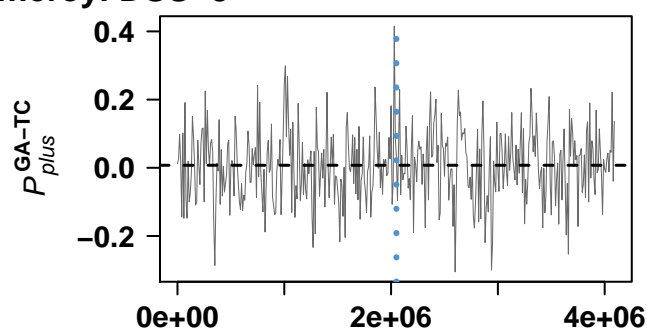
Brucella melitensis bv. 1 str. 16M



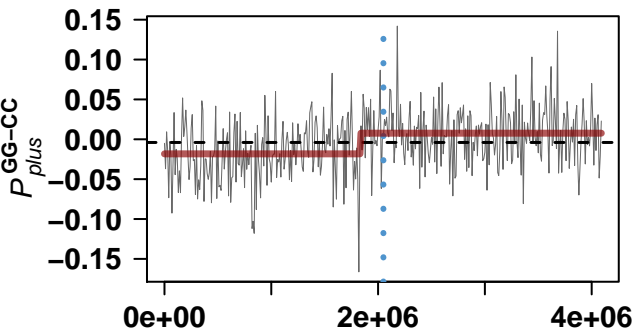
Ruegeria pomeroyi DSS-3



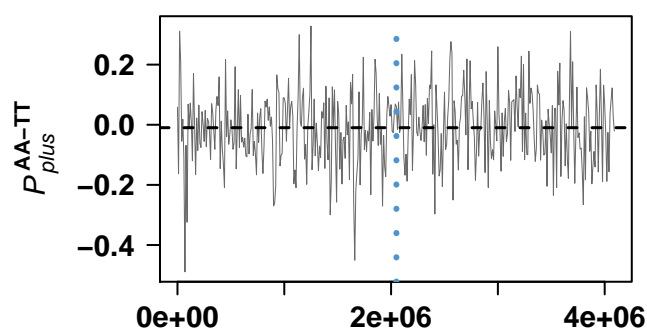
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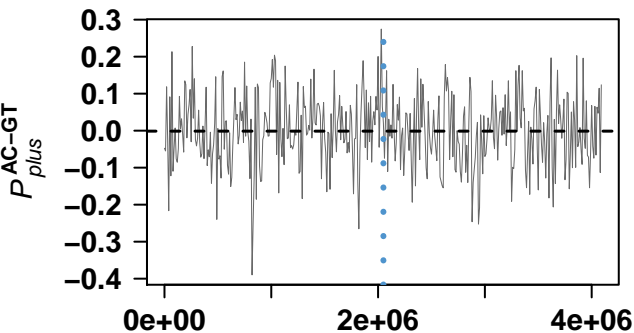
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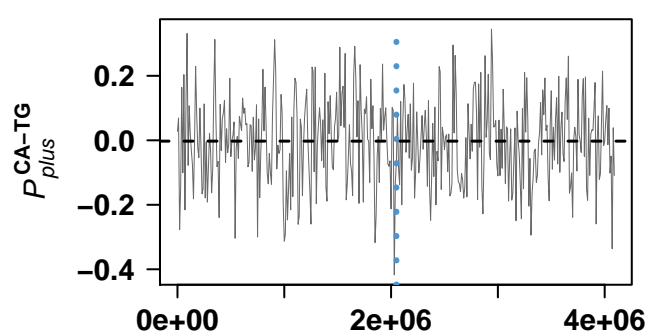
genome coordinates



genome coordinates

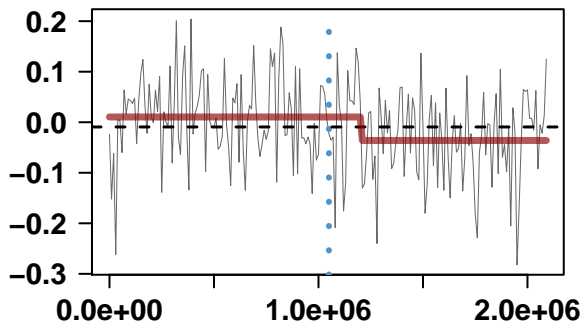


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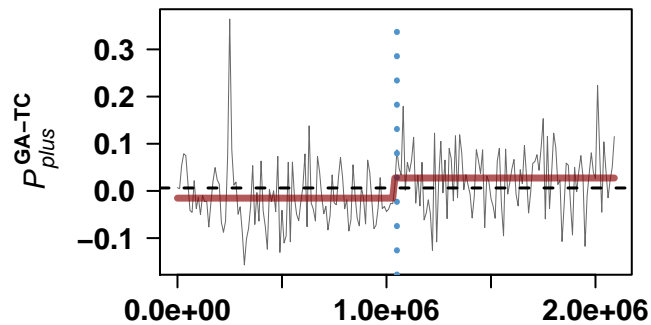


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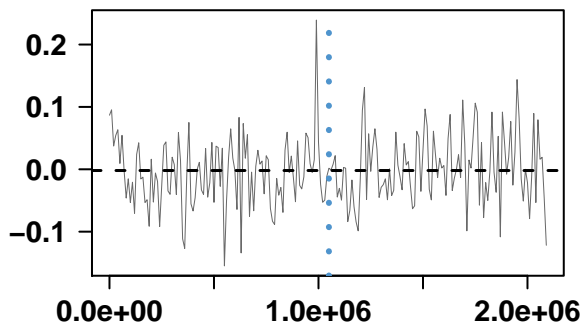
Brucella suis 1330



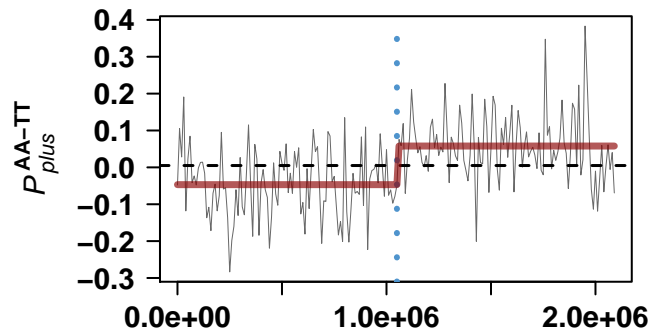
genome coordinates



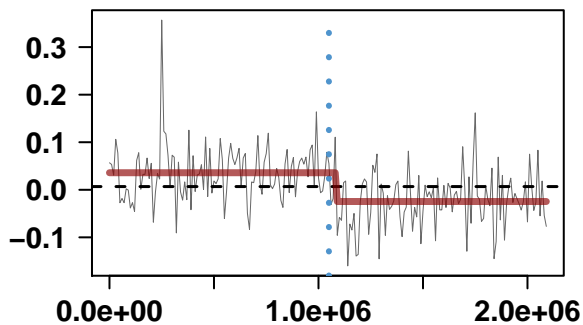
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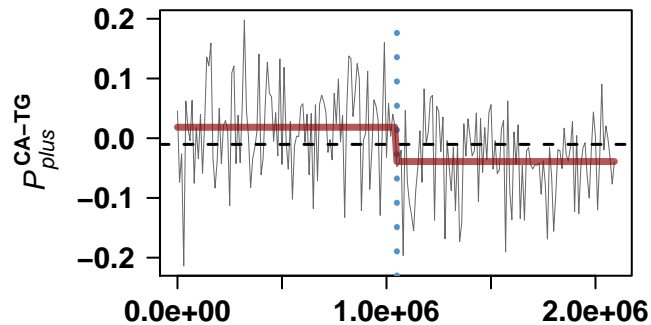
genome coordinates



genome coordinates

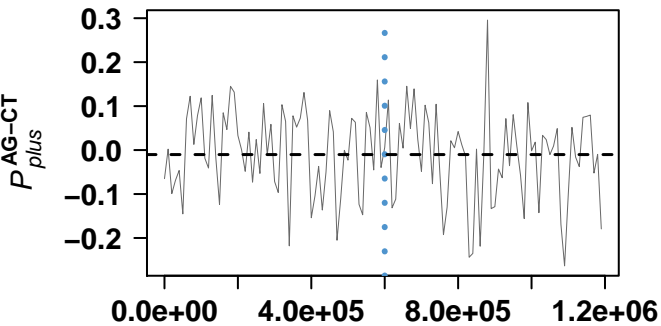


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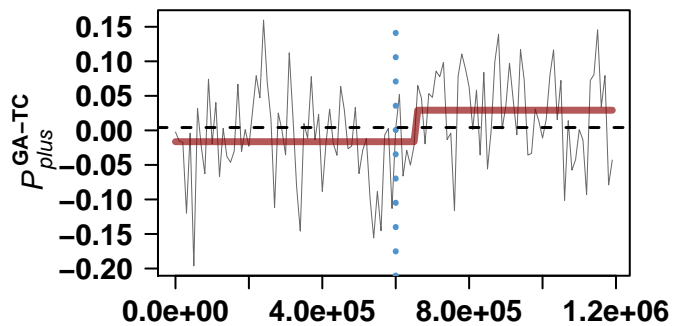


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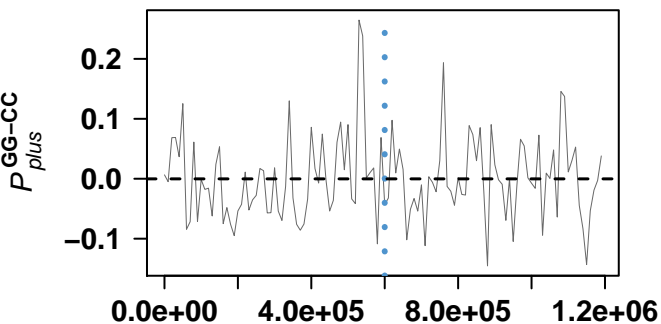
Brucella suis 1330



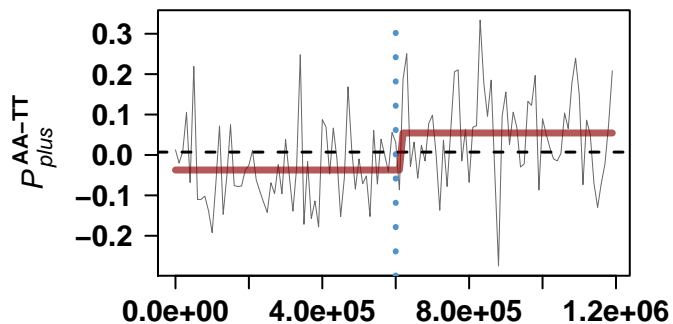
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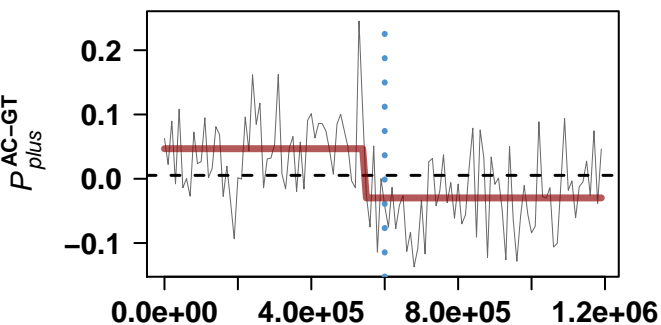
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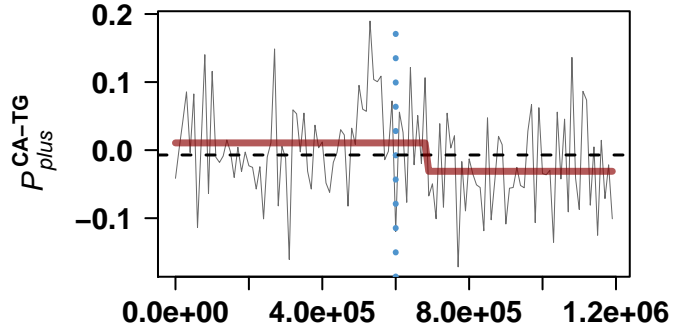
genome coordinates



genome coordinates

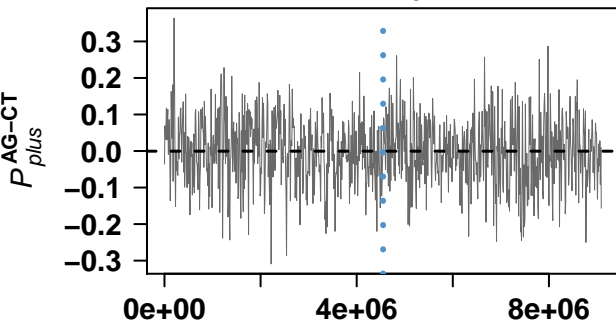


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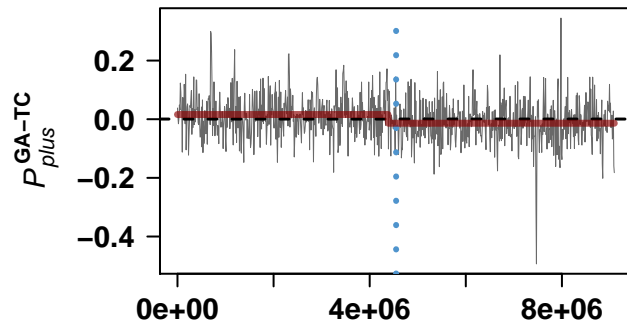


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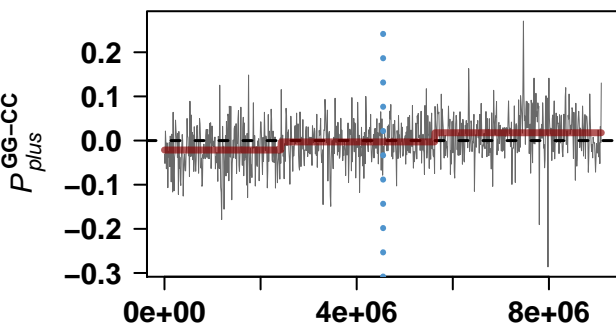
Bradyrhizobium diazoefficiens USDA 110



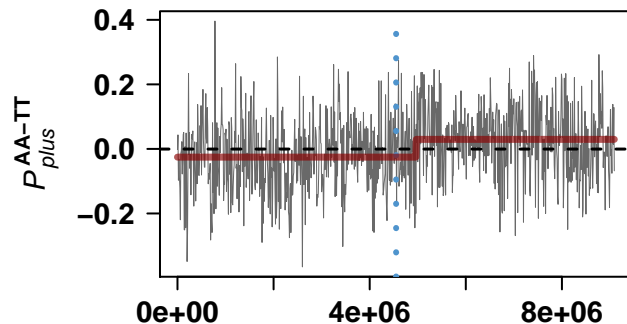
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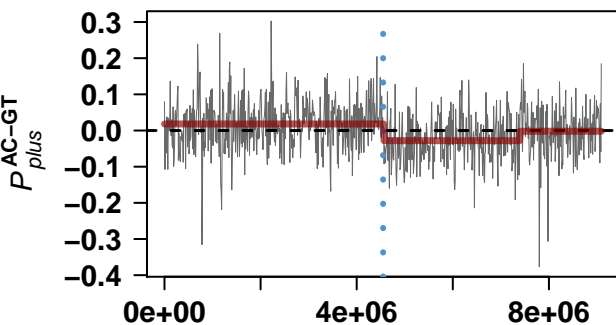
genome coordinates



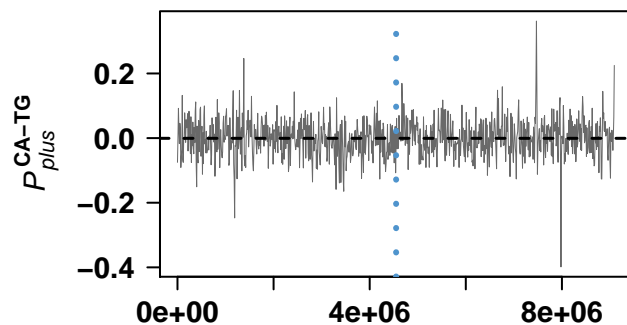
genome coordinates



genome coordinates

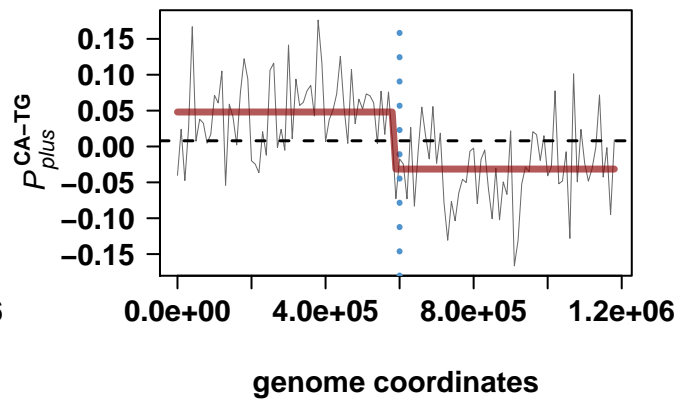
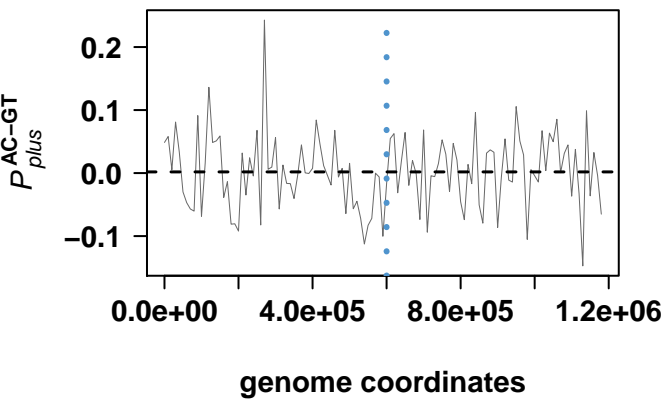
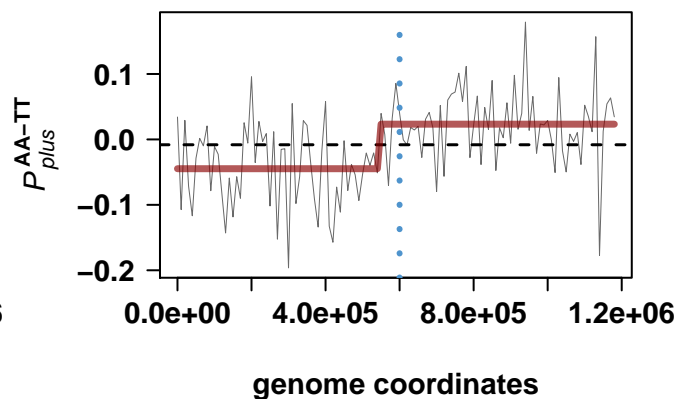
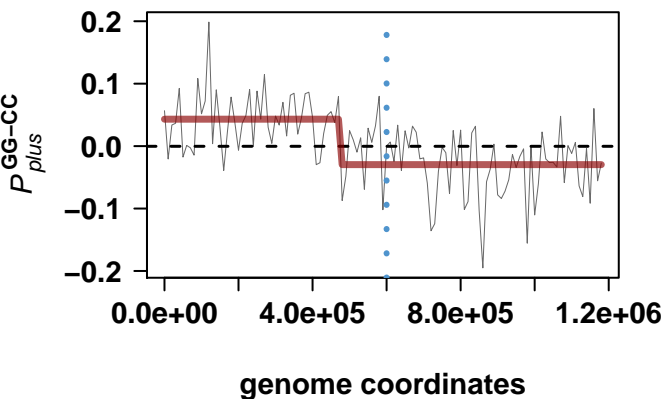
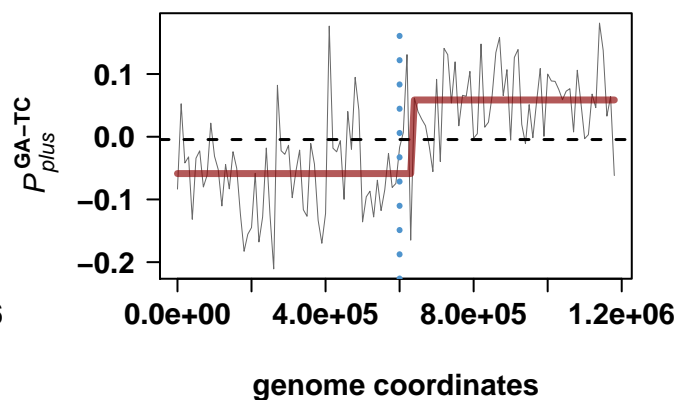
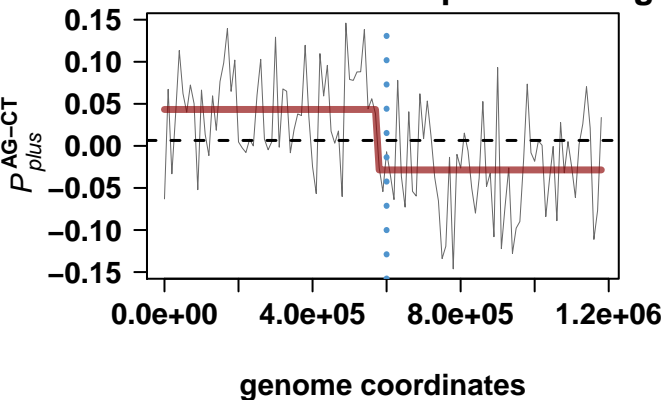


genome coordinates

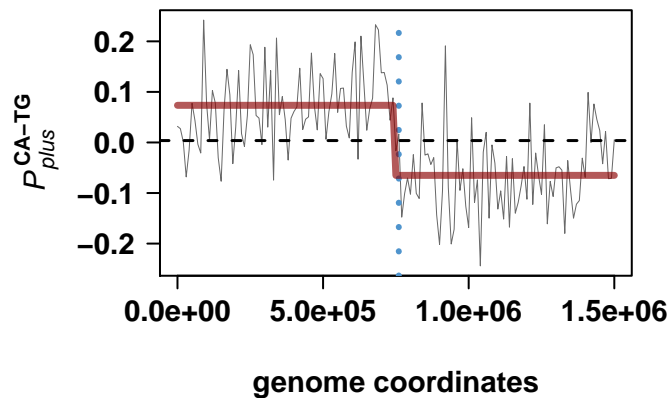
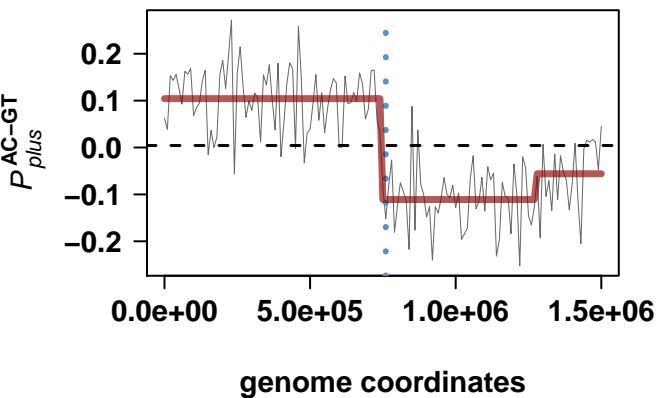
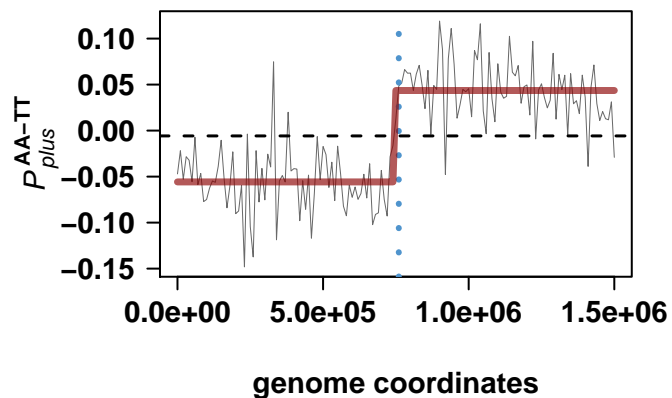
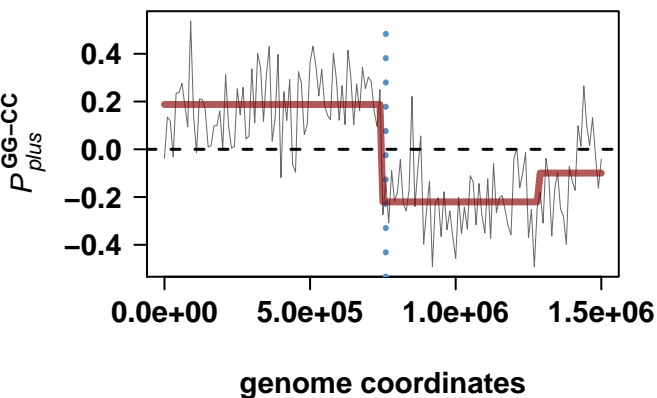
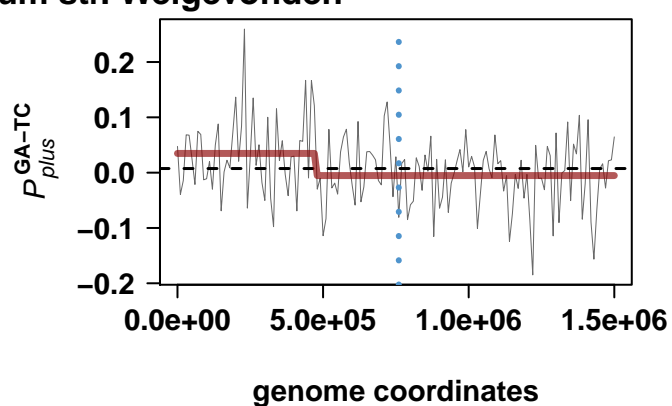
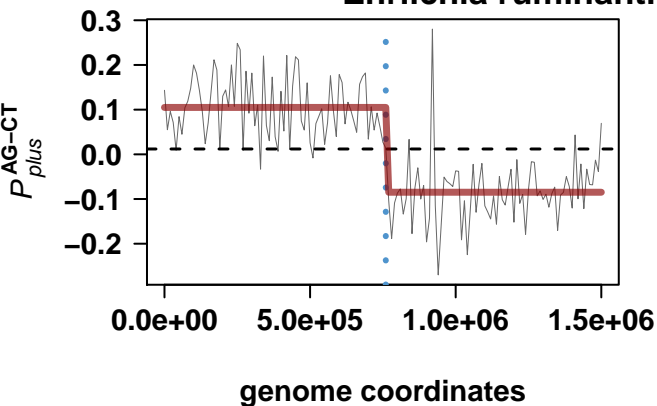


genome coordinates

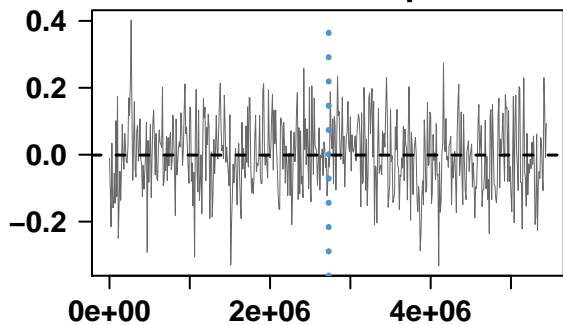
Anaplasma marginale str. St. Maries



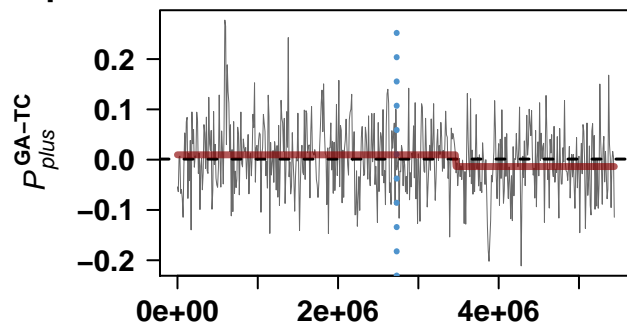
Ehrlichia ruminantium str. Welgevonden



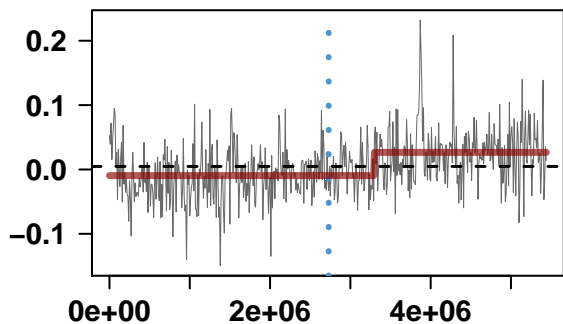
Rhodopseudomonas palustris CGA009



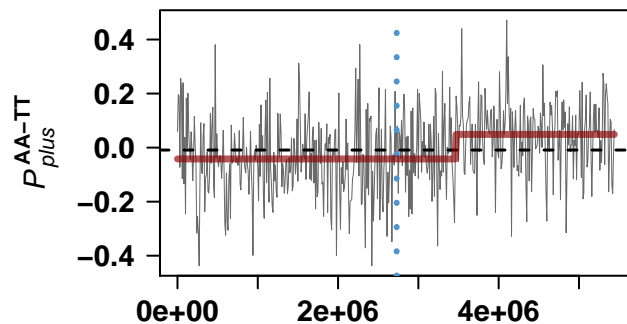
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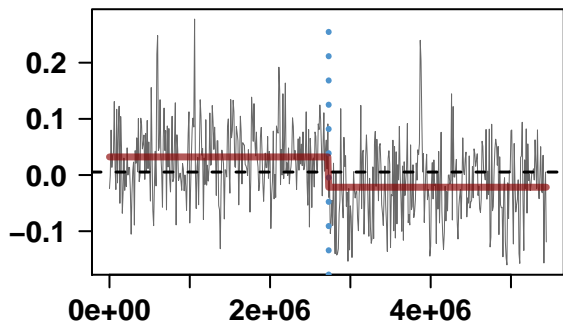
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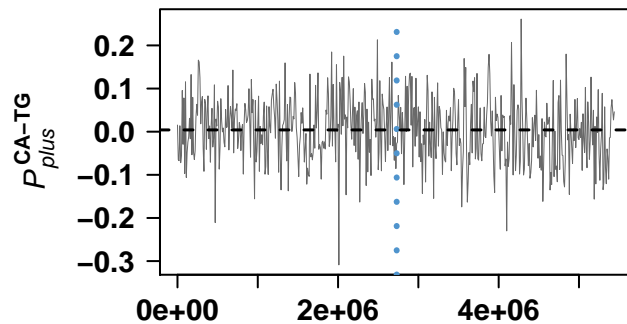
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genome coordinates

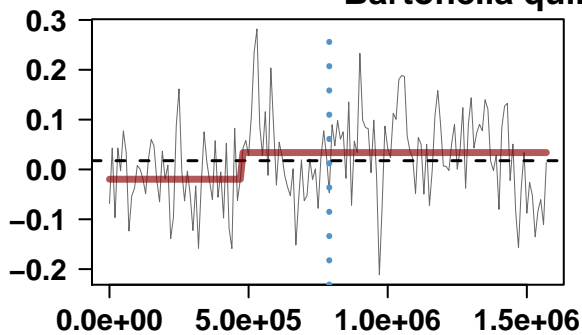


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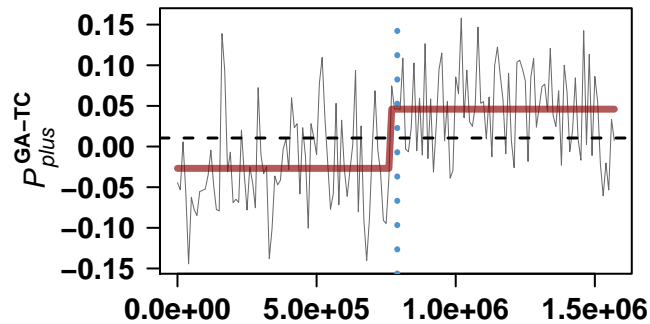


genome coordinates

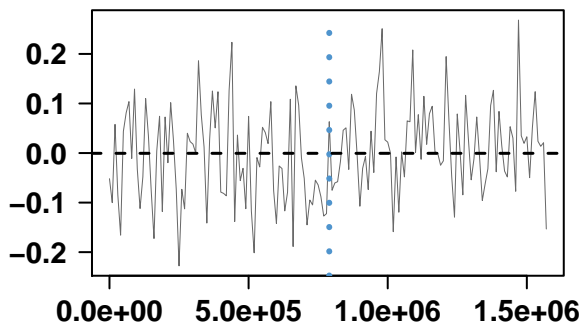
Bartonella quintana str. Toulouse



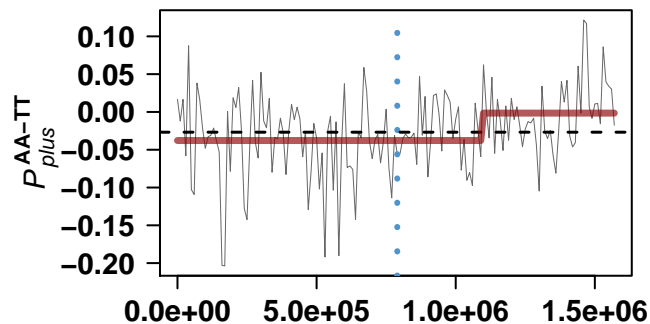
genome coordinates



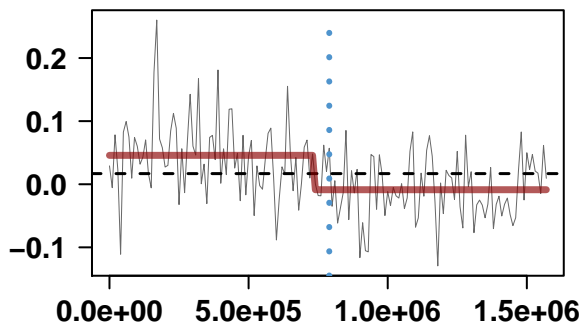
genome coordinates



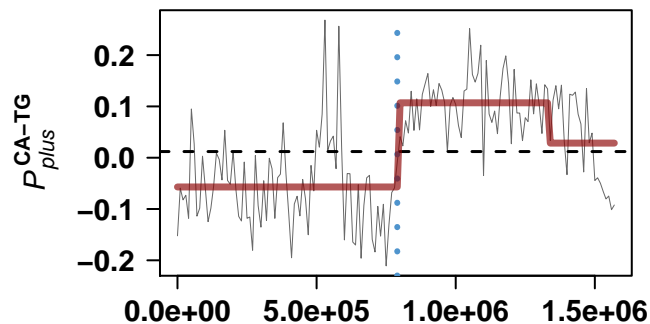
genome coordinates



genome coordinates

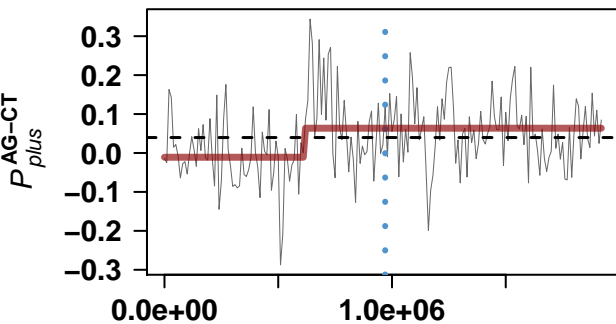


genome coordinates

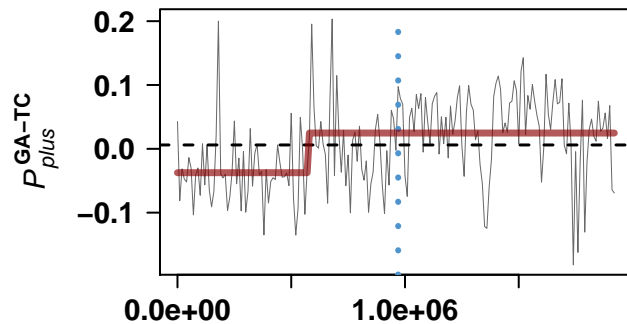


genome coordinates

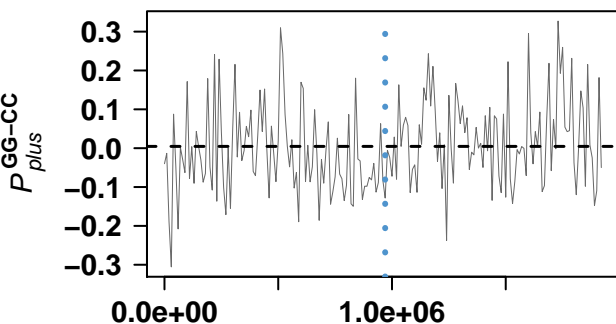
Bartonella henselae str. Houston-1



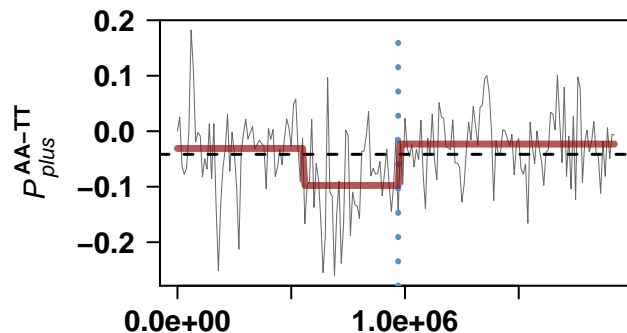
genome coordinates



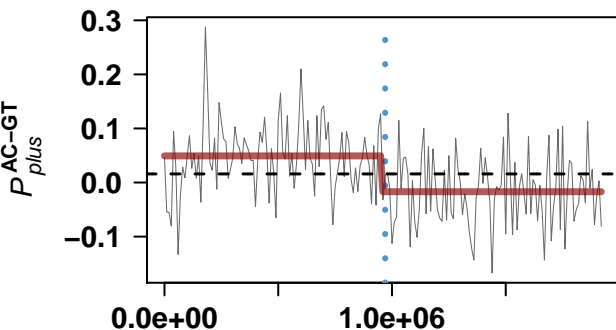
genome coordinates



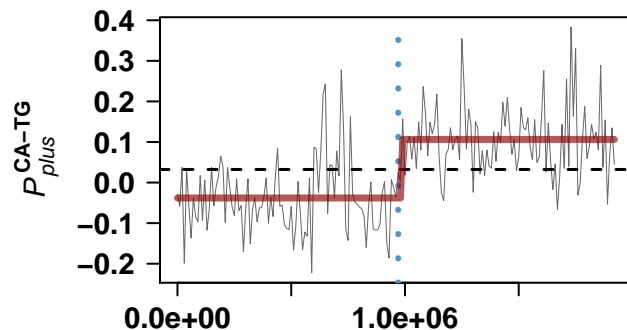
genome coordinates



genome coordinates

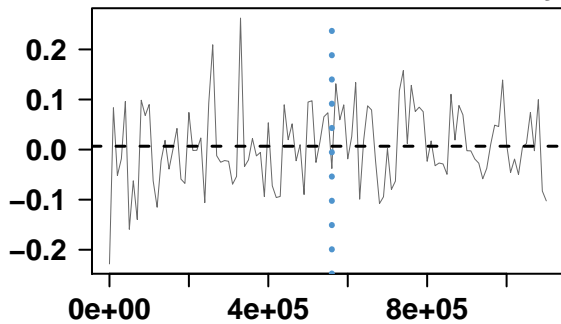


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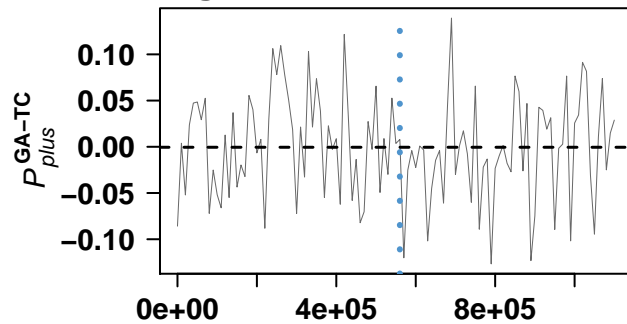


genome coordinates

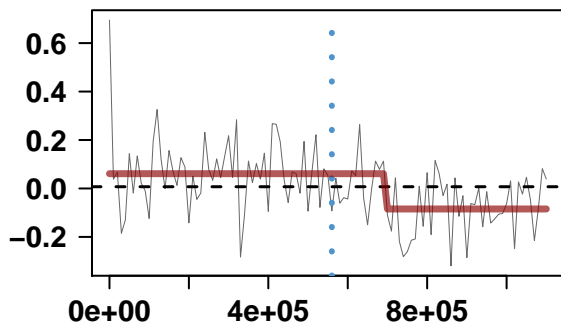
Rickettsia typhi str. Wilmington



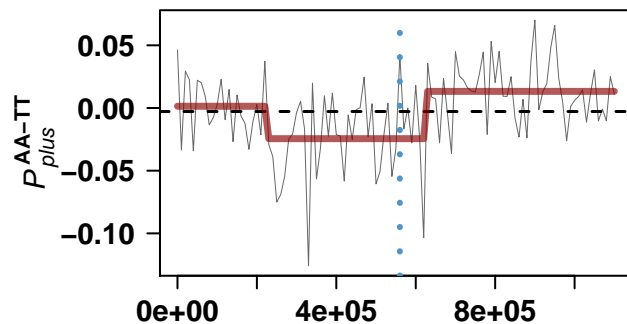
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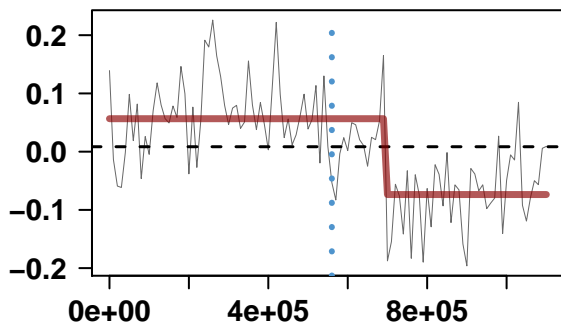
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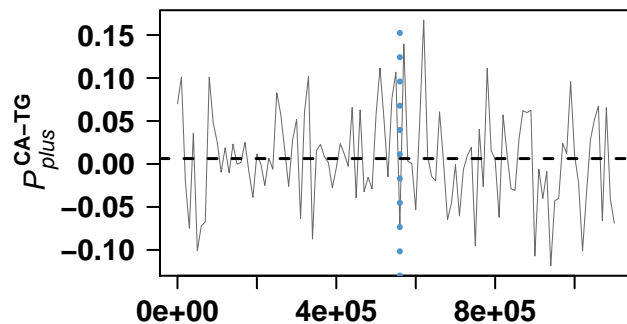
genome coordinates



genome coordinates

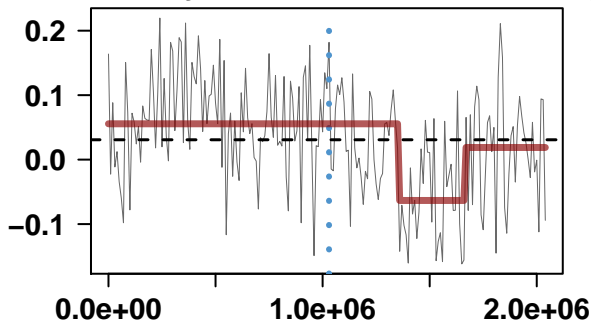


genome coordinates

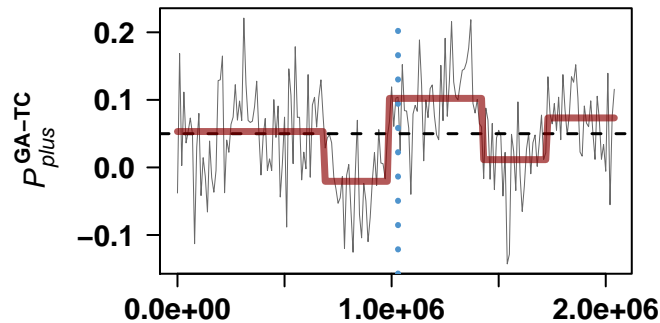


genome coordinates

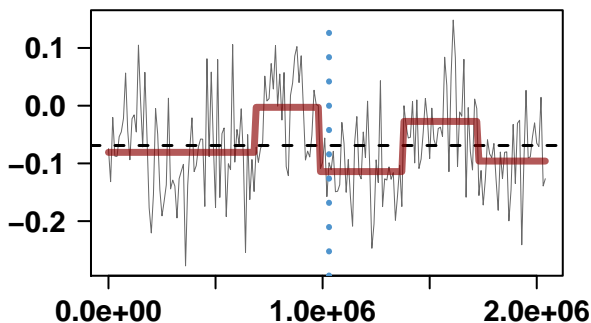
Zymomonas mobilis subsp. mobilis ZM4 = ATCC 31821



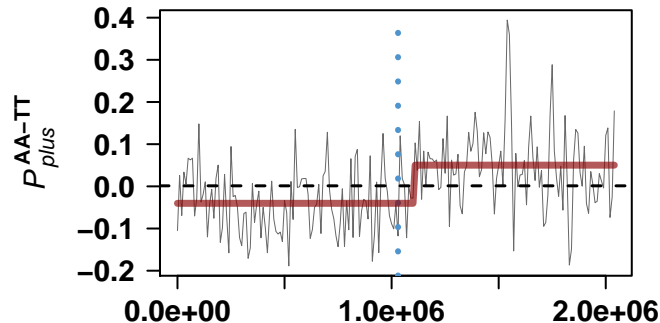
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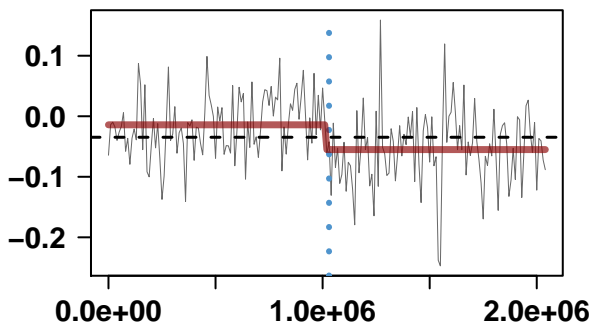
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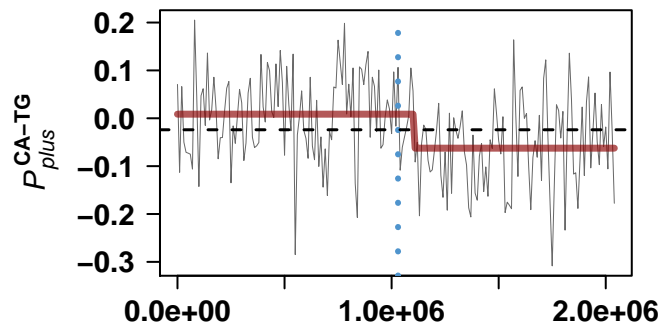
genome coordinates



genome coordinates

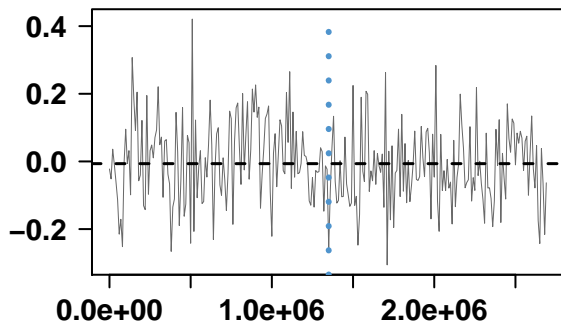


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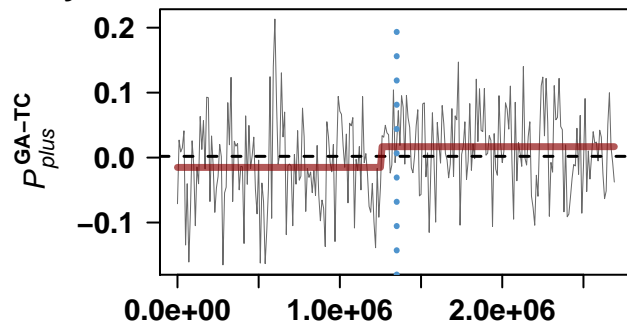


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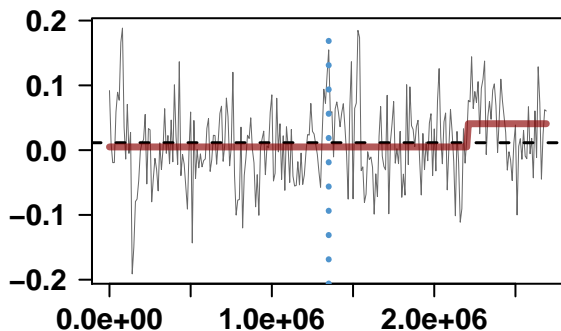
Gluconobacter oxydans 621H



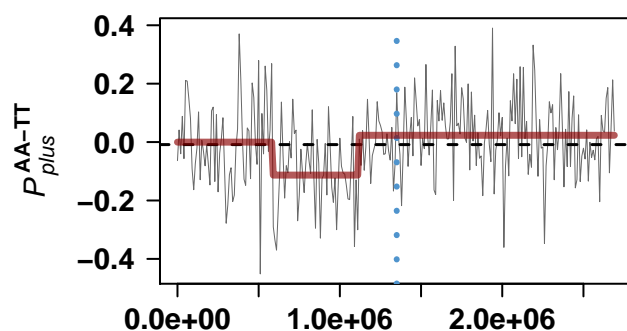
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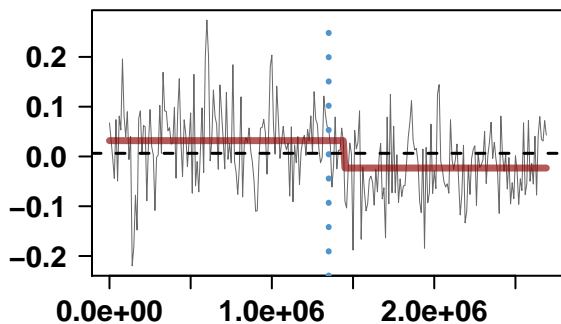
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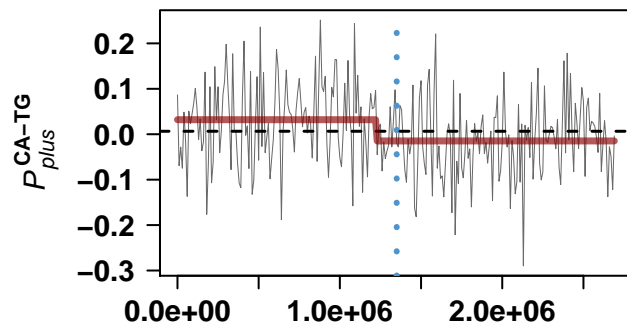
genome coordinates



genome coordinates

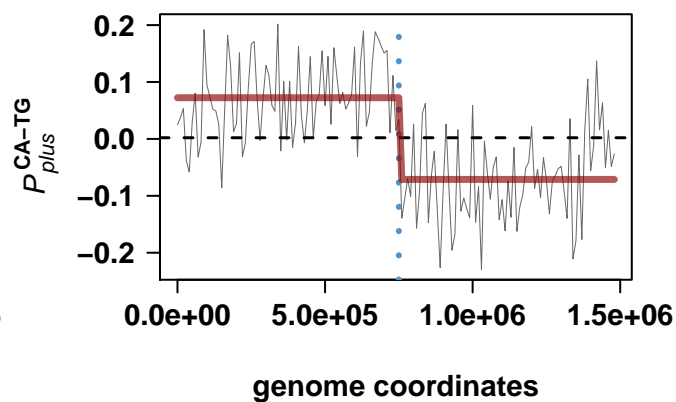
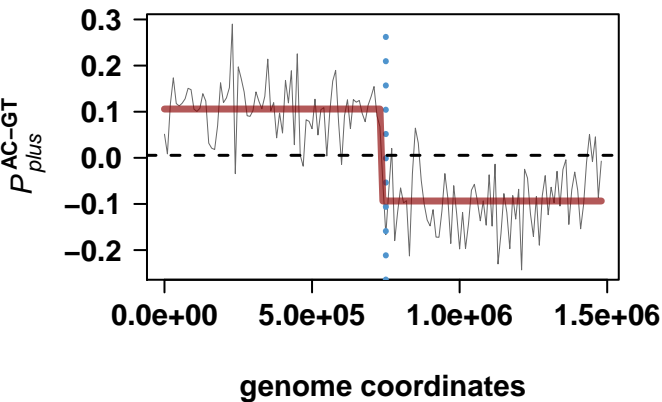
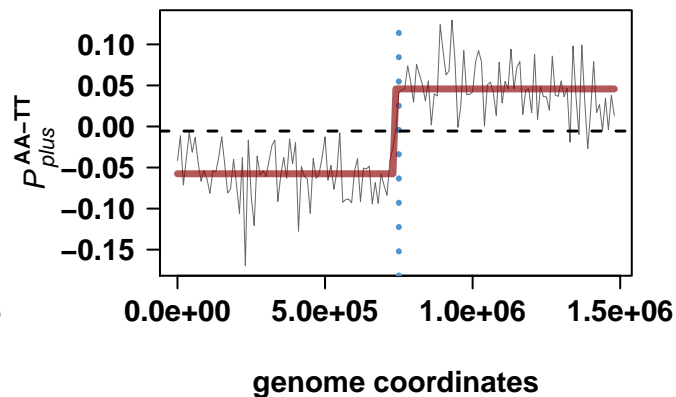
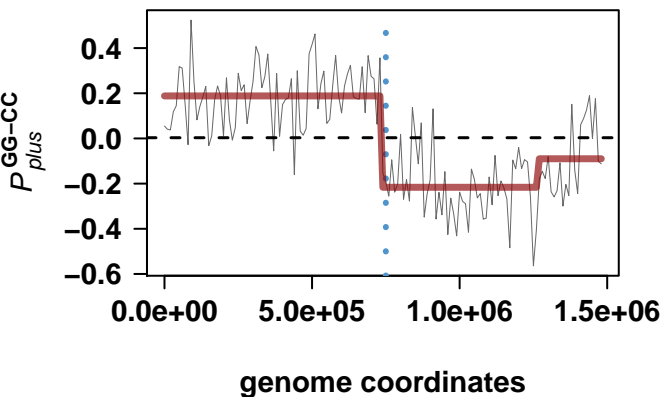
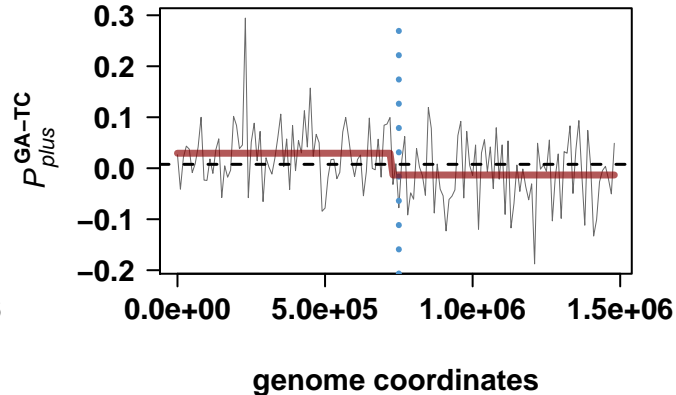
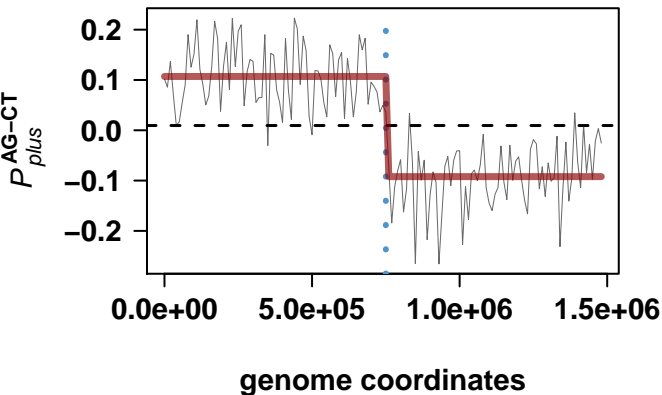


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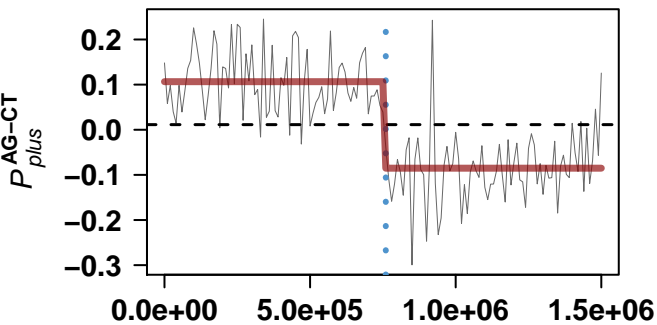


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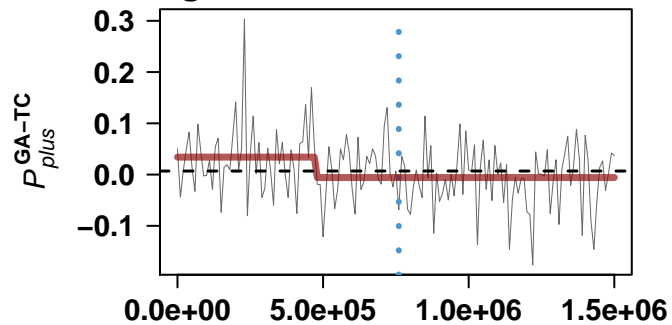
Ehrlichia ruminantium str. Gardel



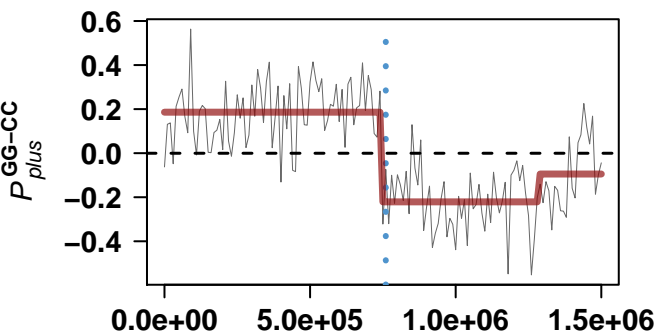
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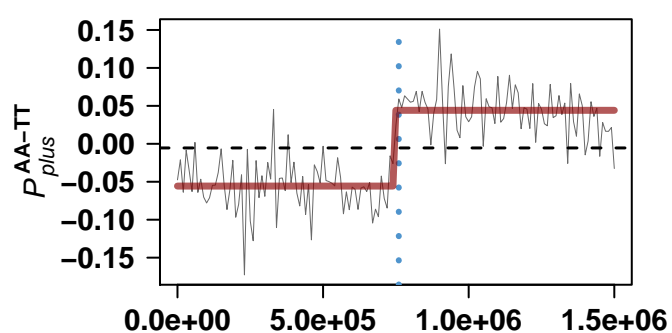
genome coordinates



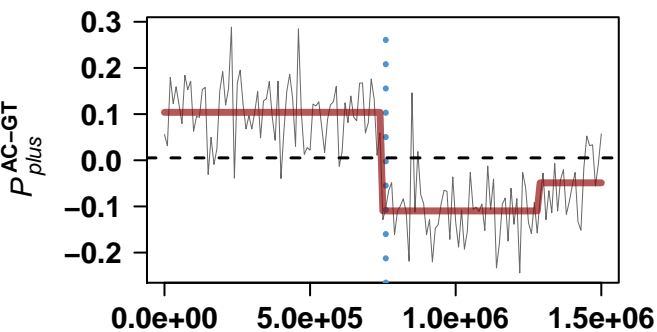
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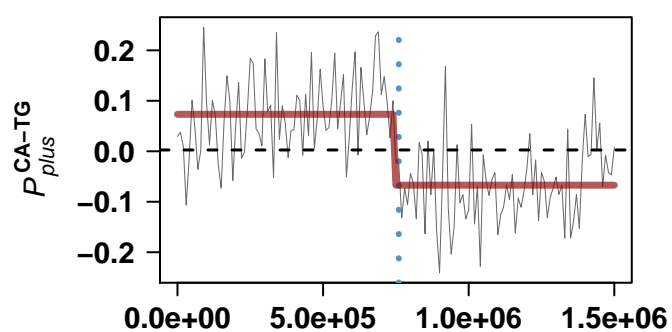
genome coordinates



genome coordinates

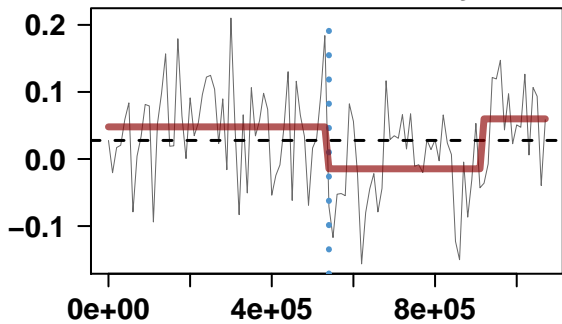


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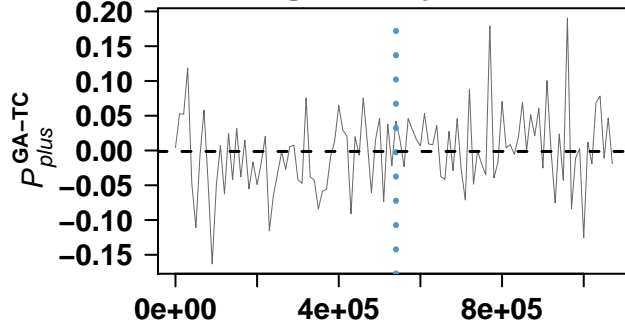


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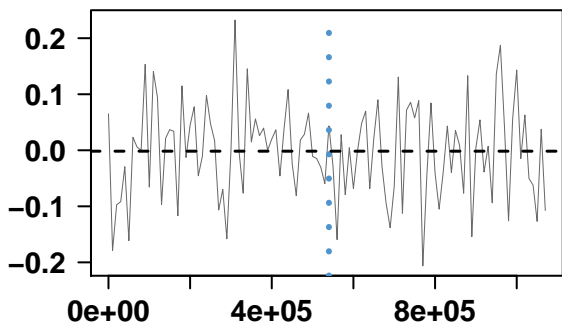
Wolbachia endosymbiont strain TRS of *Brugia malayi*



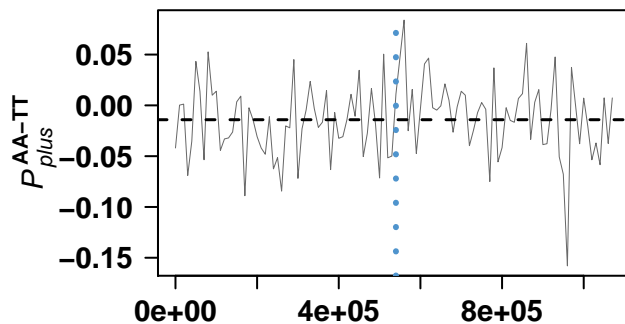
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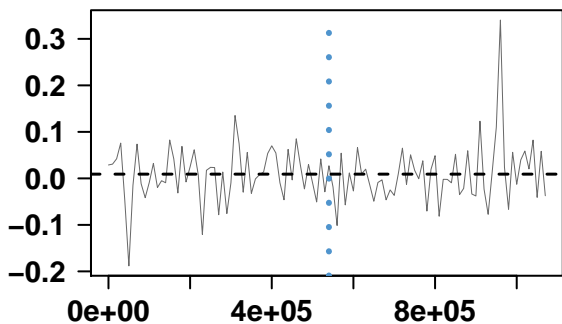
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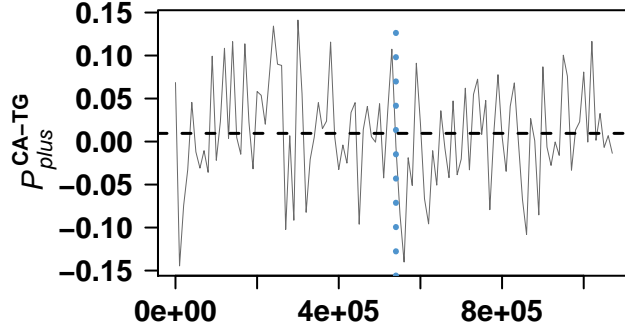
genome coordinates



genome coordinates

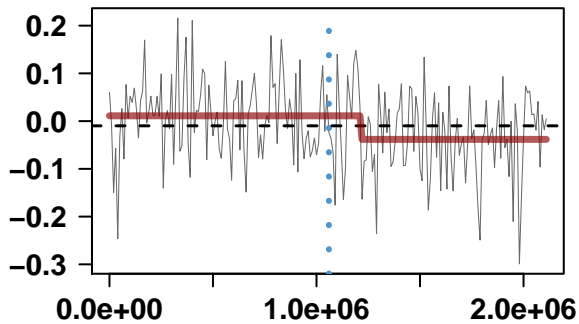


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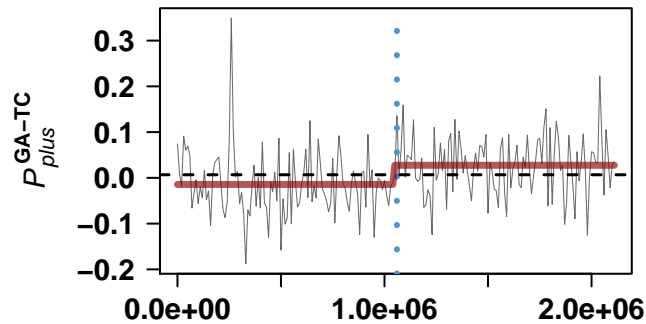


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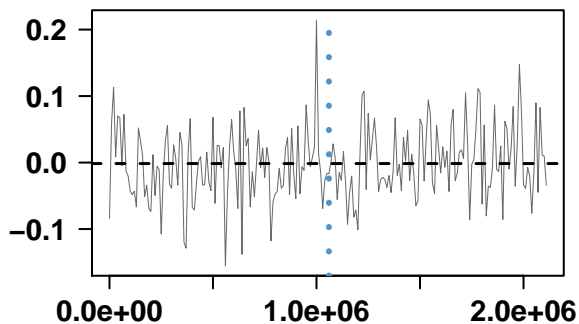
Brucella abortus bv. 1 str. 9-941



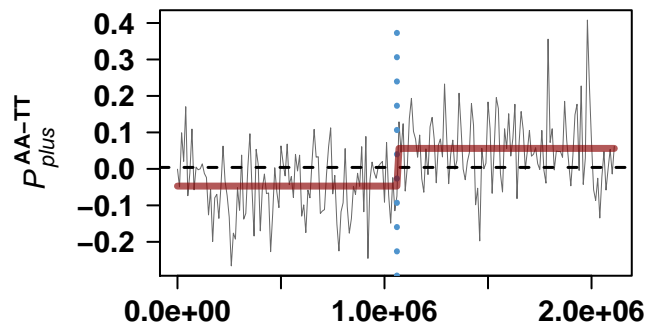
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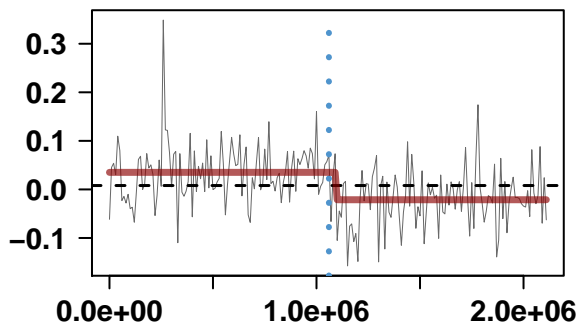
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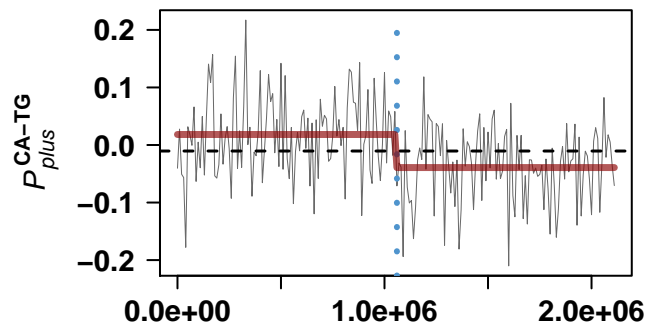
genome coordinates



genome coordinates

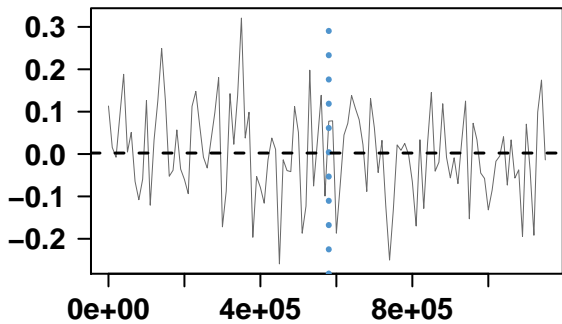


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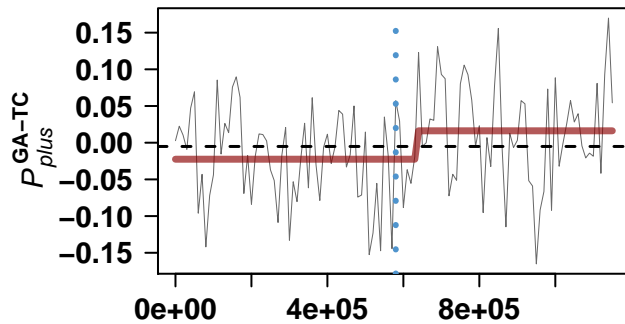


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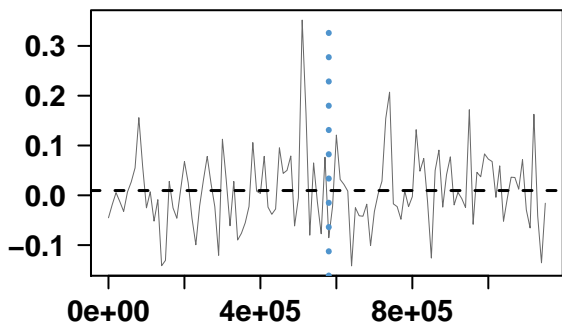
Brucella abortus bv. 1 str. 9-941



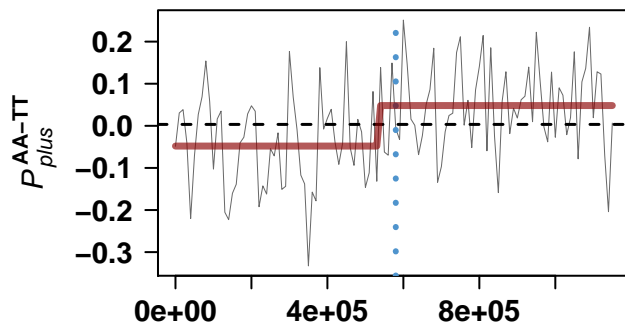
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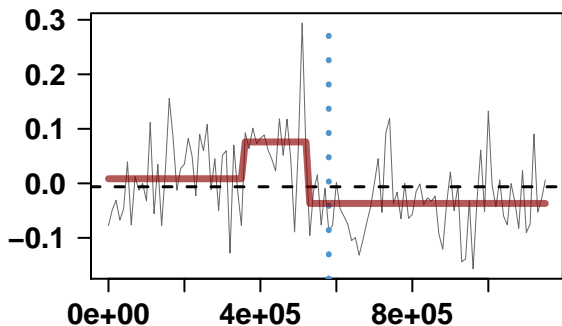
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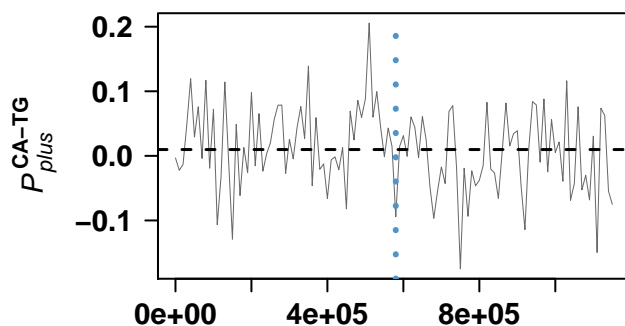
genome coordinates



genome coordinates

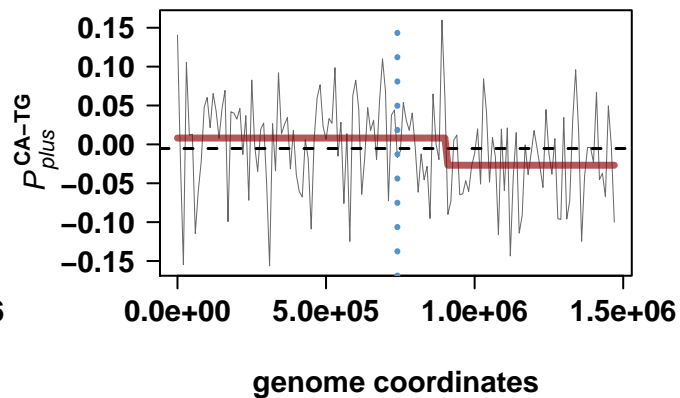
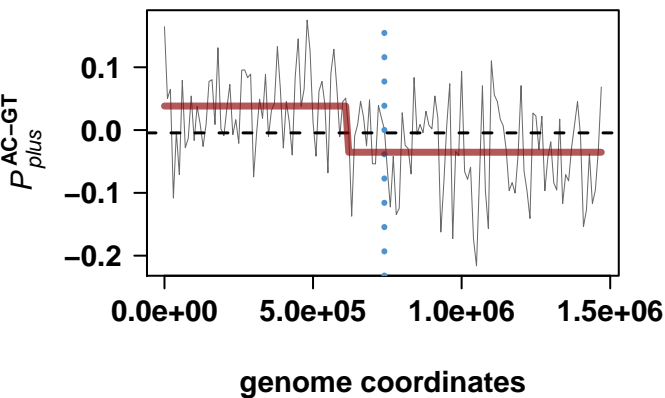
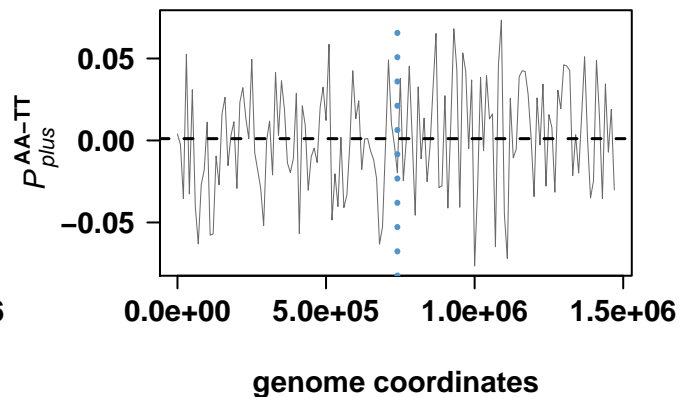
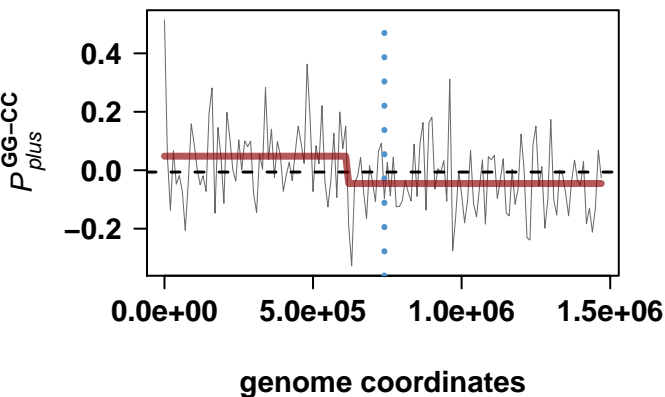
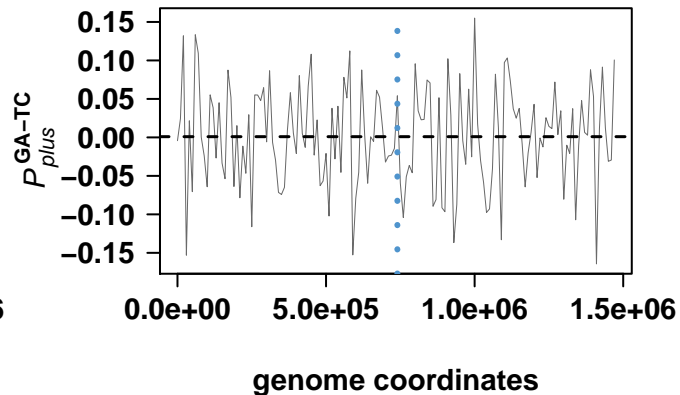
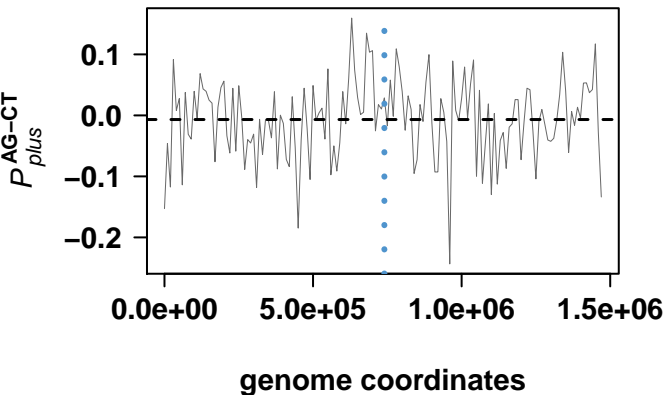


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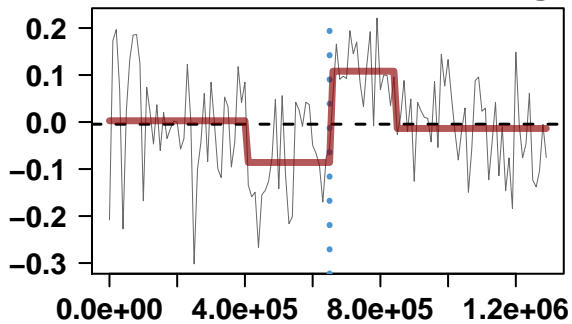


genome coordinates

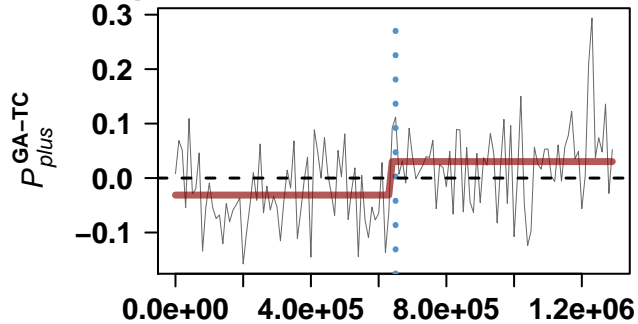
Rickettsia felis URRWXCaI2



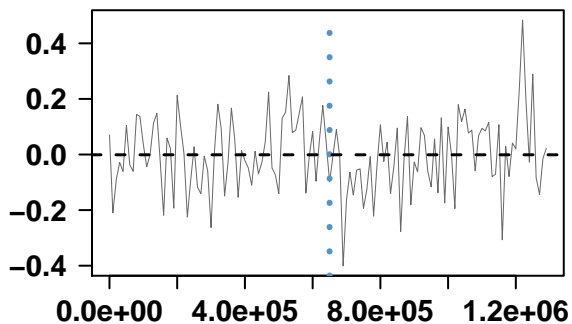
Candidatus Pelagibacter ubique HTCC1062



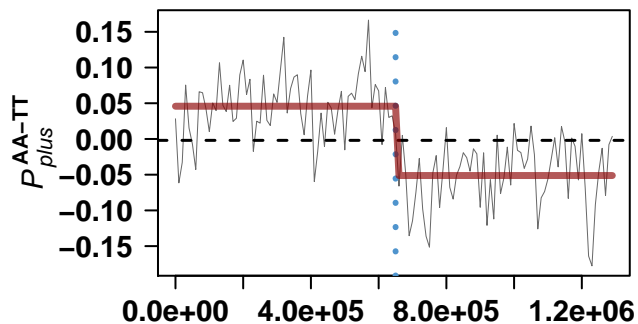
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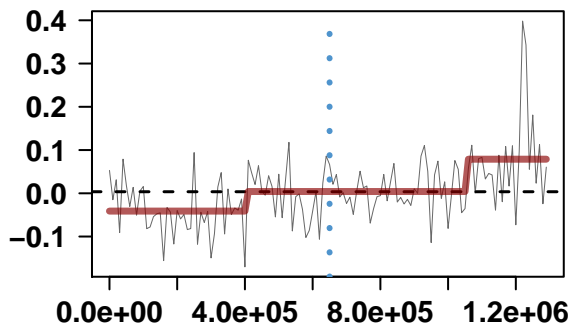
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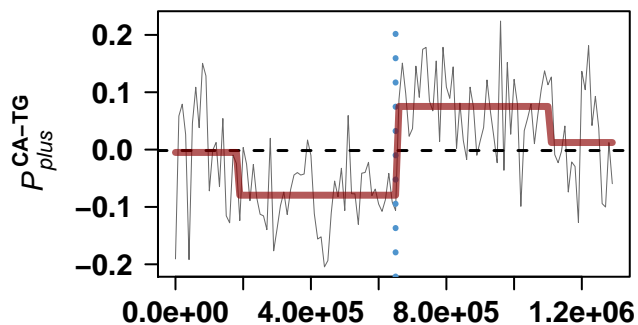
genome coordinates



genome coordinates

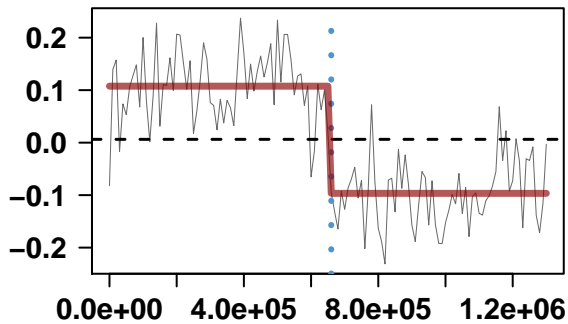


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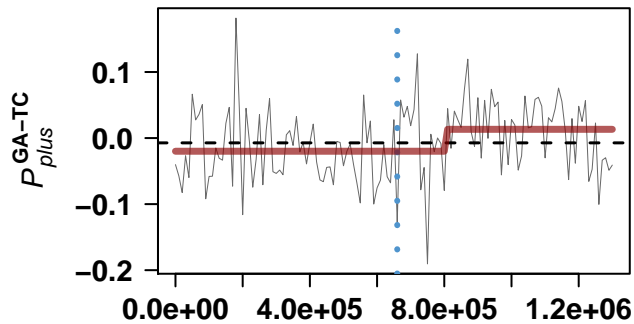


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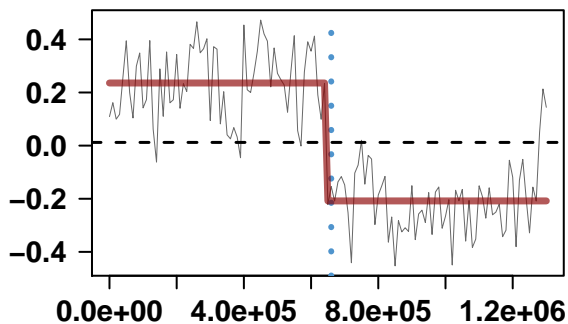
Ehrlichia canis str. Jake



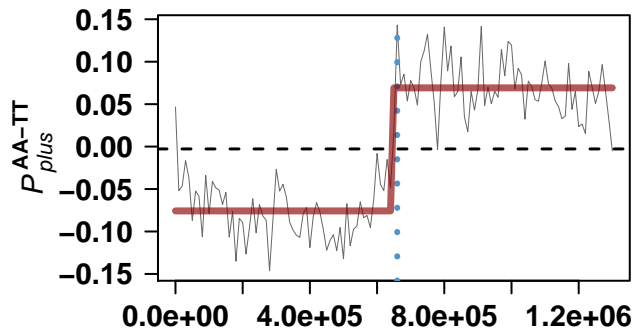
genome coordinates



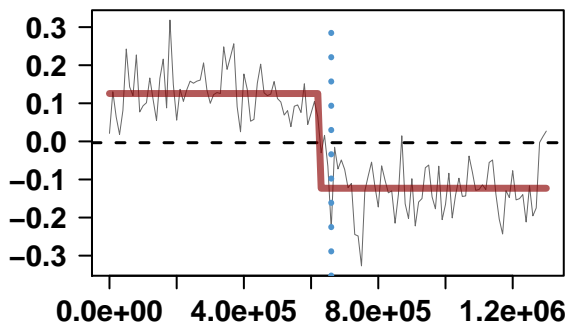
genome coordinates



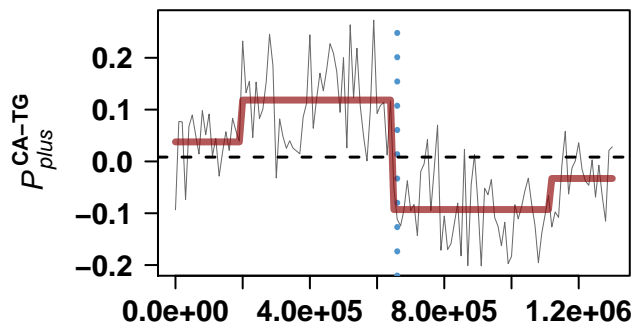
genome coordinates



genome coordinates

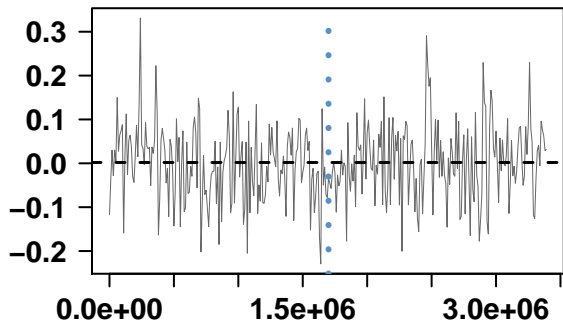


genome coordinates

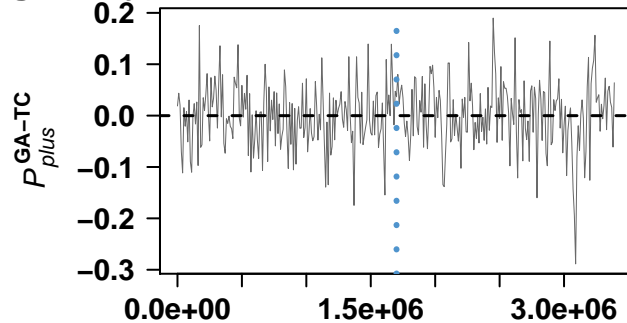


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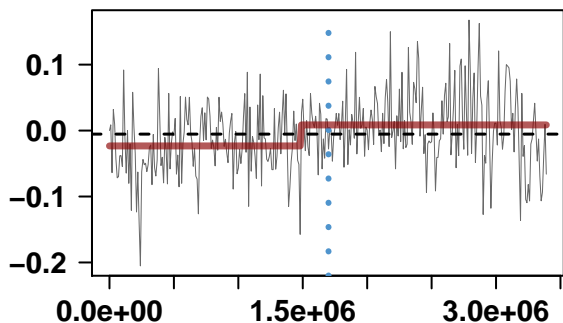
Nitrobacter winogradskyi Nb-255



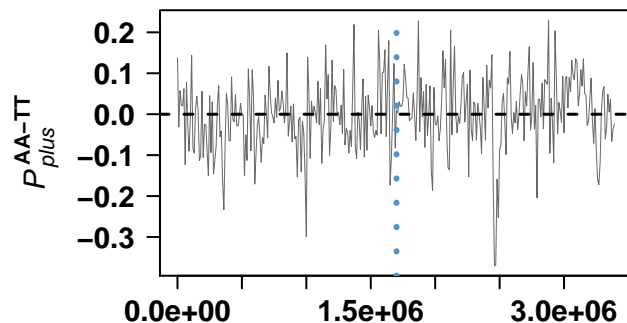
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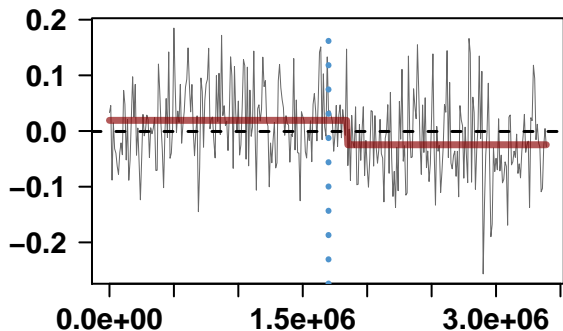
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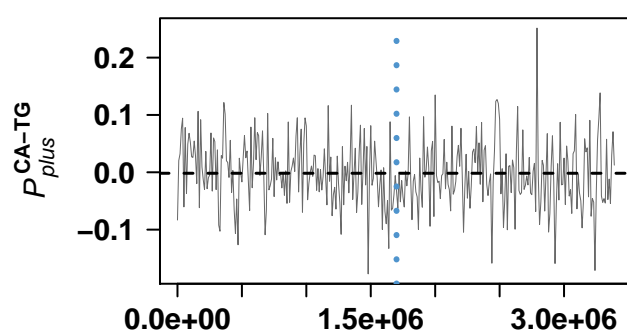
genome coordinates



genome coordinates

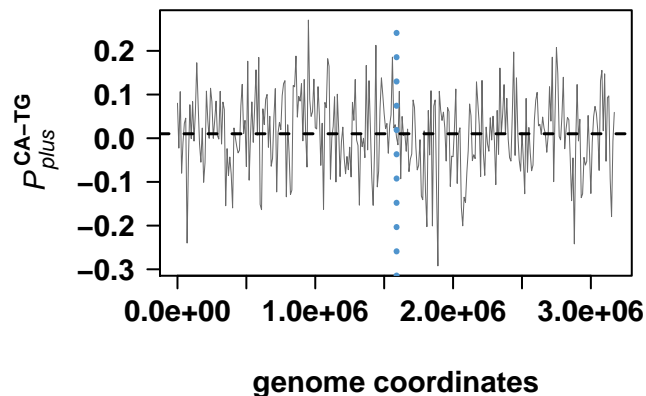
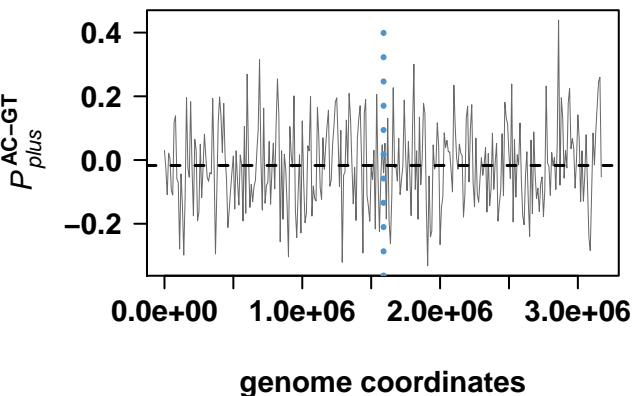
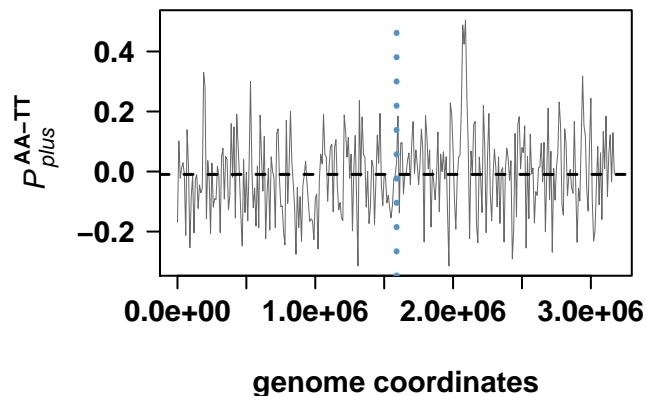
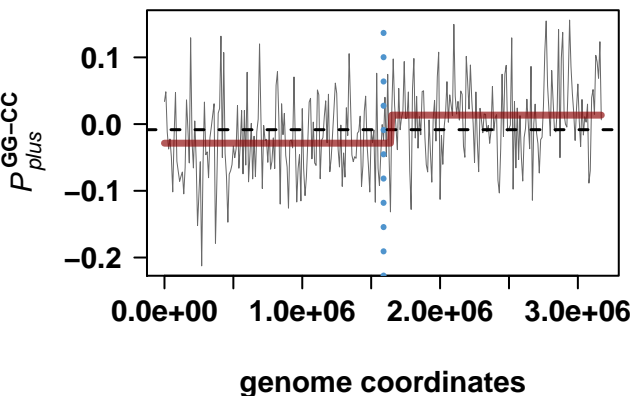
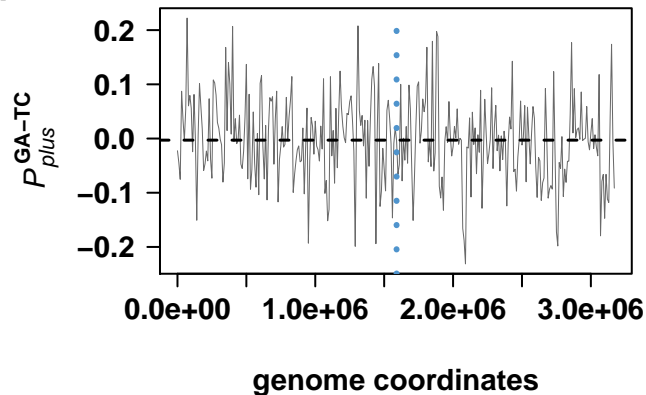
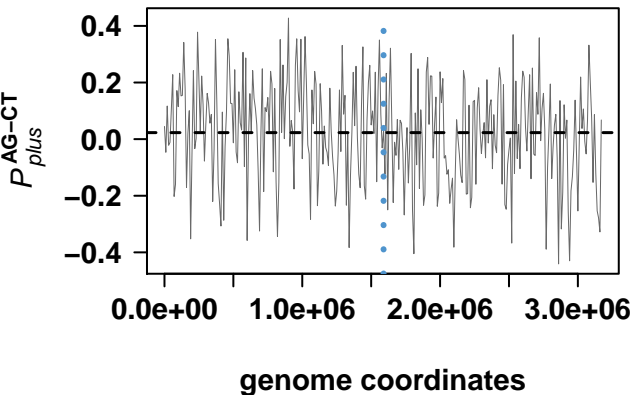


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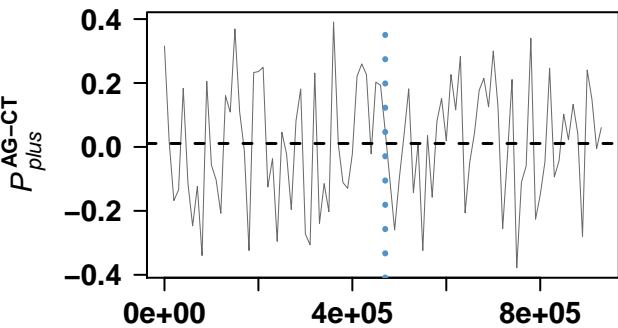


genome coordinates

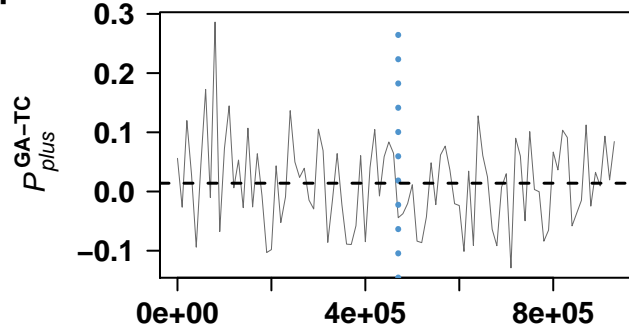
Rhodobacter sphaeroides 2.4.1



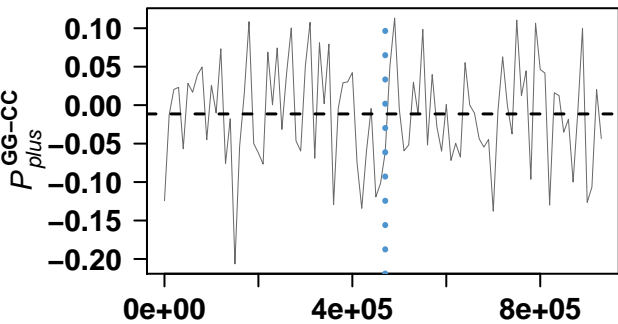
Rhodobacter sphaeroides 2.4.1



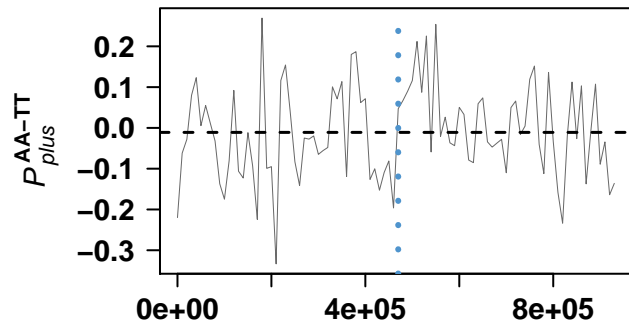
genome coordinates



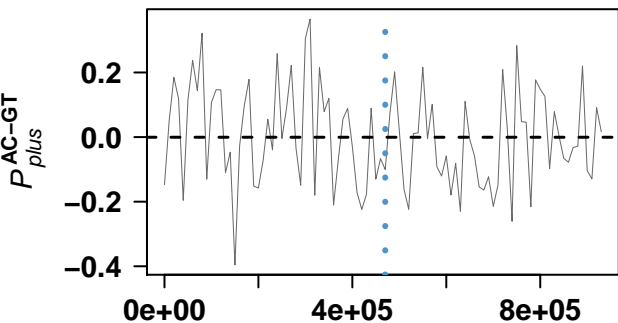
genome coordinates



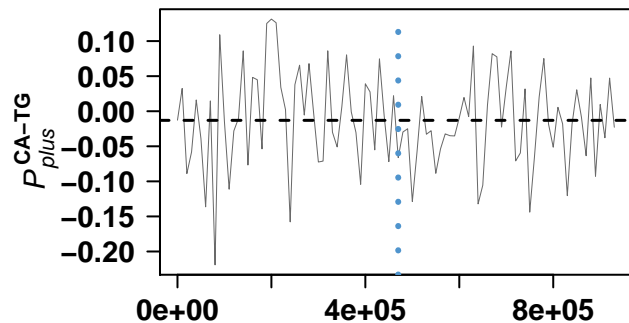
genome coordinates



genome coordinates

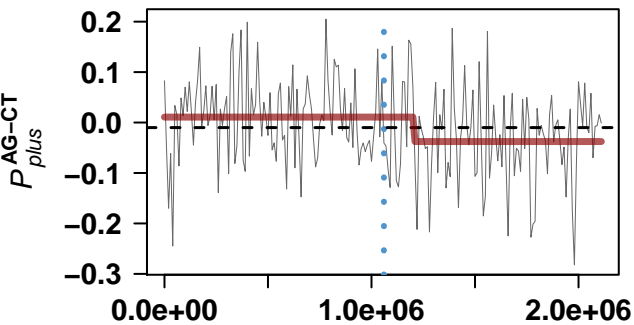


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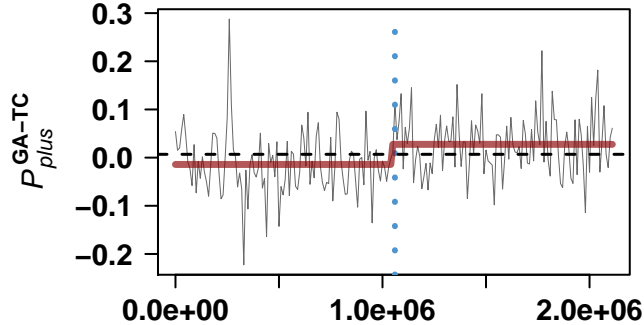


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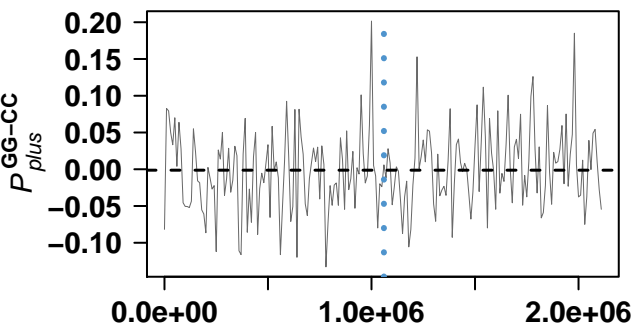
Brucella abortus 2308



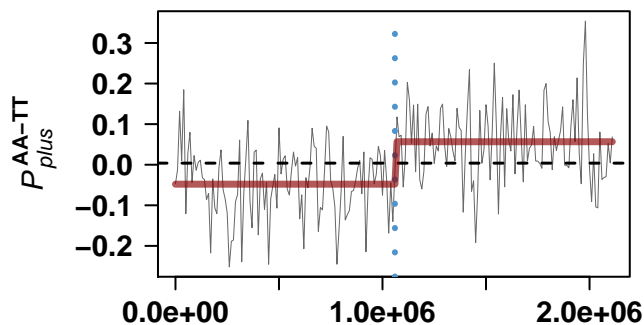
genome coordinates



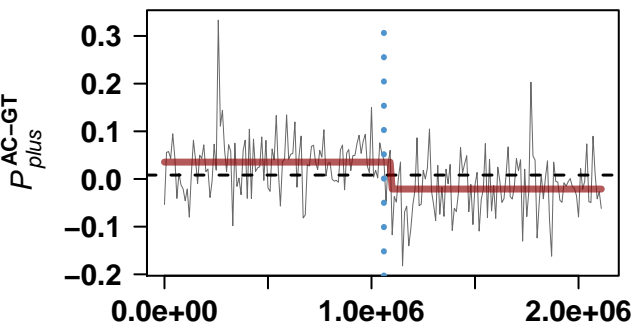
genome coordinates



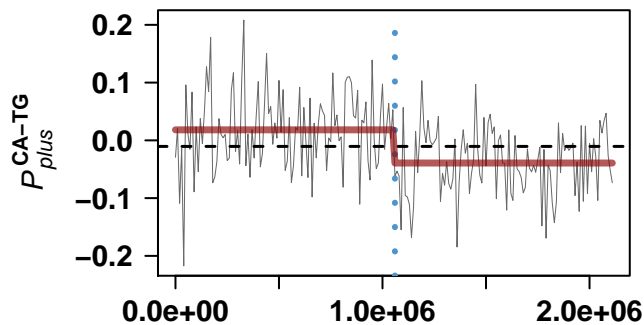
genome coordinates



genome coordinates

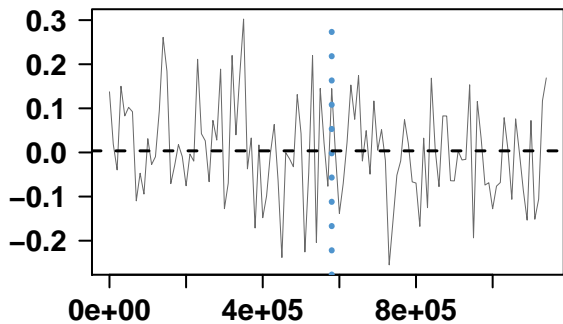


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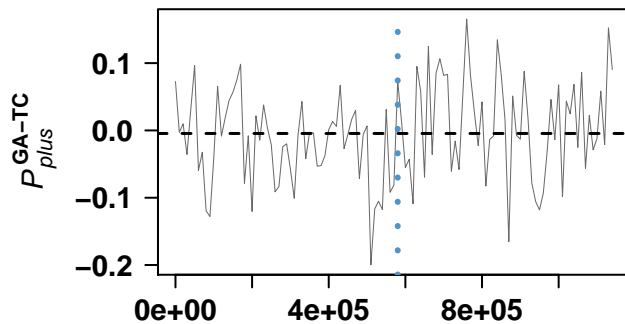


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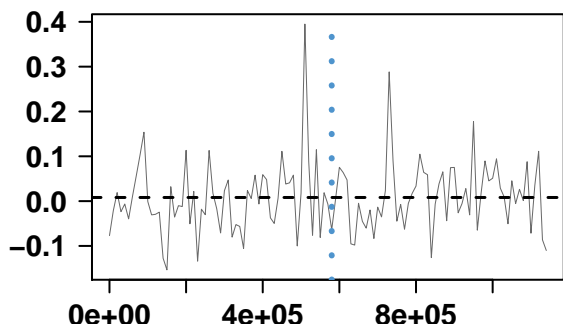
Brucella abortus 2308



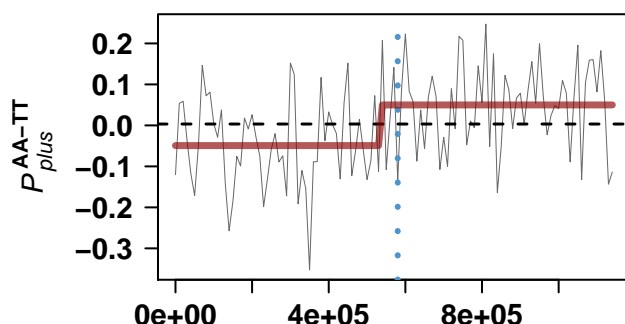
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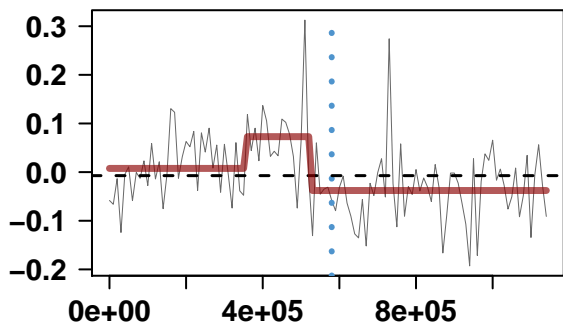
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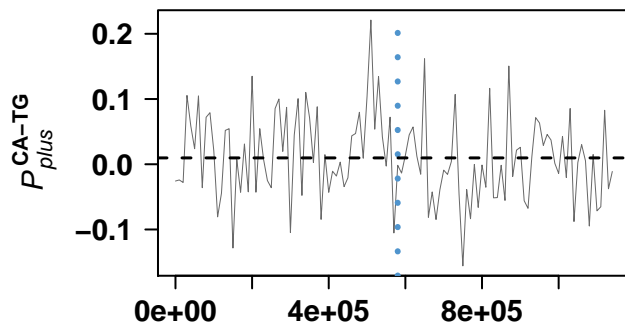
genome coordinates



genome coordinates

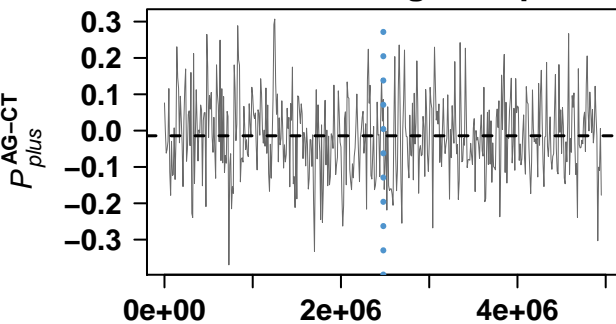


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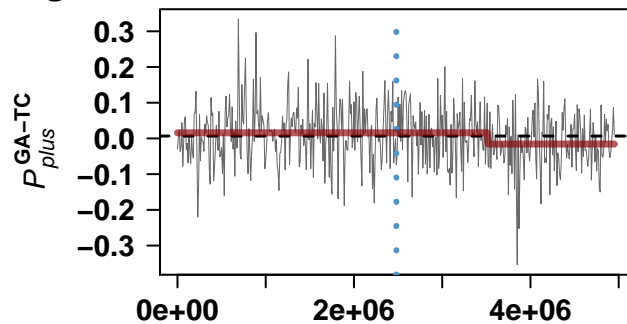


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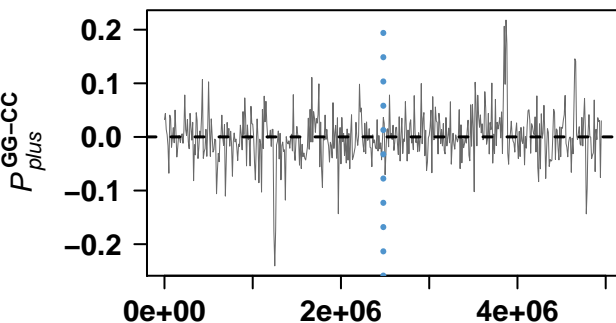
Magnetospirillum magneticum AMB-1



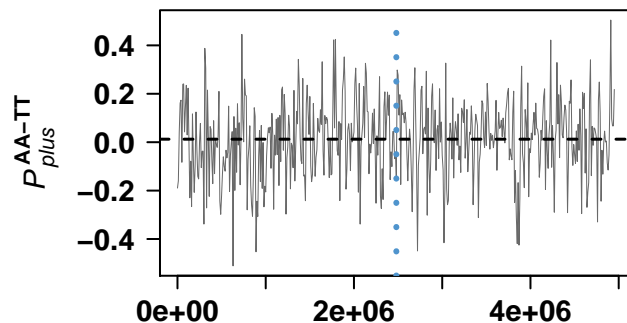
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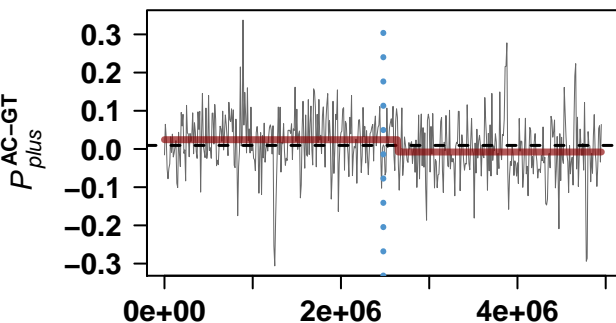
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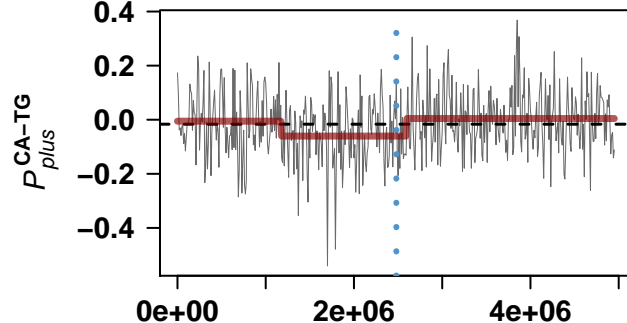
genome coordinates



genome coordinates

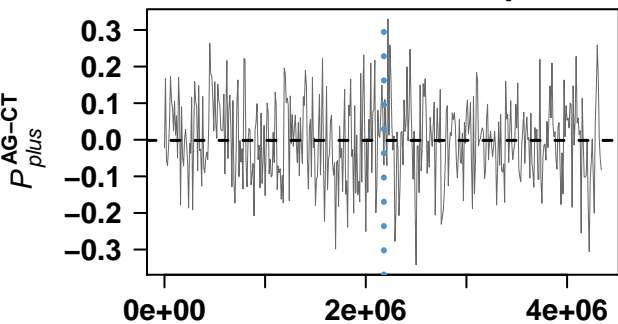


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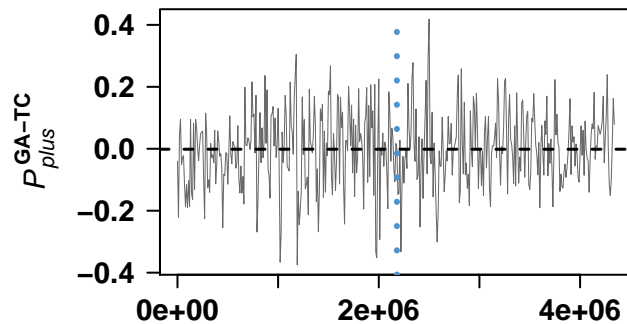


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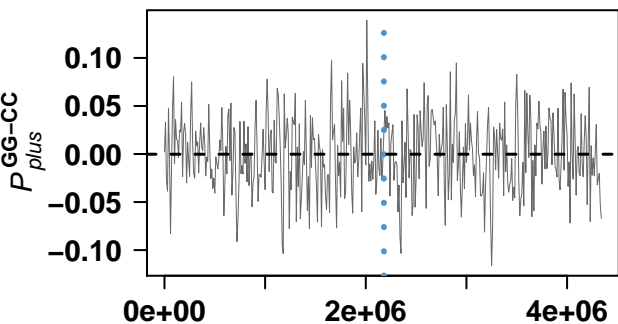
Rhodospirillum rubrum ATCC 11170



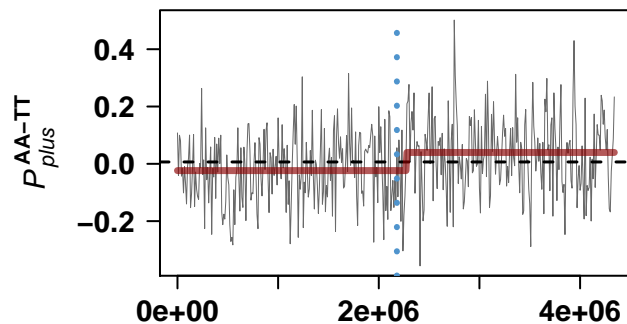
genome coordinates



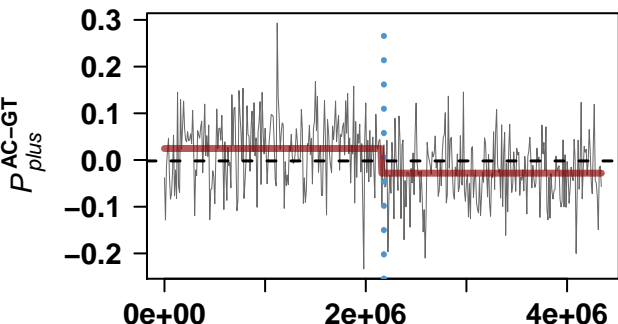
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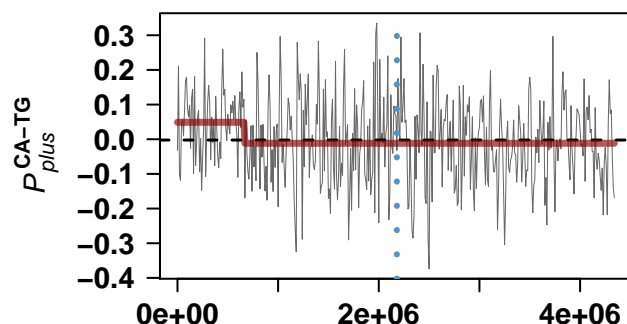
genome coordinates



genome coordinates

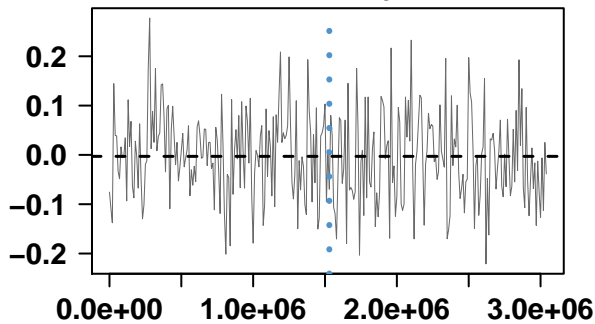


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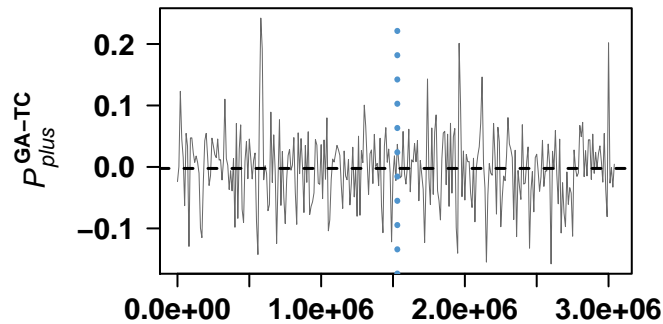


genome coordinates

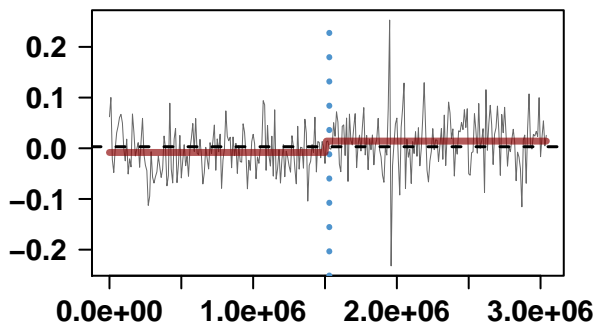
Erythrobacter litoralis HTCC2594



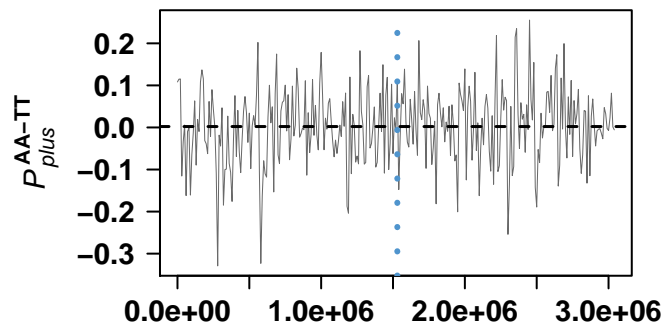
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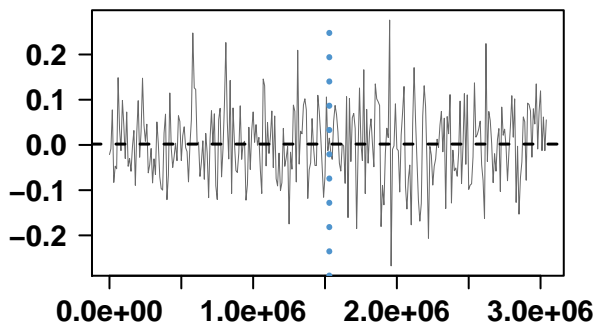
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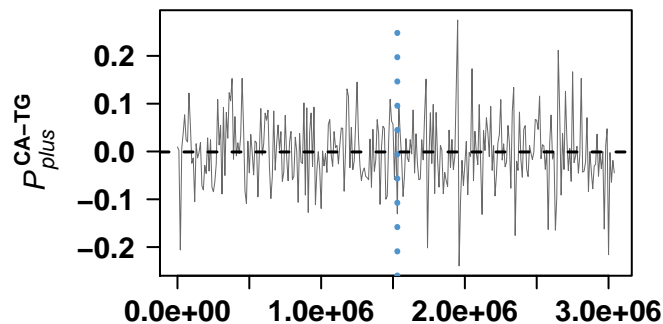
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genome coordinates

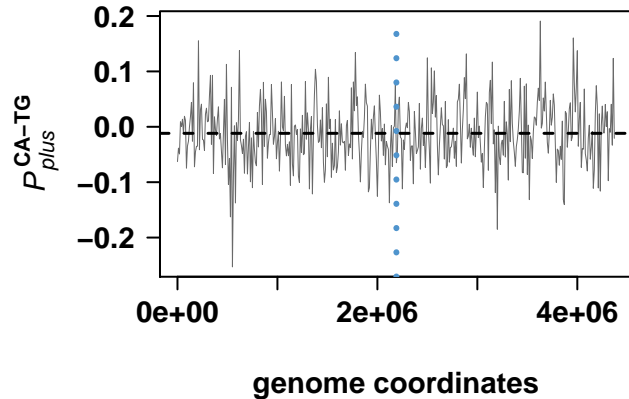
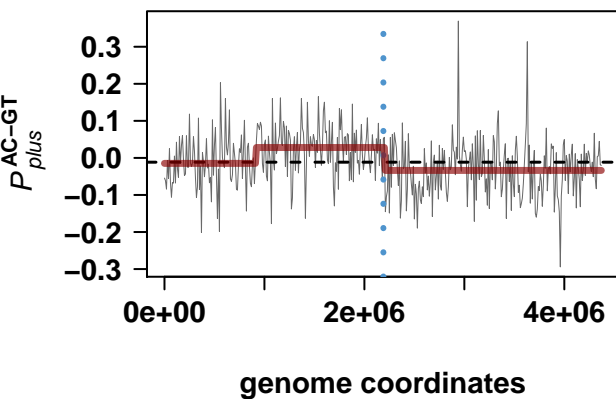
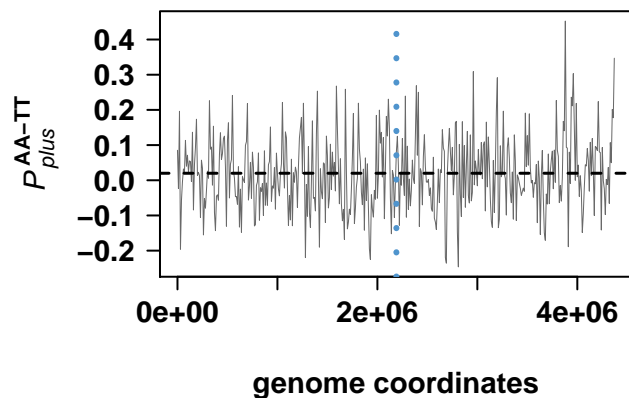
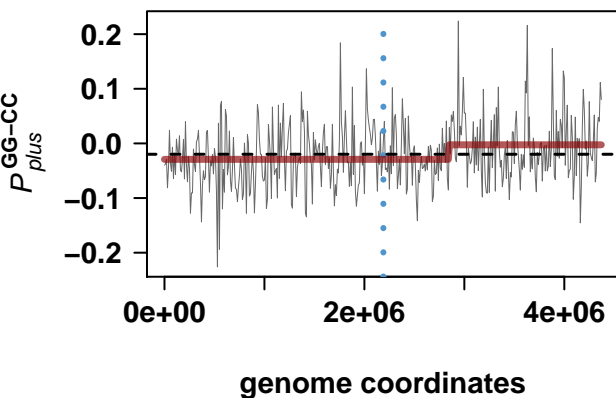
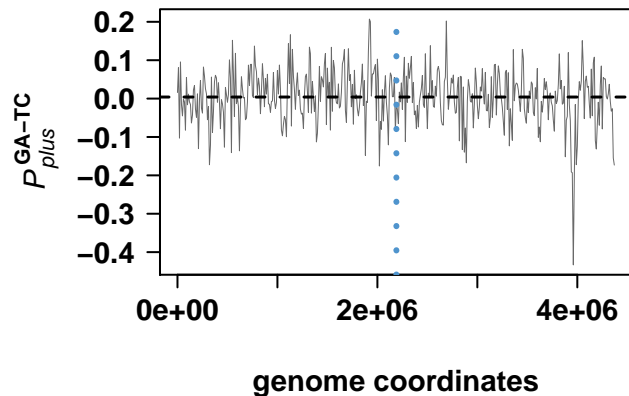
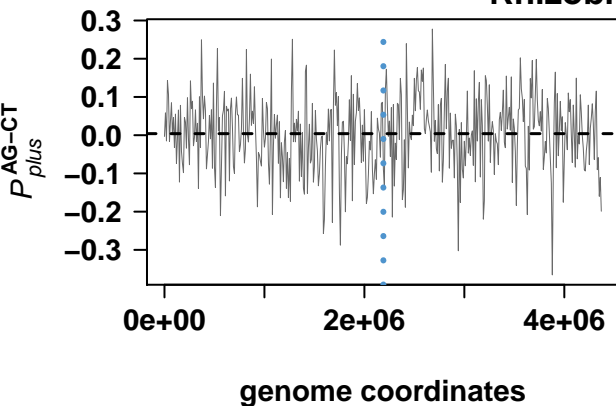


genome coordinates

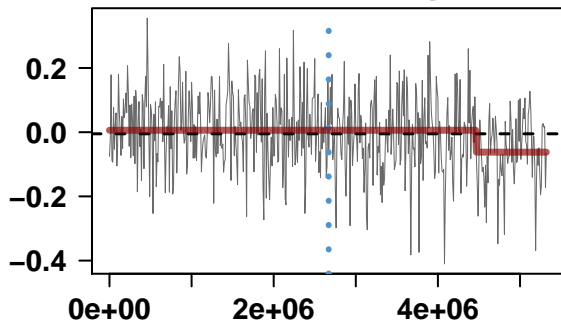


genome coordinates

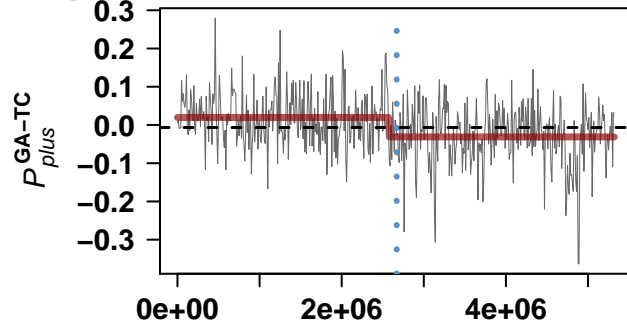
Rhizobium etli CFN 42



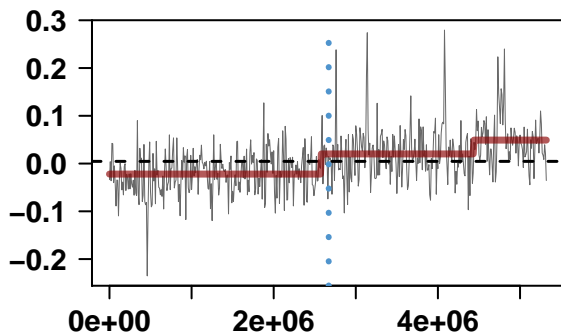
Rhodospseudomonas palustris HaA2



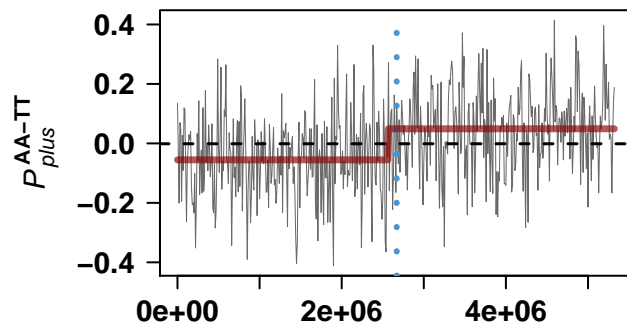
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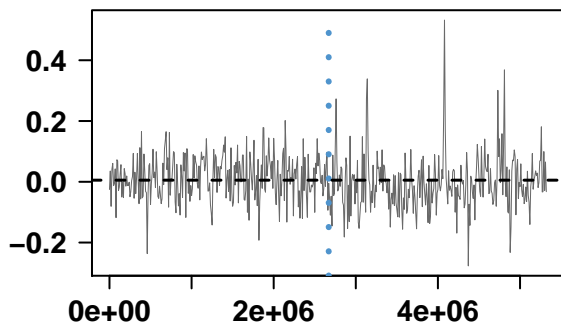
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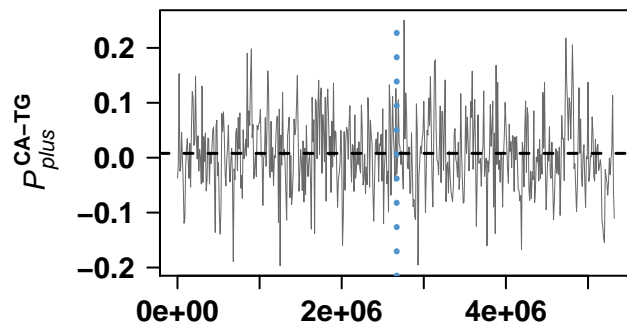
genome coordinates



genome coordinates

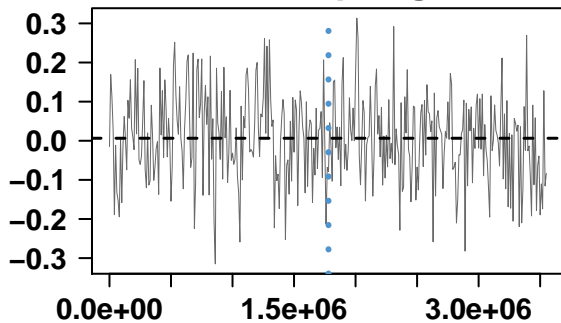


genome coordinates

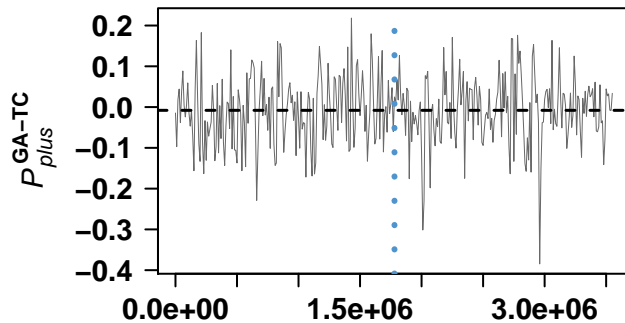


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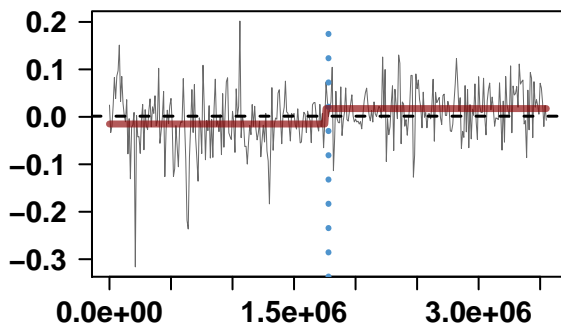
Novosphingobium aromaticivorans DSM 12444



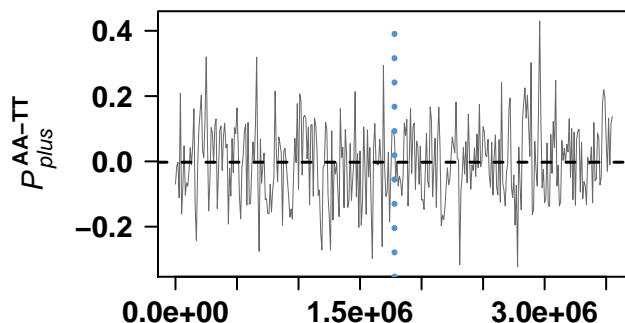
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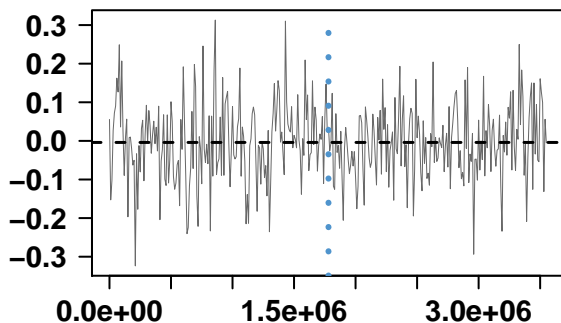
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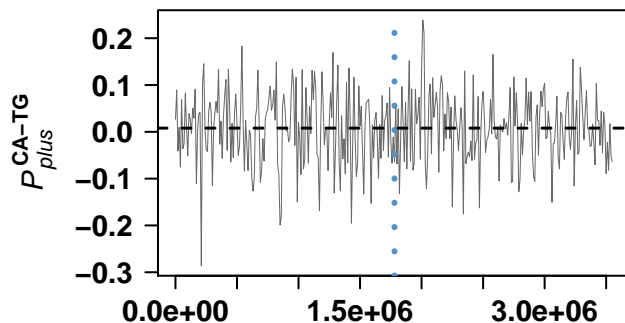
genome coordinates



genome coordinates

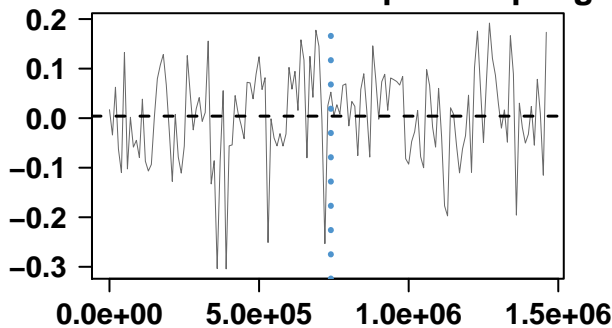


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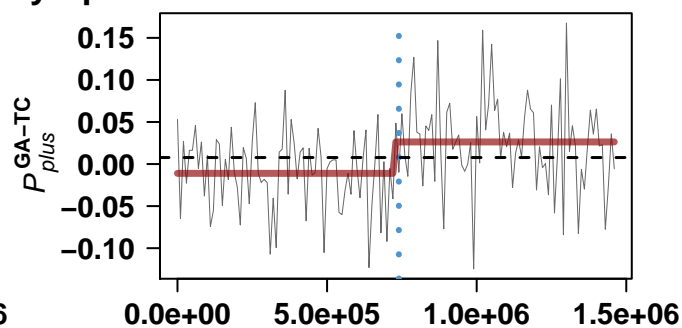


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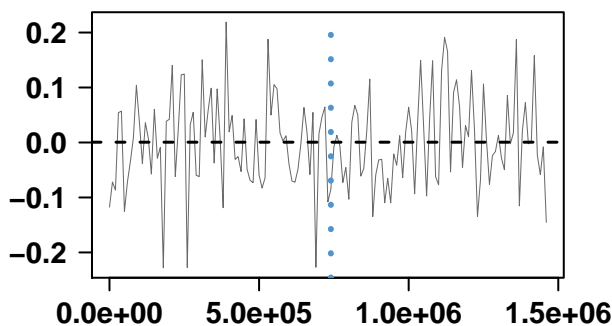
Anaplasma phagocytophilum str. HZ



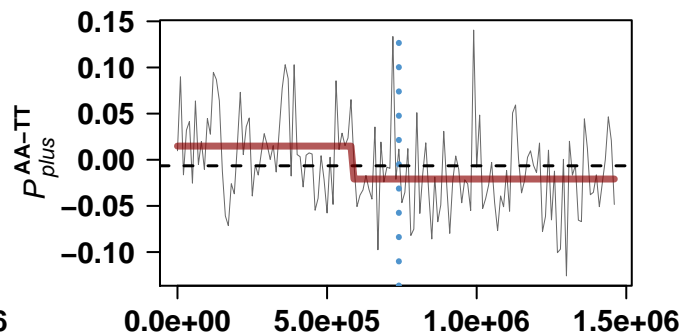
genome coordinates



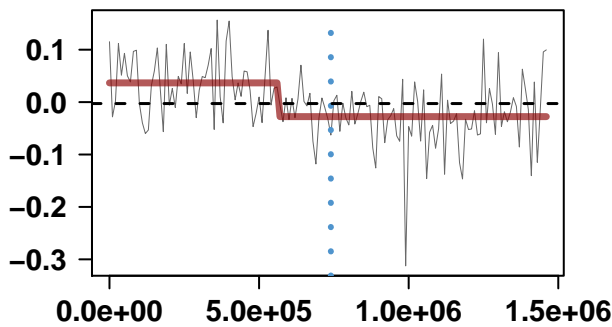
genome coordinates



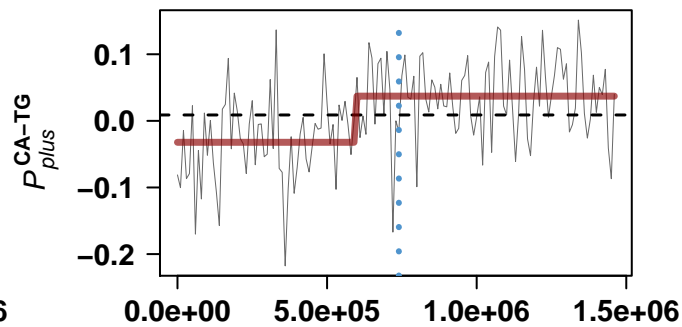
genome coordinates



genome coordinates

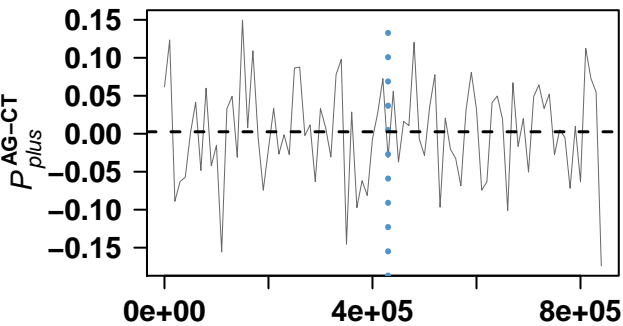


genome coordinates

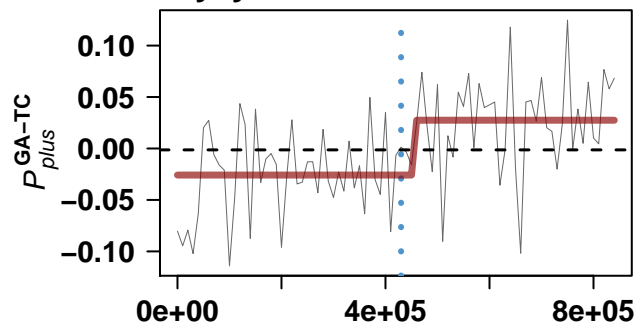


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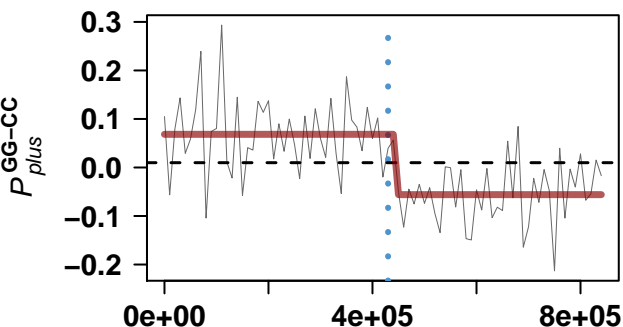
Neorickettsia sennetsu str. Miyayama



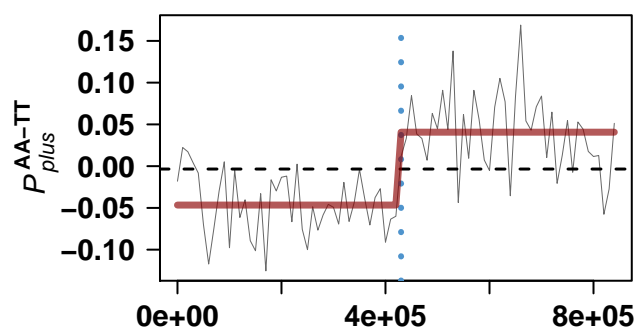
genome coordinates



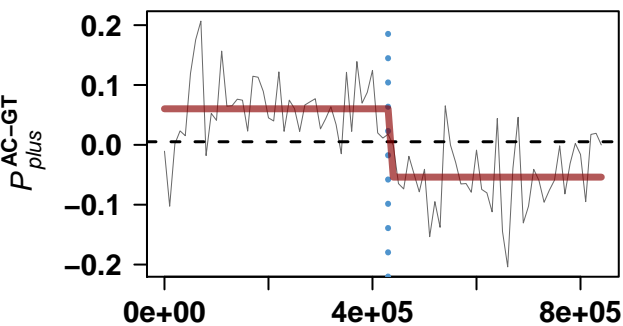
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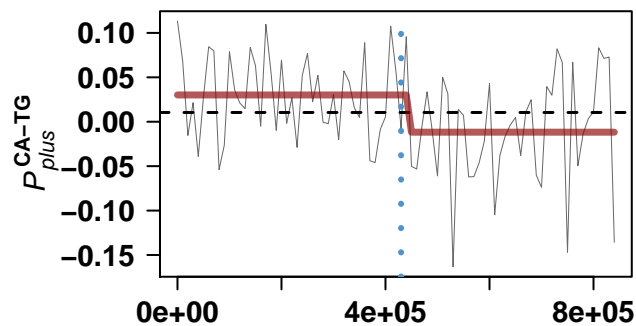
genome coordinates



genome coordinates

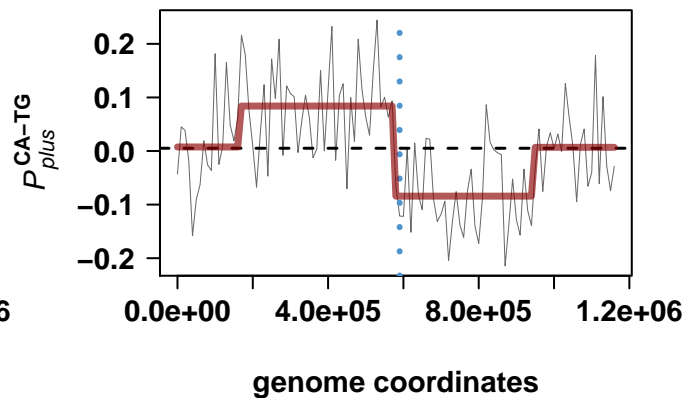
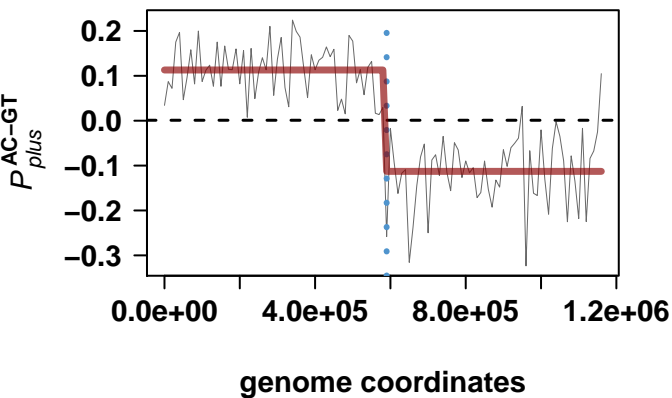
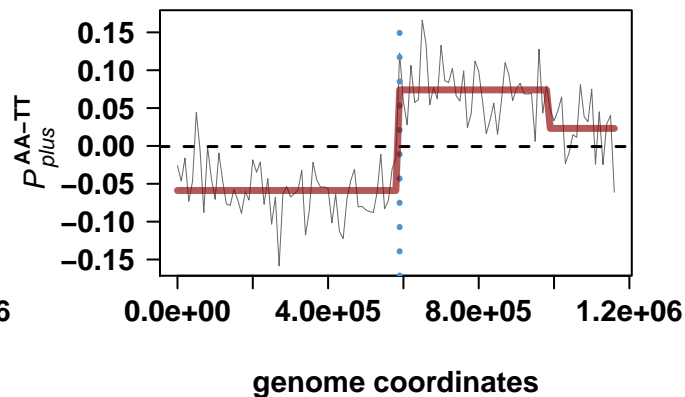
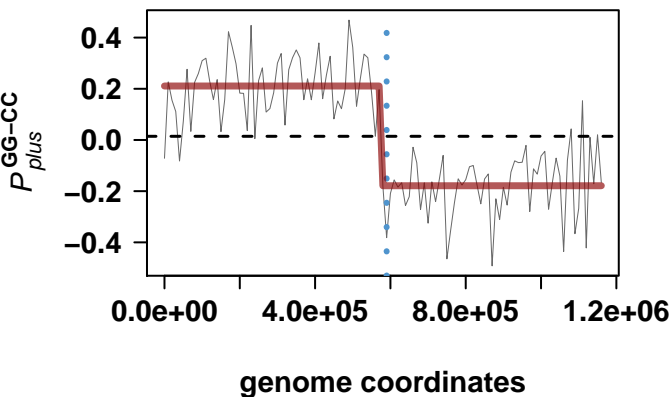
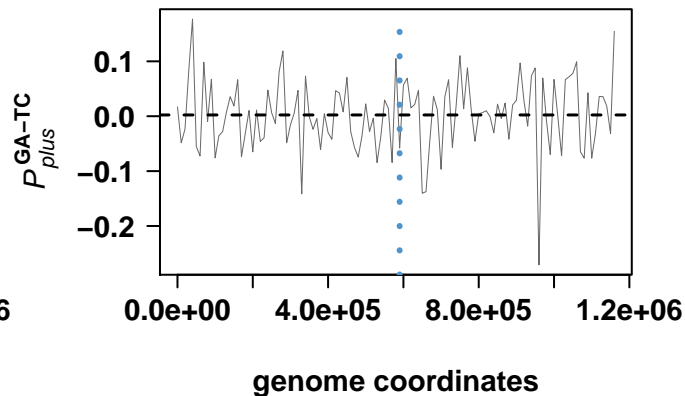
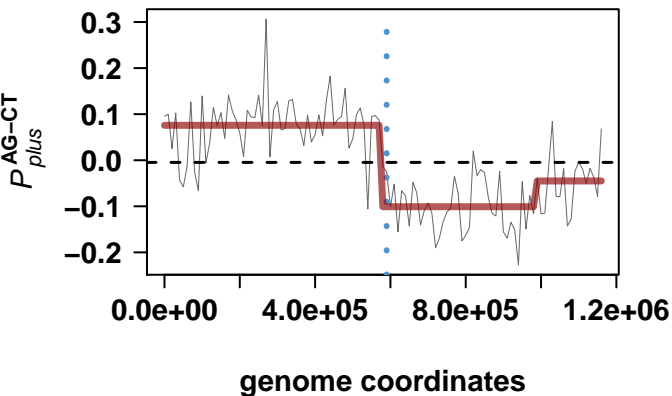


genome coordinates

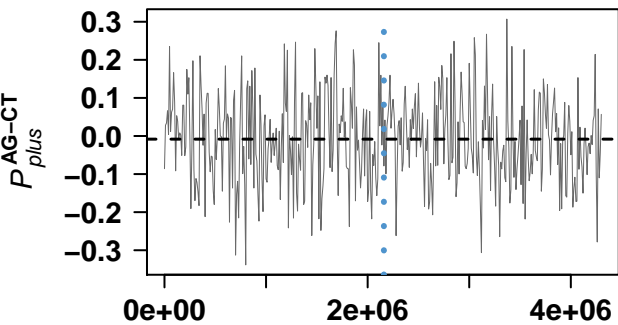


genome coordinates

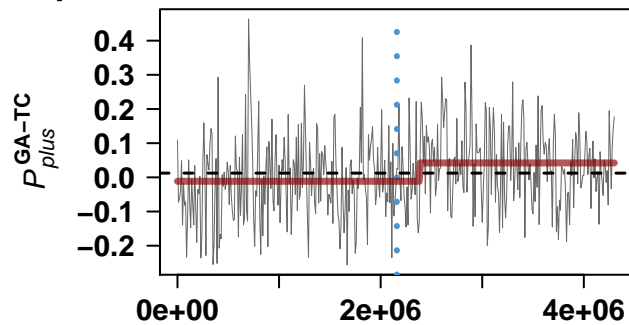
Ehrlichia chaffeensis str. Arkansas



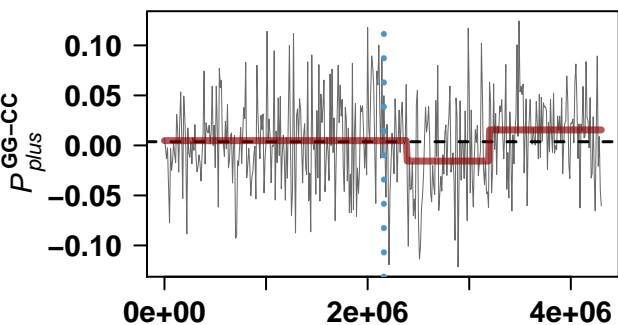
Jannaschia sp. CCS1



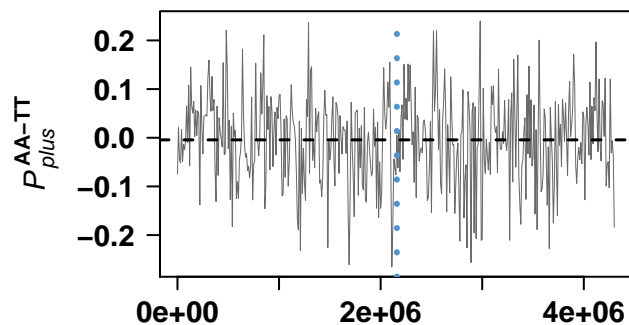
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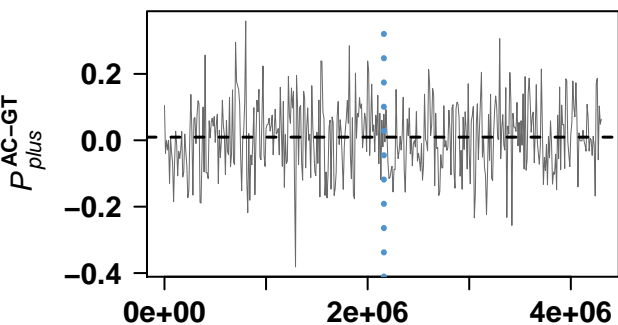
genome coordinates



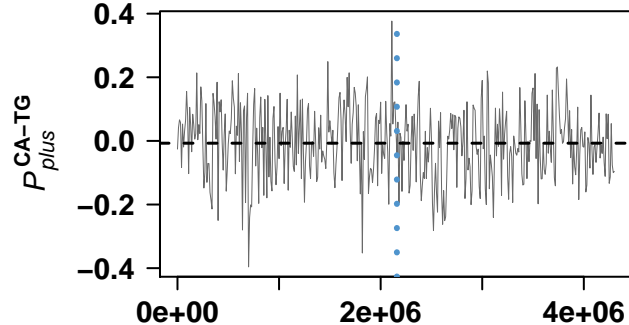
genome coordinates



genome coordinates

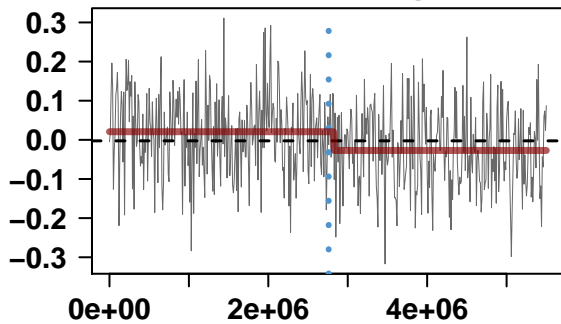


genome coordinates

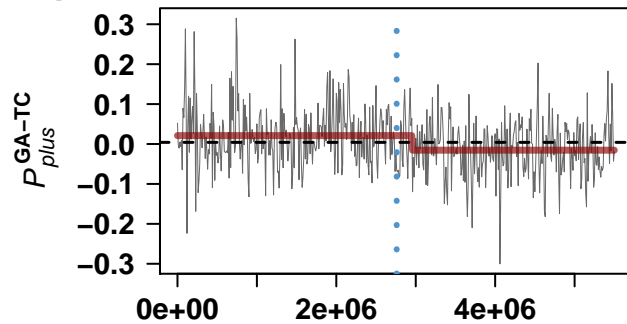


genome coordinates

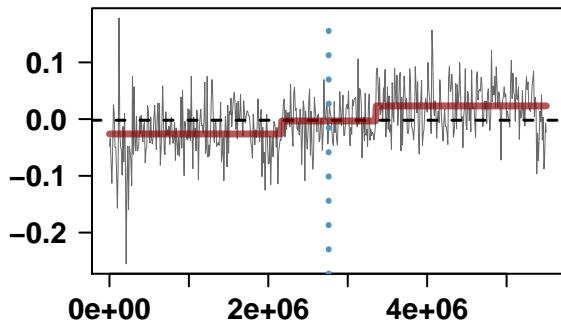
Rhodopseudomonas palustris BisB18



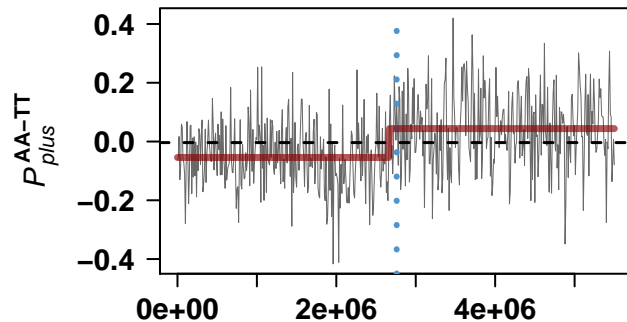
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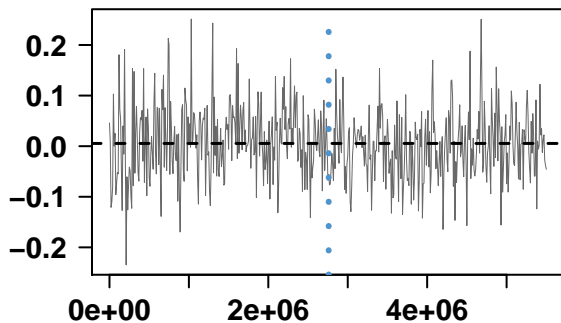
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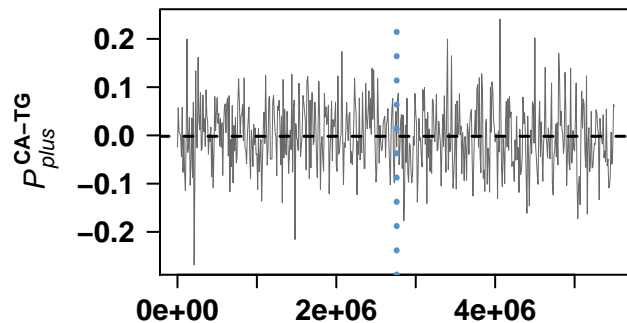
genome coordinates



genome coordinates

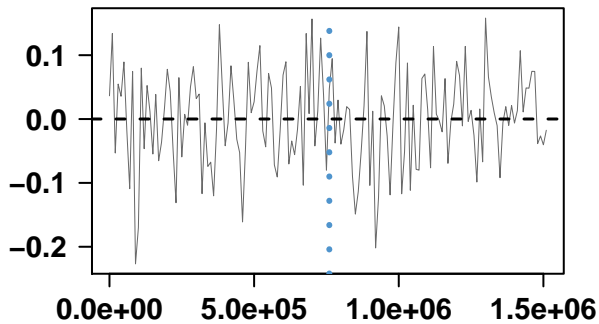


genome coordinates

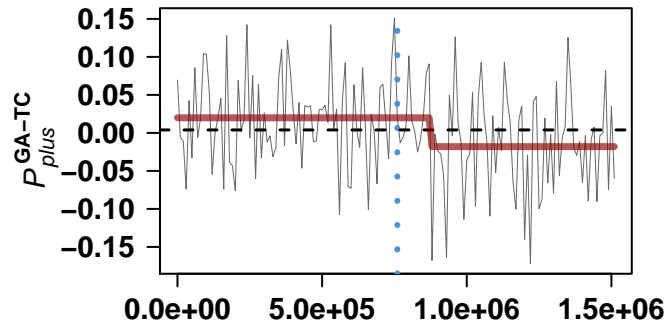


genome coordinates

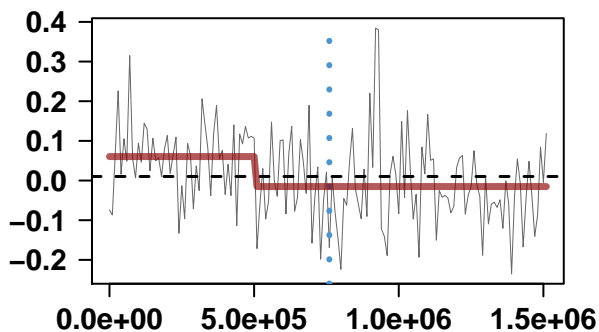
Rickettsia bellii RML369-C



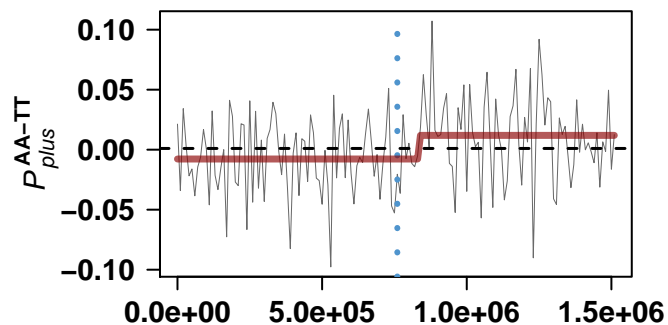
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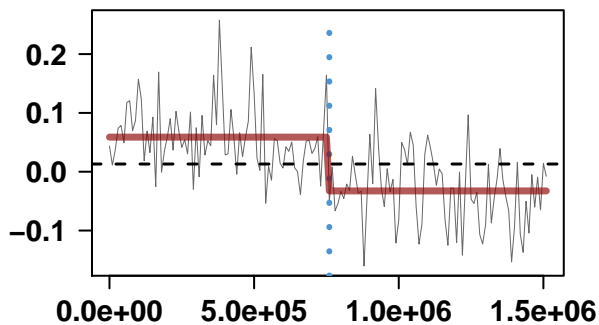
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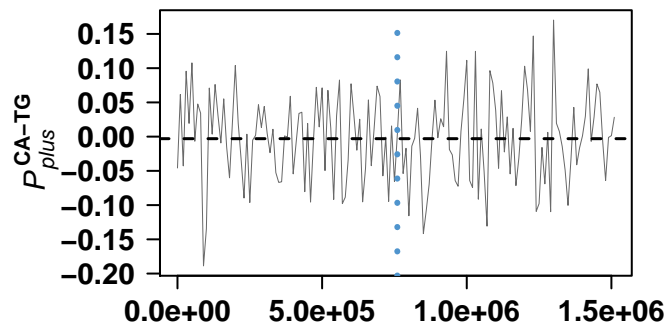
genome coordinates



genome coordinates

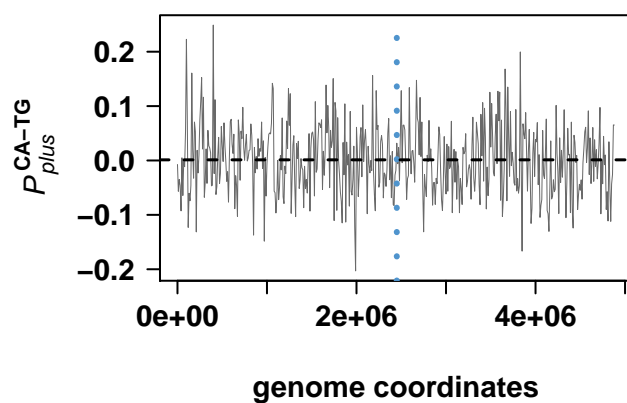
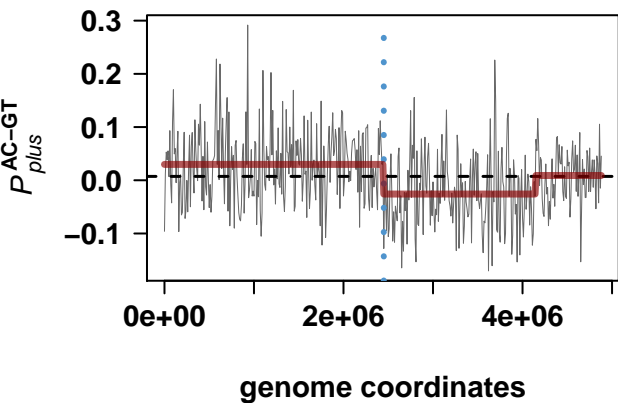
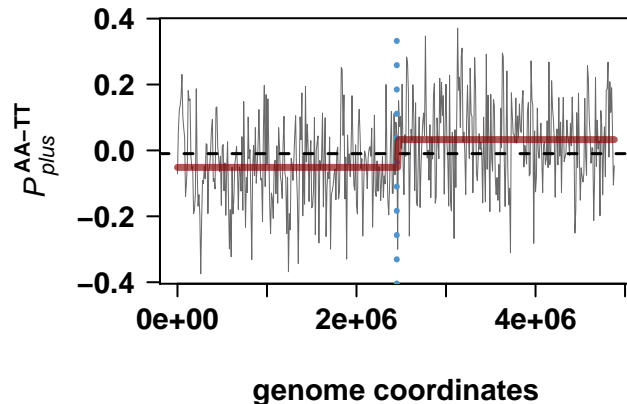
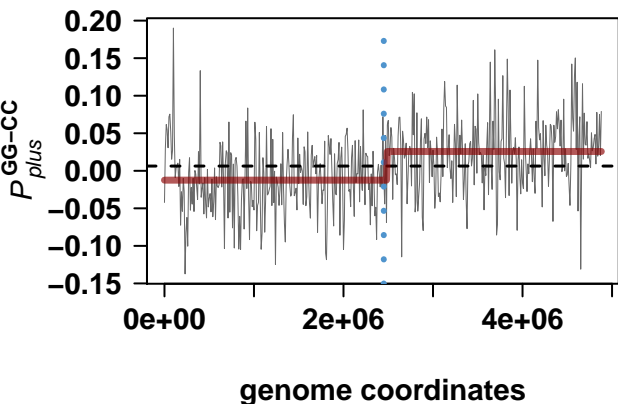
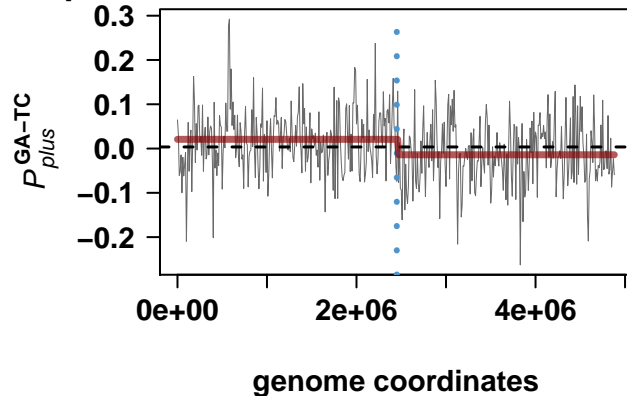
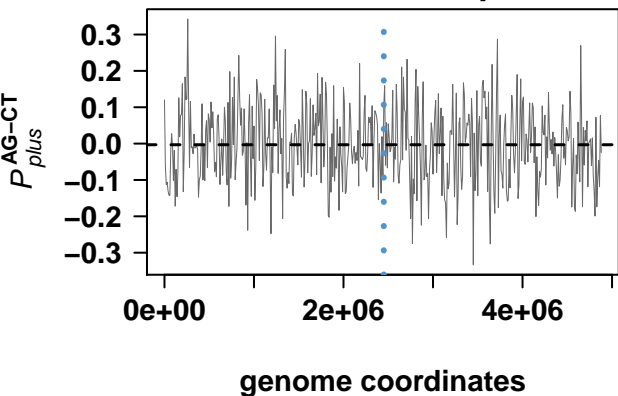


genome coordinates

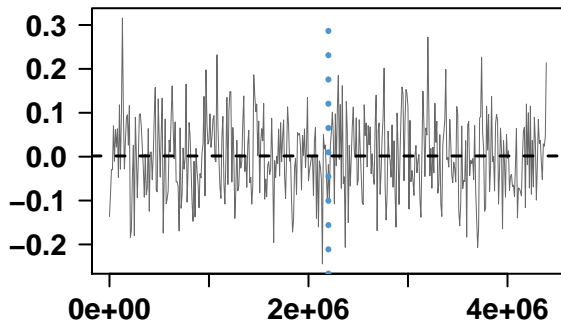


genome coordinates

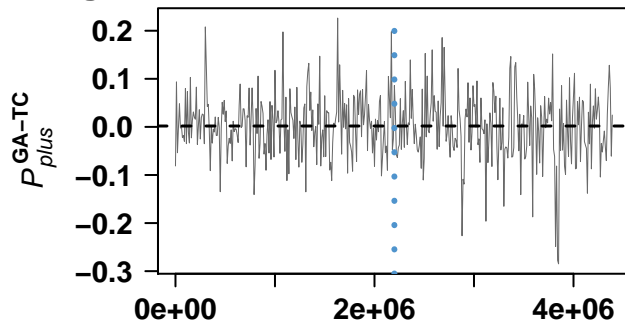
Rhodopseudomonas palustris BisB5



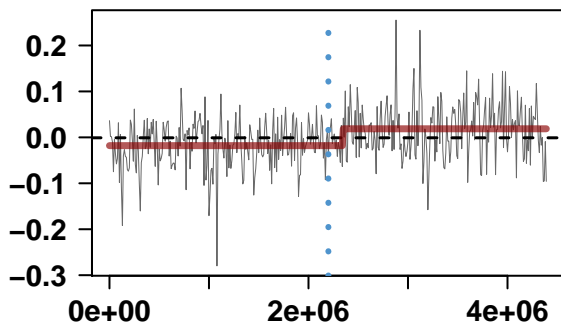
Nitrobacter hamburgensis X14



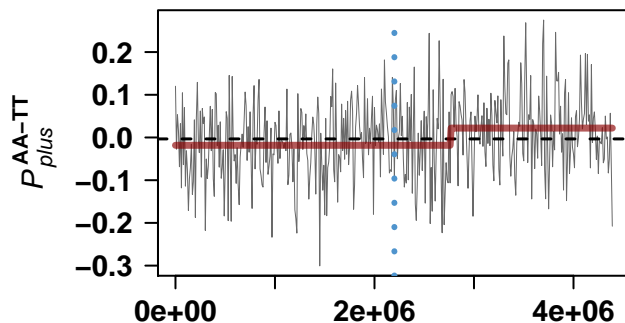
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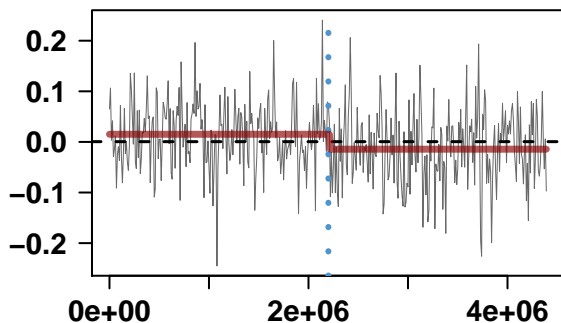
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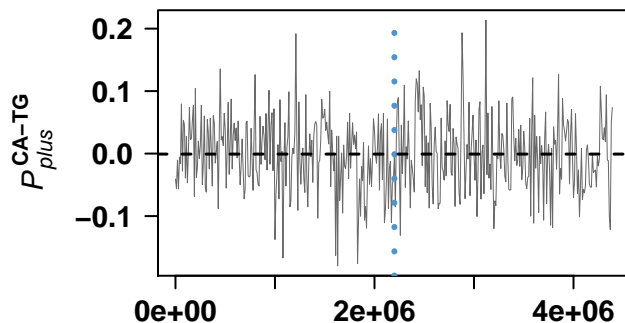
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genome coordinates

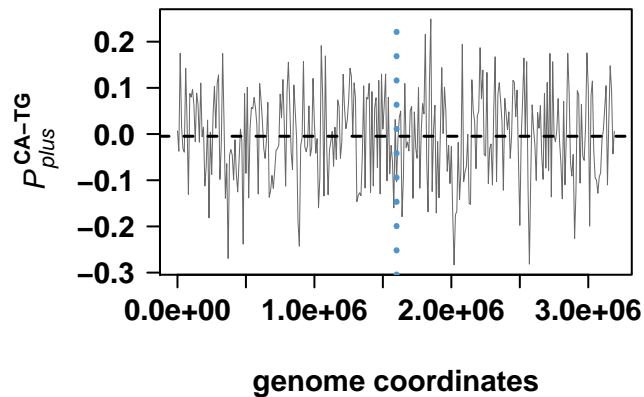
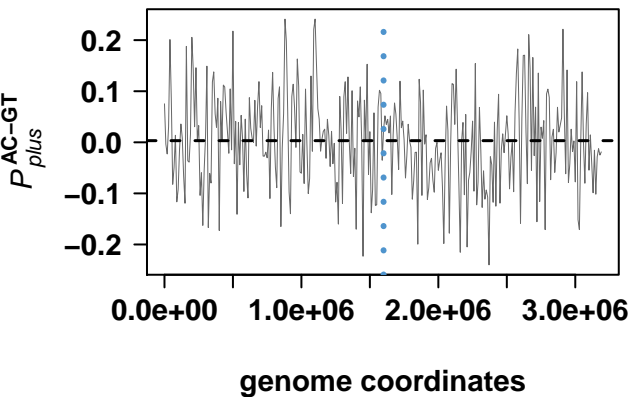
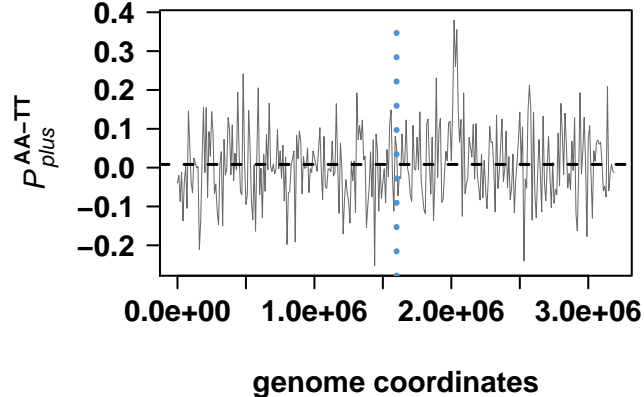
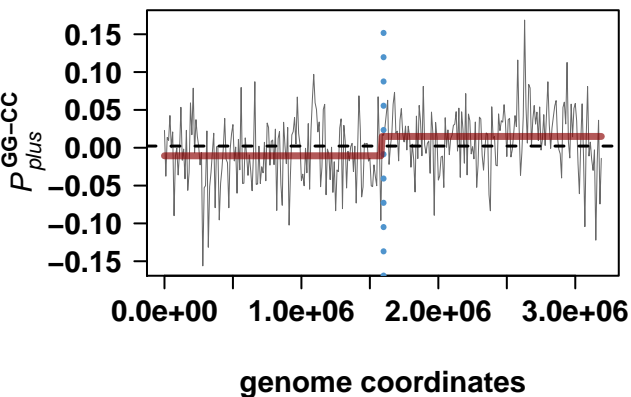
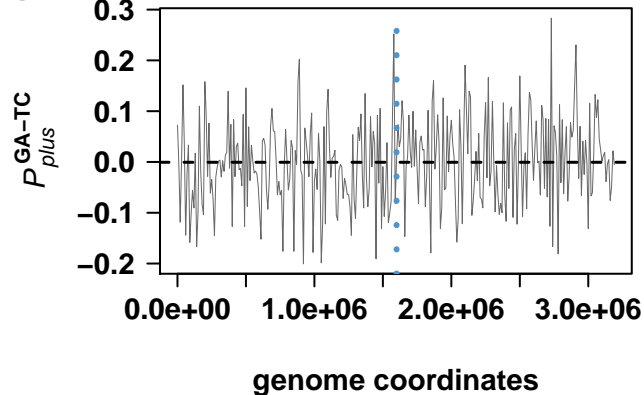
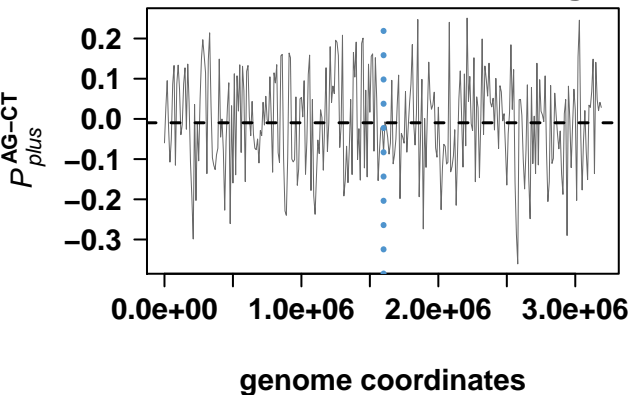


genome coordinates

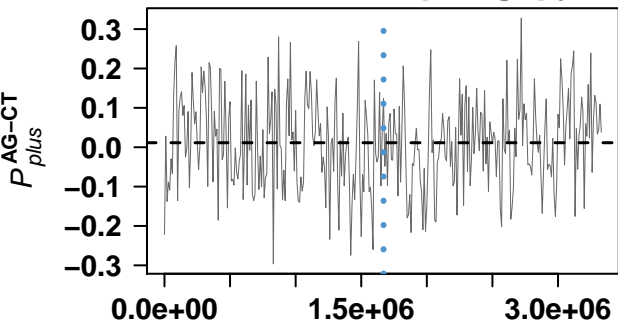


genome coordinates

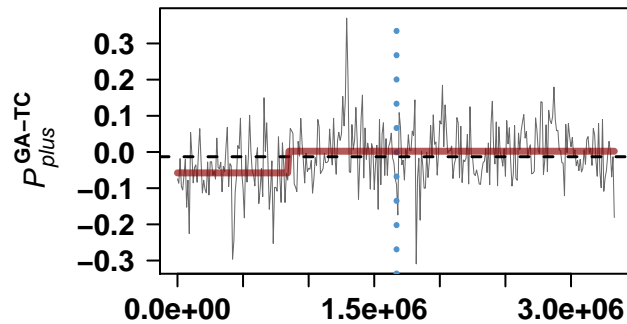
Ruegeria sp. TM1040



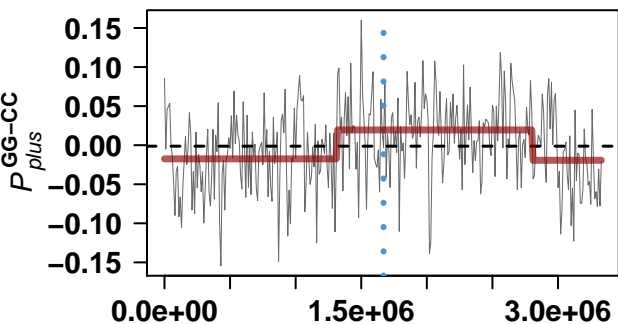
Spingopyxis alaskensis RB2256



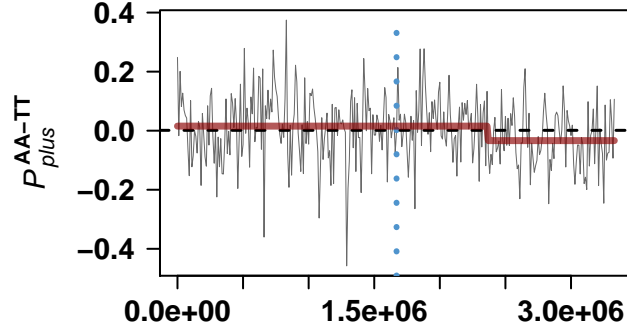
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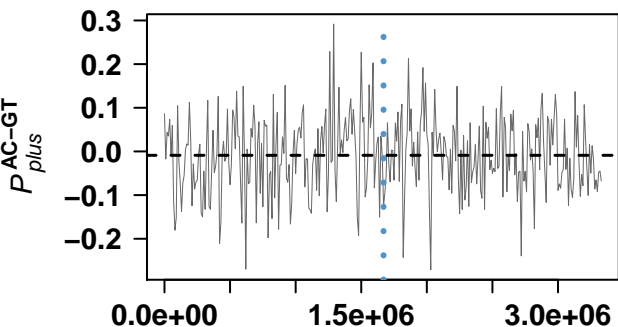
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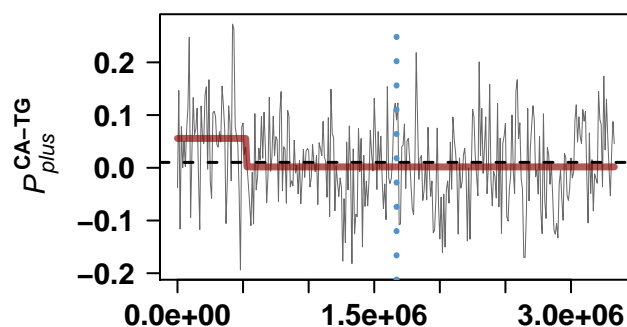
genome coordinates



genome coordinates

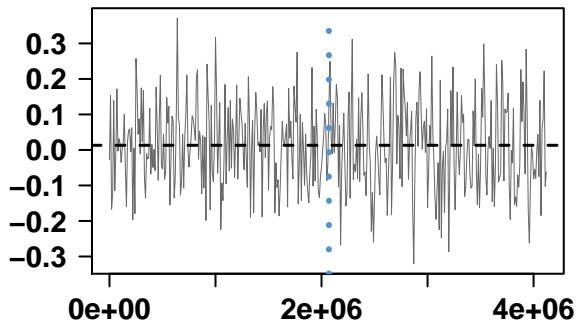


genome coordinates

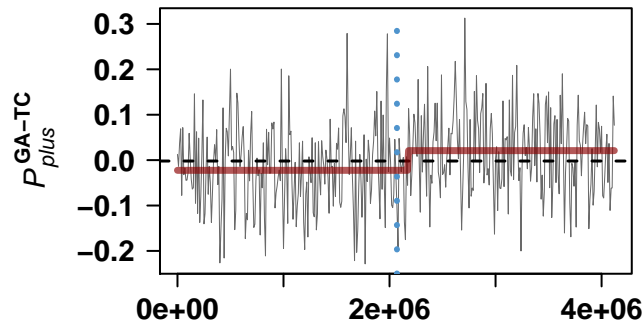


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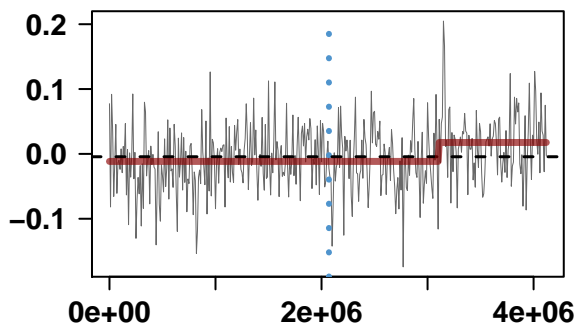
Roseobacter denitrificans OCh 114



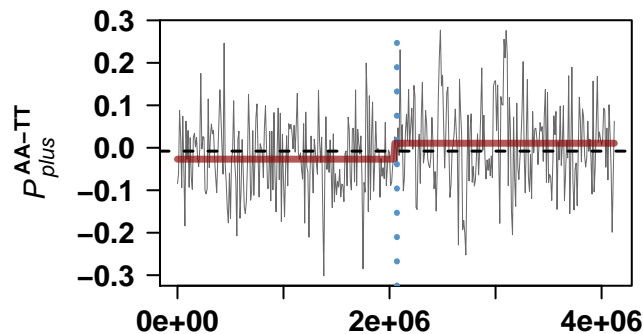
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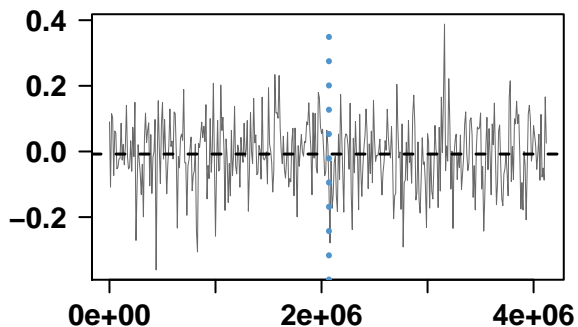
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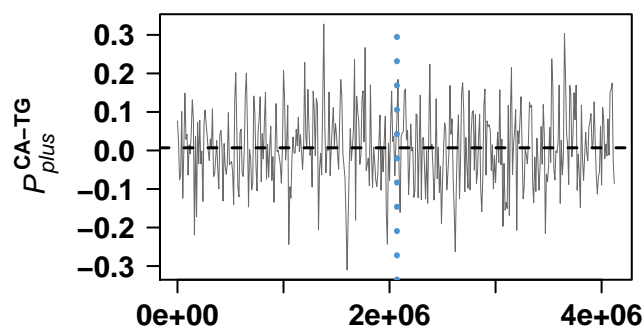
genome coordinates



genome coordinates

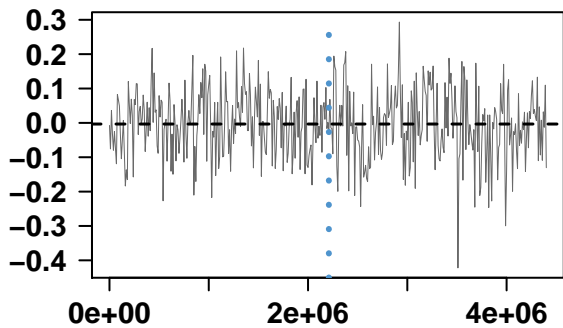


genome coordinates

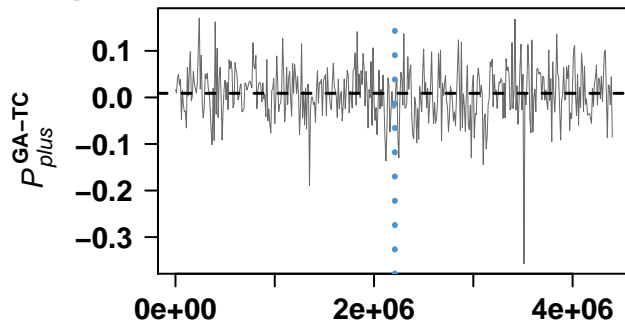


genome coordinates

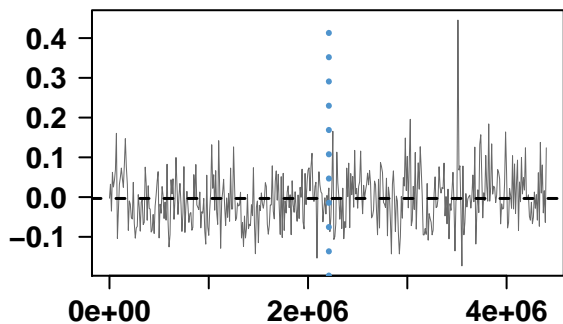
Chelativorans sp. BNC1



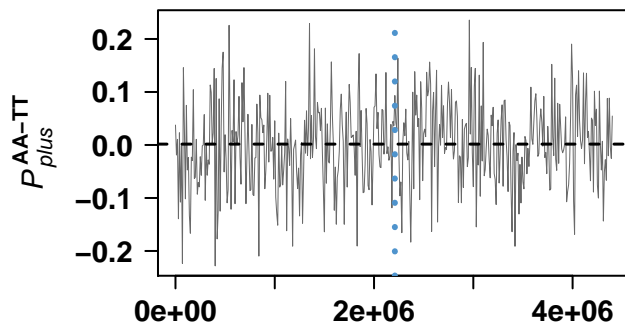
genome coordinates



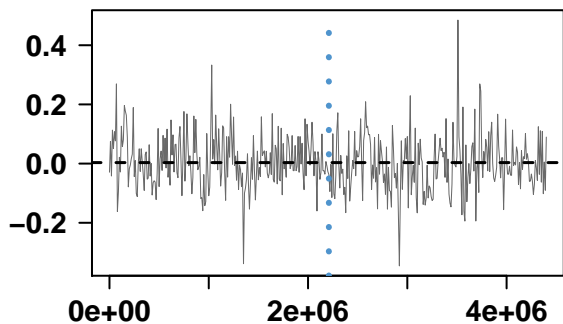
genome coordinates



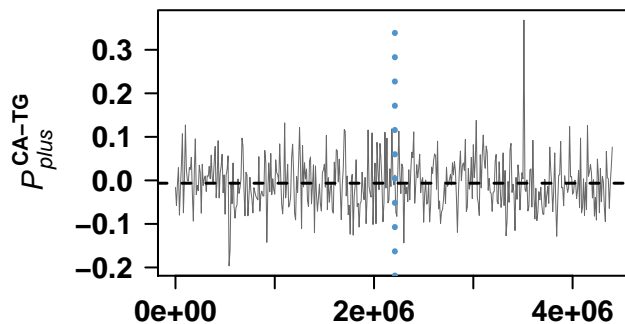
genome coordinates



genome coordinates

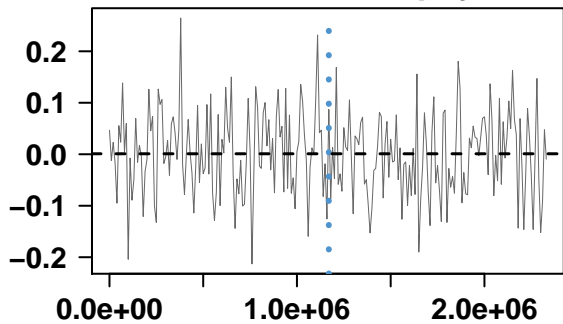


genome coordinates

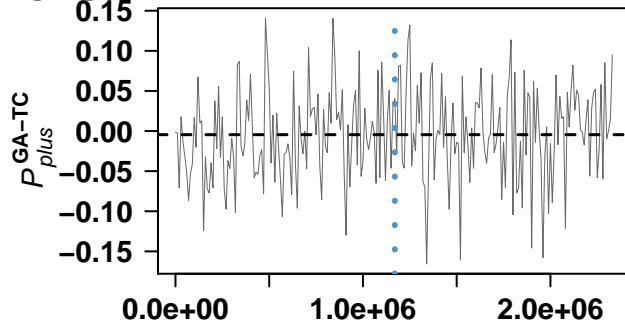


genome coordinates

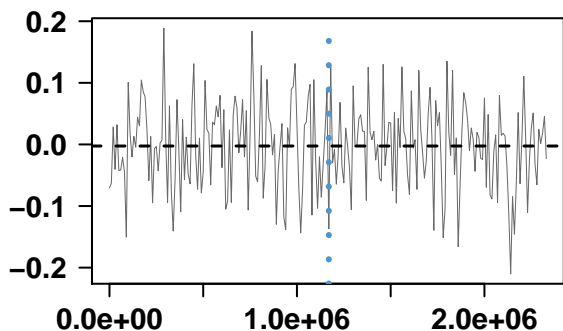
Porphyromonas gingivalis W83



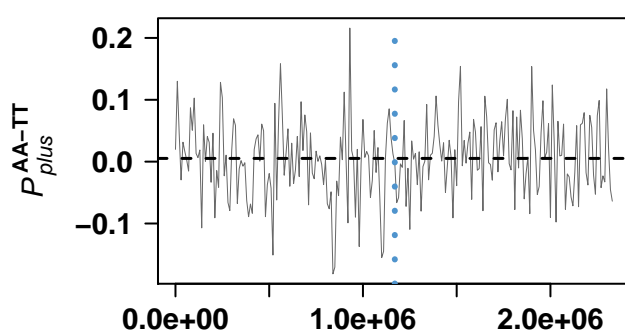
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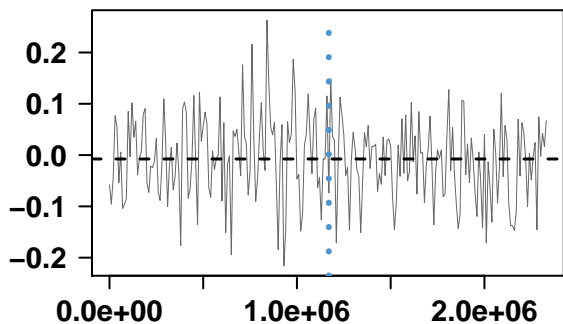
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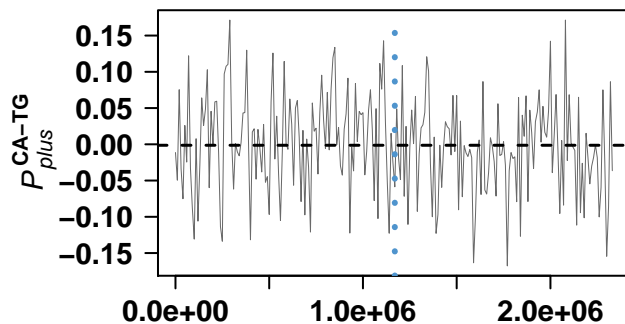
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genome coordinates

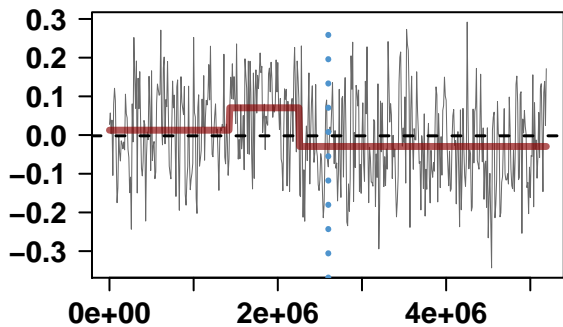


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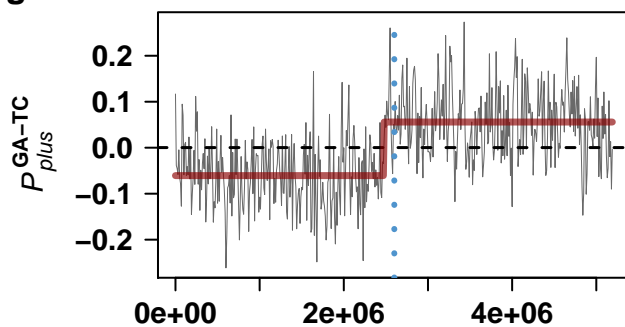


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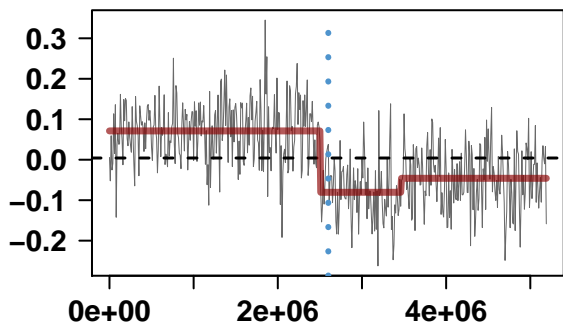
Bacteroides fragilis NCTC 9343



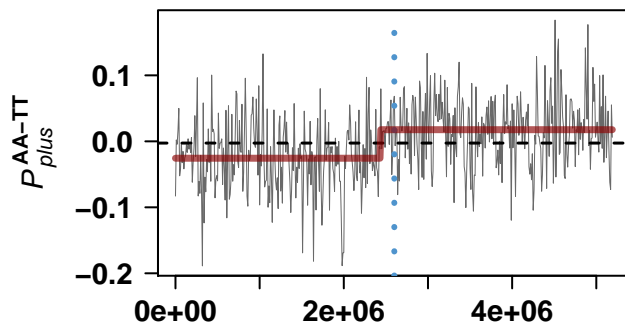
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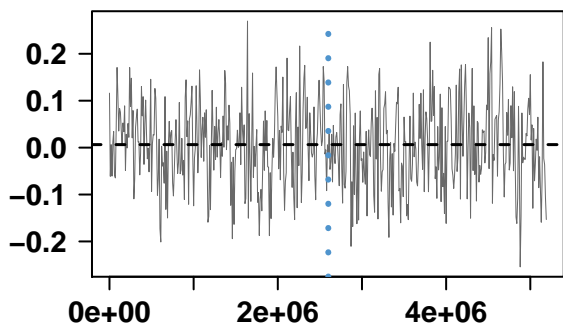
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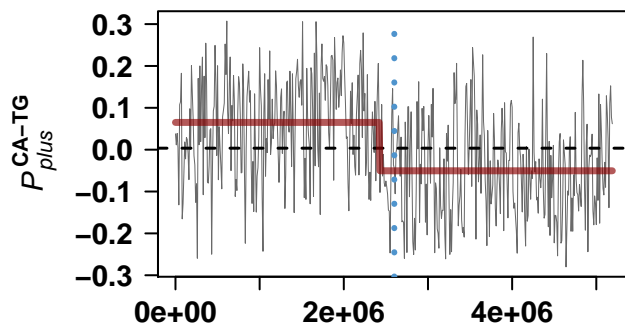
genome coordinates



genome coordinates

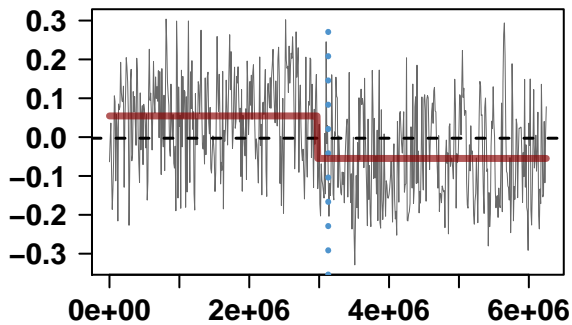


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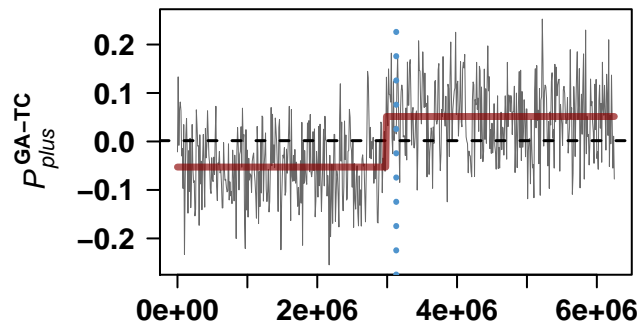


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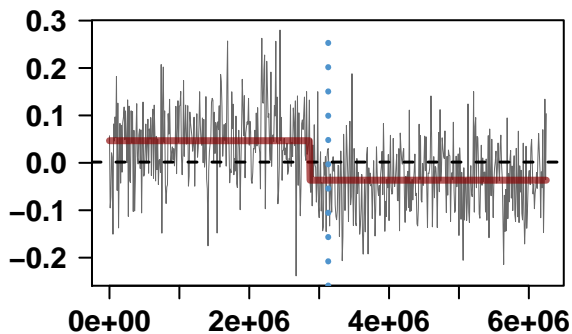
Bacteroides thetaiotaomicron VPI-5482



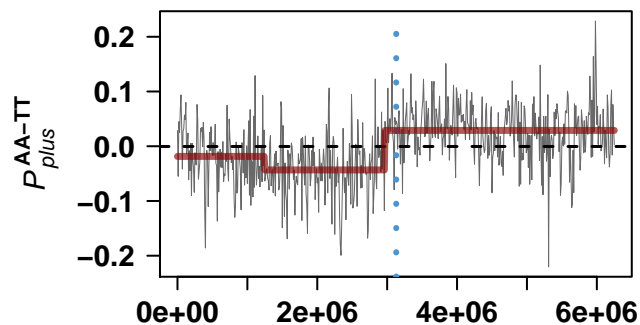
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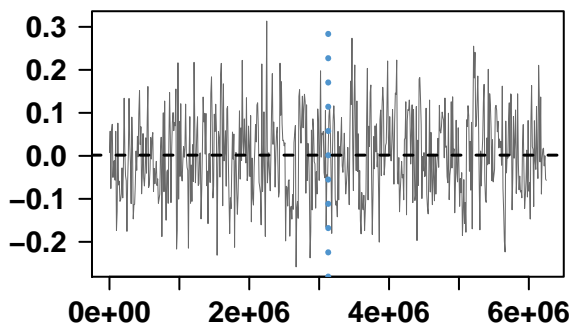
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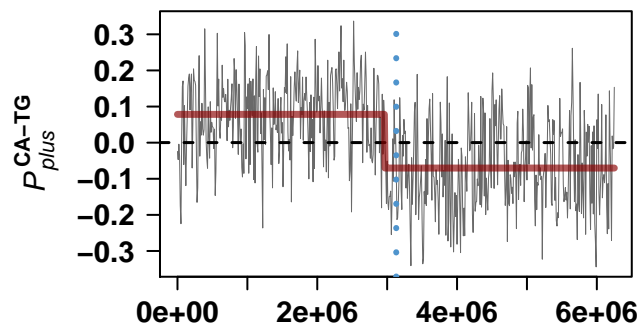
genome coordinates



genome coordinates

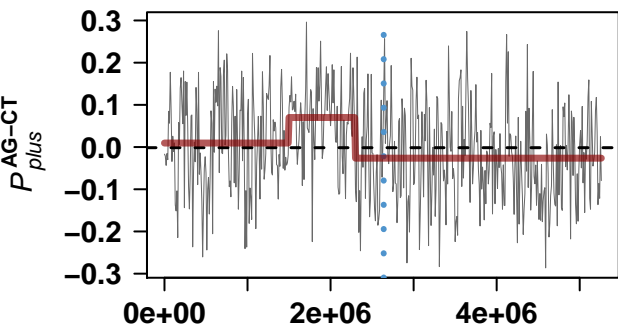


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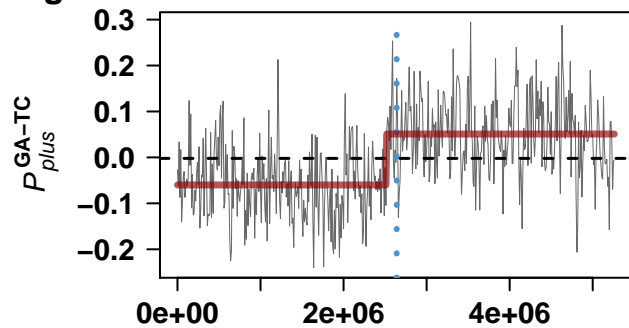


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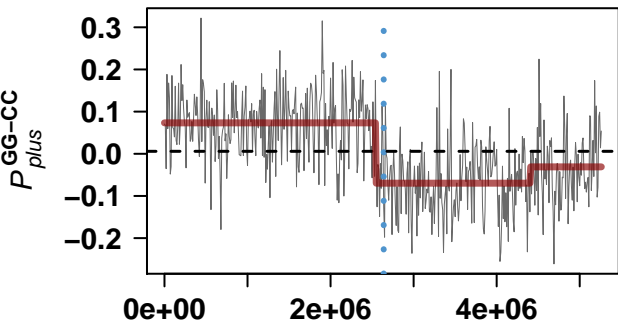
Bacteroides fragilis YCH46



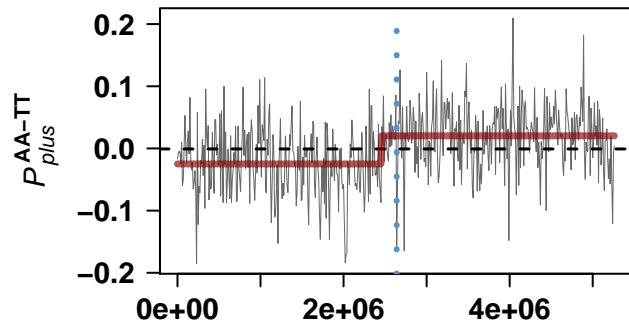
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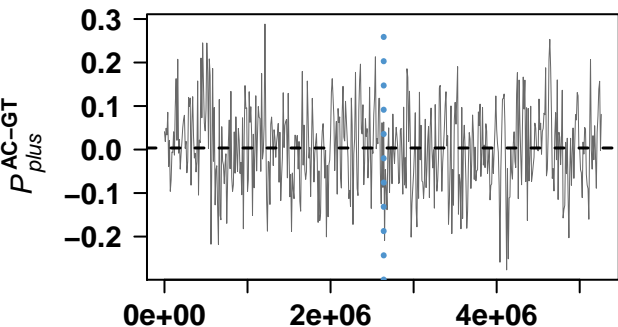
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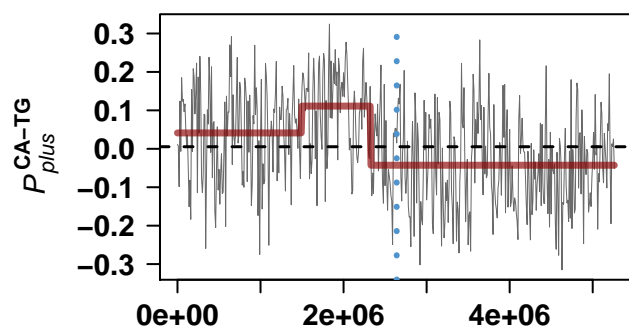
genome coordinates



genome coordinates

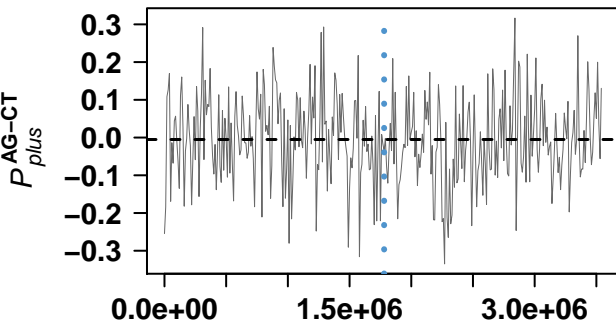


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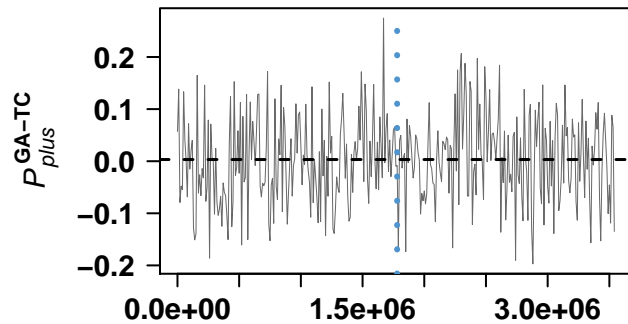


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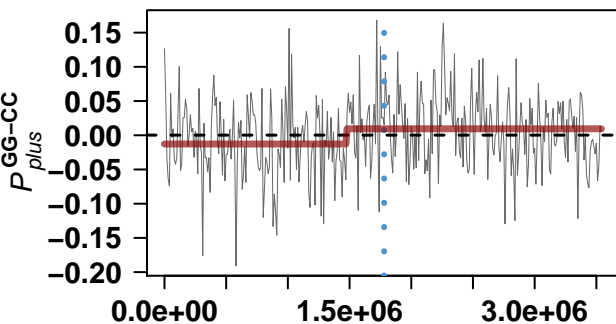
Salinibacter ruber DSM 13855



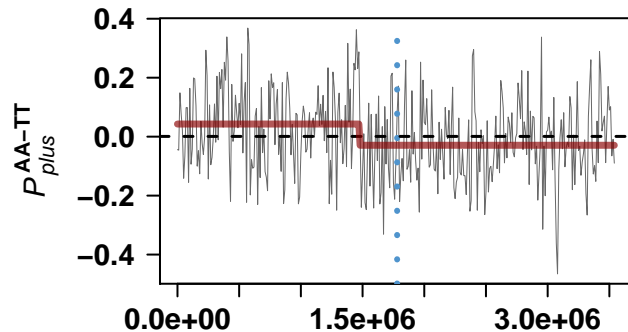
genome coordinates



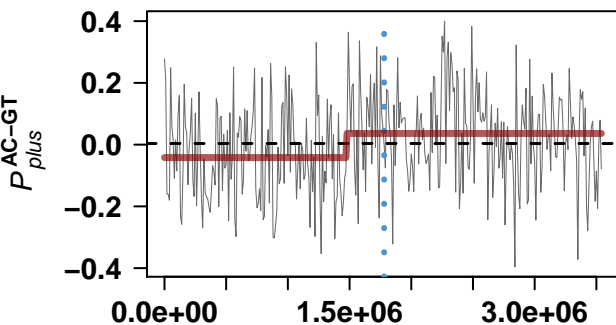
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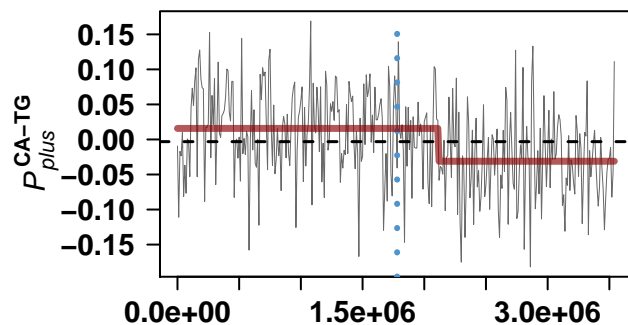
genome coordinates



genome coordinates

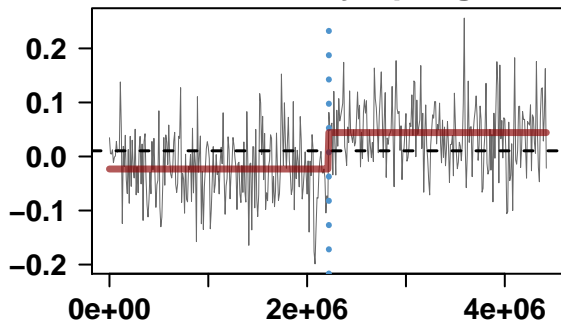


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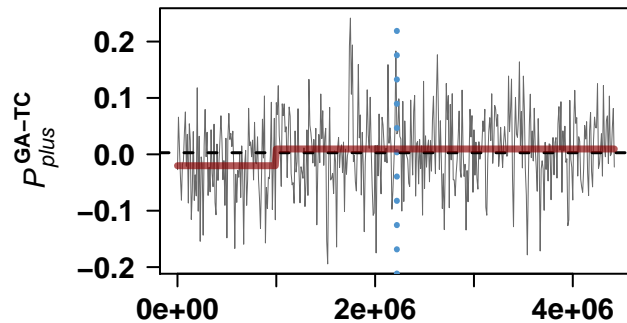


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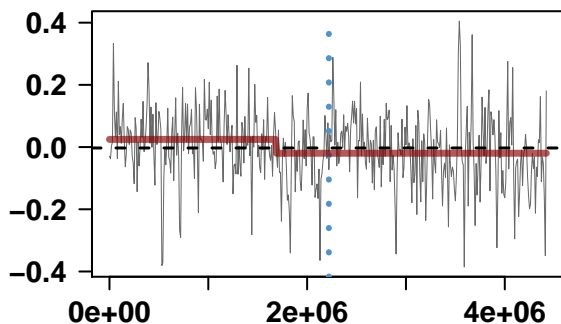
Cytophaga hutchinsonii ATCC 33406



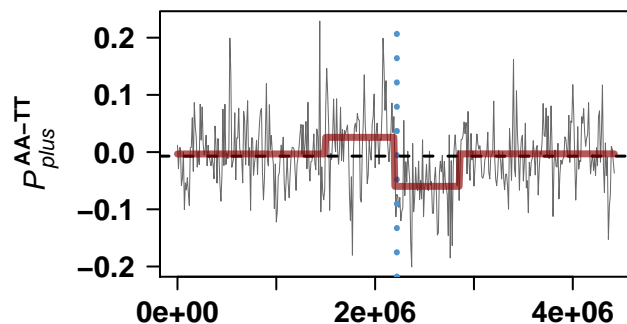
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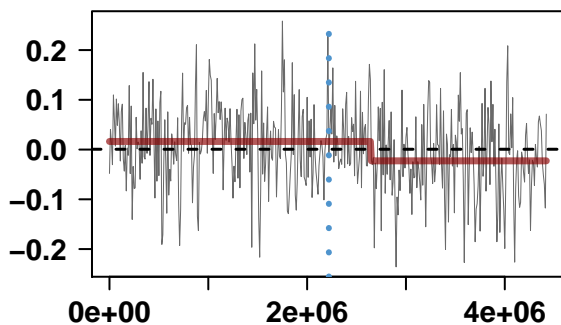
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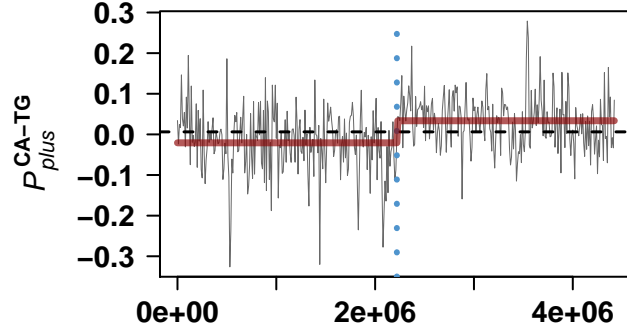
genome coordinates



genome coordinates

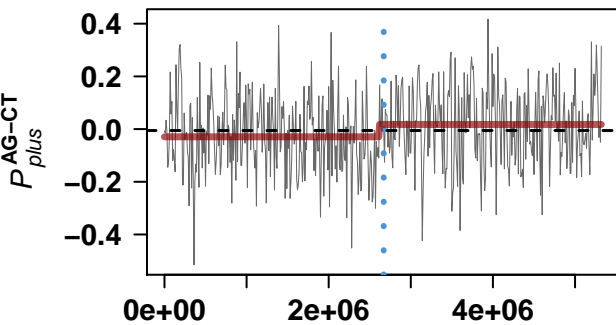


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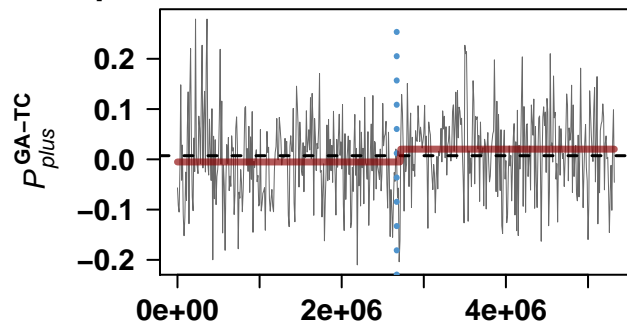


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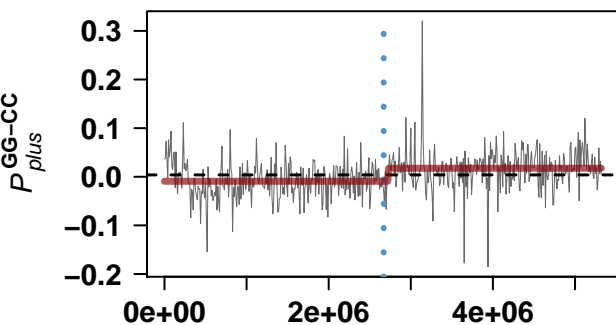
Bordetella bronchiseptica RB50



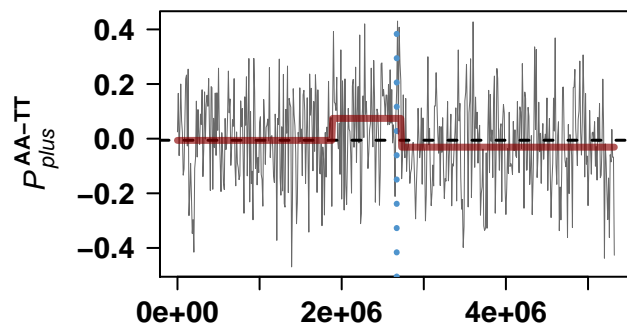
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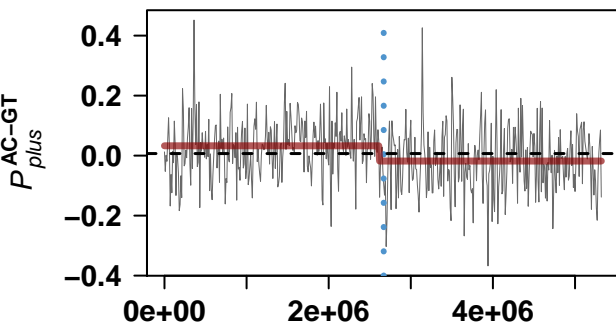
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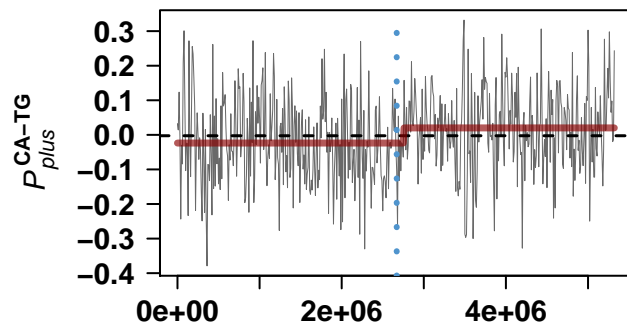
genome coordinates



genome coordinates

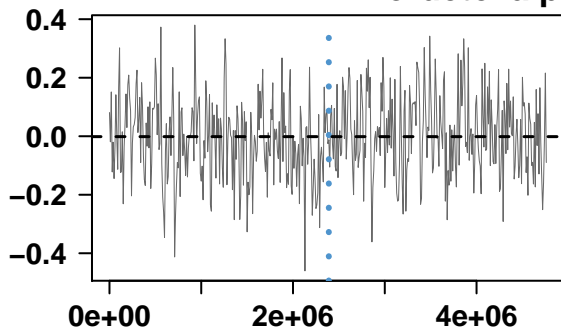


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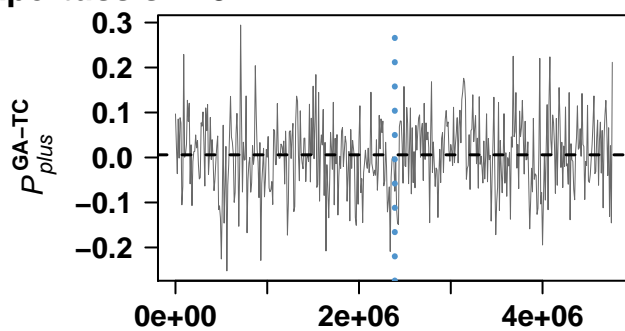


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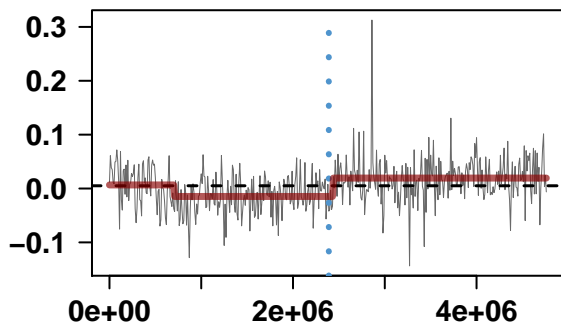
Bordetella parapertussis 12822



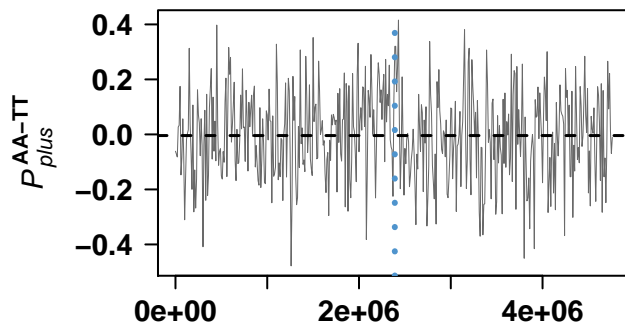
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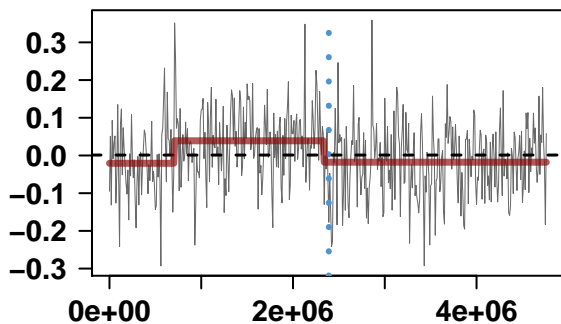
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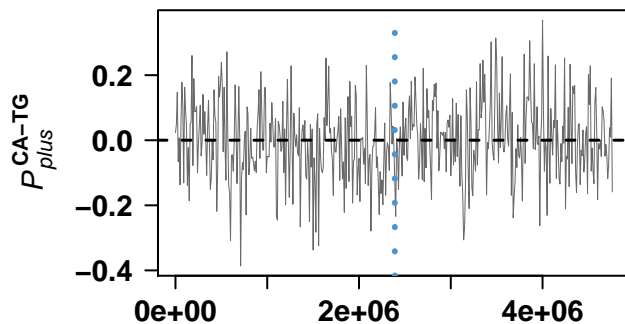
genome coordinates



genome coordinates

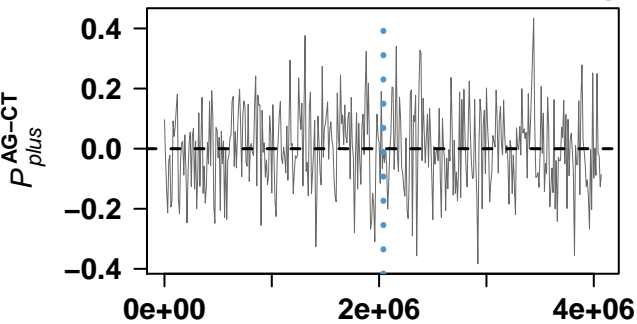


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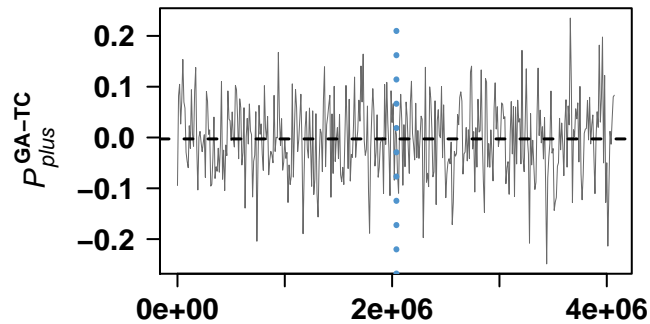


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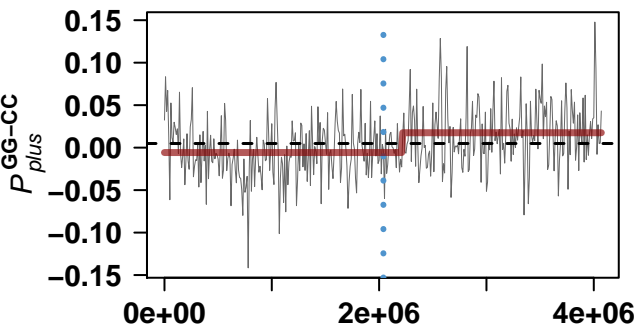
Bordetella pertussis Tohama I



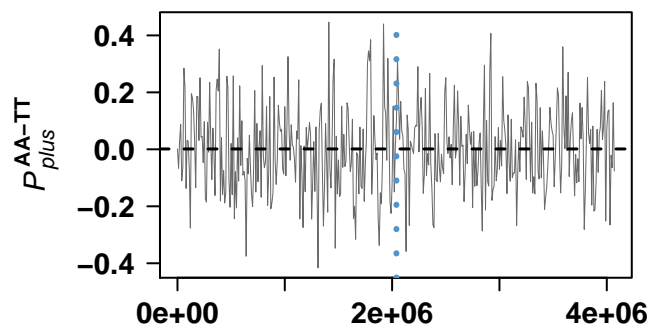
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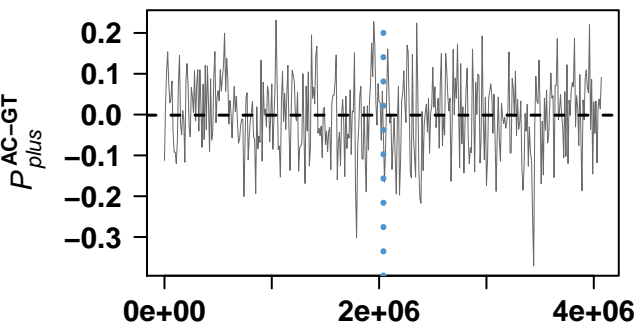
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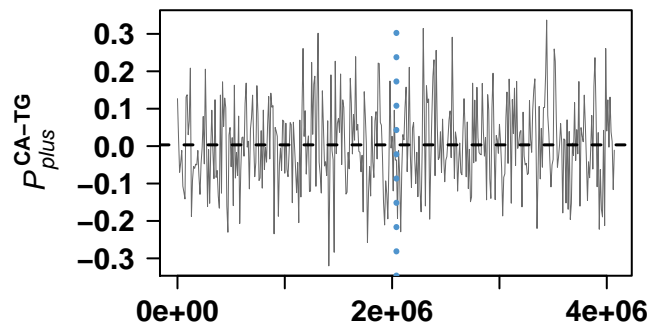
genome coordinates



genome coordinates

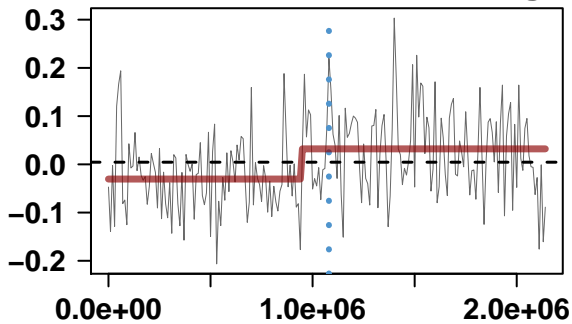


genome coordinates

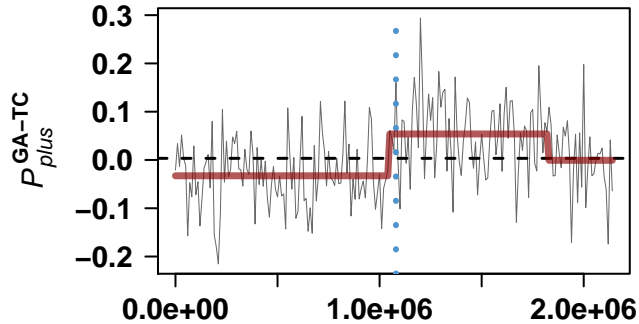


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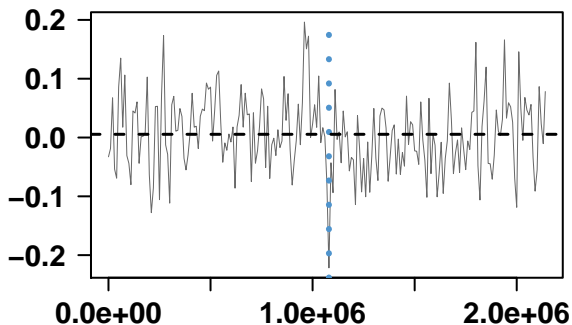
Neisseria gonorrhoeae FA 1090



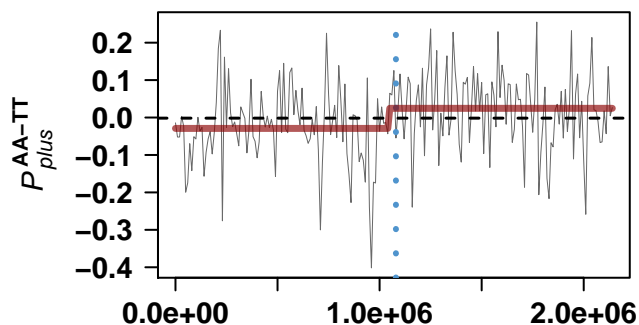
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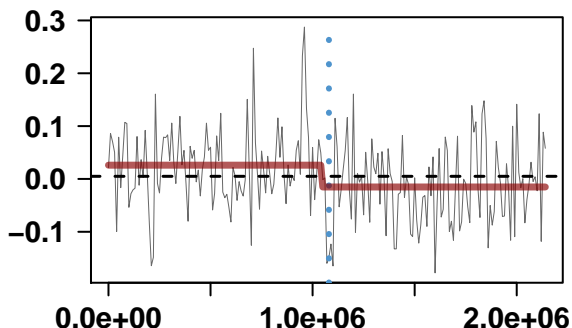
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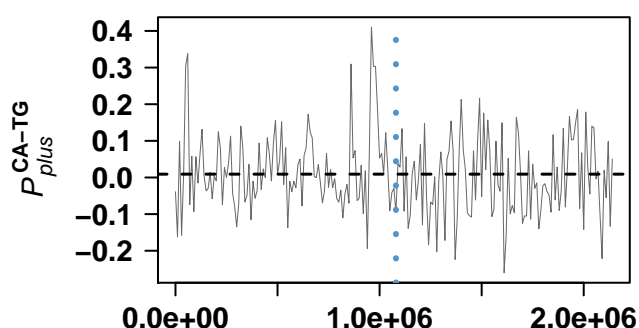
genome coordinates



genome coordinates

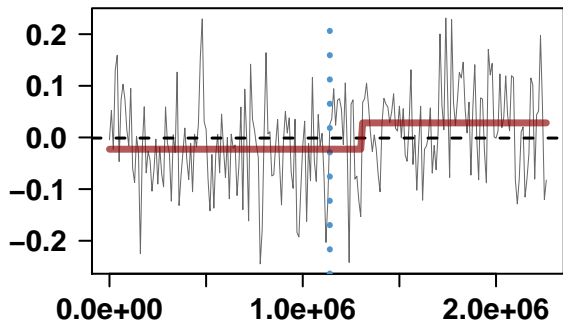


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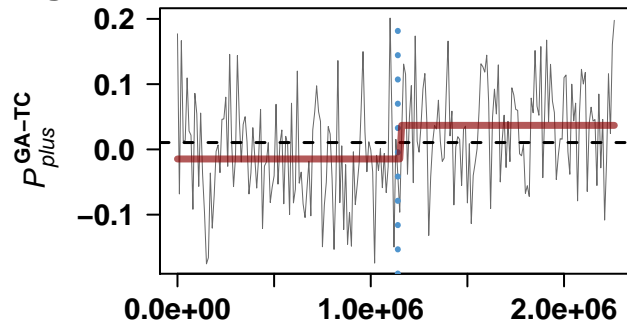


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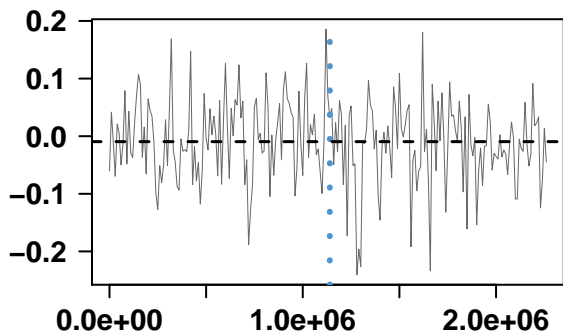
Neisseria meningitidis MC58



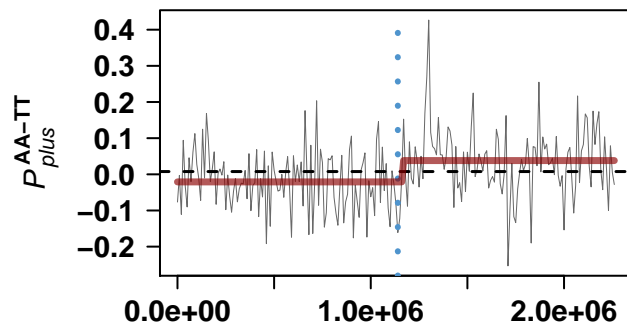
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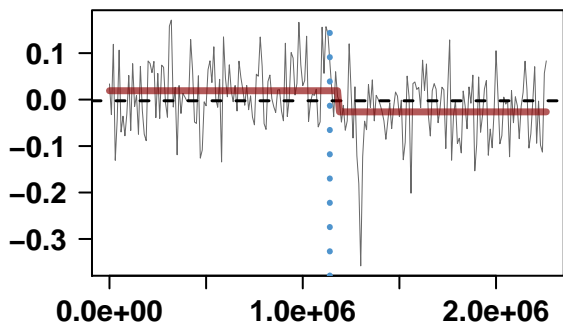
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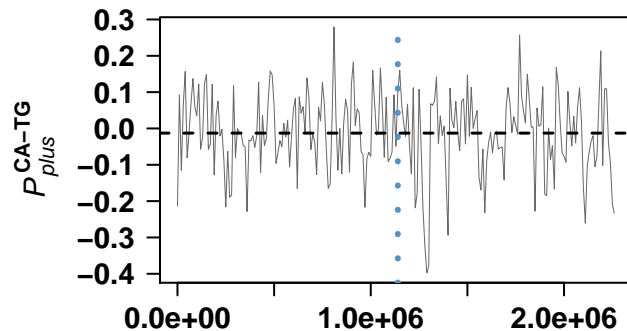
genome coordinates



genome coordinates

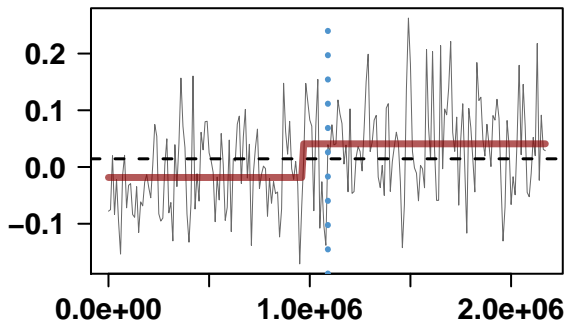


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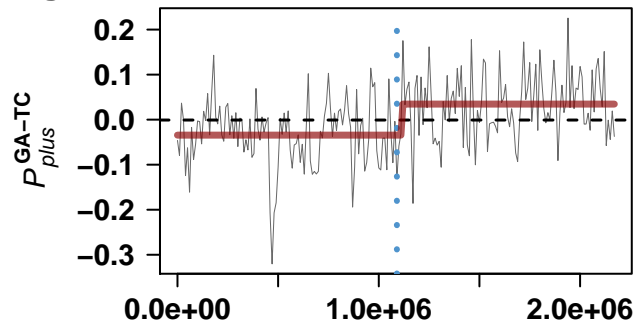


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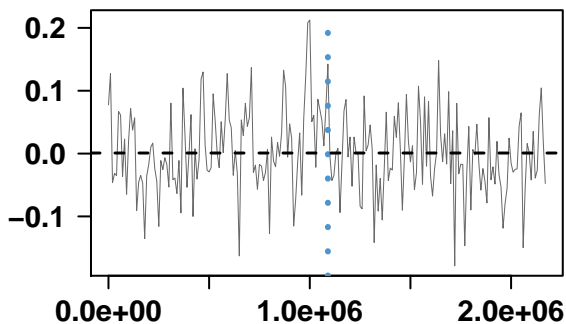
Neisseria meningitidis Z2491



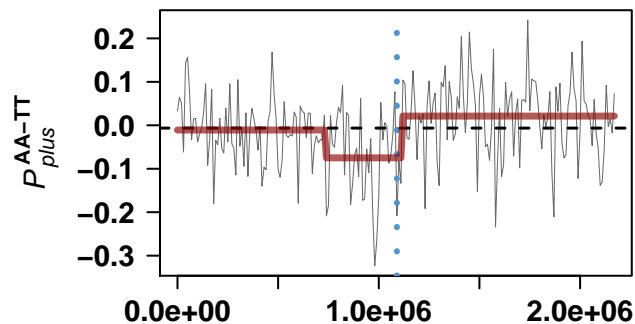
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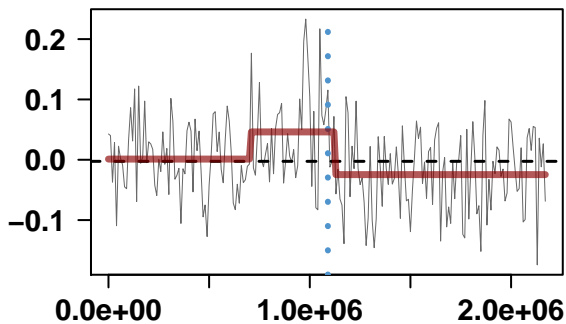
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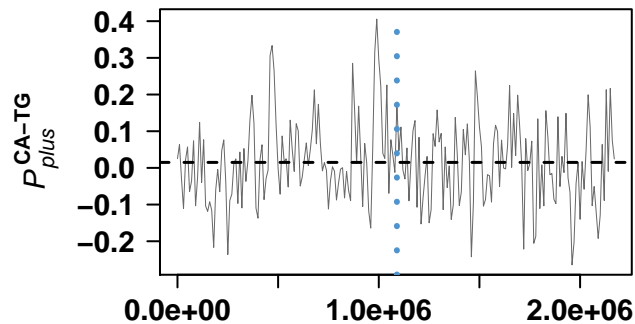
genome coordinates



genome coordinates

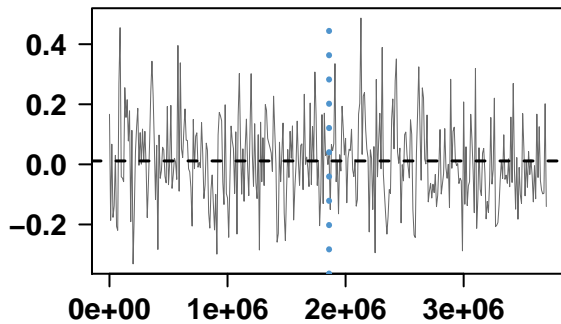


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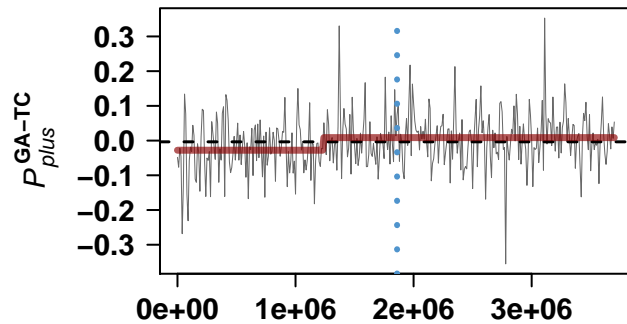


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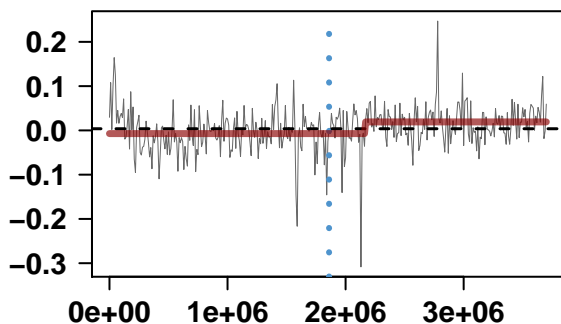
Ralstonia solanacearum GMI1000



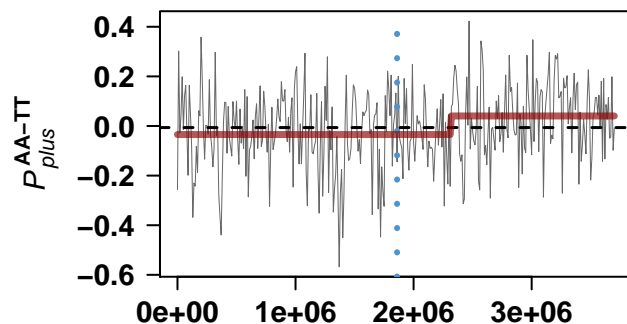
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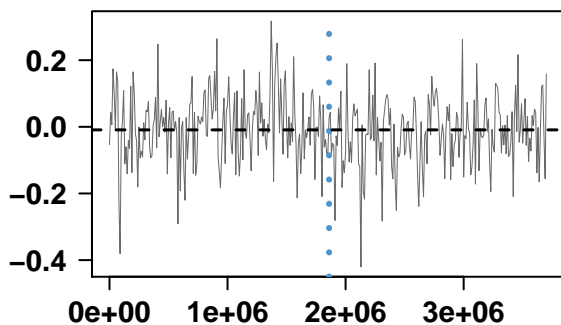
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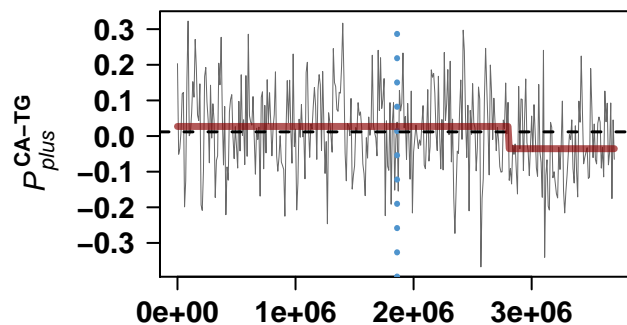
genome coordinates



genome coordinates

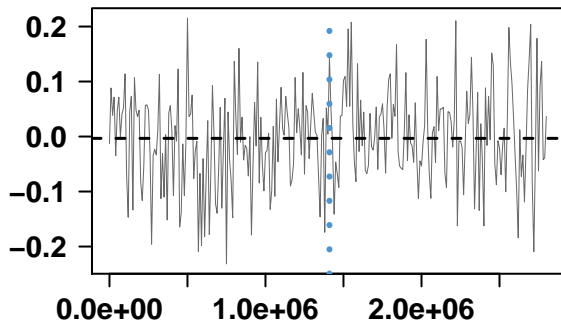


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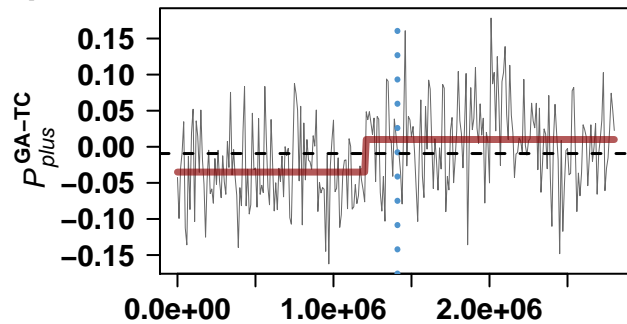


genome coordinates

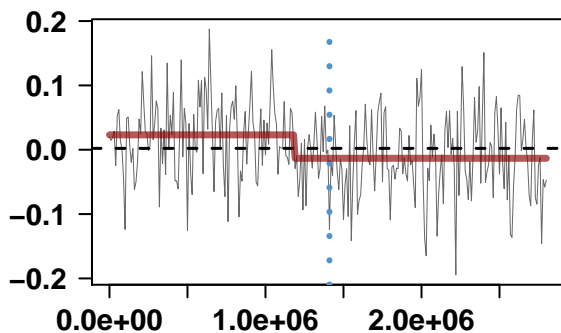
Nitrosomonas europaea ATCC 19718



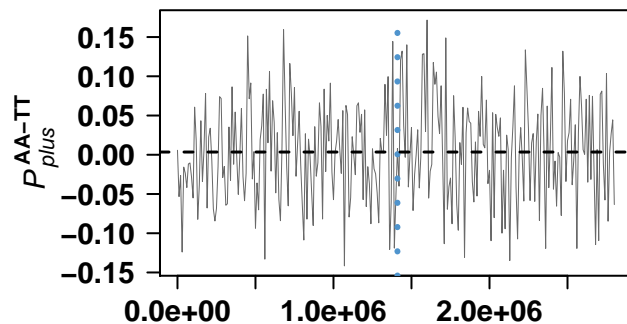
genome coordinates



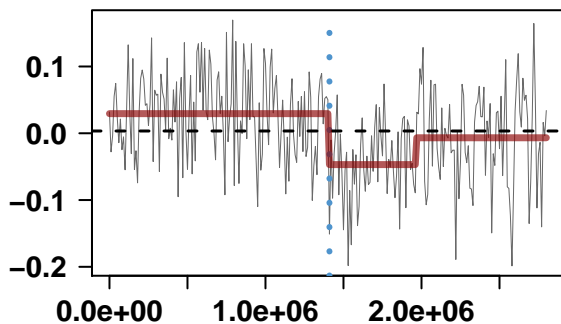
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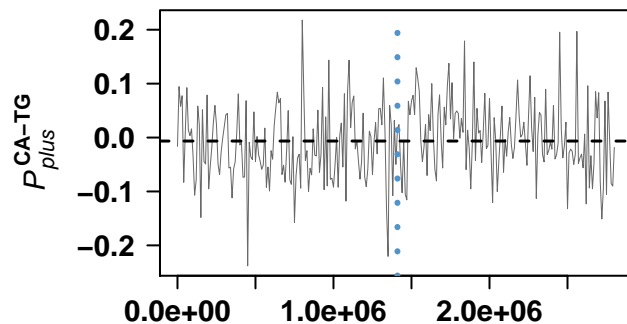
genome coordinates



genome coordinates

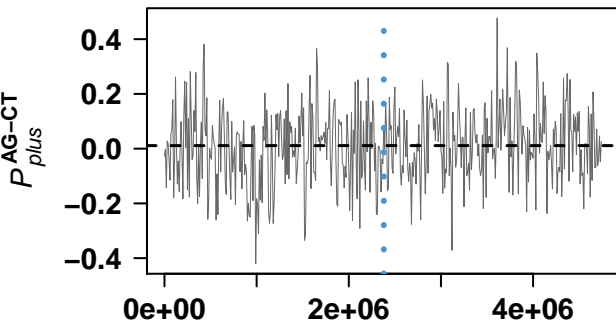


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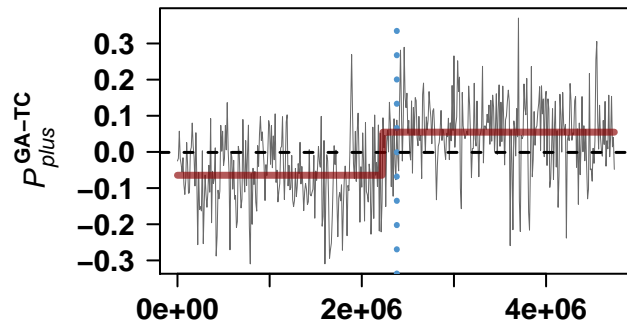


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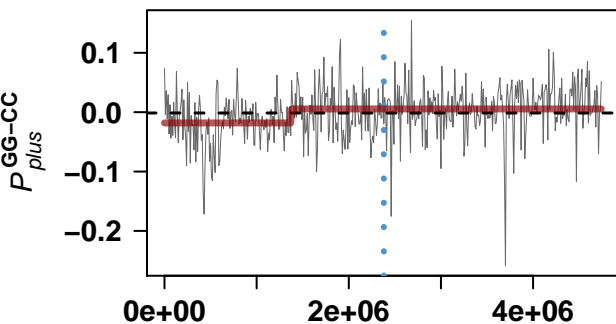
Chromobacterium violaceum ATCC 12472



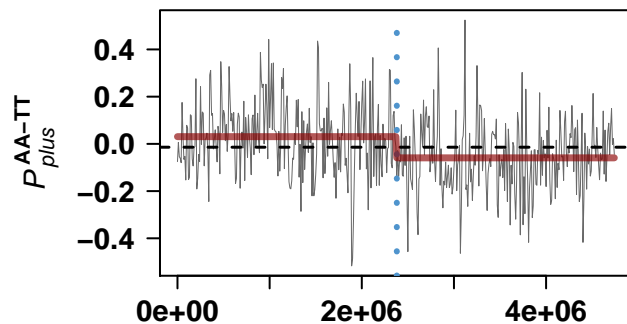
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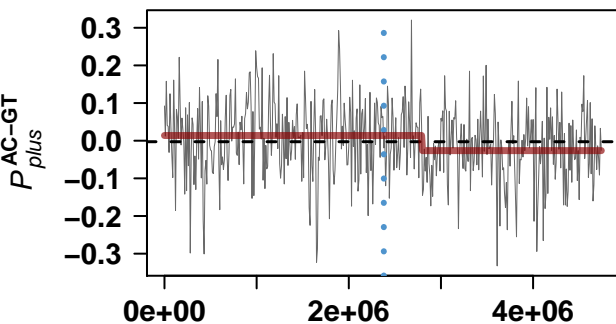
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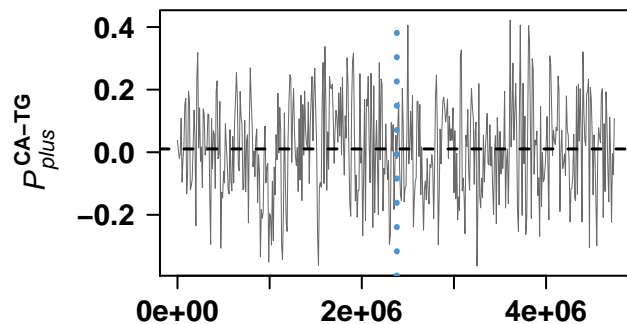
genome coordinates



genome coordinates

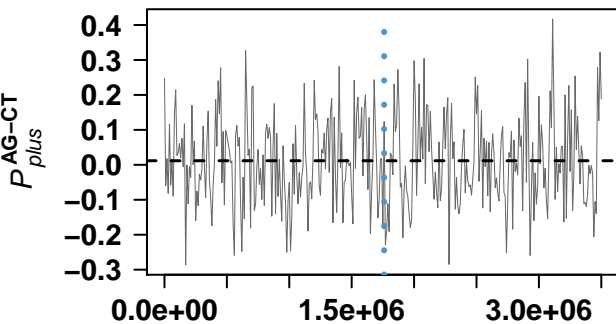


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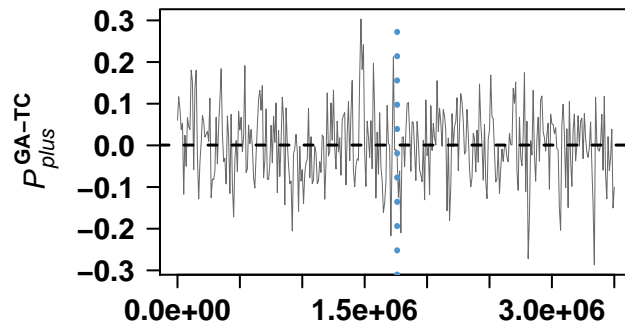


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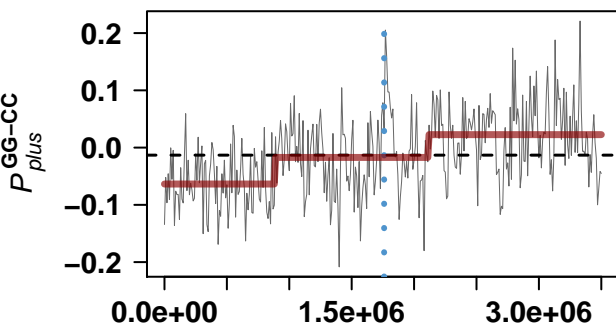
Burkholderia mallei ATCC 23344



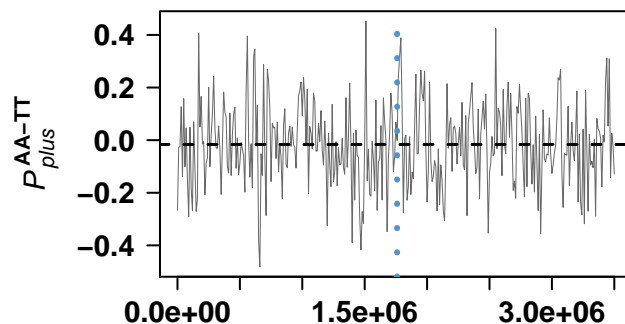
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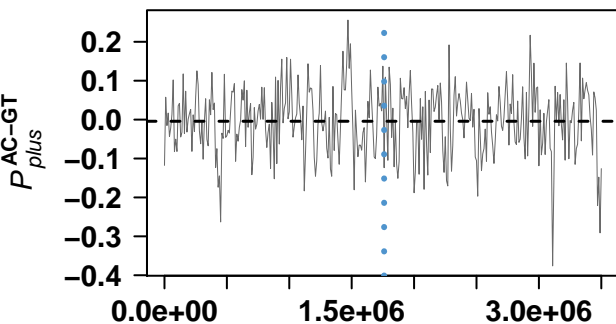
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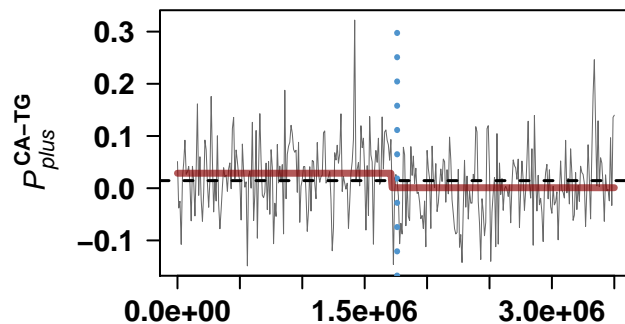
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genome coordinates

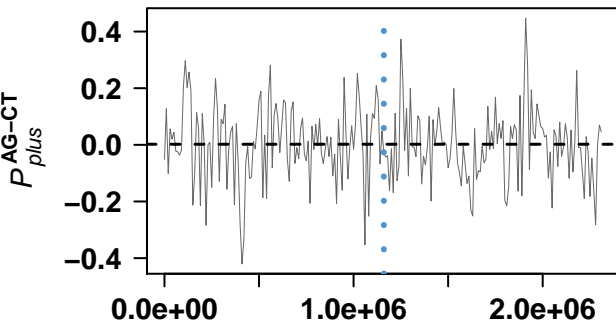


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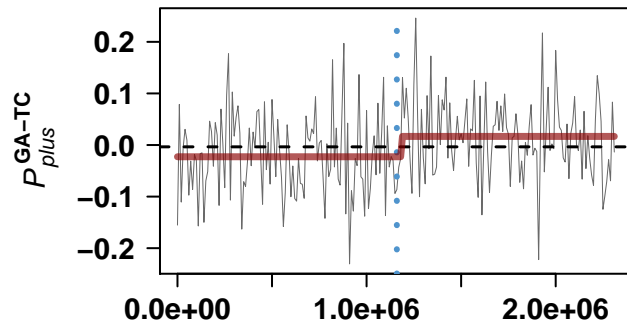


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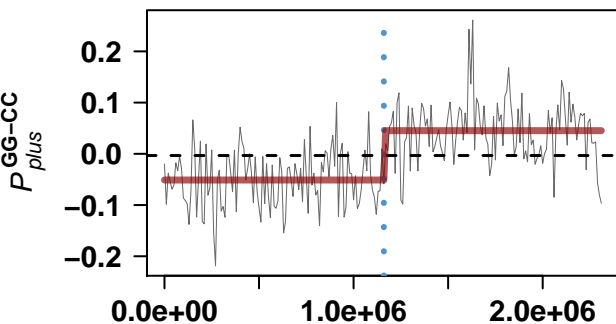
Burkholderia mallei ATCC 23344



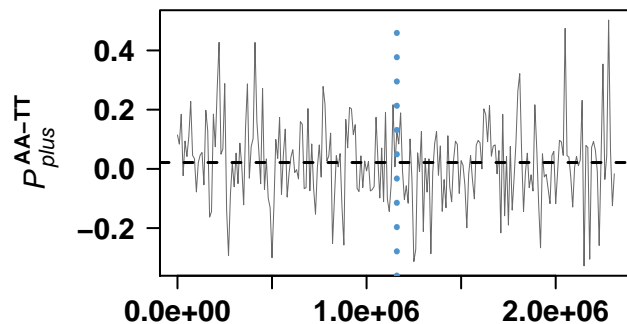
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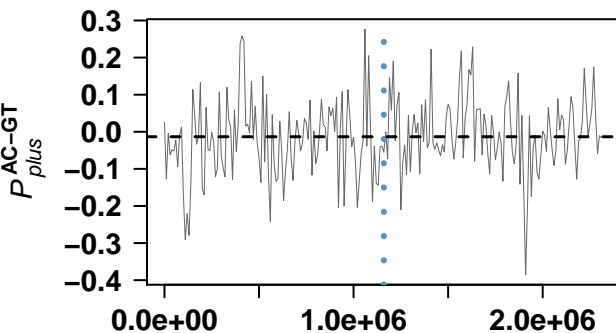
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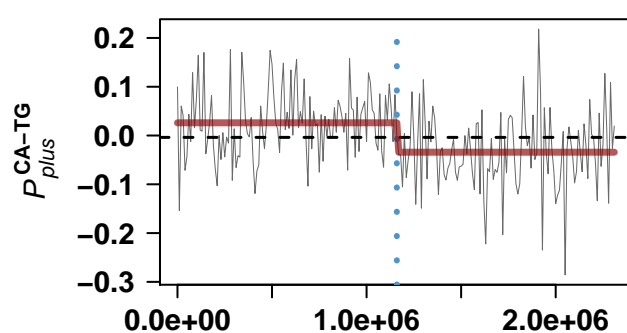
genome coordinates



genome coordinates

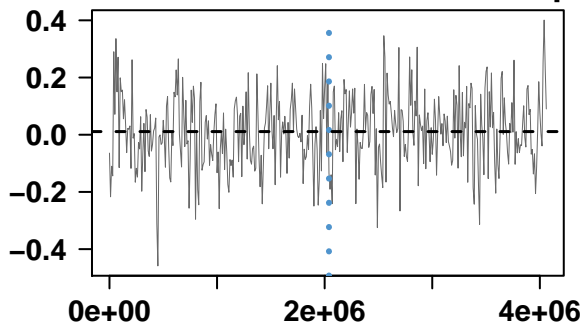


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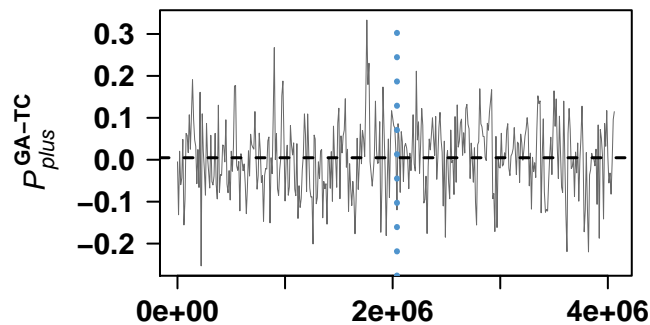


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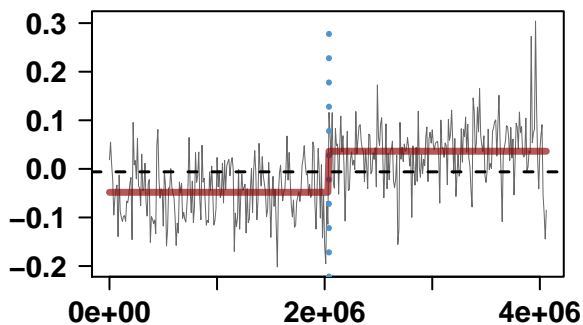
Burkholderia pseudomallei K96243



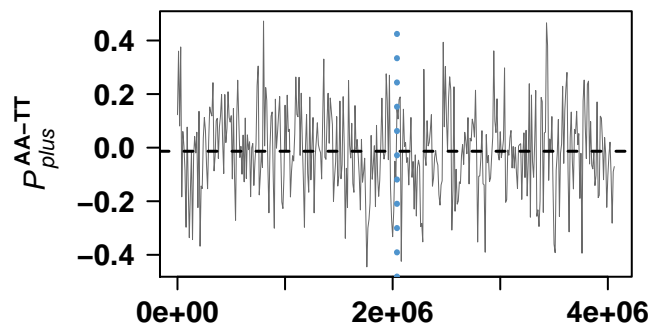
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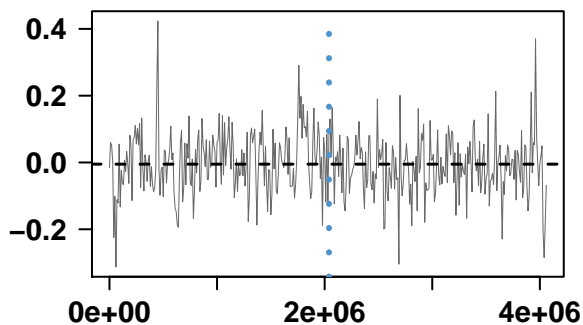
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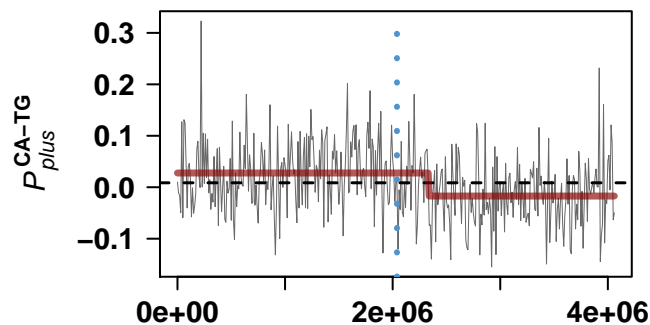
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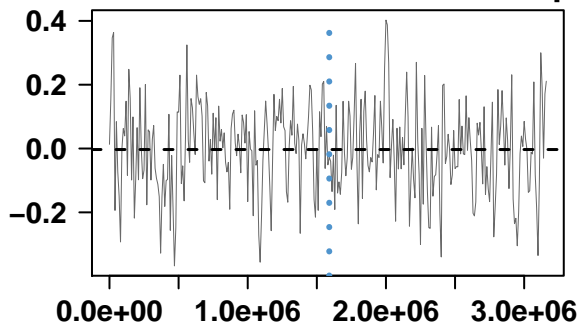


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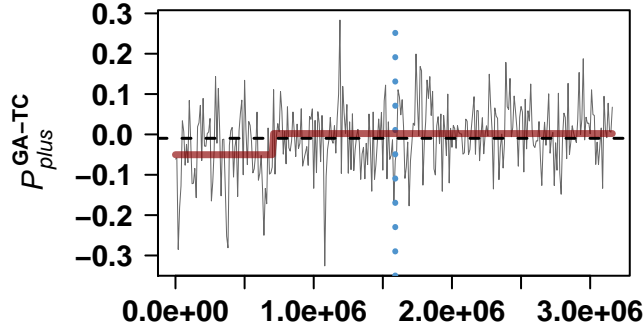


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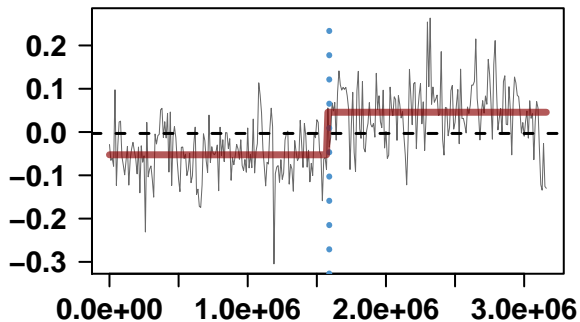
Burkholderia pseudomallei K96243



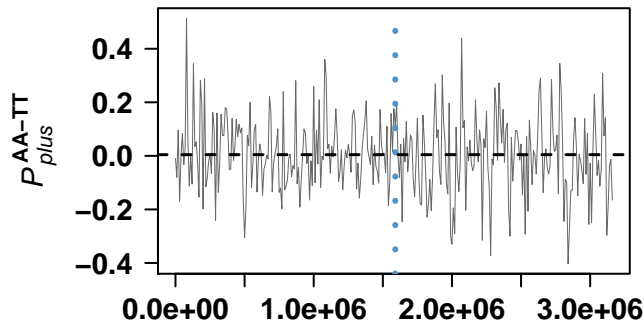
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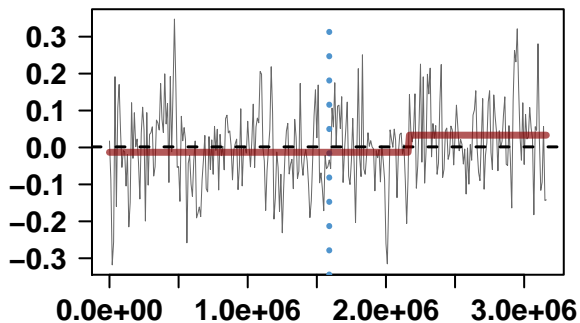
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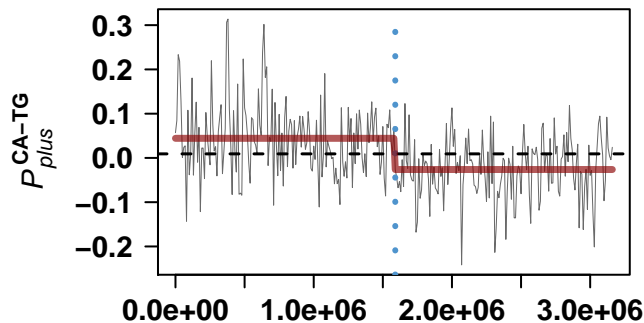
genome coordinates



genome coordinates

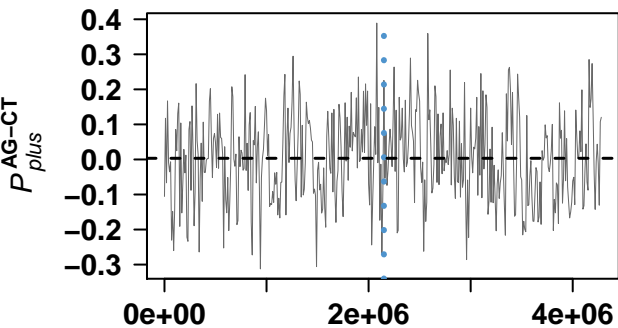


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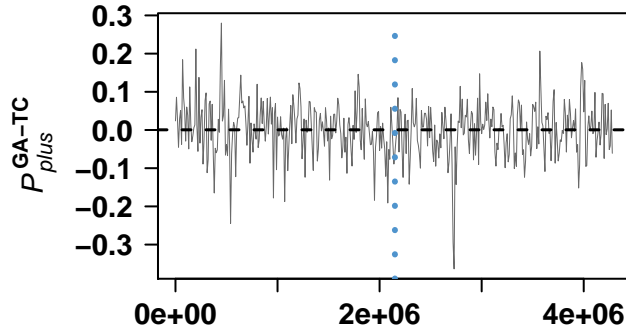


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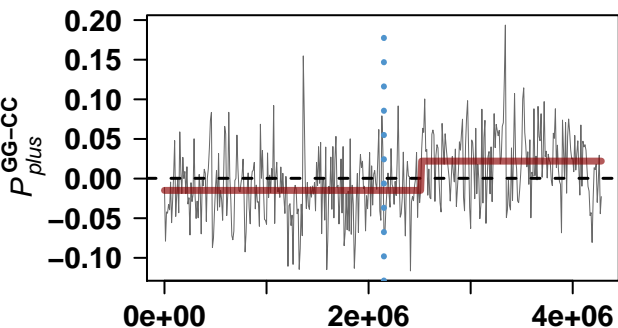
Aromatoleum aromaticum EbN1



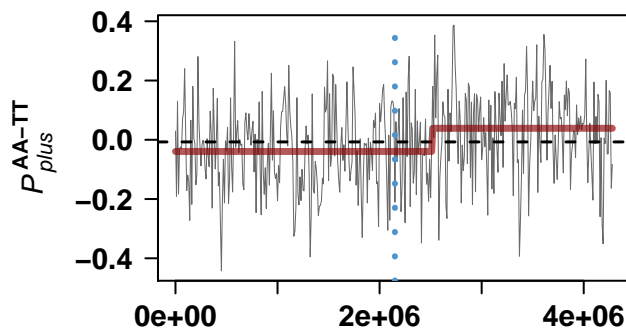
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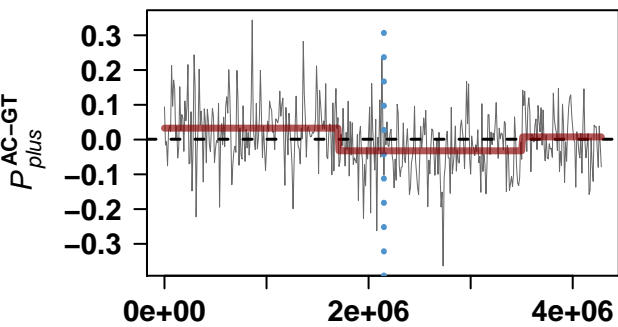
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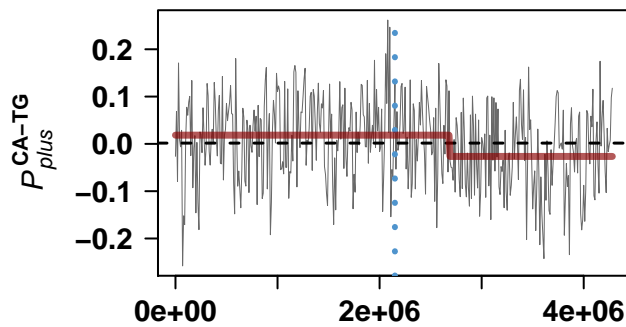
genome coordinates



genome coordinates

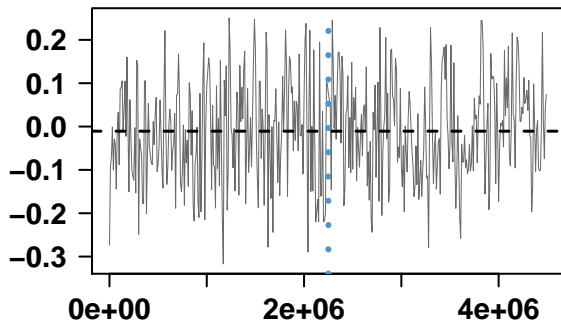


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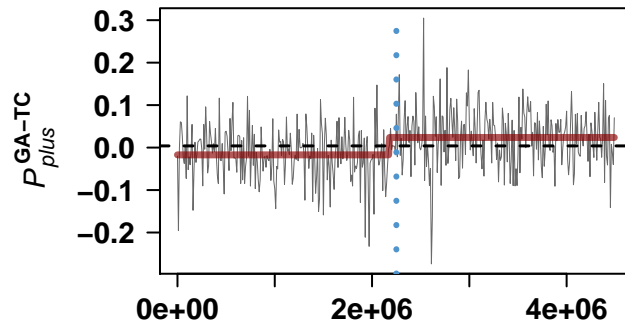


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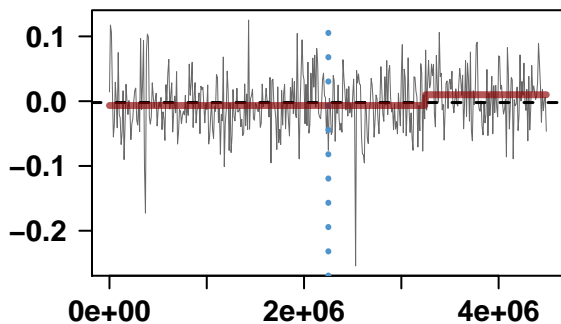
Dechloromonas aromatica RCB



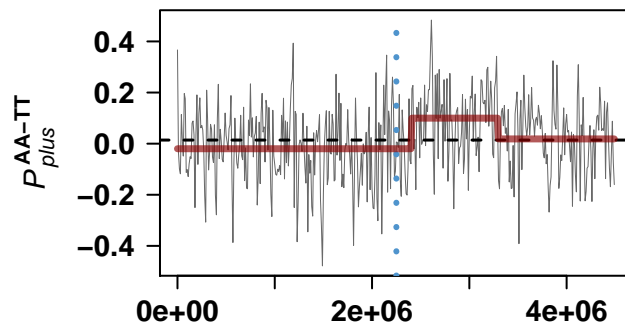
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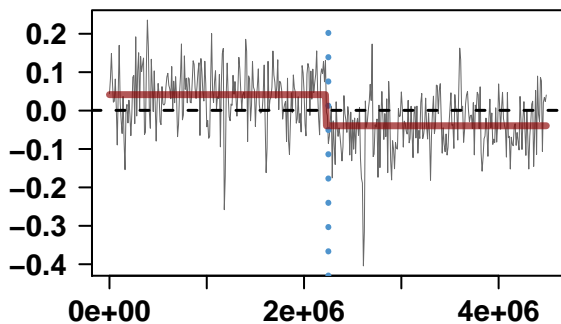
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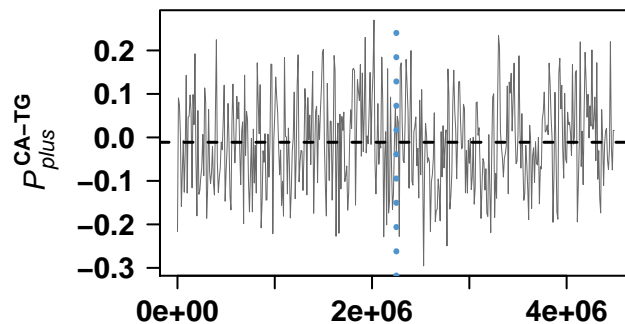
genome coordinates



genome coordinates

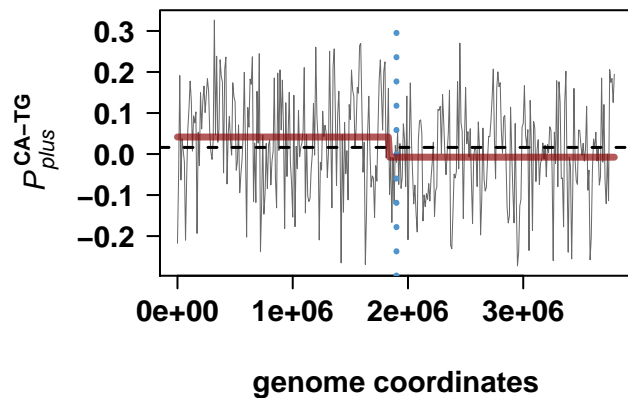
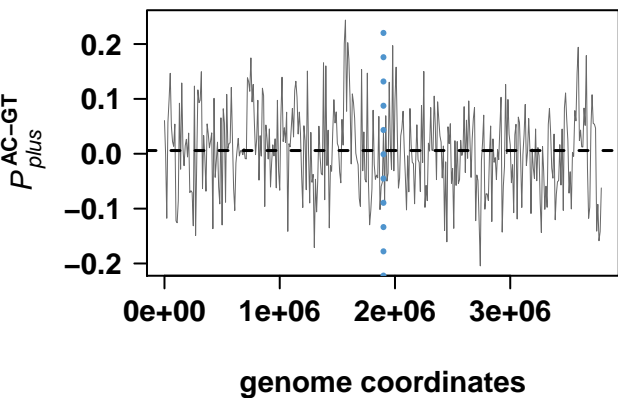
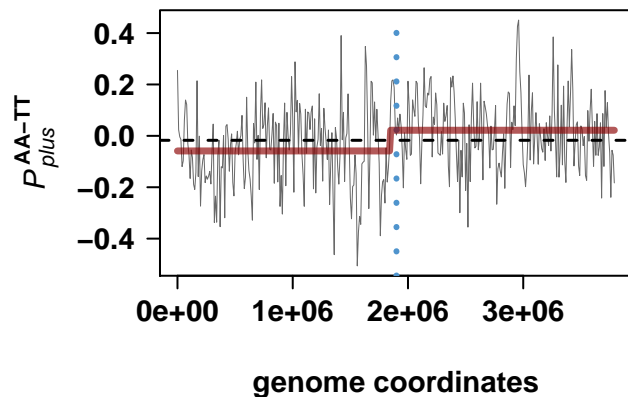
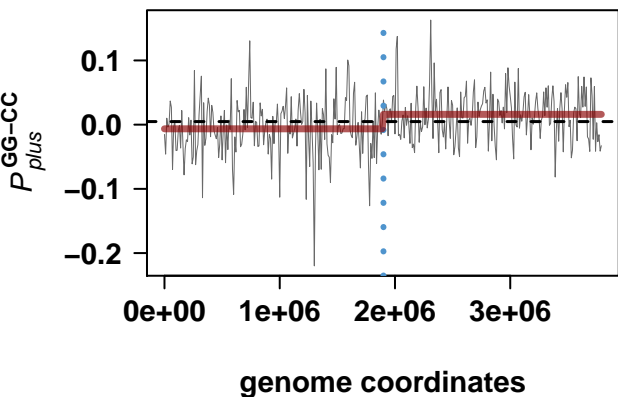
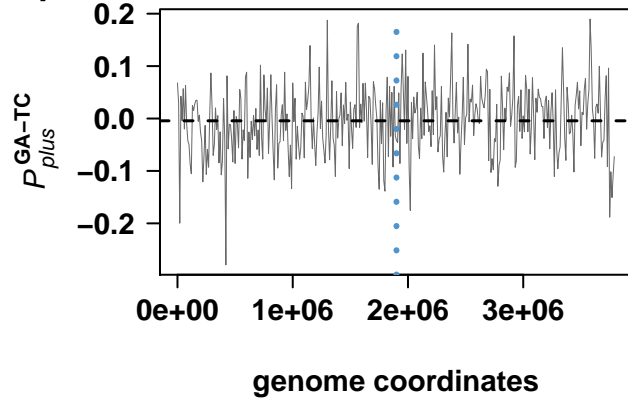
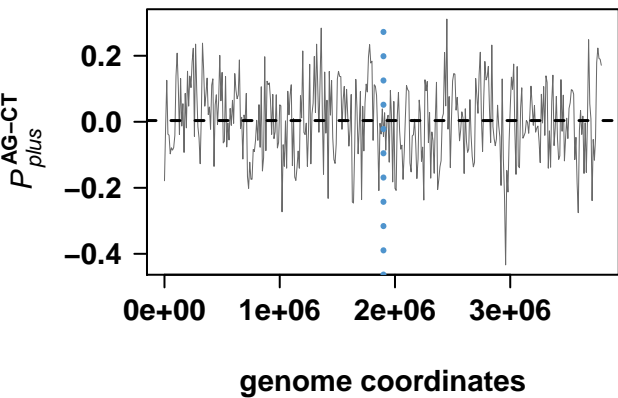


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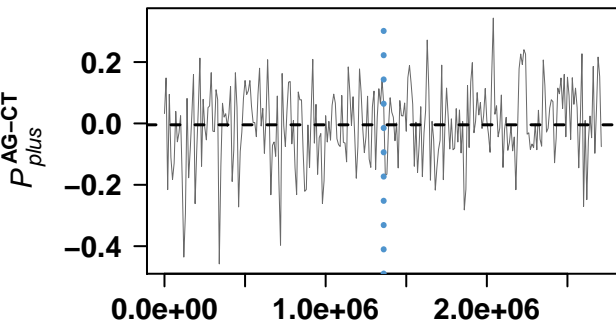


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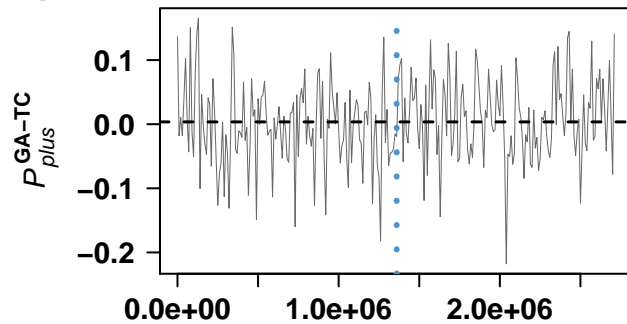
Ralstonia eutropha JMP134



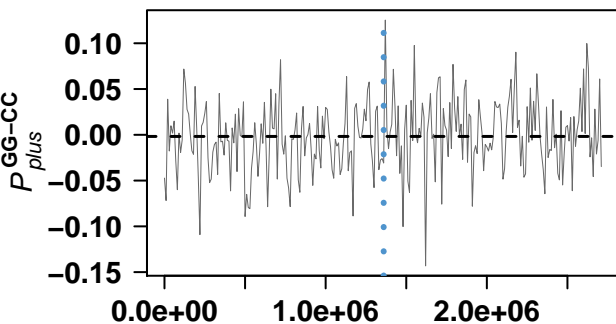
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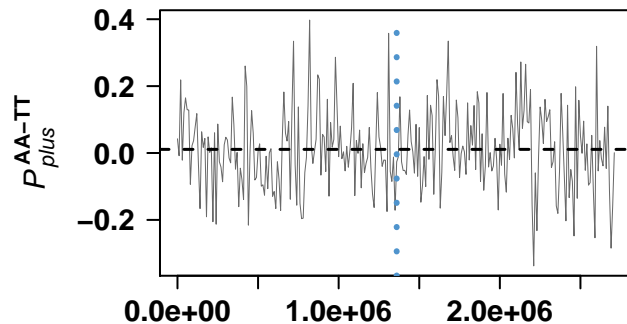
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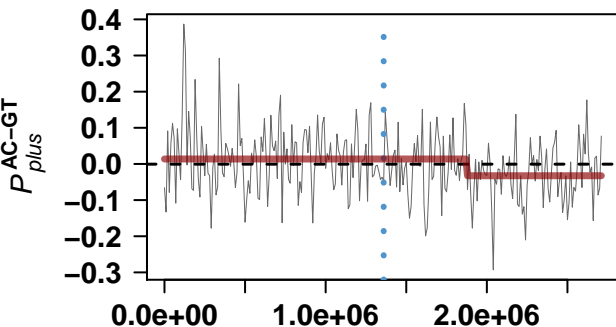
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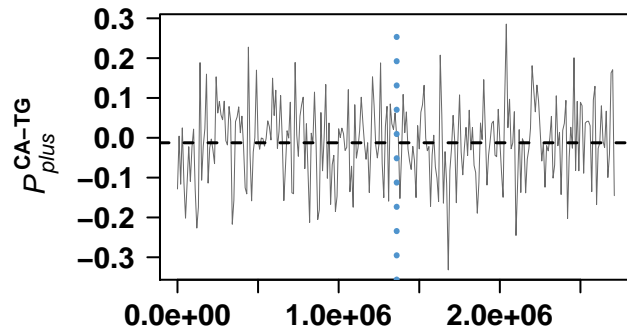
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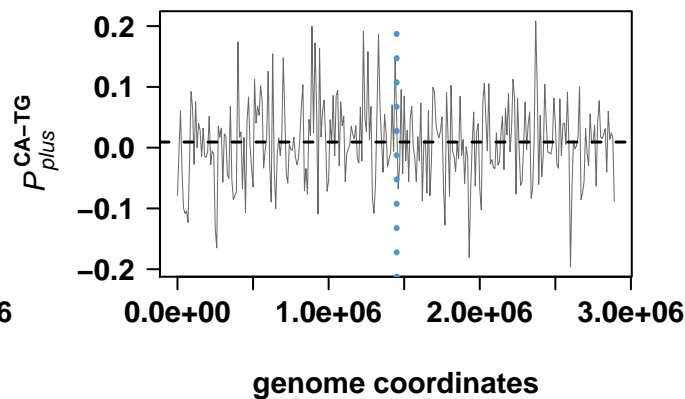
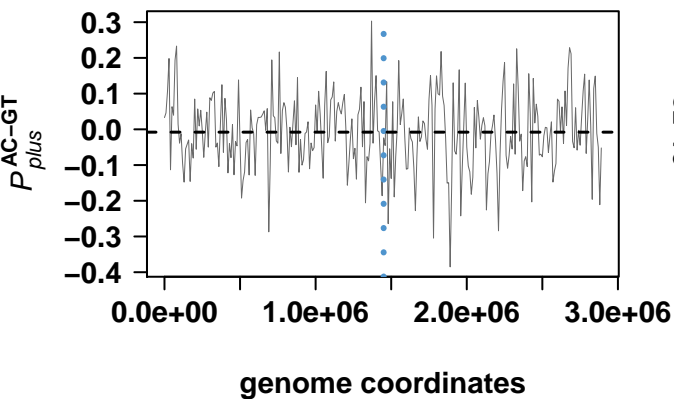
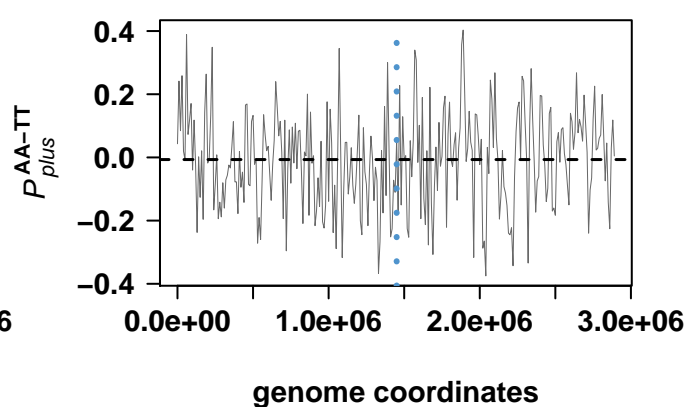
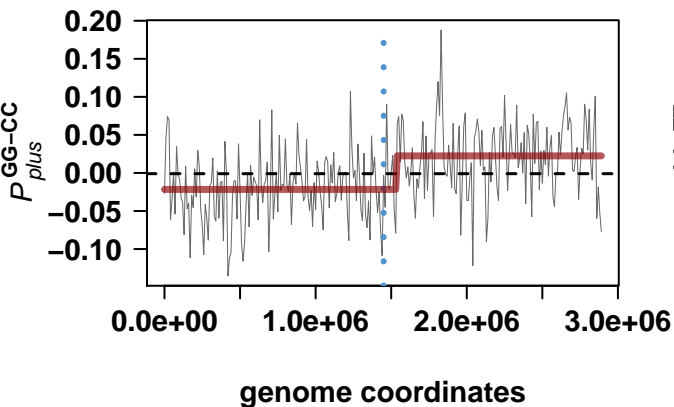
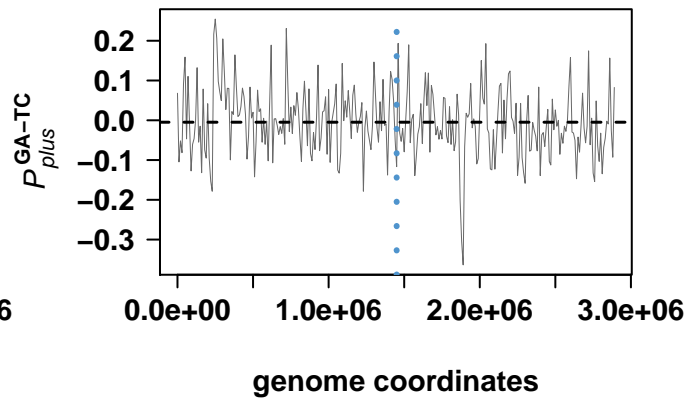
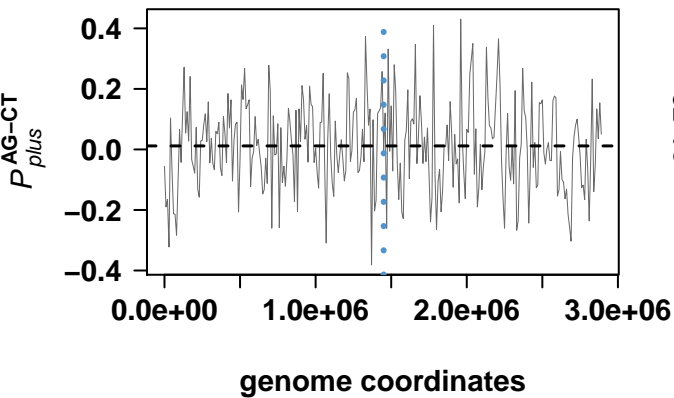


genome coordinates

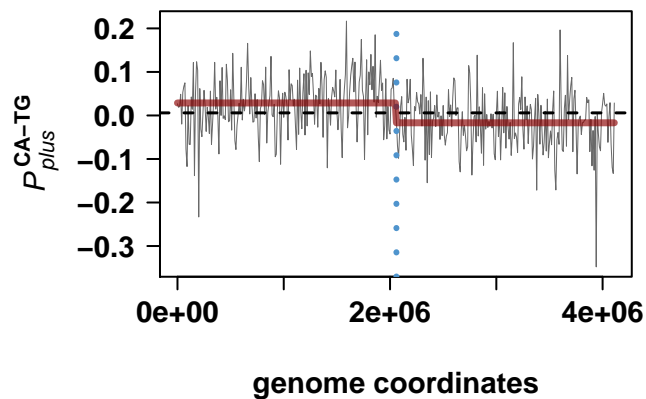
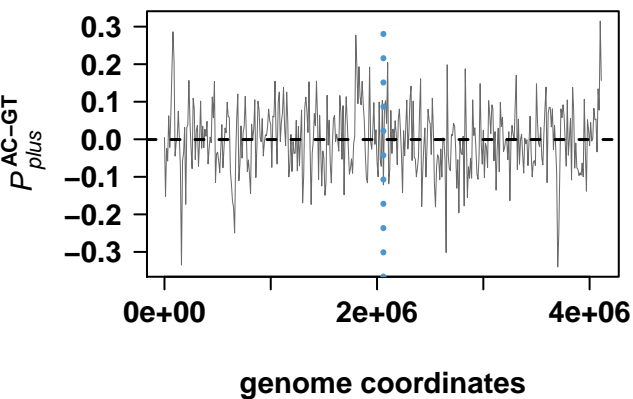
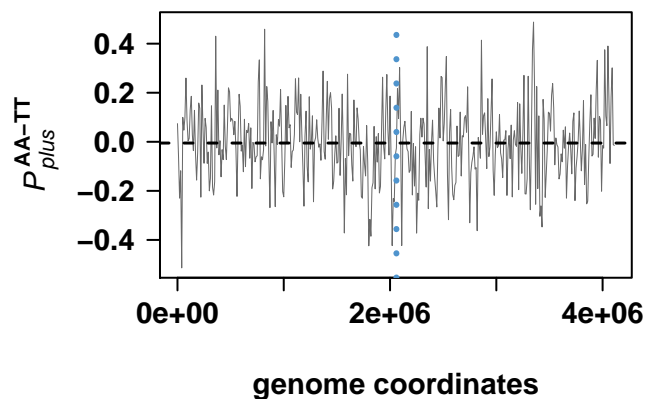
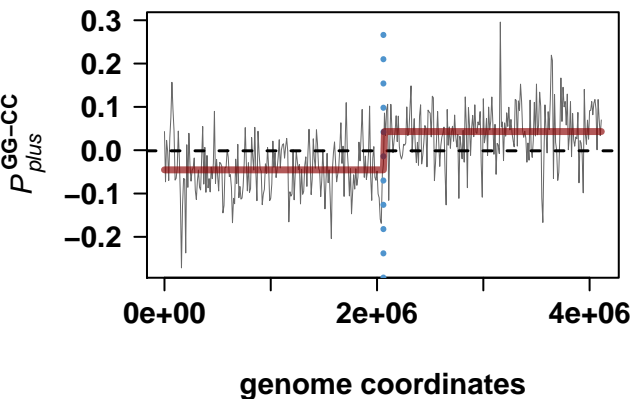
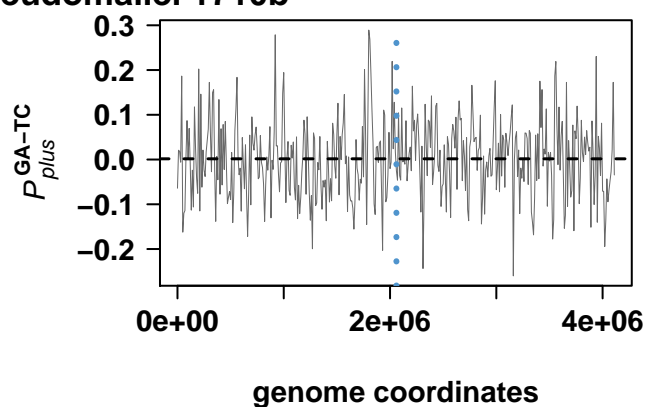
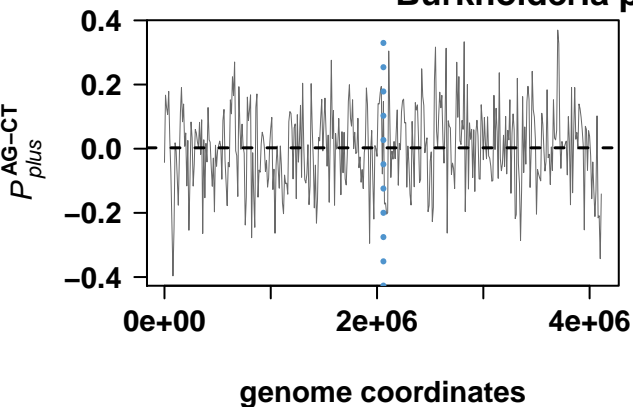


genome coordinates

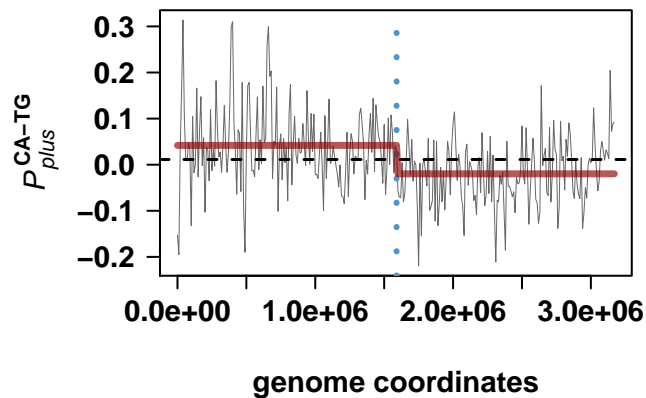
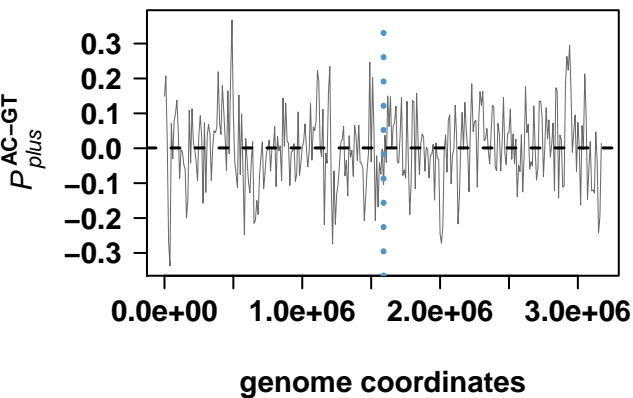
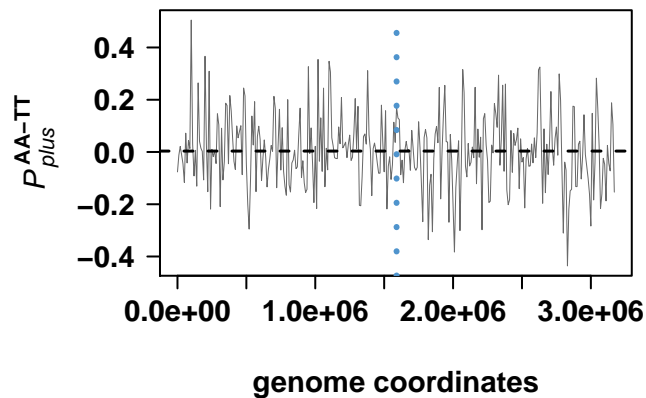
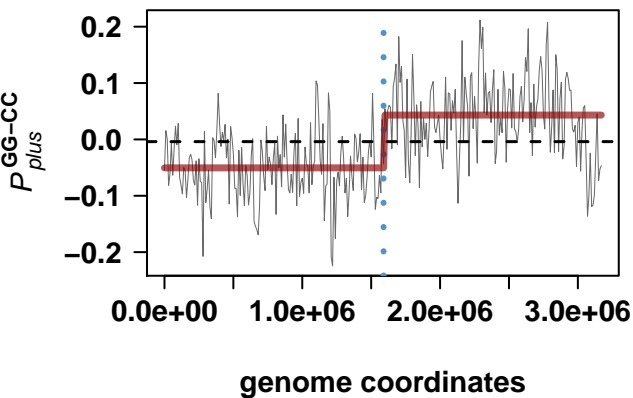
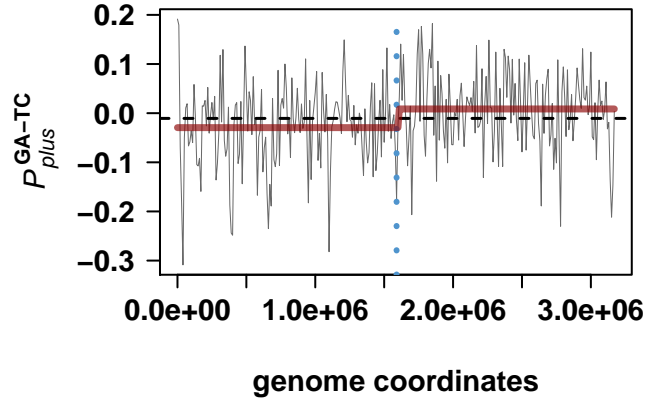
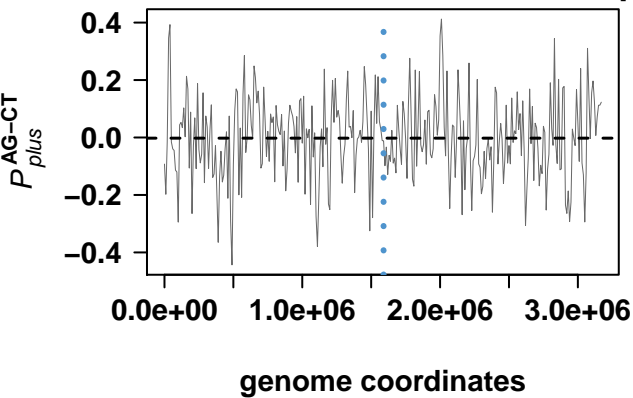
Thiobacillus denitrificans ATCC 25259



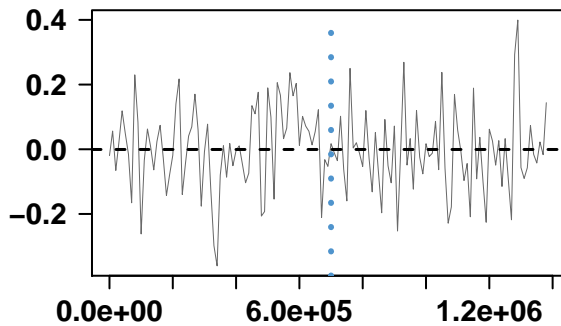
Burkholderia pseudomallei 1710b



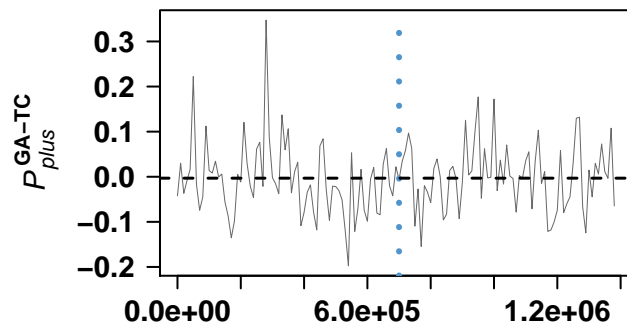
Burkholderia pseudomallei 1710b



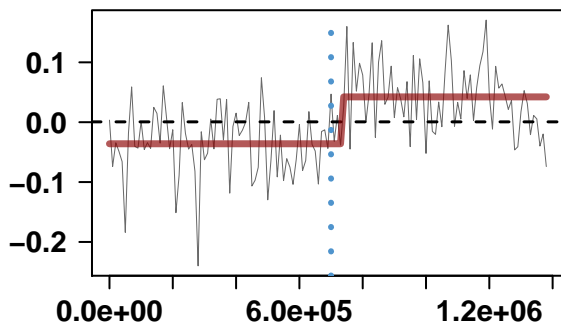
Burkholderia lata



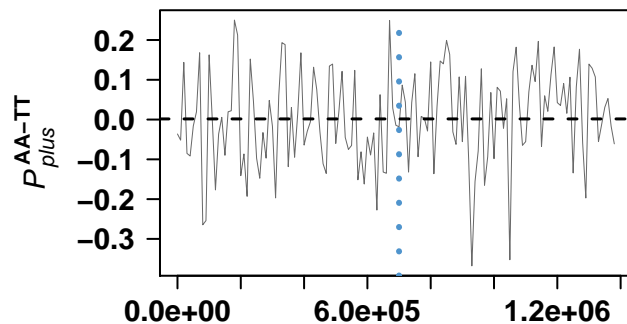
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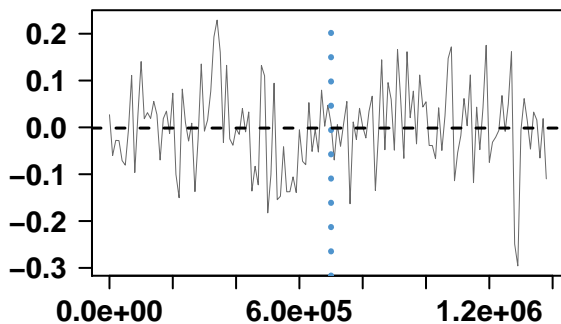
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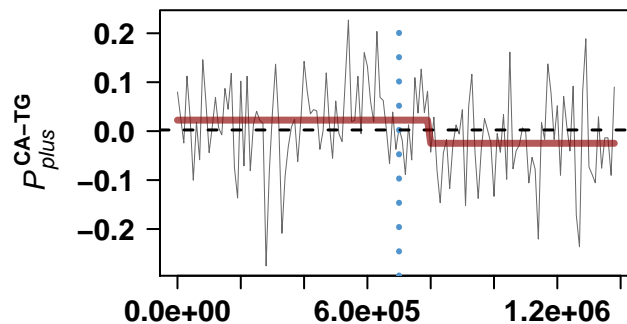
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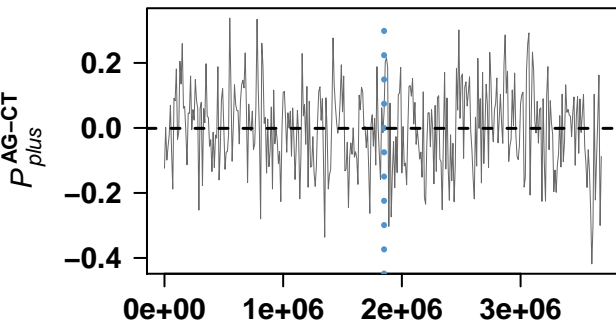


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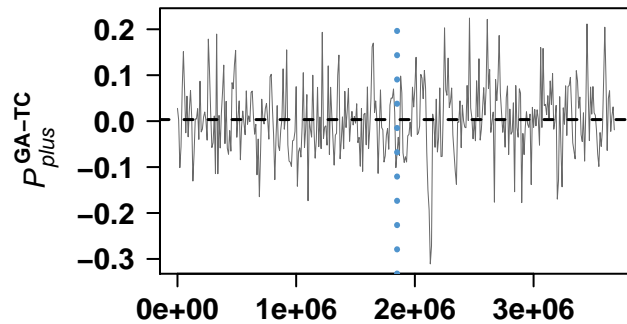


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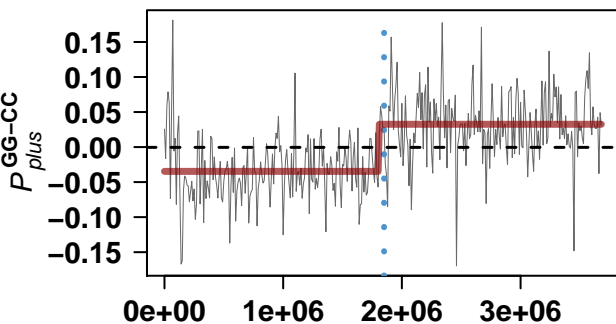
Burkholderia lata



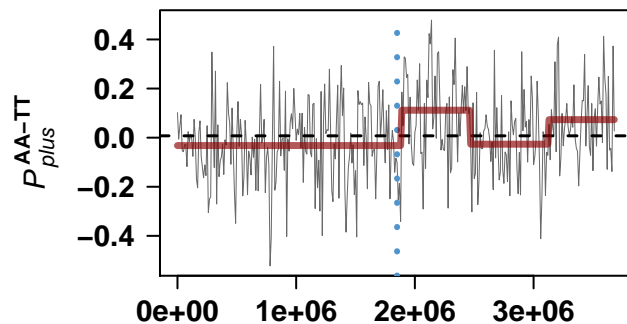
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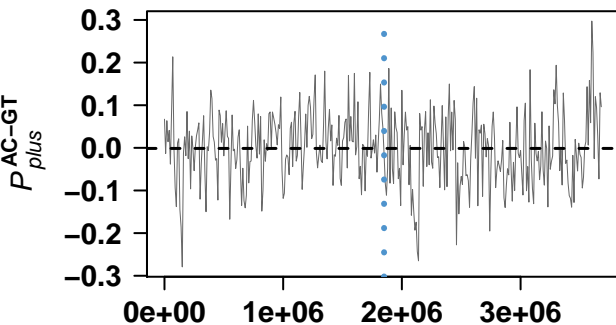
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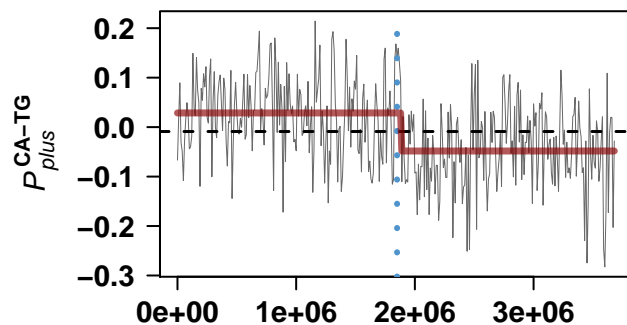
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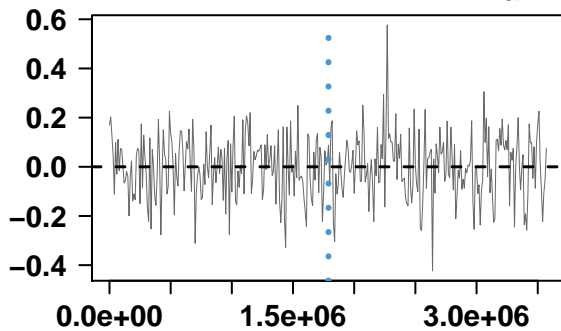


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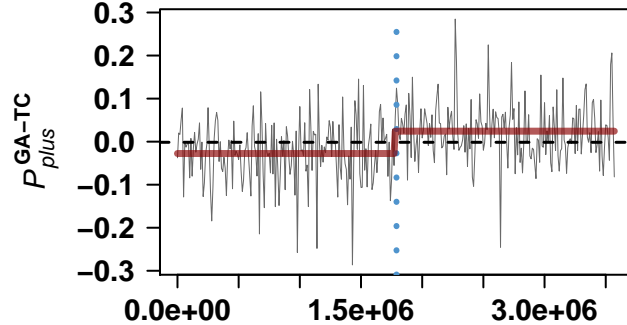


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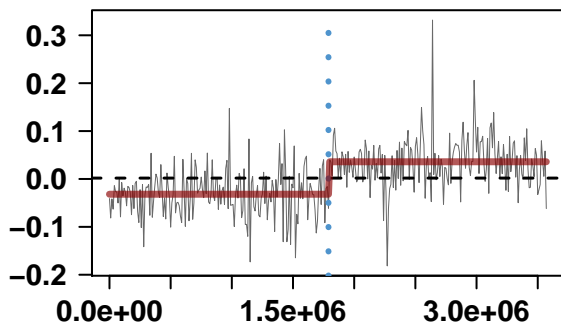
Burkholderia lata



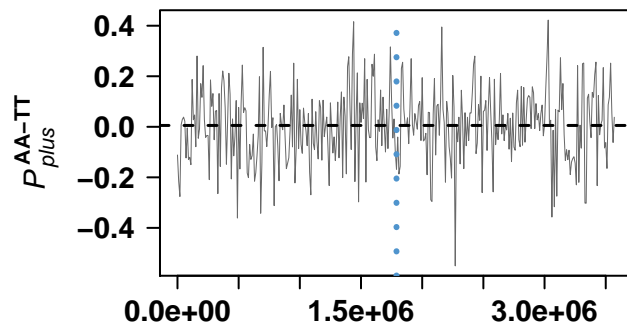
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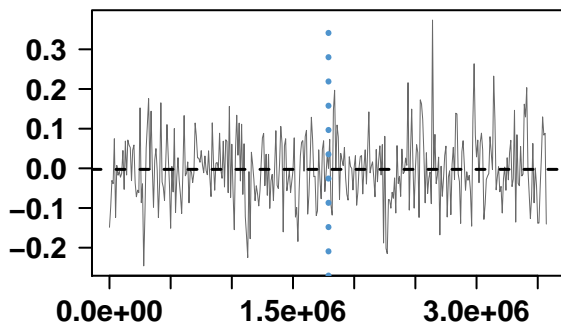
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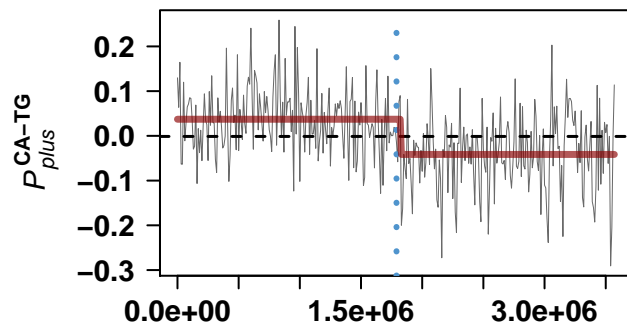
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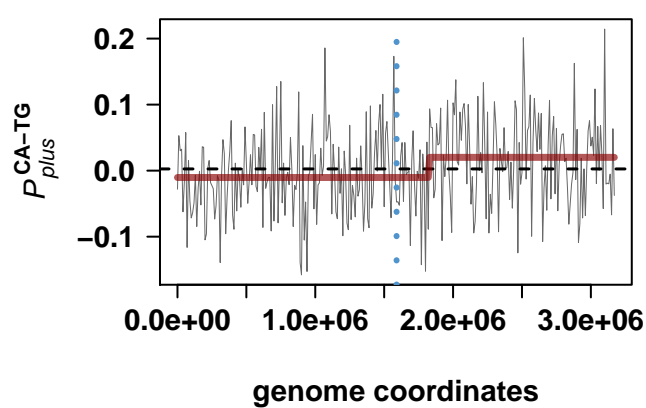
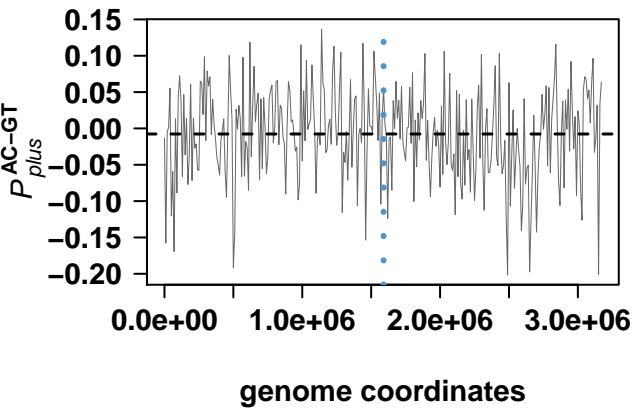
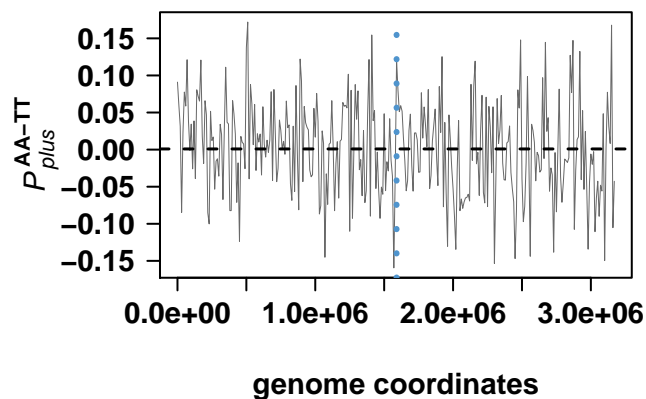
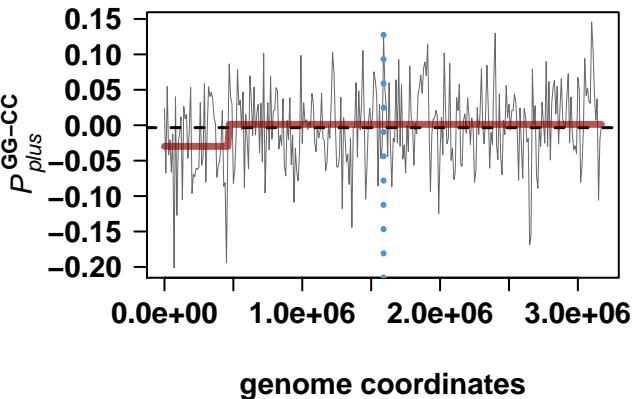
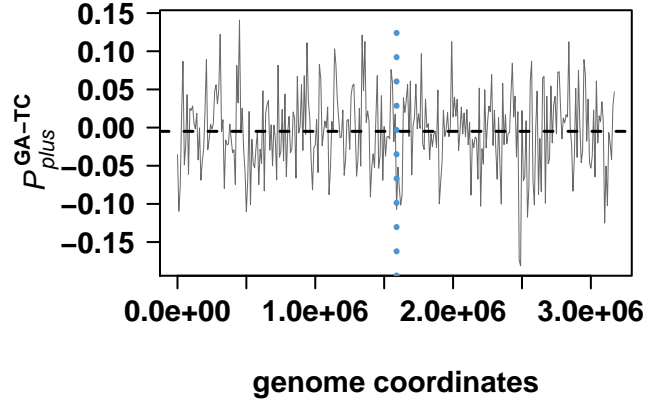
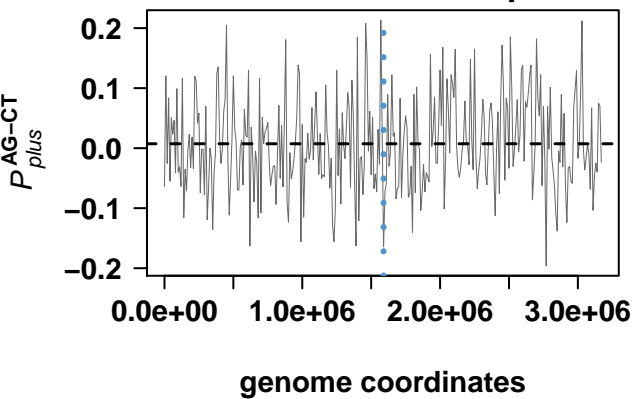


genome coordinates

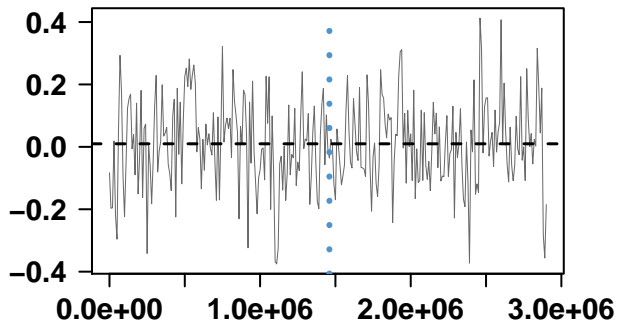


genome coordinates

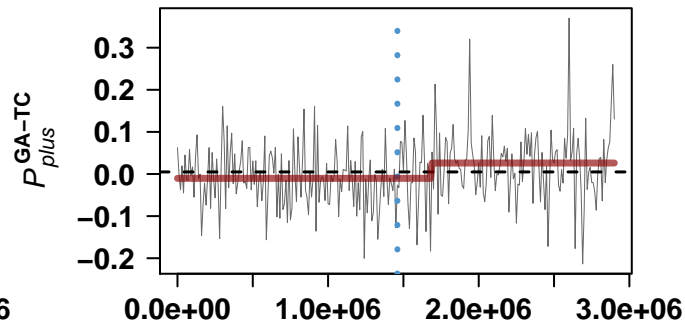
Nitrosospira multiformis ATCC 25196



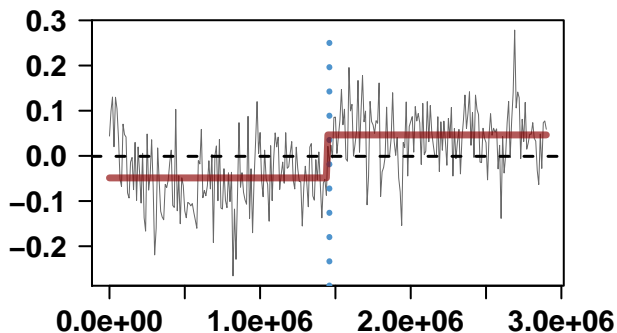
Burkholderia thailandensis E264



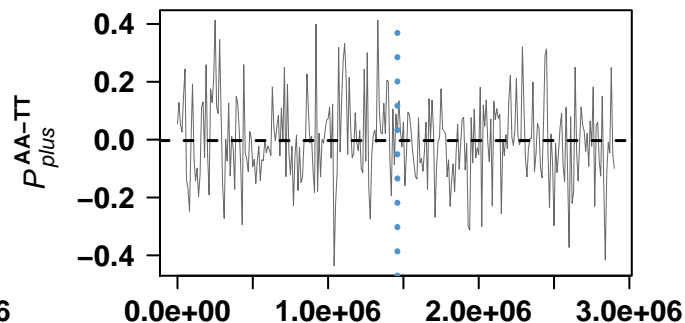
genome coordinates



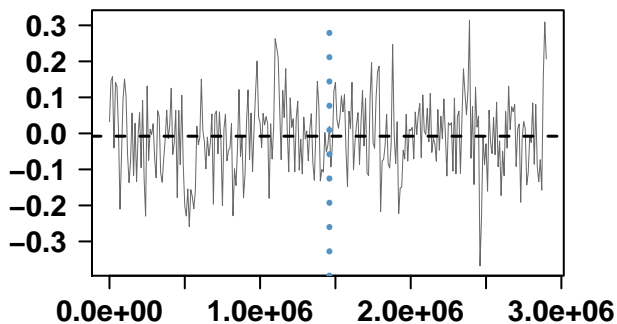
genome coordinates



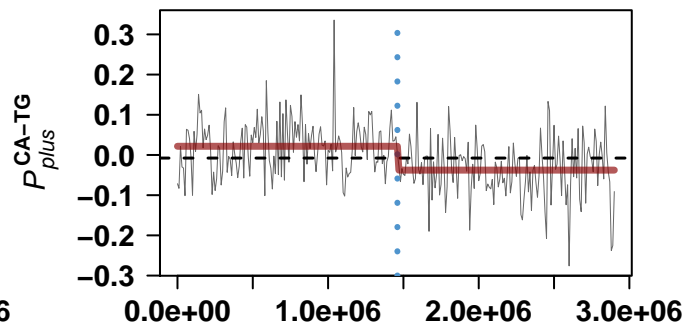
genome coordinates



genome coordinates

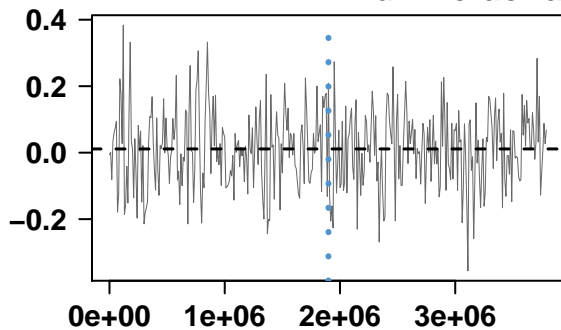


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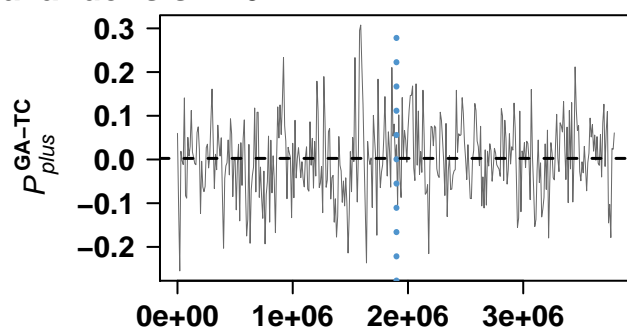


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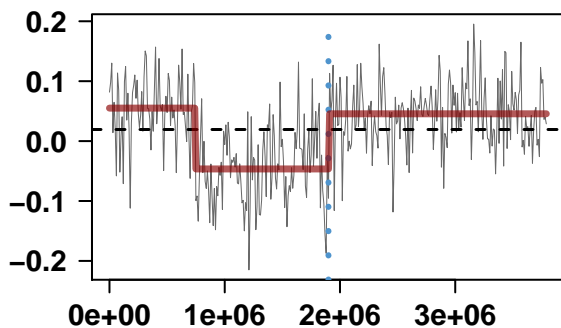
Burkholderia thailandensis E264



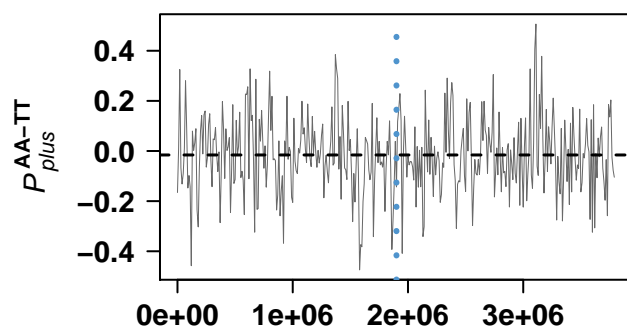
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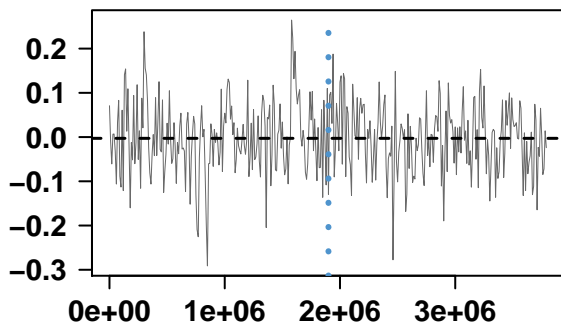
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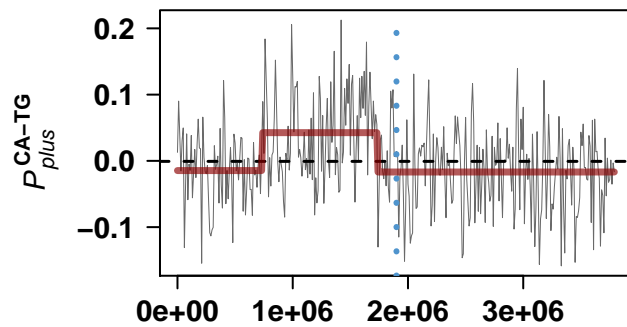
genome coordinates



genome coordinates

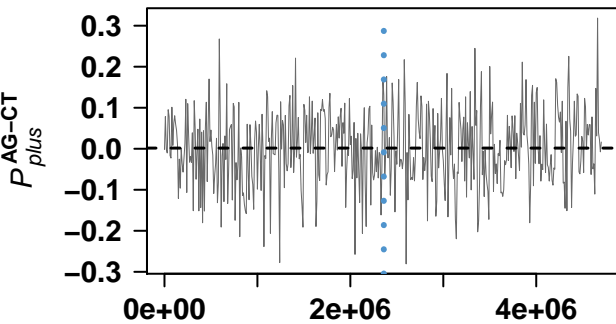


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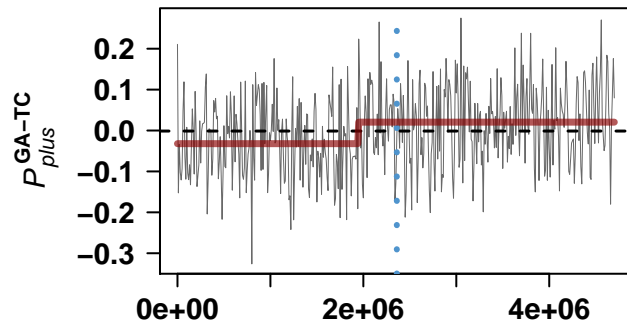


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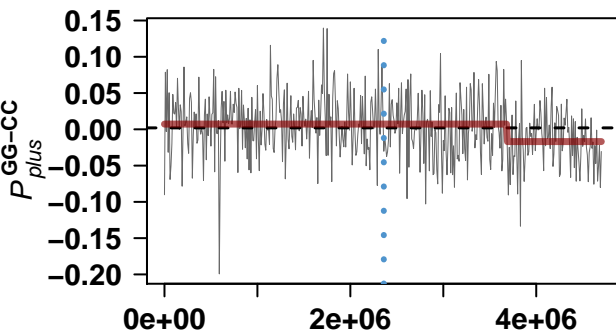
Albidiferax ferrireducens T118



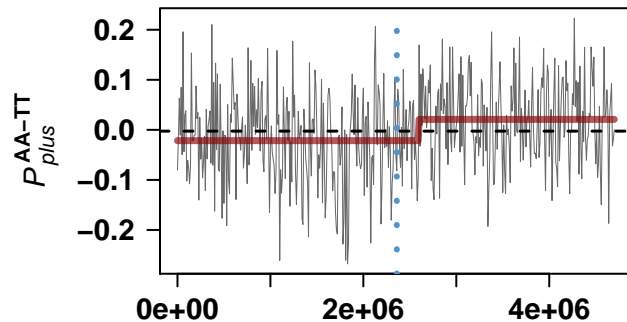
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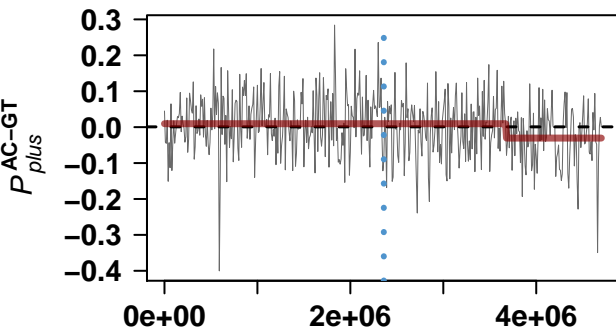
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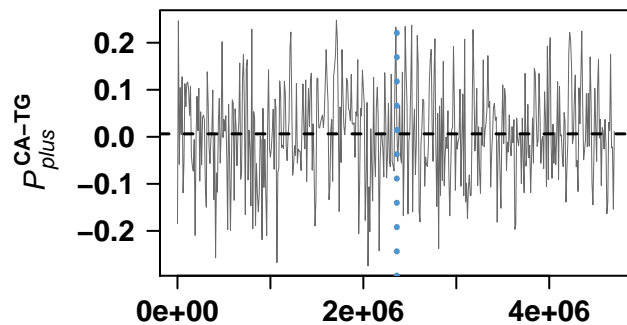
genome coordinates



genome coordinates

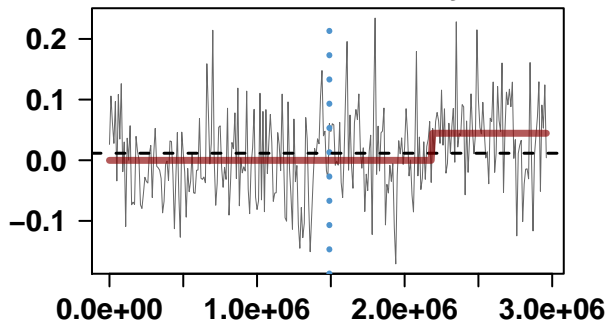


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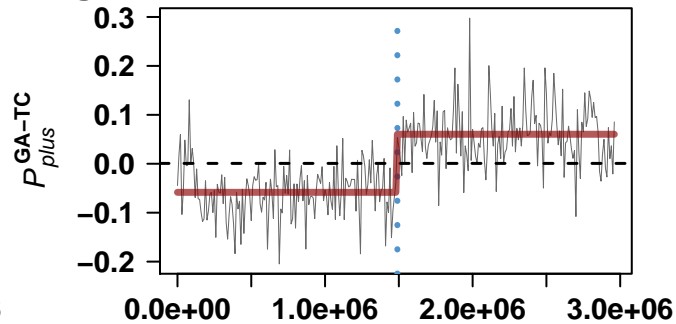


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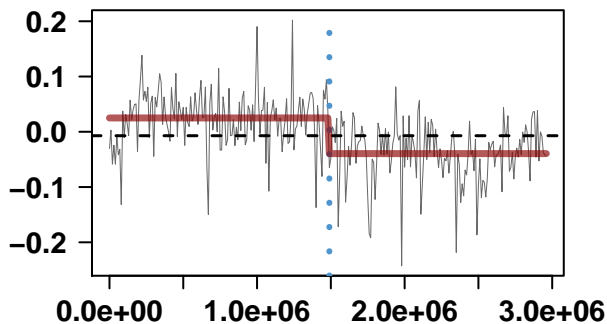
Methylobacillus flagellatus KT



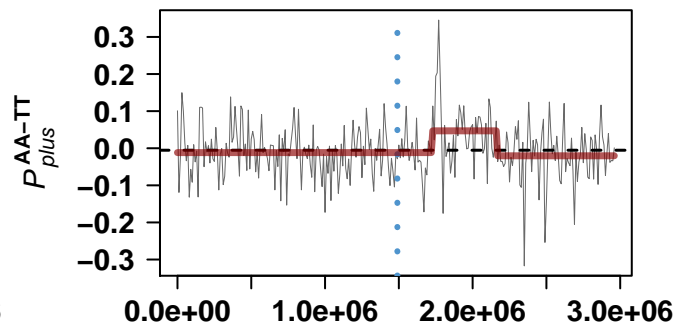
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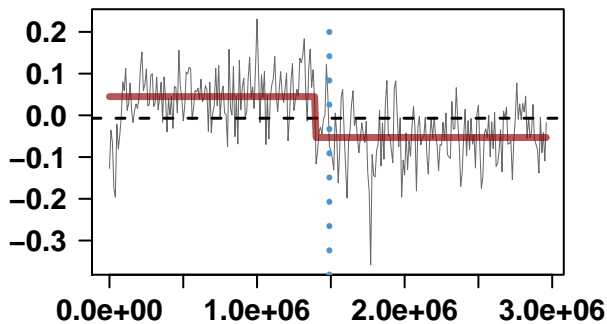
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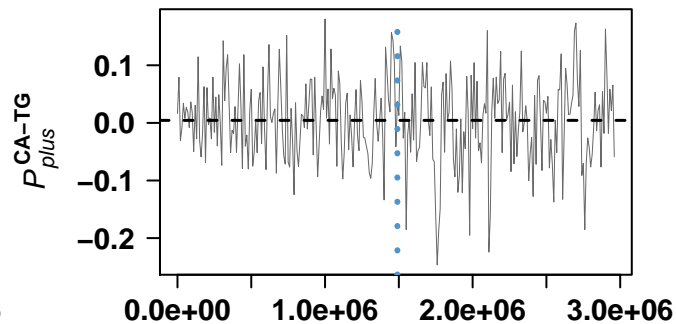
genome coordinates



genome coordinates

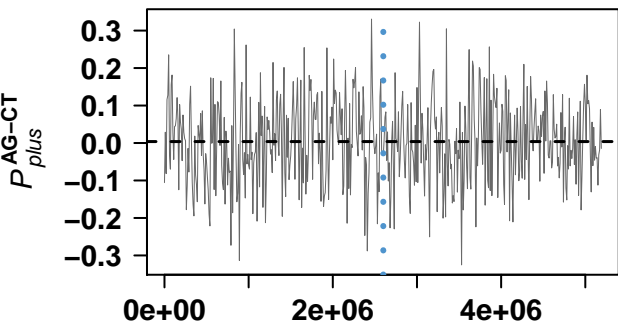


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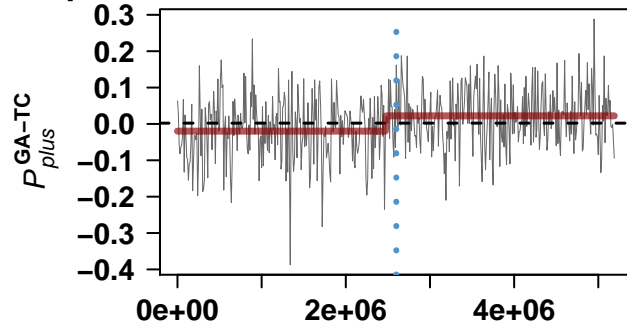


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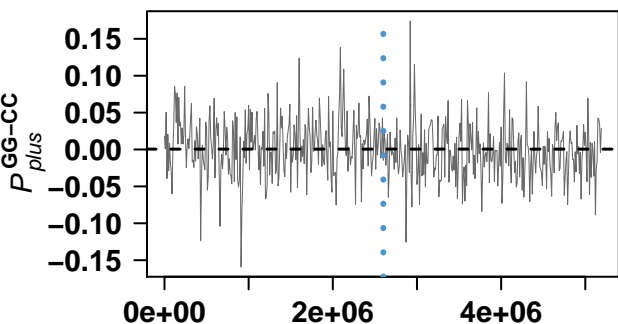
Polaromonas sp. JS666



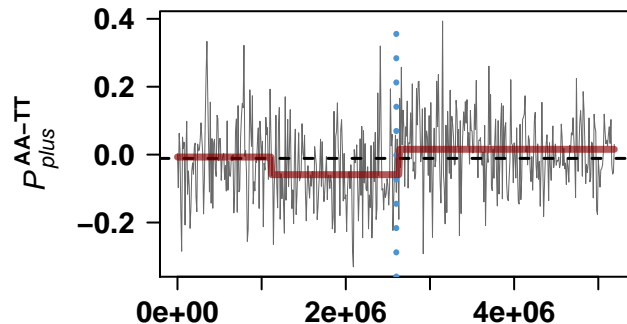
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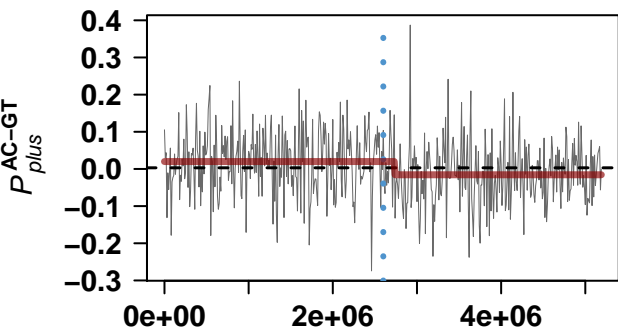
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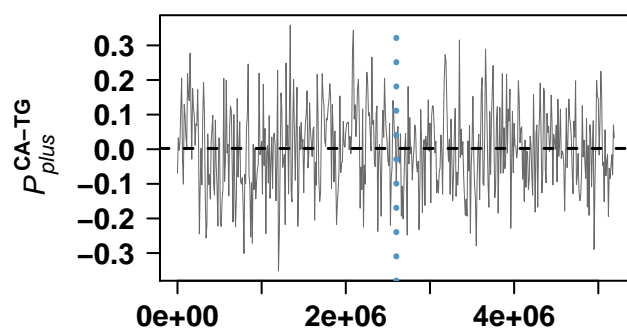
genome coordinates



genome coordinates

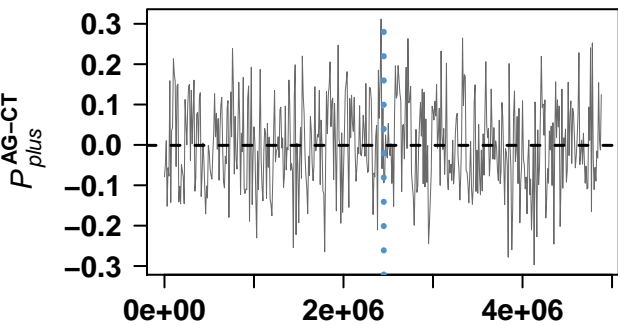


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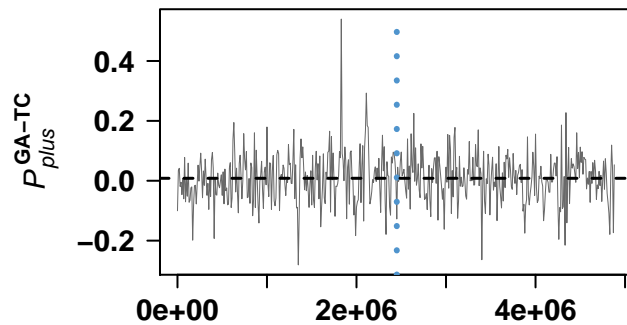


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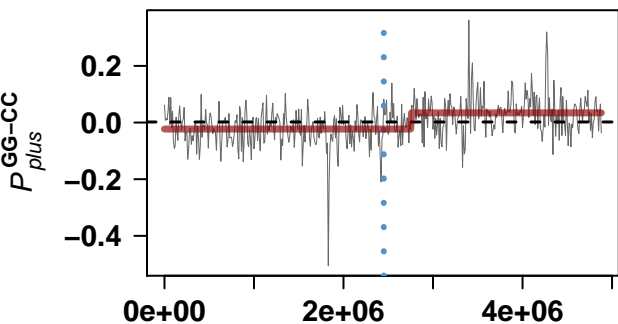
Burkholderia xenovorans LB400



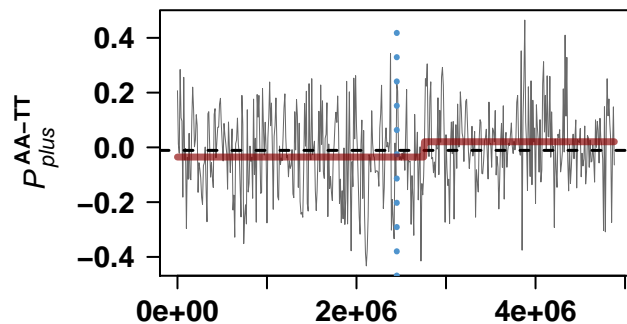
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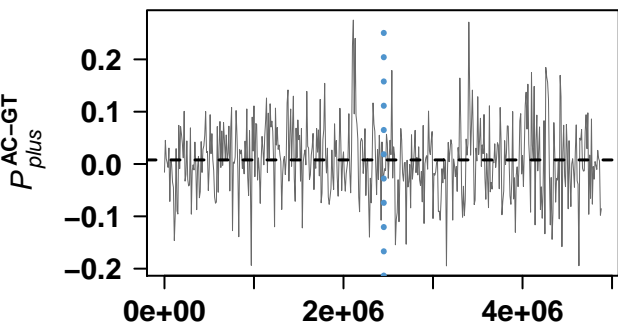
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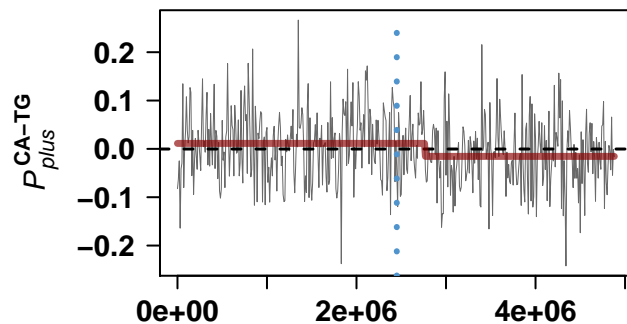
genome coordinates



genome coordinates

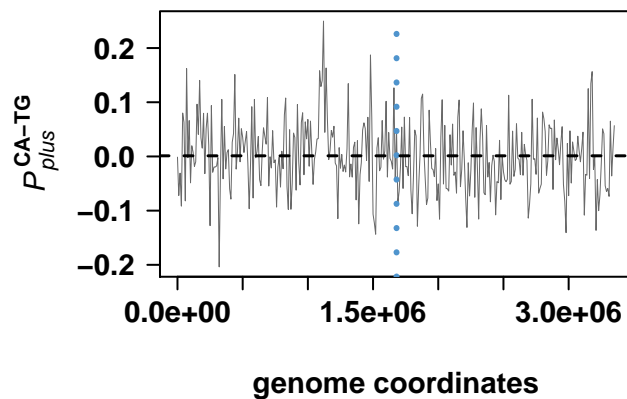
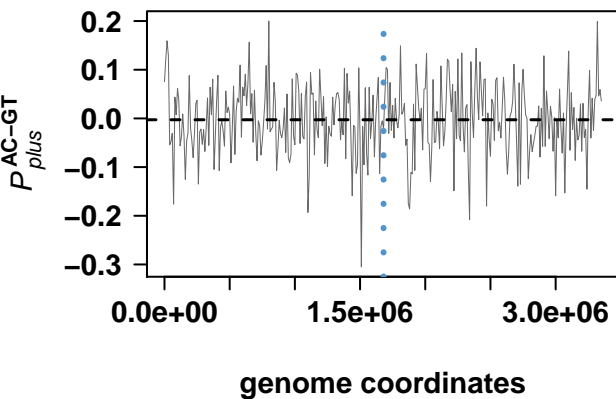
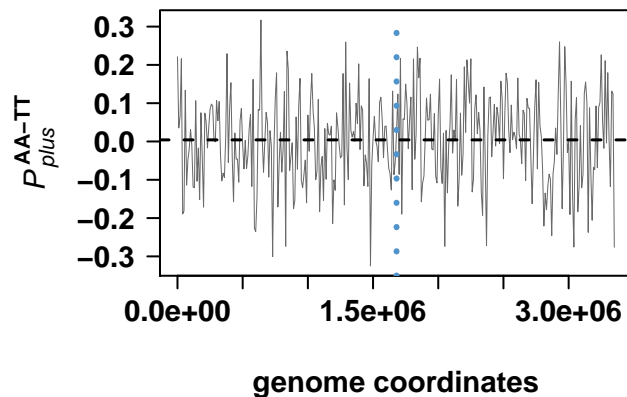
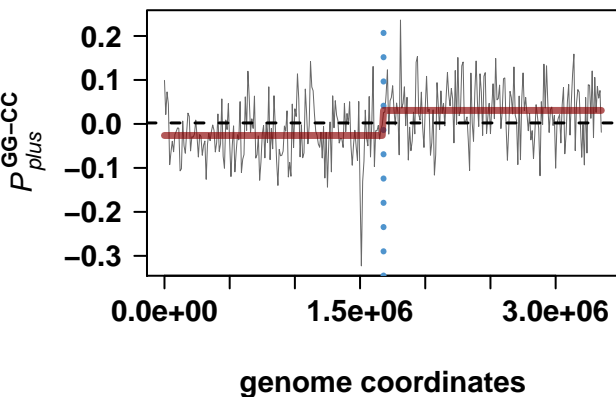
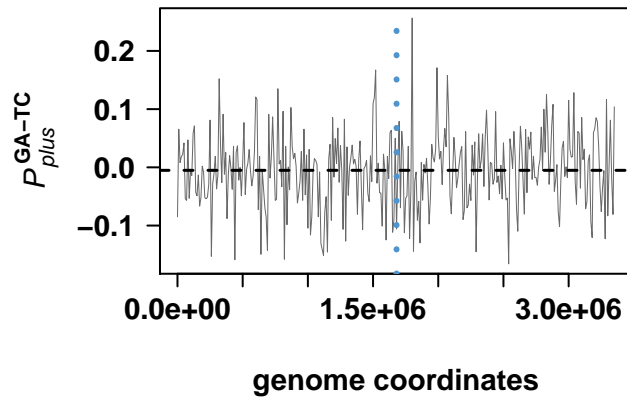
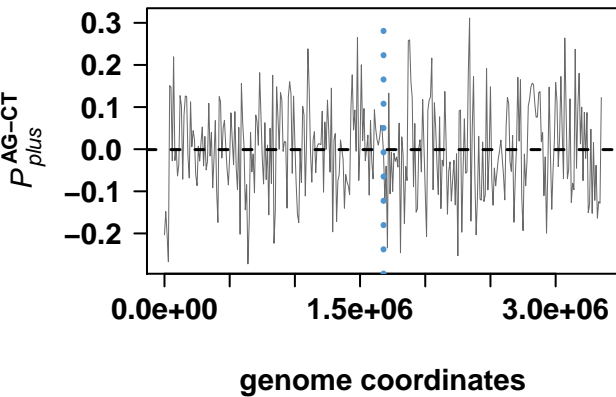


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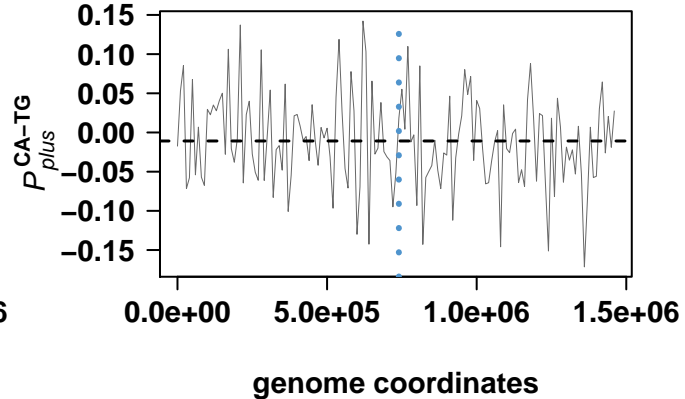
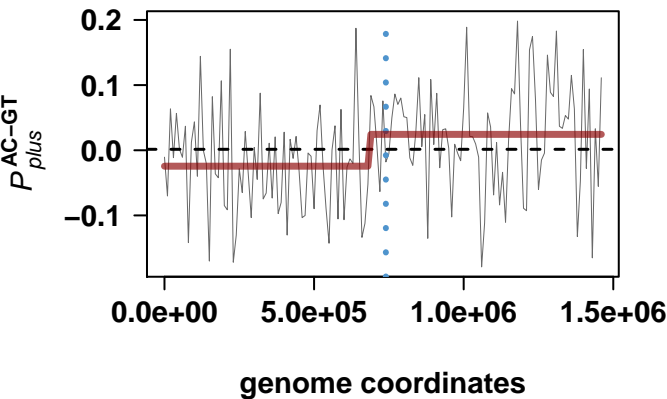
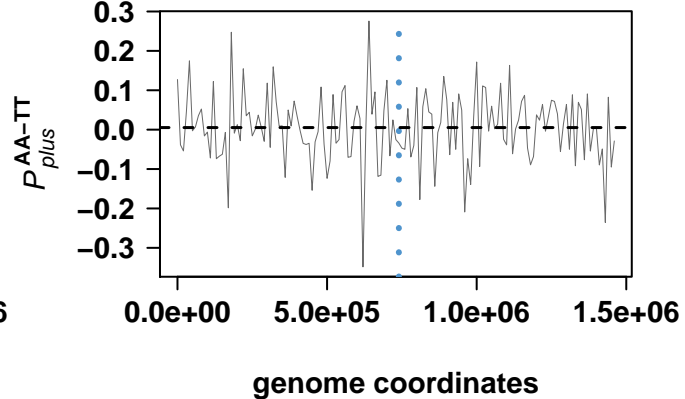
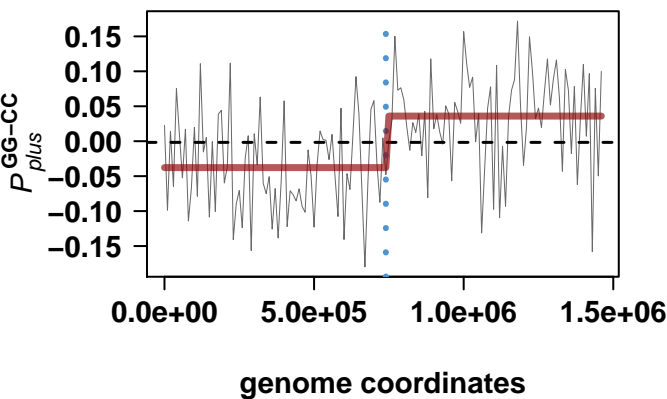
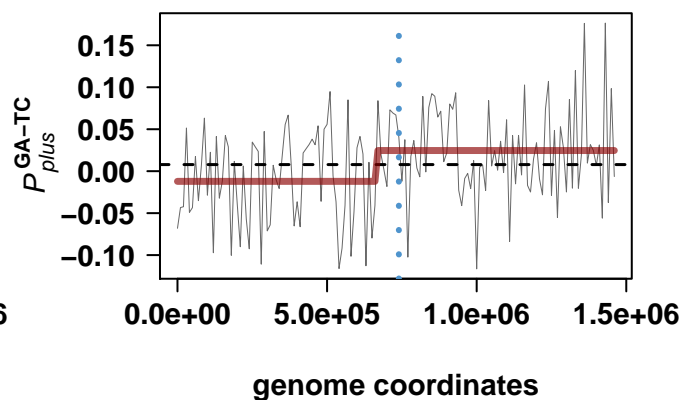
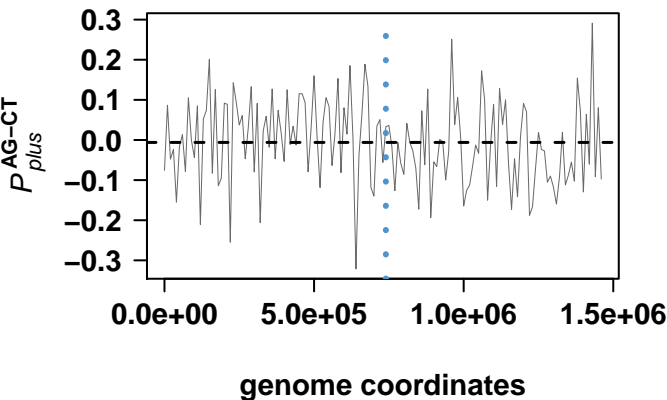


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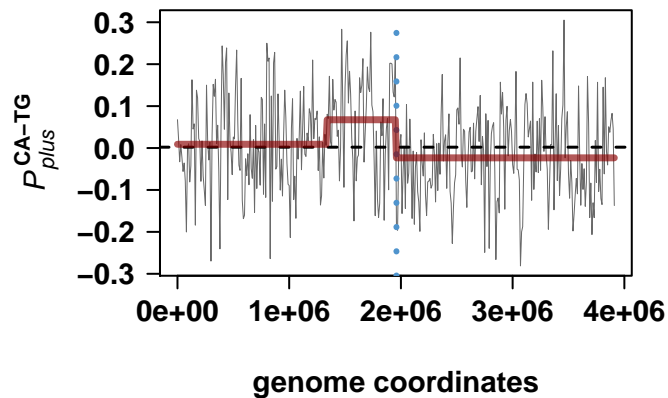
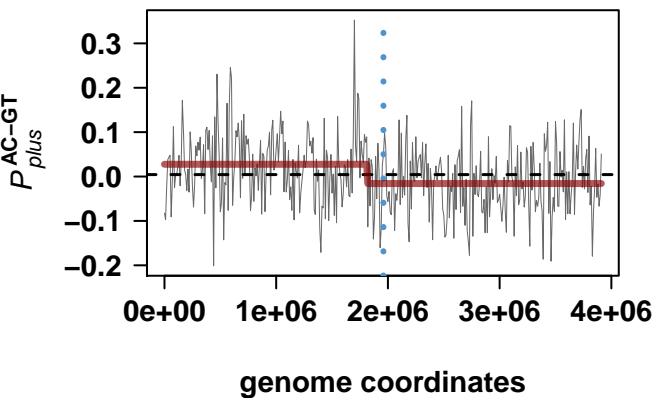
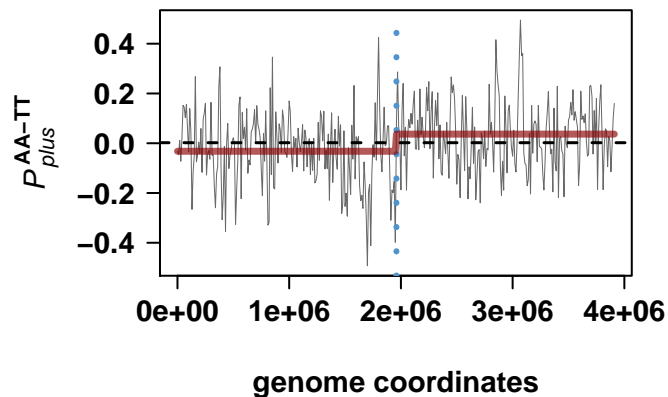
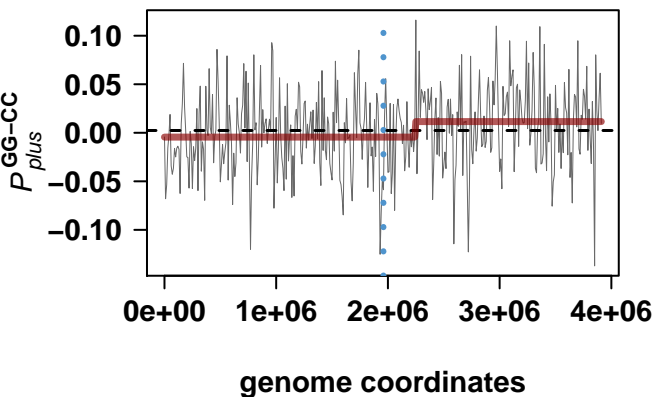
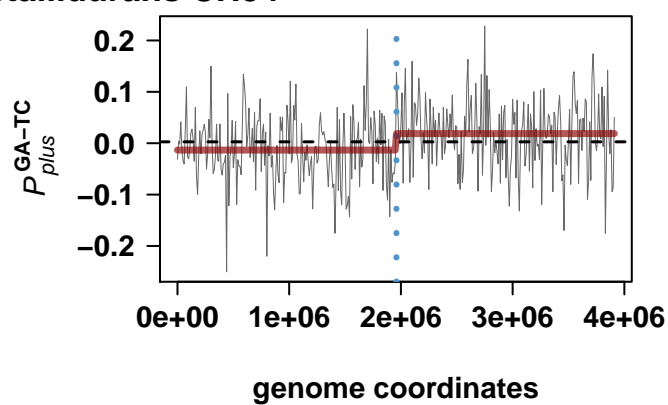
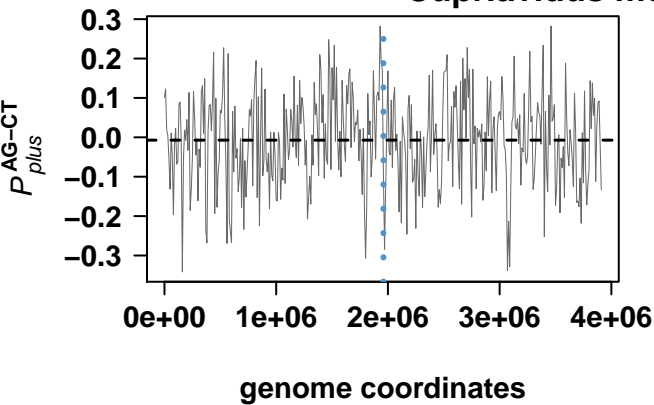
Burkholderia xenovorans LB400



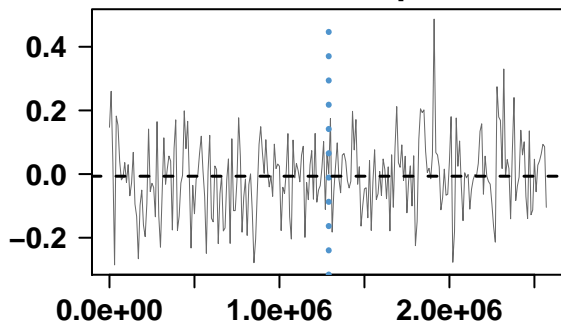
Burkholderia xenovorans LB400



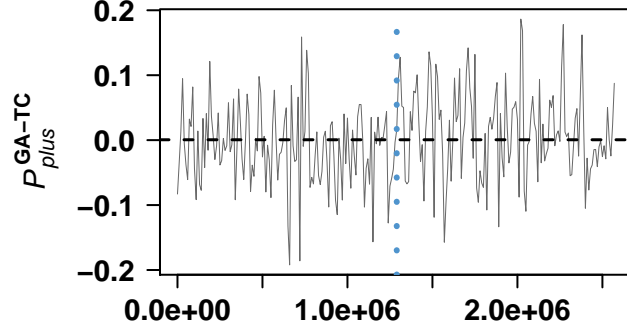
Cupriavidus metallidurans CH34



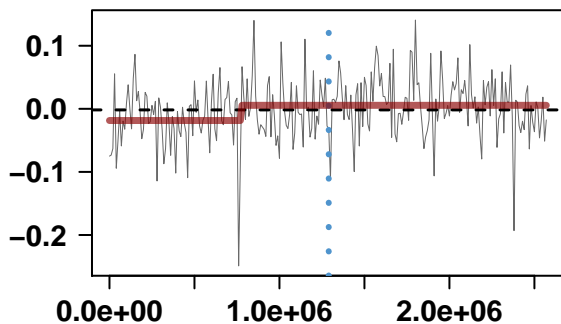
Cupriavidus metallidurans CH34



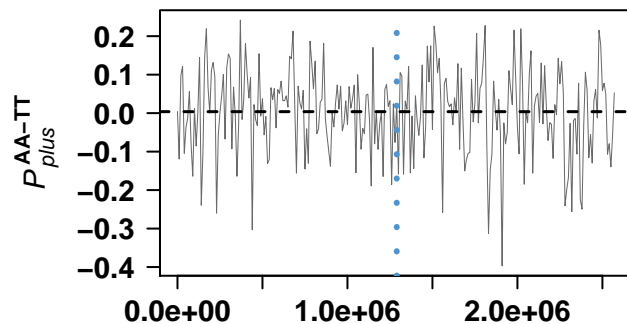
genome coordinates



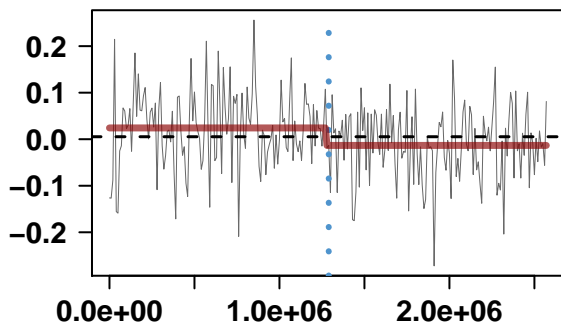
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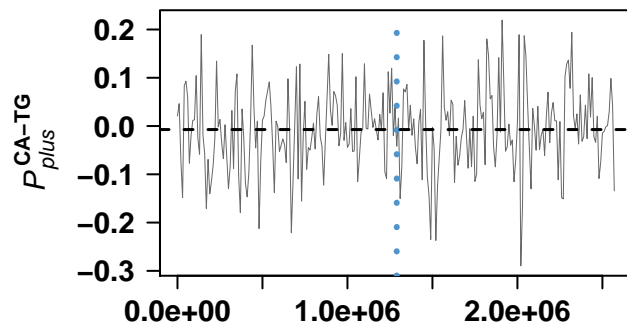
genome coordinates



genome coordinates

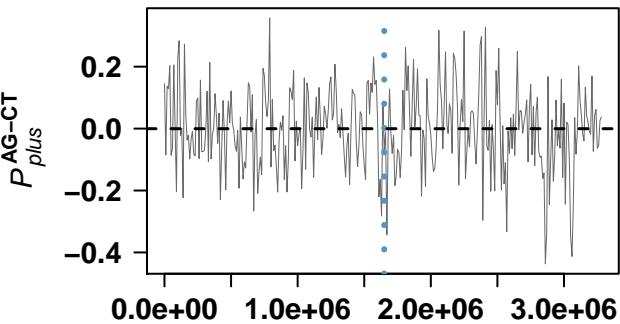


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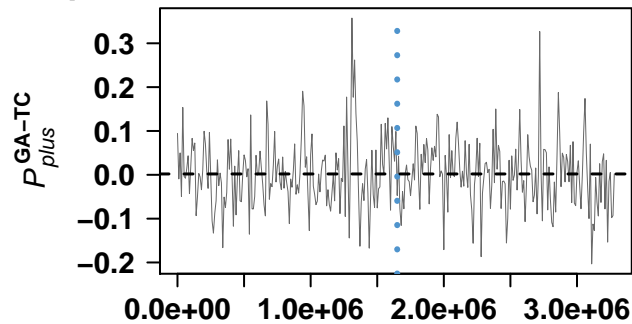


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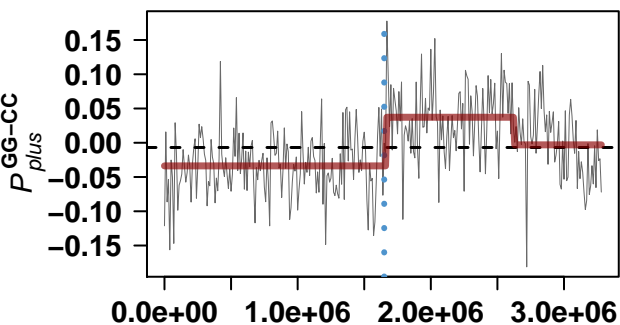
Burkholderia cenocepacia AU 1054



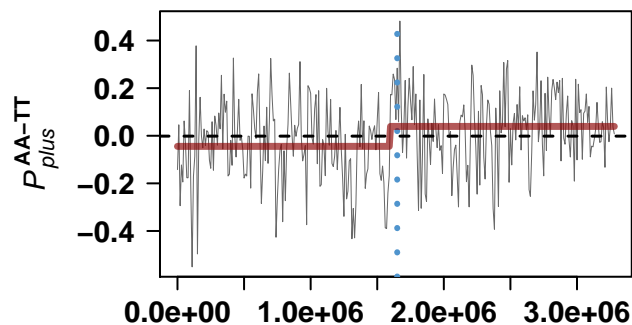
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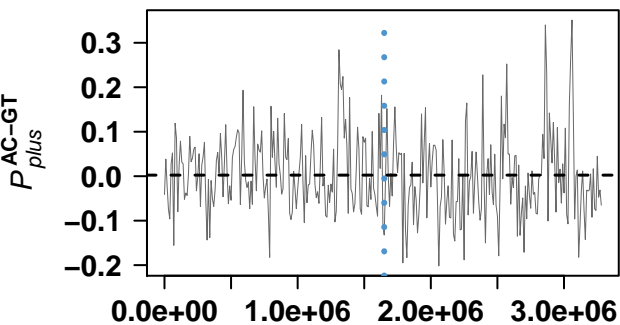
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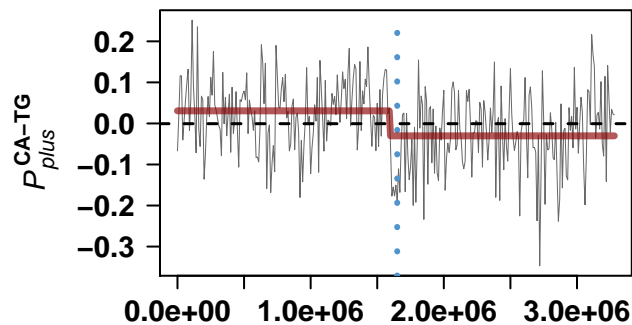
genome coordinates



genome coordinates

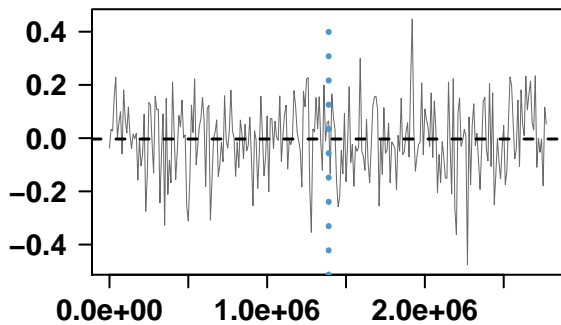


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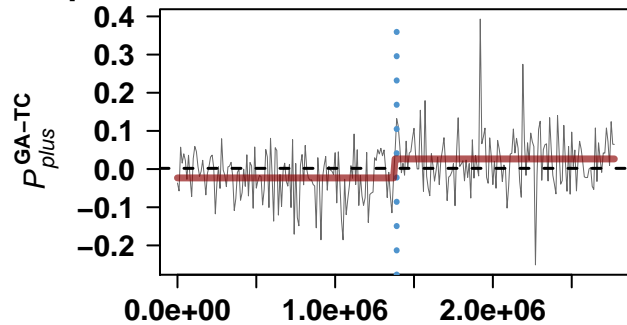


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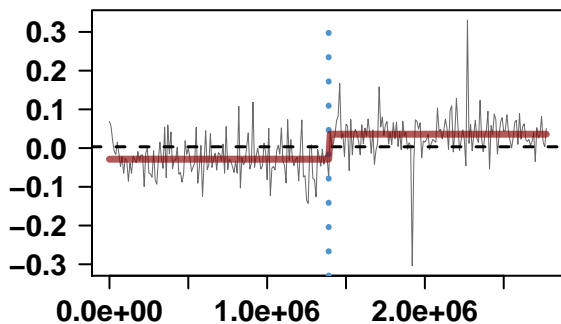
Burkholderia cenocepacia AU 1054



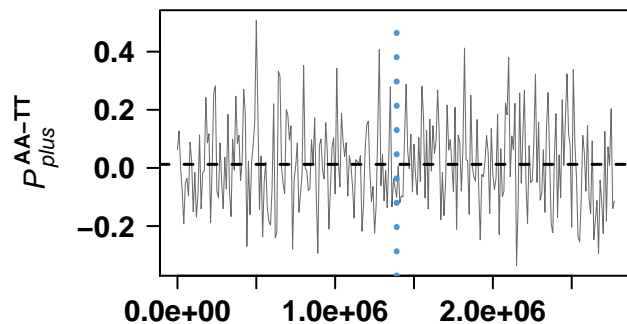
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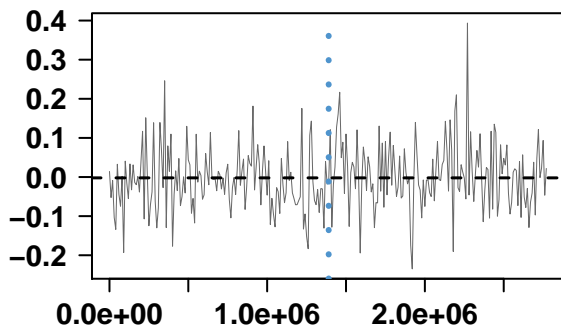
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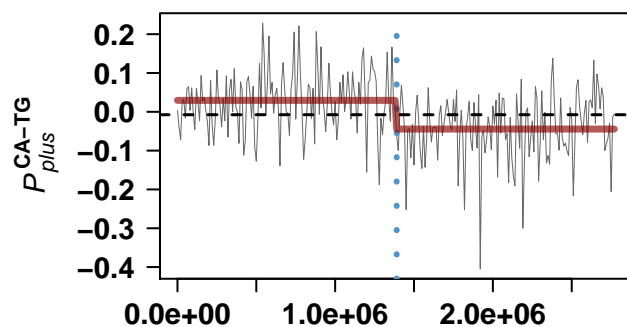
genome coordinates



genome coordinates

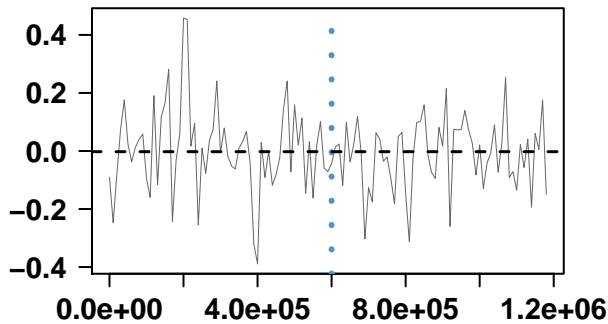


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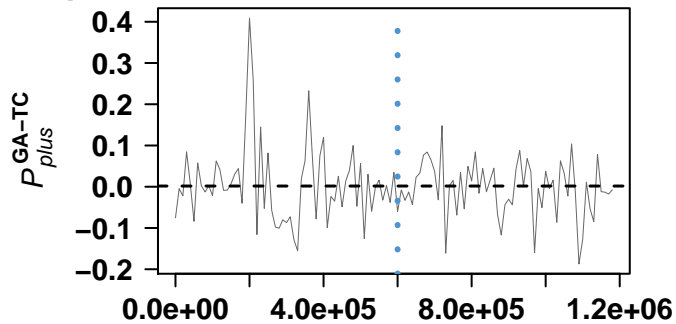


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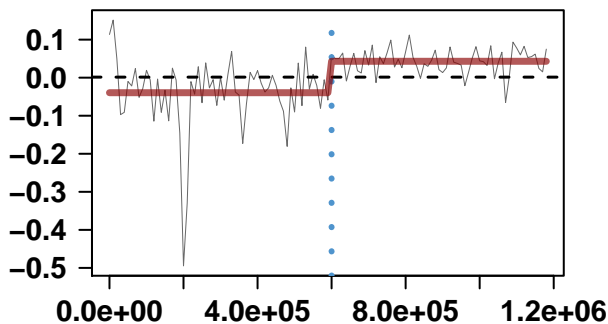
Burkholderia cenocepacia AU 1054



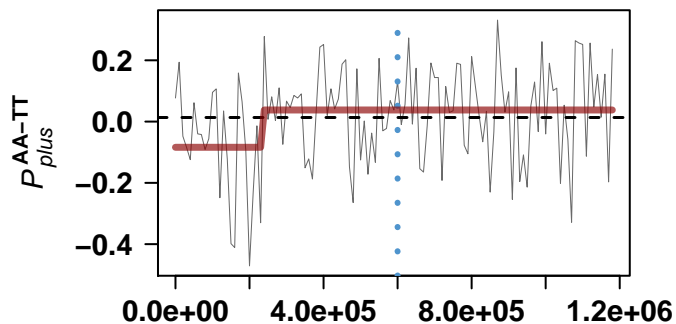
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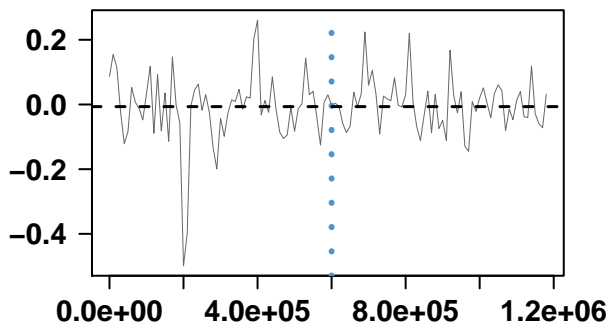
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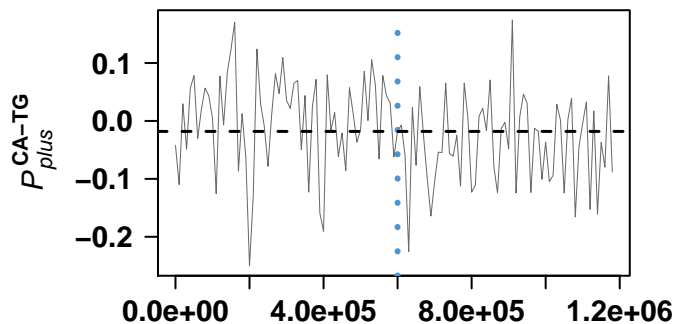
genome coordinates



genome coordinates

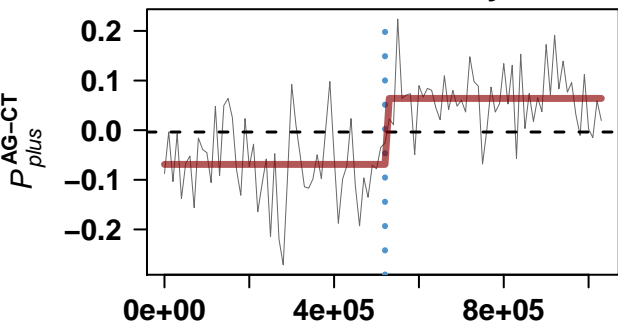


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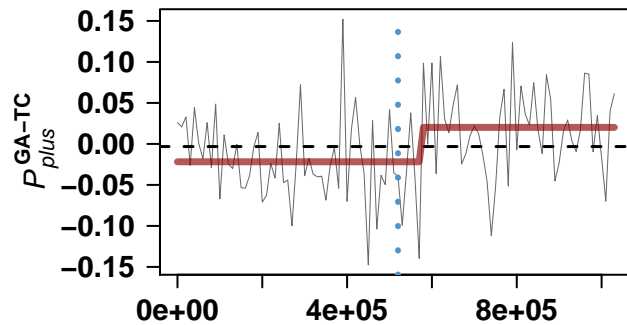


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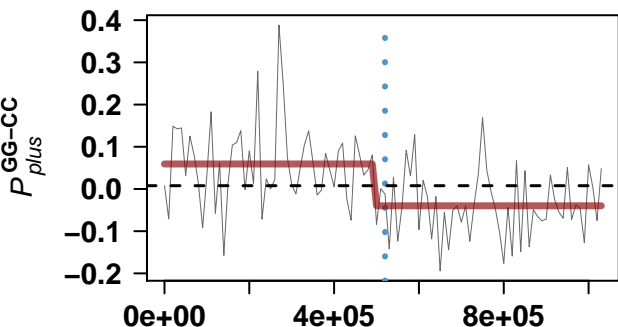
Chlamydia trachomatis D/UW-3/CX



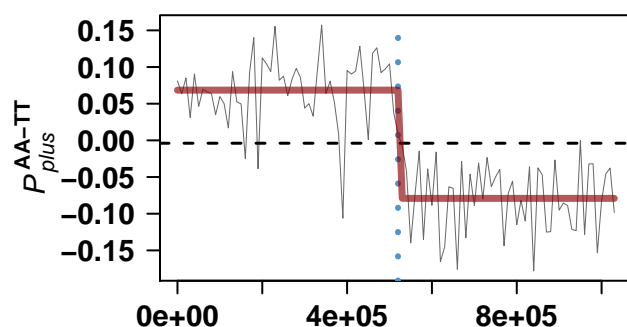
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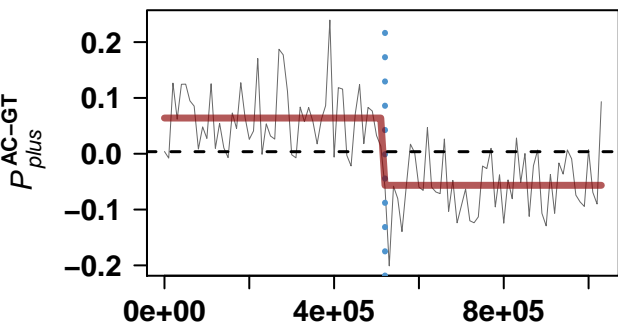
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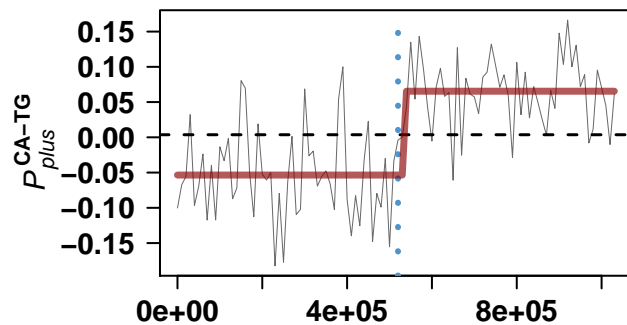
genome coordinates



genome coordinates

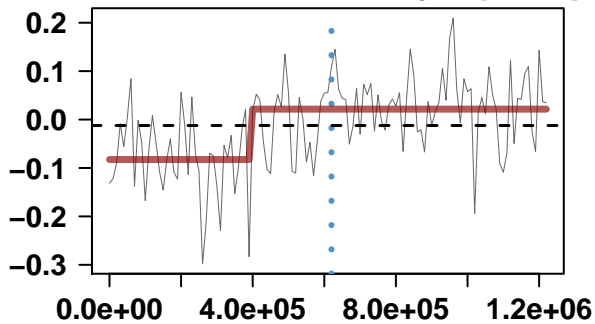


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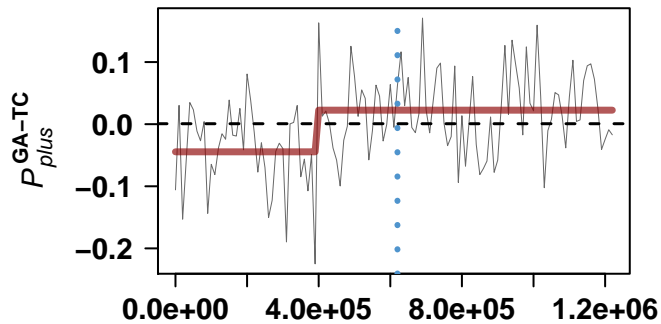


genome coordinates

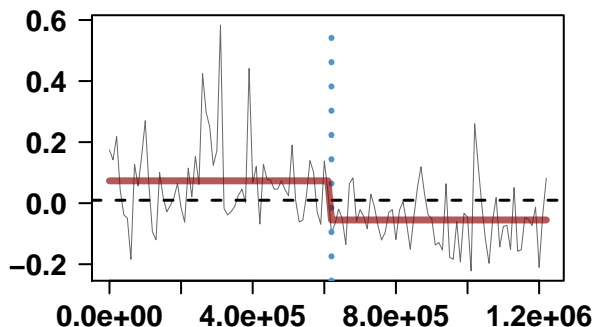
Chlamydophila pneumoniae CWL029



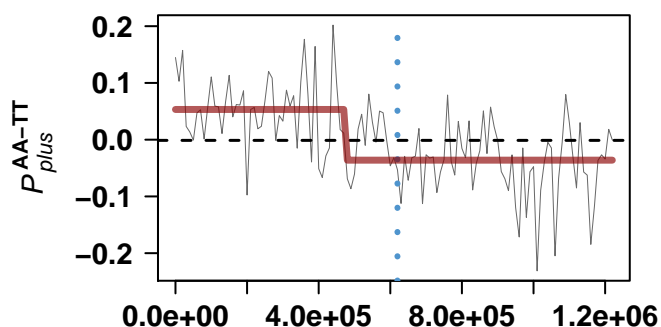
genome coordinates



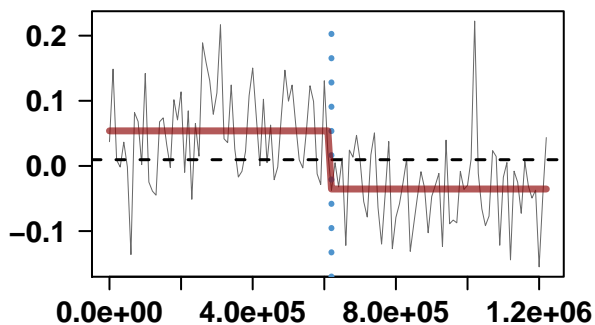
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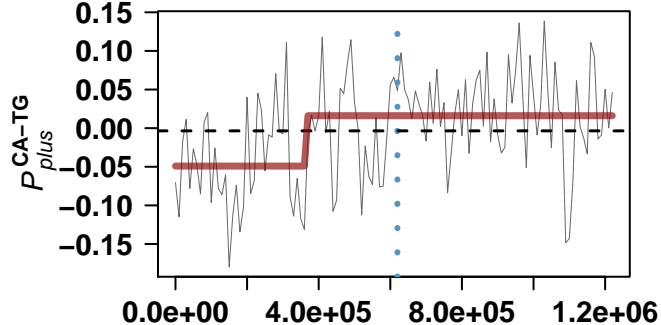
genome coordinates



genome coordinates

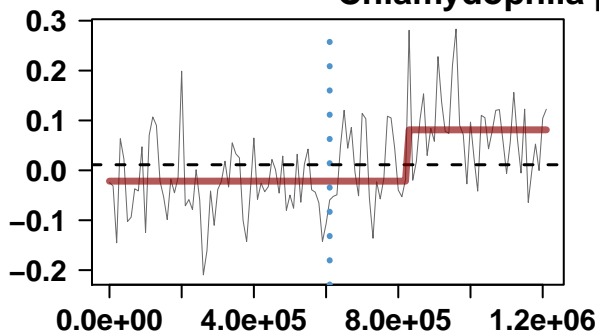


genome coordinates

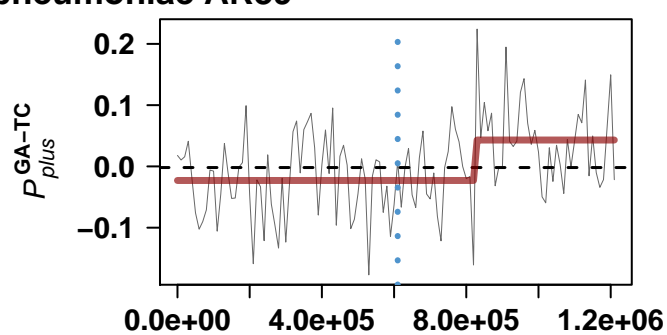


genome coordinates

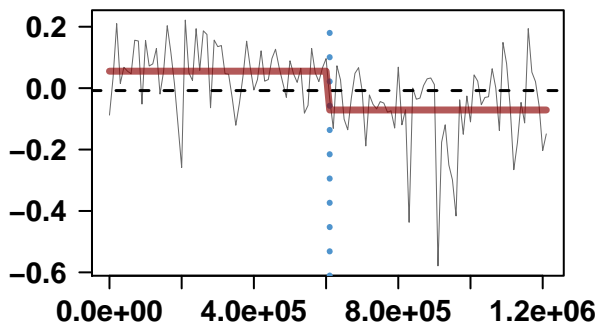
Chlamydophila pneumoniae AR39



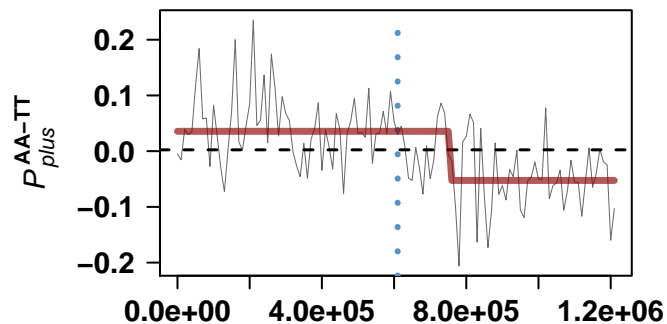
genome coordinates



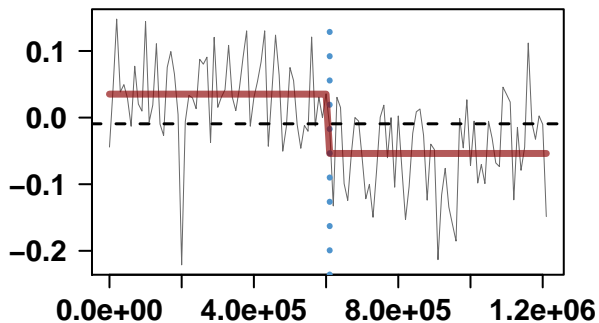
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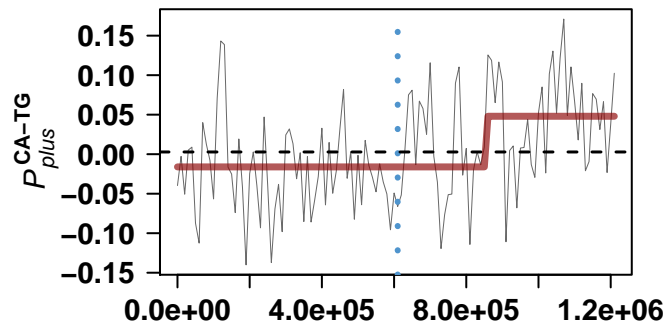
genome coordinates



genome coordinates

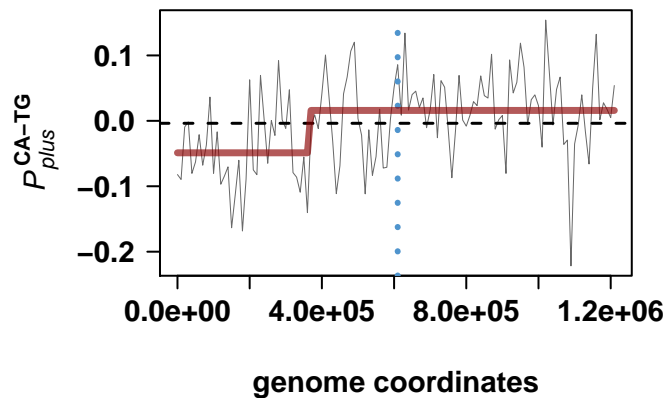
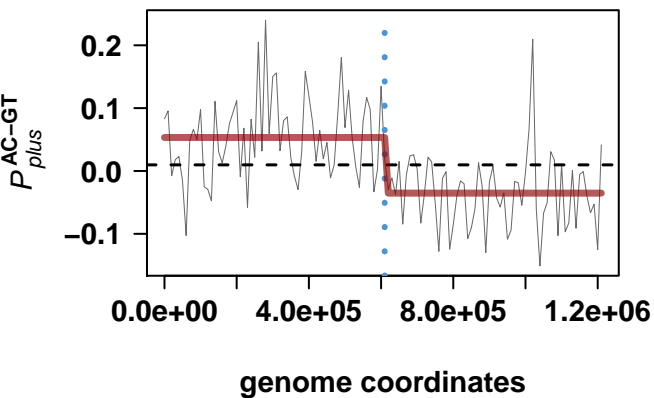
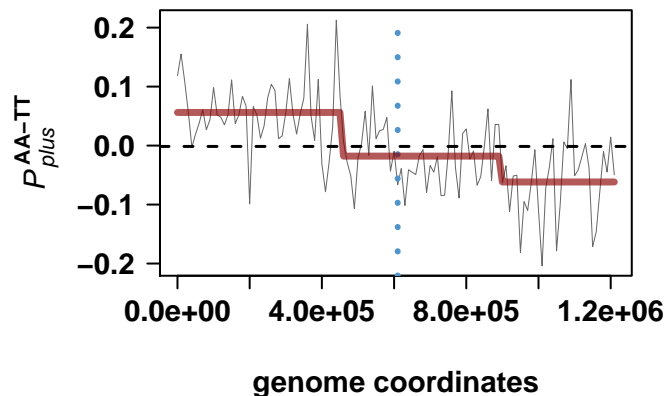
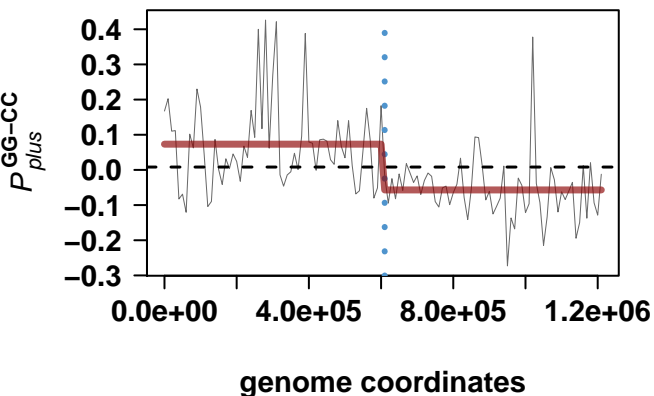
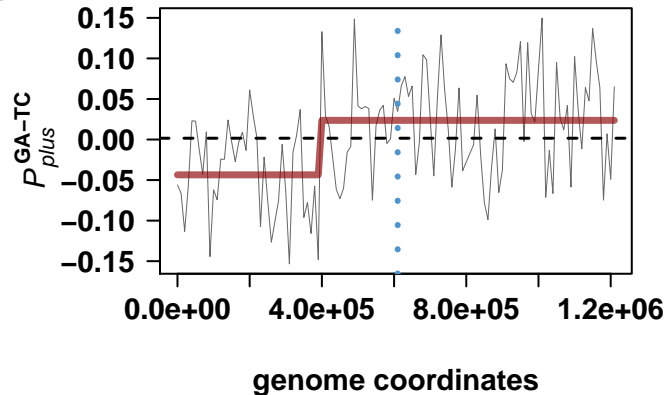
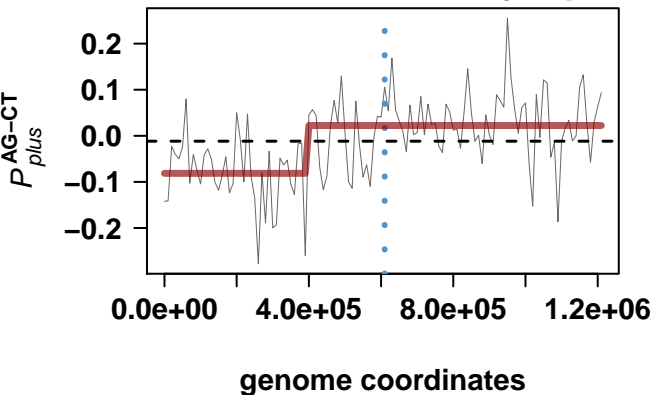


genome coordinates

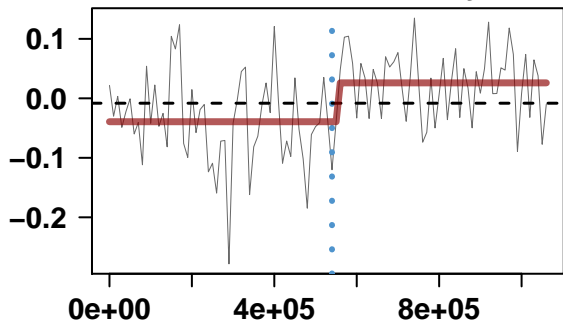


genome coordinates

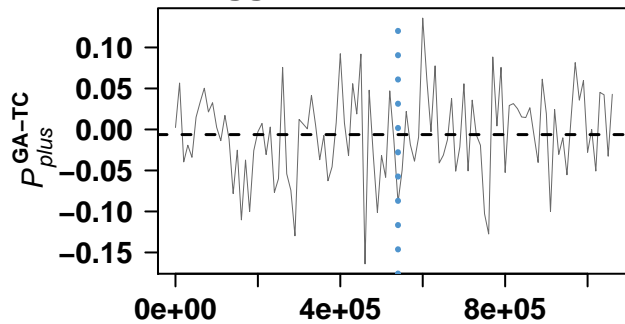
Chlamydomophila pneumoniae J138



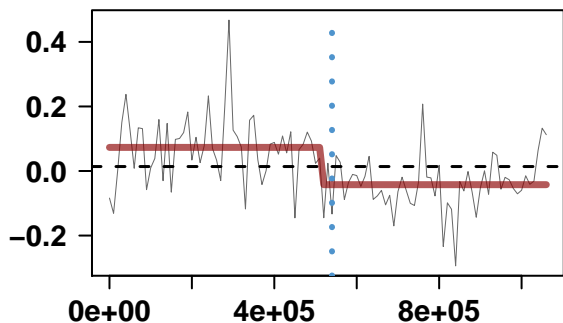
Chlamydia muridarum str. Nigg



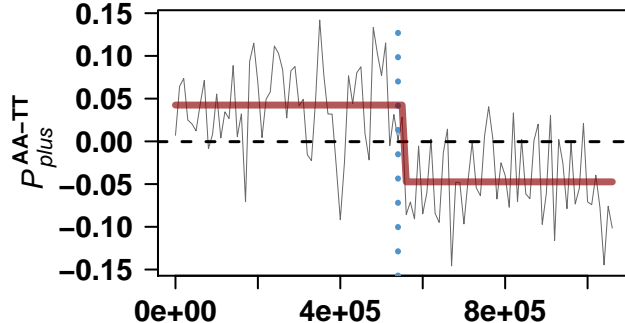
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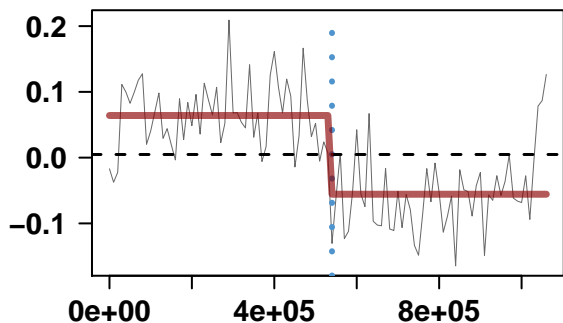
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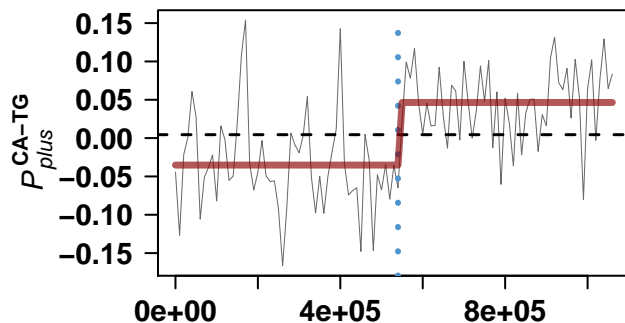
genome coordinates



genome coordinates

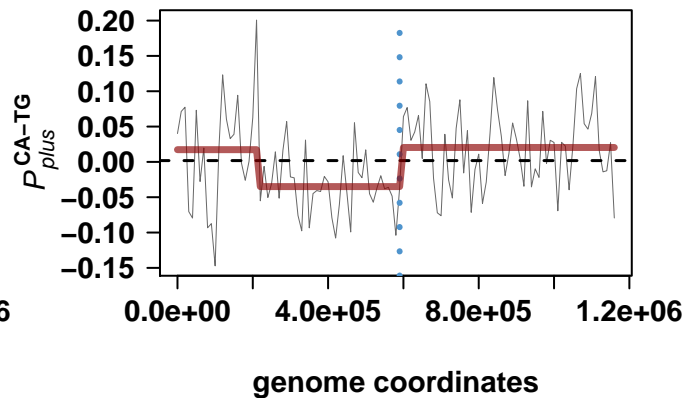
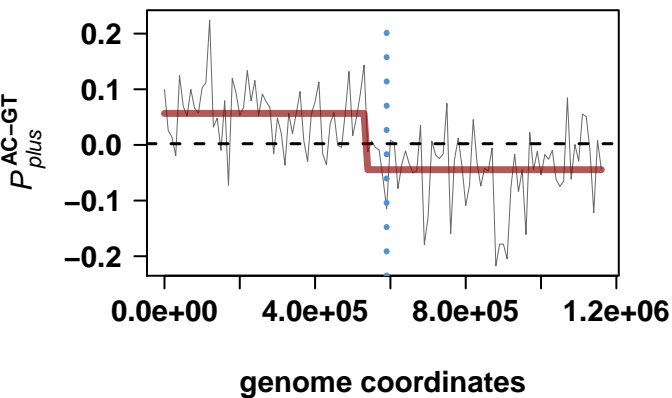
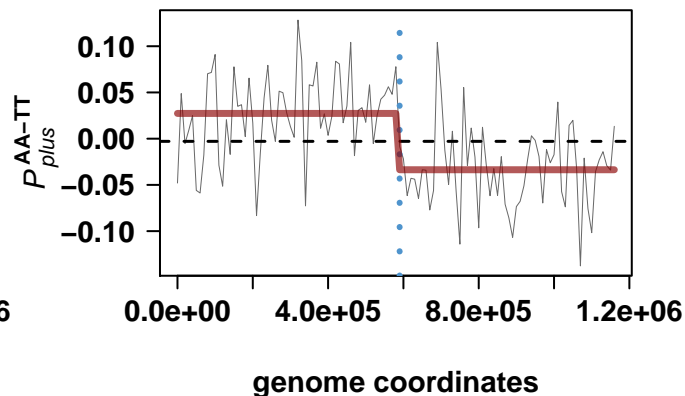
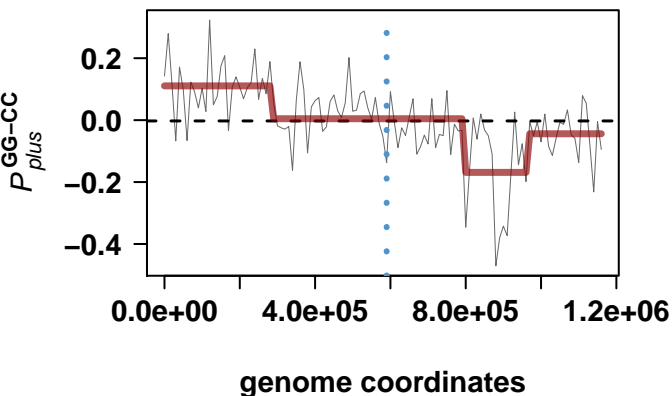
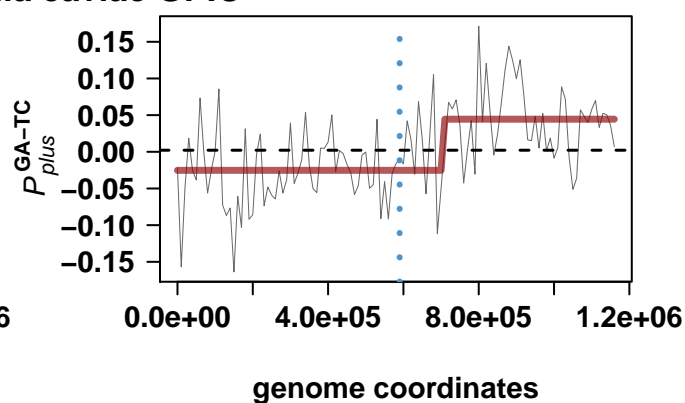
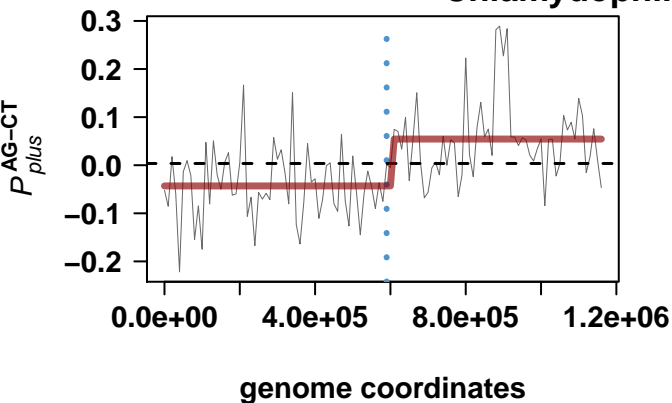


genome coordinates

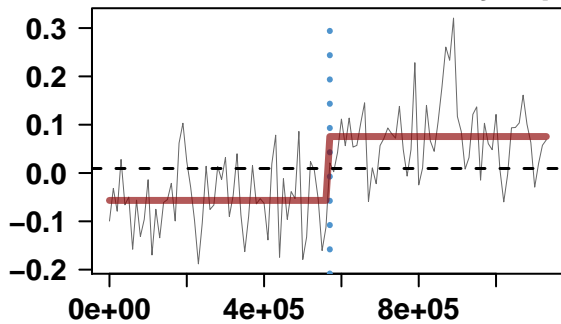


genome coordinates

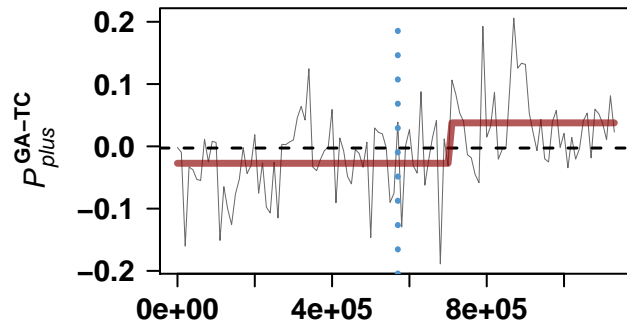
Chlamydomonas reinhardtii GPIC



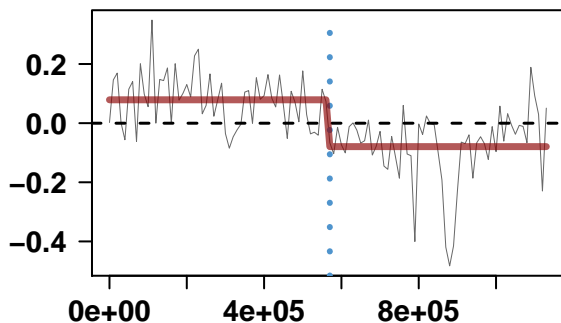
Chlamydomonas abortus S26/3



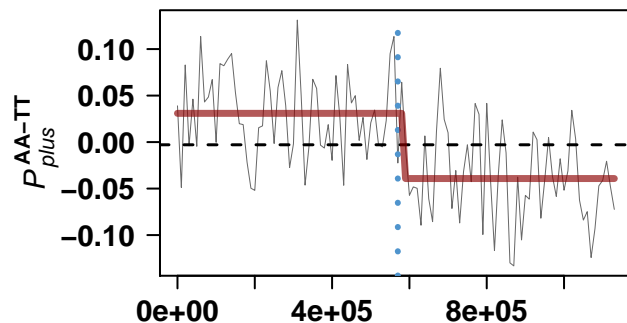
genome coordinates



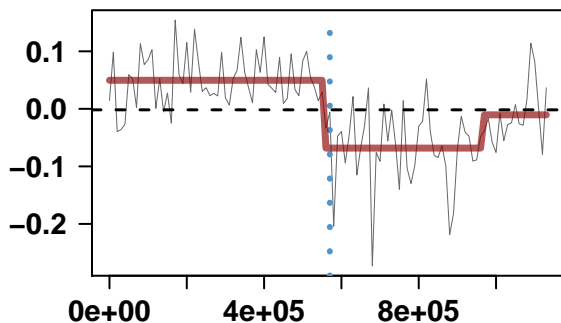
genome coordinates



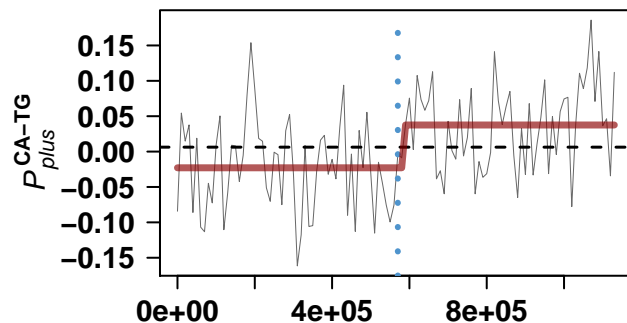
genome coordinates



genome coordinates

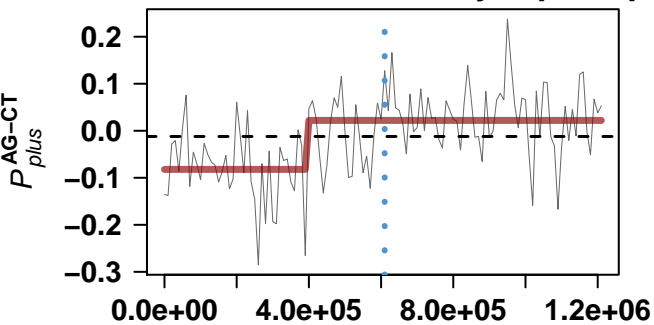


genome coordinates

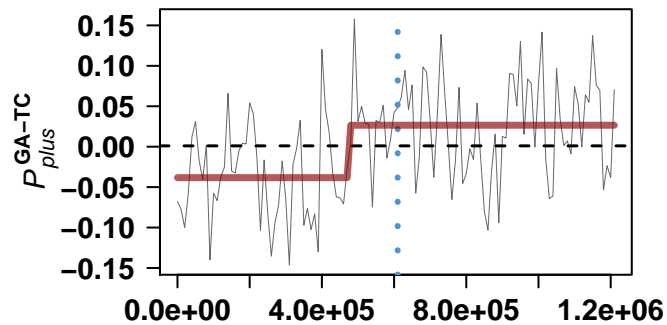


genome coordinates

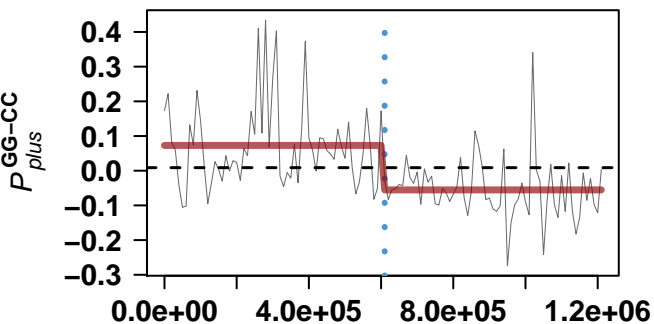
Chlamydophila pneumoniae TW-183



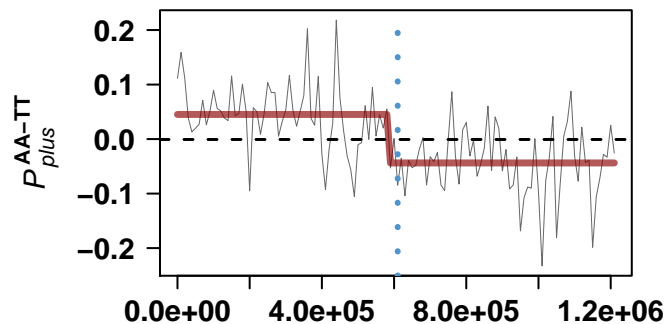
genome coordinates



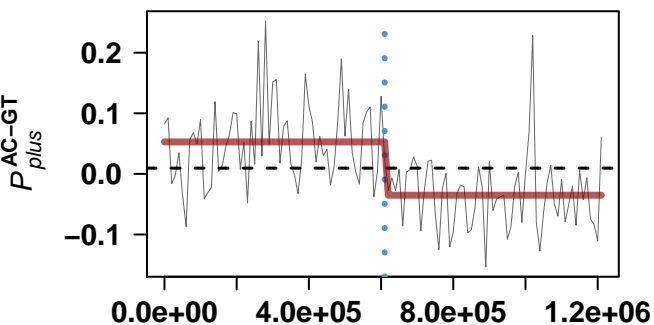
genome coordinates



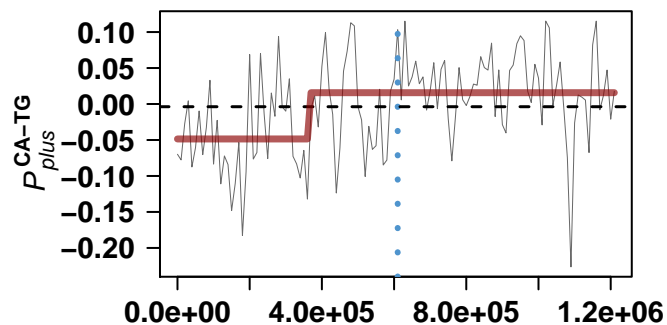
genome coordinates



genome coordinates

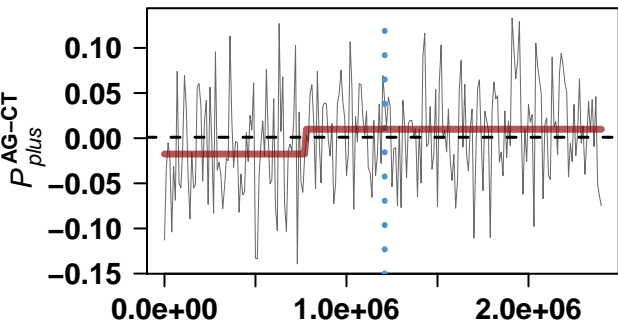


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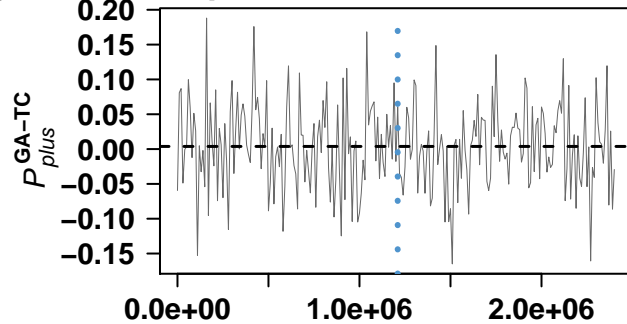


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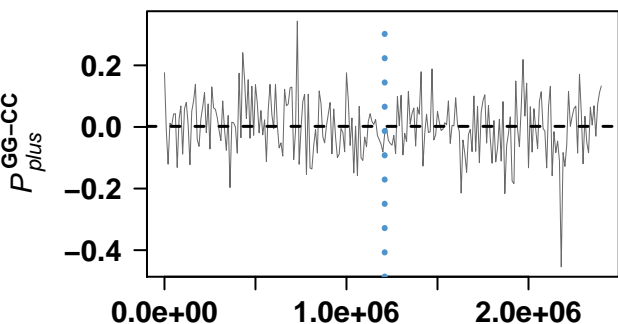
Candidatus Protochlamydia amoebophila UWE25



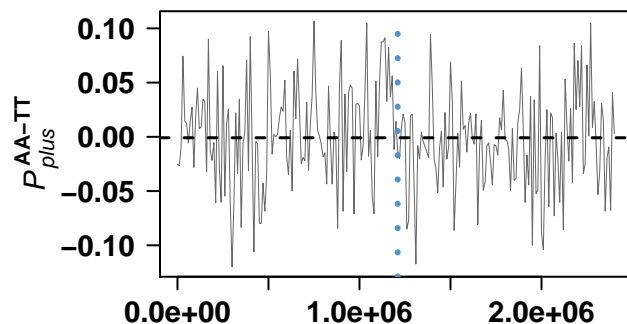
genome coordinates



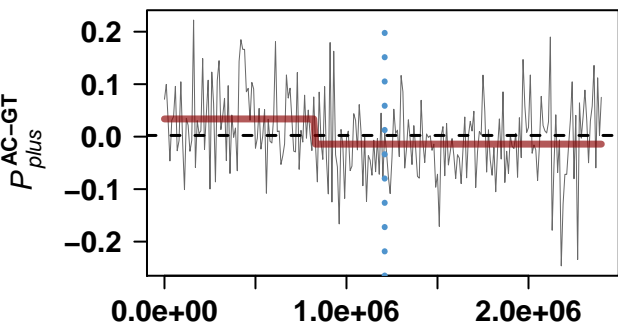
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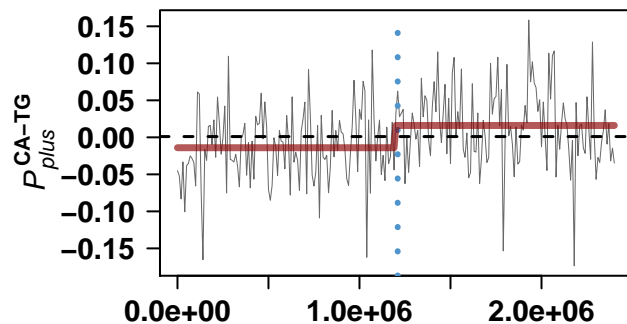
genome coordinates



genome coordinates

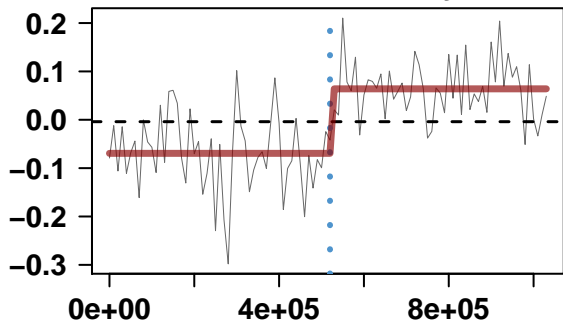


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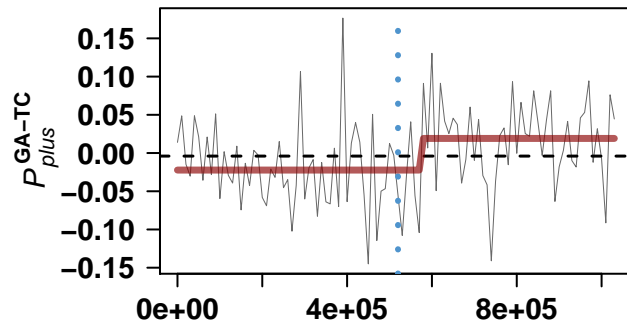


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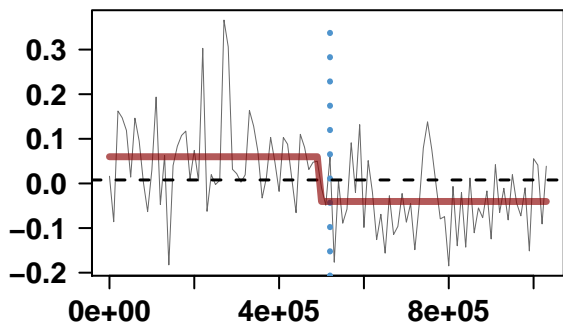
Chlamydia trachomatis A/HAR-13



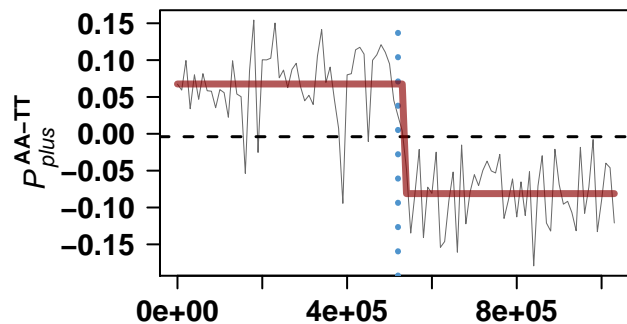
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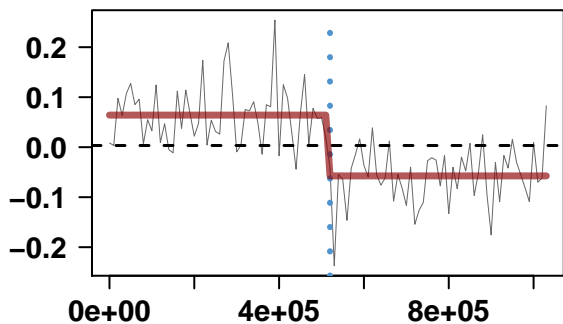
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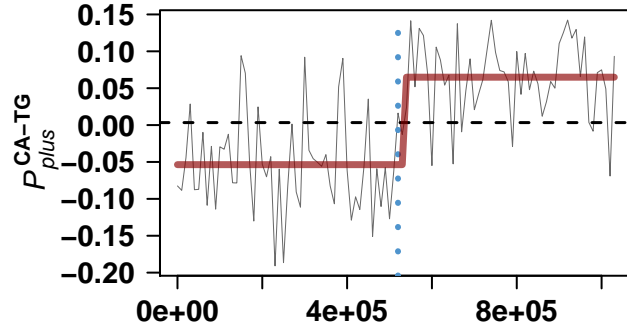
genome coordinates



genome coordinates

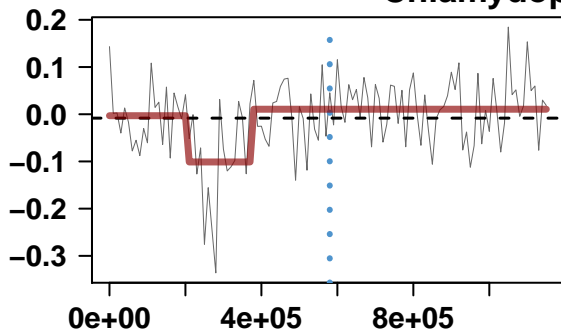


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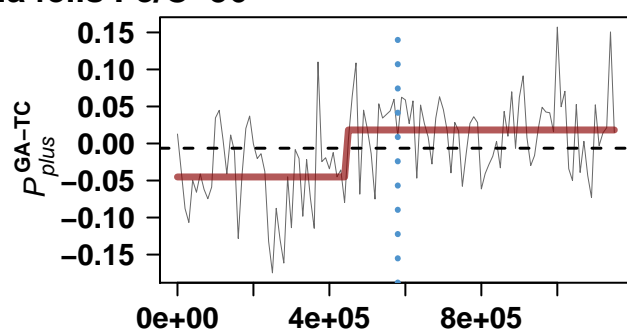


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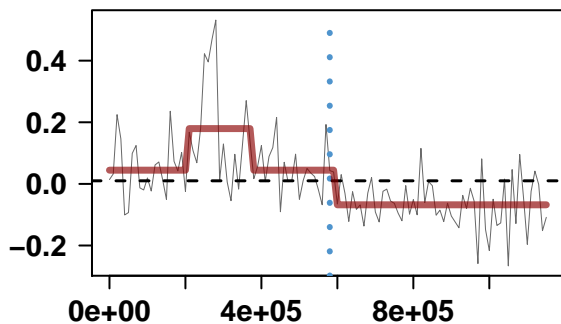
Chlamydophila felis Fe/C-56



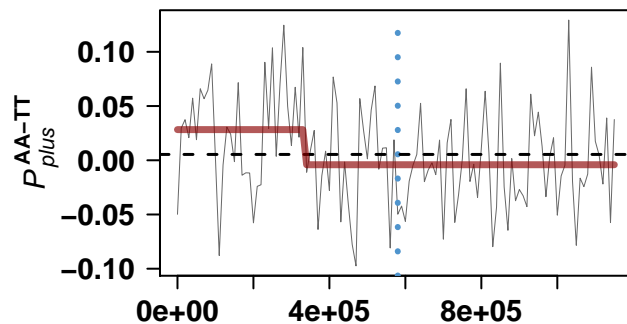
genome coordinates



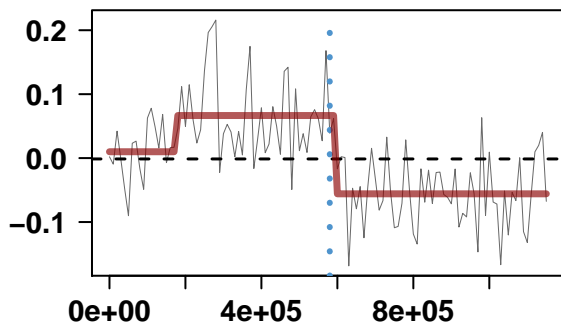
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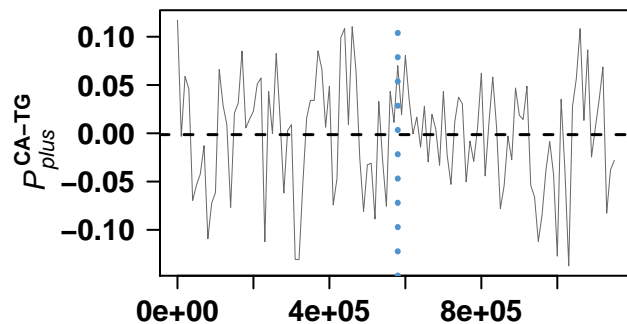
genome coordinates



genome coordinates

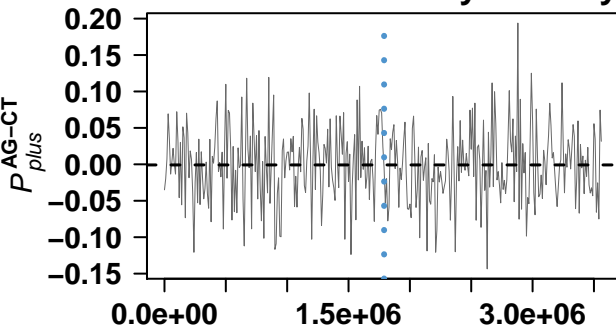


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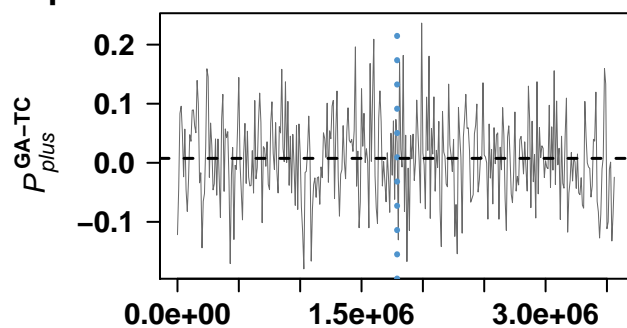


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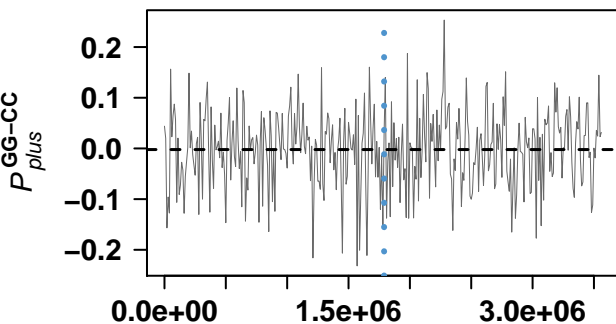
Synechocystis sp. PCC 6803



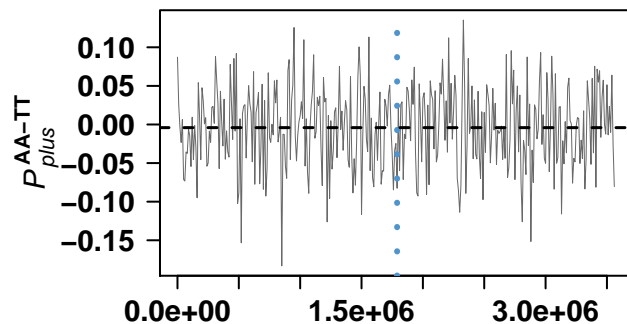
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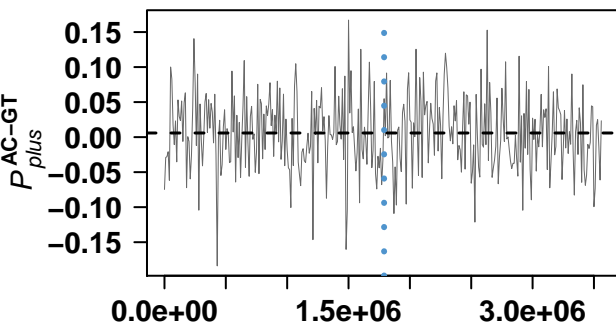
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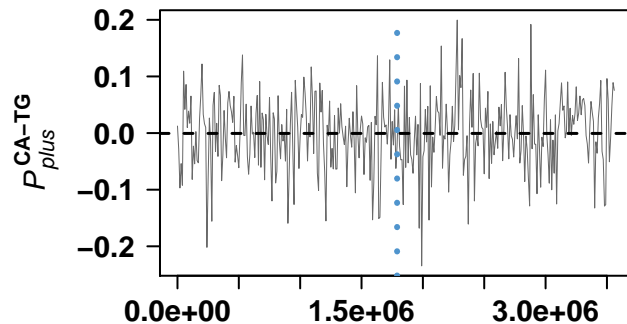
genome coordinates



genome coordinates

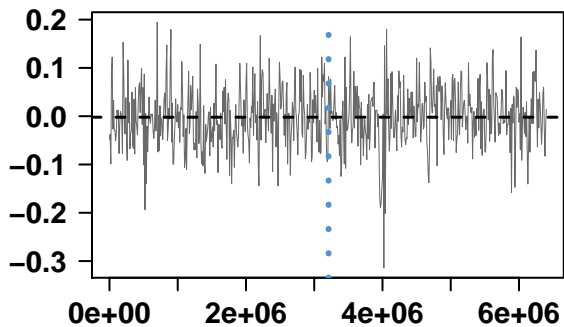


genome coordinates

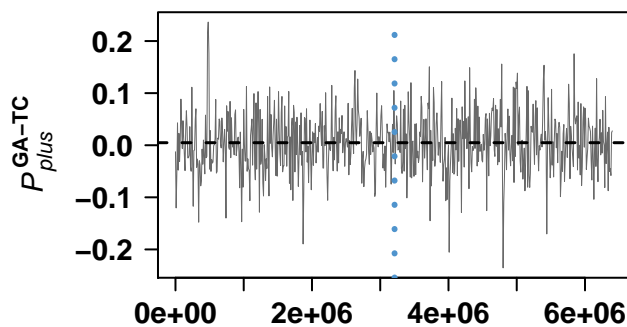


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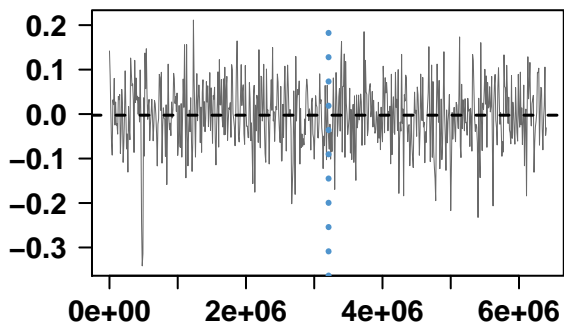
Nostoc sp. PCC 7120



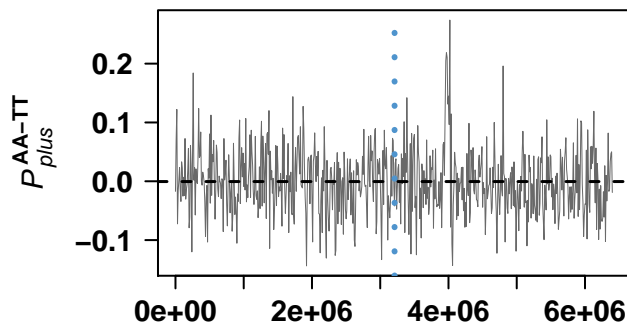
genome coordinates



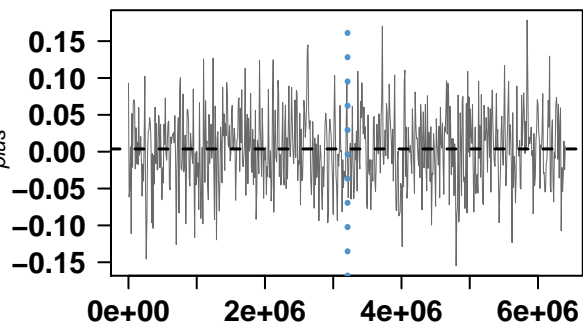
genome coordinates



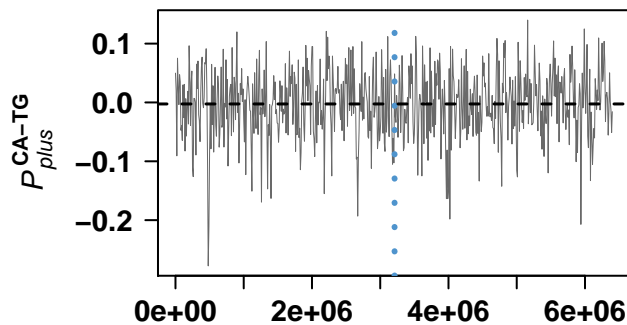
genome coordinates



genome coordinates

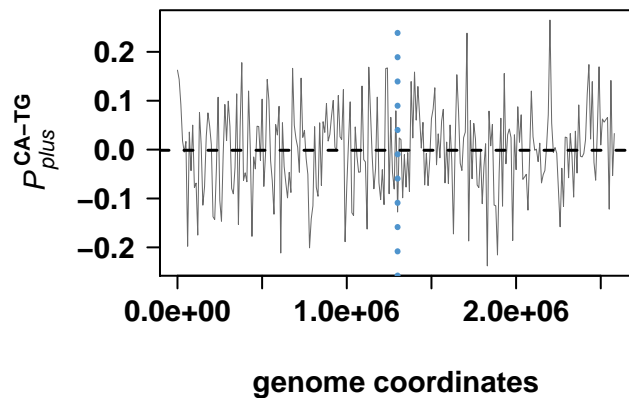
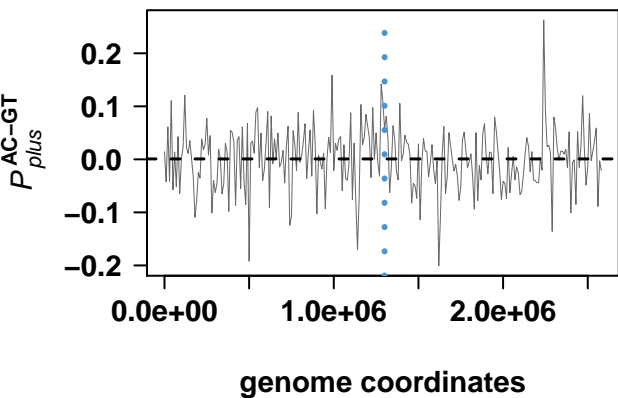
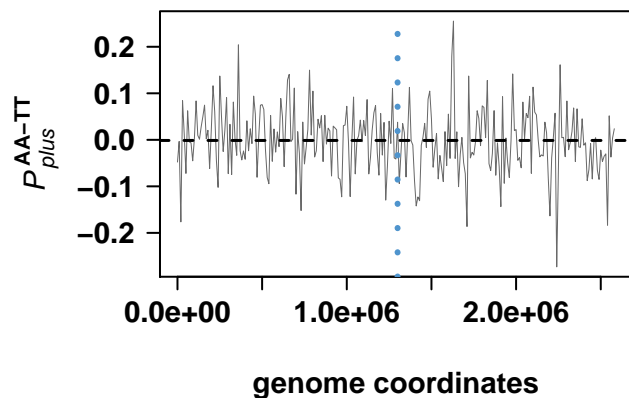
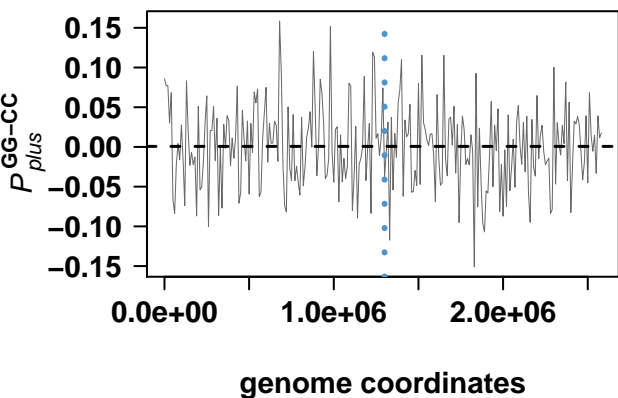
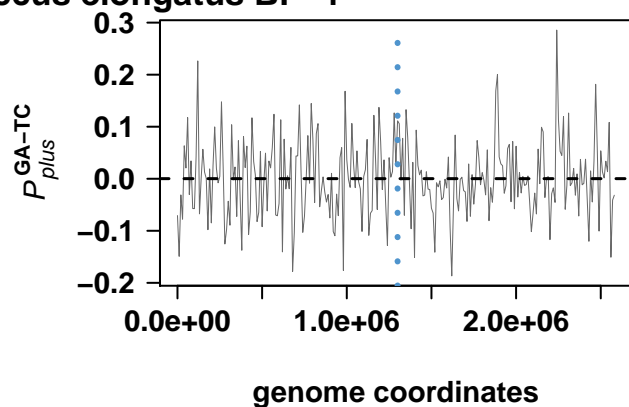
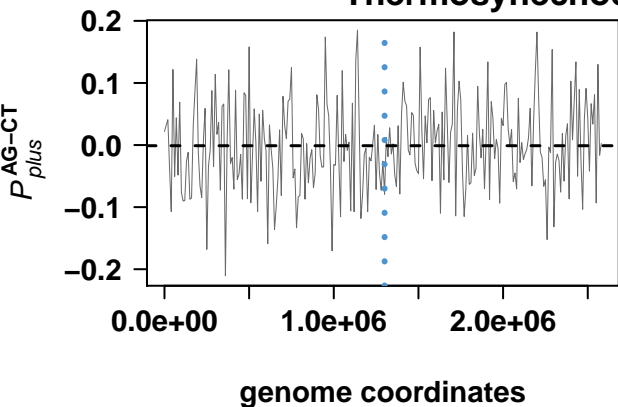


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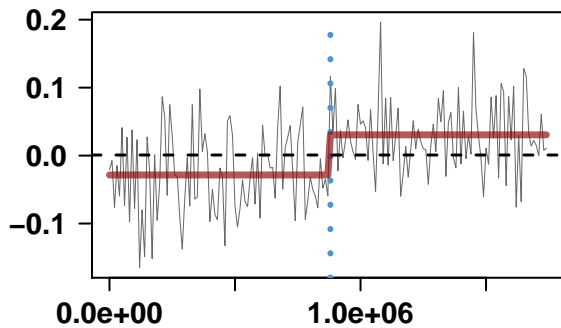


genome coordinates

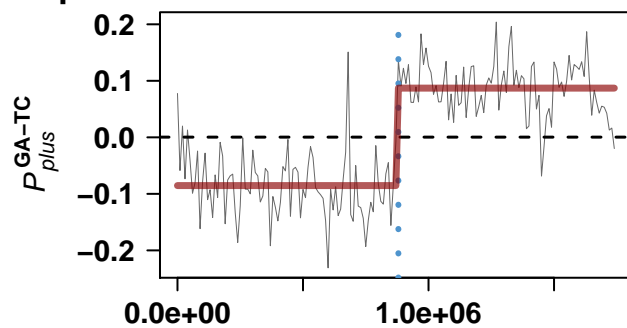
Thermosynechococcus elongatus BP-1



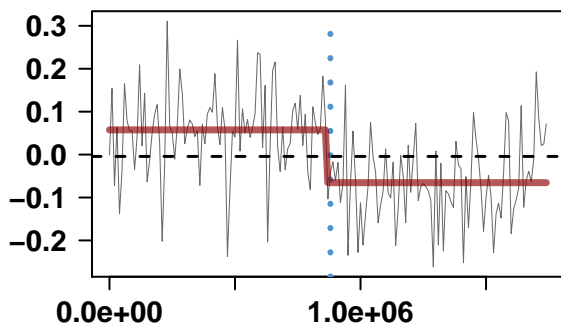
Prochlorococcus marinus subsp. marinus str. CCMP1375



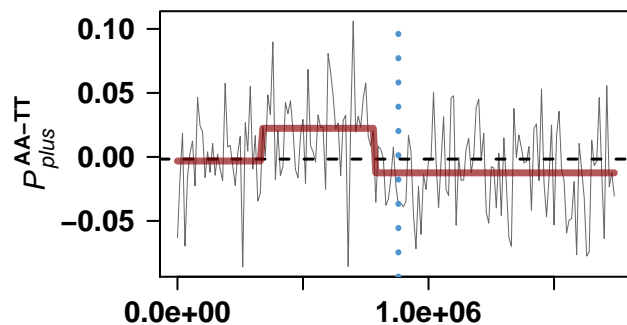
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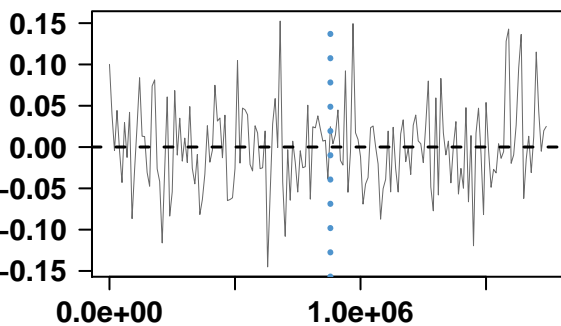
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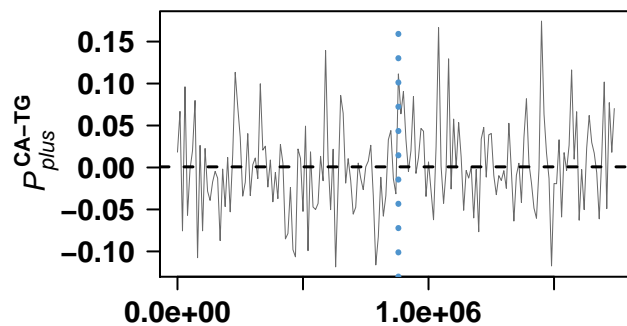
genome coordinates



genome coordinates

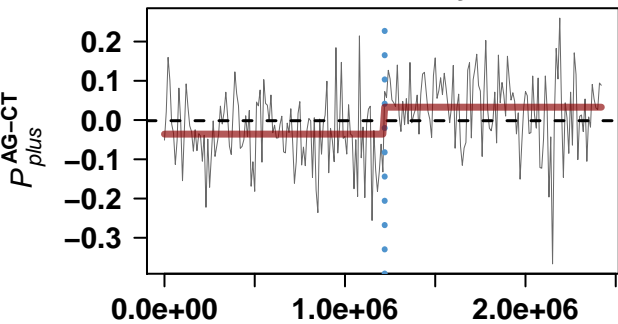


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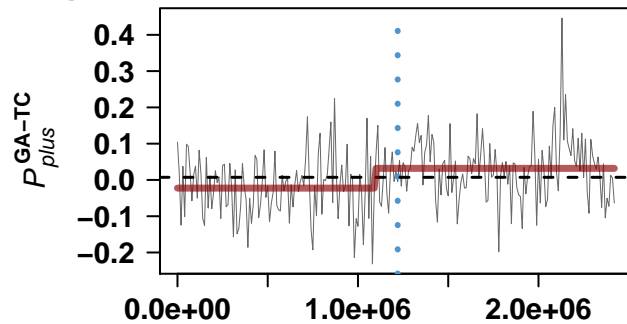


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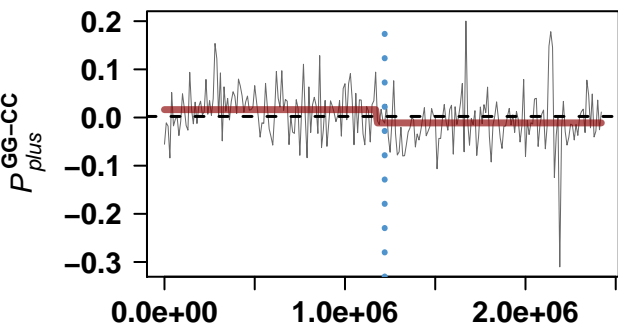
Synechococcus sp. WH 8102



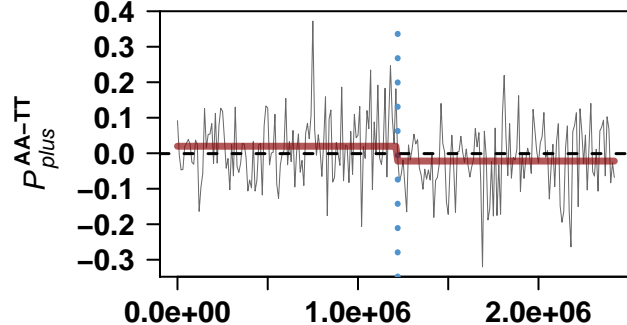
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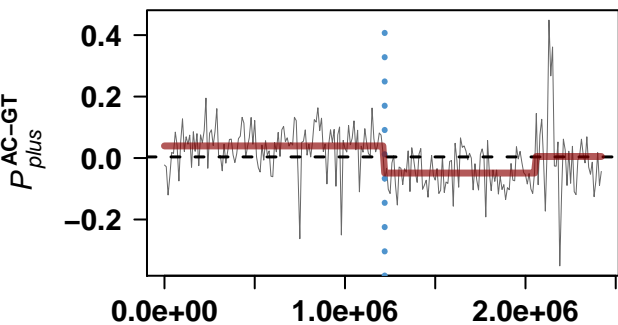
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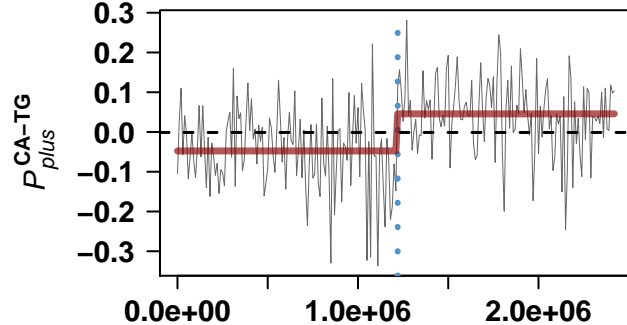
genome coordinates



genome coordinates

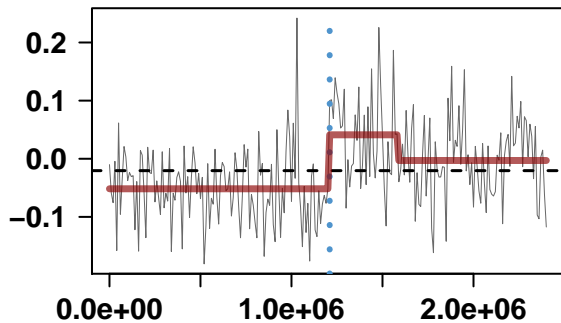


genome coordinates

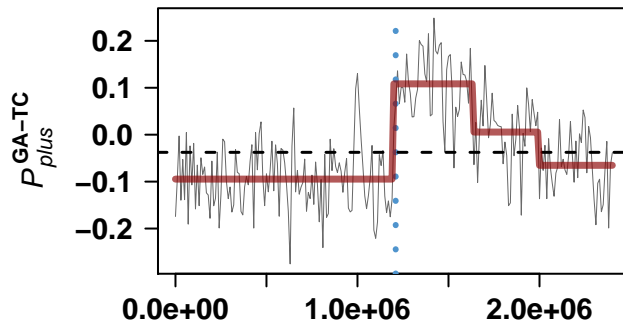


genome coordinates

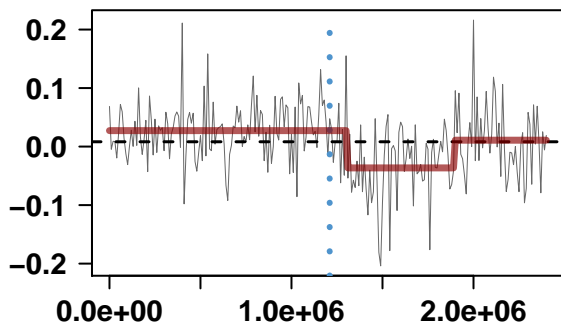
Prochlorococcus marinus str. MIT 9313



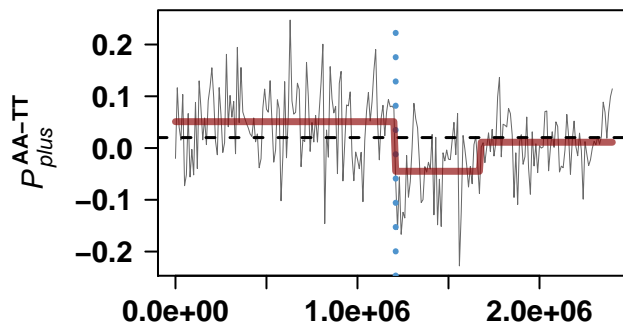
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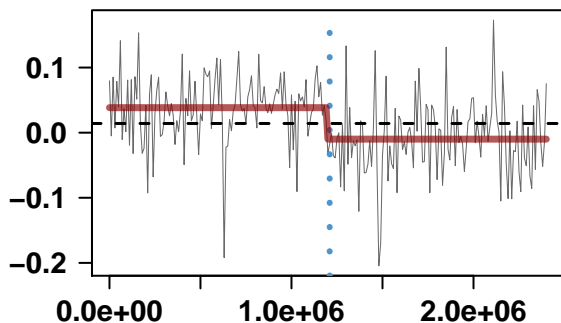
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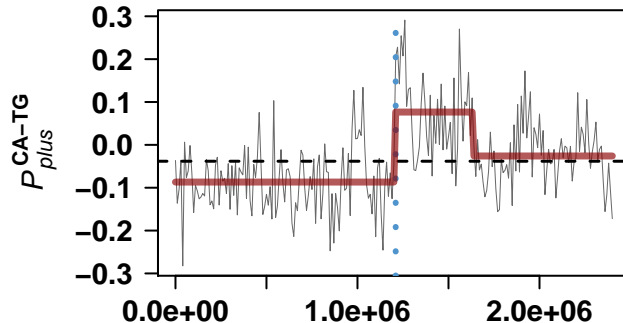
genome coordinates



genome coordinates

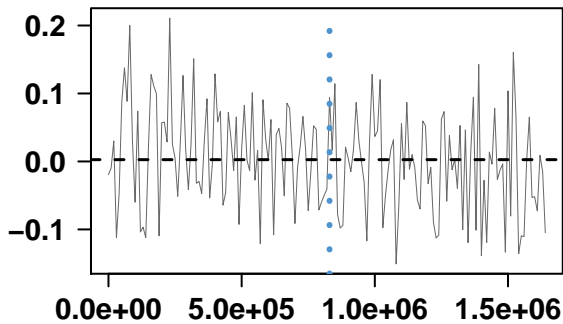


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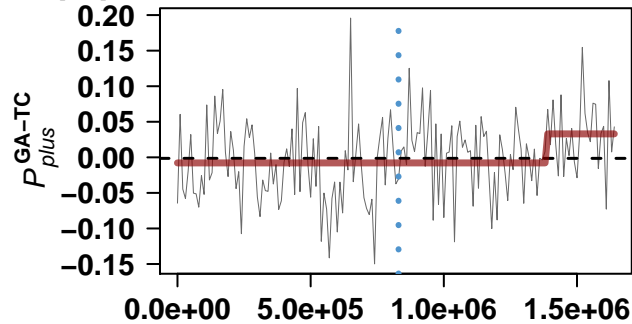


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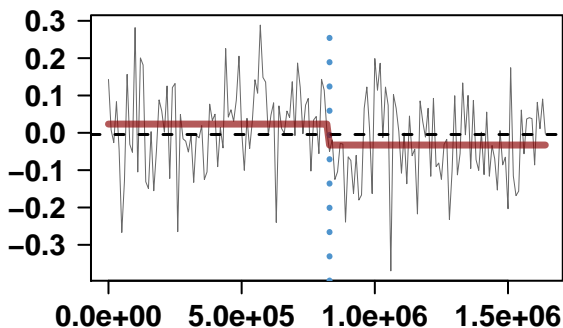
Prochlorococcus marinus subsp. pastoris str. CCMP1986



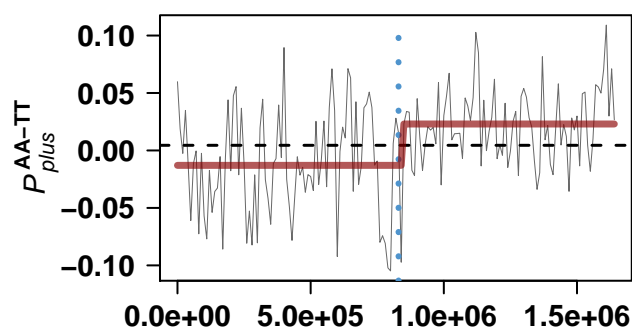
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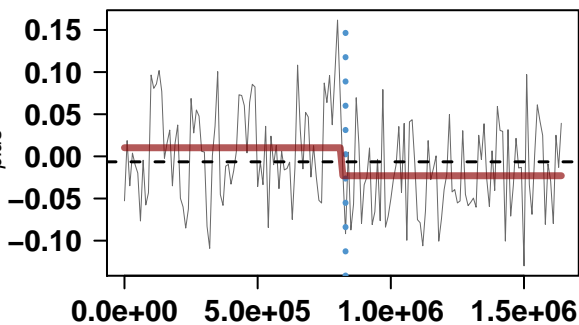
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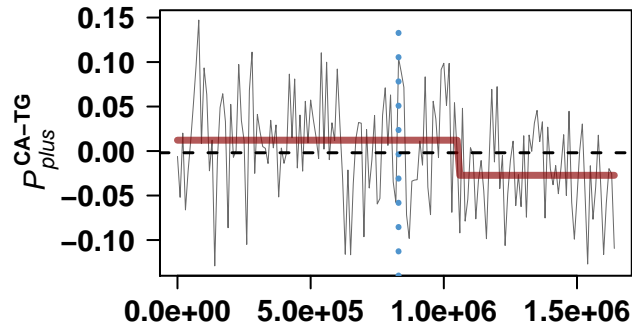
genome coordinates



genome coordinates

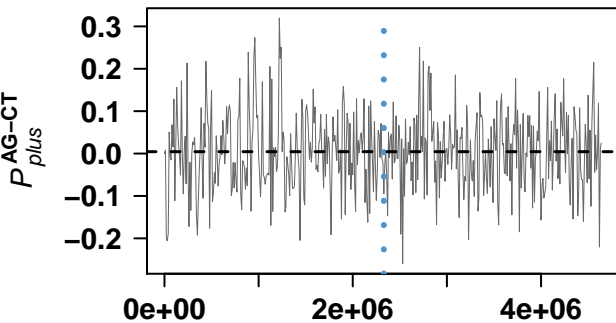


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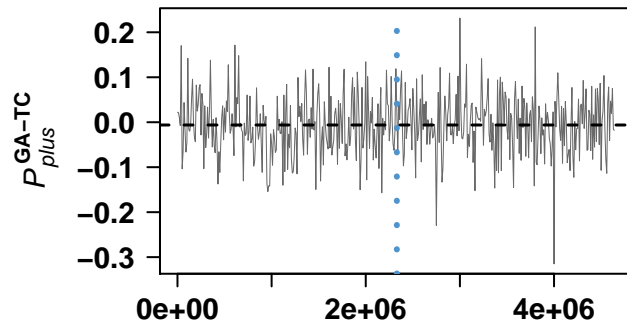


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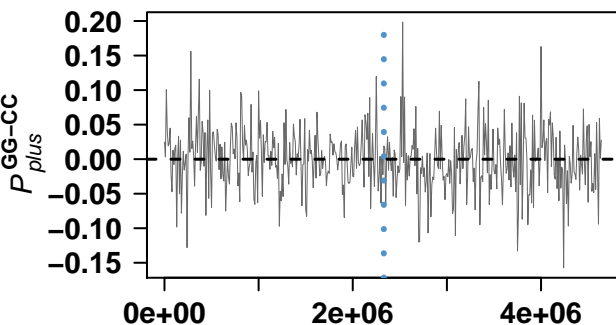
Gloeobacter violaceus PCC 7421



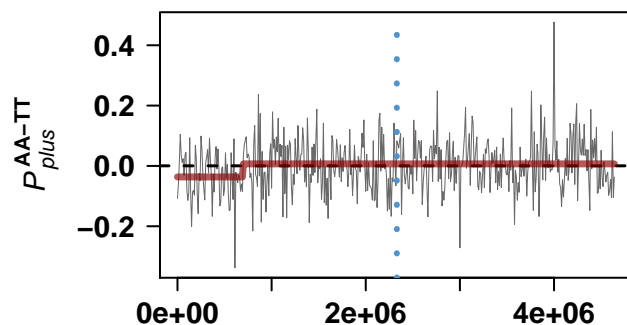
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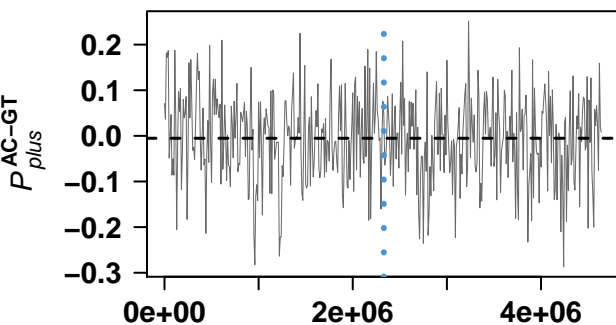
genome coordinates



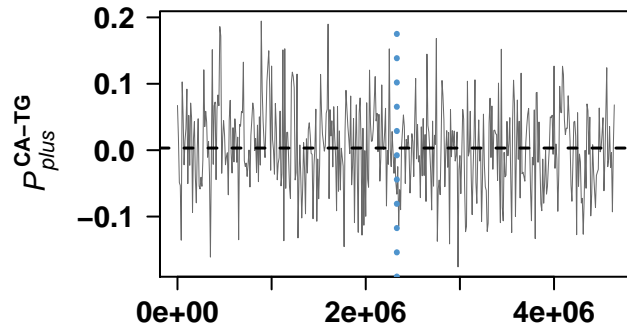
genome coordinates



genome coordinates

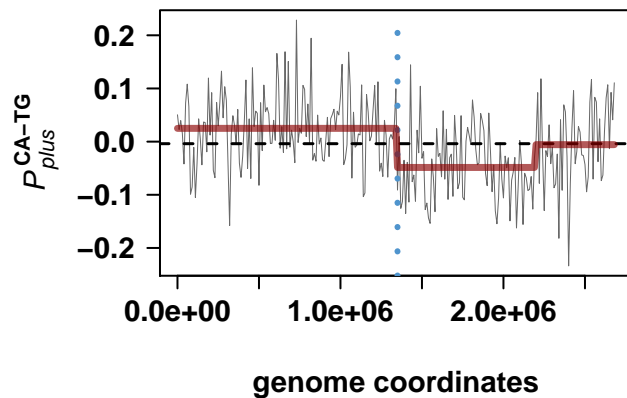
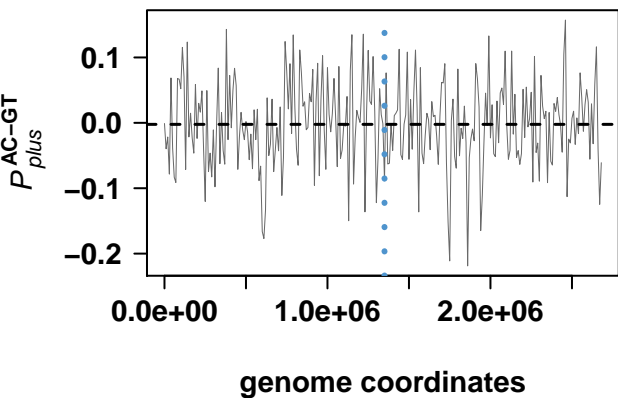
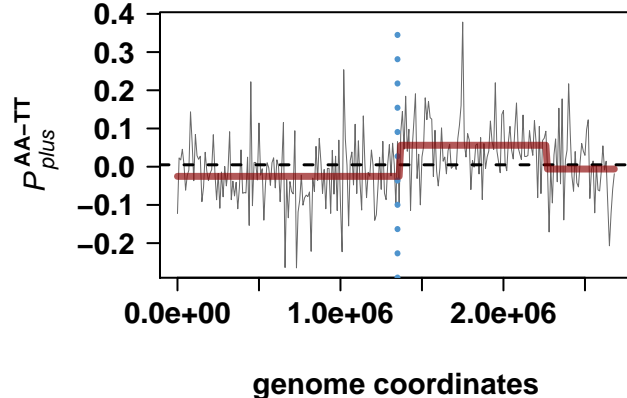
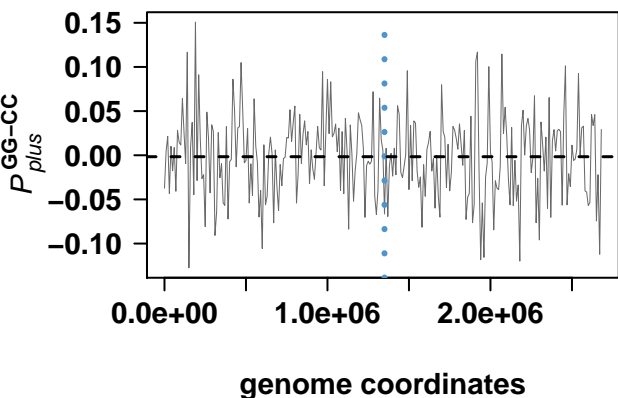
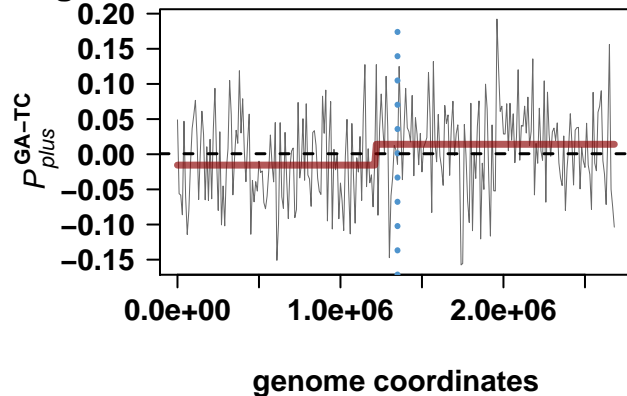
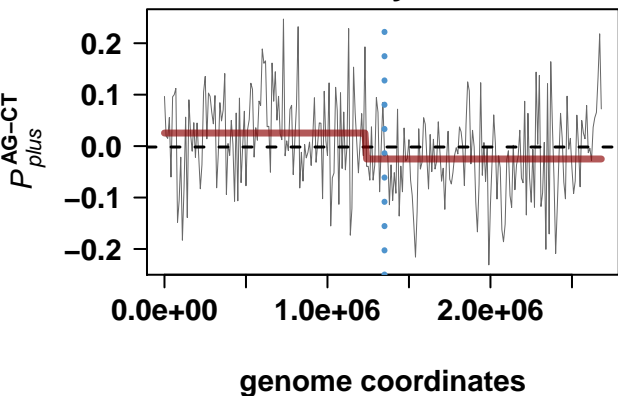


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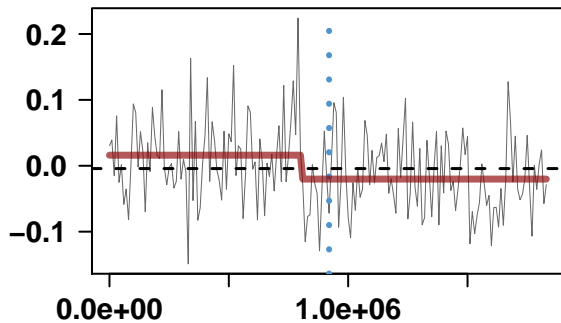


genome coordinates

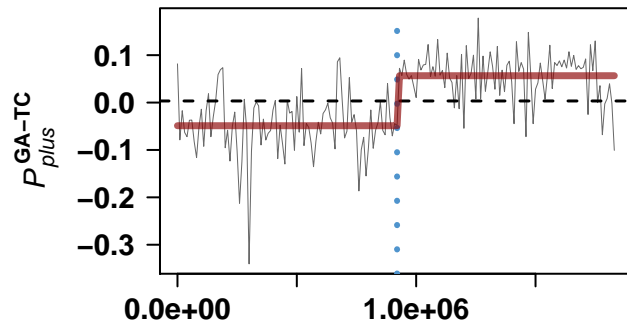
Synechococcus elongatus PCC 6301



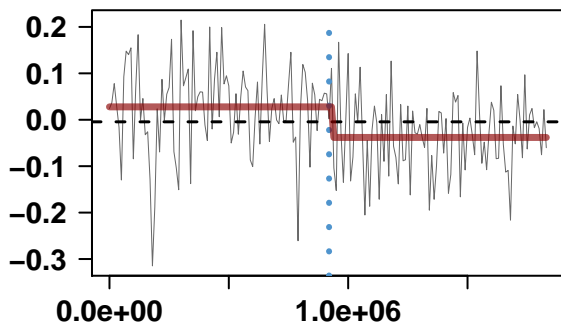
Prochlorococcus marinus str. NATL2A



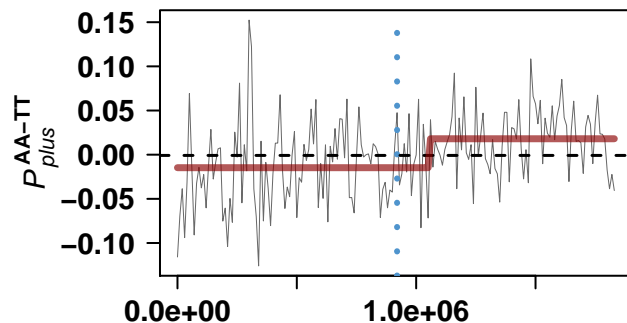
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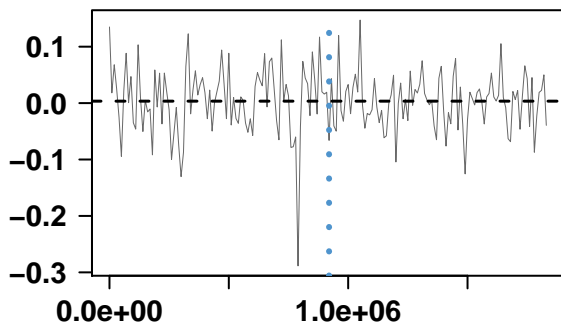
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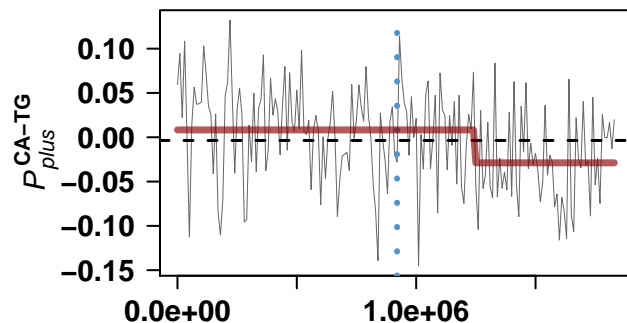
genome coordinates



genome coordinates

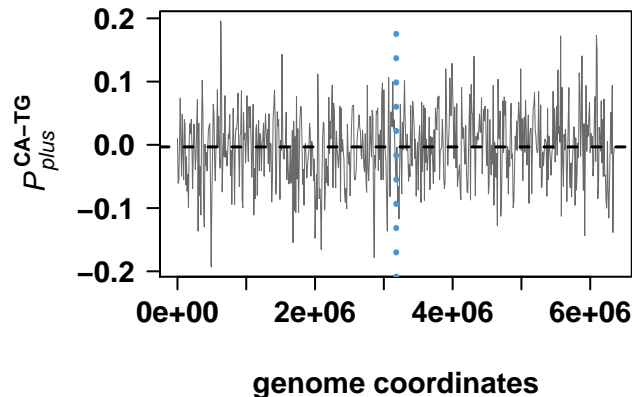
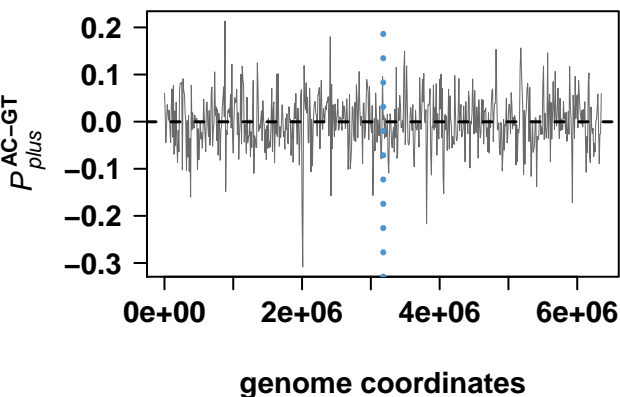
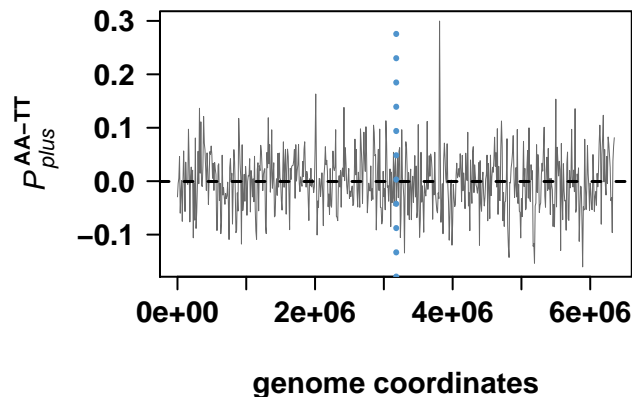
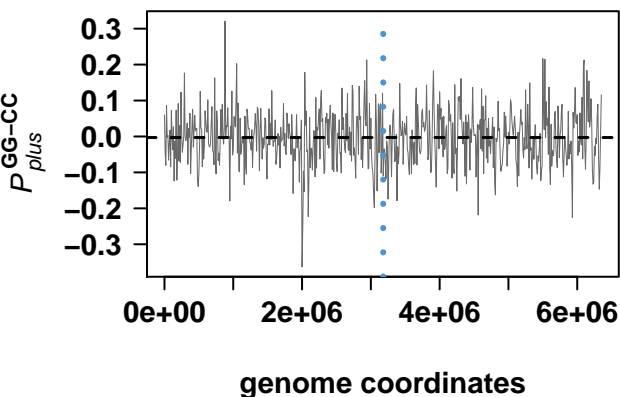
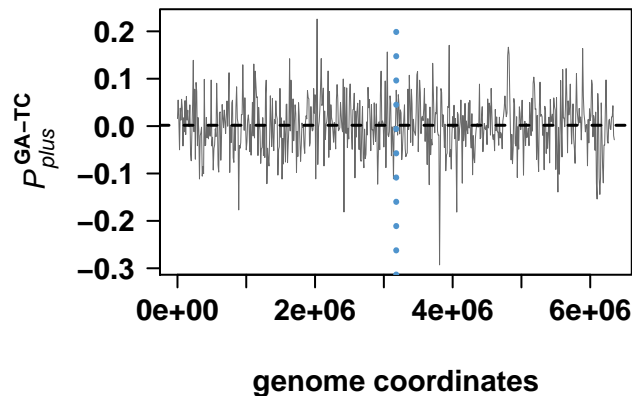
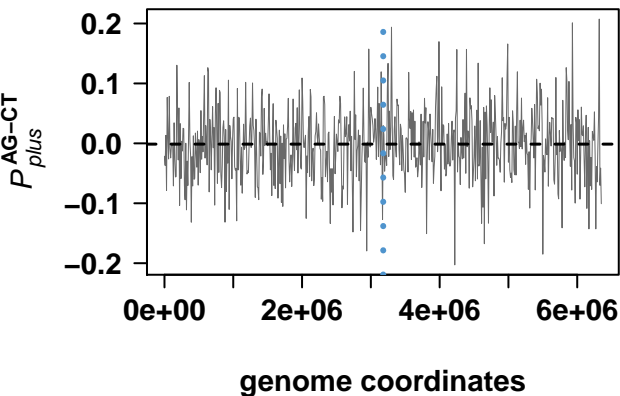


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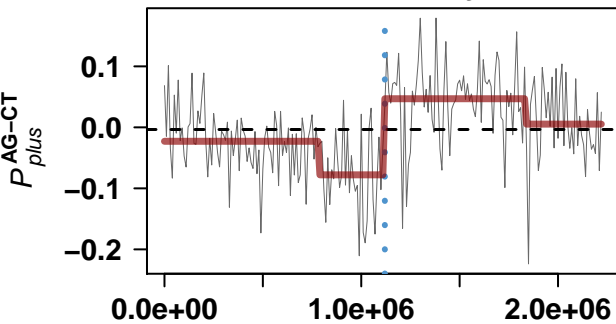


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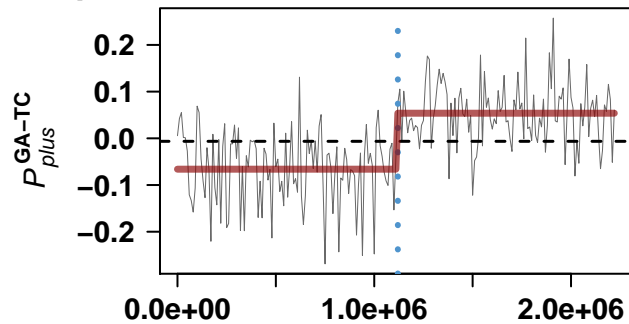
Anabaena variabilis ATCC 29413



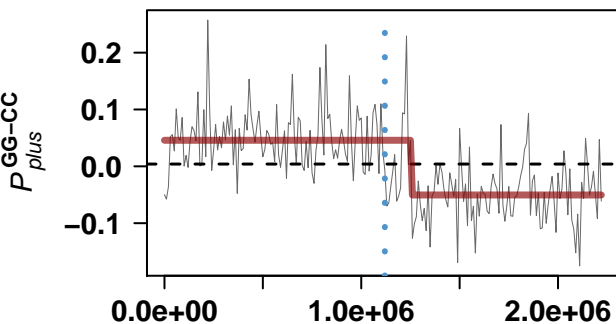
Synechococcus sp. CC9902



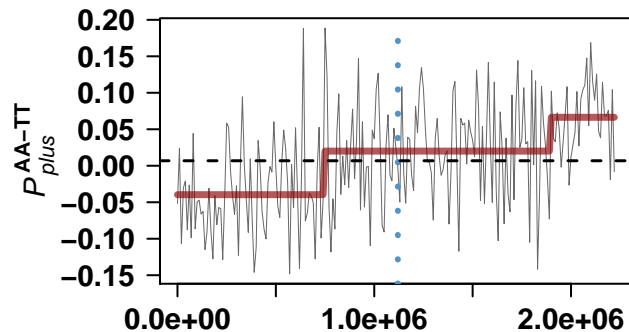
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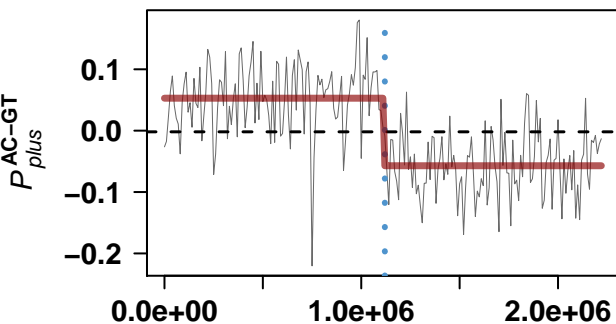
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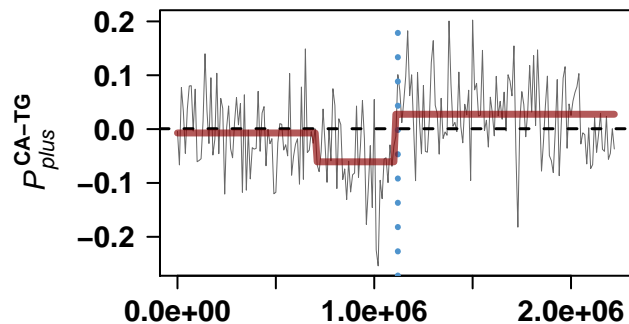
genome coordinates



genome coordinates

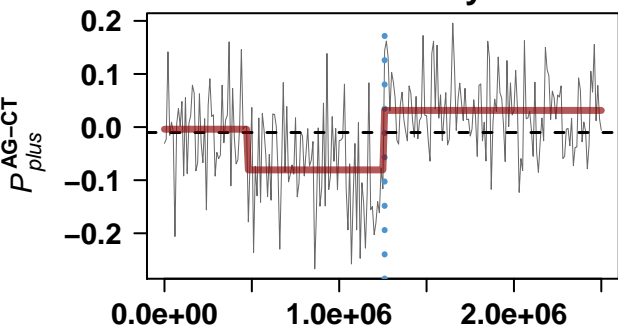


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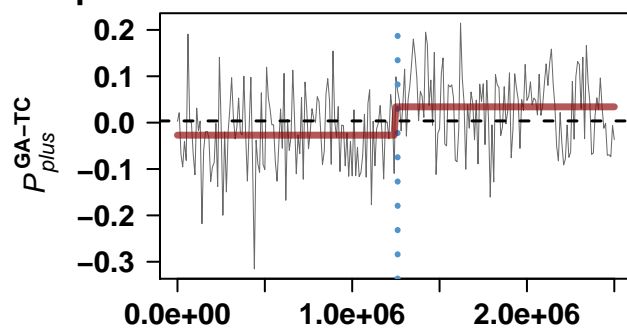


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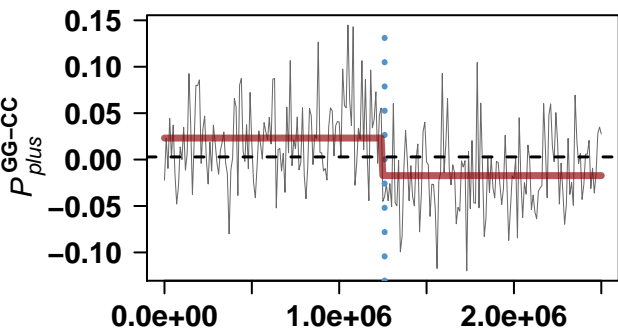
Synechococcus sp. CC9605



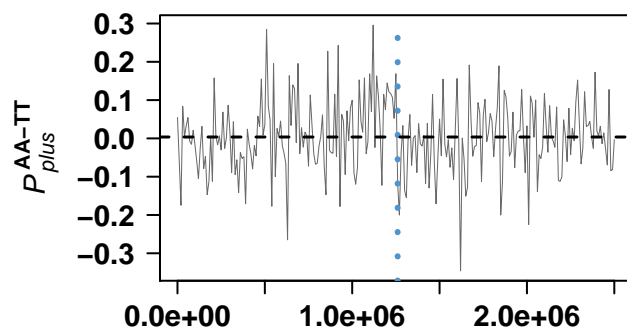
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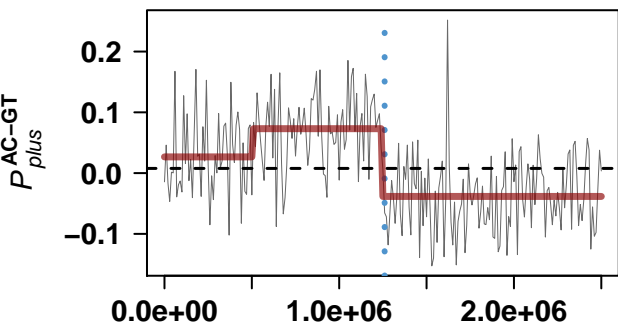
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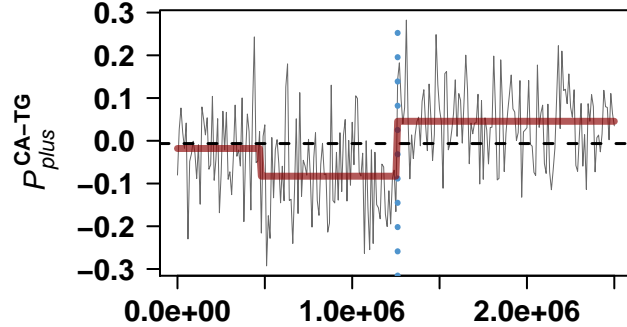
genome coordinates



genome coordinates

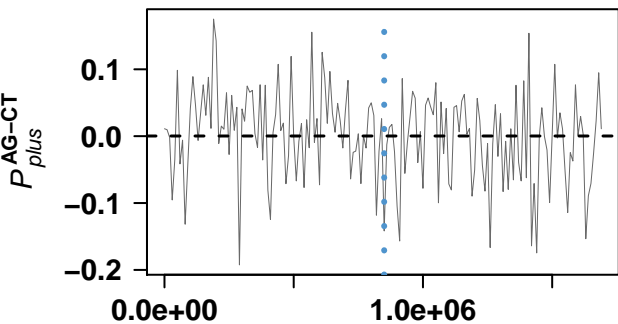


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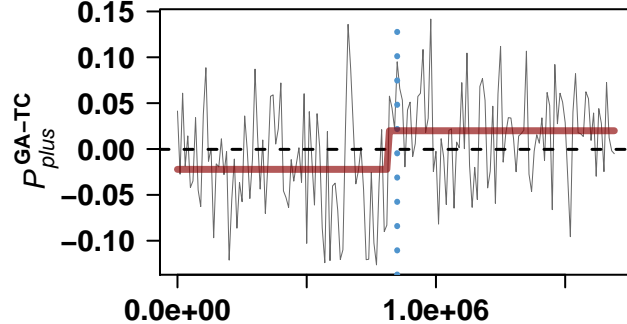


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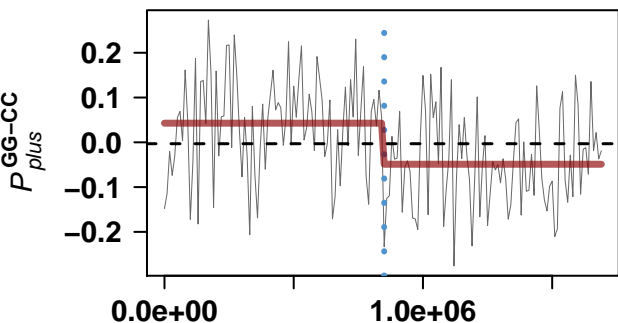
Prochlorococcus marinus str. MIT 9312



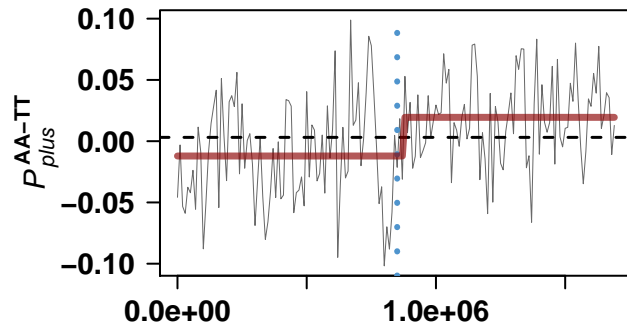
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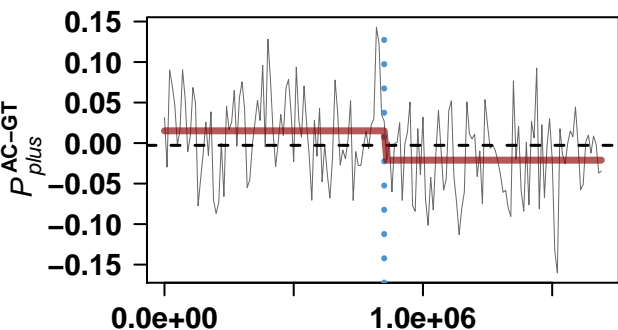
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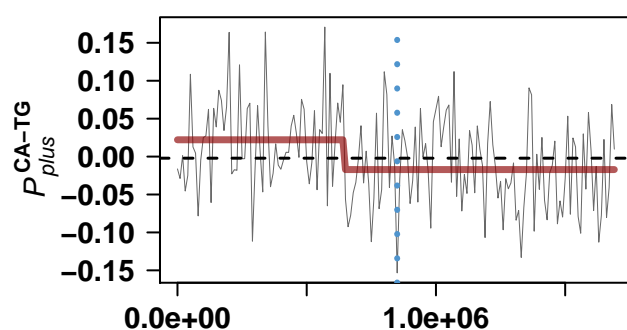
genome coordinates



genome coordinates

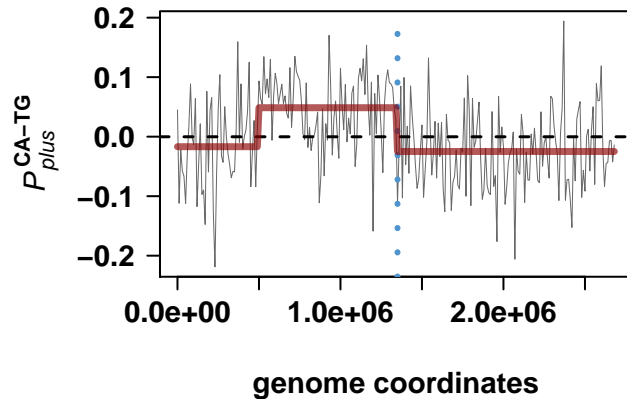
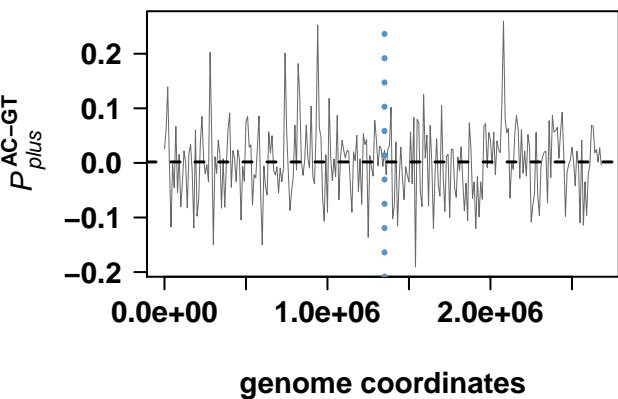
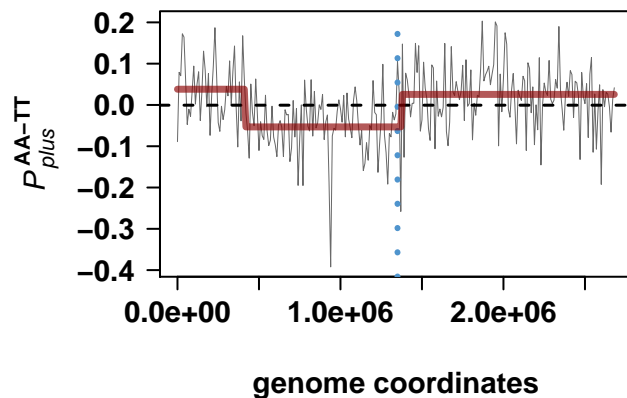
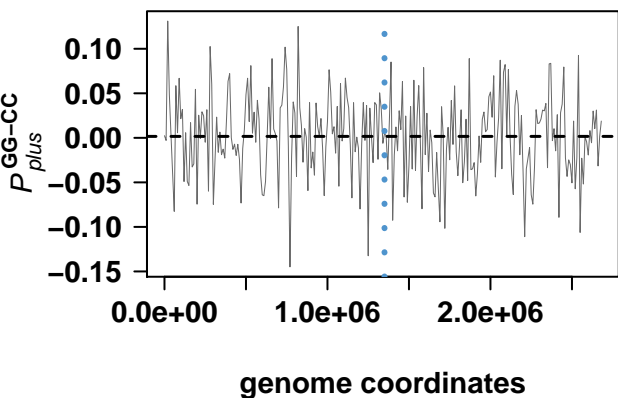
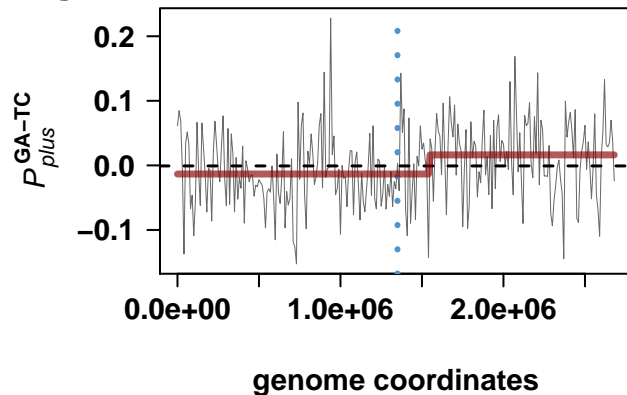
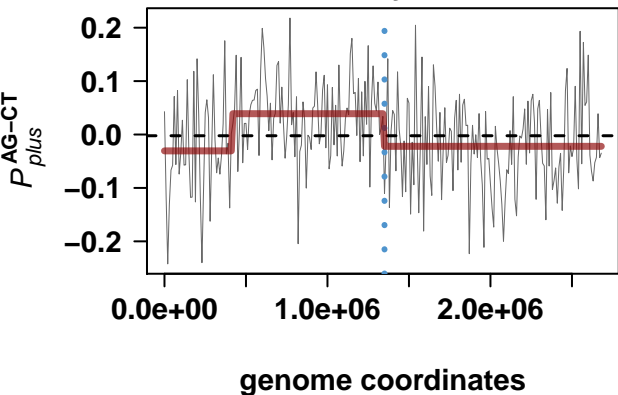


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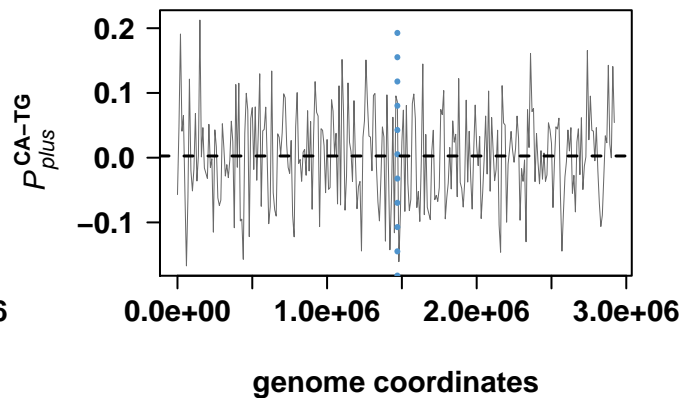
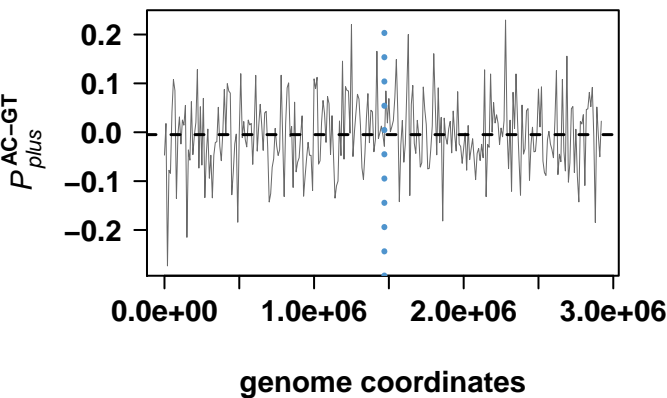
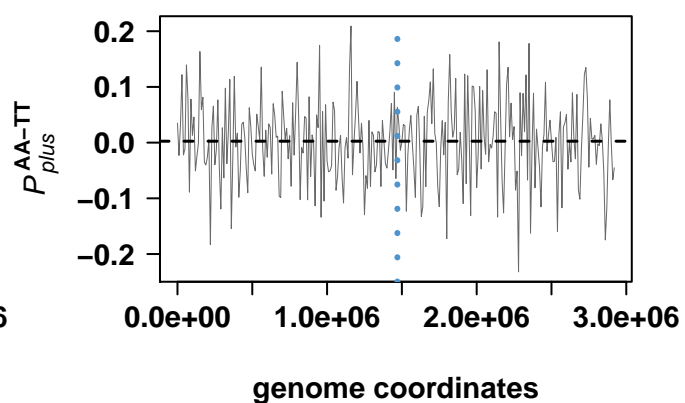
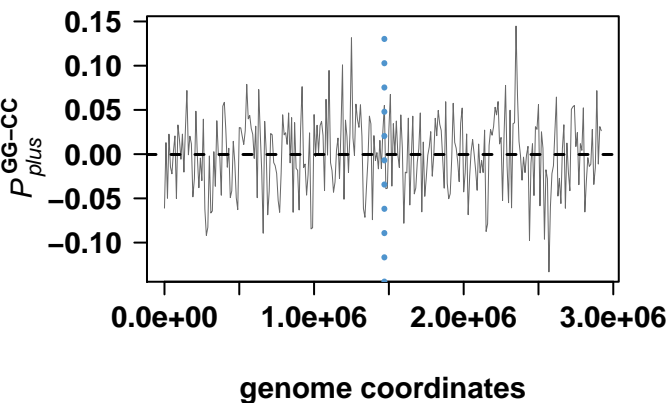
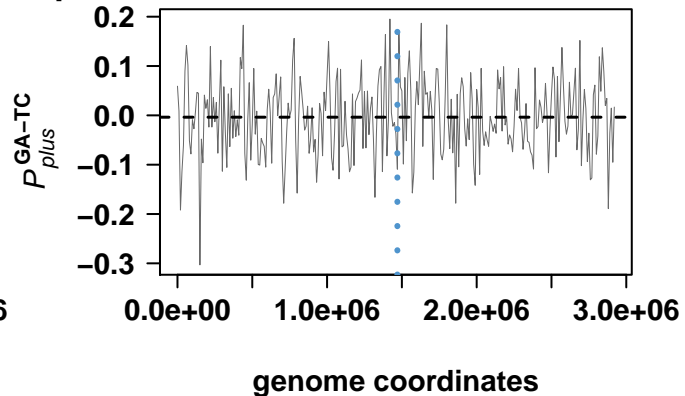
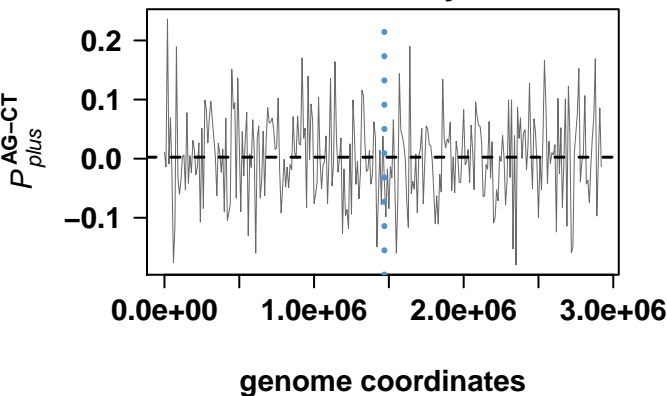


genome coordinates

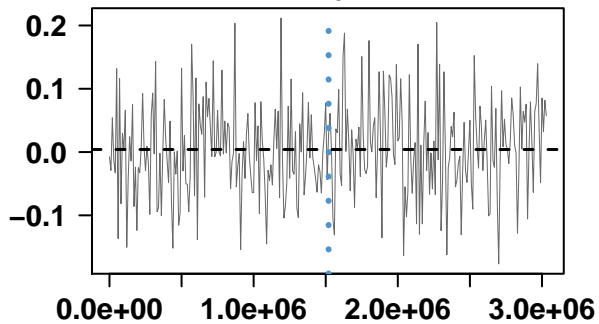
Synechococcus elongatus PCC 7942



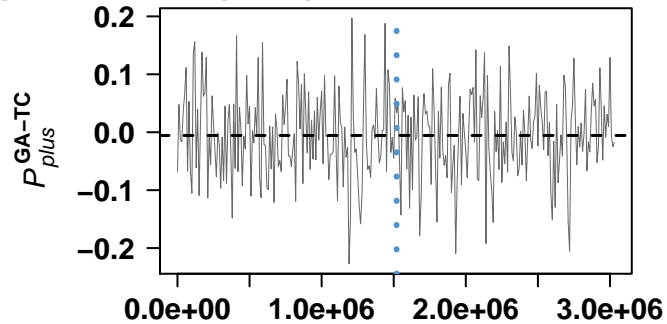
Synechococcus sp. JA-3-3Ab



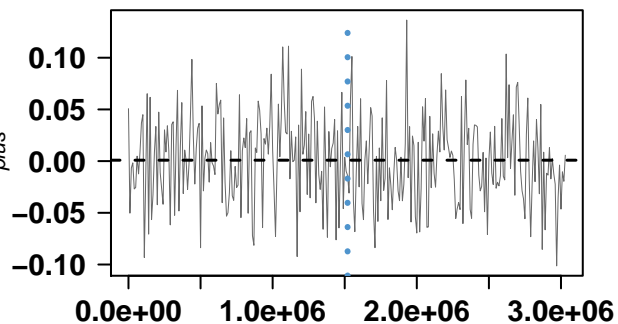
Synechococcus sp. JA-2-3B'a(2-13)



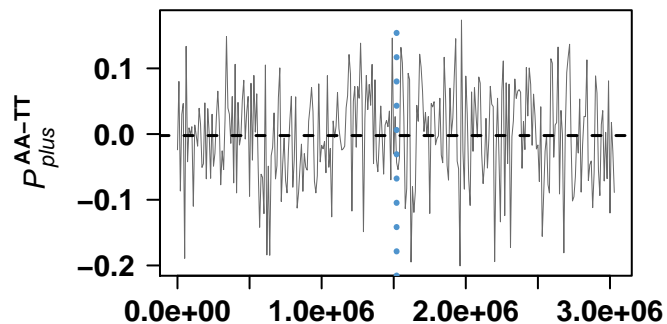
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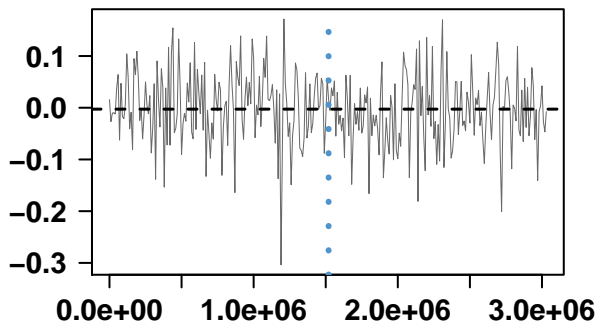
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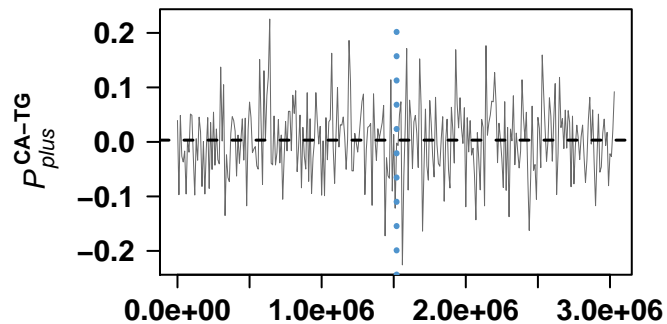
genome coordinates



genome coordinates

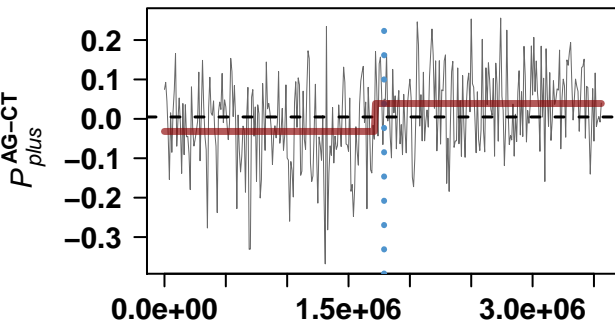


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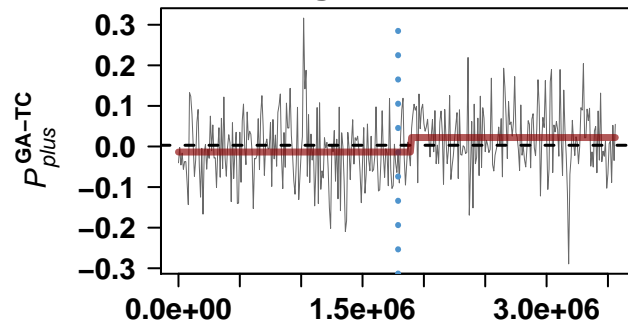


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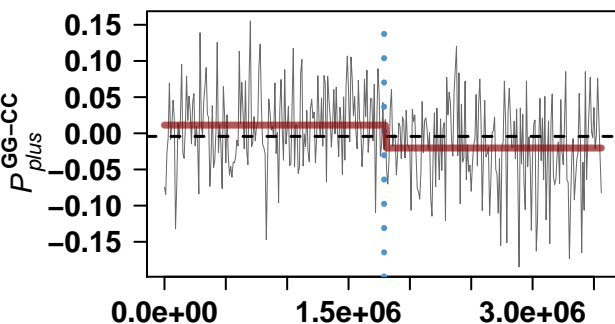
Desulfovibrio vulgaris str. Hildenborough



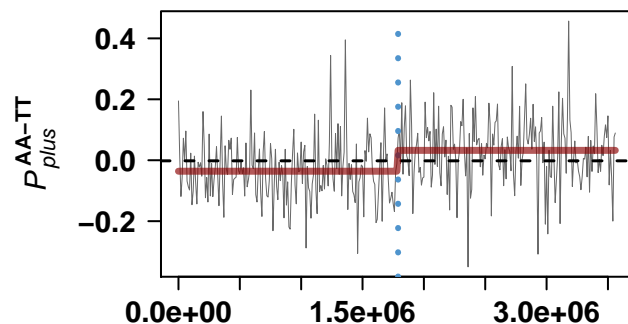
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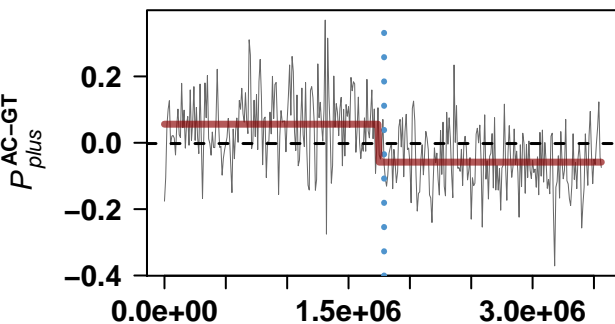
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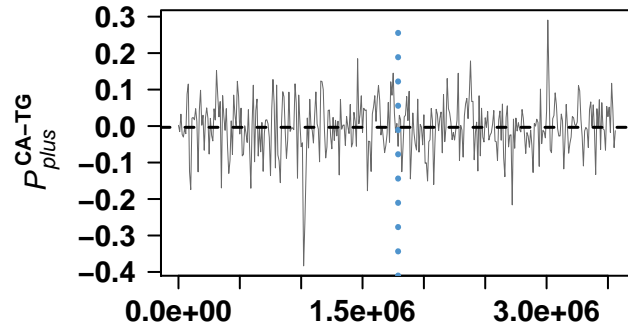
genome coordinates



genome coordinates

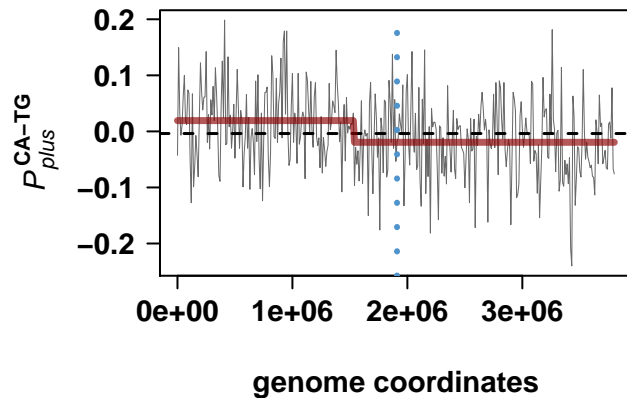
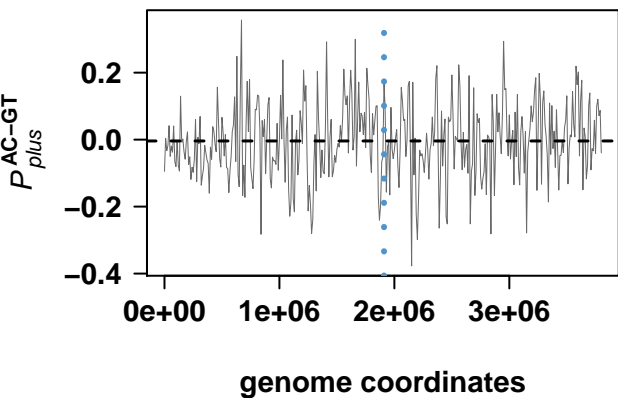
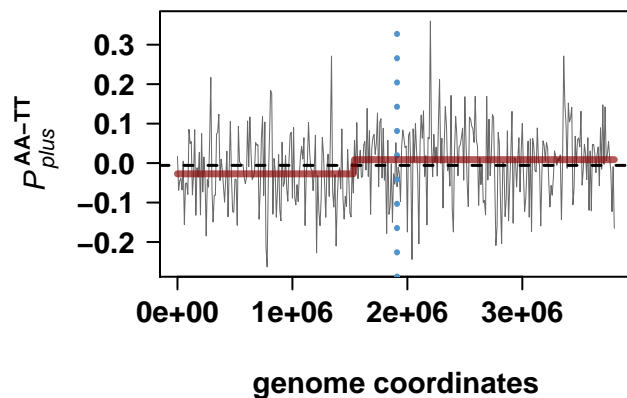
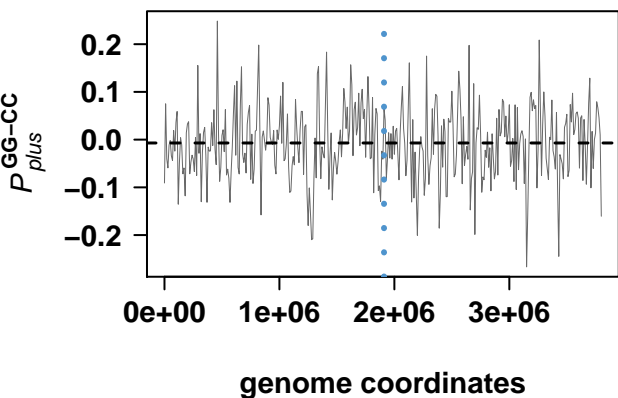
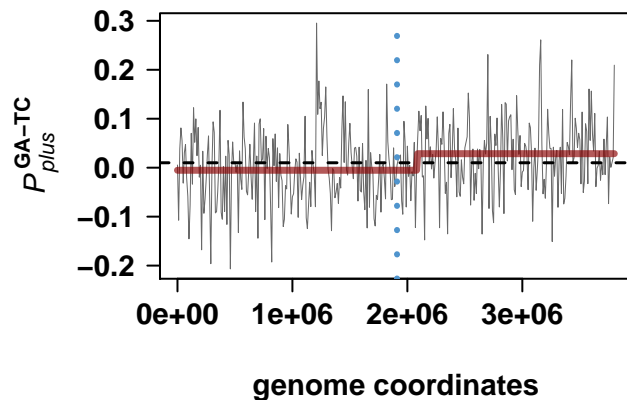
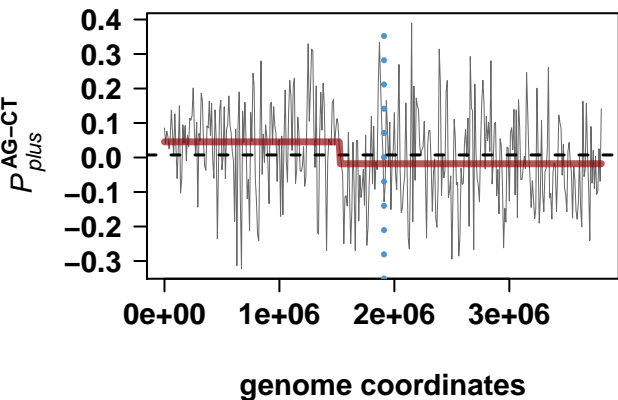


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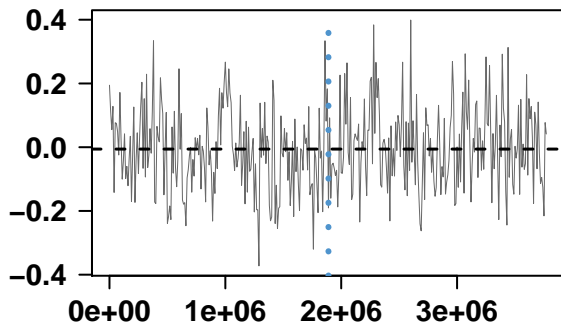


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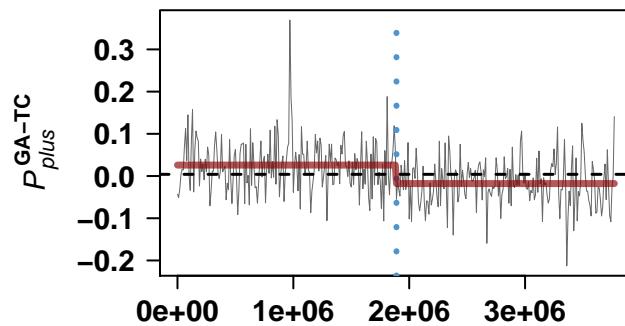
Geobacter sulfurreducens PCA



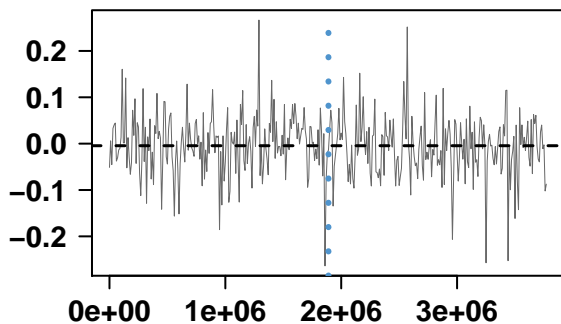
Bdellovibrio bacteriovorus HD100



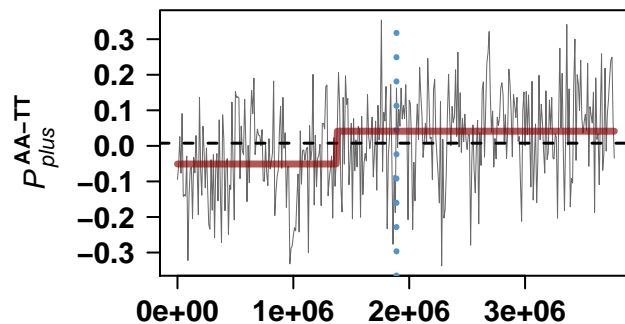
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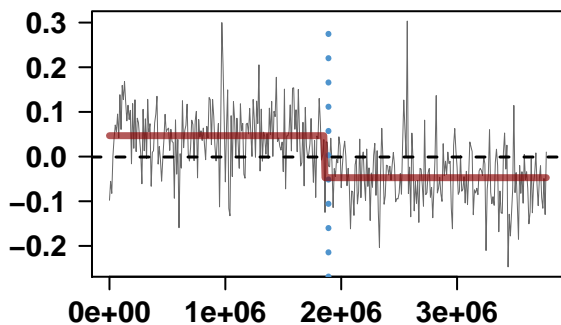
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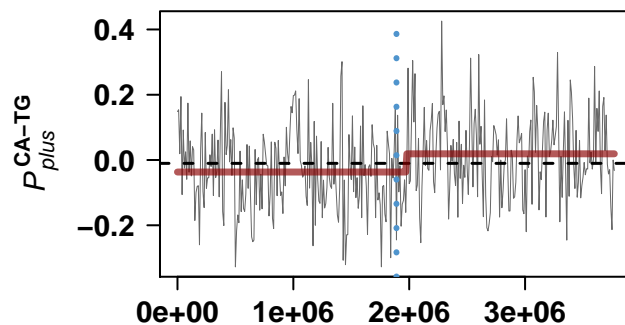
genome coordinates



genome coordinates

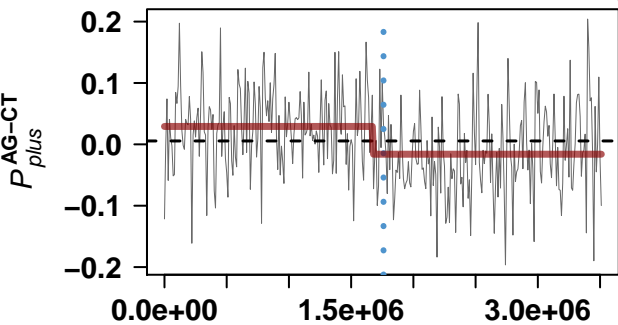


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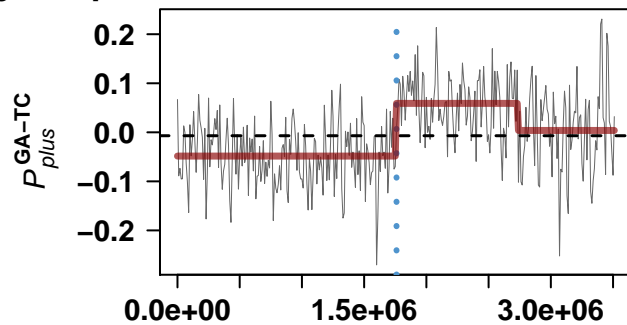


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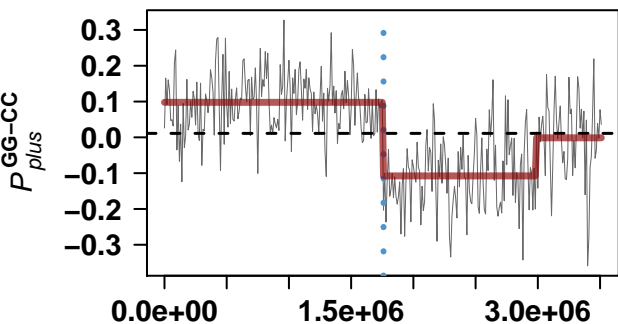
Desulfotalea psychrophila LSv54



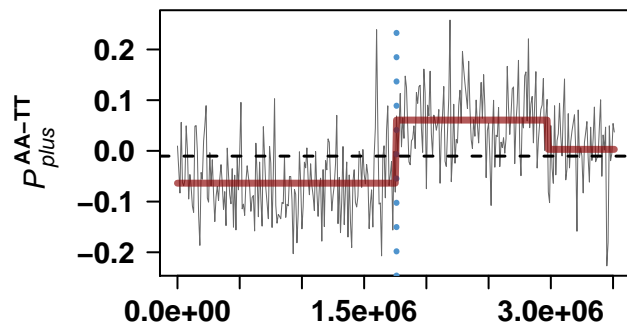
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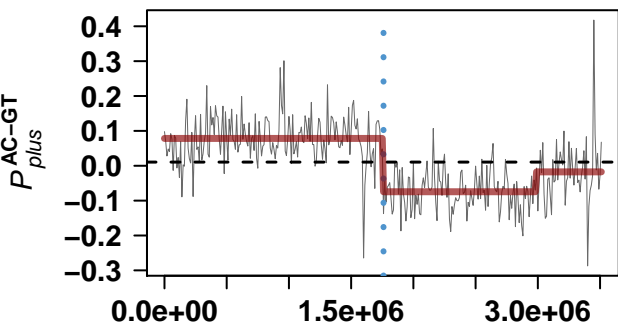
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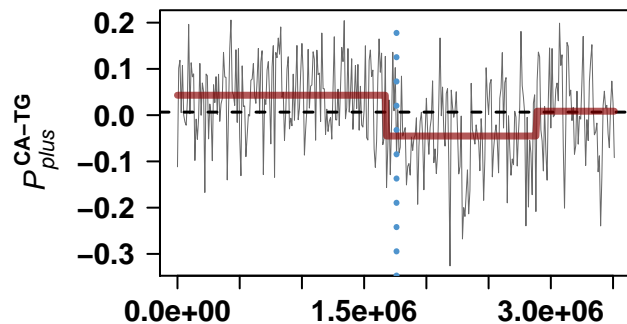
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genome coordinates

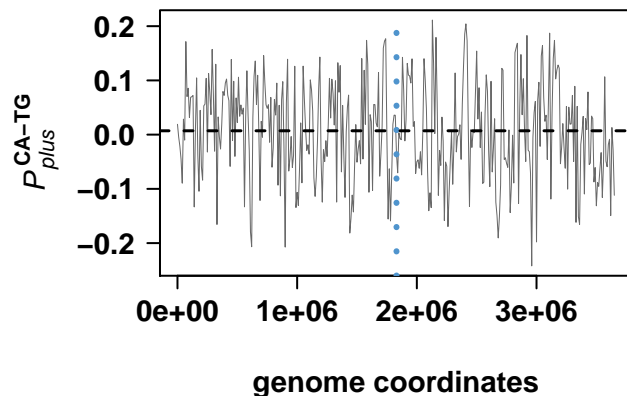
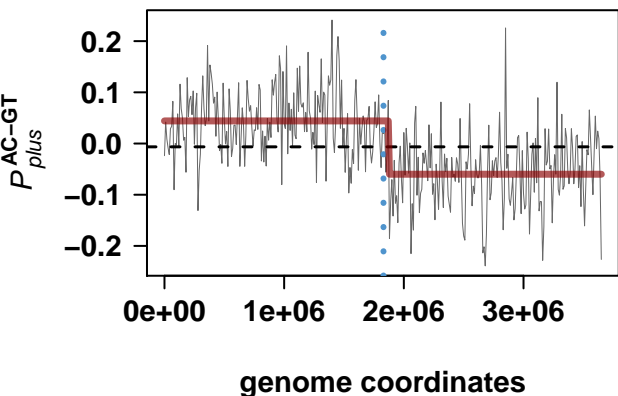
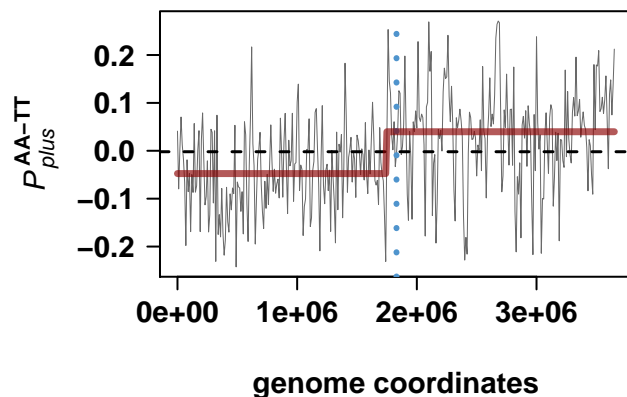
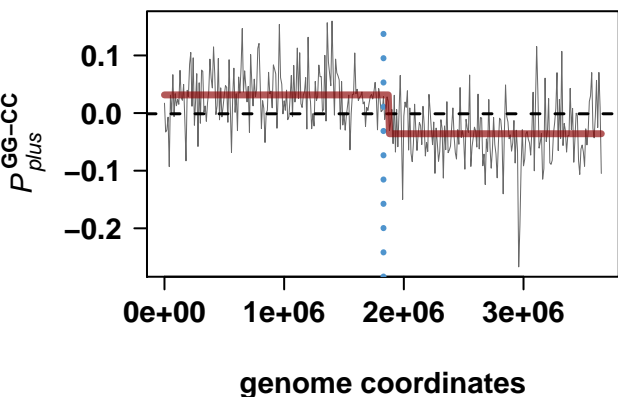
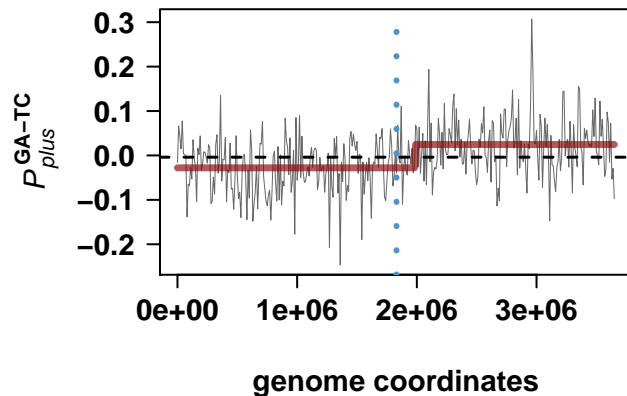
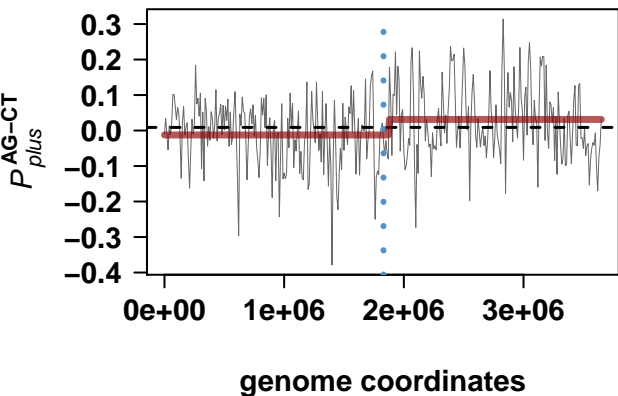


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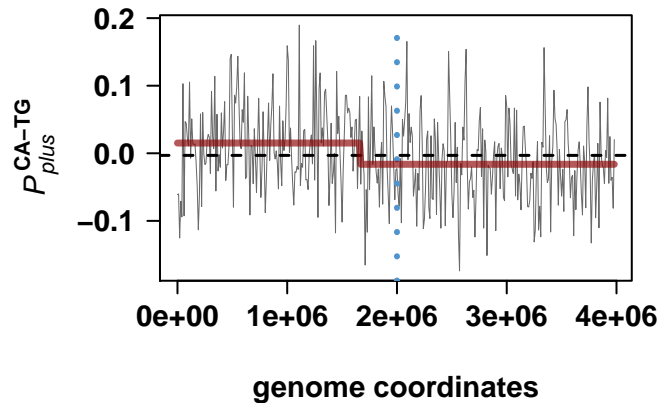
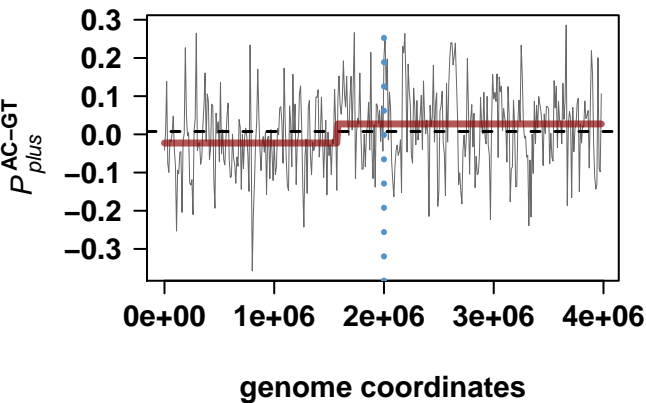
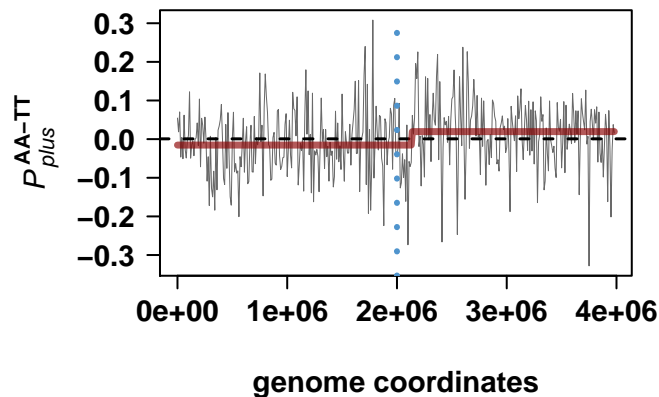
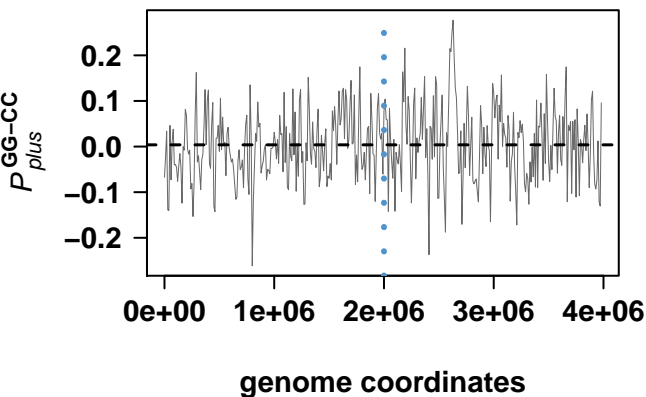
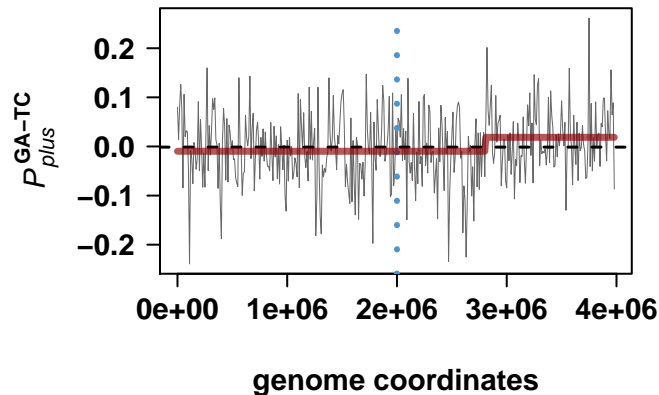
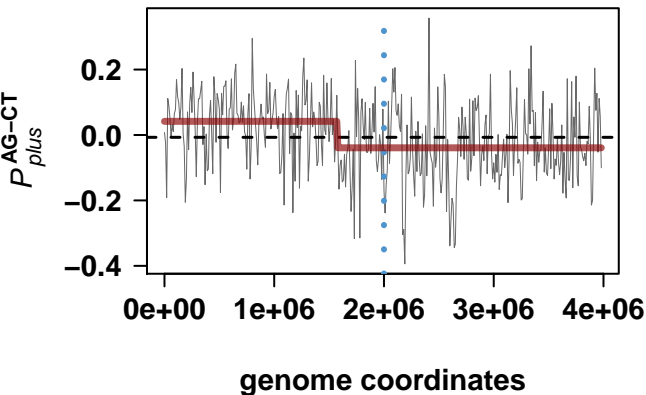


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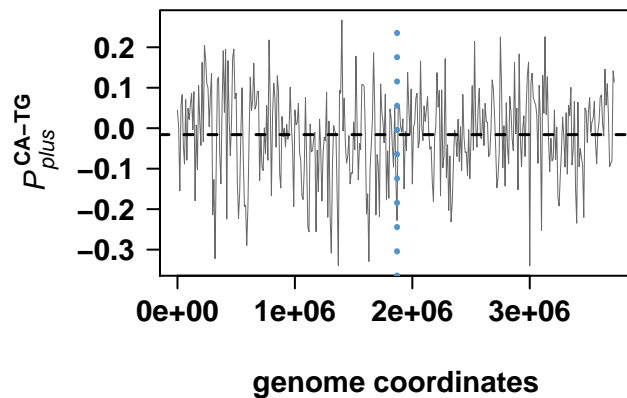
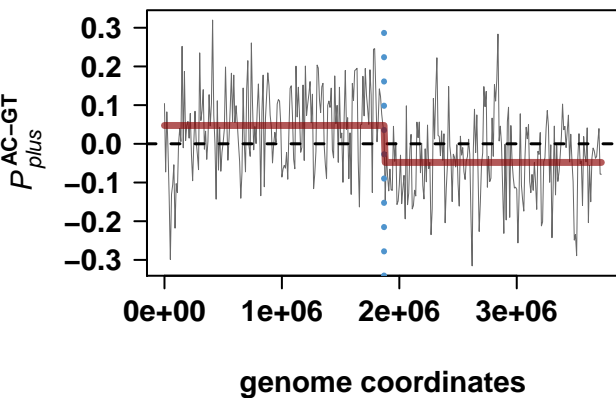
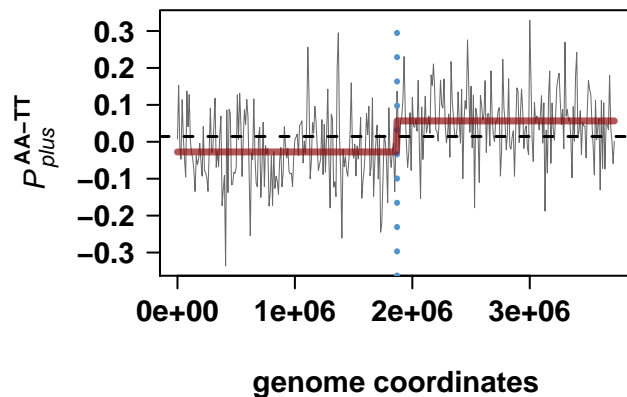
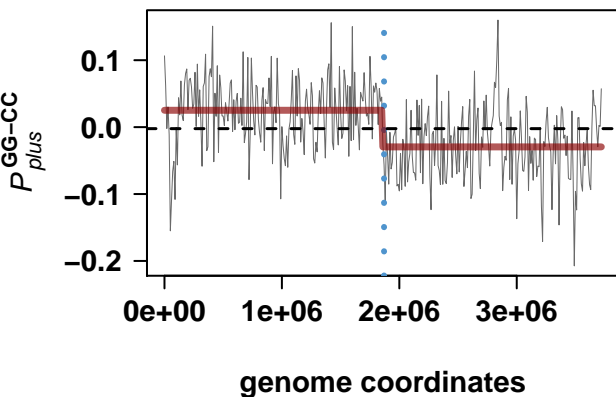
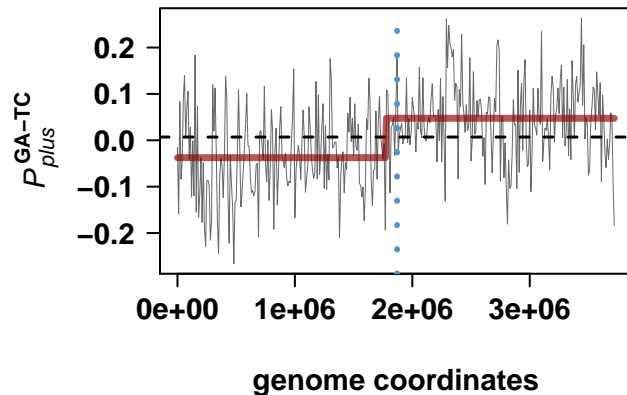
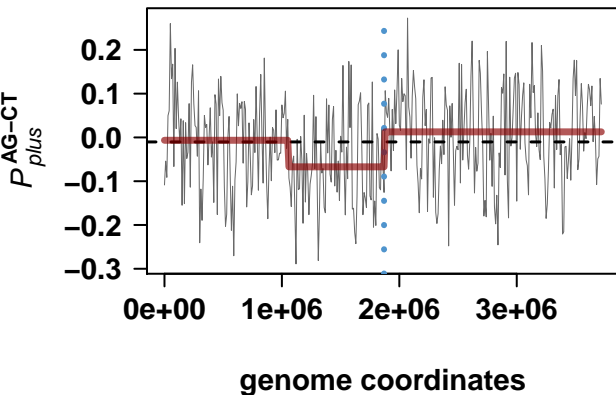
Pelobacter carbinolicus DSM 2380



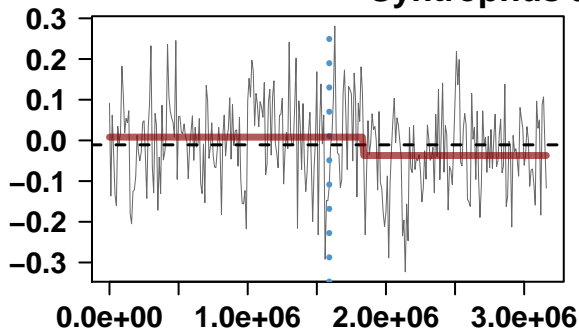
Geobacter metallireducens GS-15



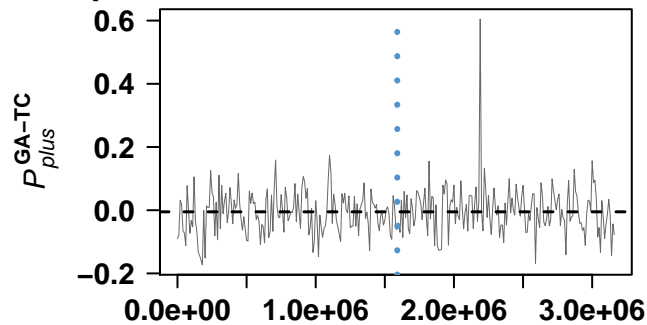
Desulfovibrio alaskensis G20



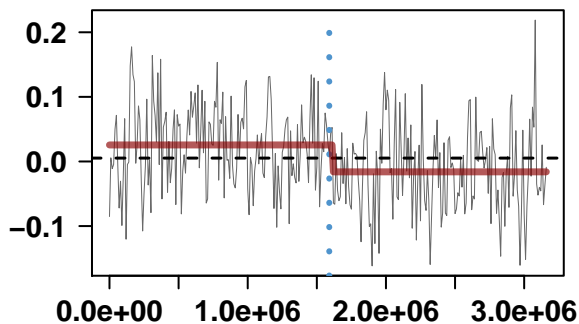
Syntrophus aciditrophicus SB



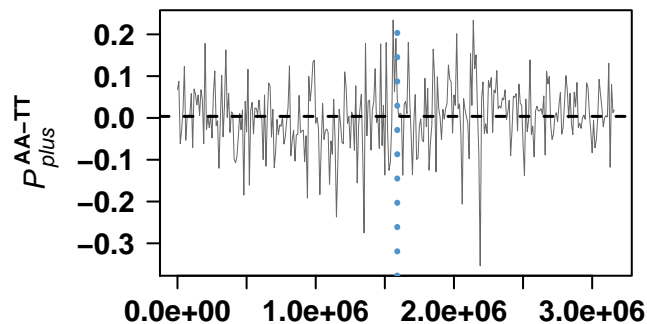
genome coordinates



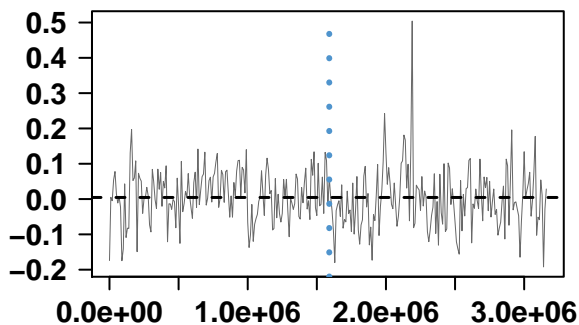
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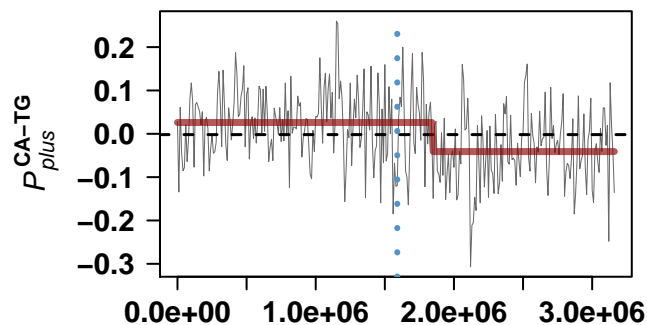
genome coordinates



genome coordinates

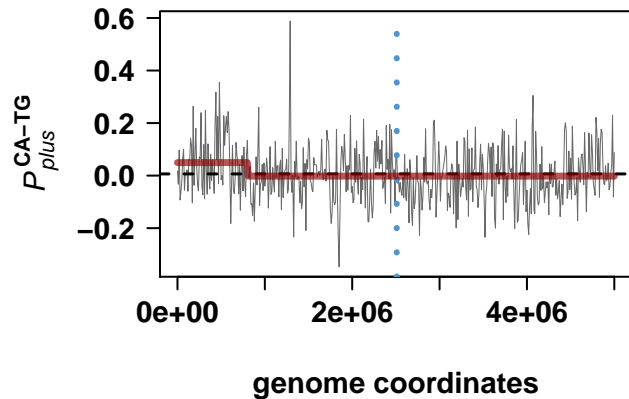
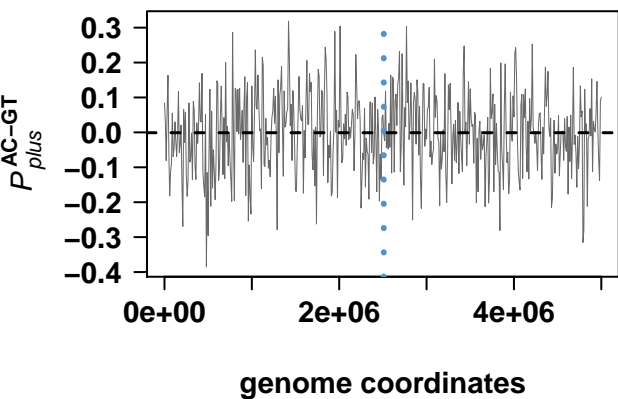
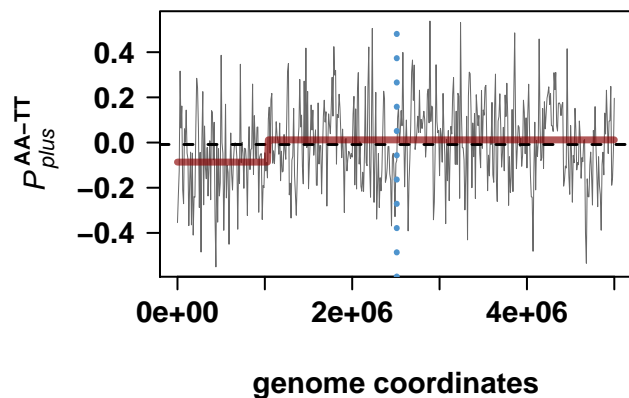
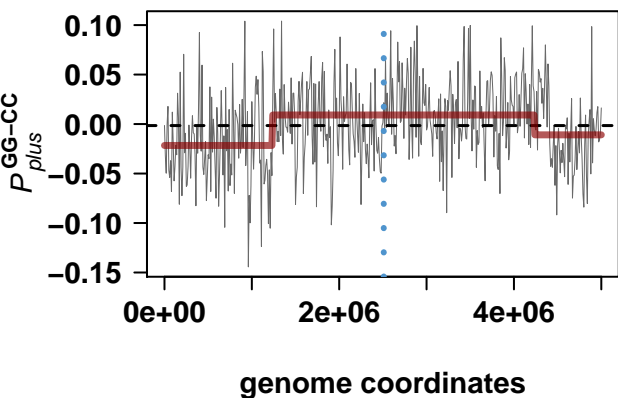
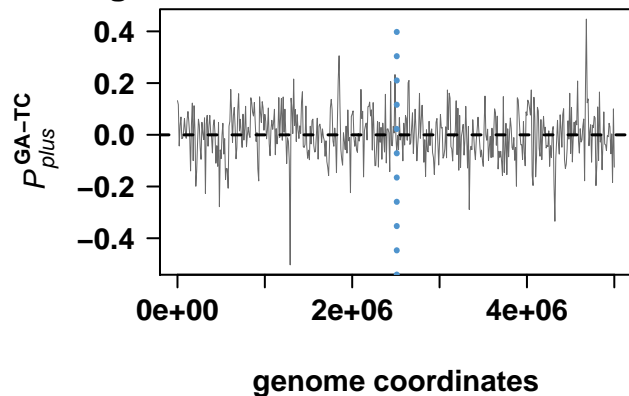
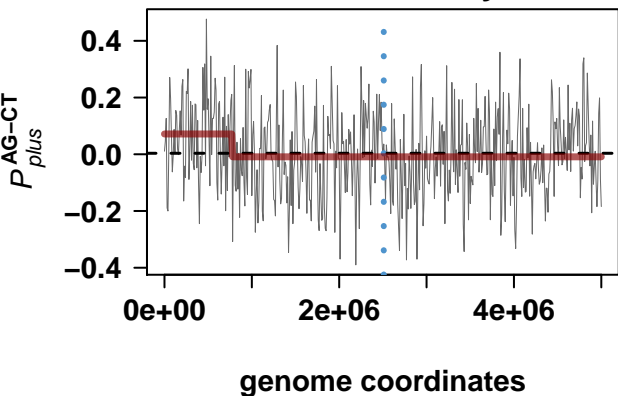


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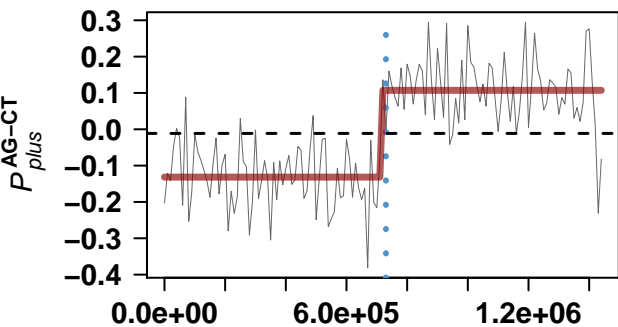


genome coordinates

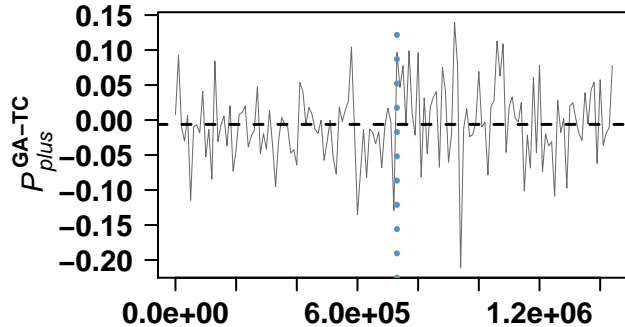
Anaeromyxobacter dehalogenans 2CP-C



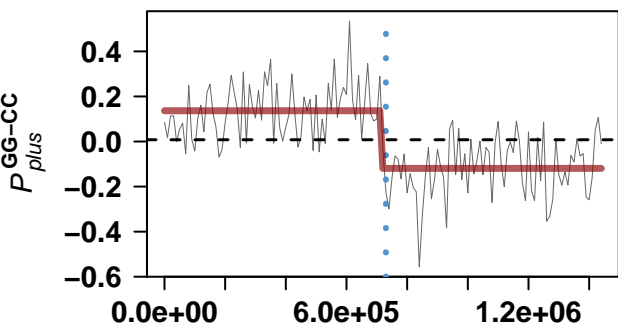
Lawsonia intracellularis PHE/MN1-00



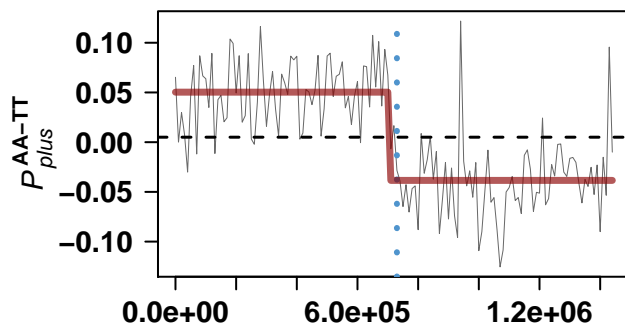
genome coordinates



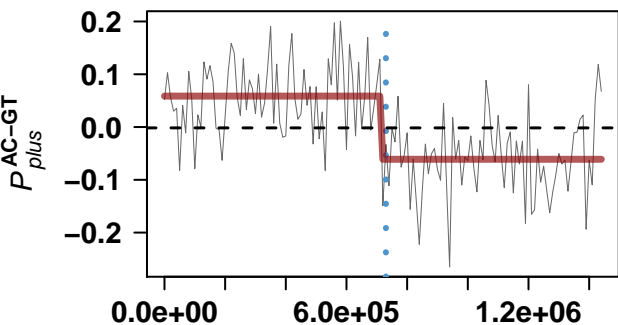
genome coordinates



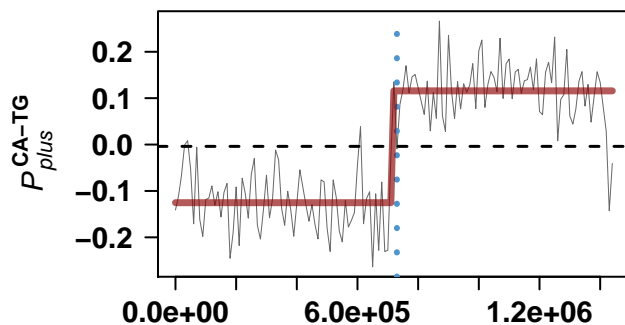
genome coordinates



genome coordinates

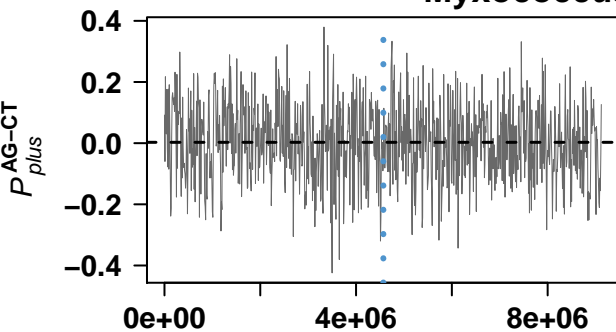


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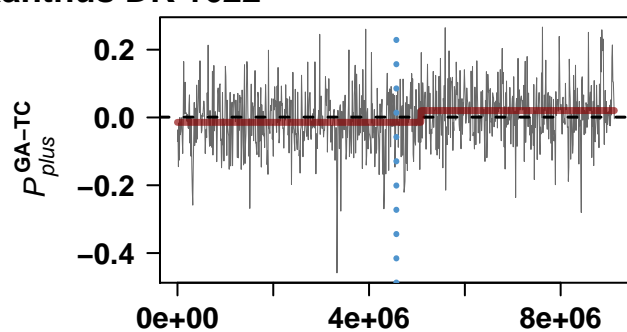


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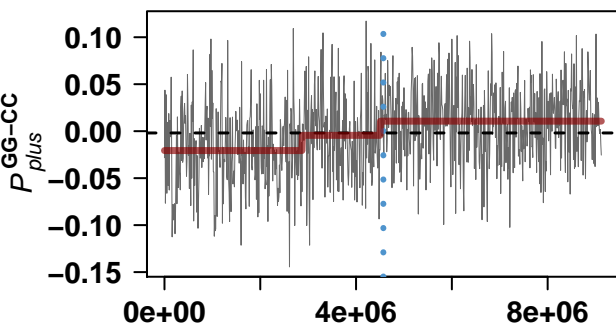
Myxococcus xanthus DK 1622



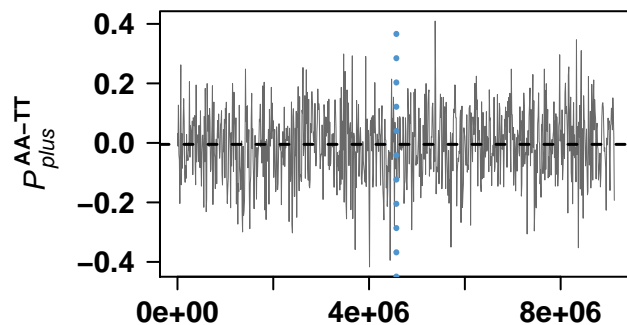
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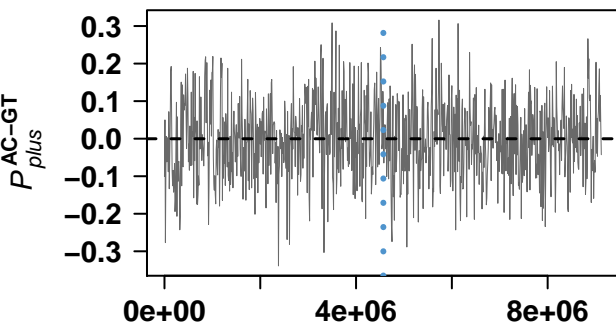
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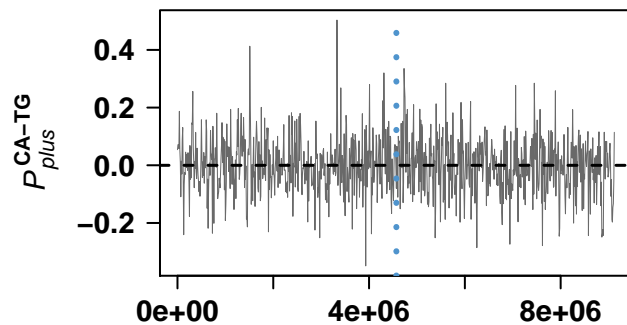
genome coordinates



genome coordinates

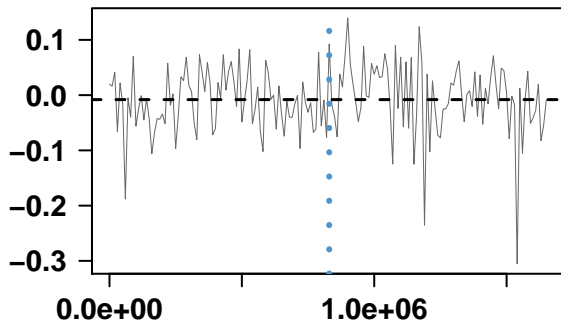


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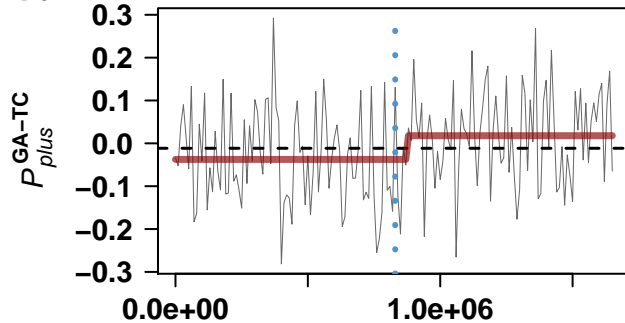


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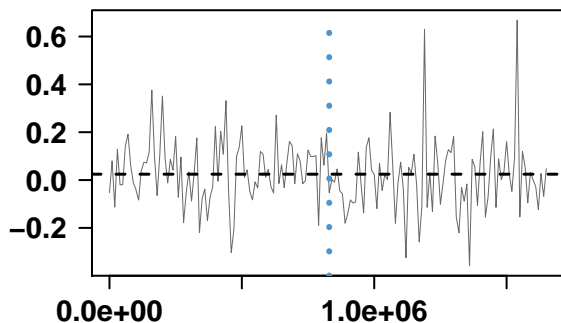
Helicobacter pylori 26695



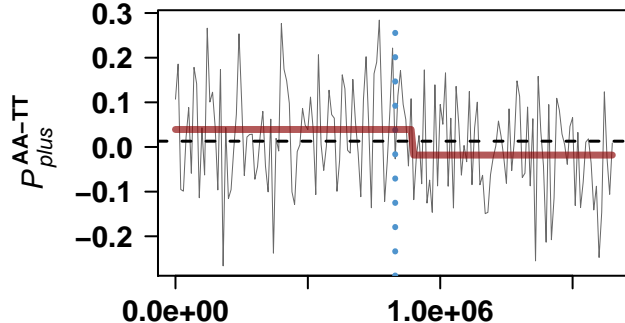
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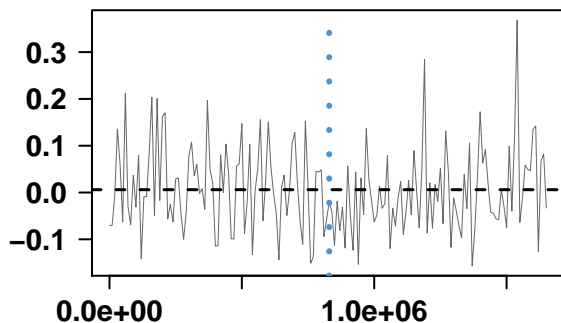
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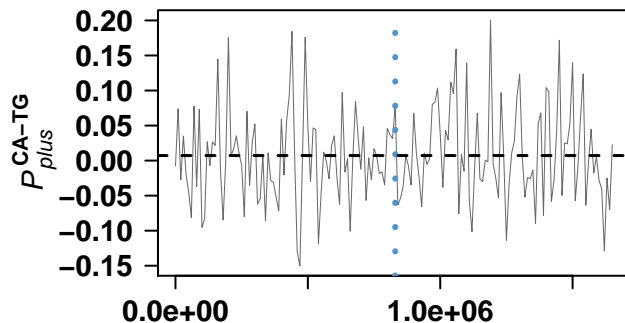
genome coordinates



genome coordinates

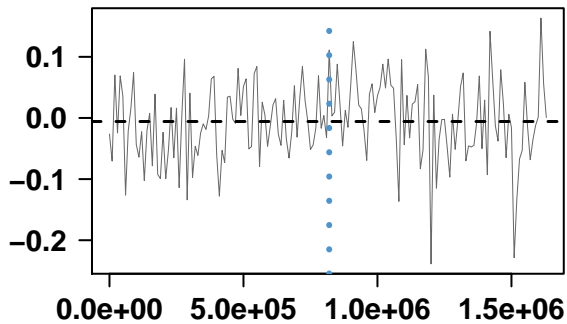


genome coordinates

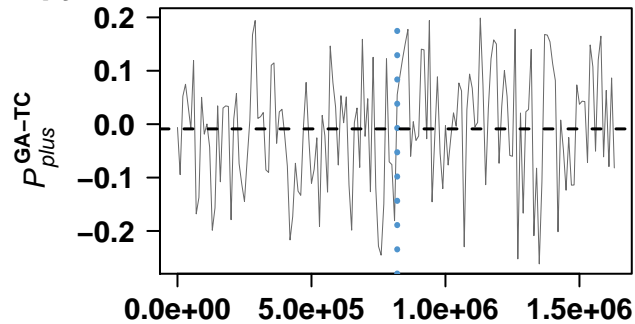


genome coordinates

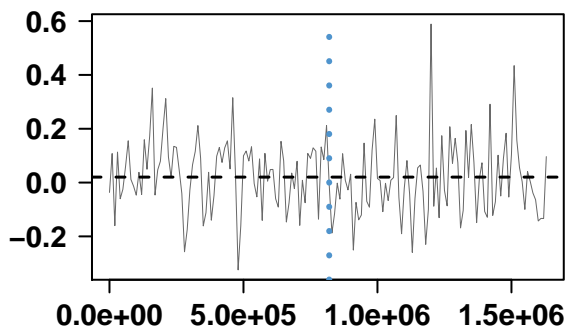
Helicobacter pylori J99



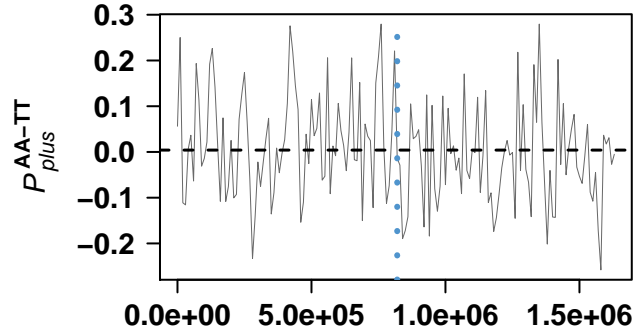
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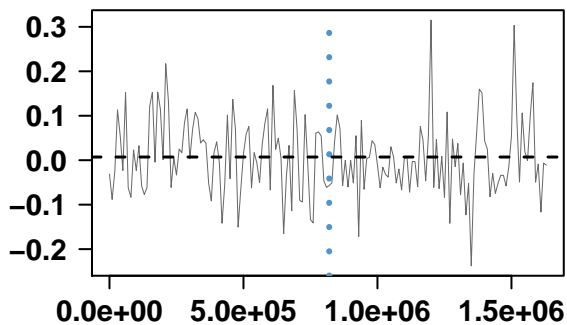
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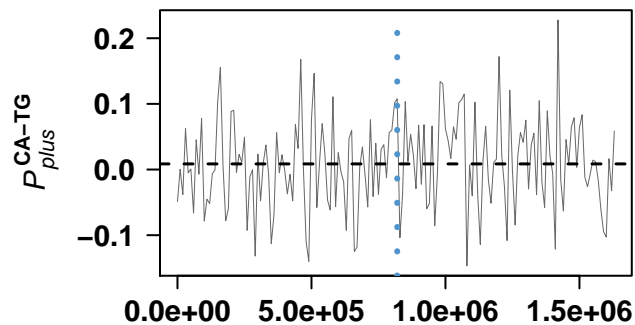
genome coordinates



genome coordinates

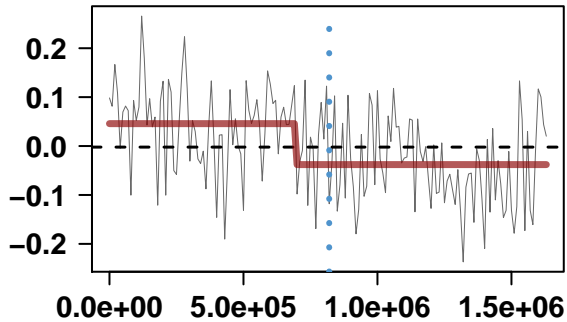


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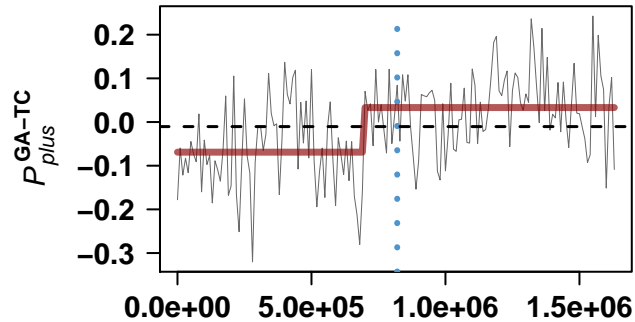


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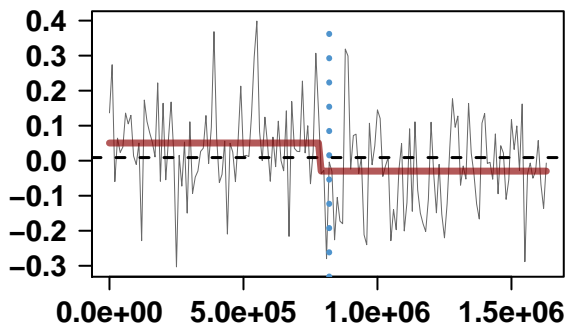
Campylobacter jejuni subsp. jejuni NCTC 11168 = ATCC 700819



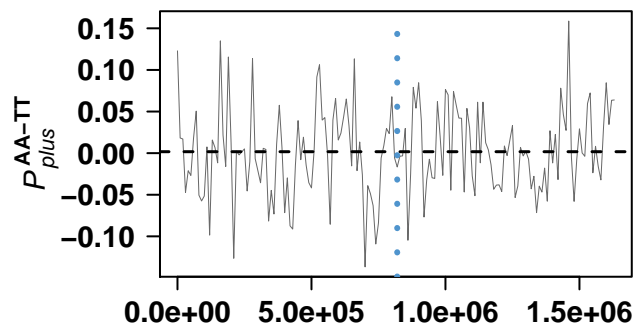
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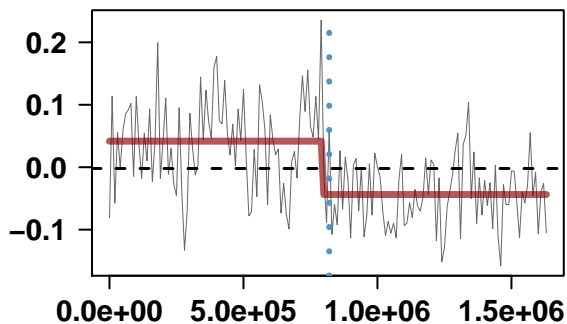
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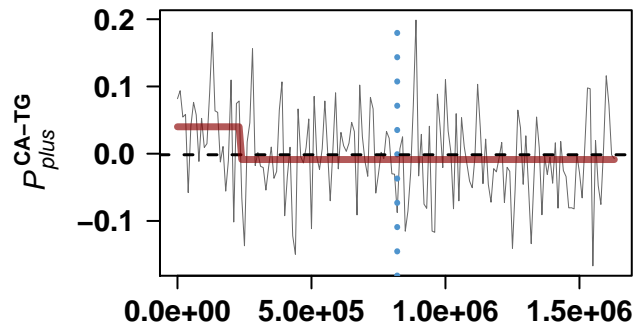
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genome coordinates

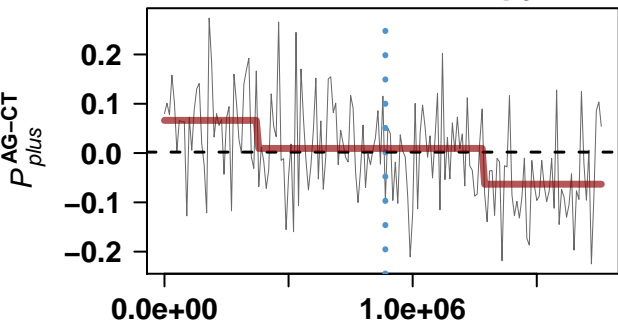


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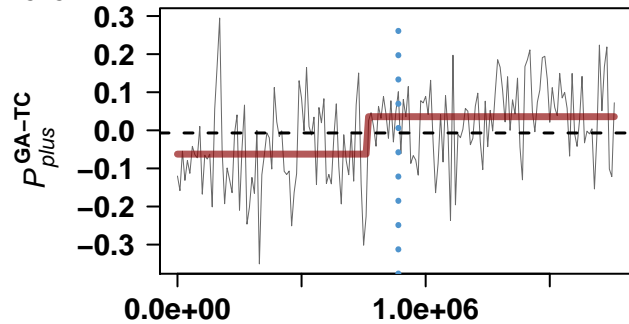


genome coordinates

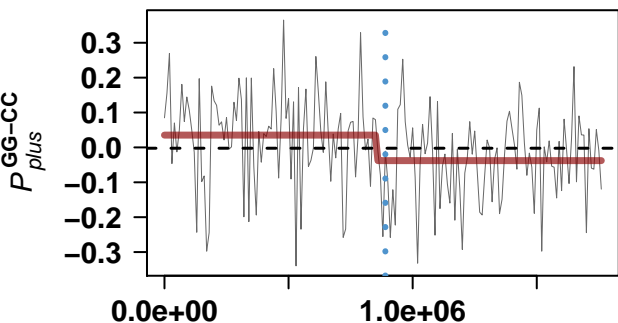
Campylobacter jejuni RM1221



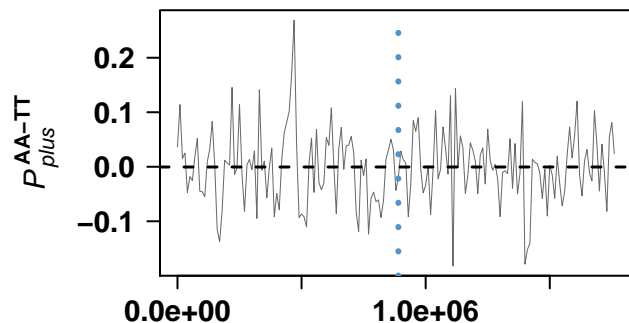
genome coordinates



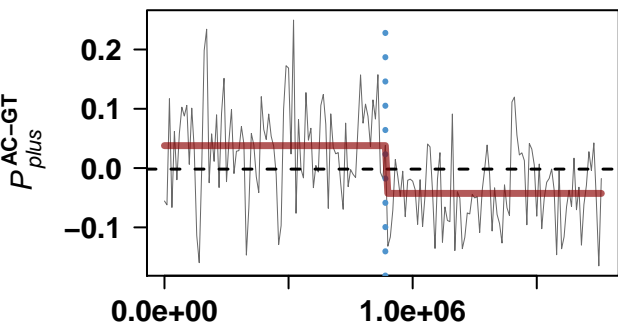
genome coordinates



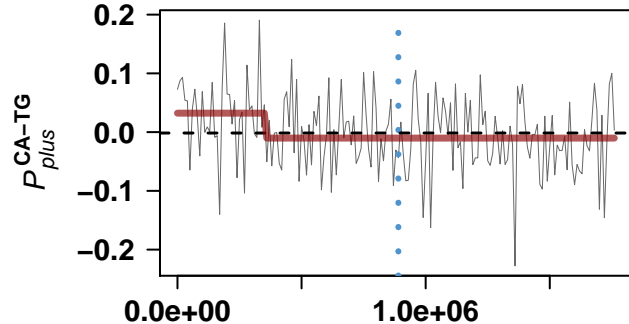
genome coordinates



genome coordinates

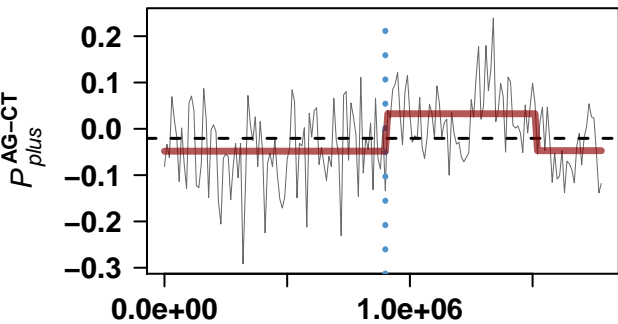


genome coordinates

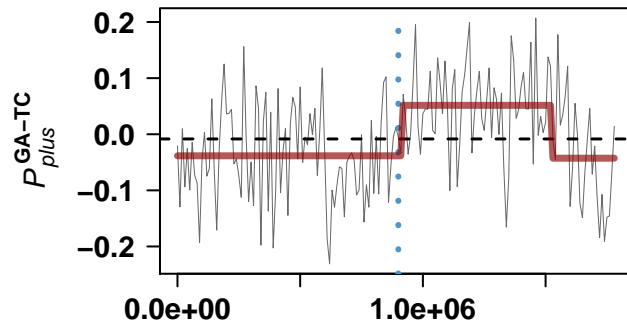


genome coordinates

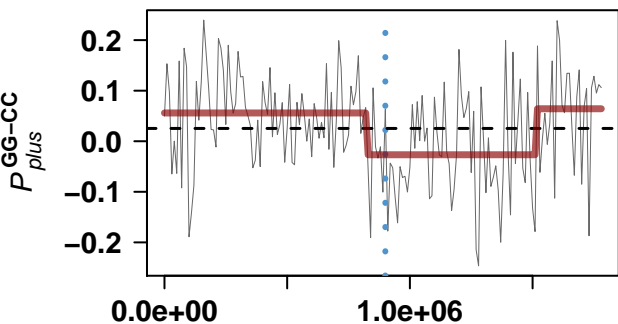
Helicobacter hepaticus ATCC 51449



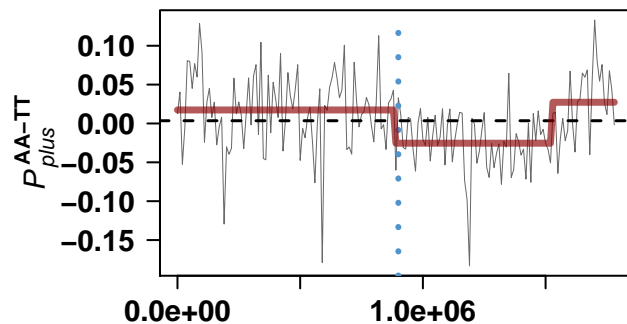
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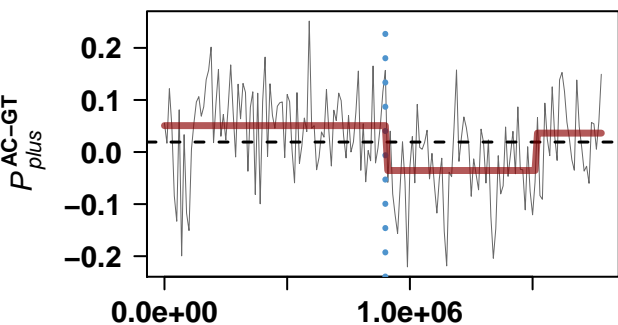
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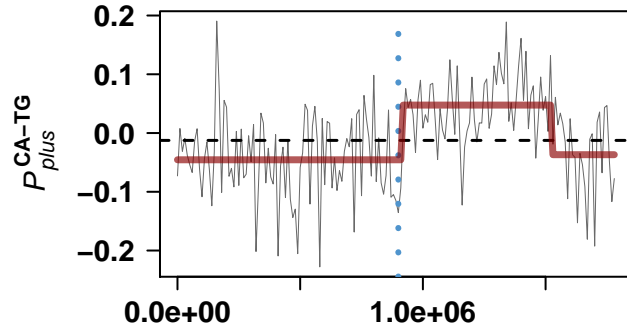
genome coordinates



genome coordinates

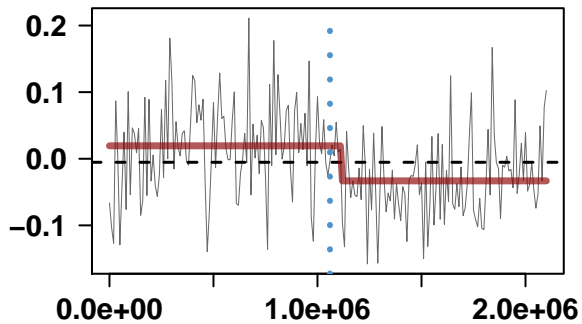


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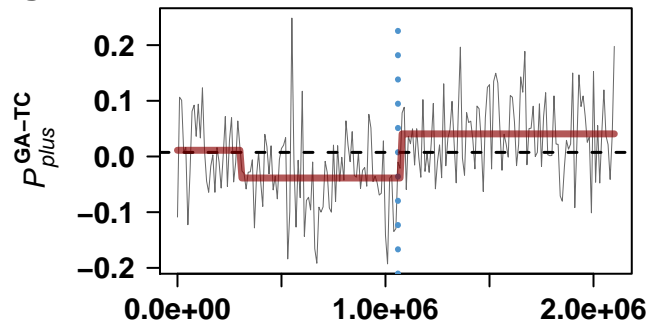


genome coordinates

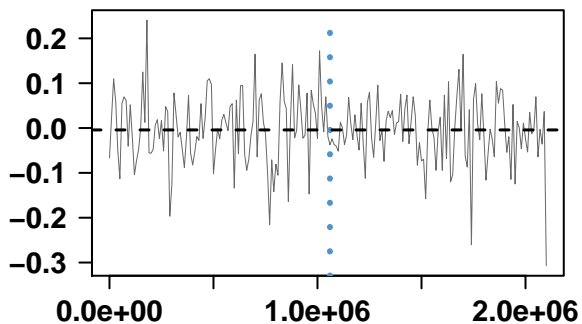
Wolinella succinogenes DSM 1740



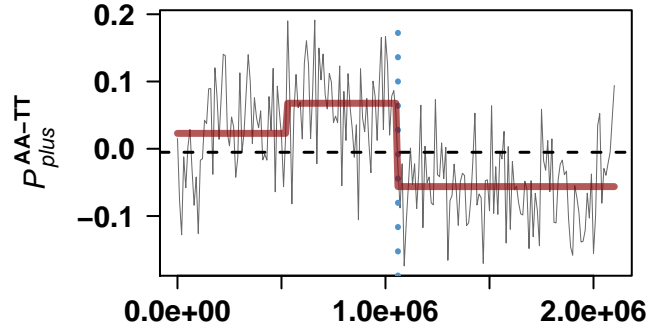
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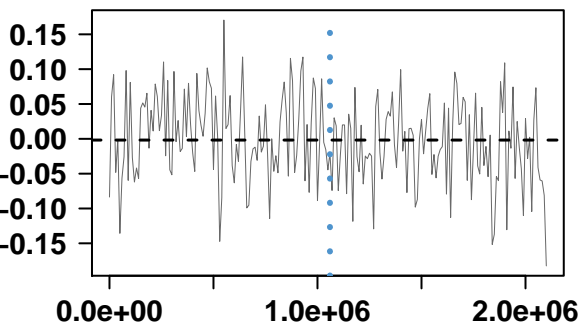
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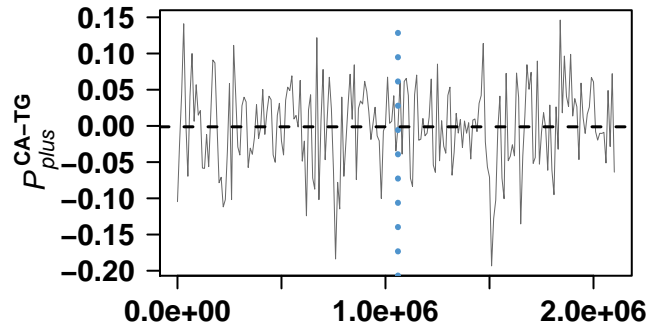
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genome coordinates

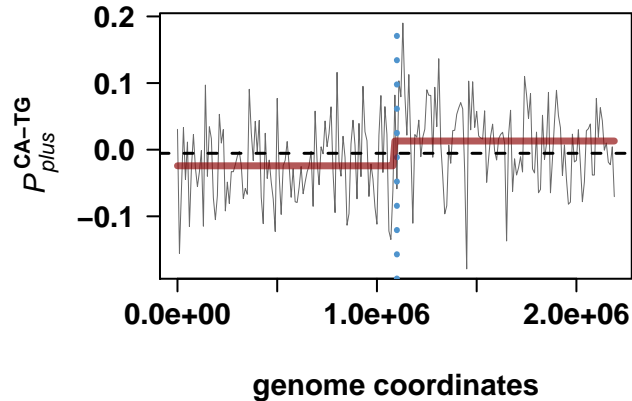
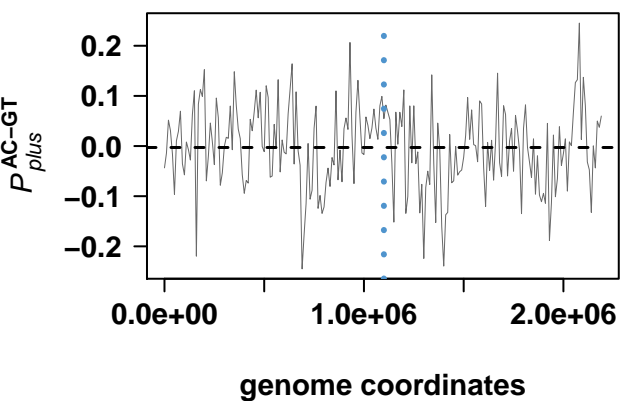
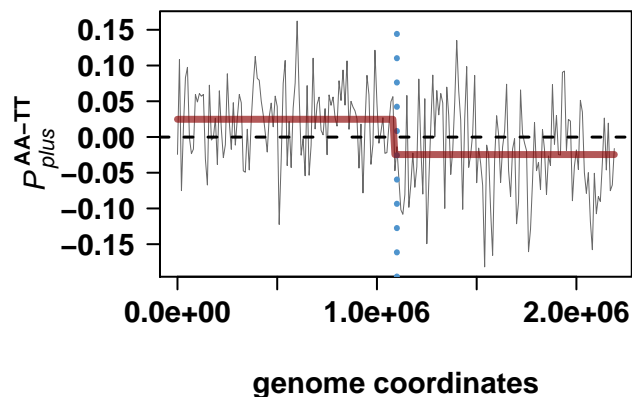
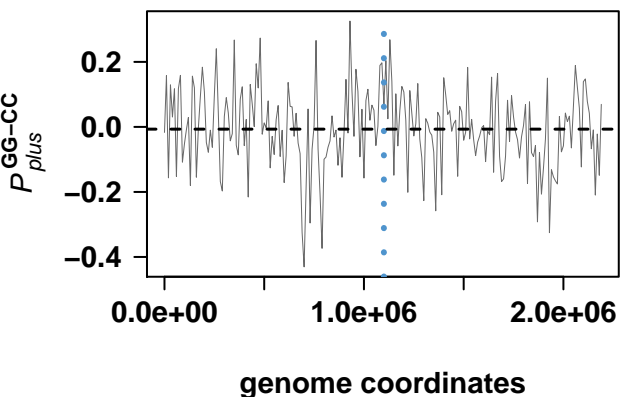
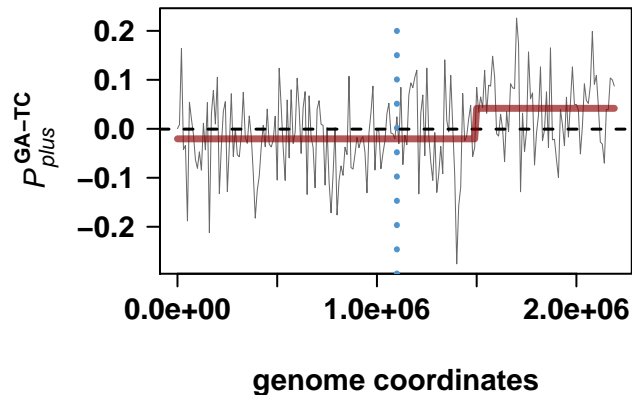
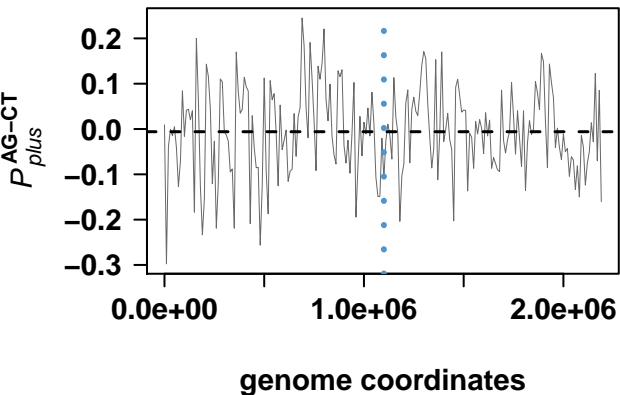


genome coordinates

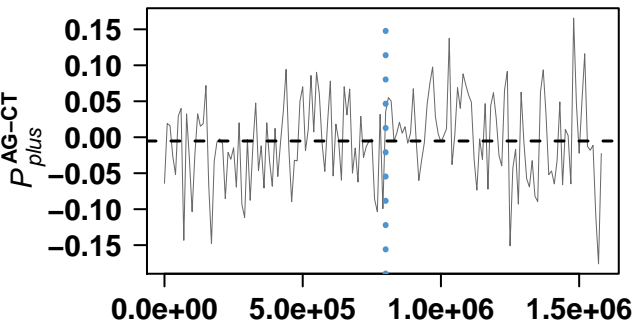


genome coordinates

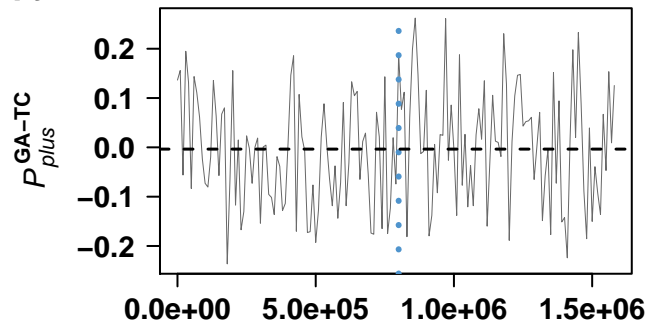
Sulfurimonas denitrificans DSM 1251



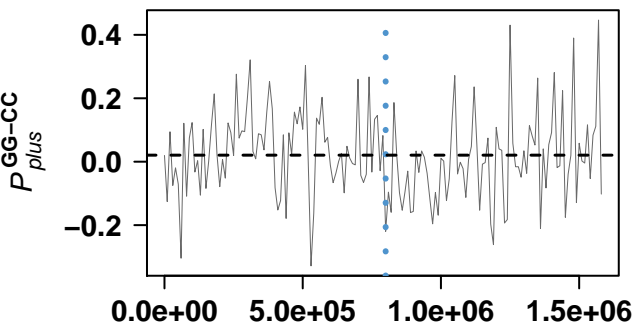
Helicobacter pylori HPAG1



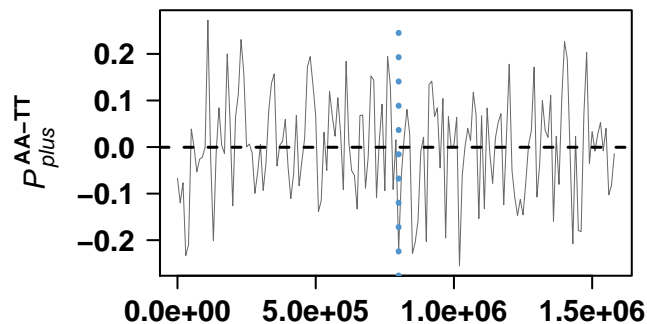
genome coordinates



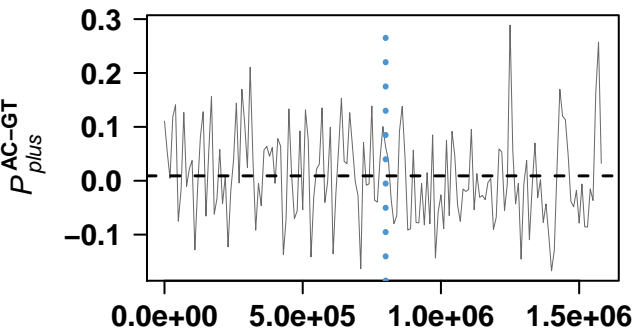
genome coordinates



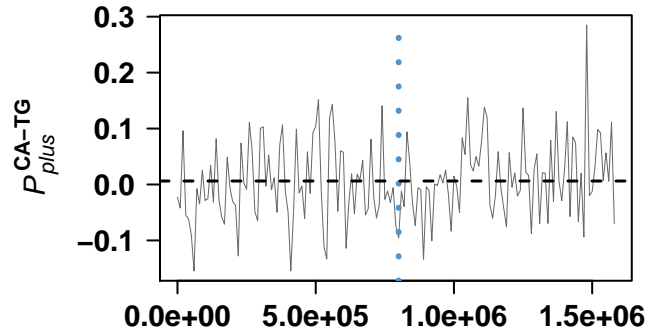
genome coordinates



genome coordinates

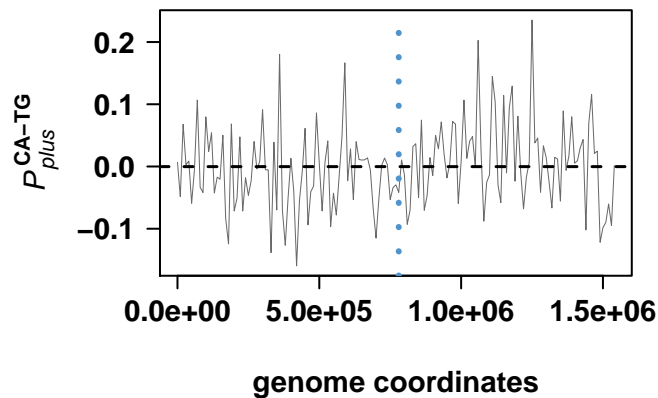
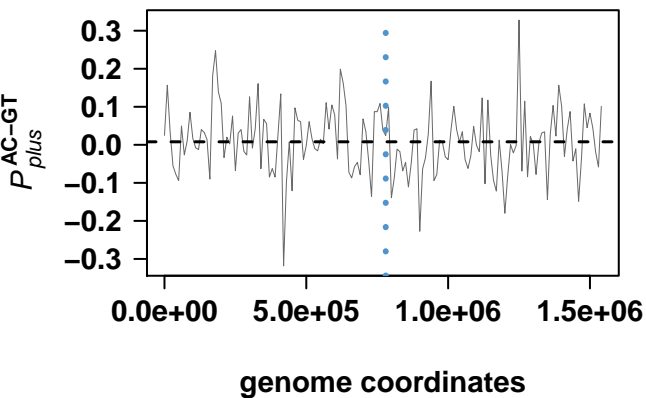
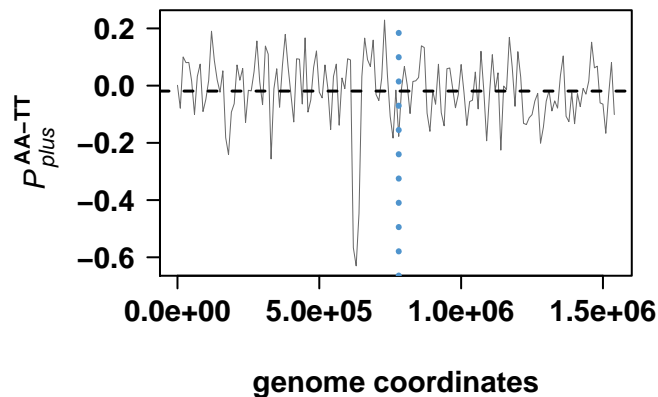
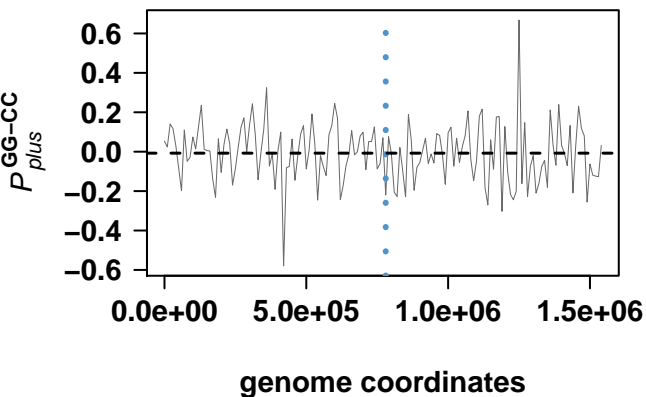
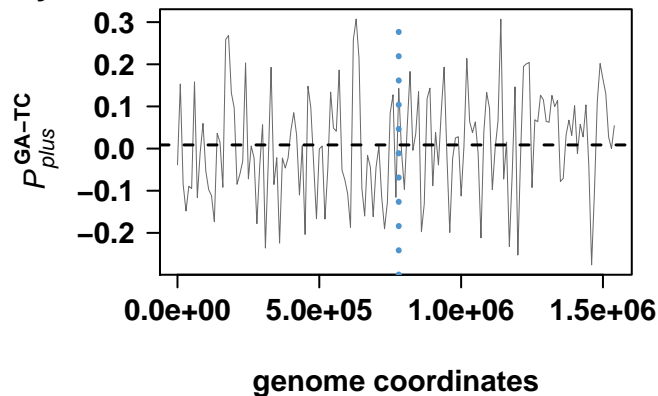
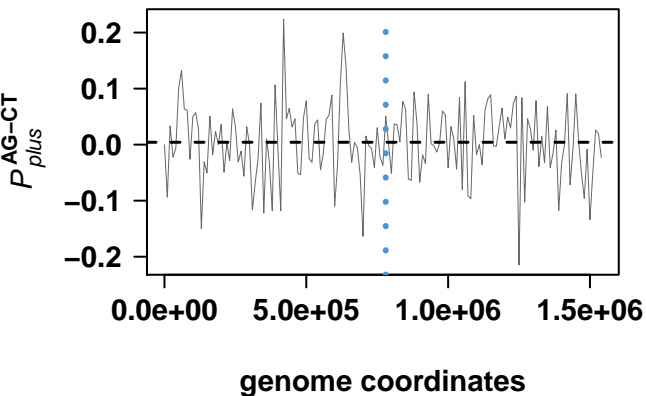


genome coordinates

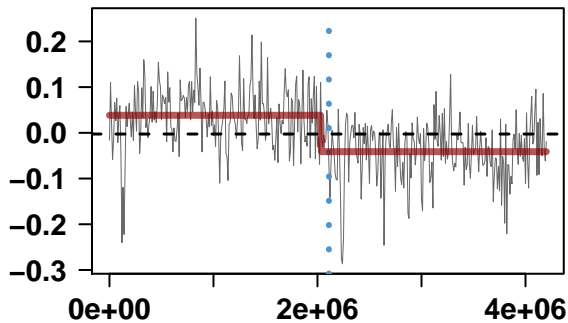


genome coordinates

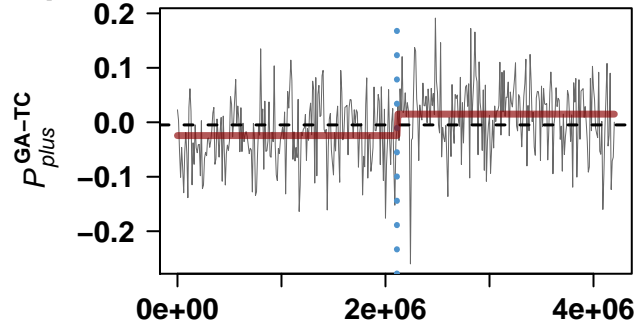
Helicobacter acinonychis str. Sheeba



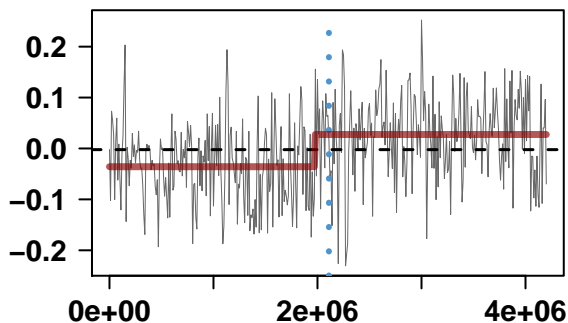
Bacillus subtilis subsp. subtilis str. 168



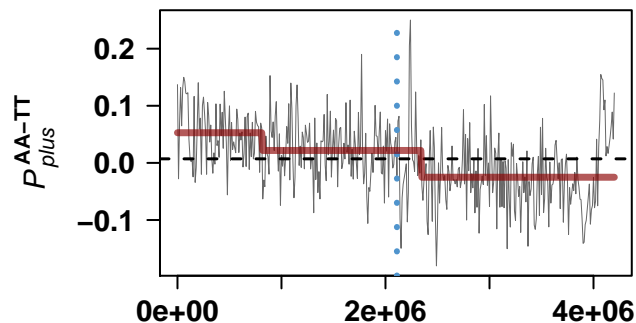
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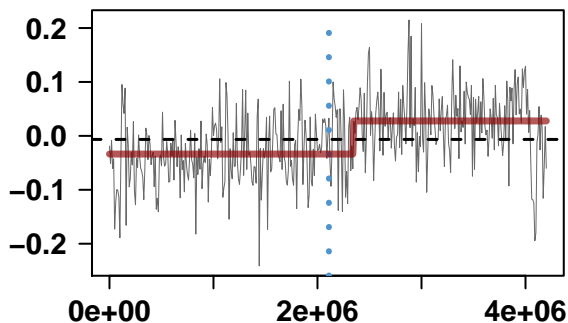
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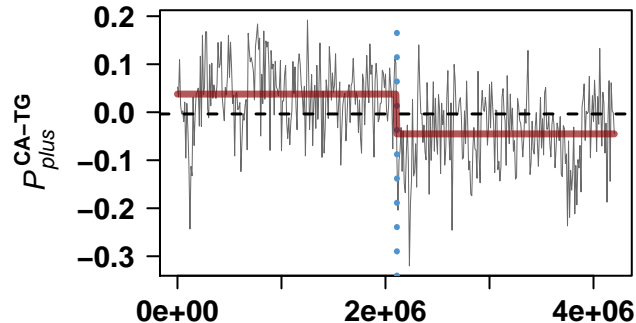
genome coordinates



genome coordinates

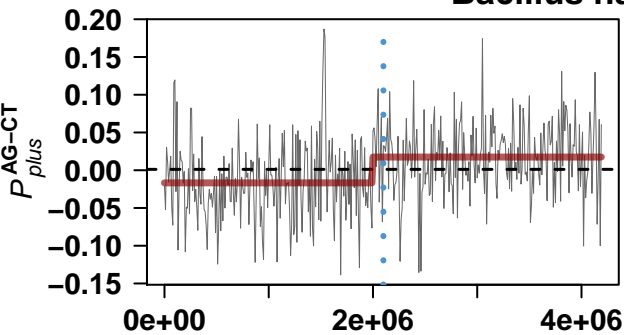


genome coordinates

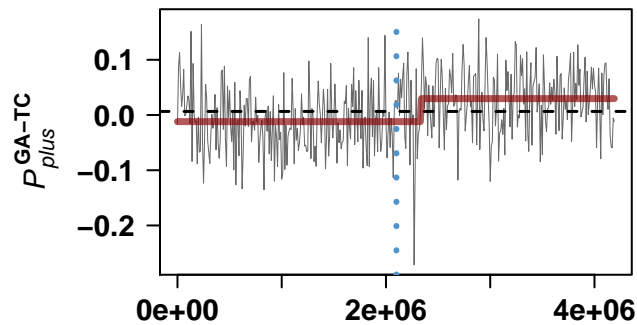


genome coordinates

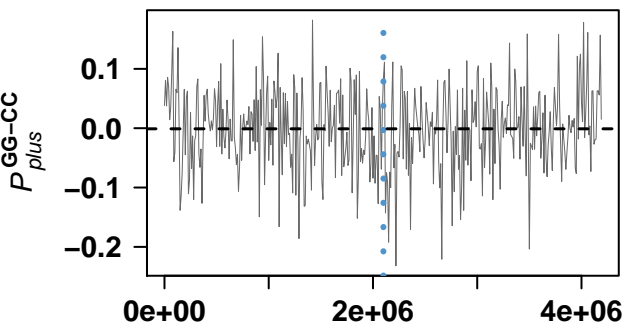
Bacillus halodurans C-125



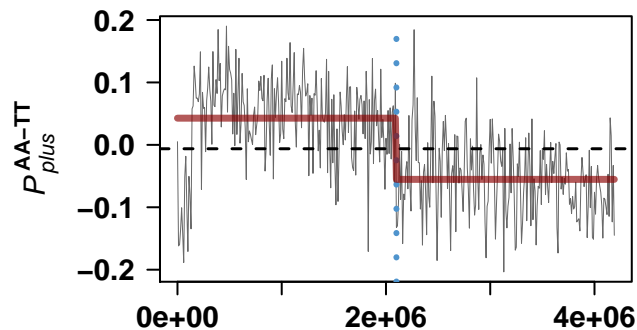
genome coordinates



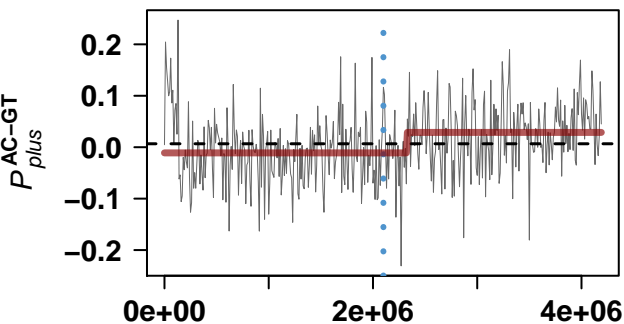
genome coordinates



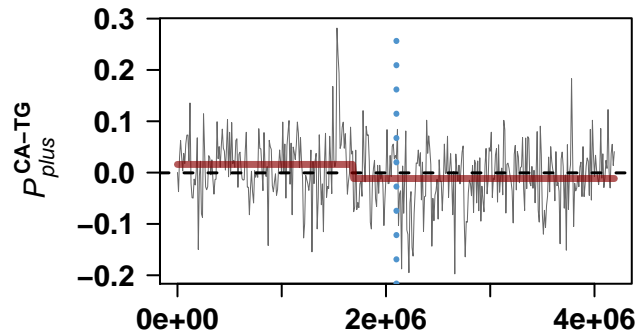
genome coordinates



genome coordinates

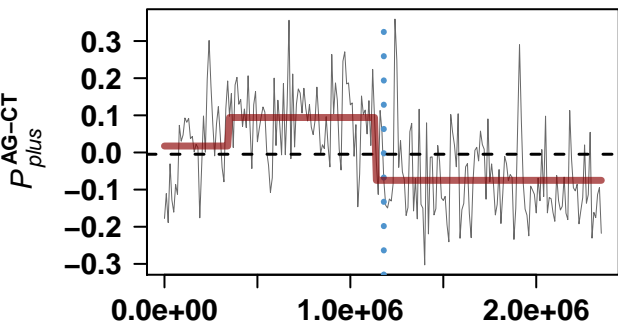


genome coordinates

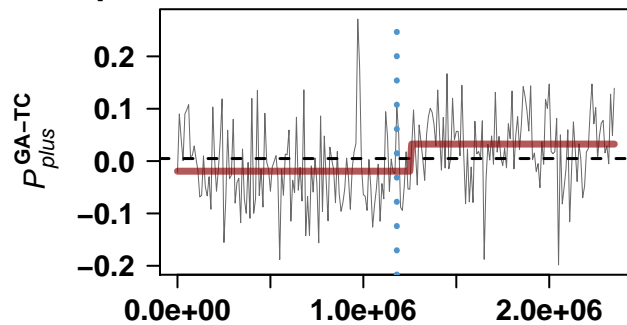


genome coordinates

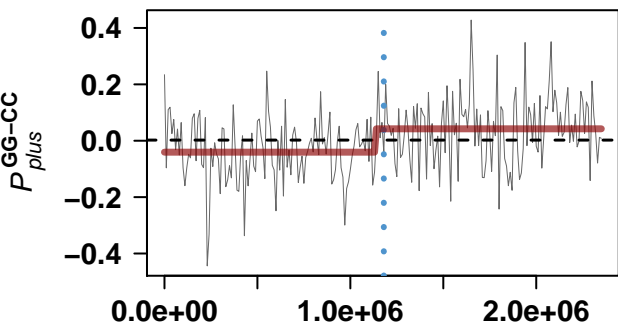
Lactococcus lactis subsp. lactis II1403



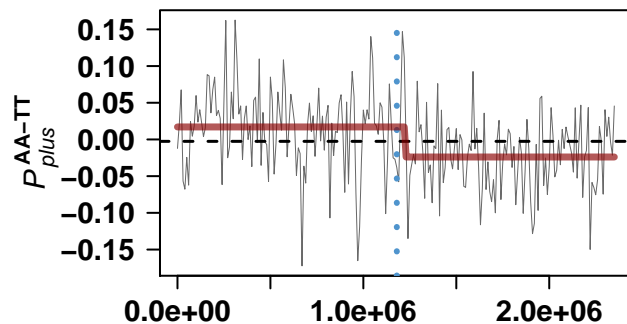
genome coordinates



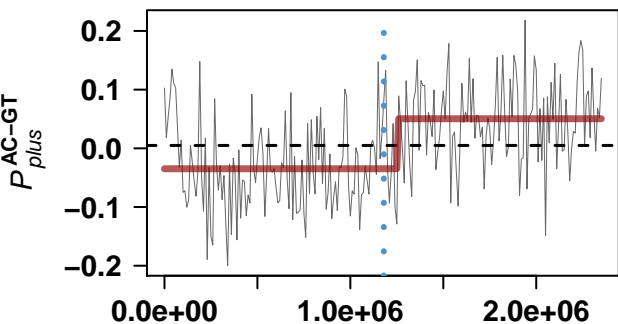
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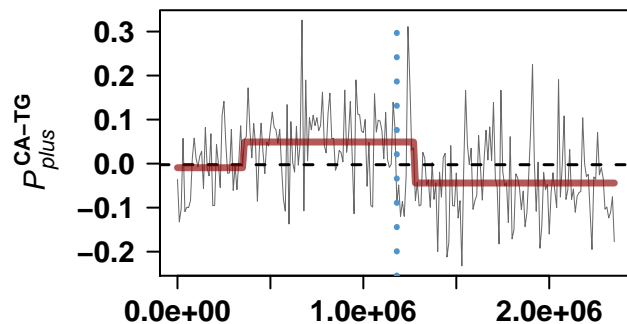
genome coordinates



genome coordinates

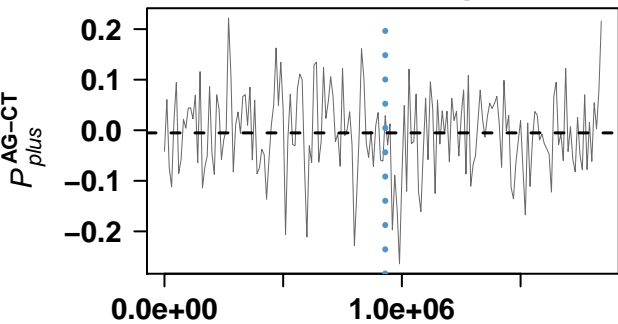


genome coordinates

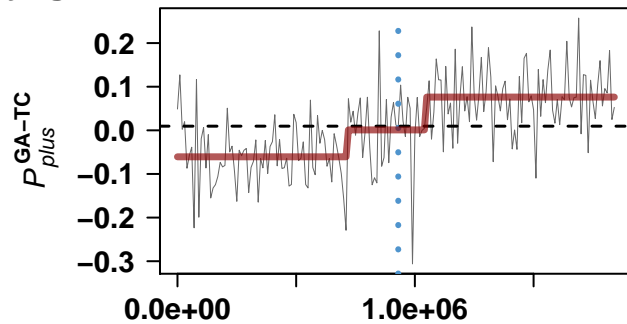


genome coordinates

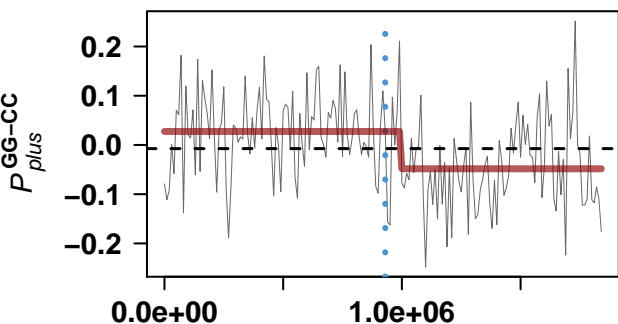
Streptococcus pyogenes M1 GAS



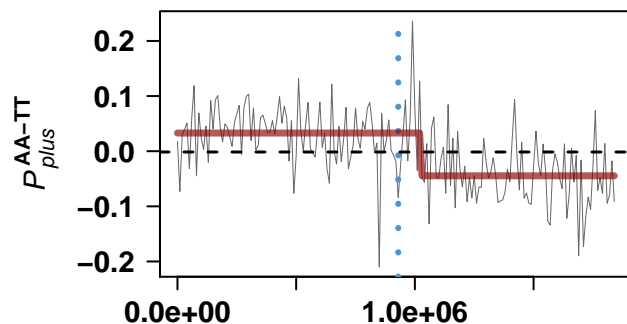
genome coordinates



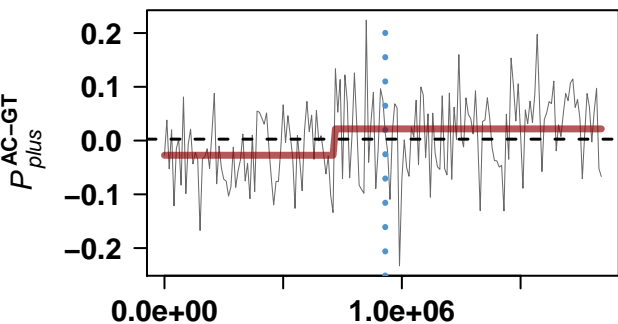
genome coordinates



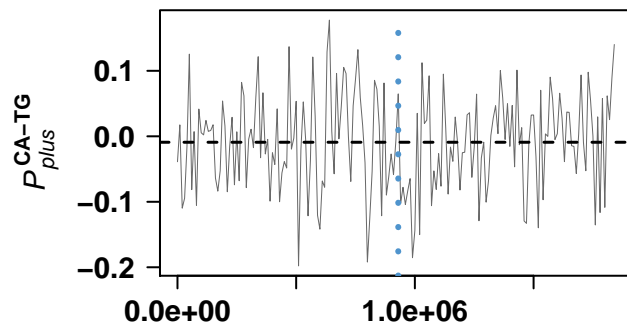
genome coordinates



genome coordinates

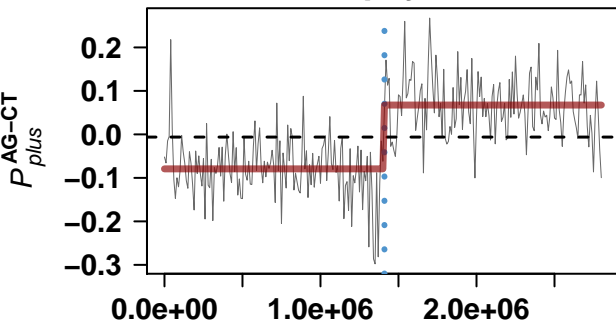


genome coordinates

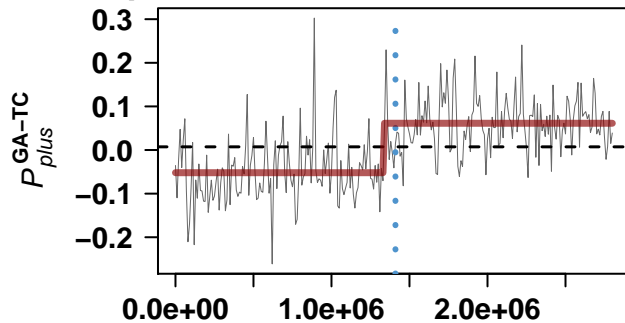


genome coordinates

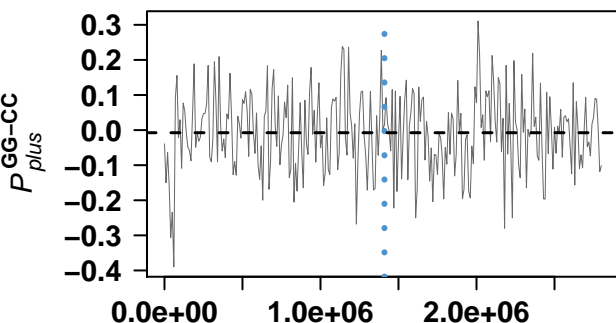
Staphylococcus aureus subsp. aureus N315



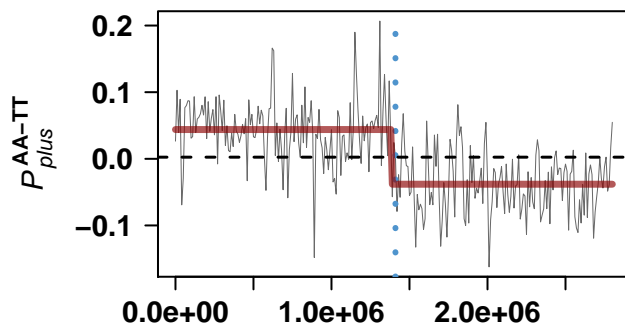
genome coordinates



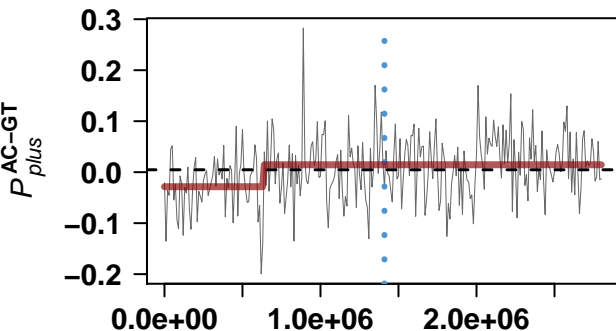
genome coordinates



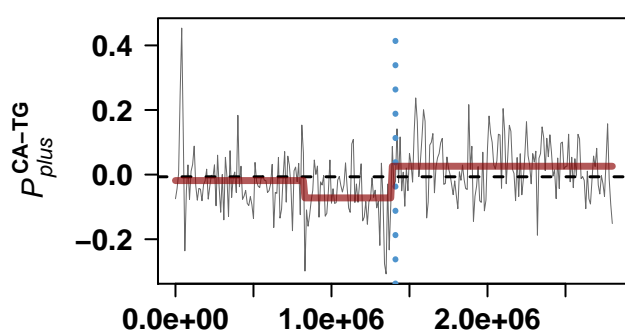
genome coordinates



genome coordinates

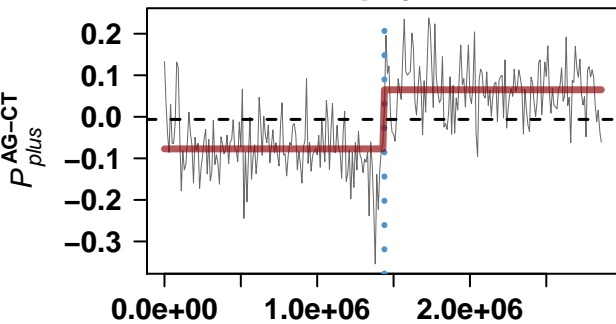


genome coordinates

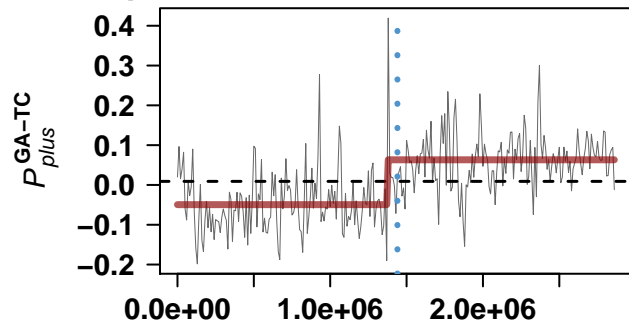


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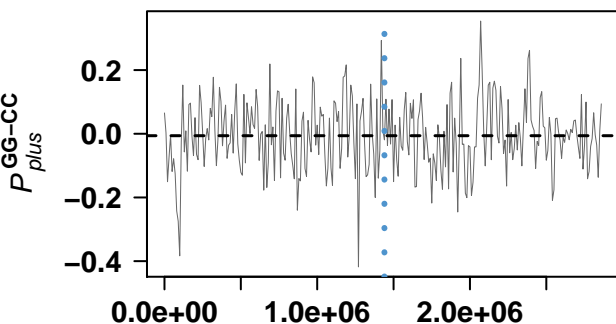
Staphylococcus aureus subsp. aureus Mu50



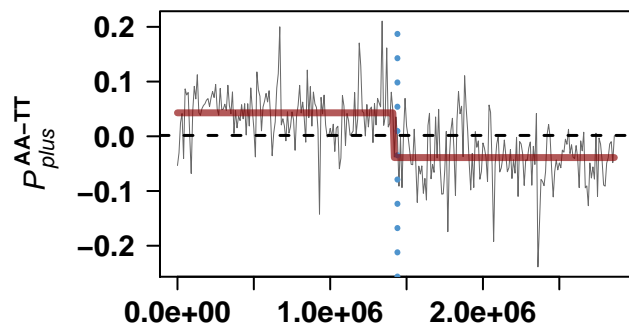
genome coordinates



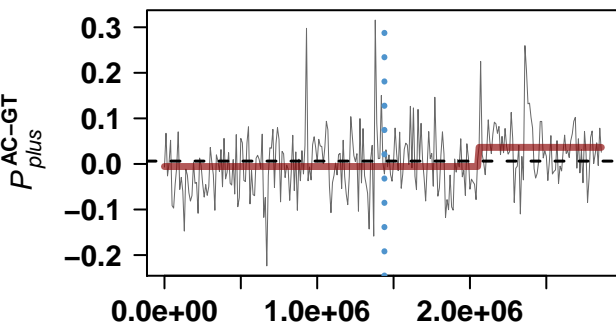
genome coordinates



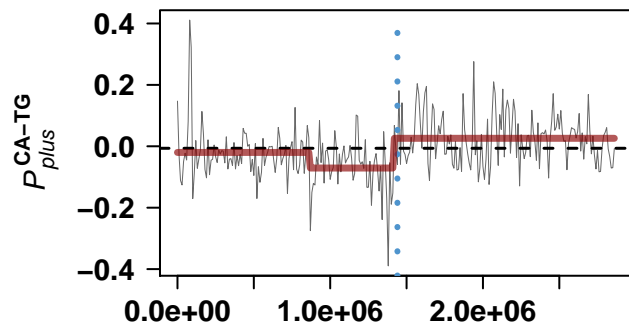
genome coordinates



genome coordinates

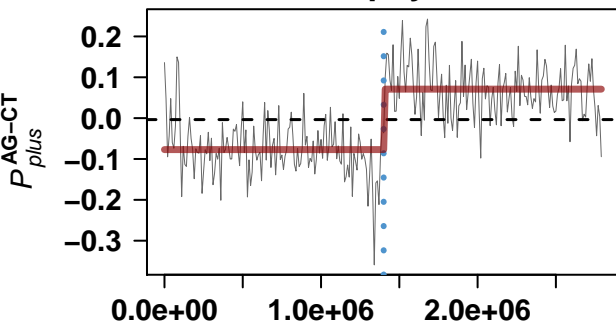


genome coordinates

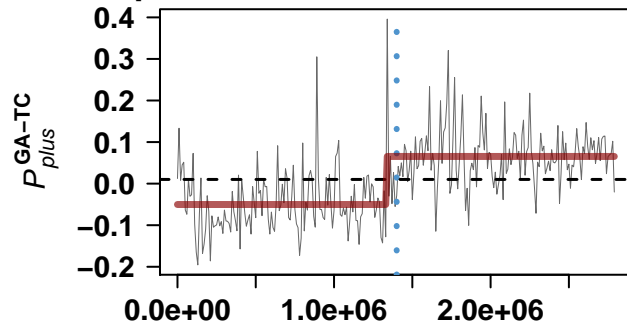


genome coordinates

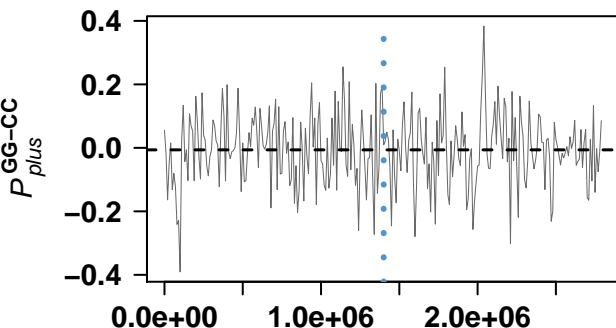
Staphylococcus aureus subsp. aureus COL



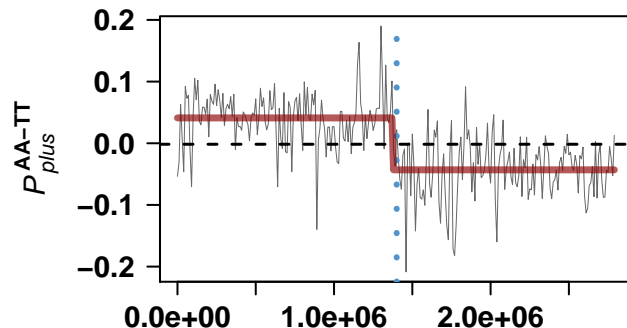
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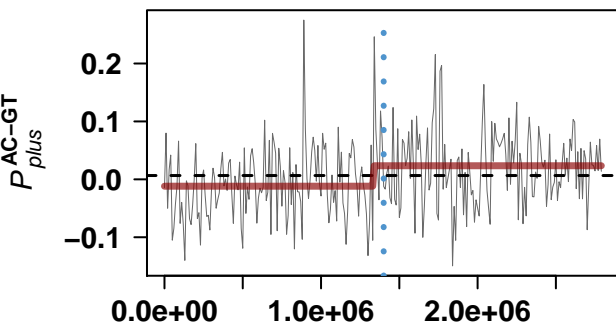
genome coordinates



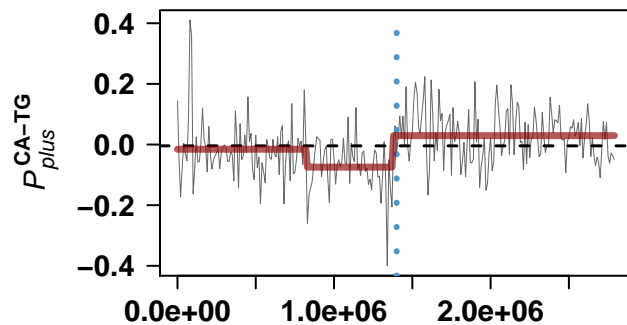
genome coordinates



genome coordinates

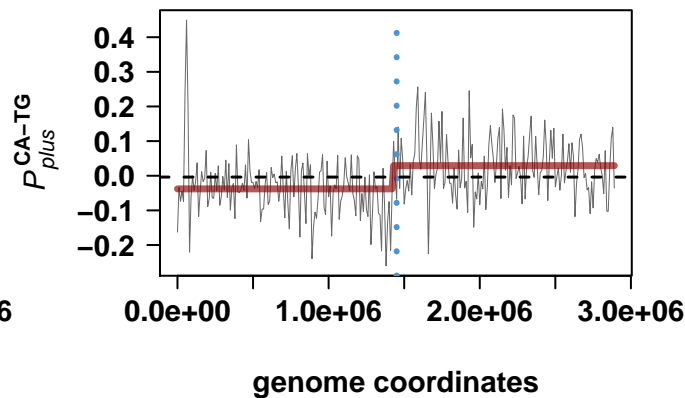
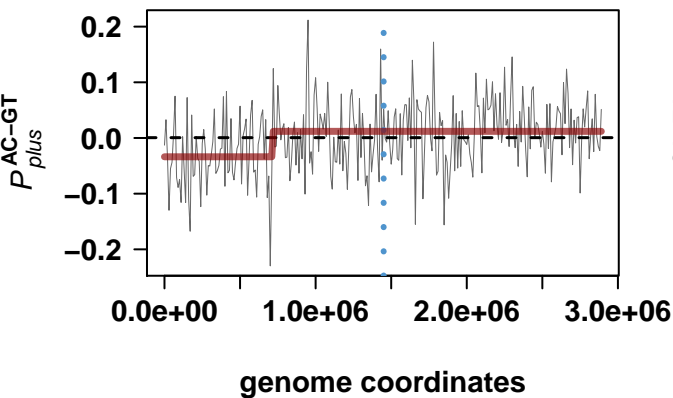
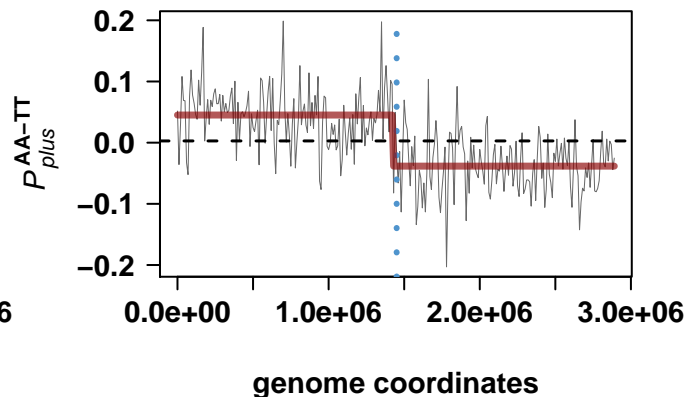
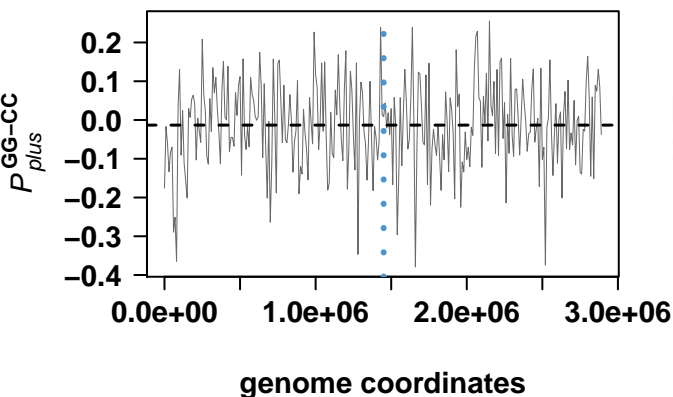
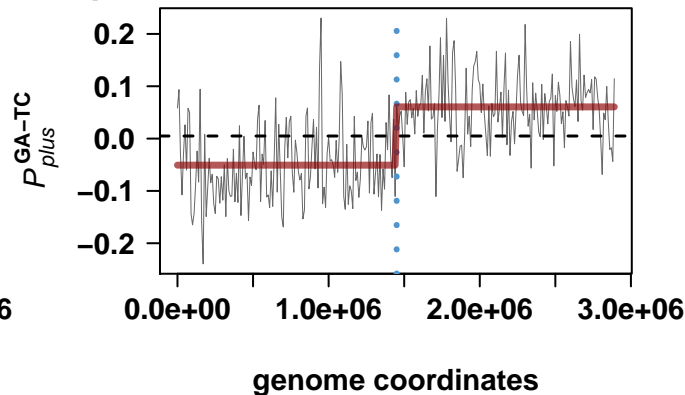
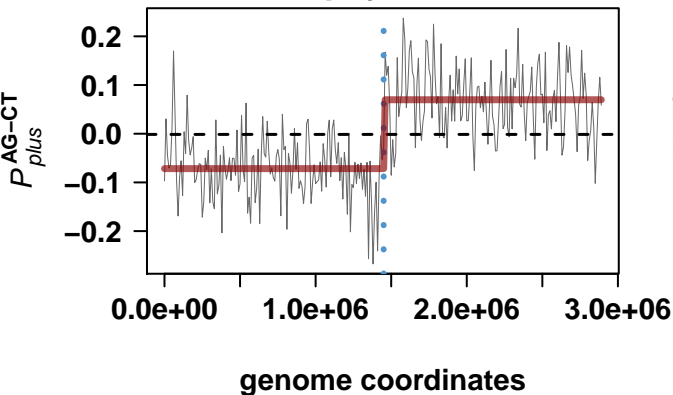


genome coordinates

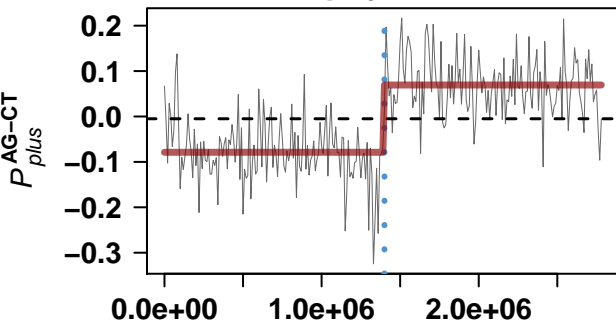


genome coordinates

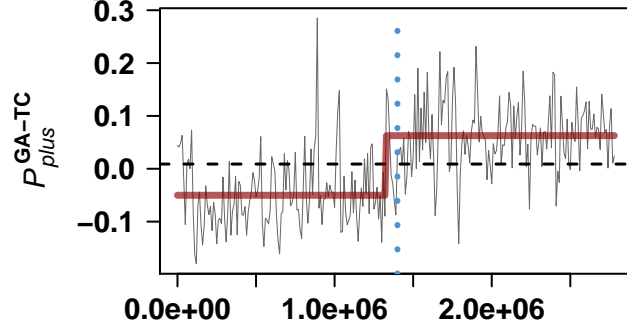
Staphylococcus aureus subsp. aureus MRSA252



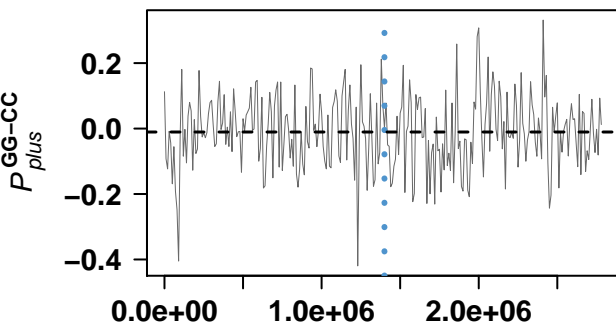
Staphylococcus aureus subsp. aureus MSSA476



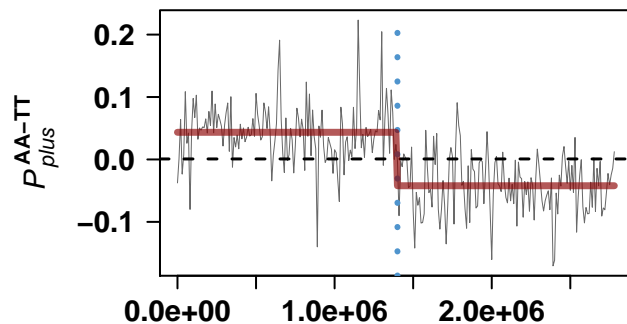
genome coordinates



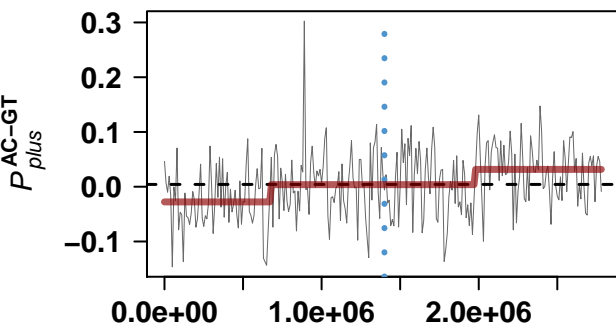
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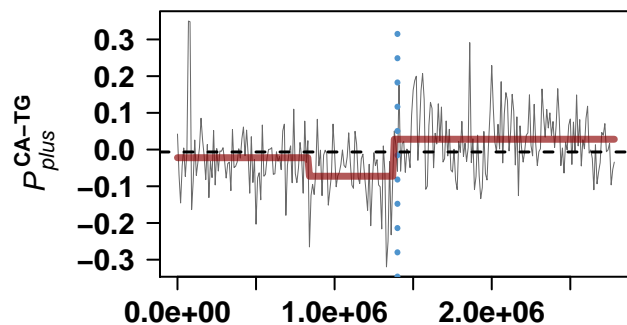
genome coordinates



genome coordinates

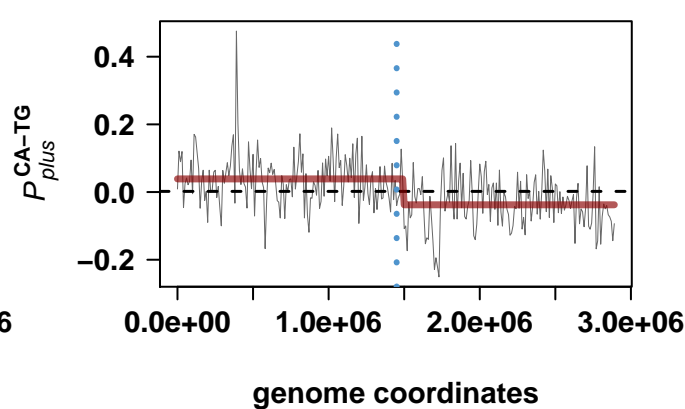
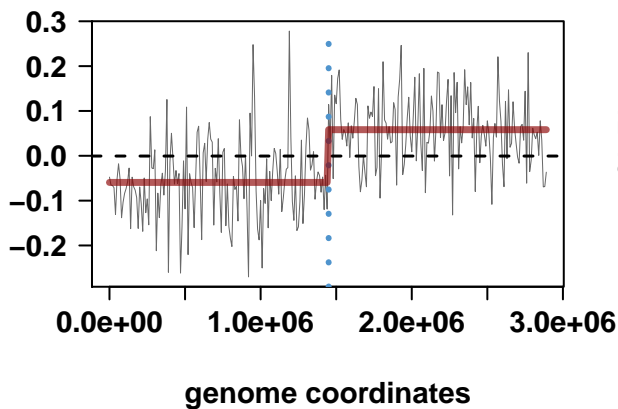
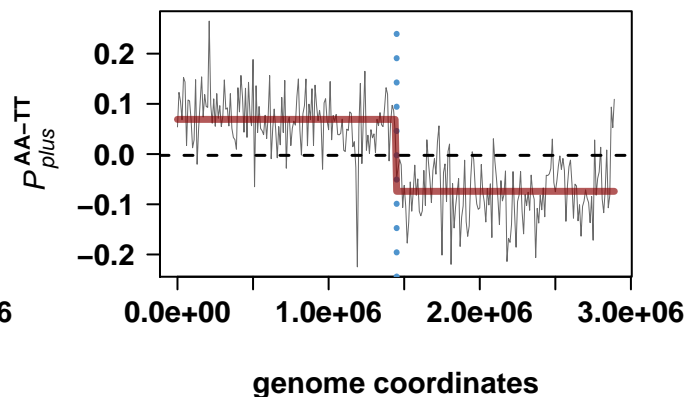
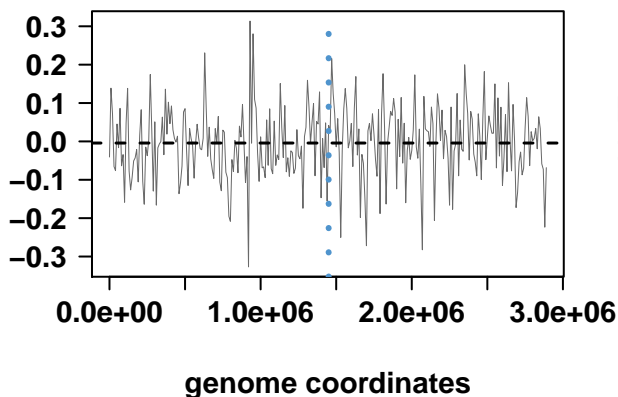
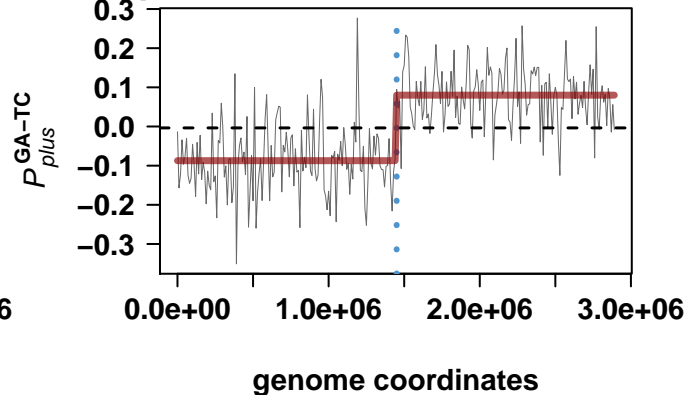
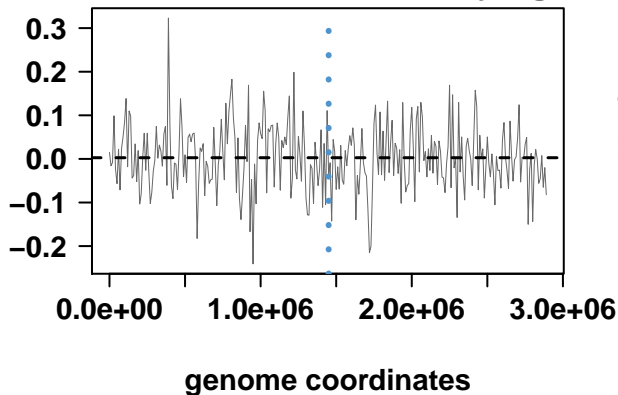


genome coordinates

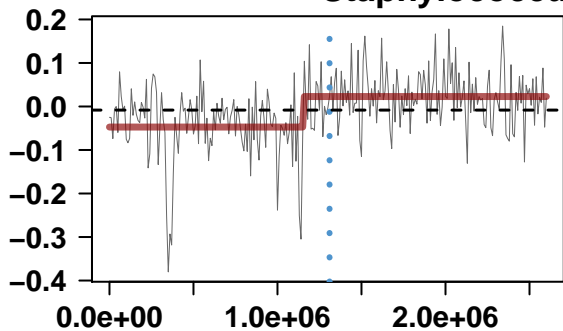


genome coordinates

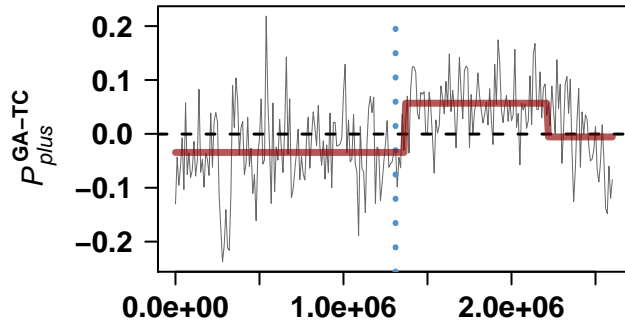
Listeria monocytogenes serotype 4b str. F2365



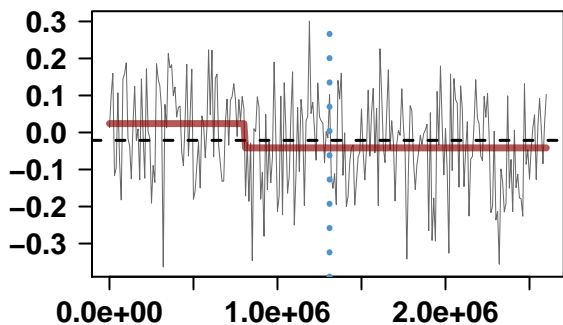
Staphylococcus epidermidis RP62A



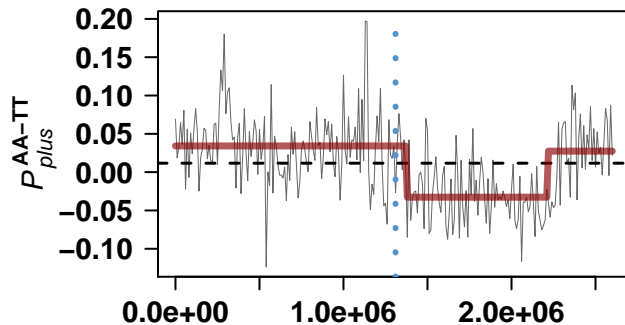
genome coordinates



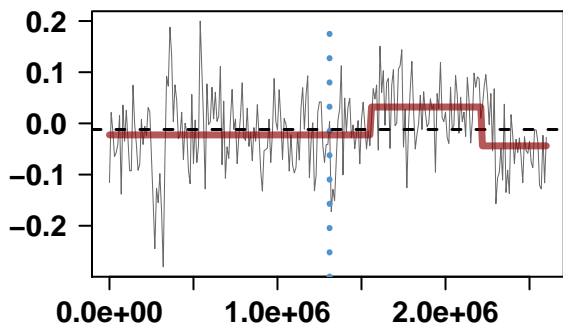
genome coordinates



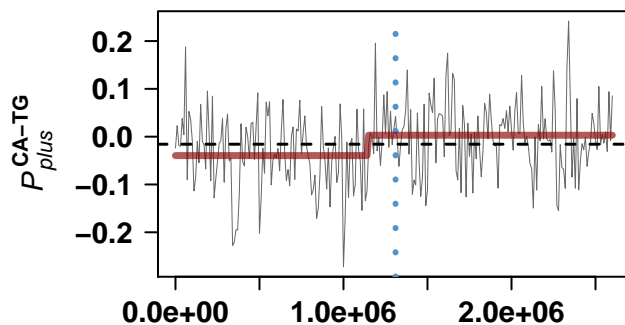
genome coordinates



genome coordinates

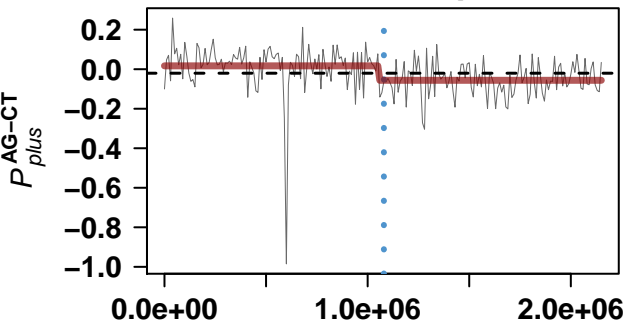


genome coordinates

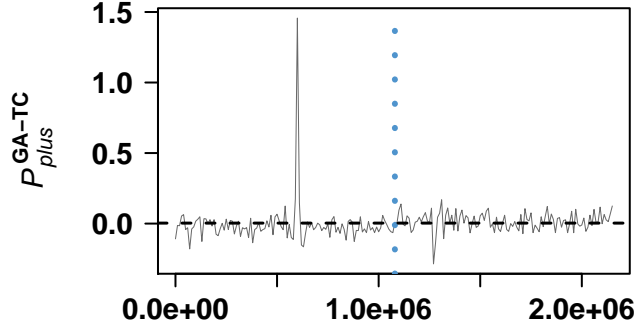


genome coordinates

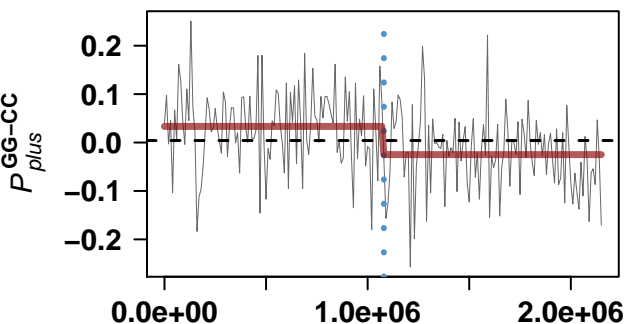
Streptococcus pneumoniae TIGR4



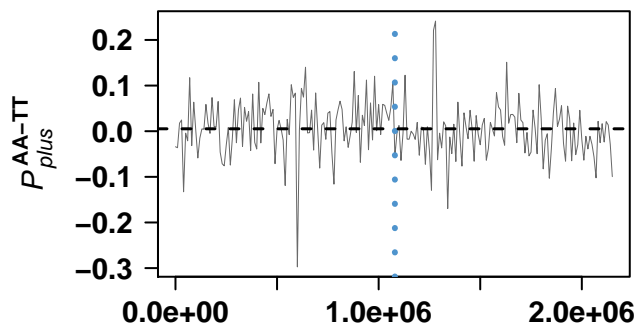
genome coordinates



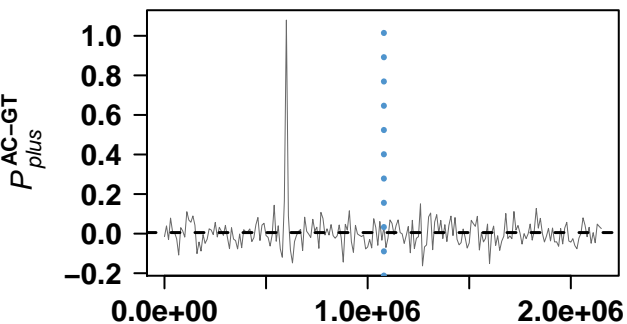
genome coordinates



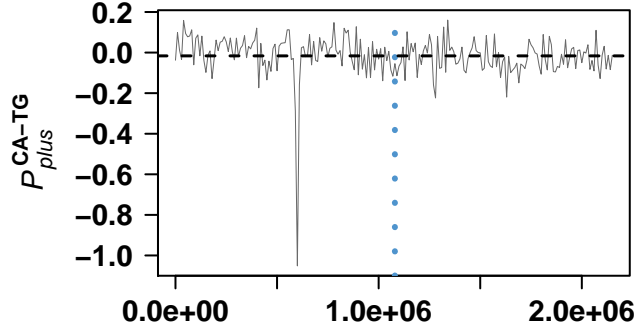
genome coordinates



genome coordinates

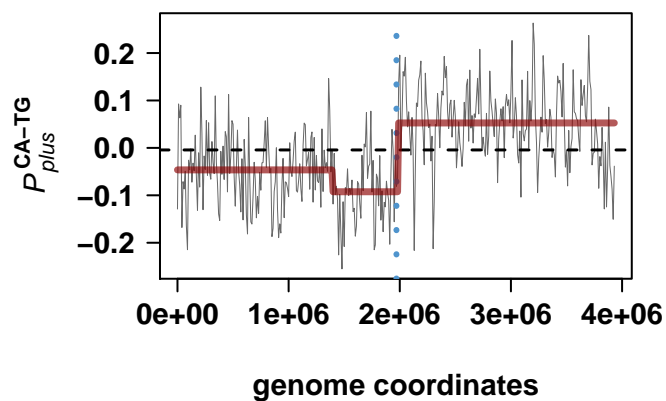
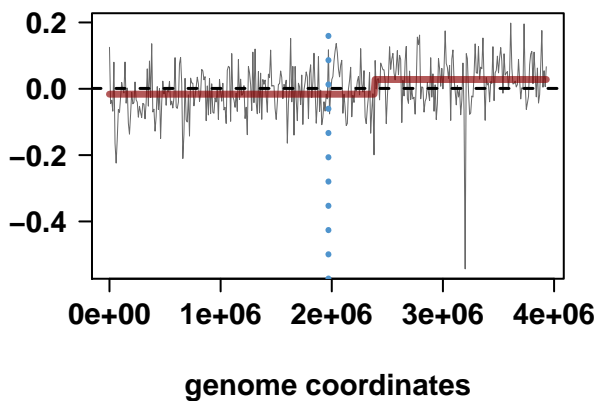
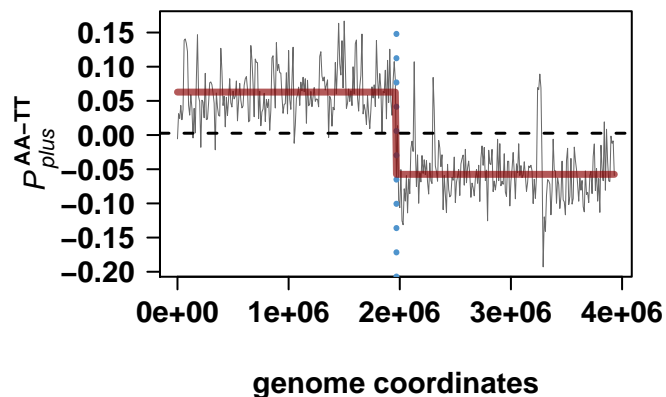
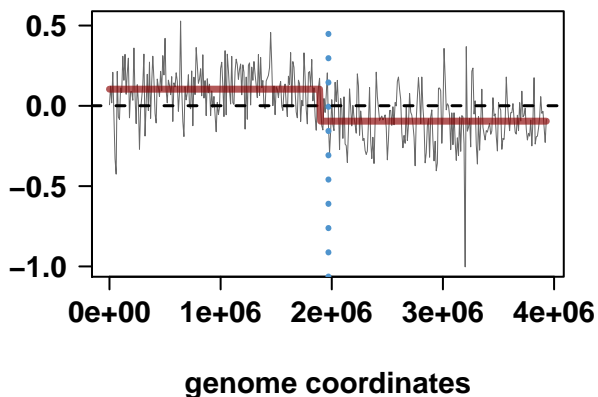
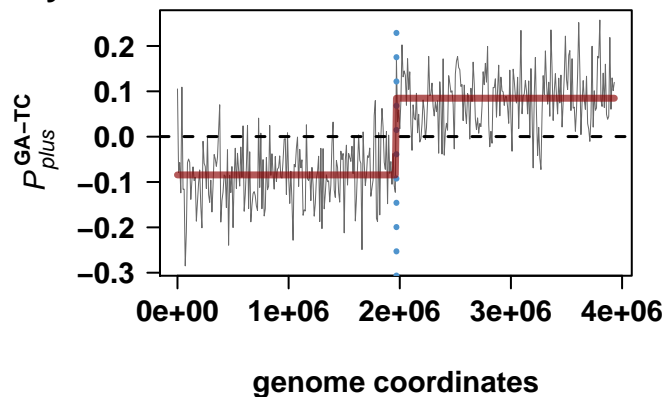
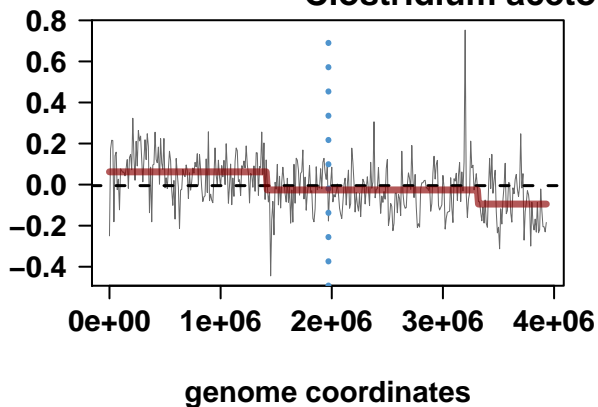


genome coordinates

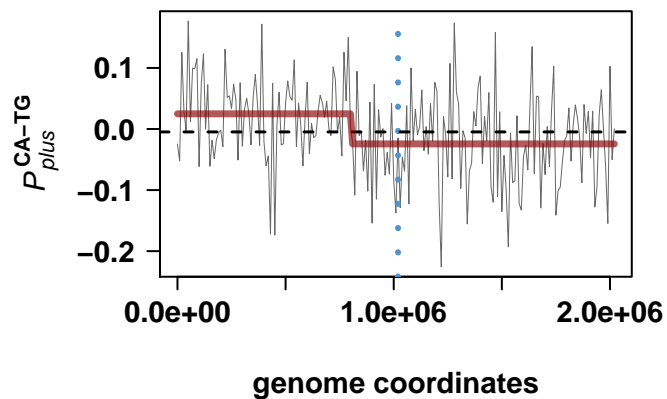
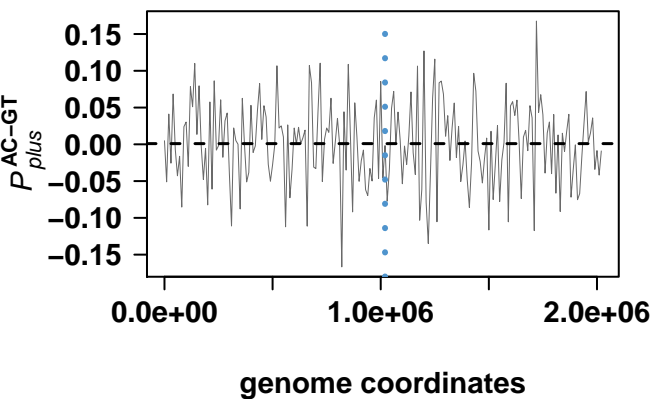
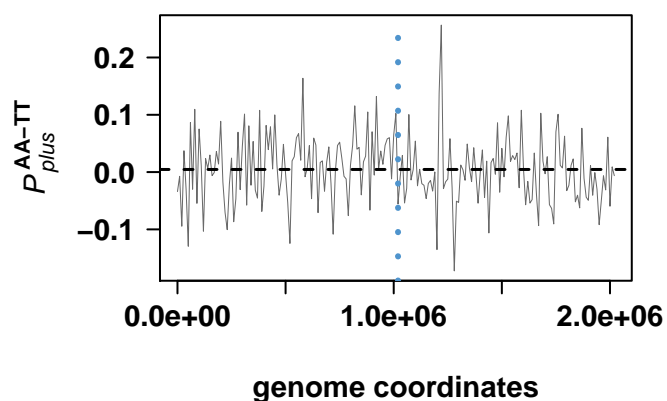
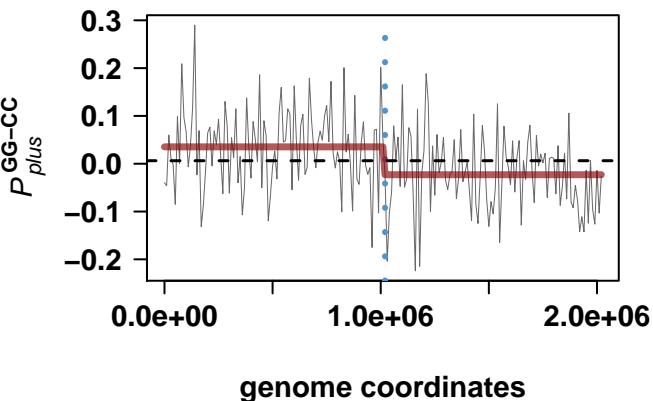
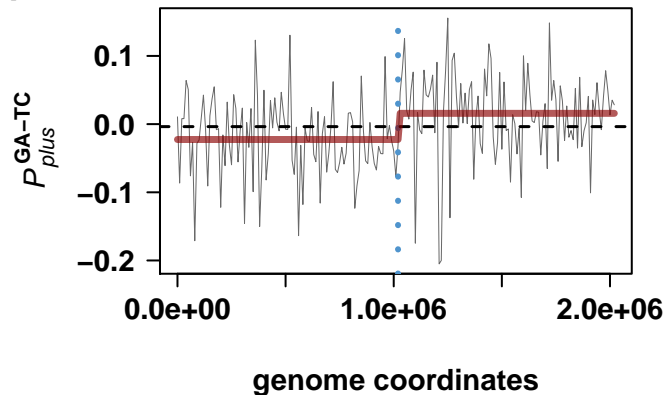
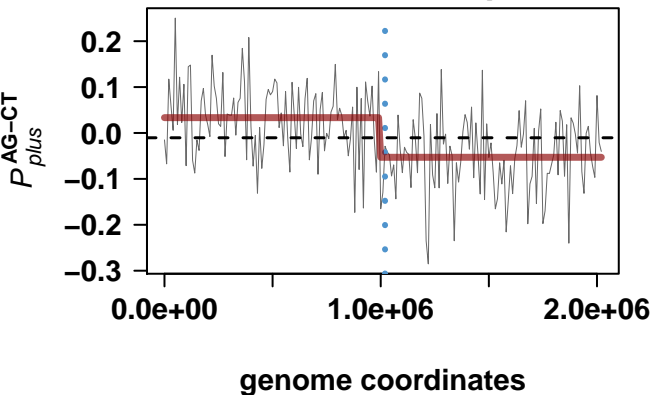


genome coordinates

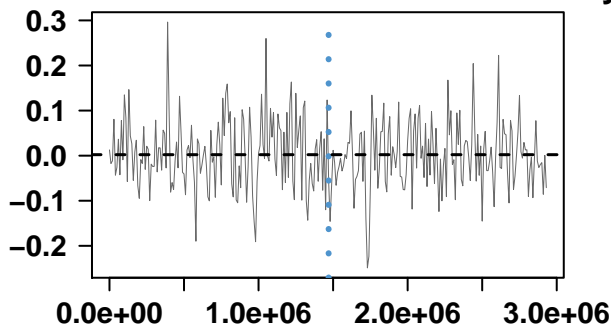
Clostridium acetobutylicum ATCC 824



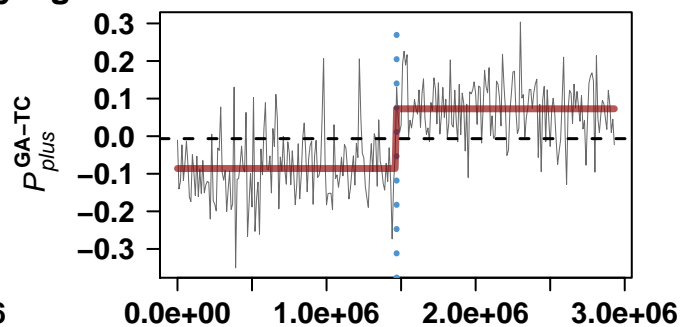
Streptococcus pneumoniae R6



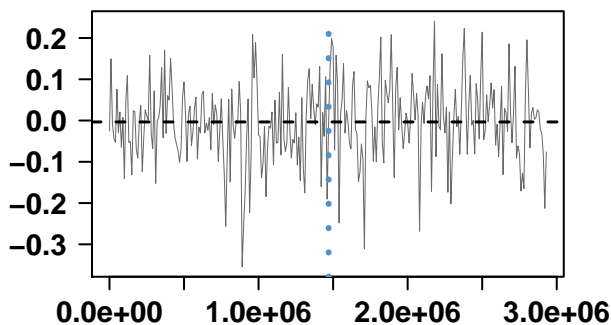
Listeria monocytogenes EGD-e



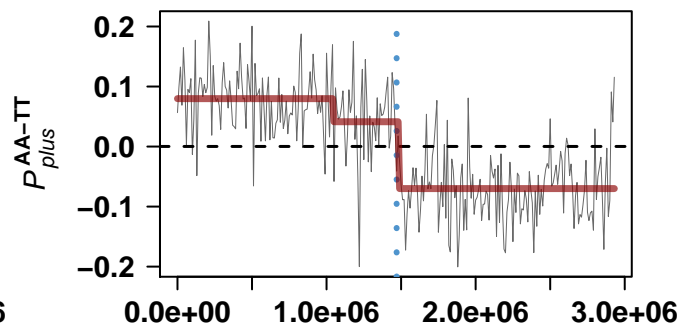
genome coordinates



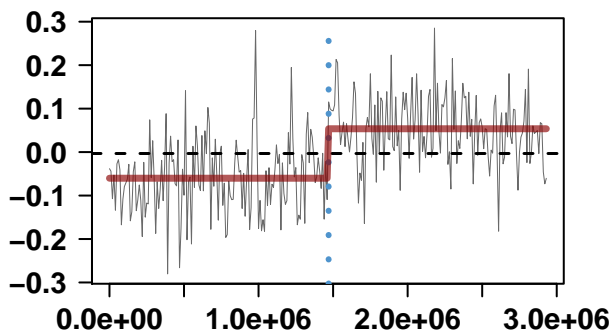
genome coordinates



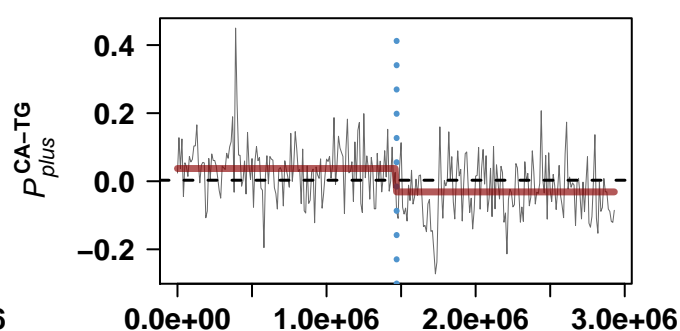
genome coordinates



genome coordinates

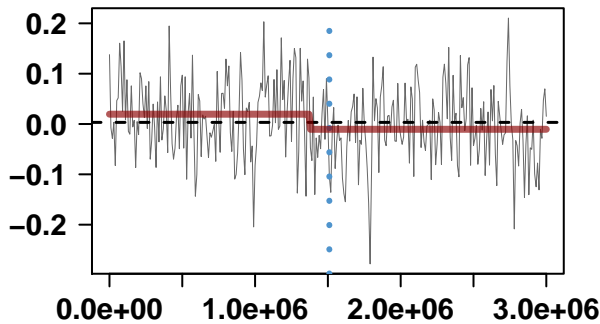


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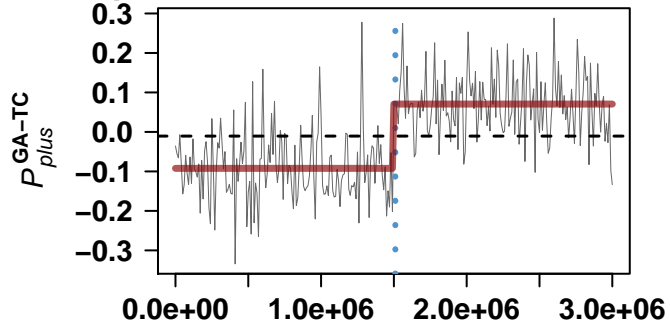


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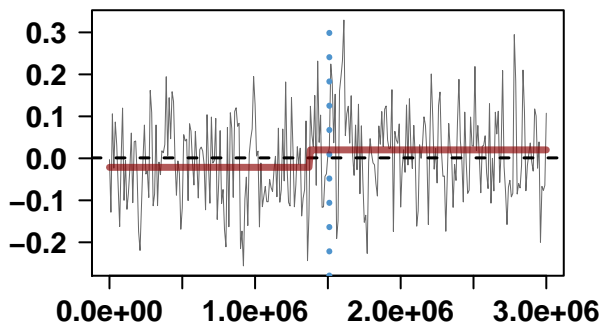
Listeria innocua Clip11262



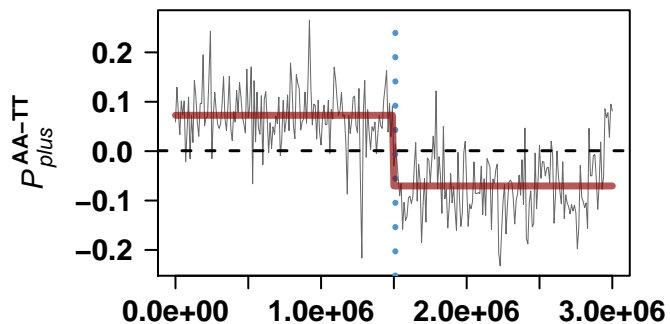
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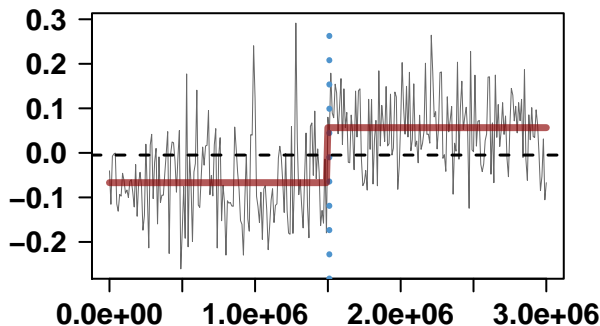
genome coordinates



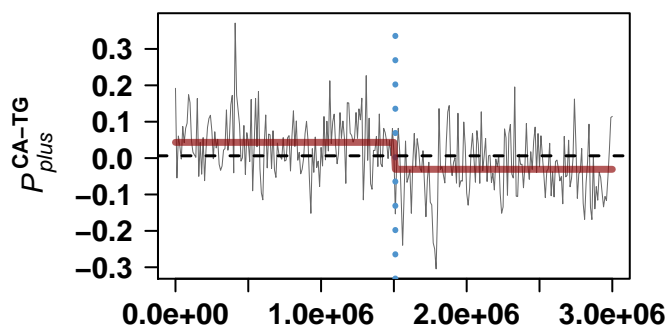
genome coordinates



genome coordinates

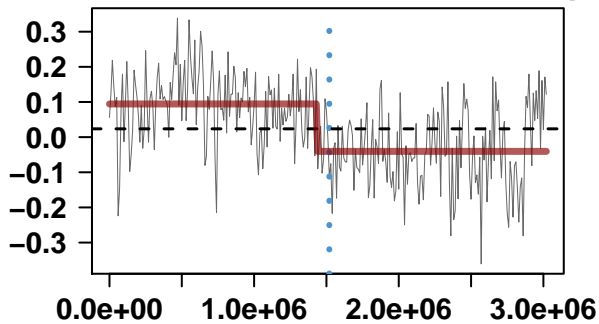


genome coordinates

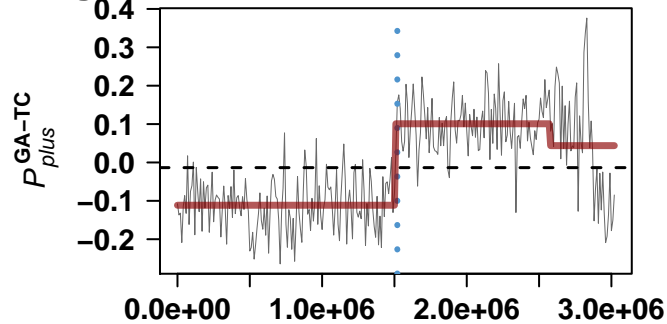


genome coordinates

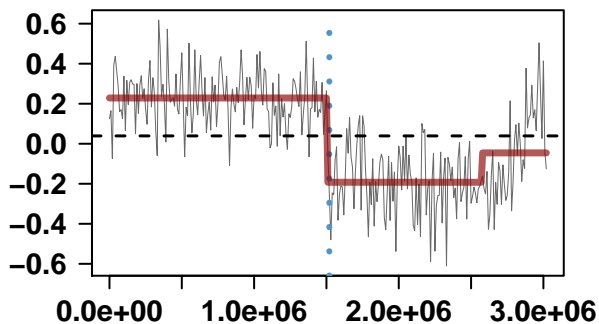
Clostridium perfringens str. 13



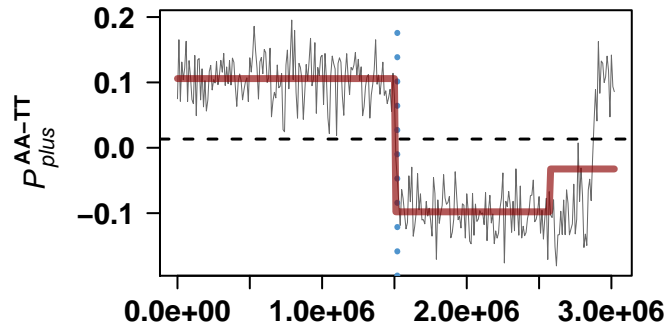
genome coordinates



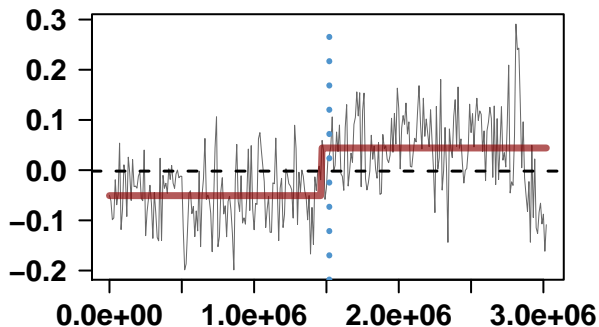
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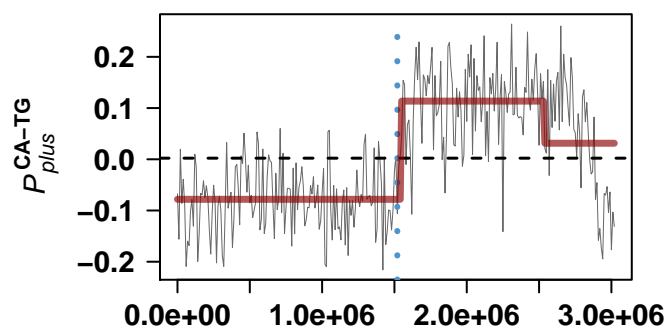
genome coordinates



genome coordinates

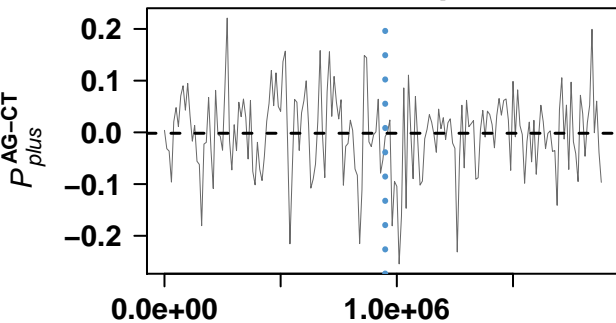


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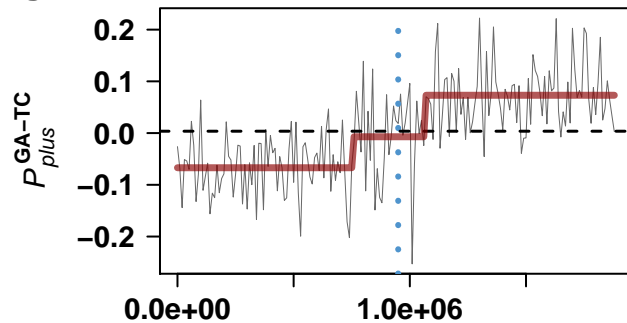


genome coordinates

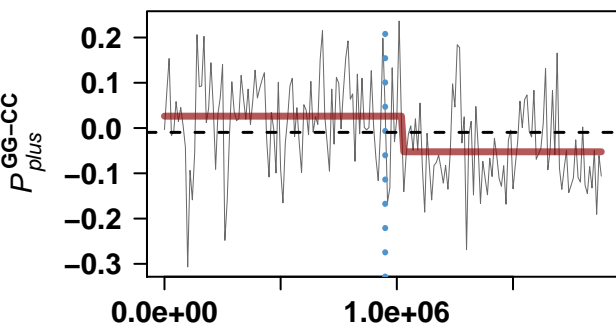
Streptococcus pyogenes MGAS8232



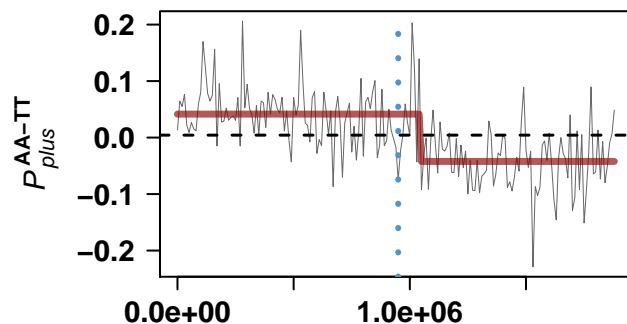
genome coordinates



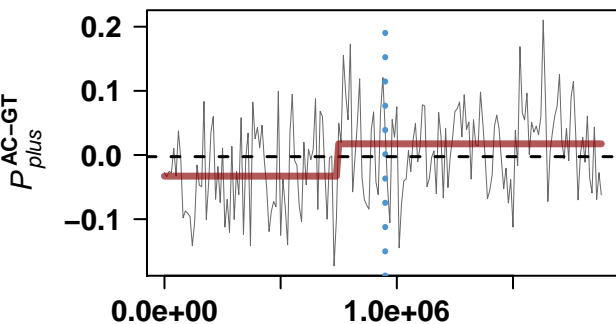
genome coordinates



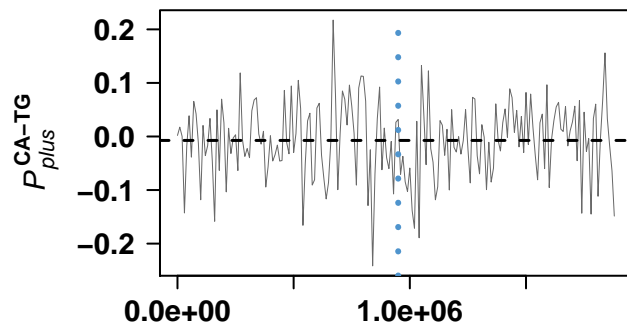
genome coordinates



genome coordinates

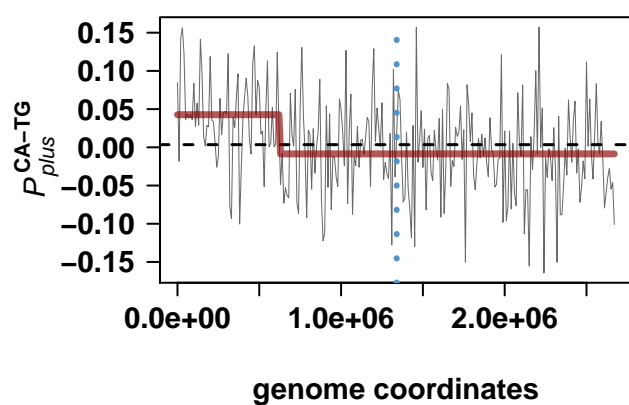
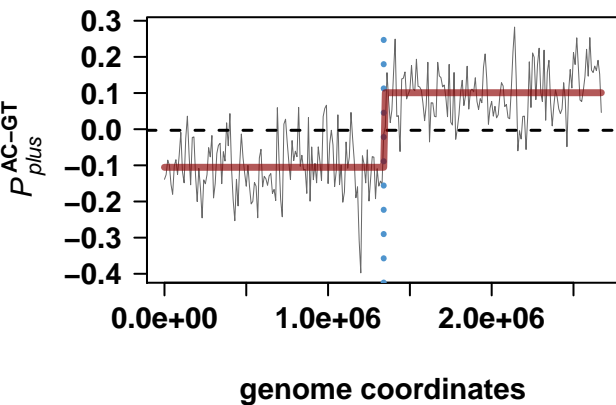
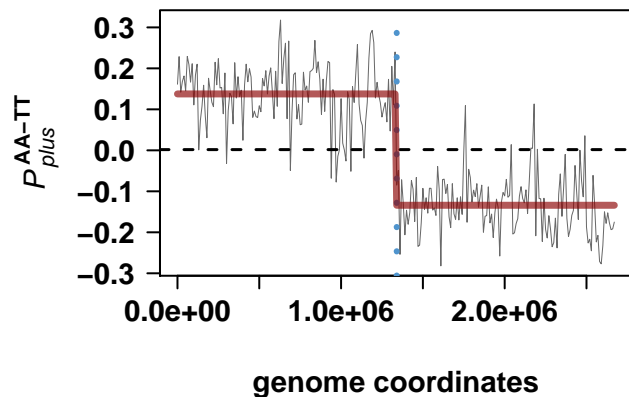
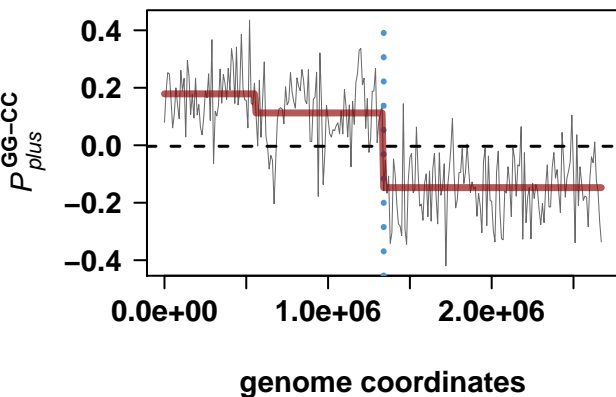
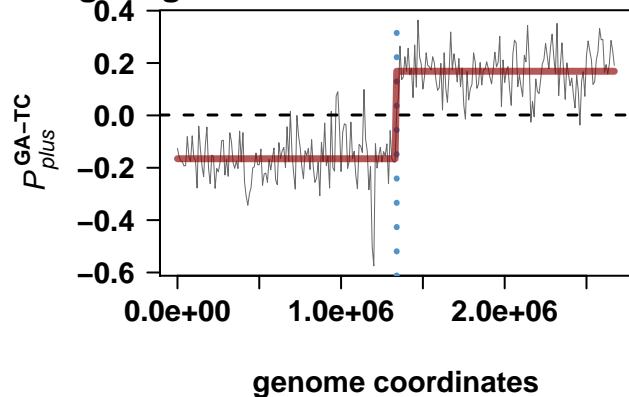
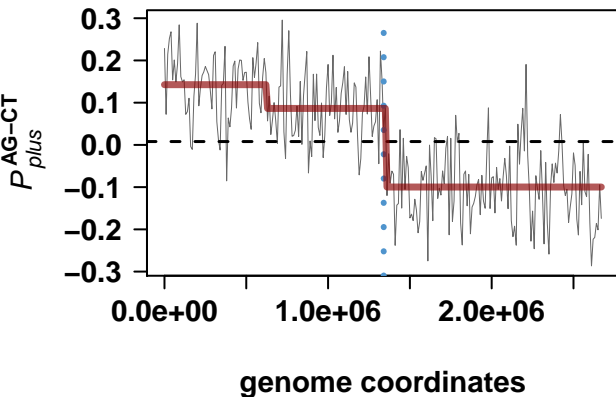


genome coordinates

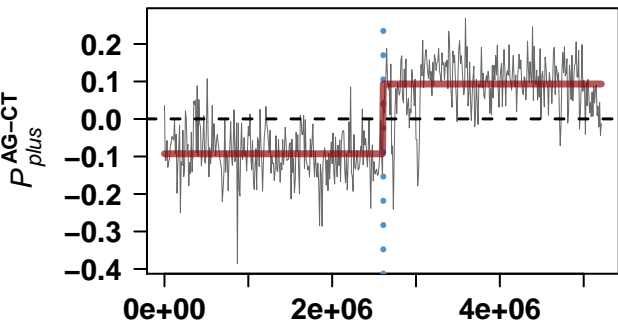


genome coordinates

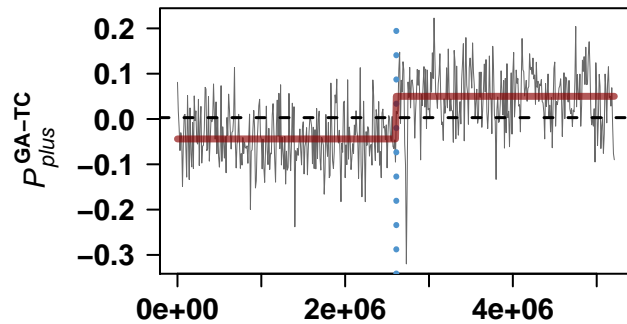
Thermoanaerobacter tengcongensis MB4



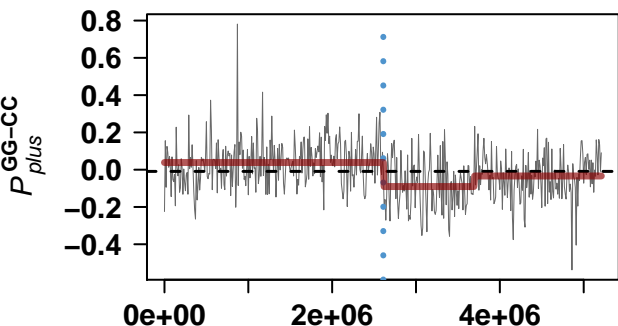
Bacillus cereus ATCC 10987



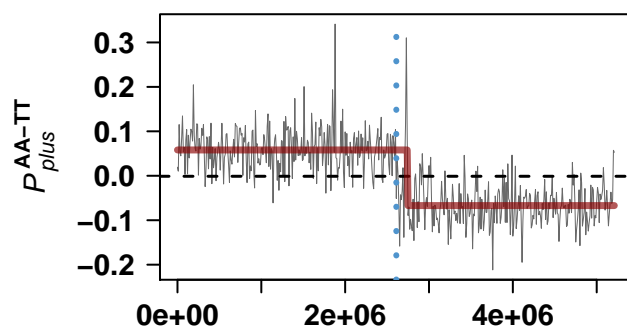
genome coordinates



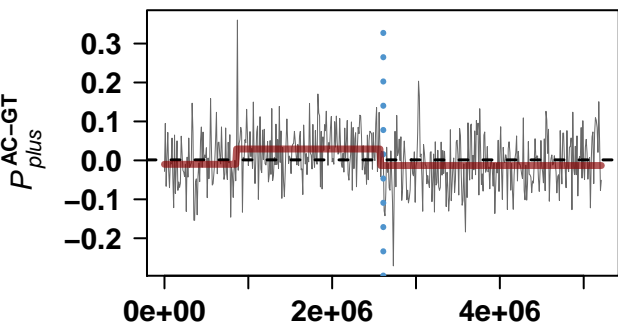
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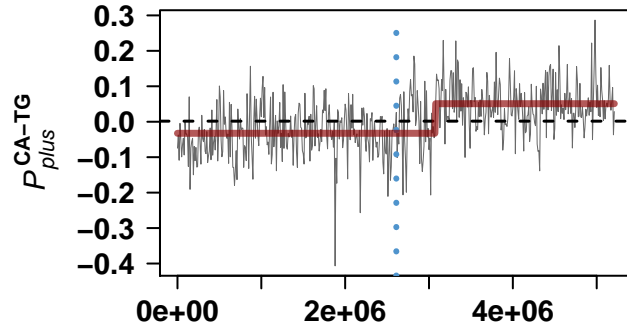
genome coordinates



genome coordinates

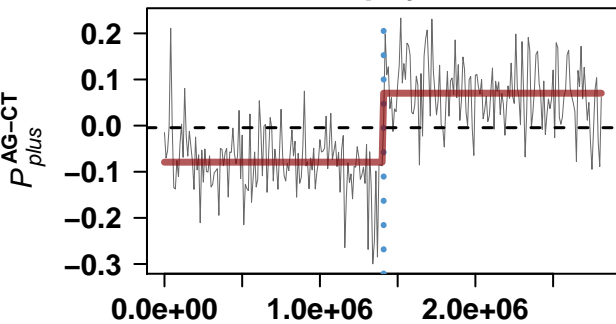


genome coordinates

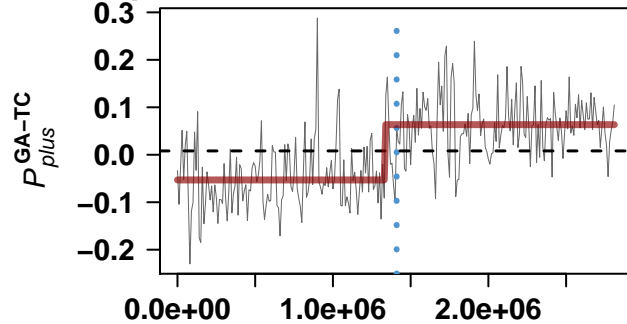


genome coordinates

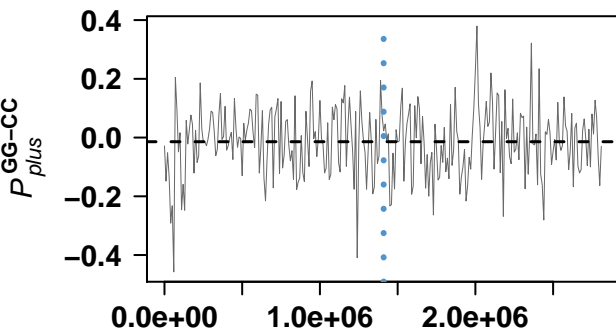
Staphylococcus aureus subsp. aureus MW2



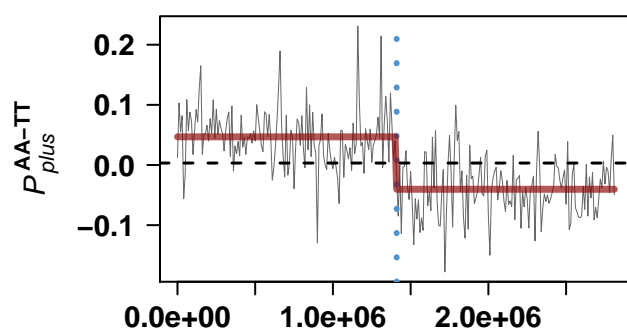
genome coordinates



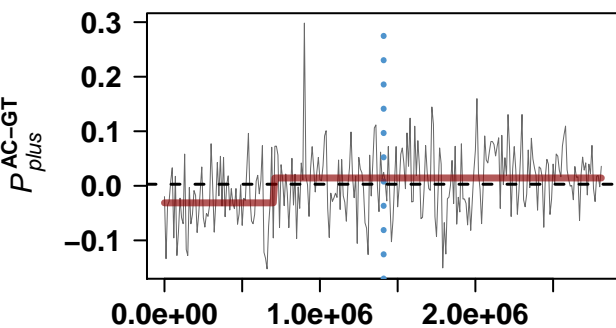
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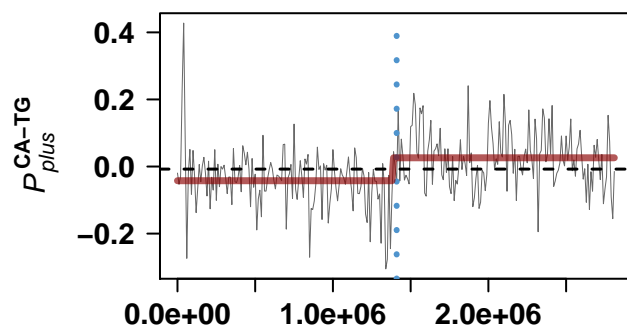
genome coordinates



genome coordinates

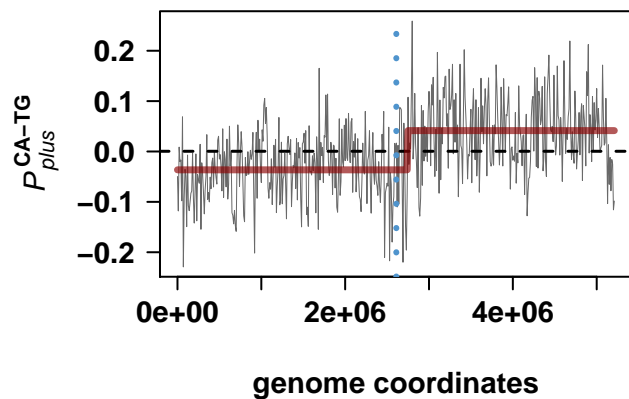
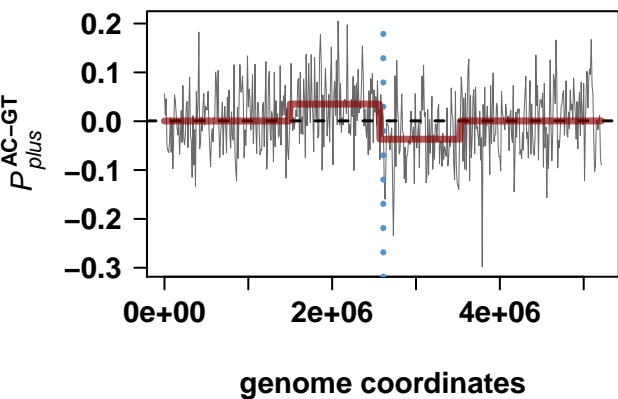
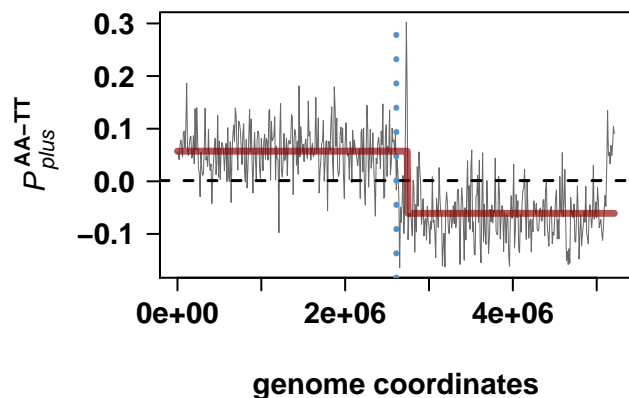
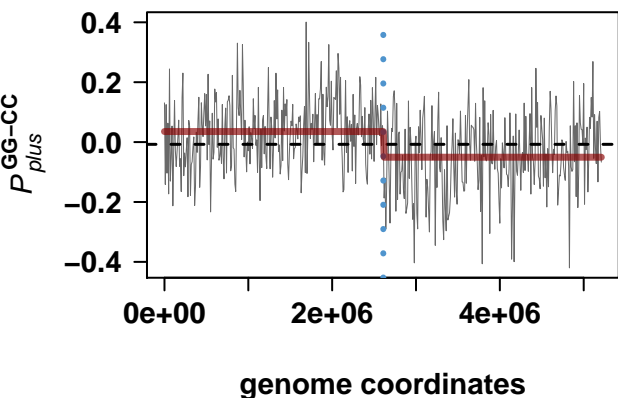
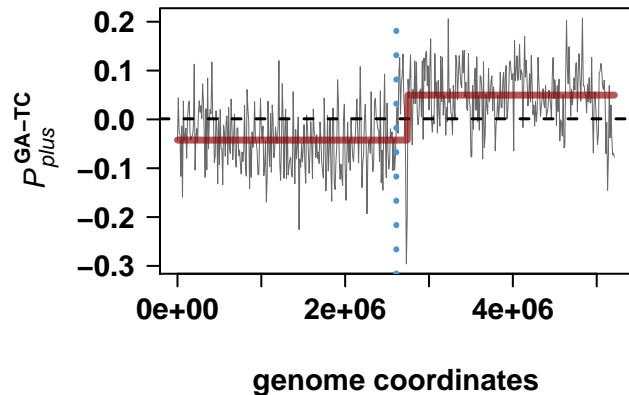
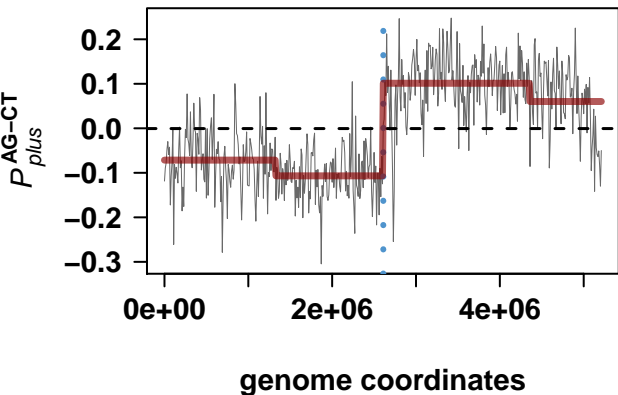


genome coordinates

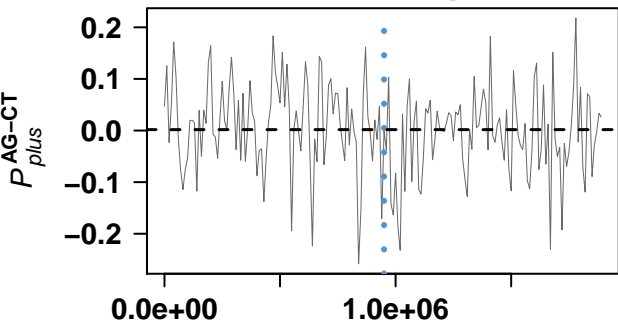


genome coordinates

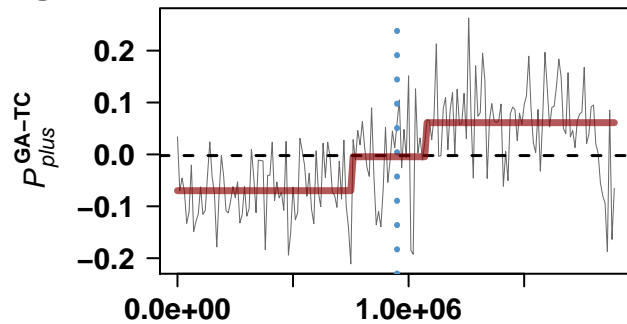
Bacillus anthracis str. Ames



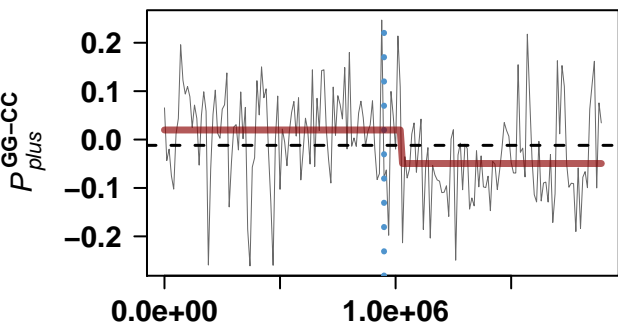
Streptococcus pyogenes MGAS315



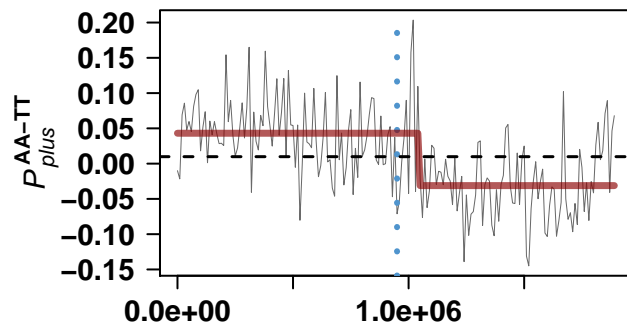
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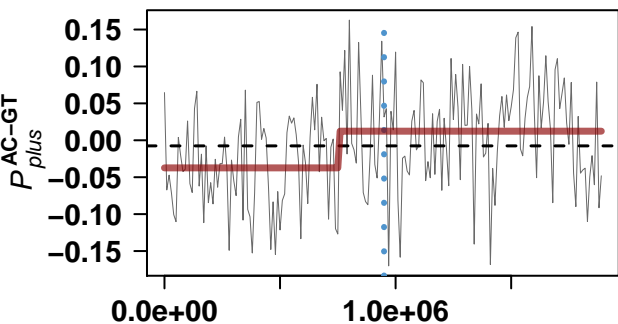
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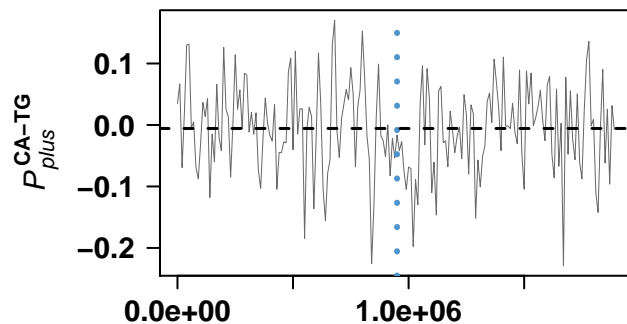
genome coordinates



genome coordinates

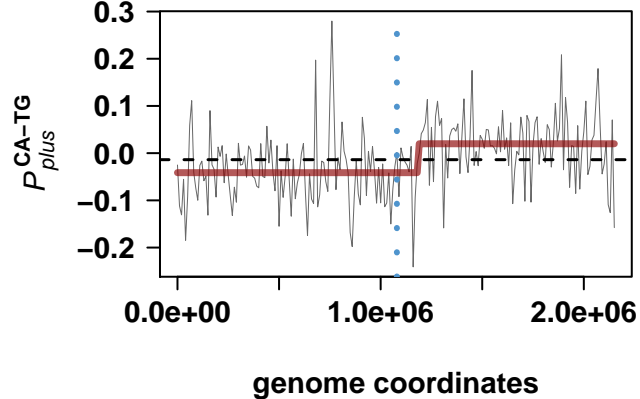
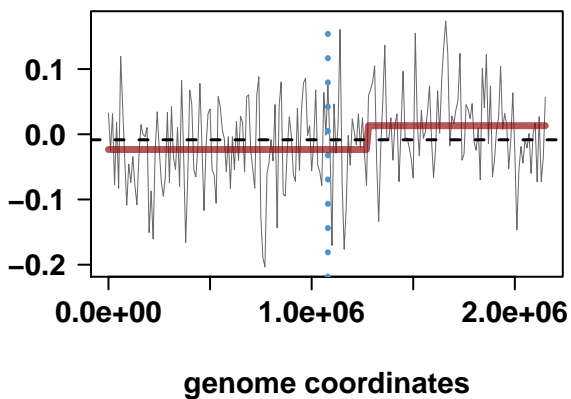
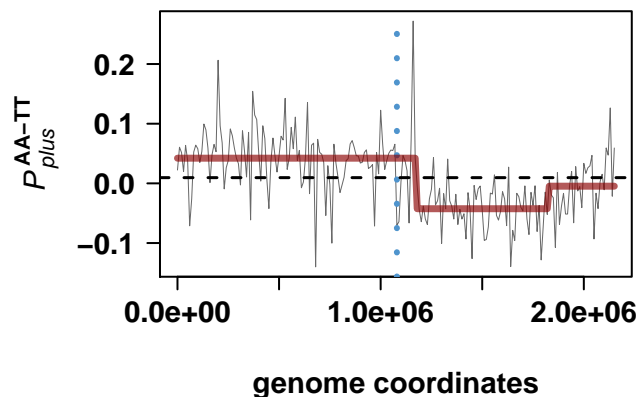
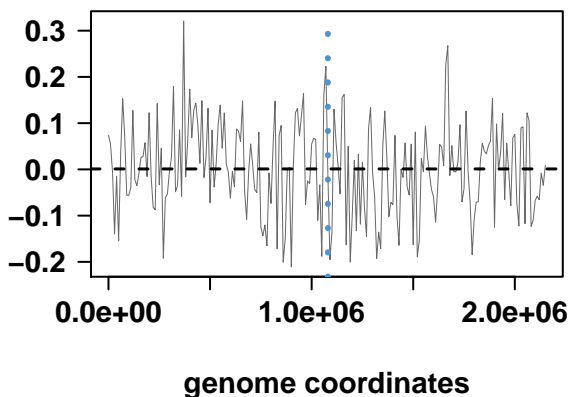
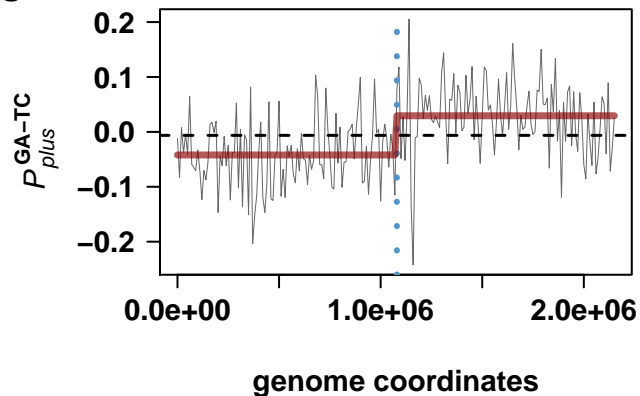
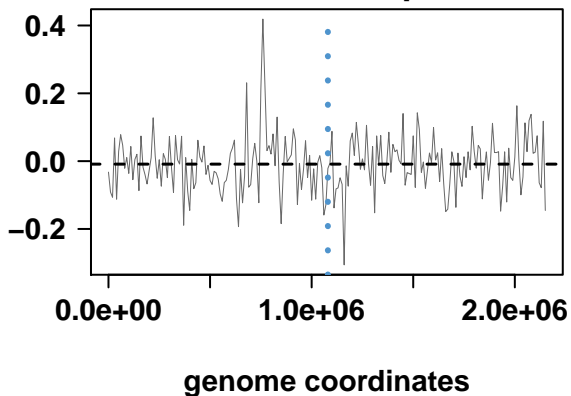


genome coordinates

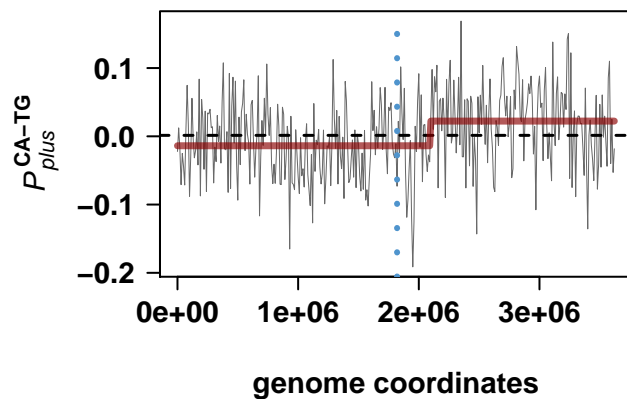
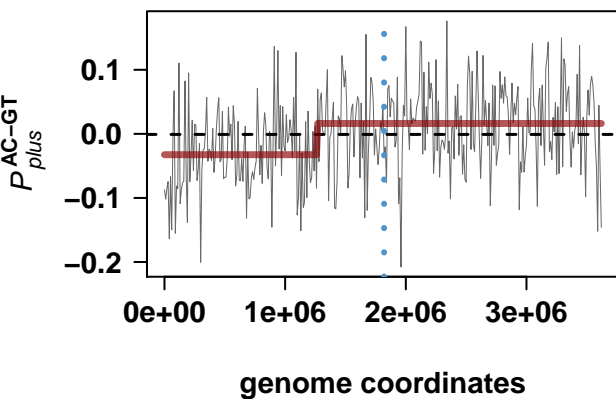
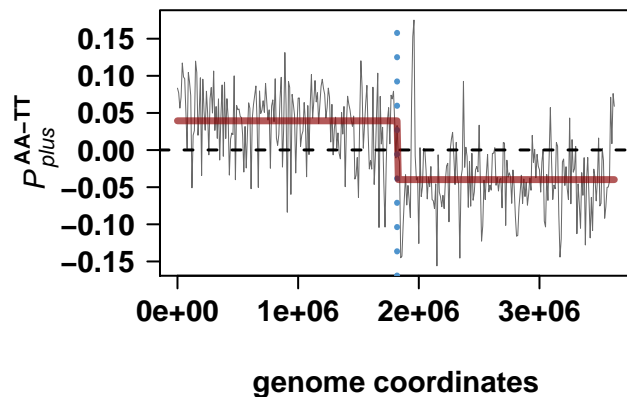
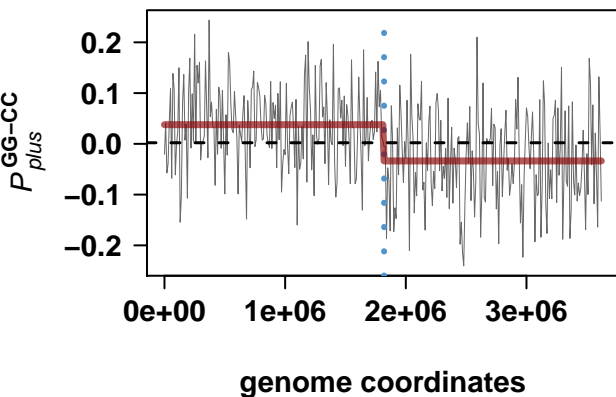
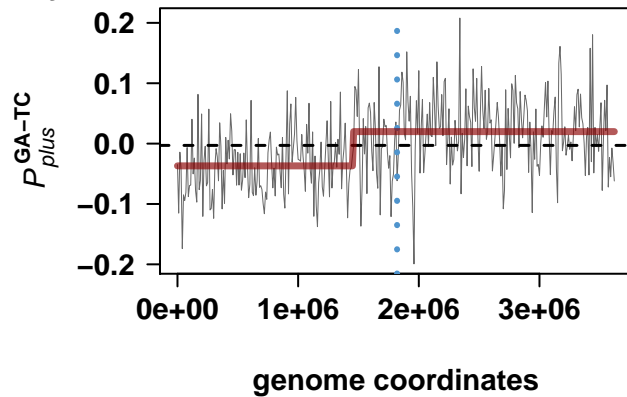
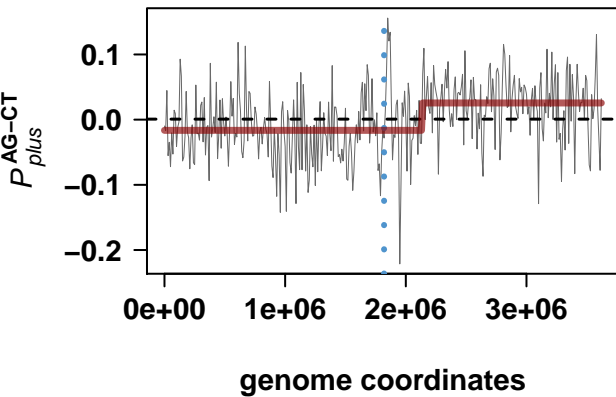


genome coordinates

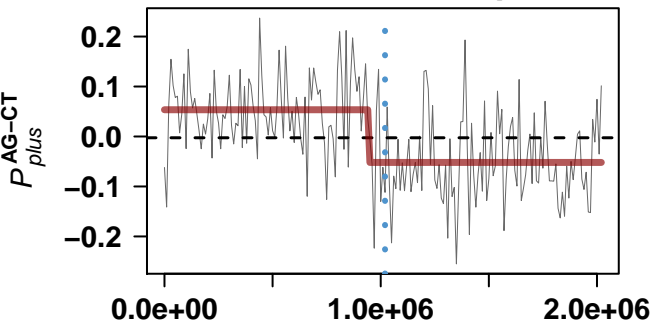
Streptococcus agalactiae 2603V/R



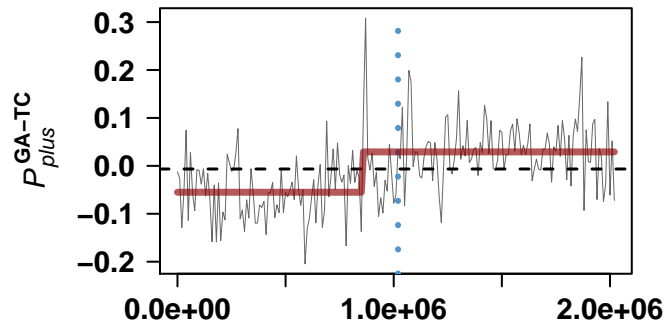
Oceanobacillus hieyensis HTE831



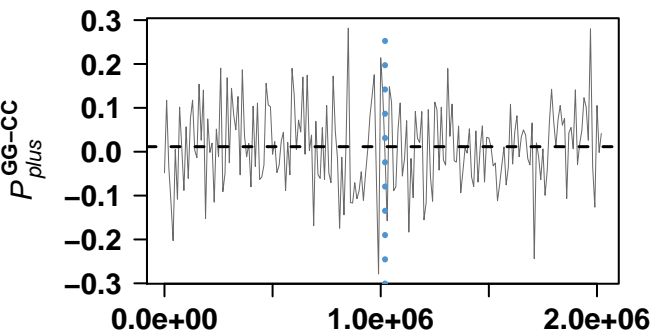
Streptococcus mutans UA159



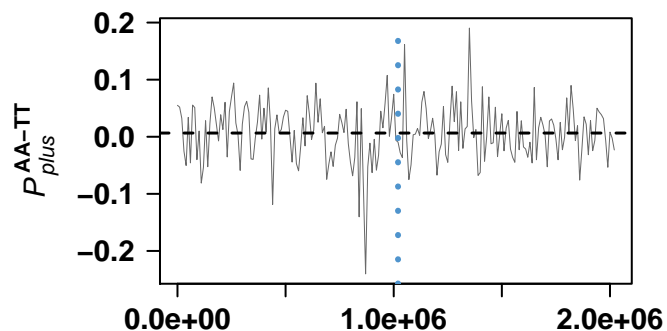
genome coordinates



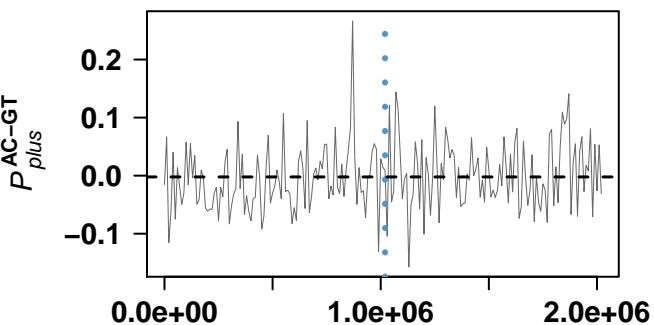
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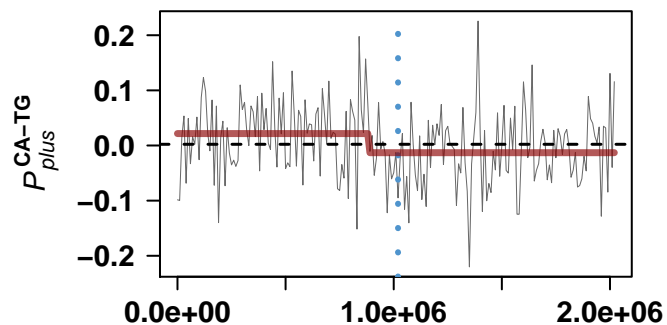
genome coordinates



genome coordinates

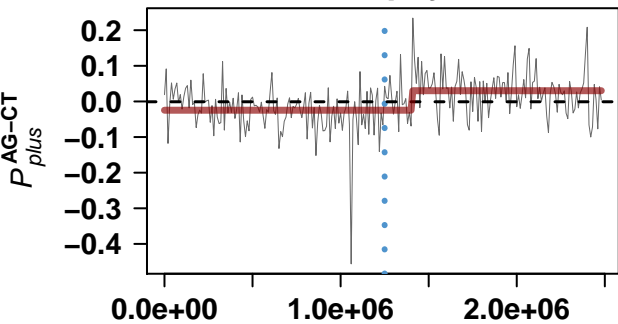


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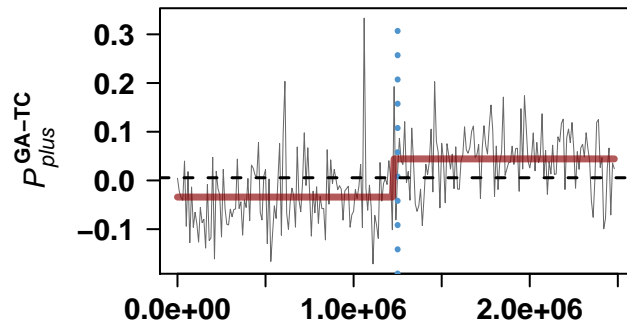


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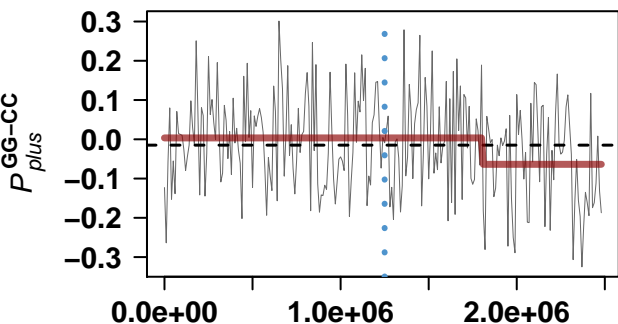
Staphylococcus epidermidis ATCC 12228



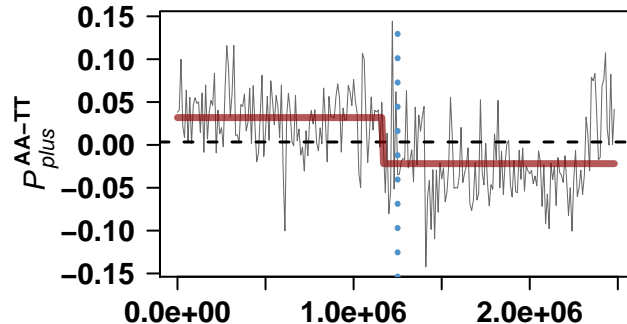
genome coordinates



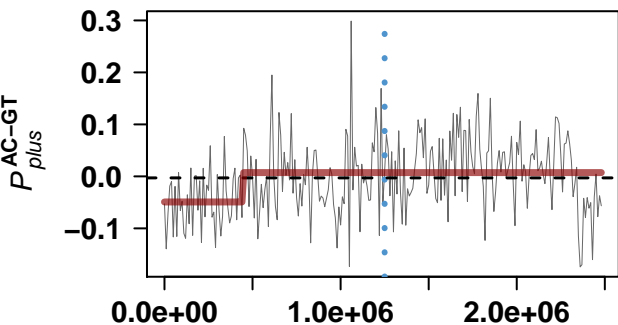
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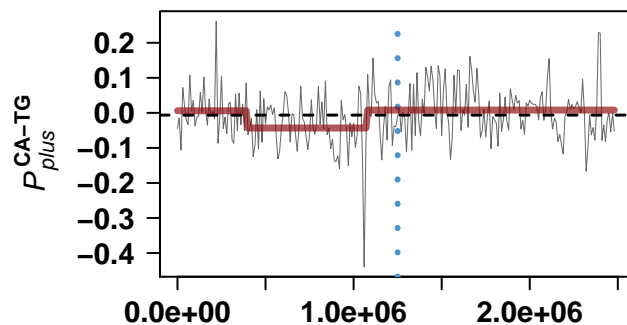
genome coordinates



genome coordinates

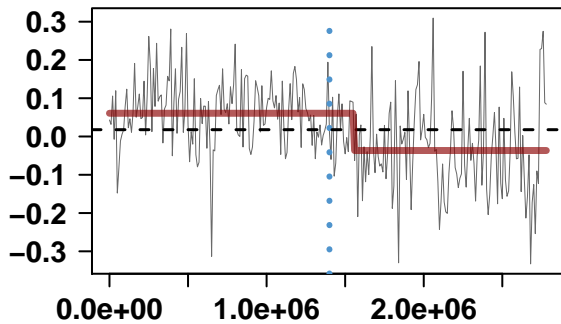


genome coordinates

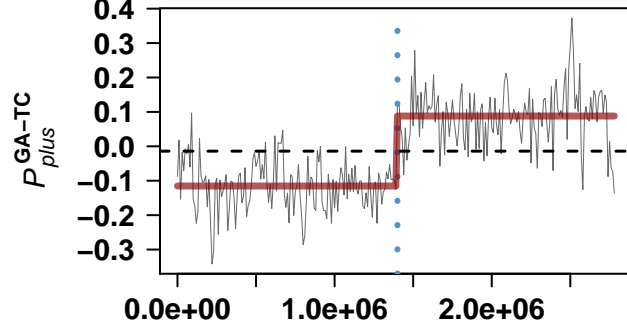


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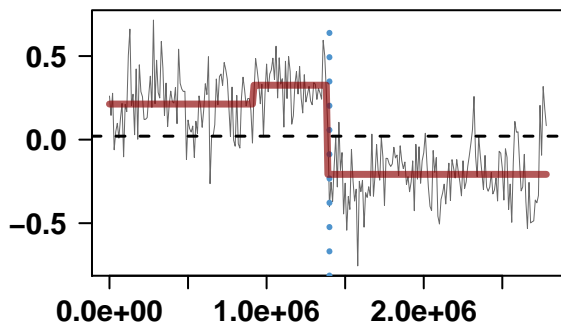
Clostridium tetani E88



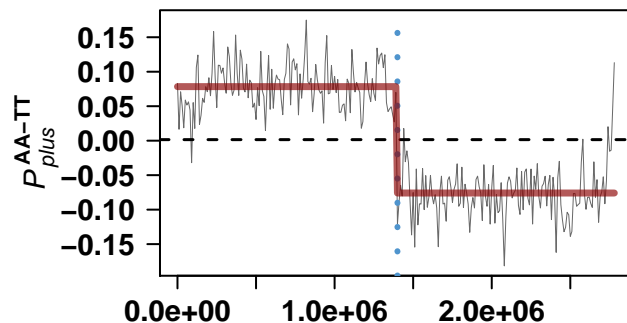
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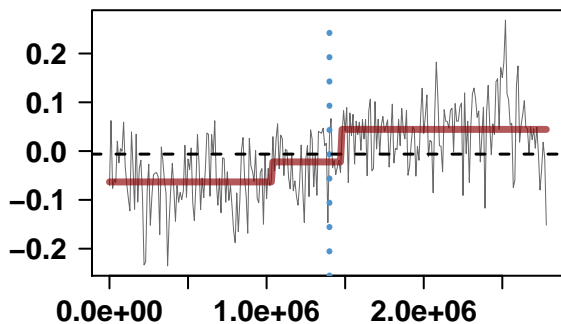
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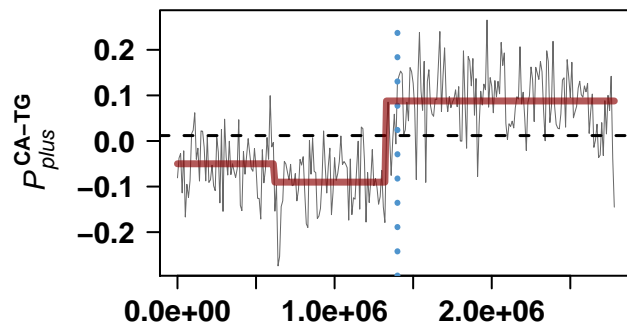
genome coordinates



genome coordinates

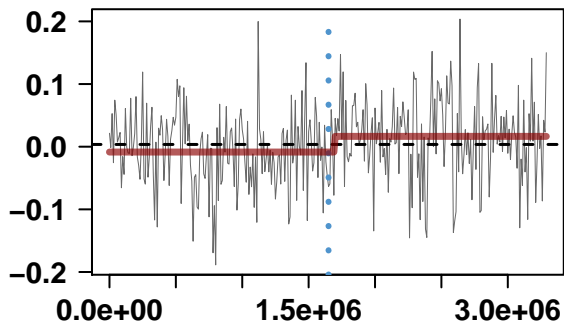


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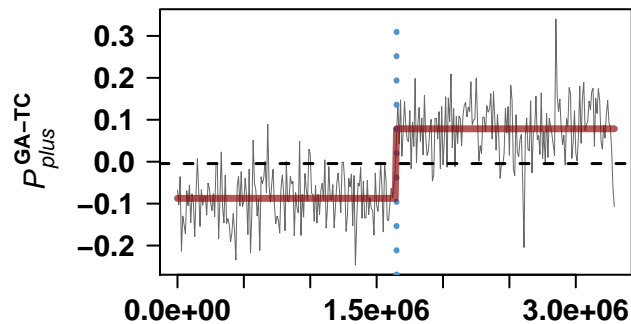


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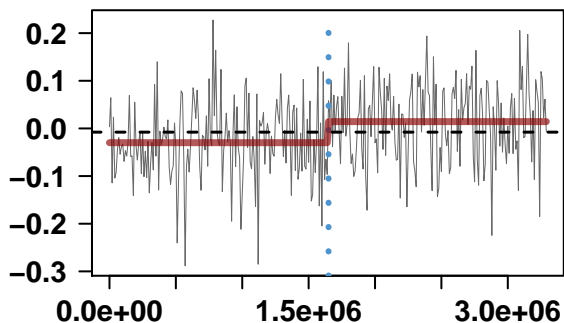
Lactobacillus plantarum WCFS1



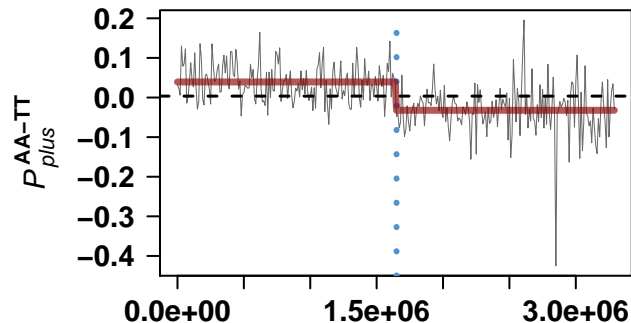
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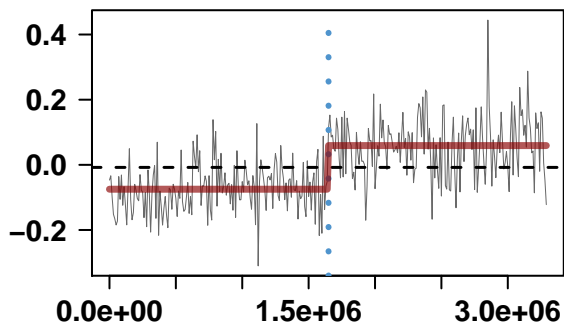
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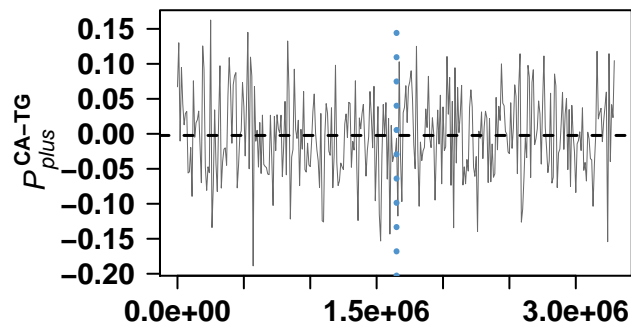
genome coordinates



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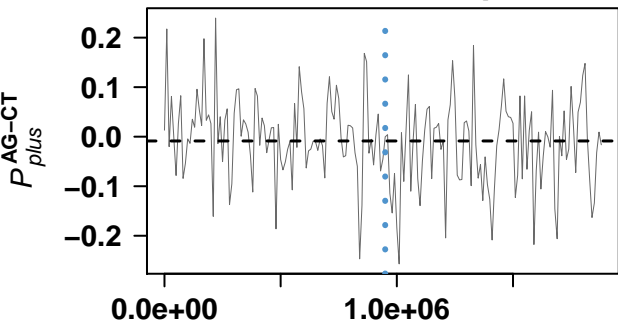


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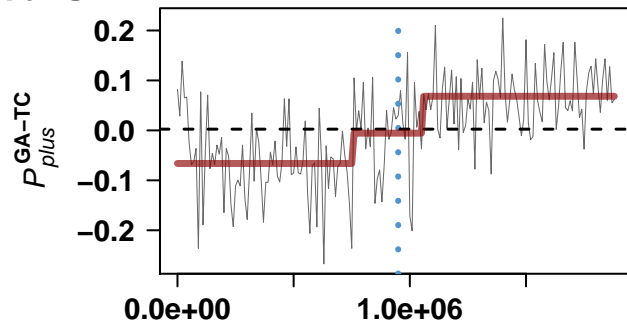


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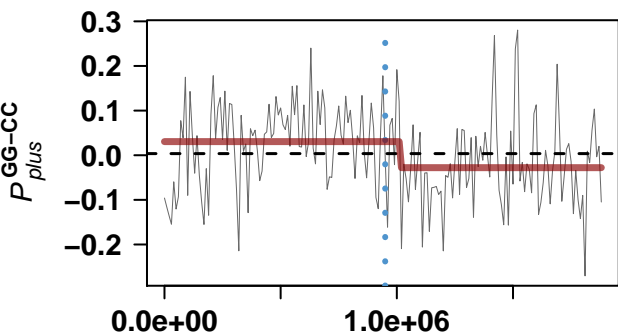
Streptococcus pyogenes SSI-1



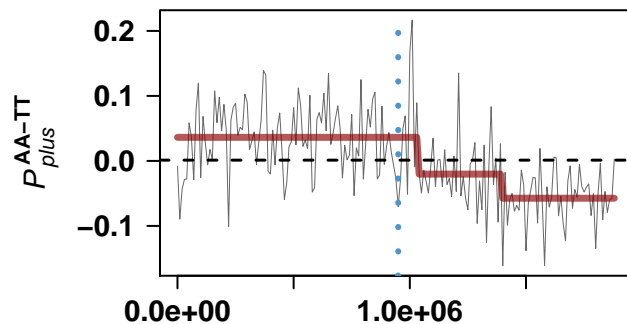
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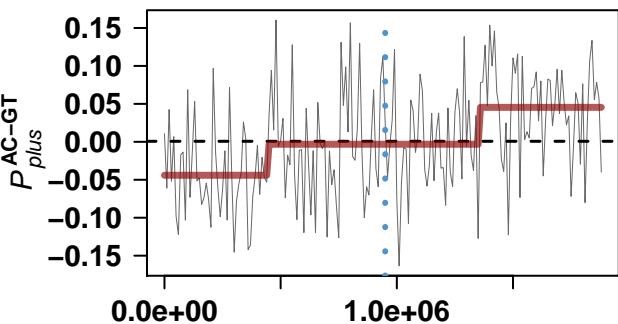
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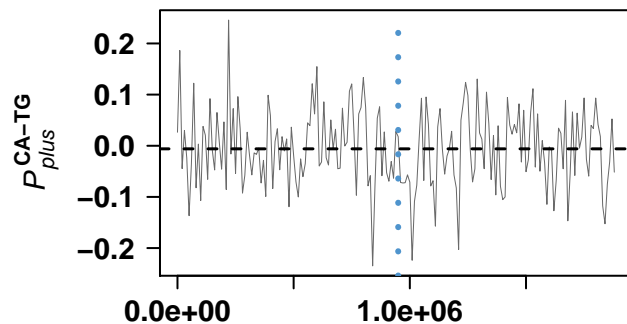
genome coordinates



genome coordinates

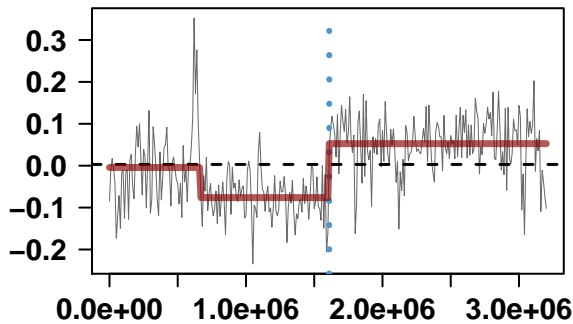


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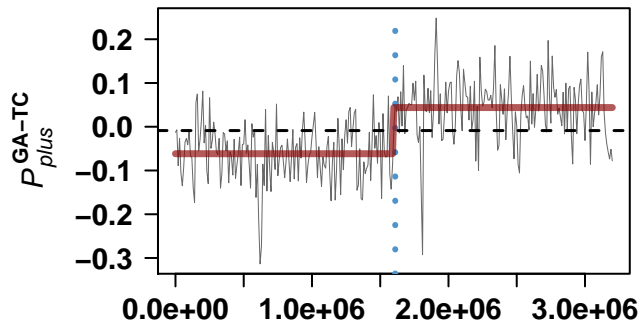


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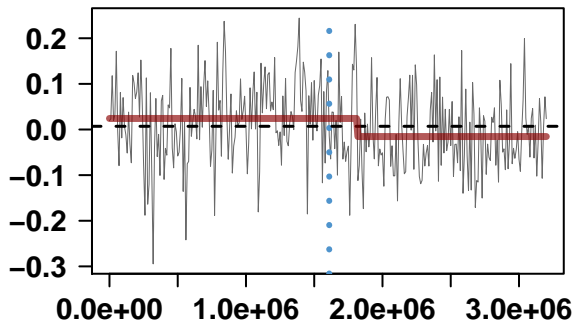
Enterococcus faecalis V583



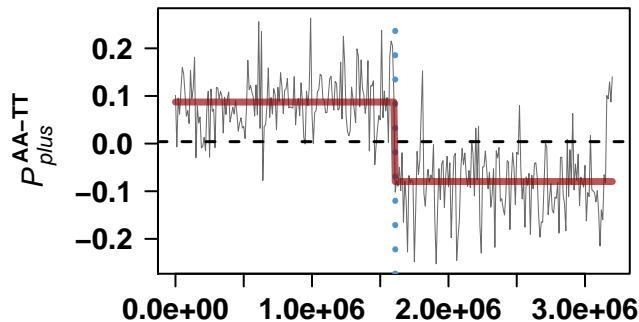
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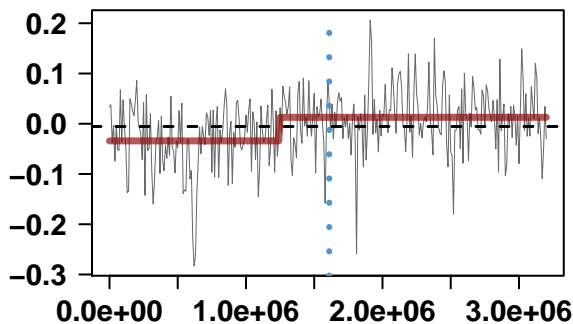
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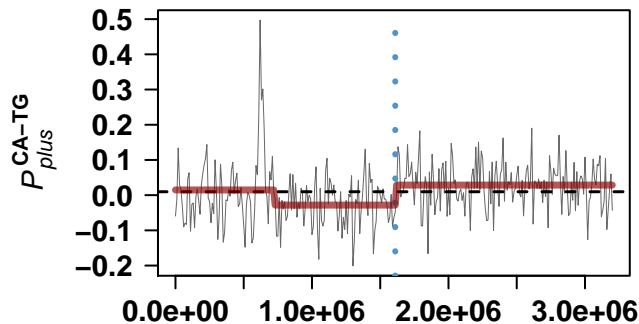
genome coordinates



genome coordinates

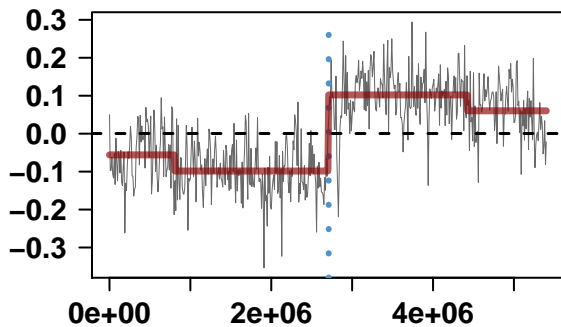


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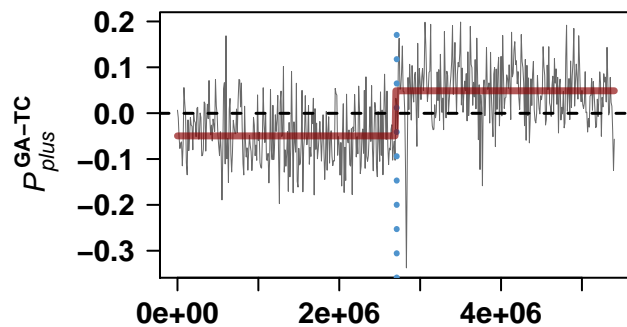


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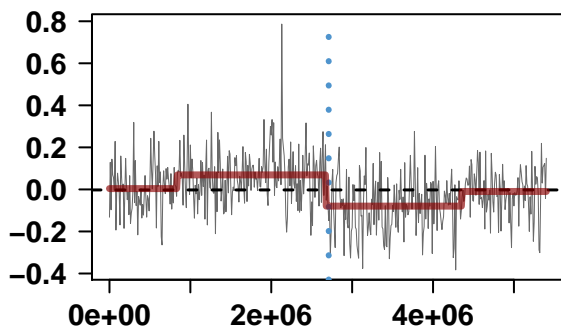
Bacillus cereus ATCC 14579



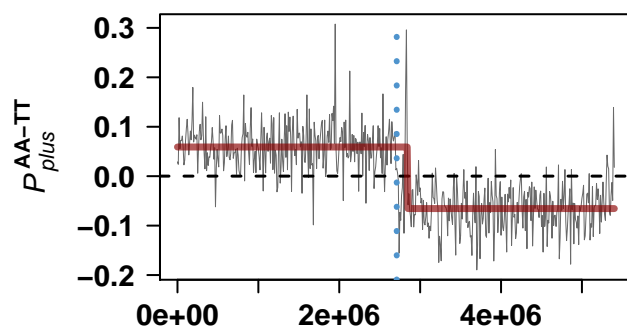
genome coordinates



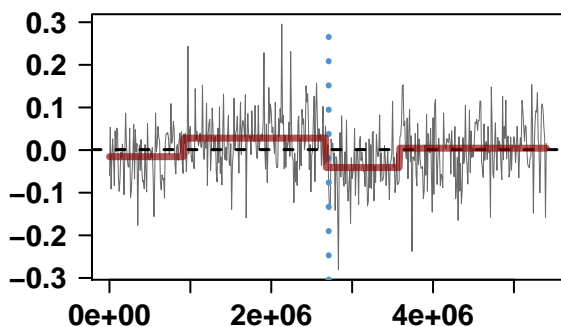
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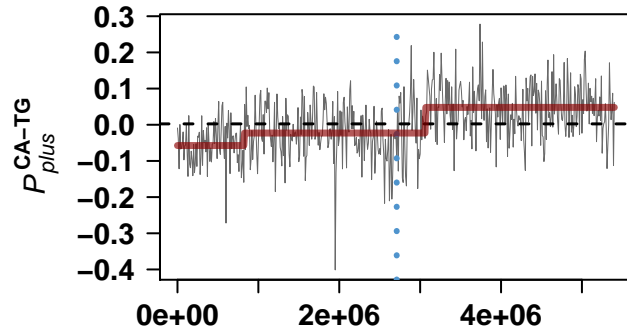
genome coordinates



genome coordinates

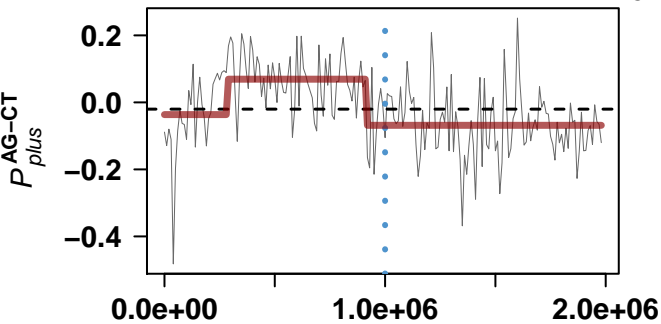


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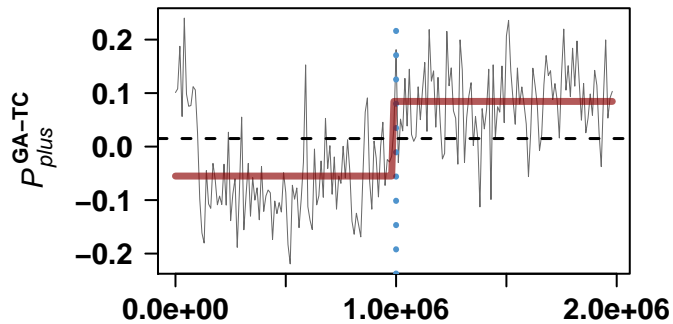


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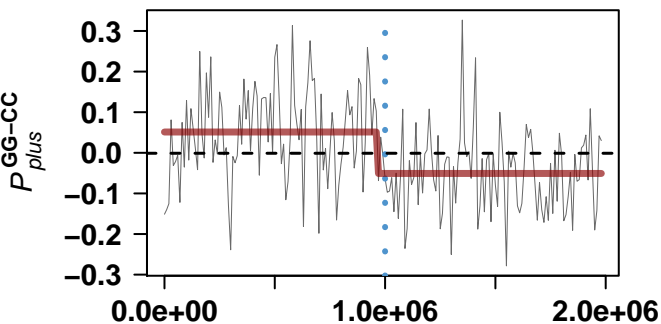
Lactobacillus johnsonii NCC 533



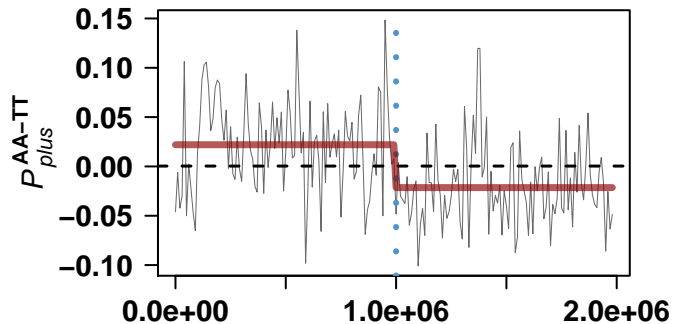
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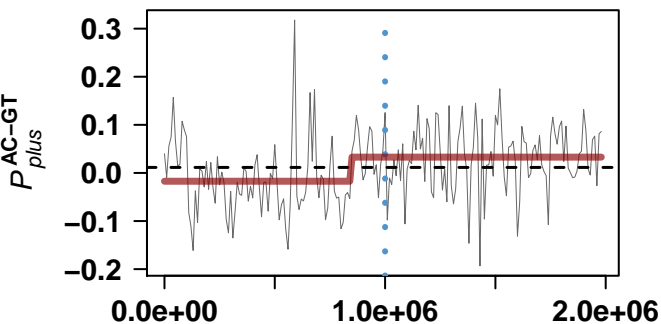
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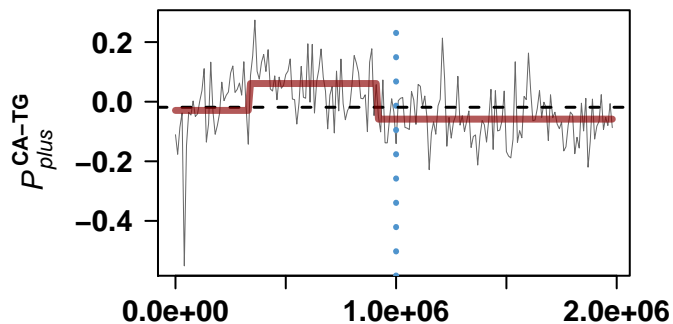
genome coordinates



genome coordinates

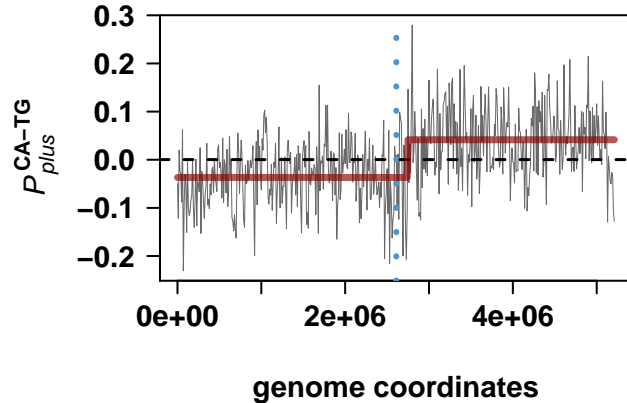
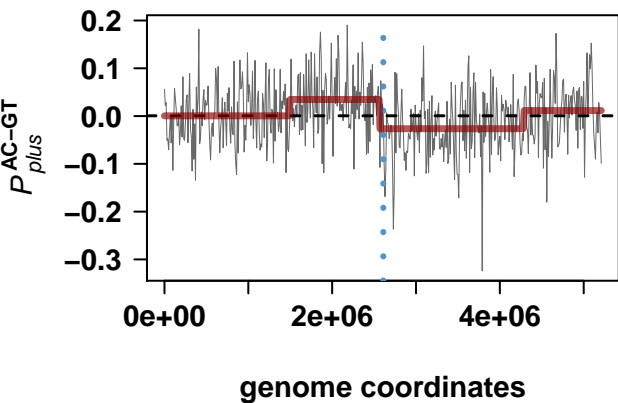
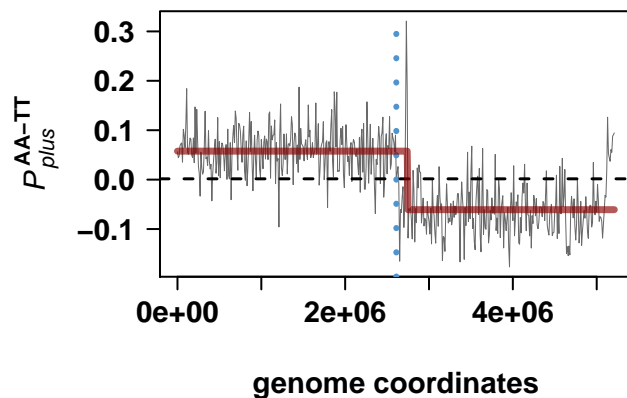
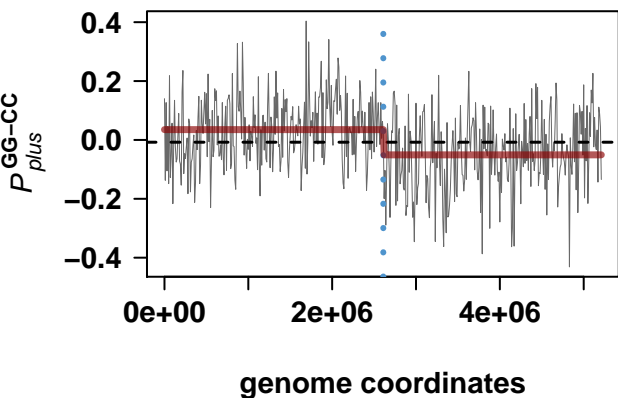
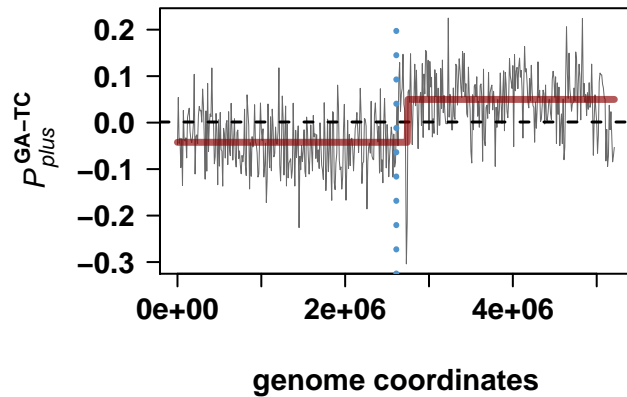
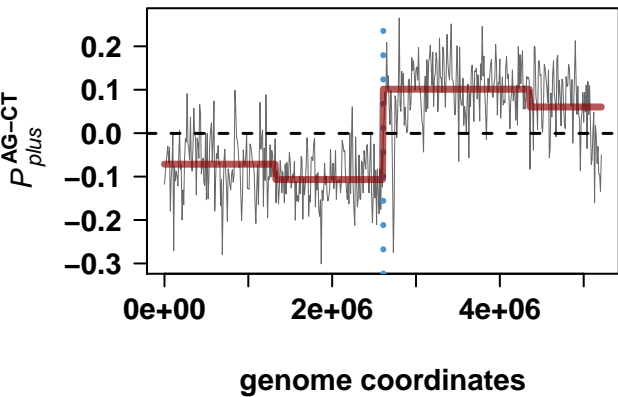


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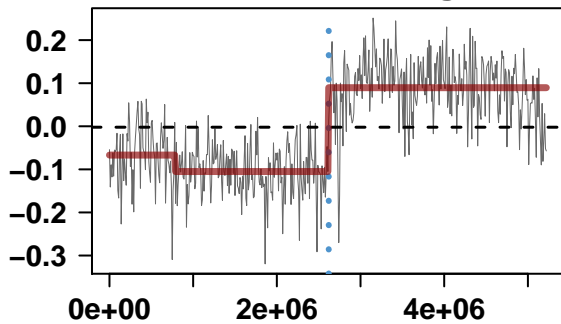


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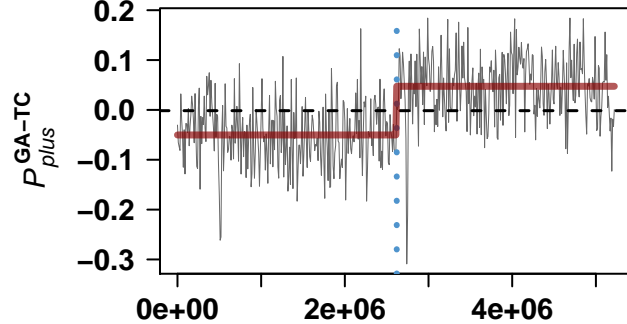
Bacillus anthracis str. Sterne



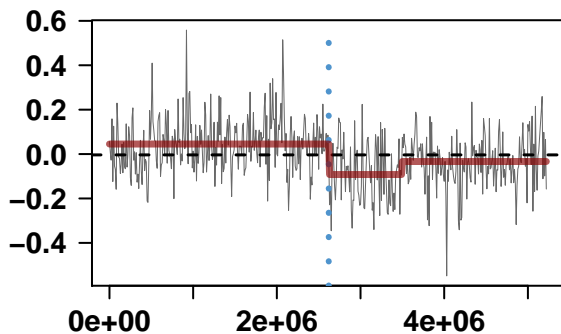
Bacillus thuringiensis serovar konkukian str. 97-27



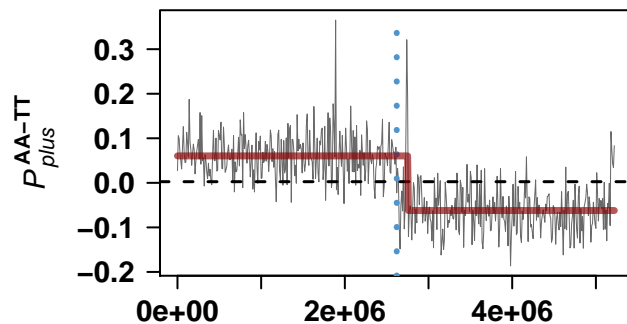
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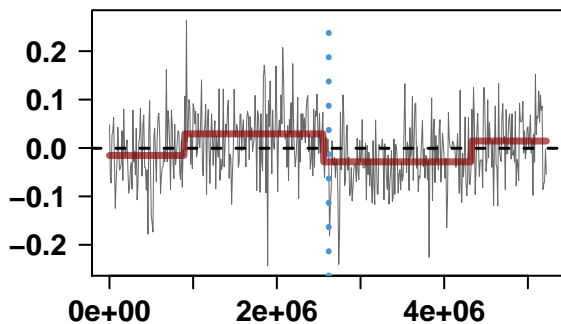
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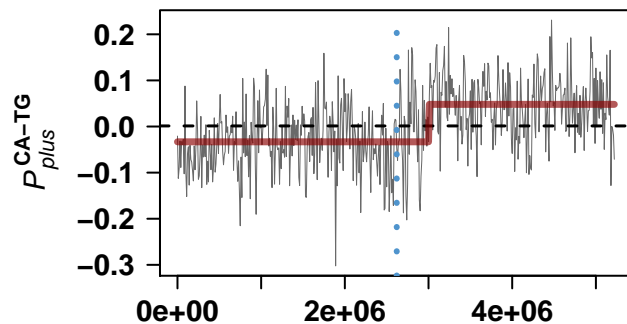
genome coordinates



genome coordinates

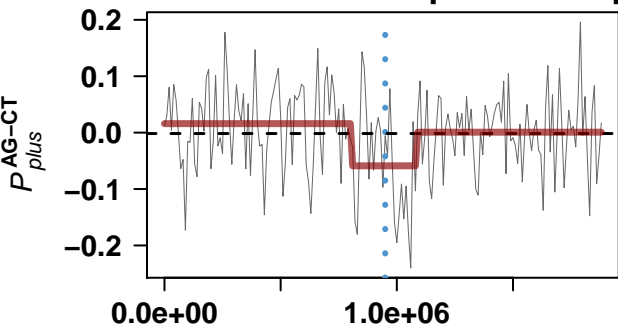


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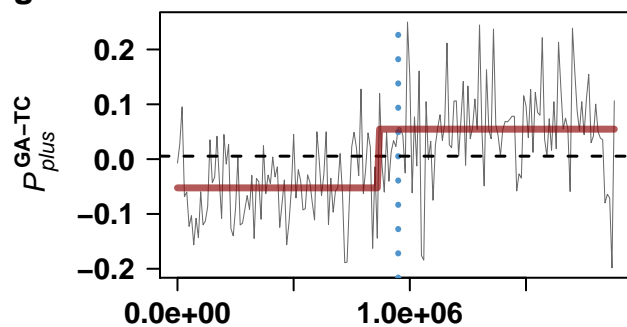


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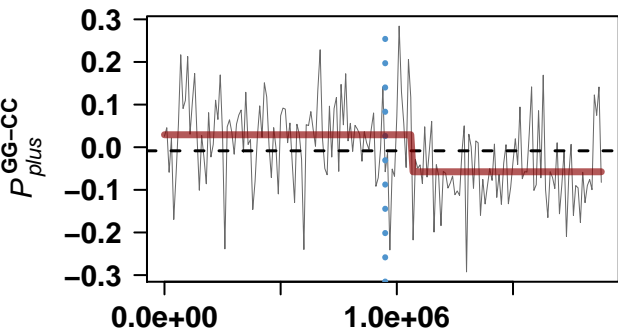
Streptococcus pyogenes MGAS10394



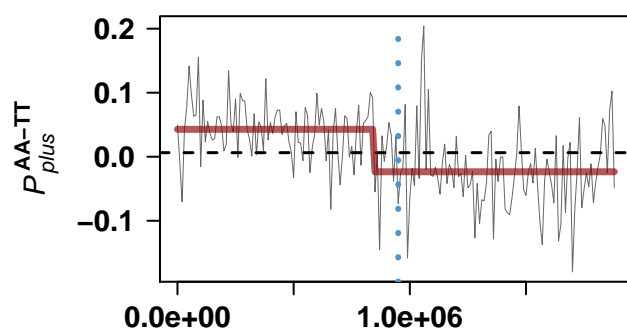
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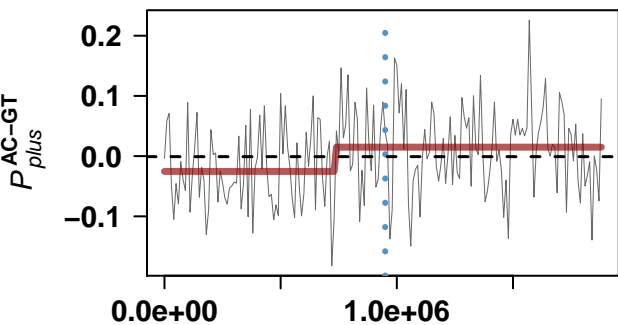
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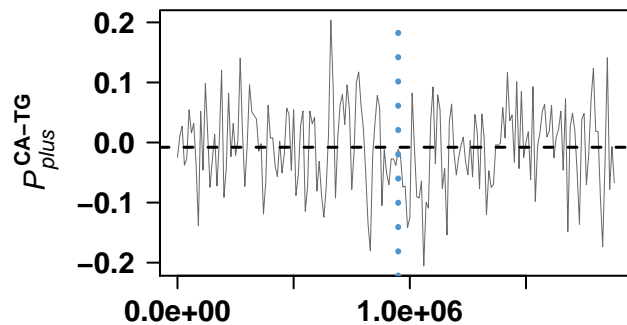
genome coordinates



genome coordinates

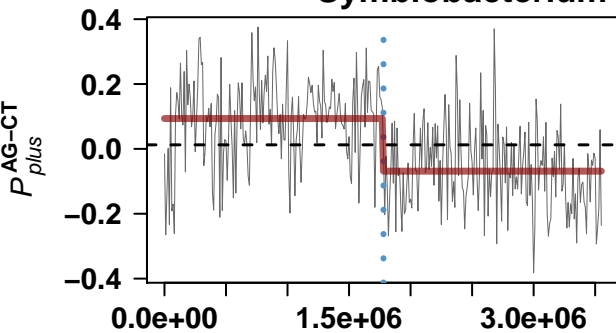


genome coordinates

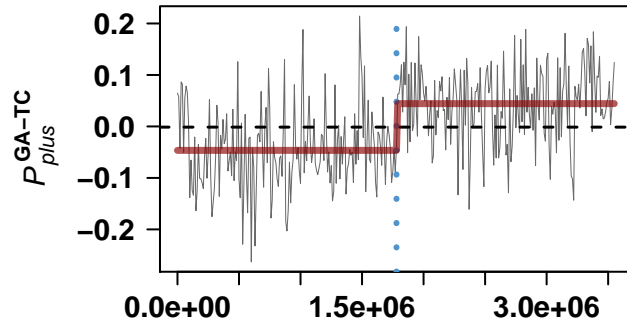


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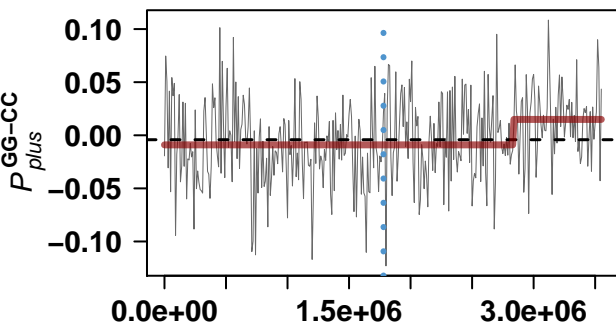
Symbiobacterium thermophilum IAM 14863



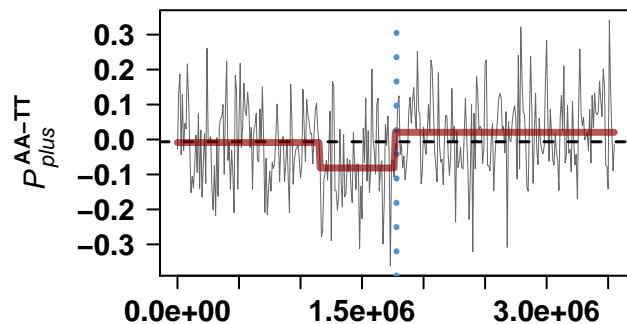
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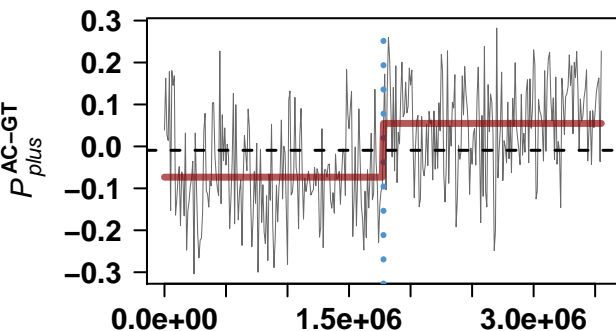
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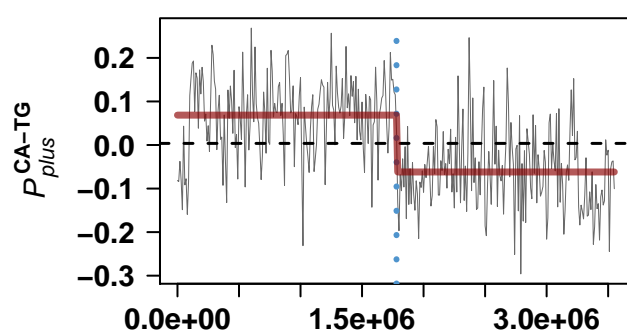
genome coordinates



genome coordinates

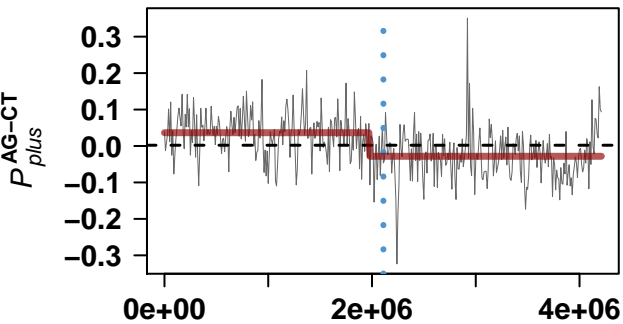


genome coordinates

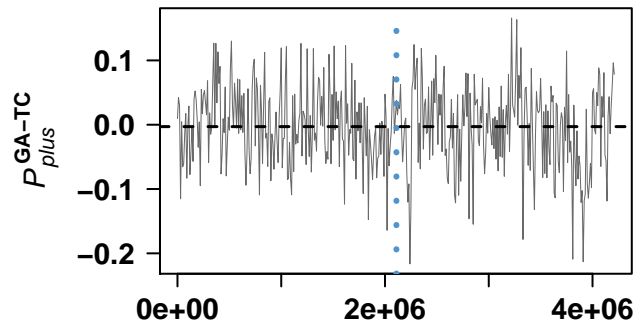


genome coordinates

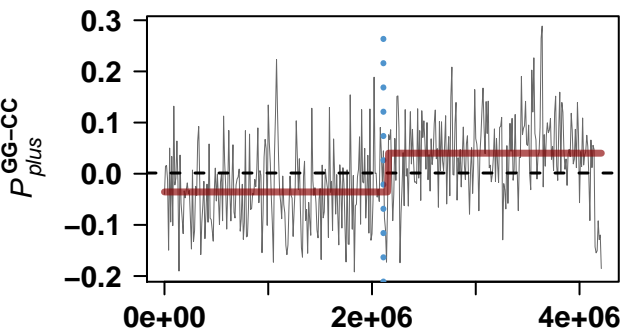
Bacillus licheniformis DSM 13 = ATCC 14580



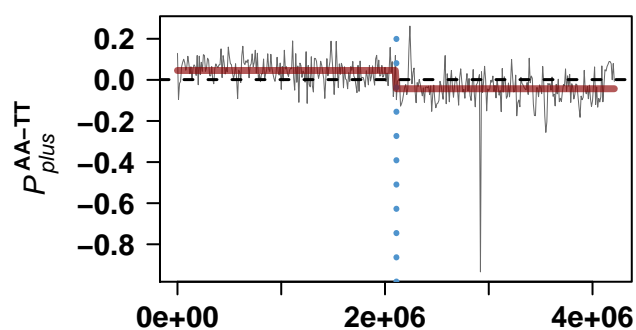
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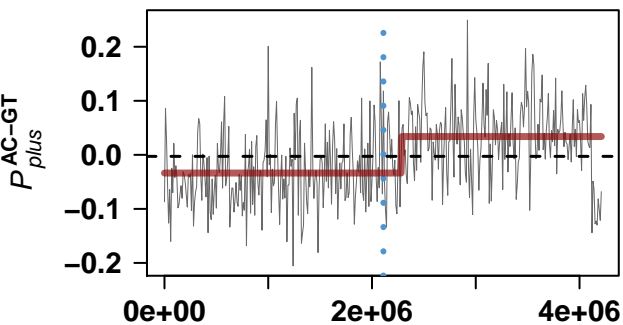
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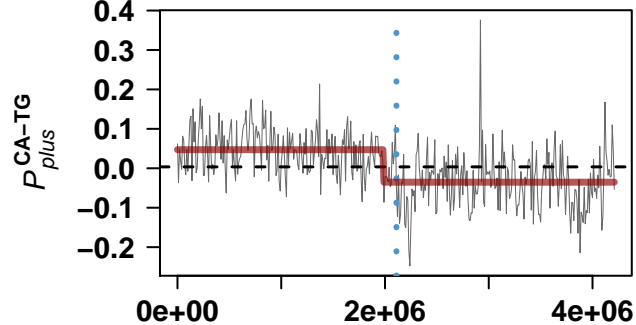
genome coordinates



genome coordinates

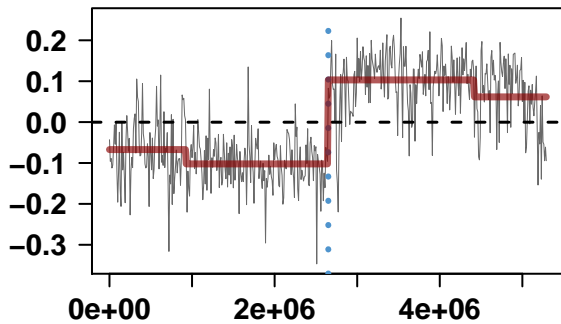


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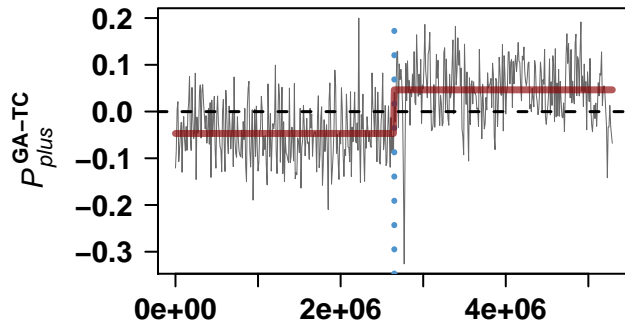


genome coordinates

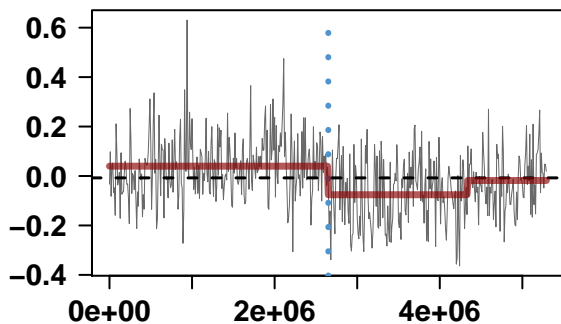
Bacillus cereus E33L



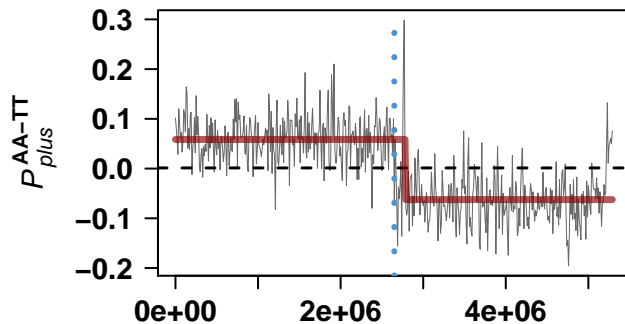
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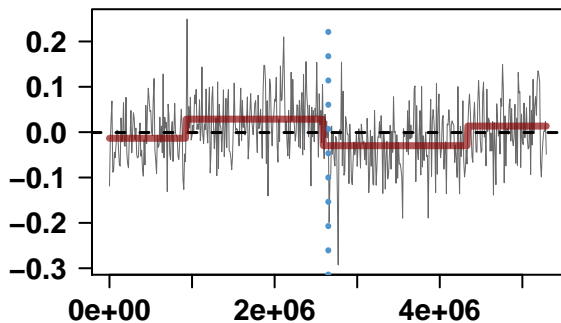
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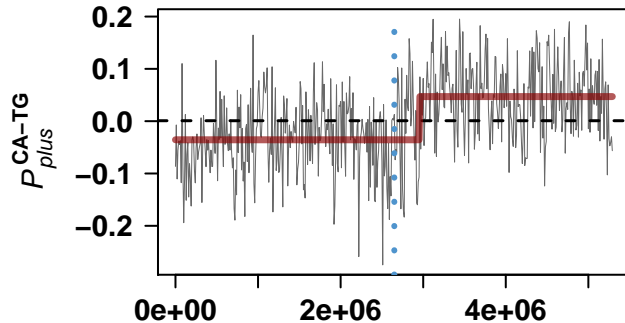
genome coordinates



genome coordinates

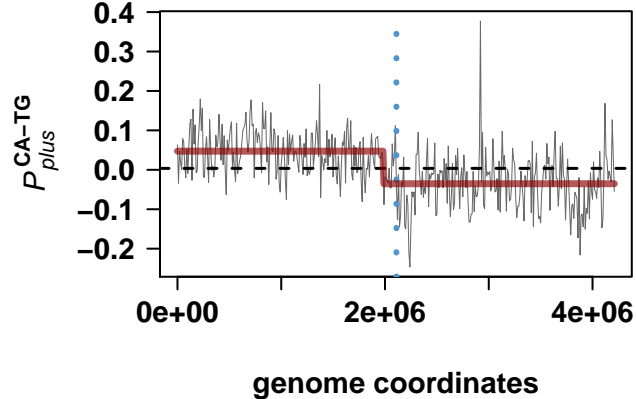
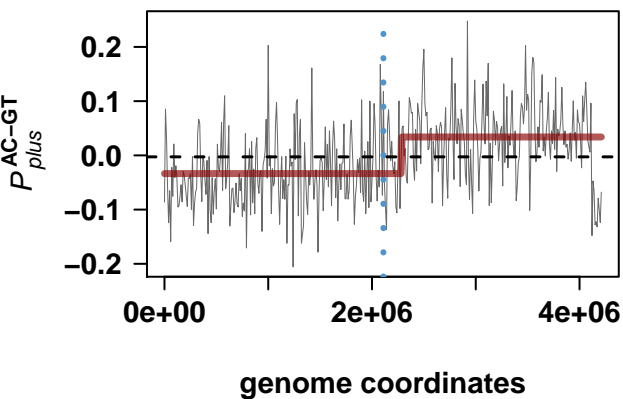
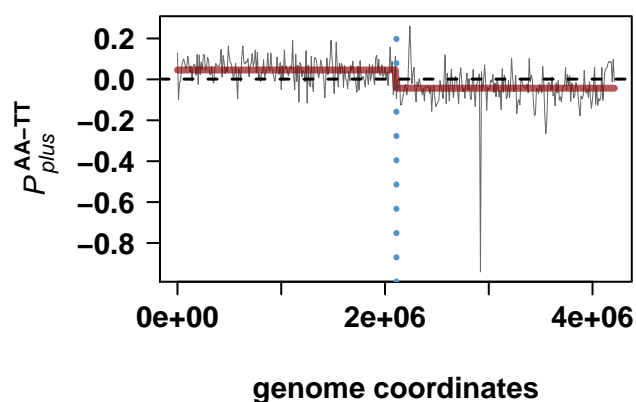
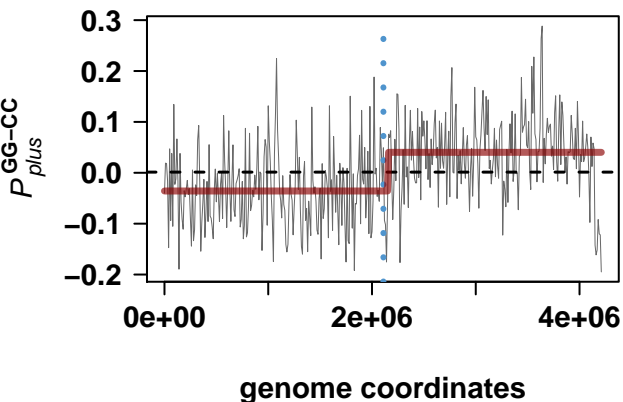
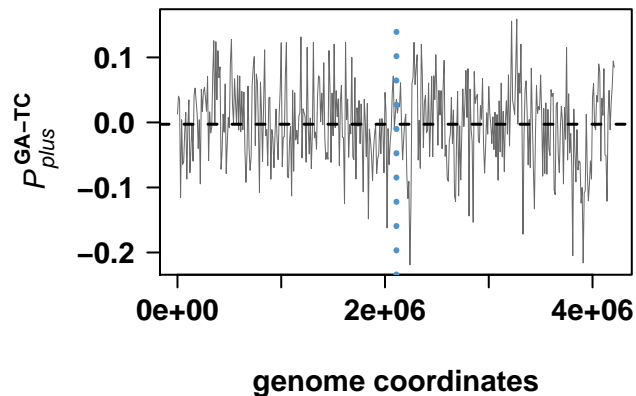
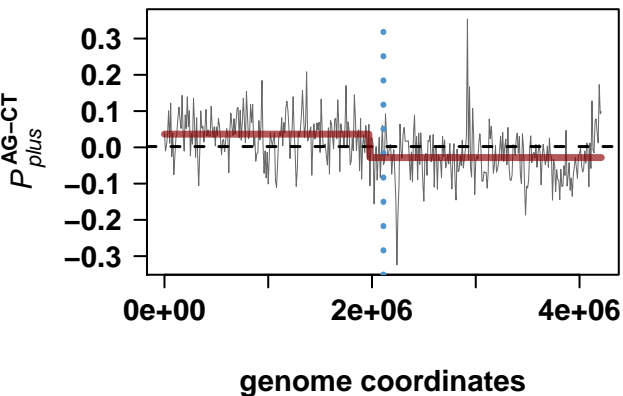


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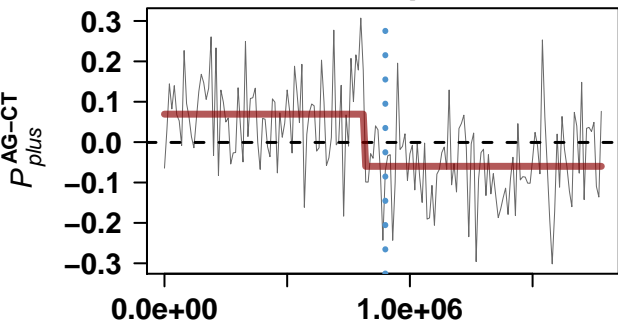


genome coordinates

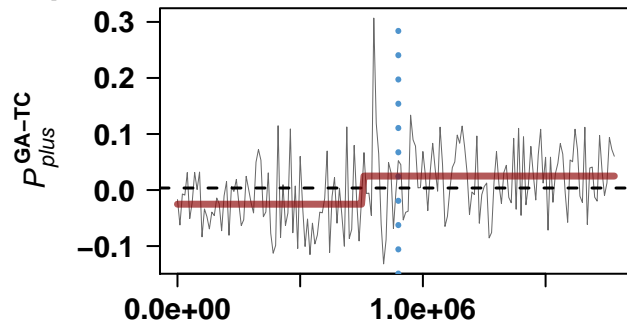
Bacillus licheniformis DSM 13 = ATCC 14580



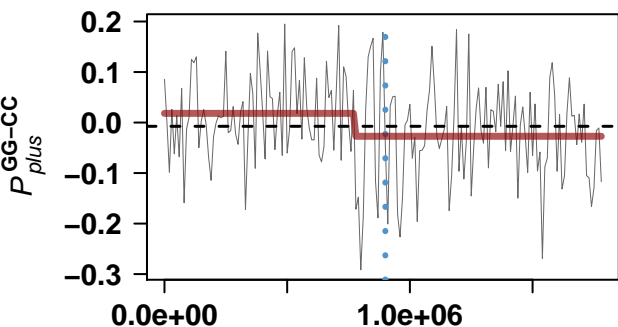
Streptococcus thermophilus LMG 18311



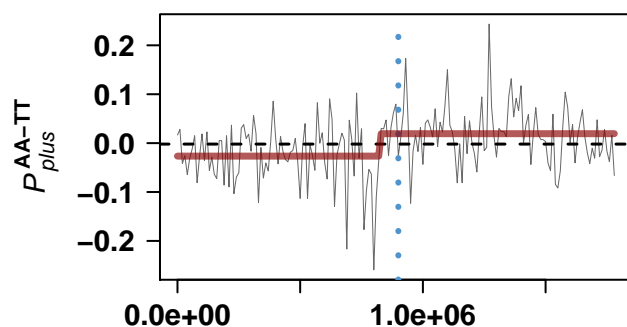
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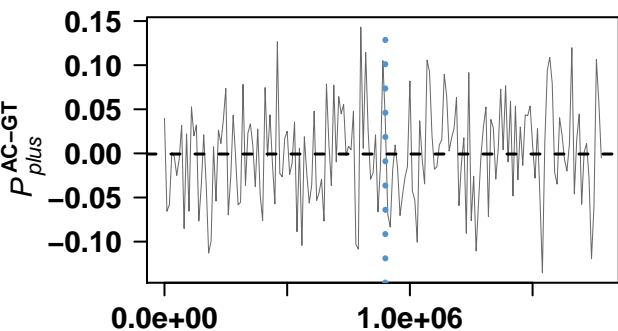
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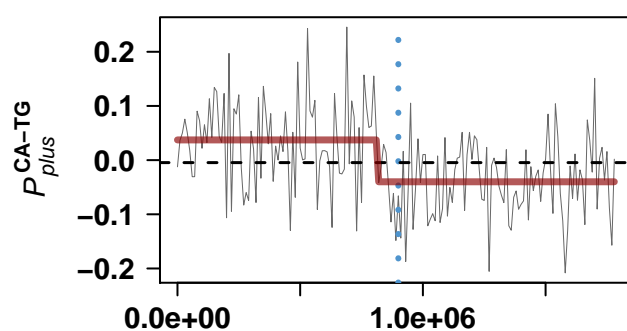
genome coordinates



genome coordinates

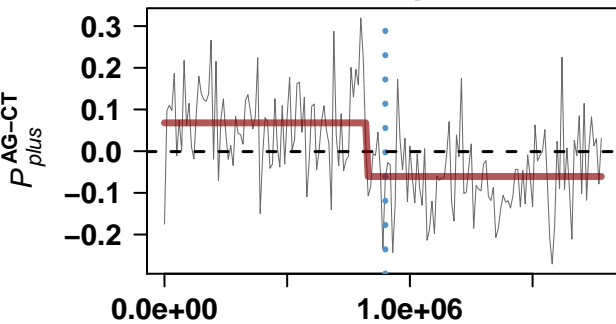


genome coordinates

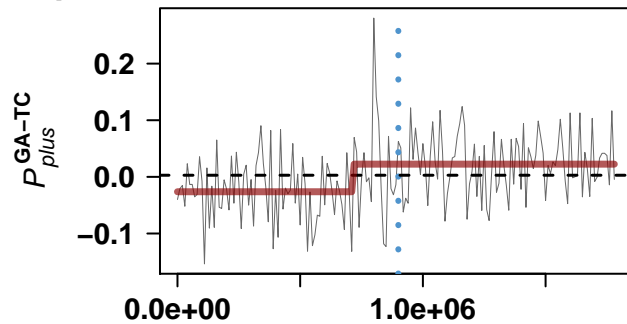


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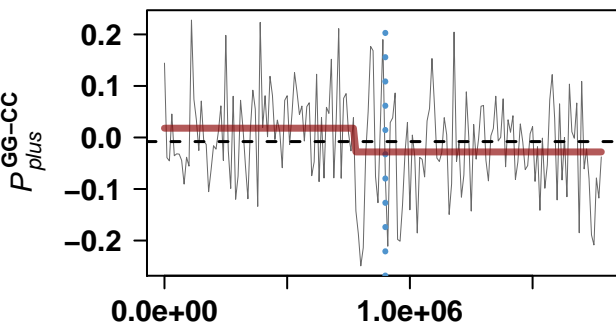
Streptococcus thermophilus CNRZ1066



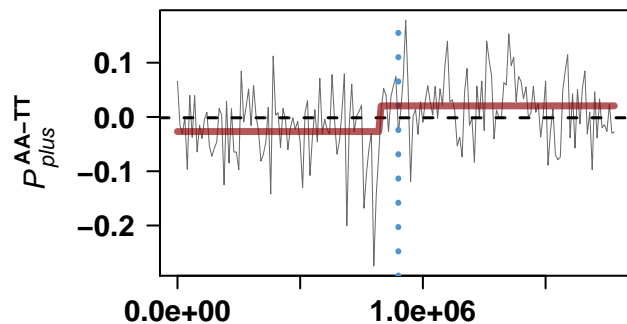
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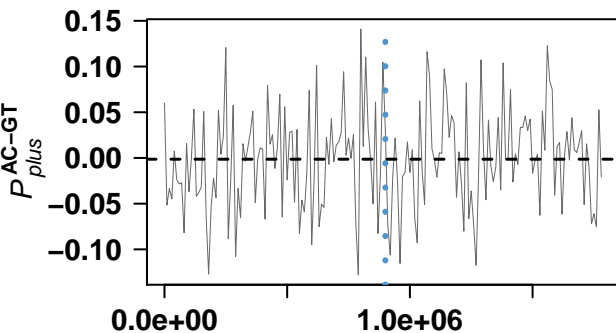
genome coordinates



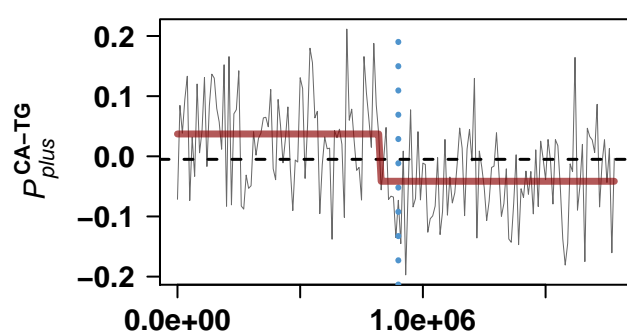
genome coordinates



genome coordinates

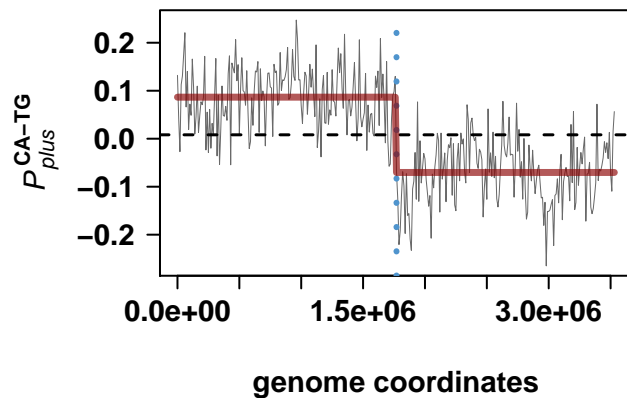
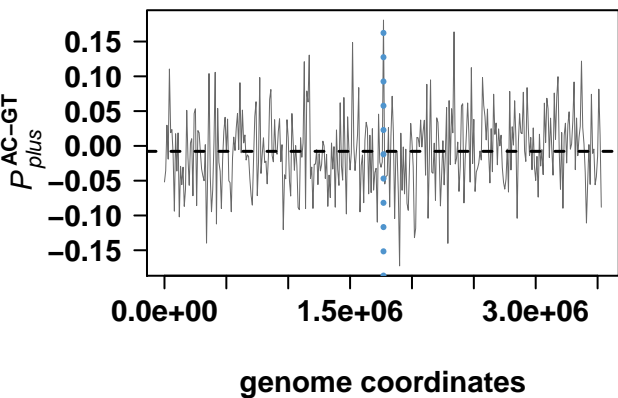
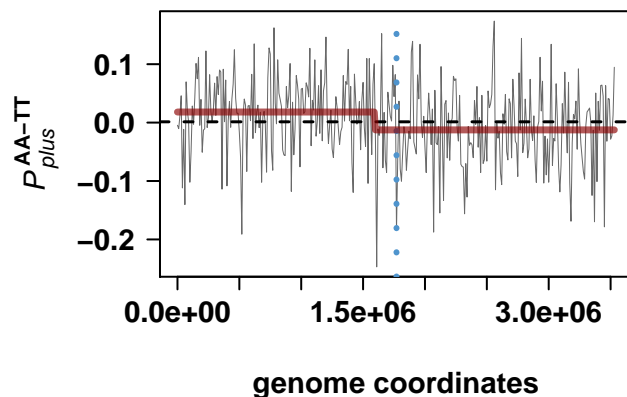
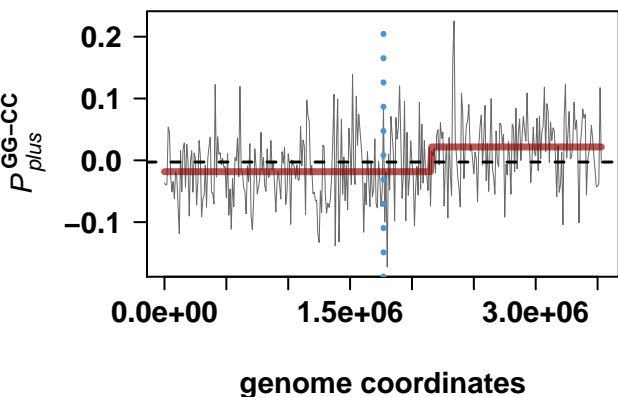
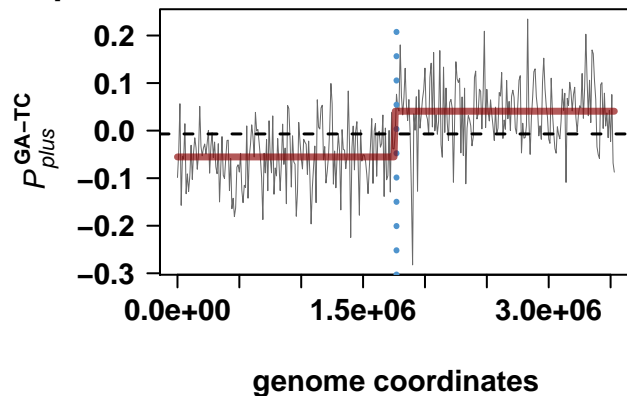
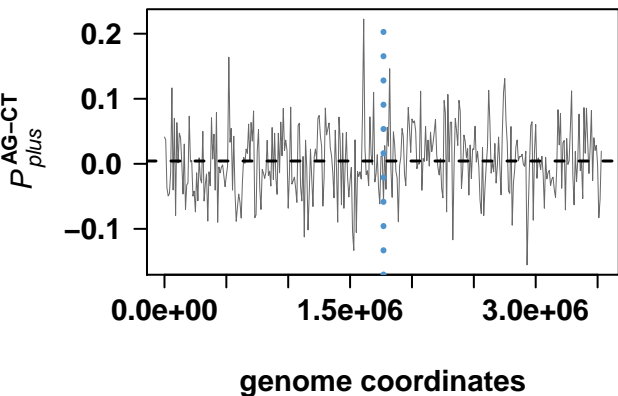


genome coordinates

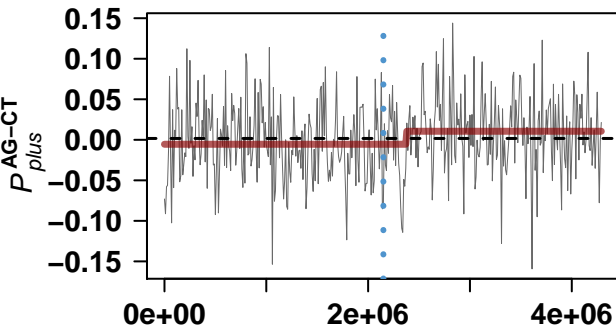


genome coordinates

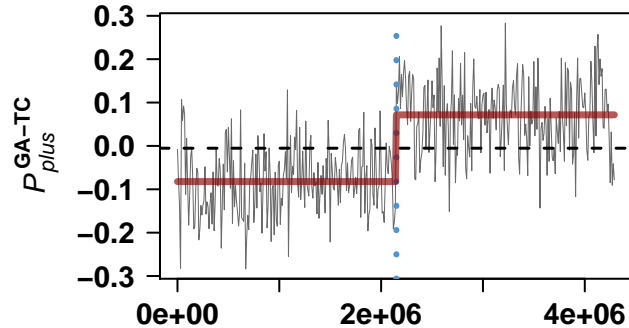
Geobacillus kaustophilus HTA426



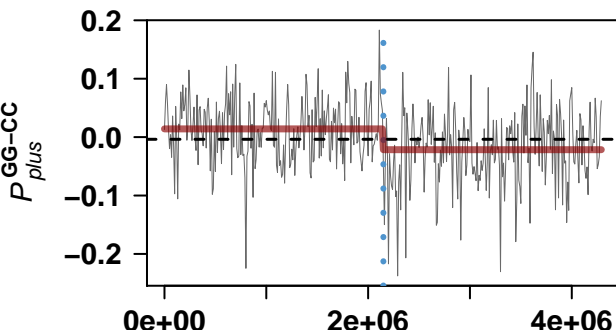
Bacillus clausii KSM-K16



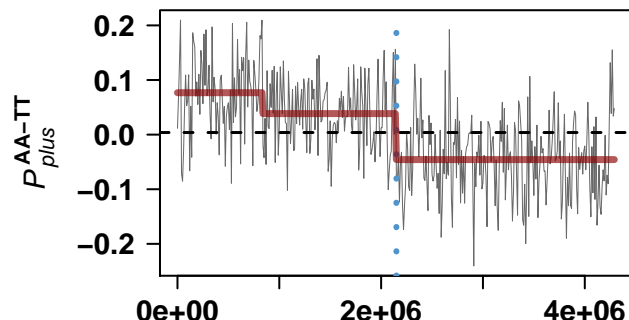
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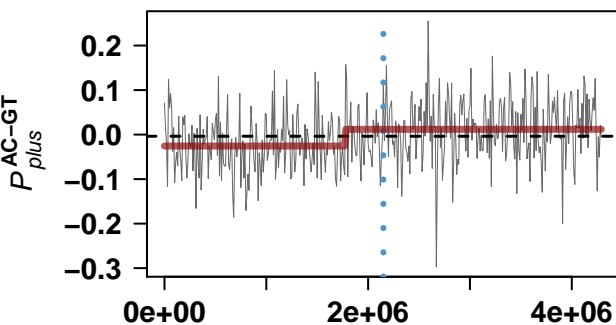
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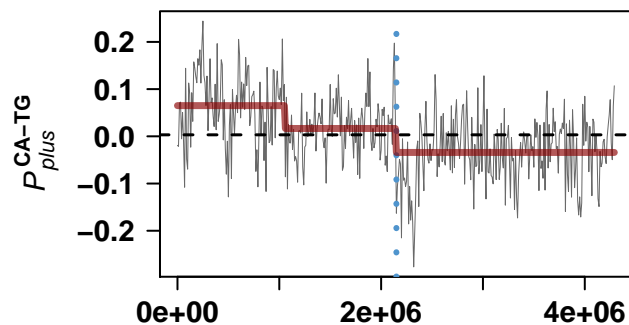
genome coordinates



genome coordinates

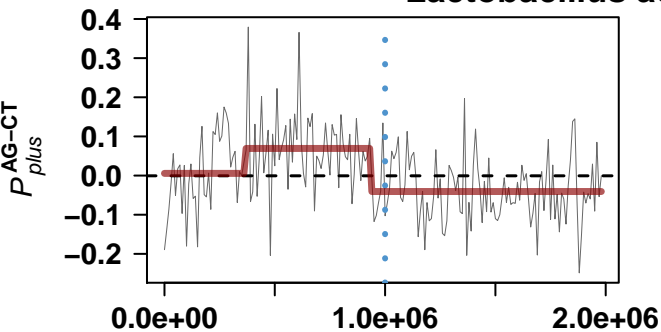


genome coordinates

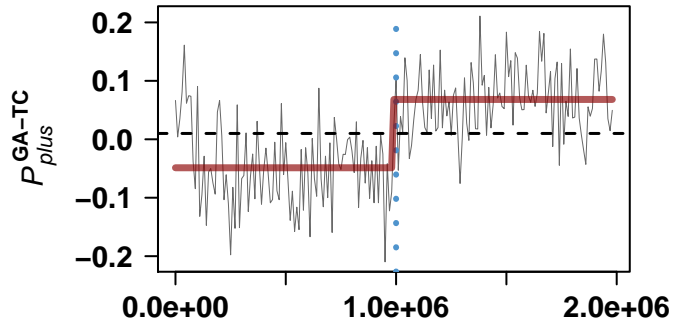


genome coordinates

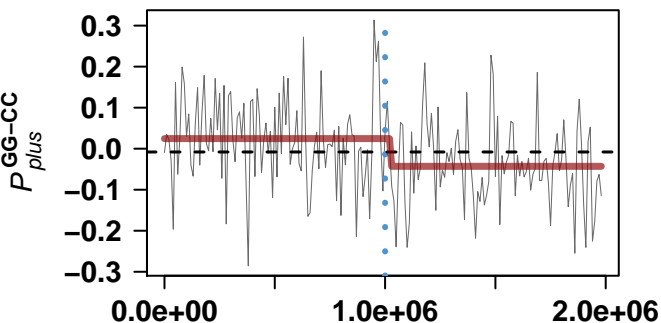
Lactobacillus acidophilus NCFM



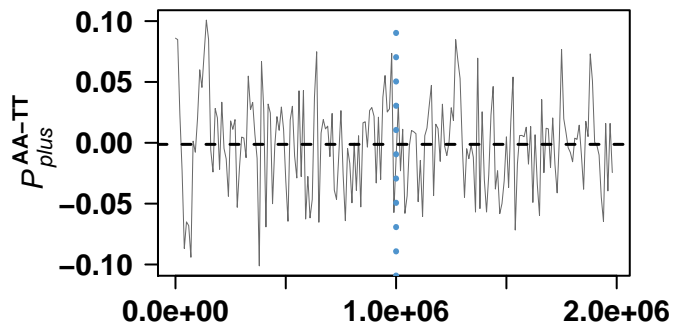
genome coordinates



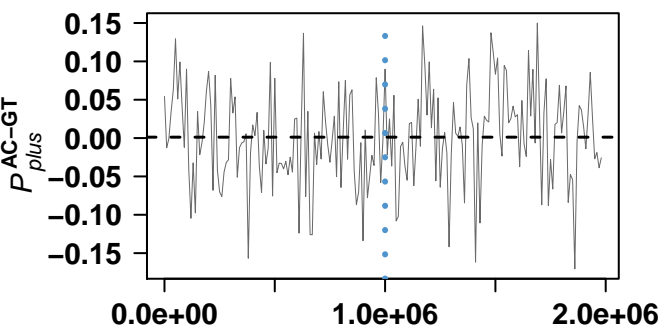
genome coordinates



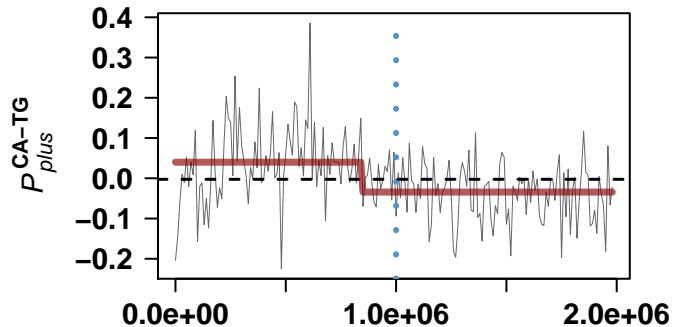
genome coordinates



genome coordinates

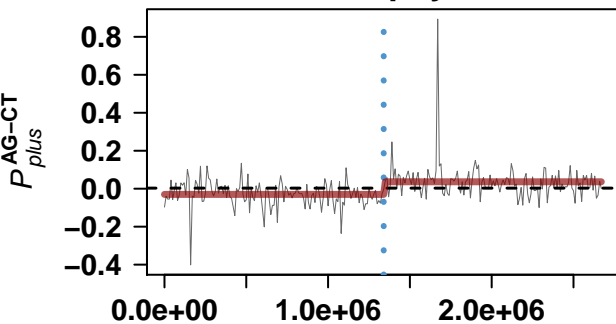


genome coordinates

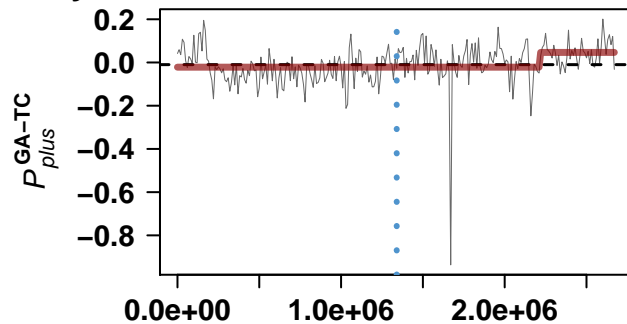


genome coordinates

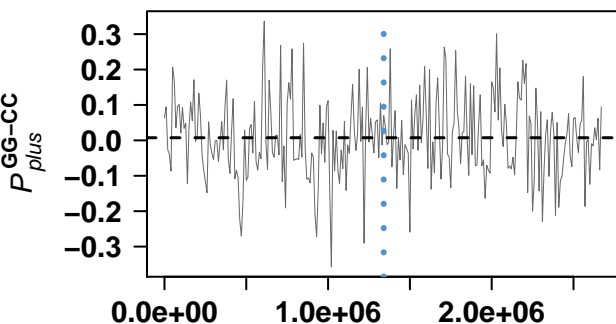
Staphylococcus haemolyticus JCSC1435



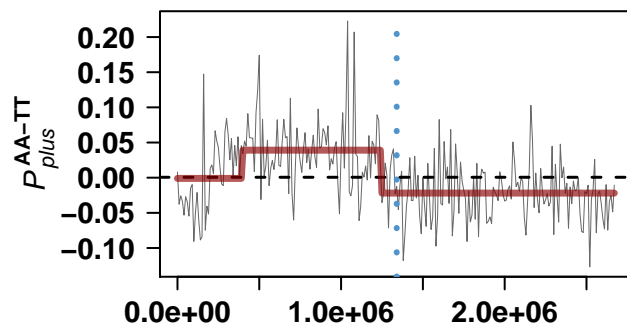
genome coordinates



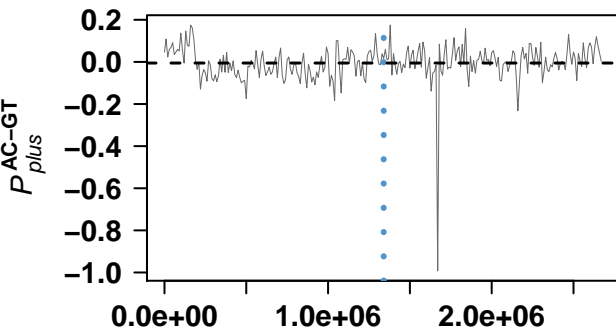
genome coordinates



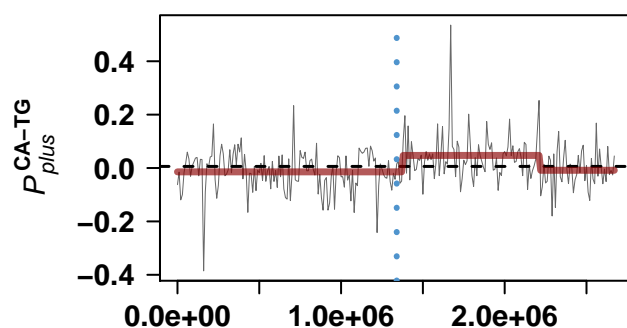
genome coordinates



genome coordinates

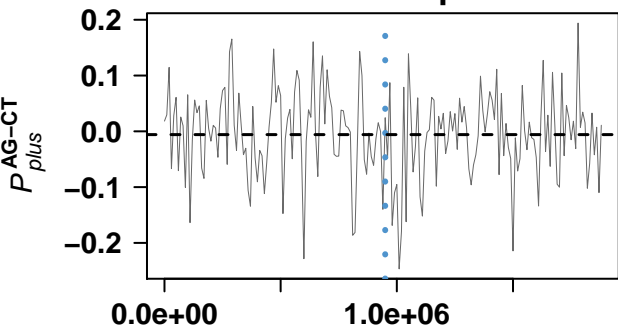


genome coordinates

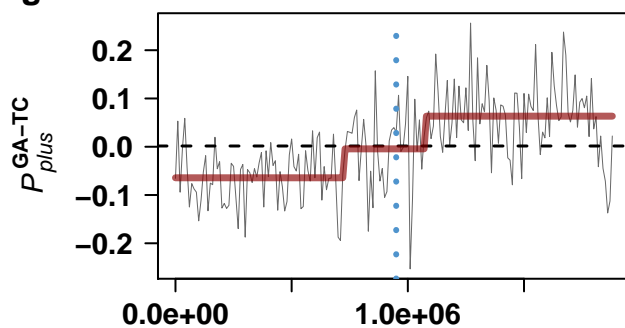


genome coordinates

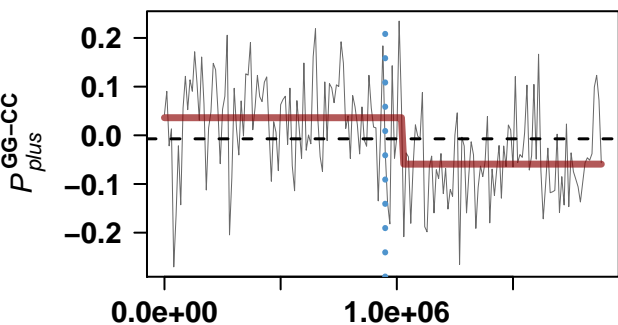
Streptococcus pyogenes MGAS6180



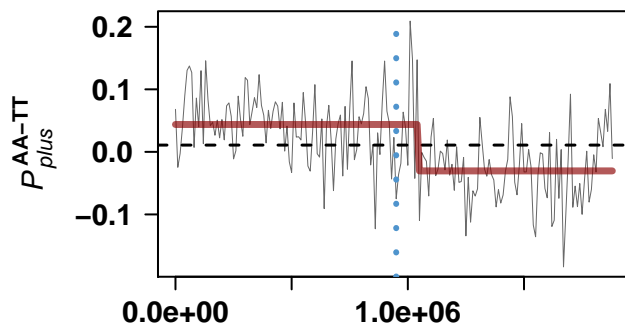
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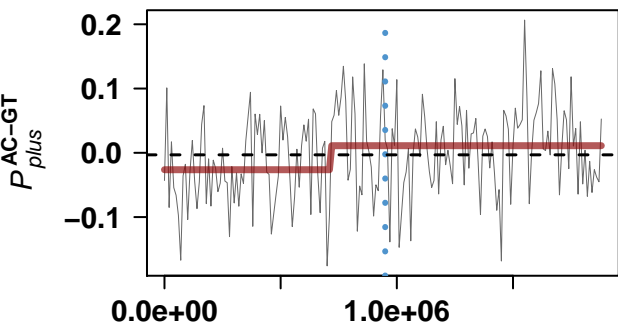
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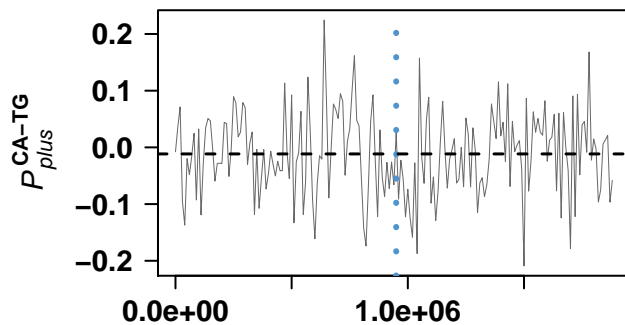
genome coordinates



genome coordinates

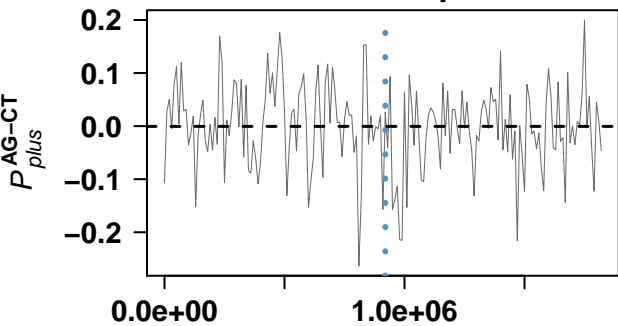


genome coordinates

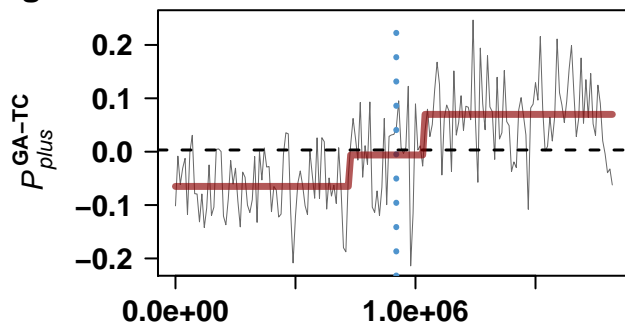


genome coordinates

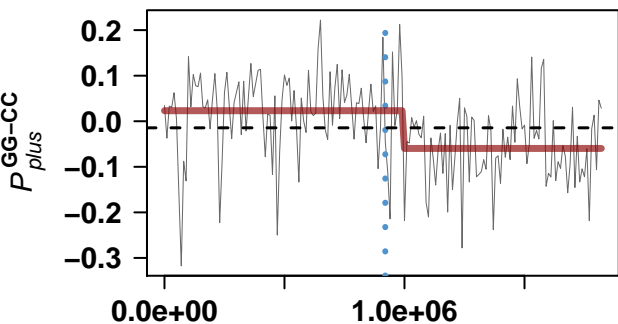
Streptococcus pyogenes MGAS5005



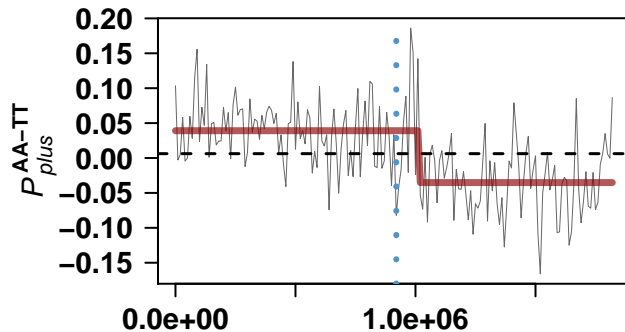
genome coordinates



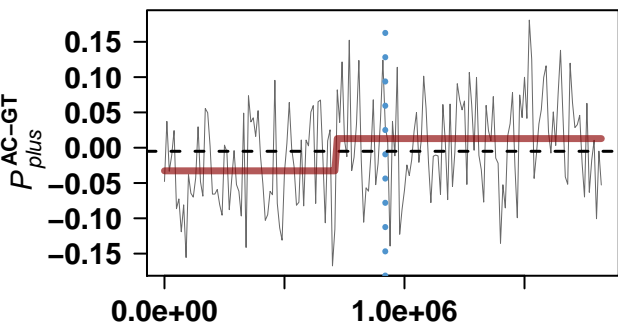
genome coordinates



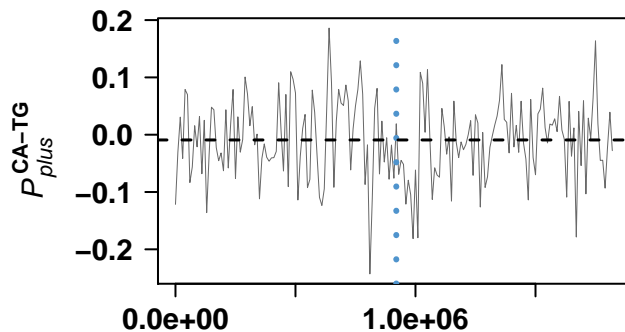
genome coordinates



genome coordinates

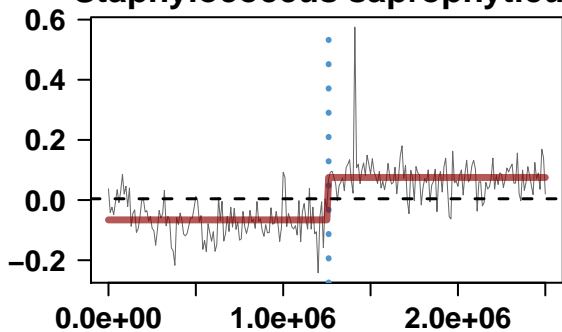


genome coordinates

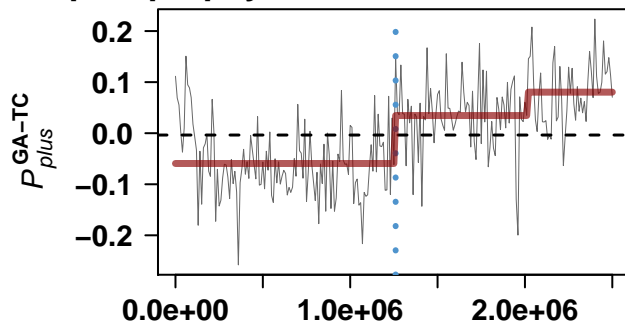


genome coordinates

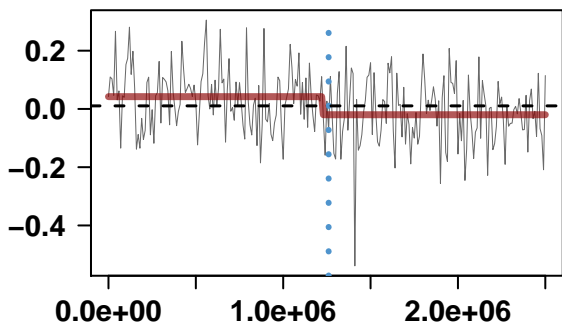
Staphylococcus saprophyticus subsp. saprophyticus ATCC 15305



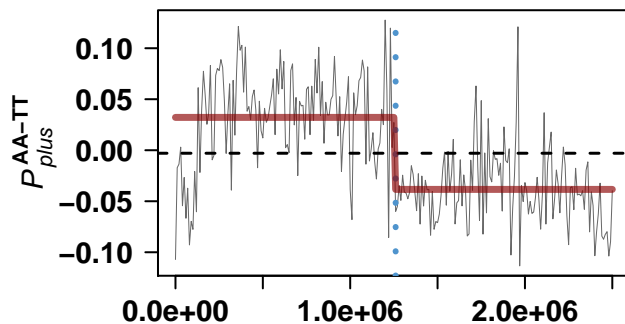
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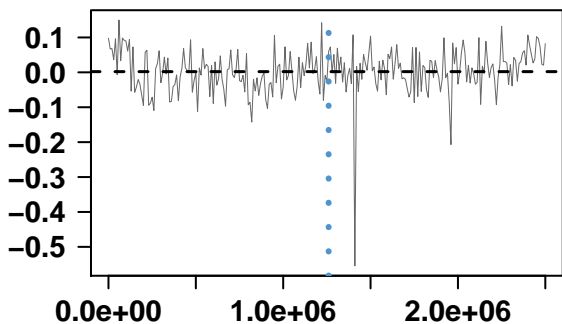
genome coordinates



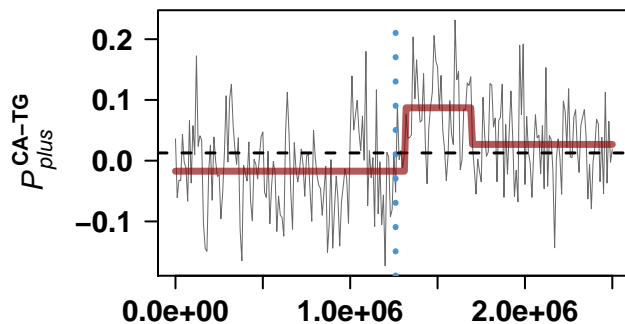
genome coordinates



genome coordinates

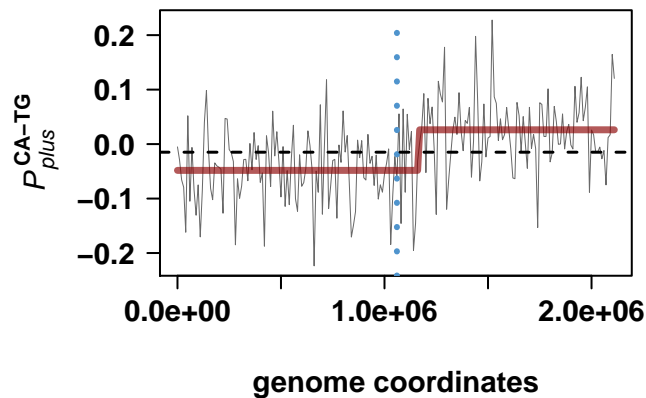
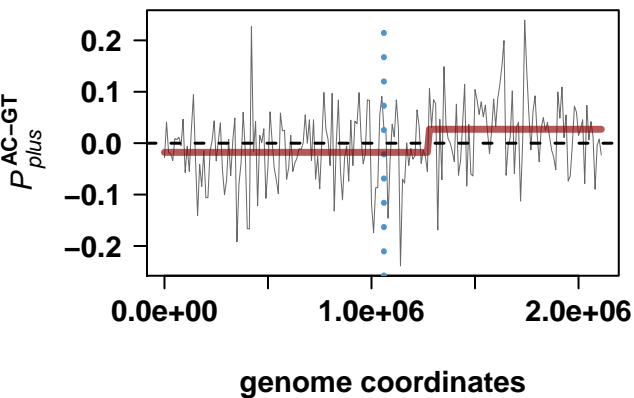
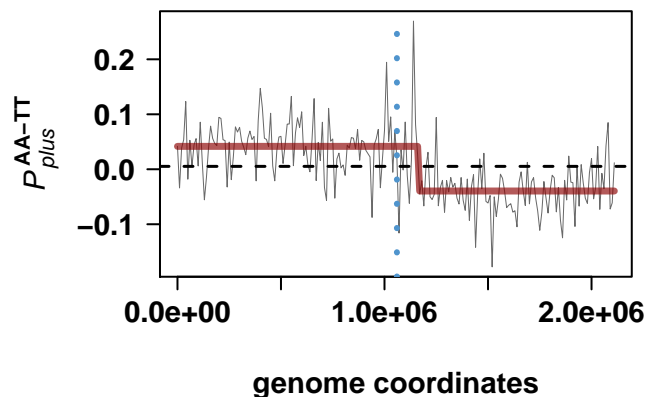
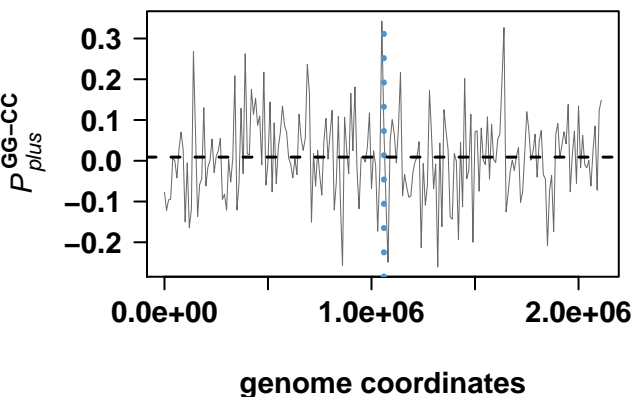
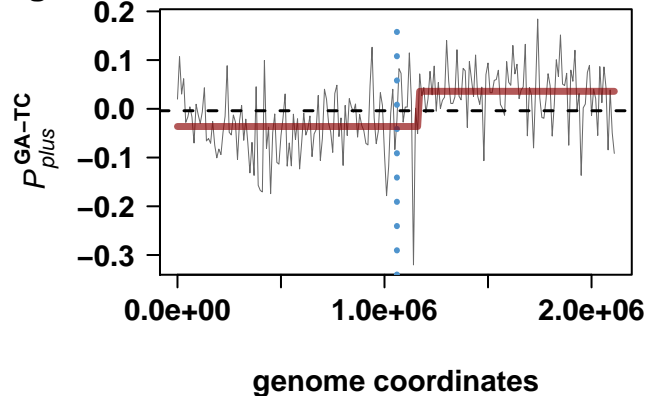
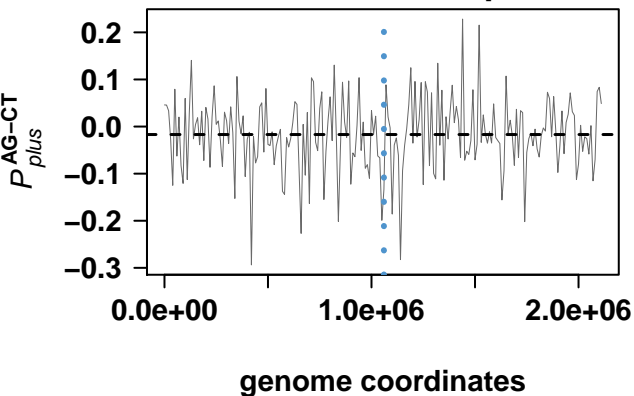


genome coordinates

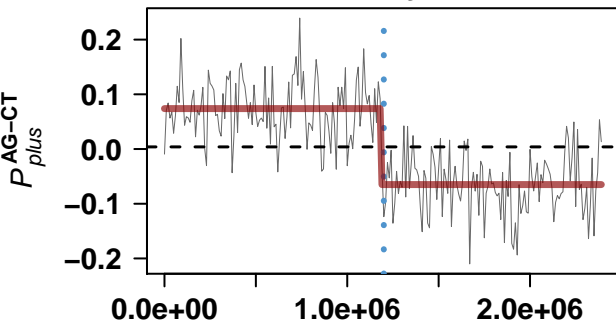


genome coordinates

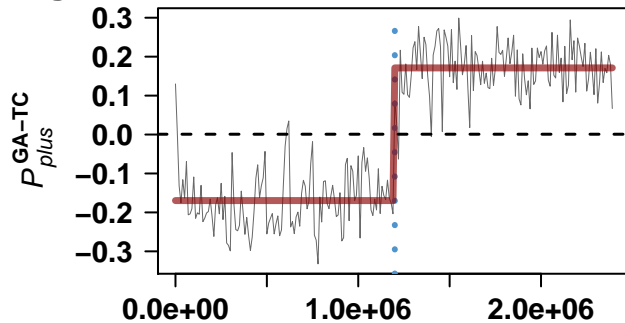
Streptococcus agalactiae A909



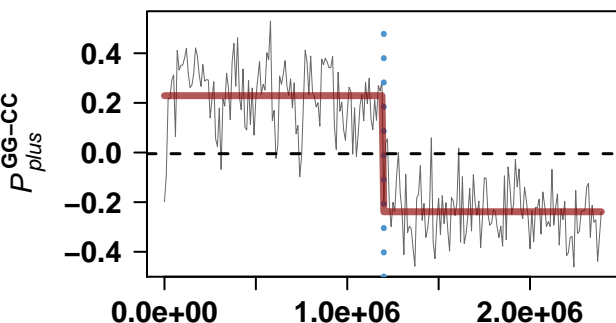
Carboxydotherrmus hydrogenoformans Z-2901



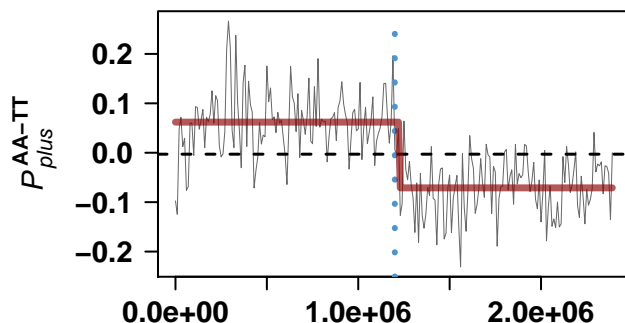
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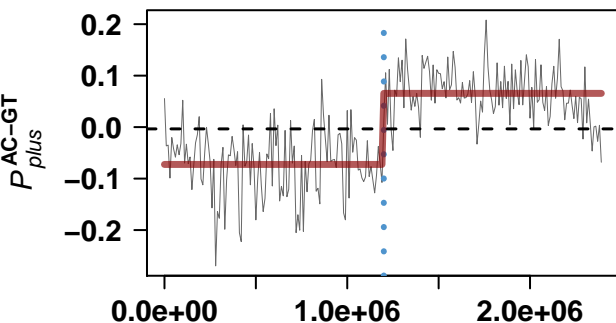
genome coordinates



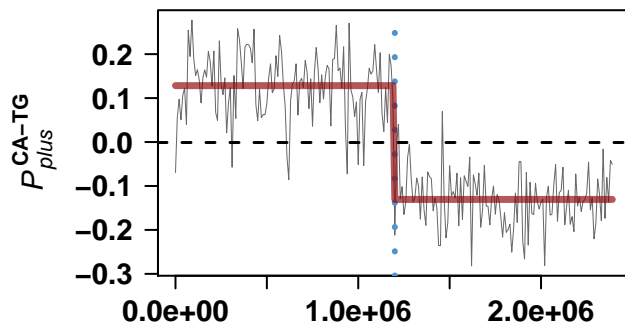
genome coordinates



genome coordinates

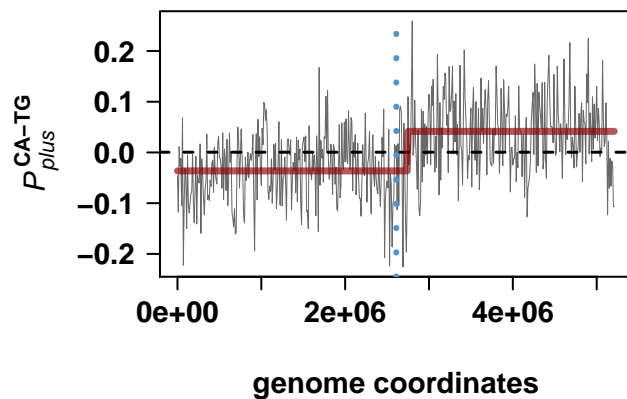
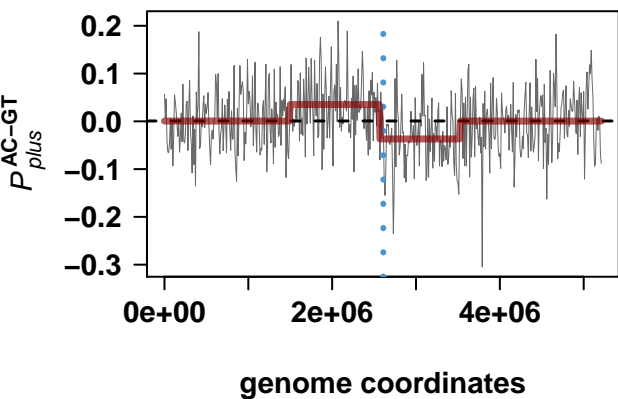
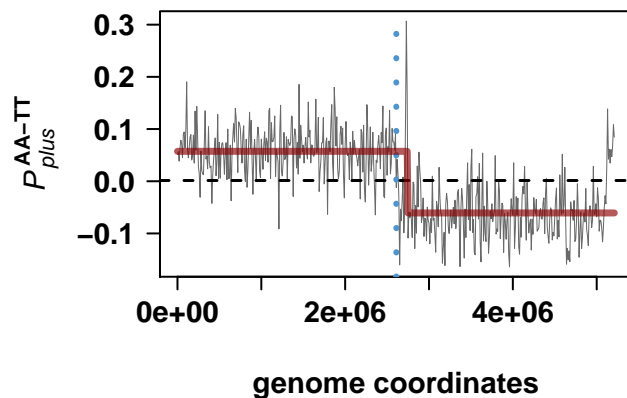
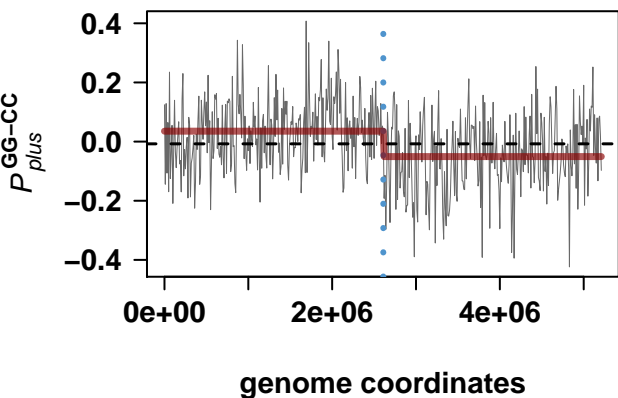
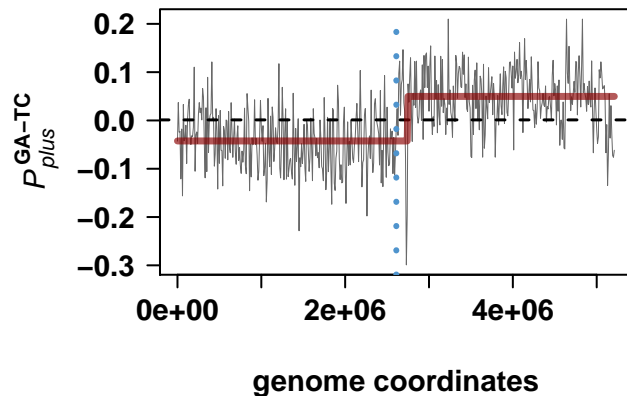
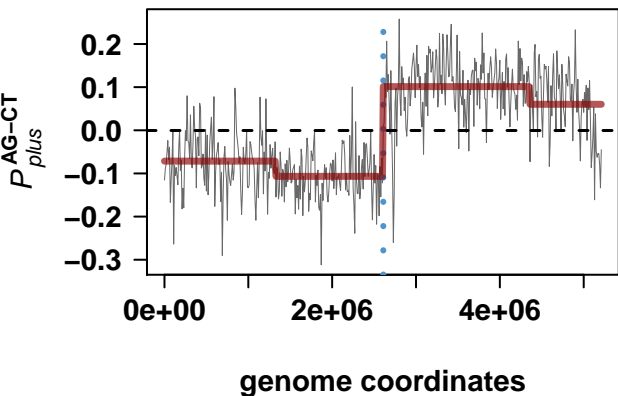


genome coordinates

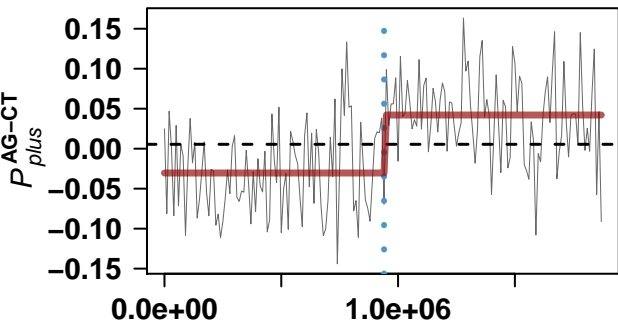


genome coordinates

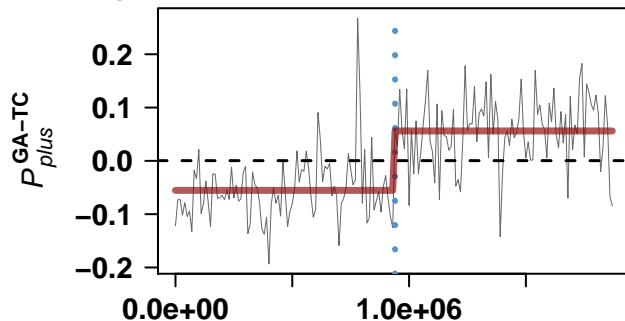
Bacillus anthracis str. 'Ames Ancestor'



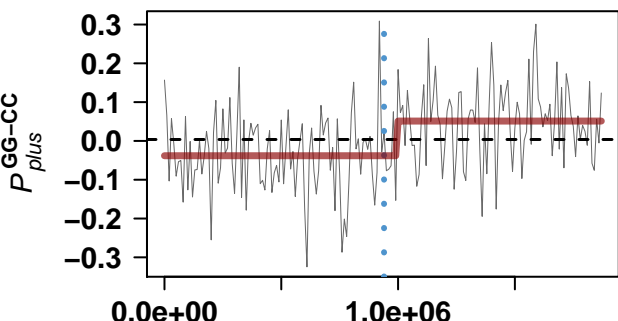
Lactobacillus sakei subsp. sakei 23K



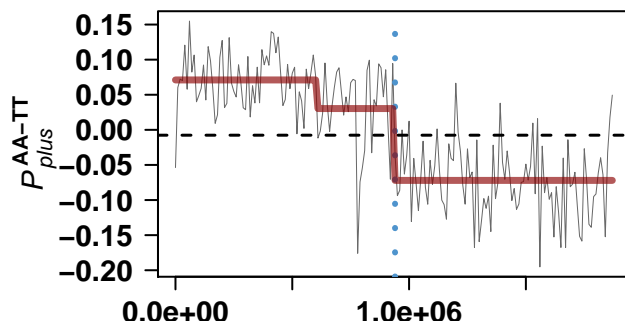
genome coordinates



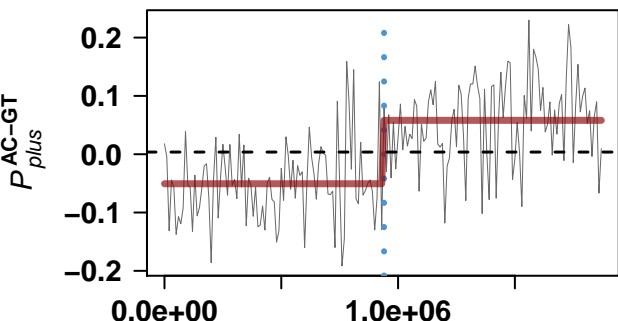
genome coordinates



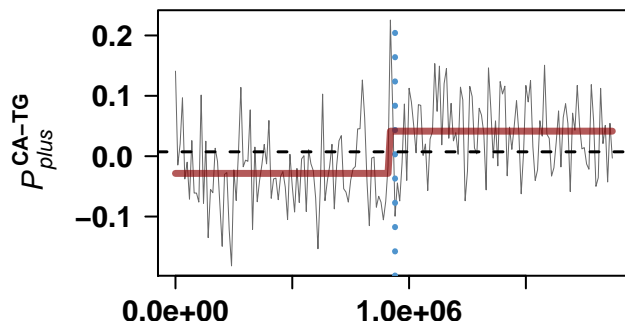
genome coordinates



genome coordinates

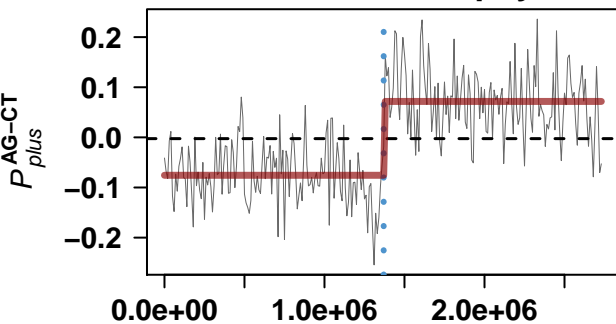


genome coordinates

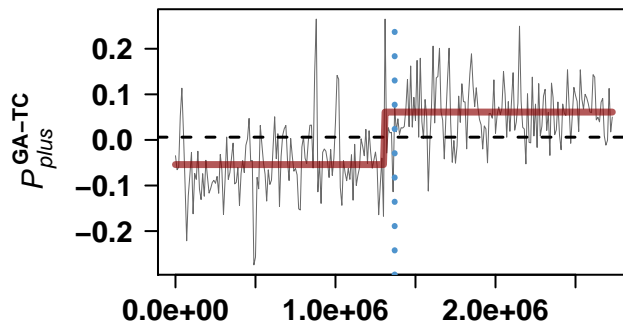


genome coordinates

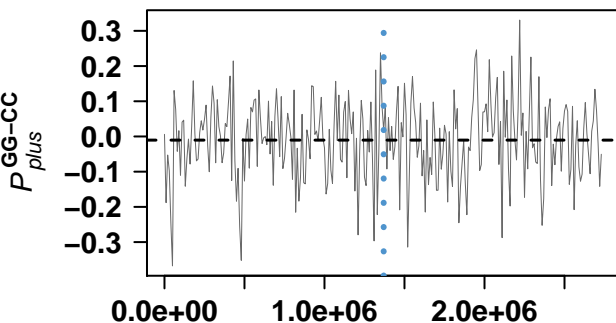
Staphylococcus aureus RF122



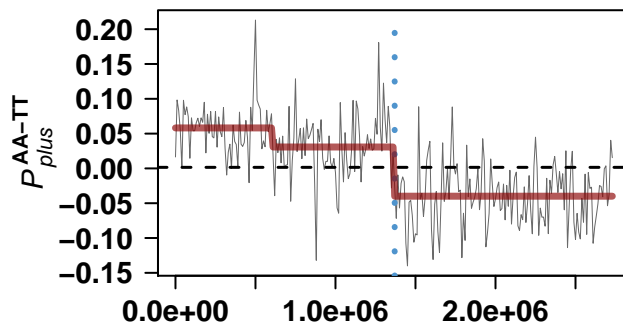
genome coordinates



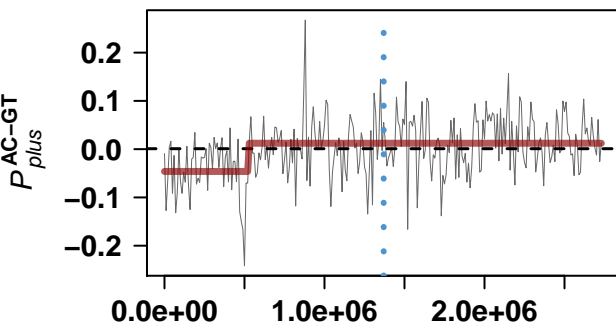
genome coordinates



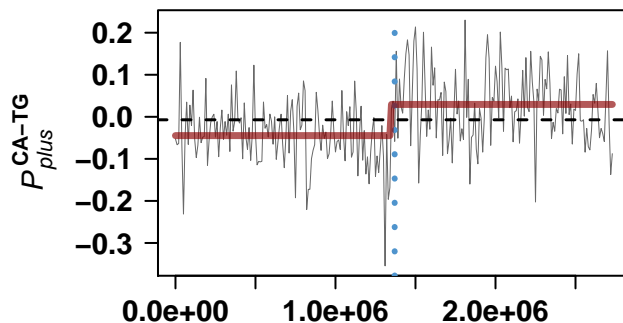
genome coordinates



genome coordinates

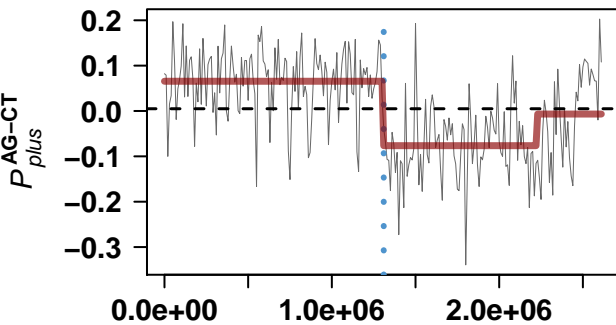


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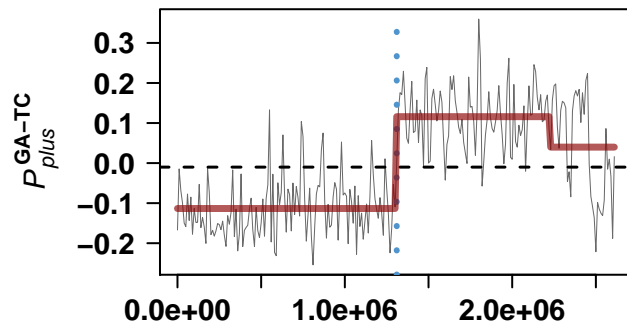


genome coordinates

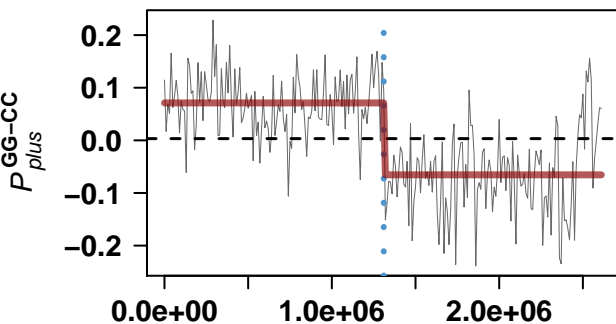
Moorella thermoacetica ATCC 39073



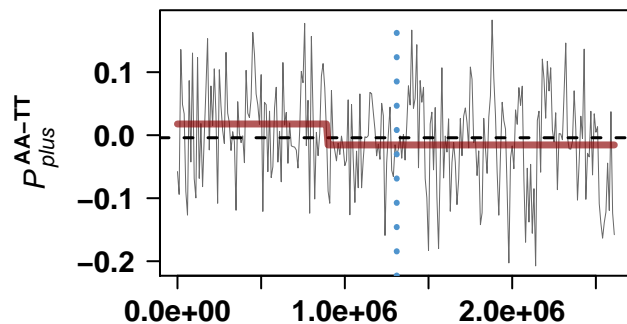
genome coordinates



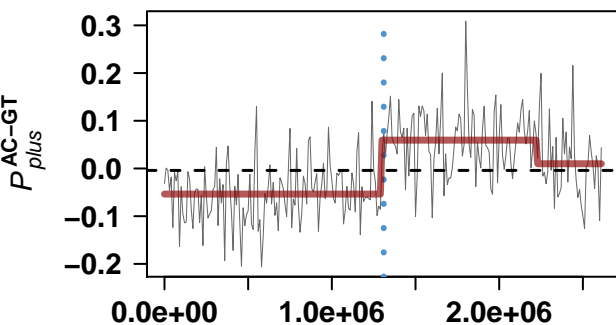
genome coordinates



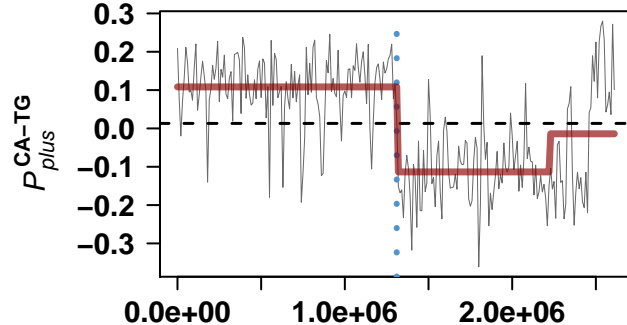
genome coordinates



genome coordinates

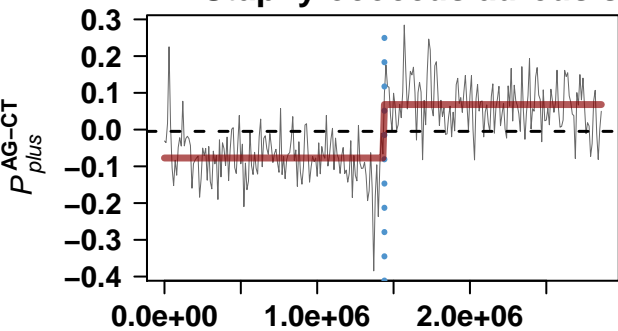


genome coordinates

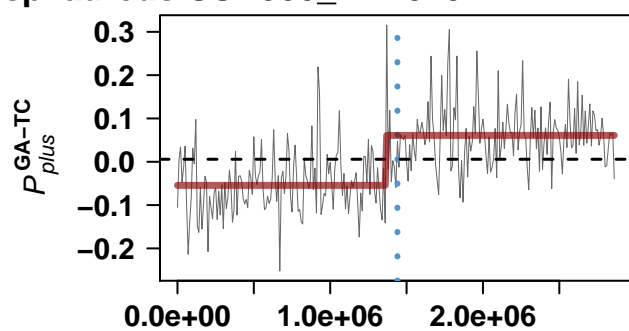


genome coordinates

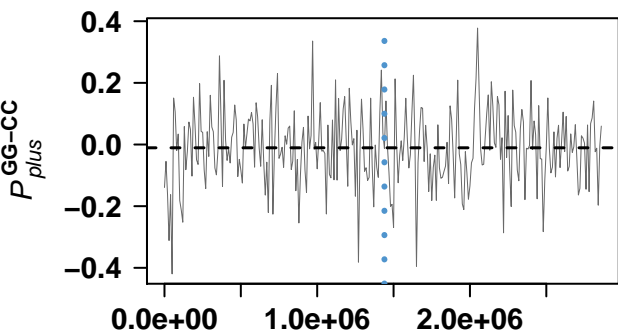
Staphylococcus aureus subsp. aureus USA300_FPR3757



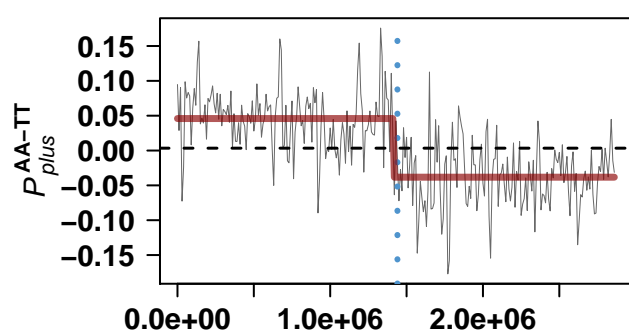
genome coordinates



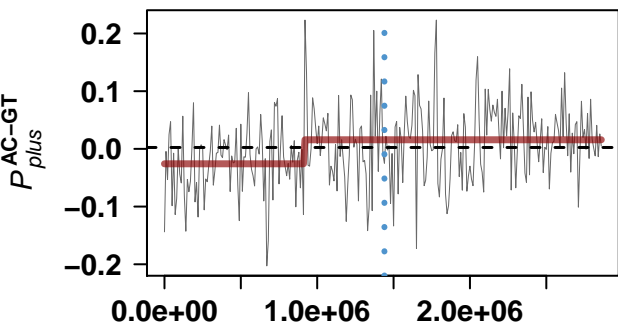
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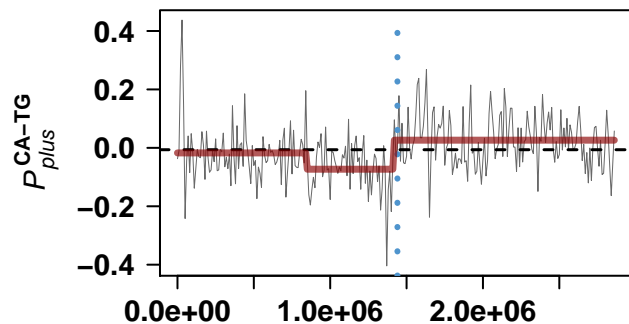
genome coordinates



genome coordinates

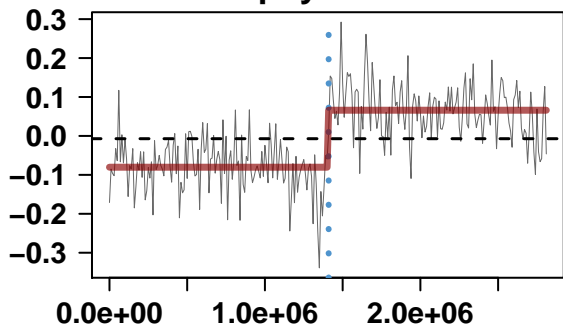


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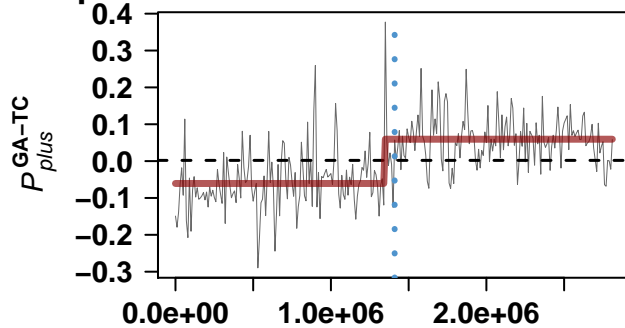


genome coordinates

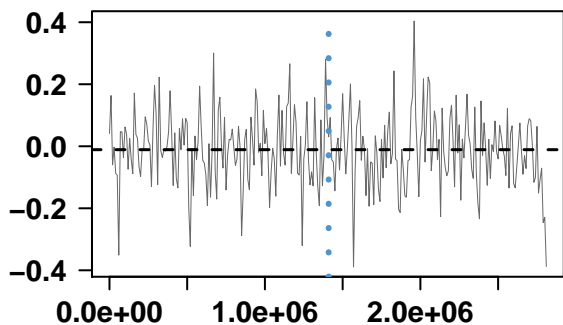
Staphylococcus aureus subsp. aureus NCTC 8325



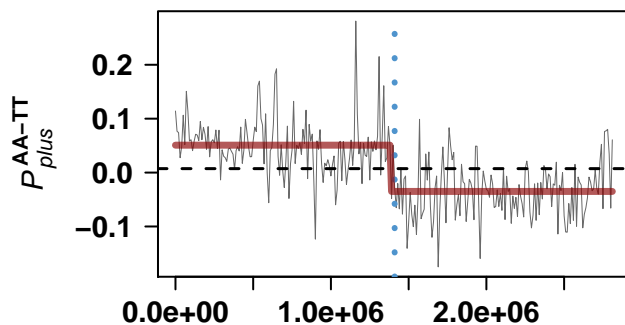
genome coordinates



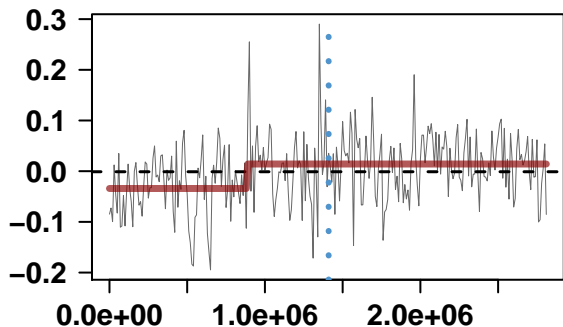
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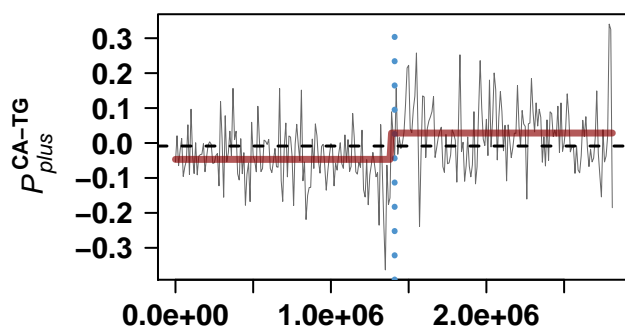
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genome coordinates

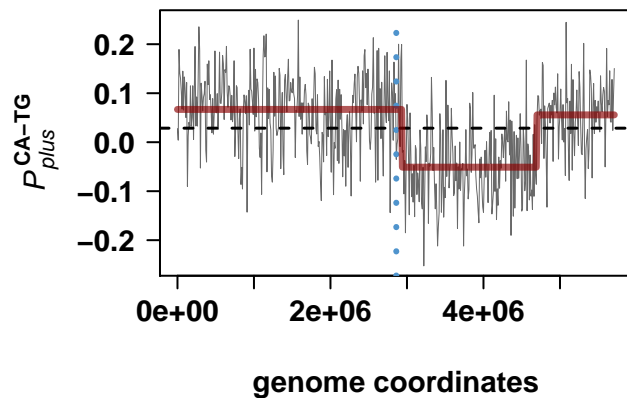
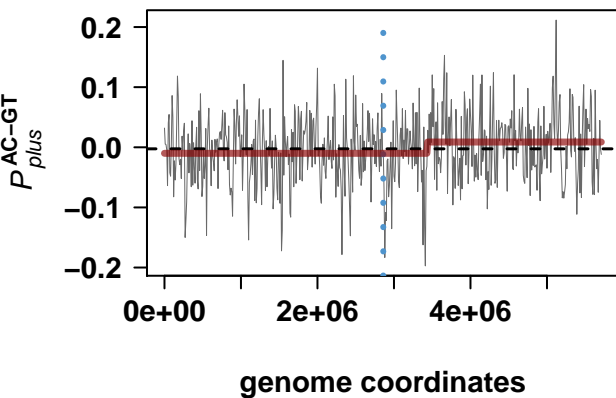
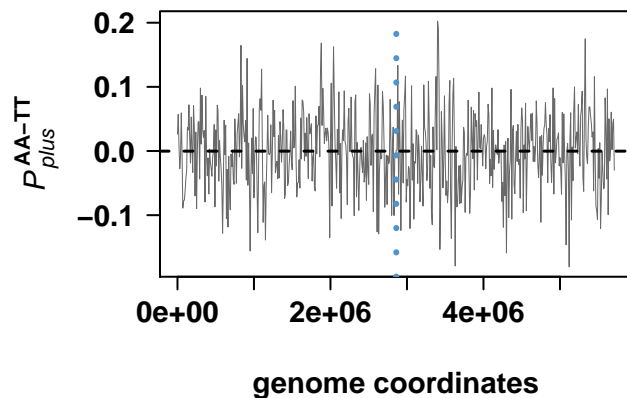
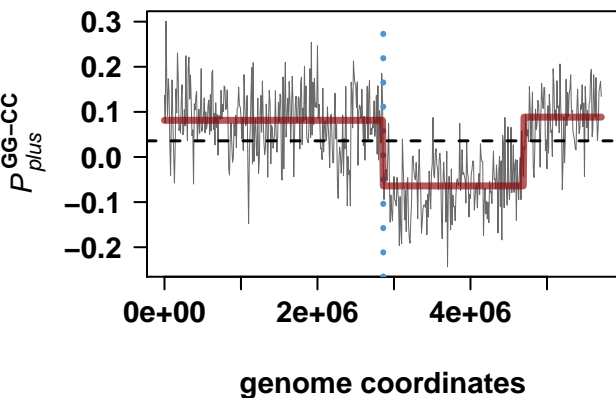
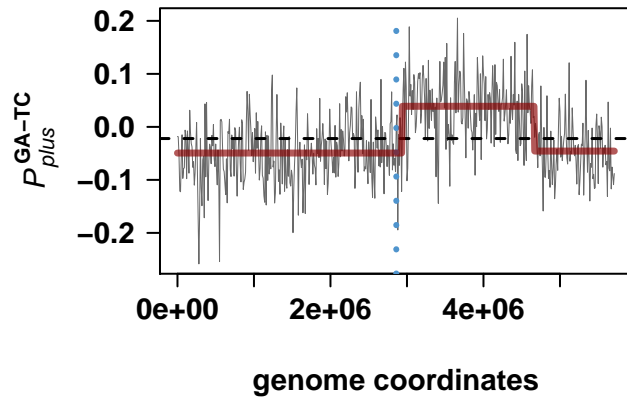
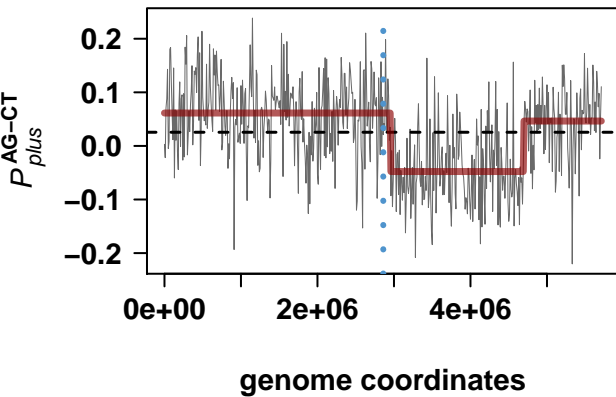


genome coordinates

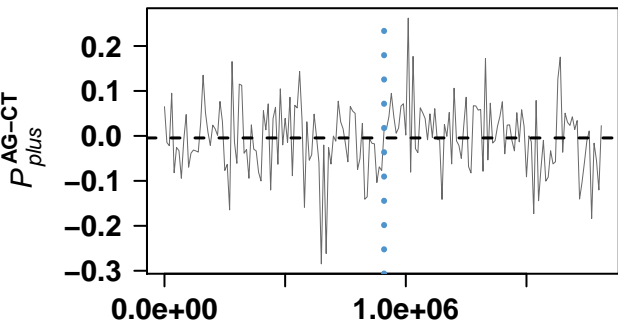


genome coordinates

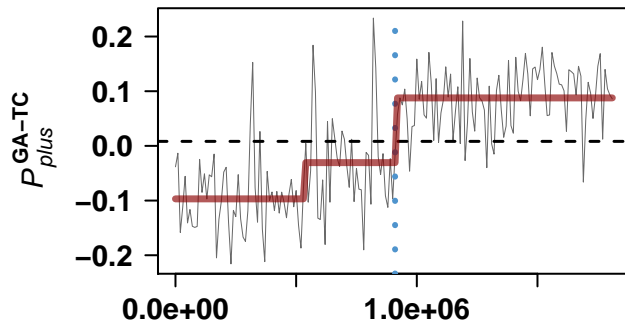
Desulfitobacterium hafniense Y51



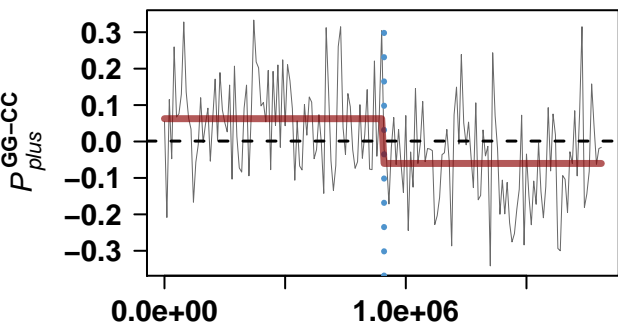
Lactobacillus salivarius UCC118



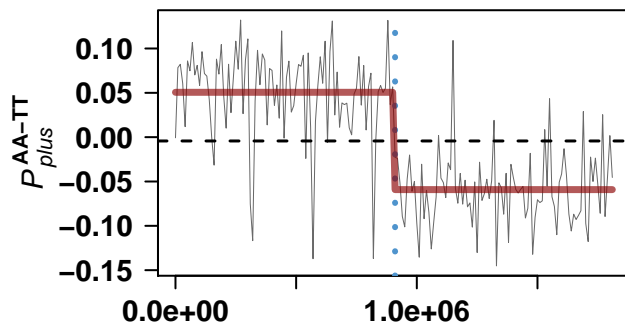
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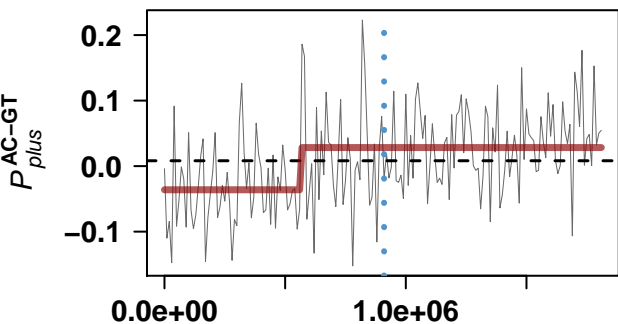
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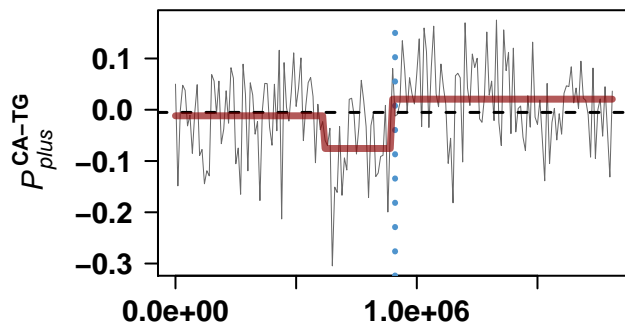
genome coordinates



genome coordinates

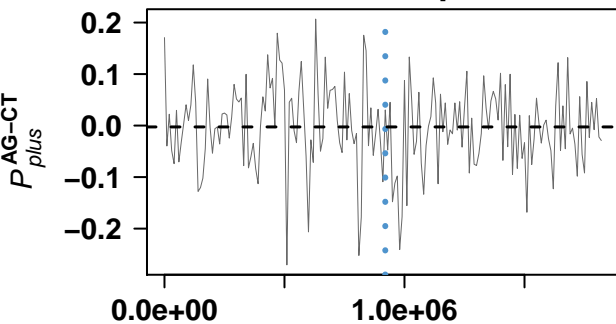


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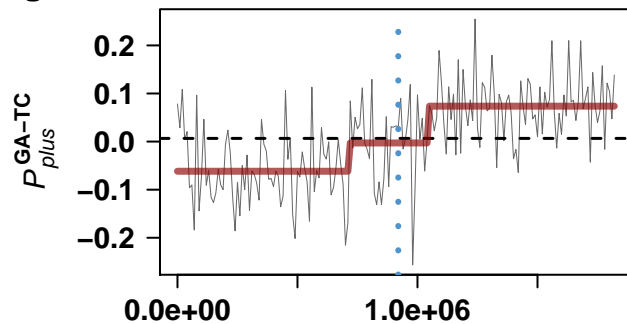


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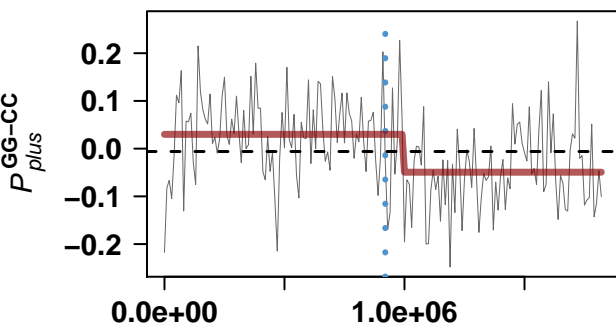
Streptococcus pyogenes MGAS9429



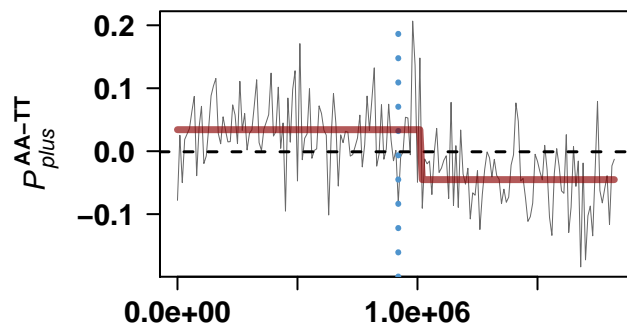
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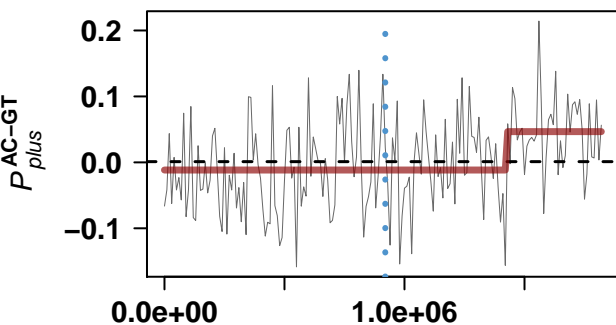
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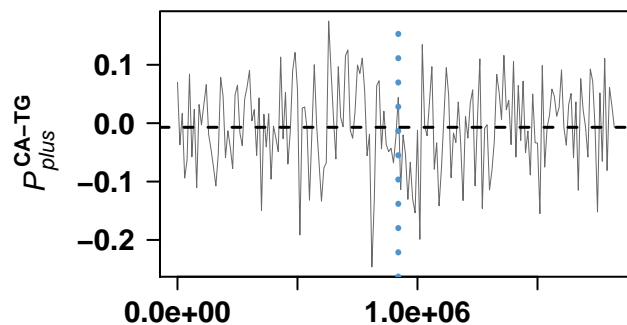
genome coordinates



genome coordinates

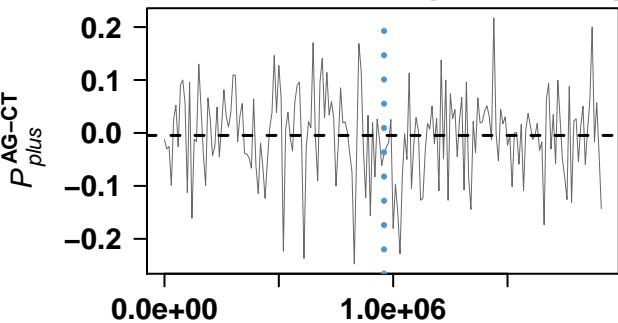


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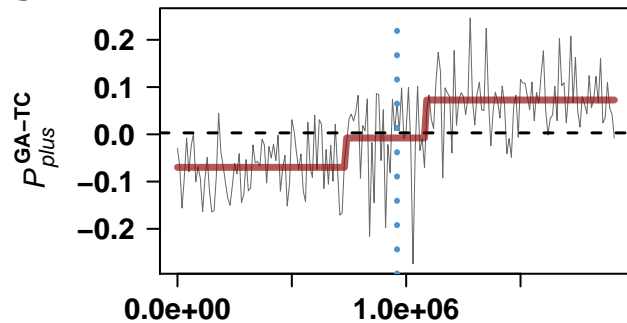


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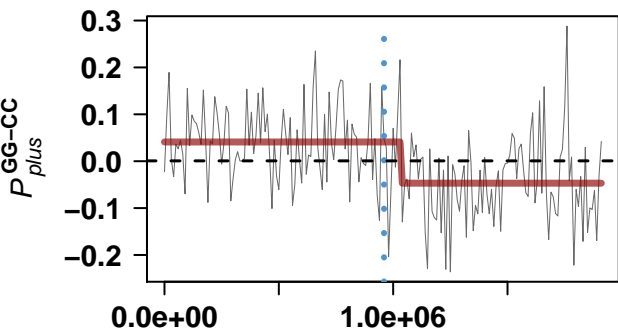
Streptococcus pyogenes MGAS10270



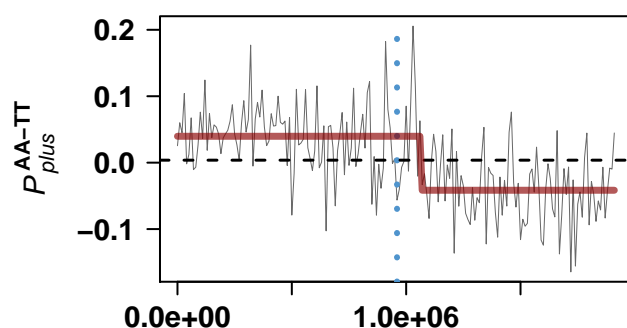
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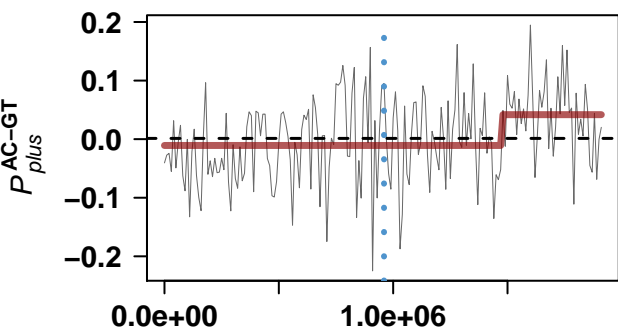
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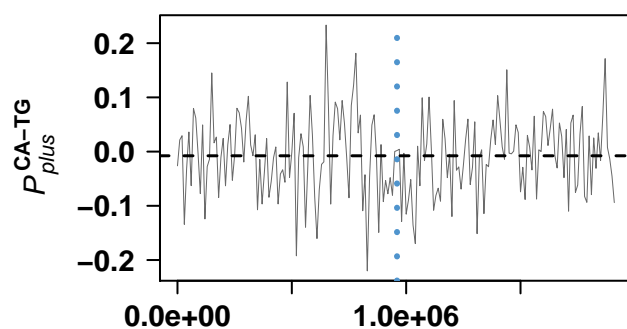
genome coordinates



genome coordinates

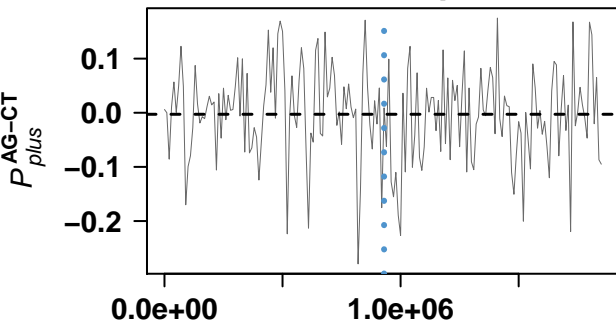


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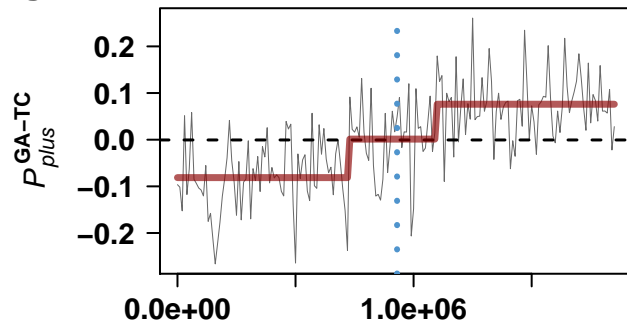


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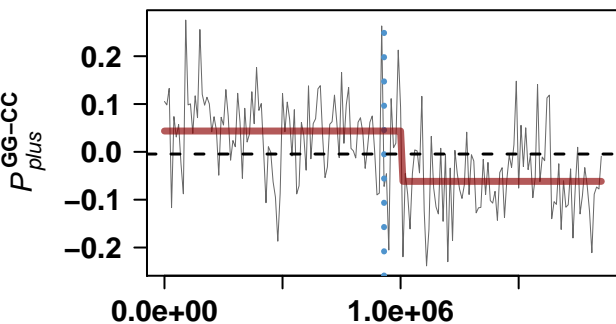
Streptococcus pyogenes MGAS2096



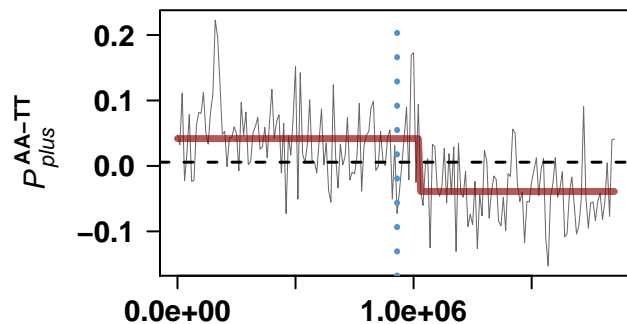
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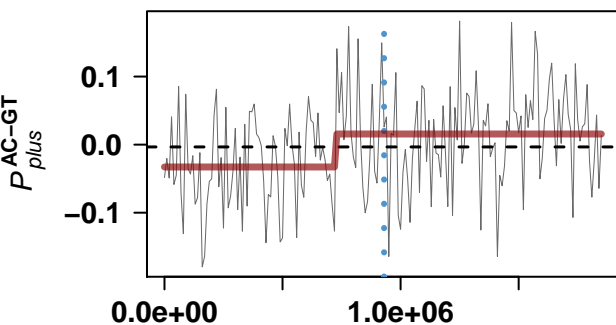
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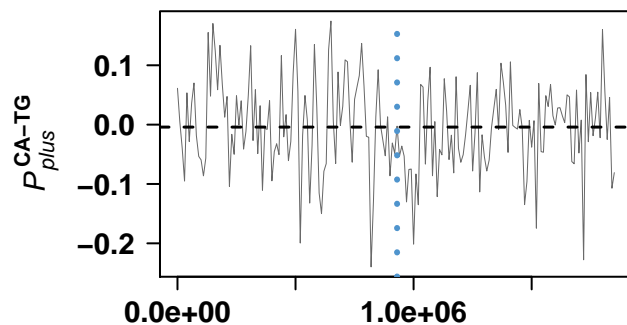
genome coordinates



genome coordinates

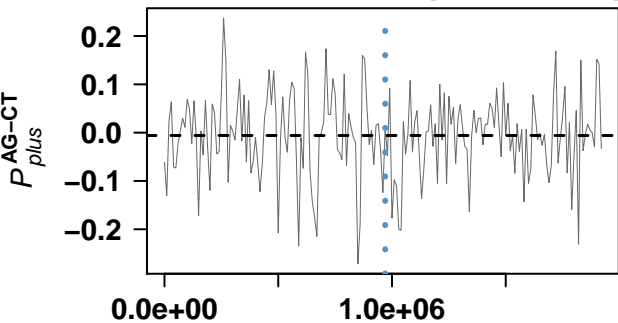


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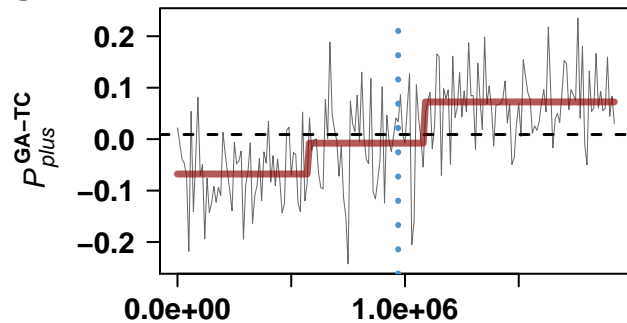


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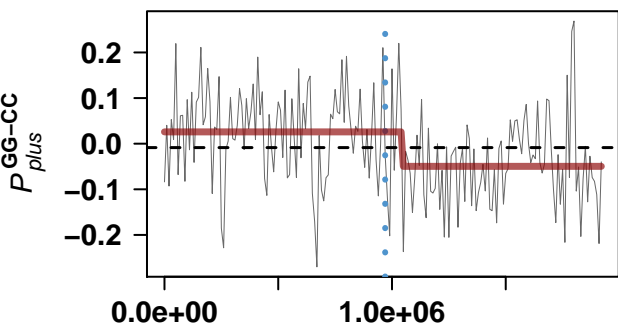
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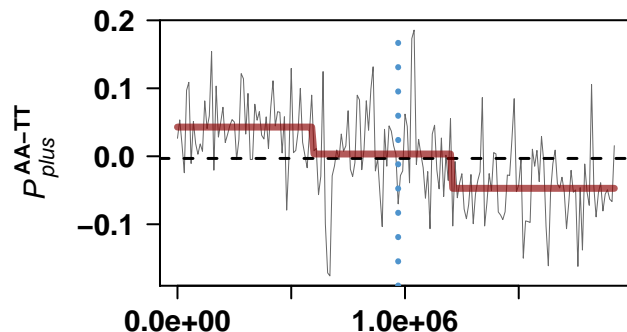
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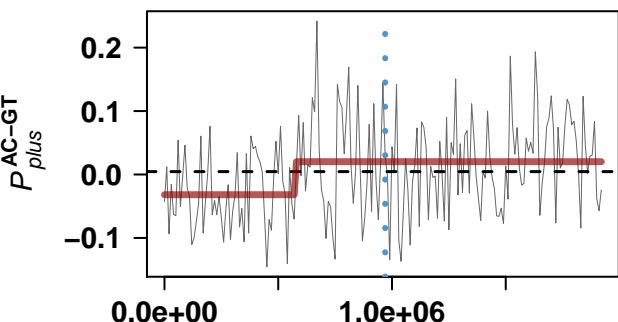
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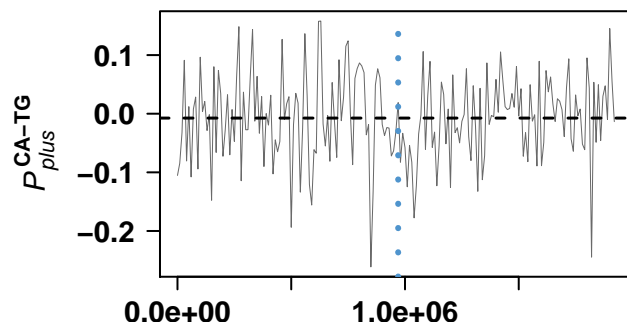
genome coordinates



genome coordinates

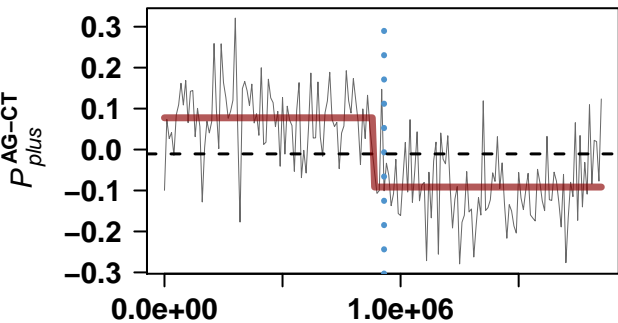


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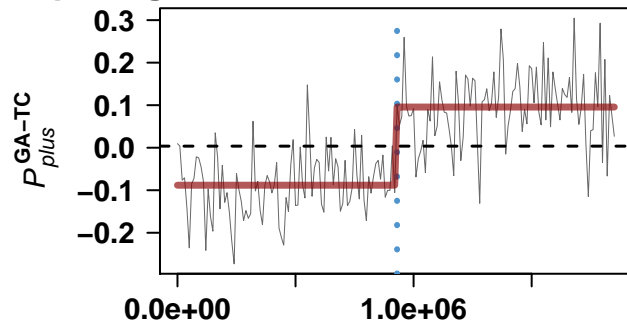


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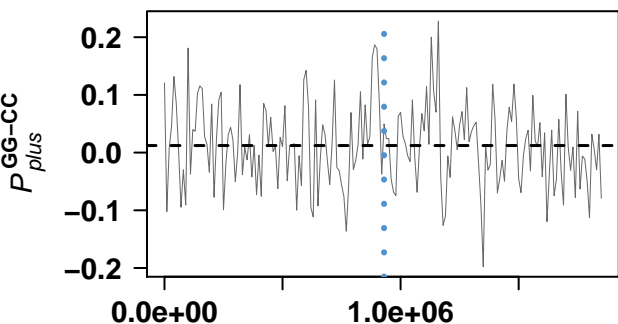
Lactobacillus delbrueckii subsp. bulgaricus ATCC 11842



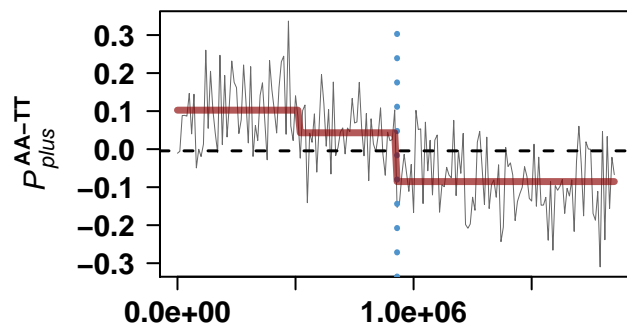
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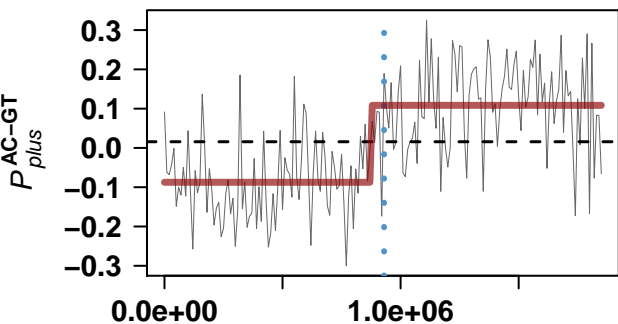
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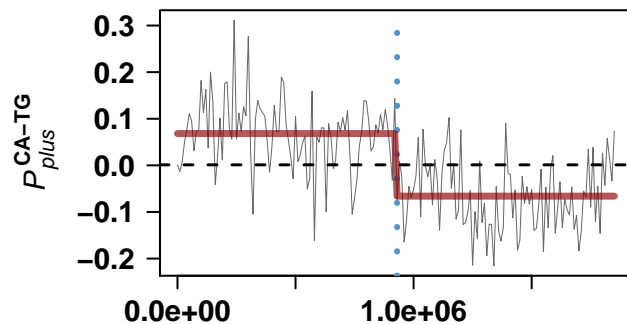
genome coordinates



genome coordinates

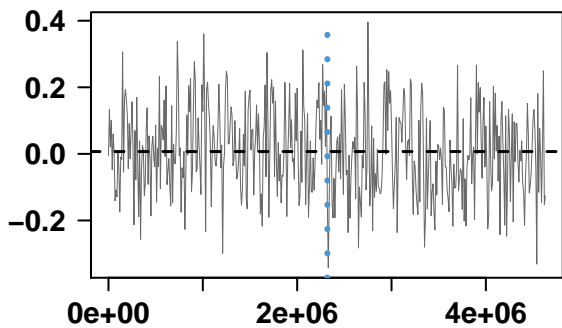


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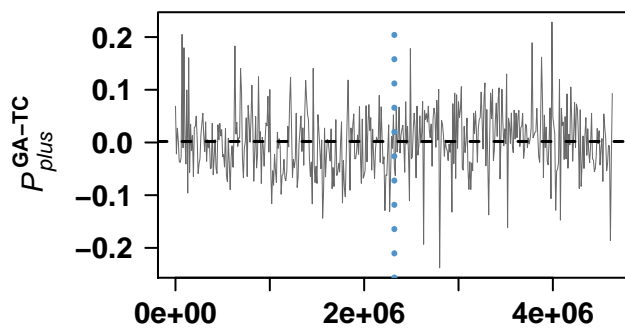


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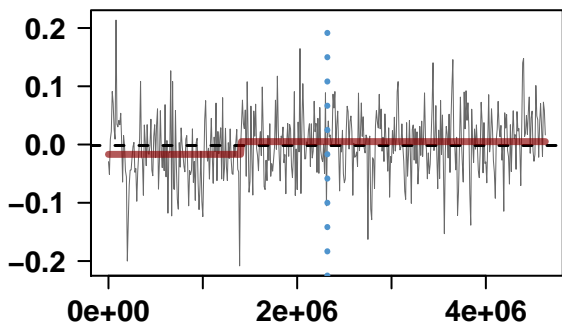
Escherichia coli str. K-12 substr. W3110



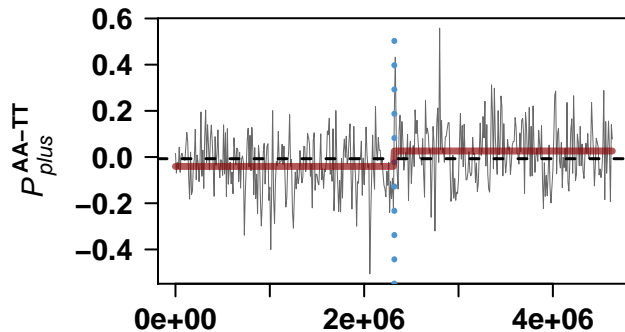
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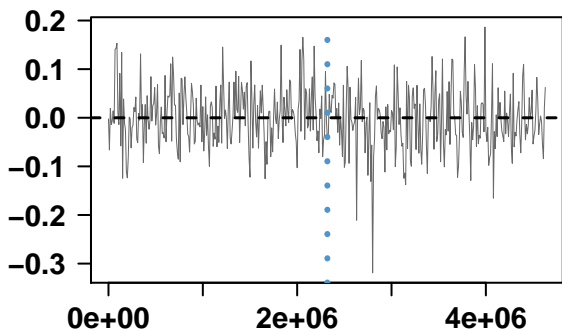
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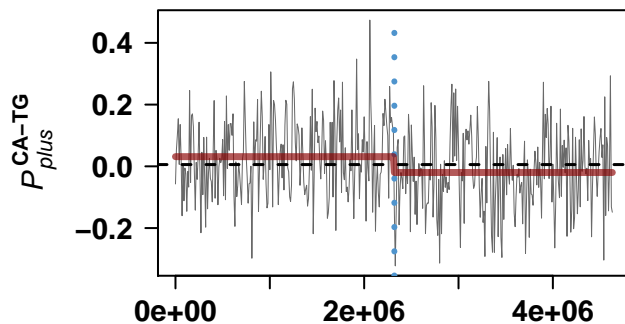
genome coordinates



genome coordinates

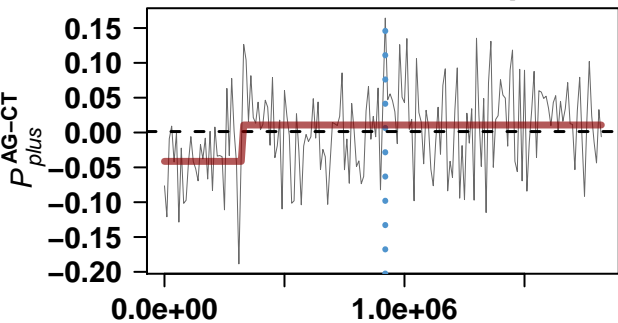


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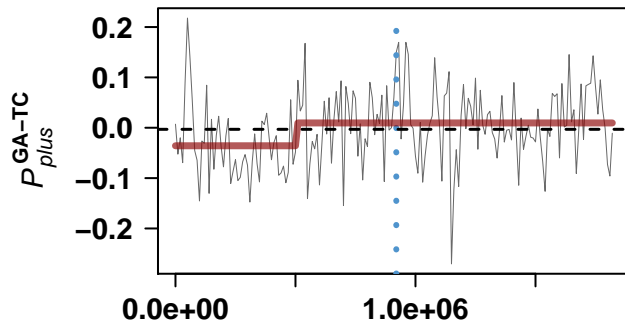


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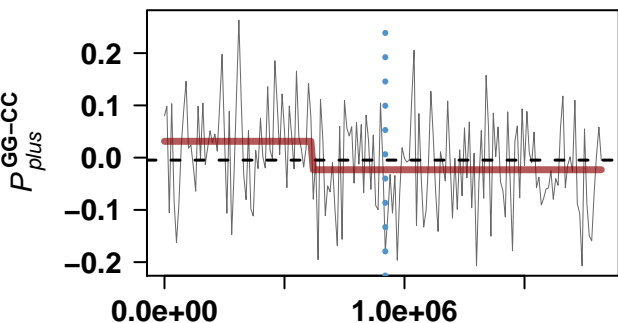
Haemophilus influenzae Rd KW20



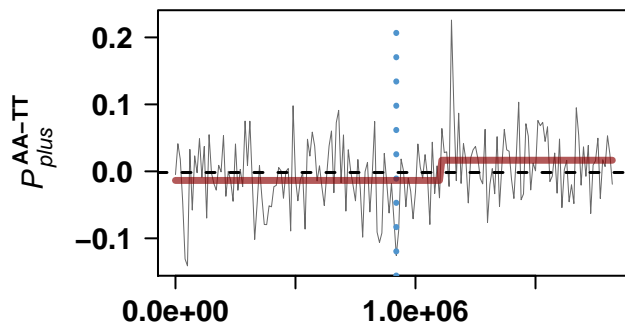
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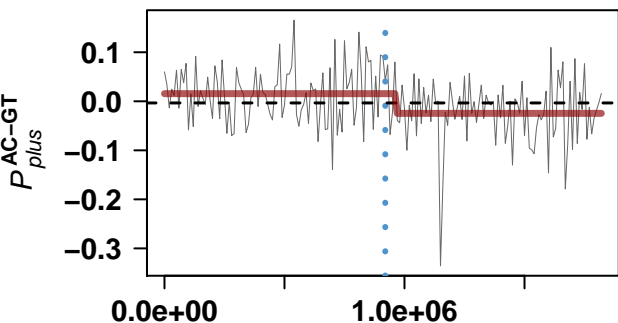
genome coordinates



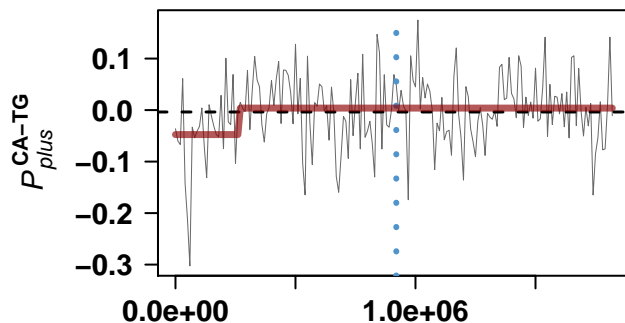
genome coordinates



genome coordinates

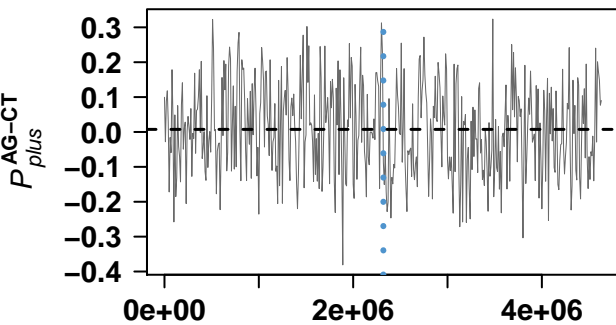


genome coordinates

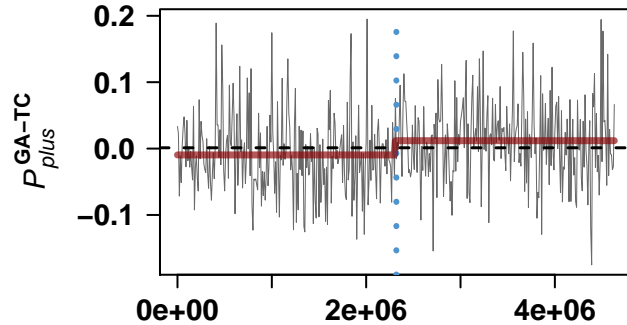


genome coordinates

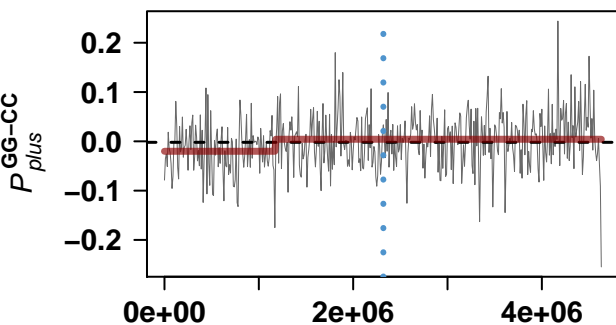
Escherichia coli str. K-12 substr. MG1655



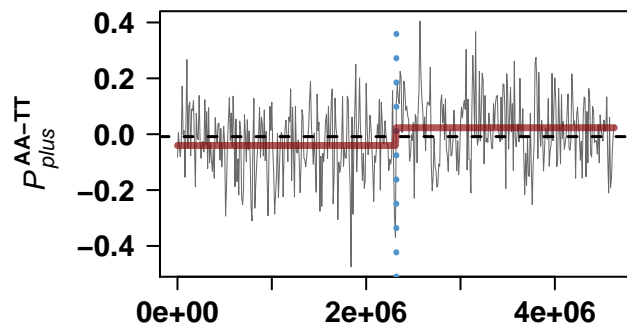
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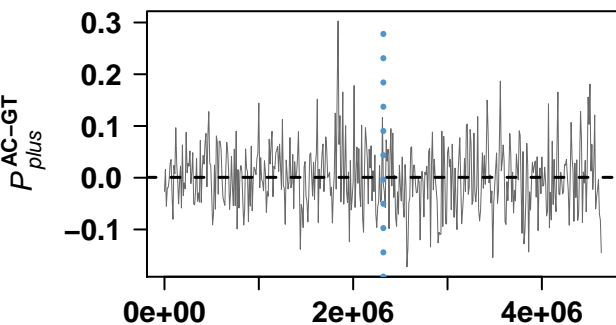
genome coordinates



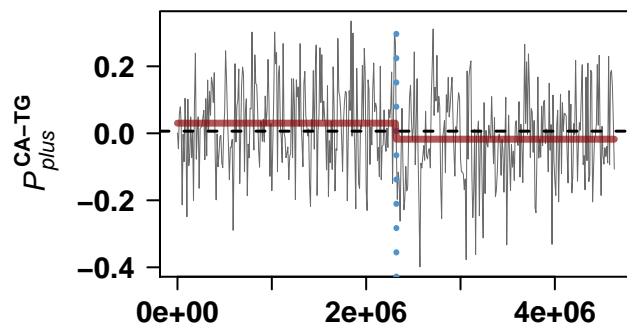
genome coordinates



genome coordinates

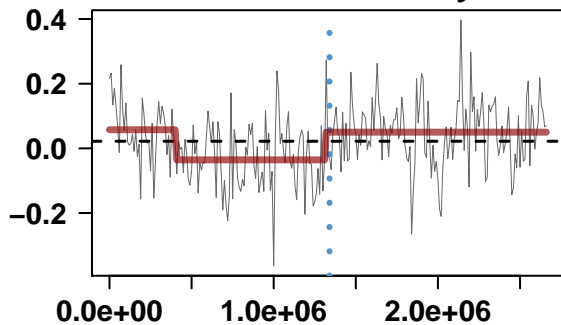


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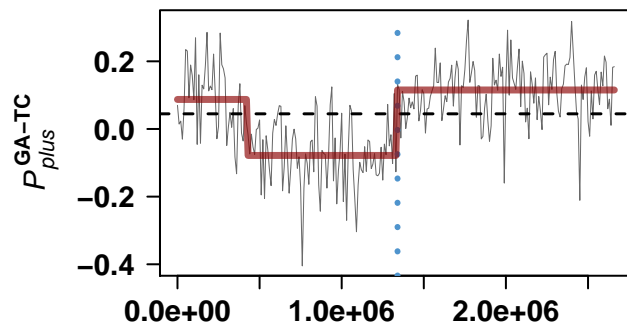


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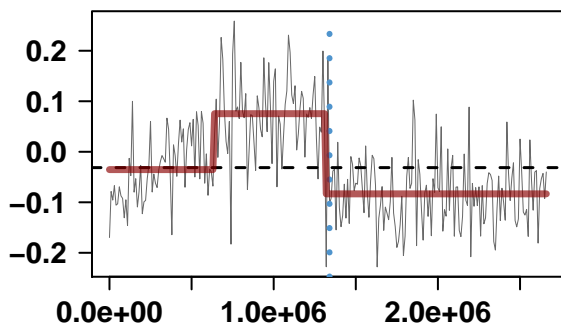
Xylella fastidiosa 9a5c



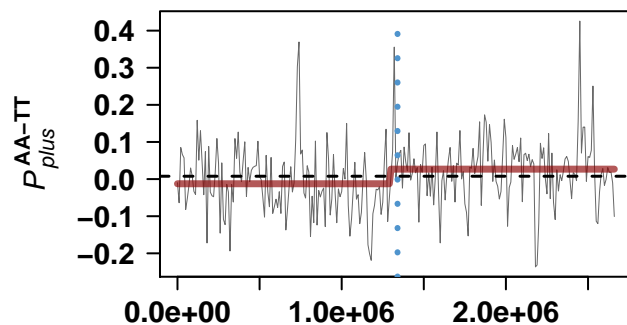
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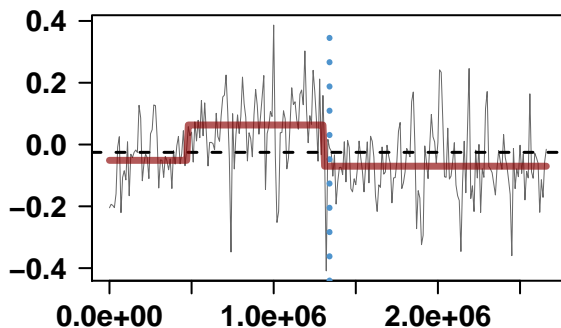
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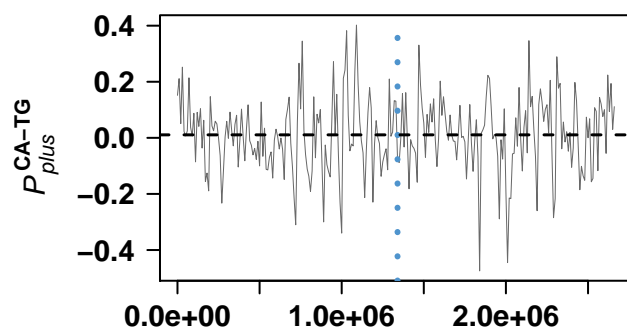
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genome coordinates

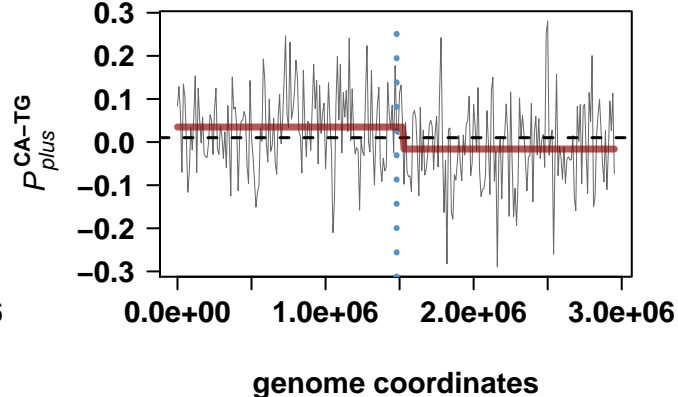
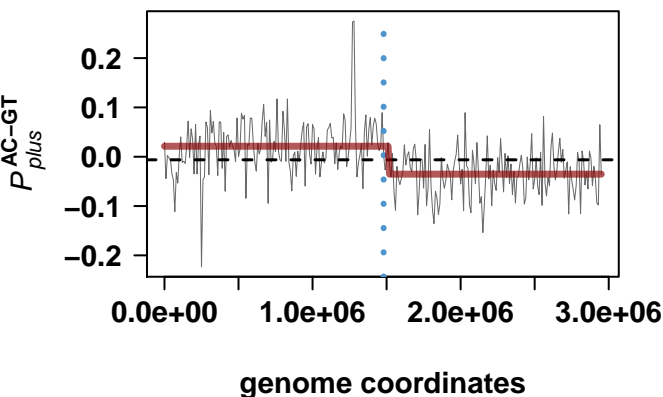
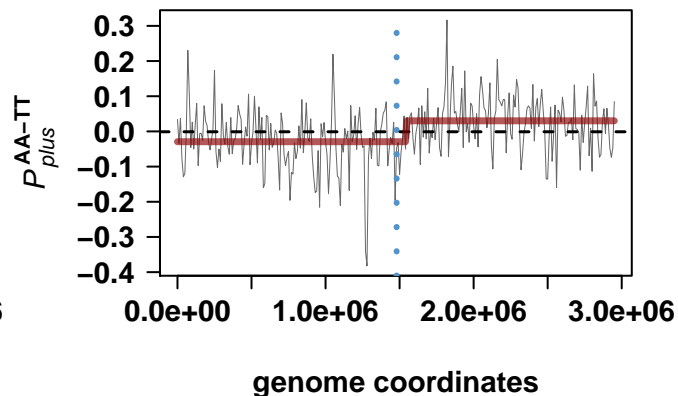
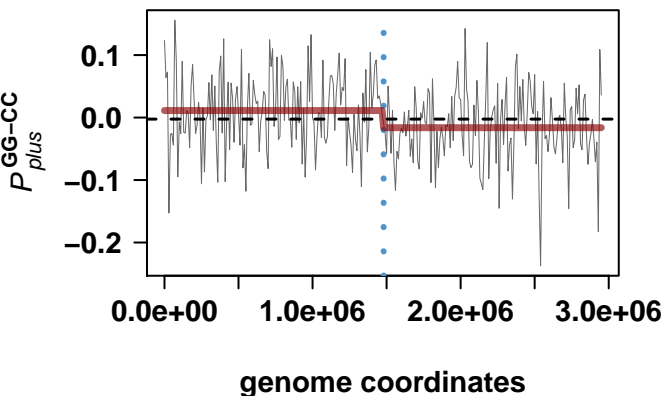
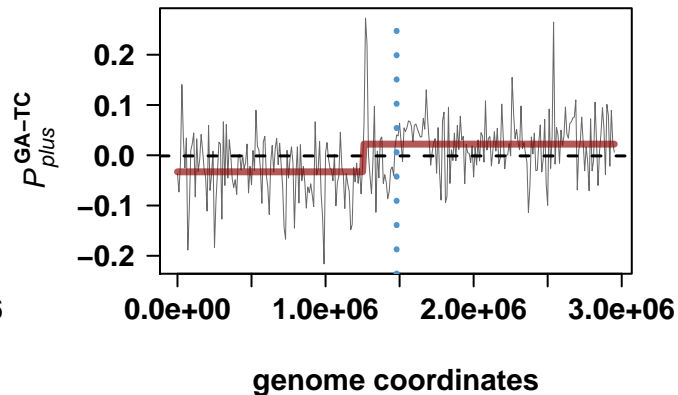
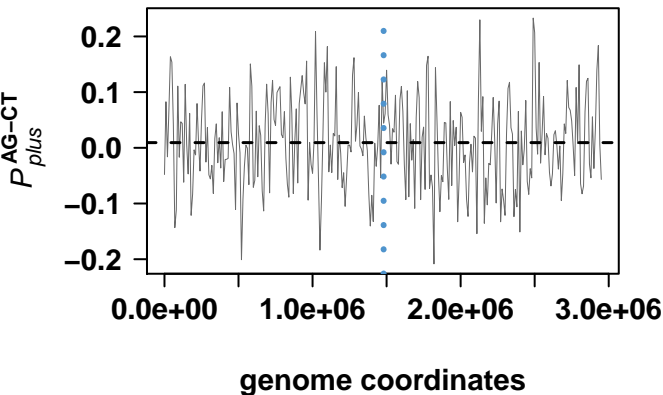


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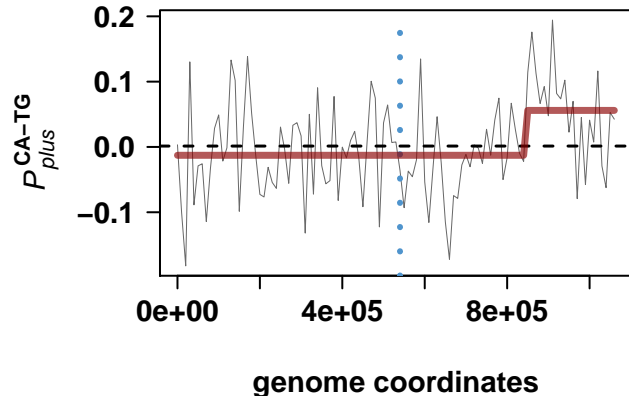
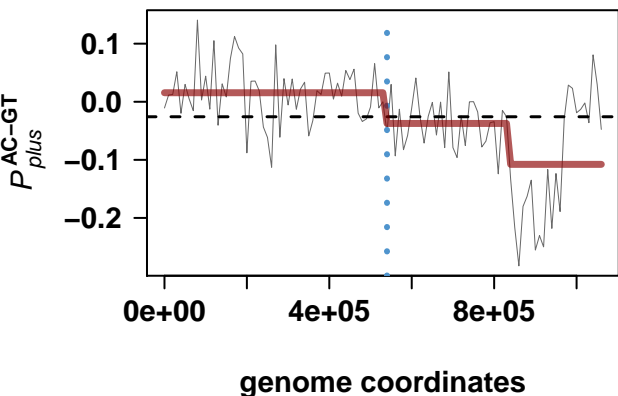
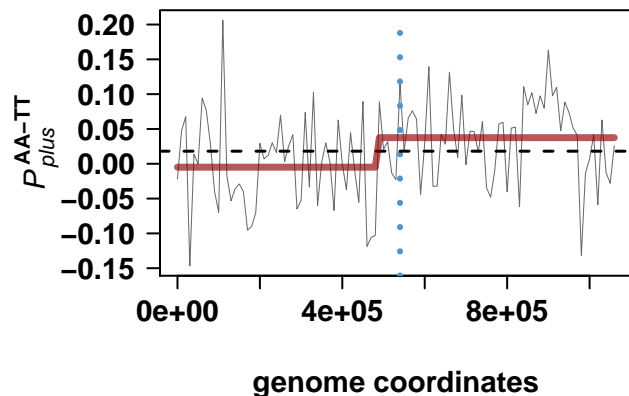
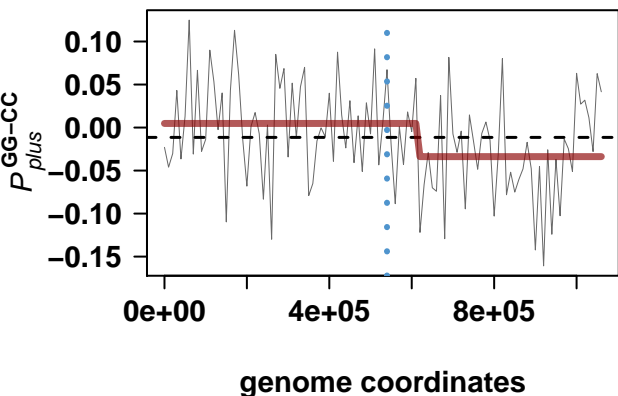
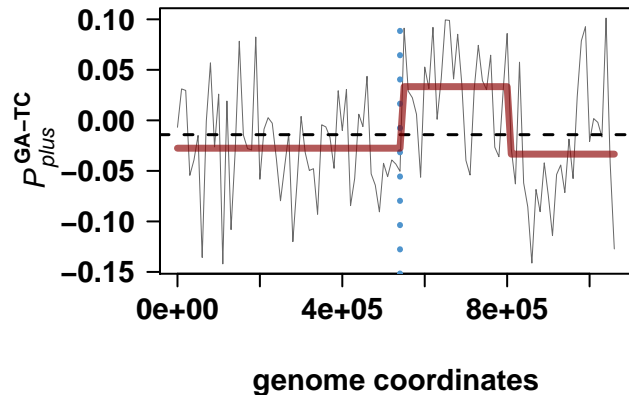
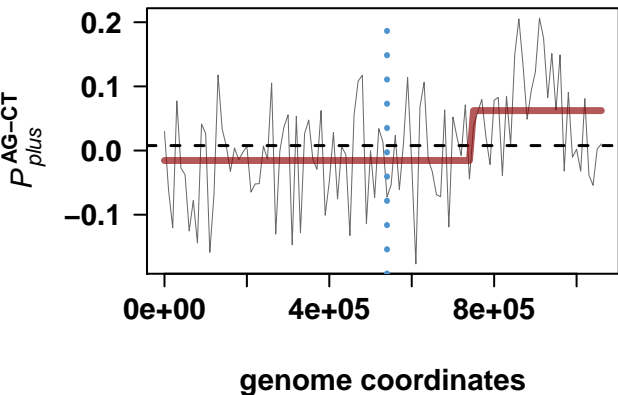


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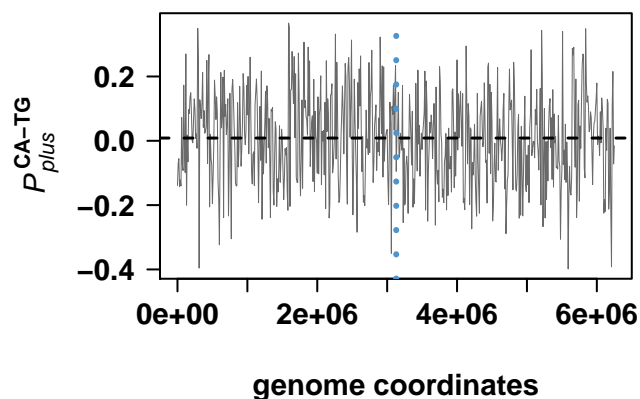
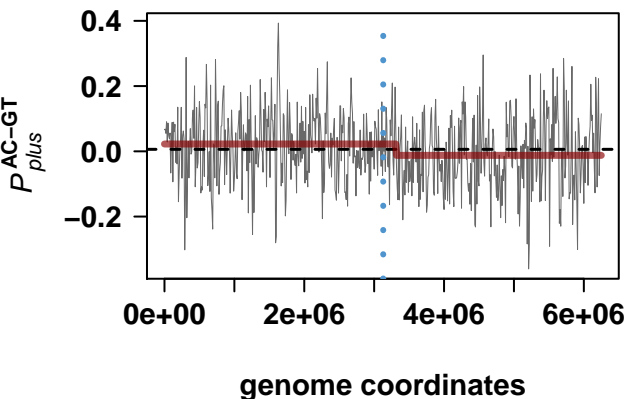
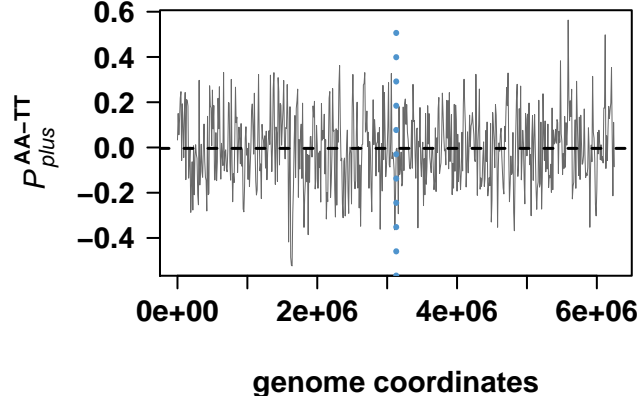
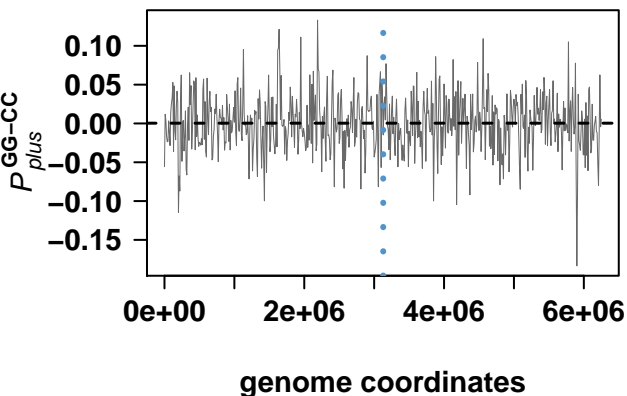
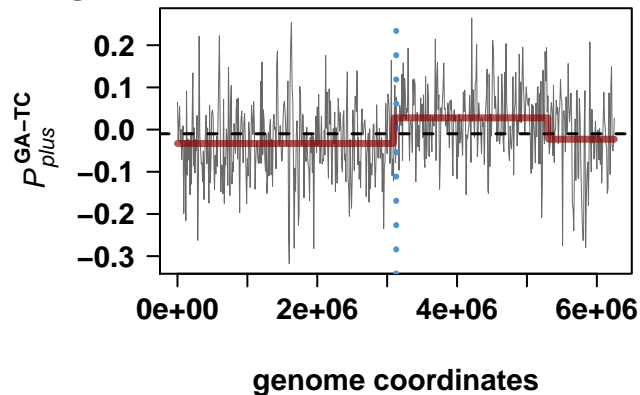
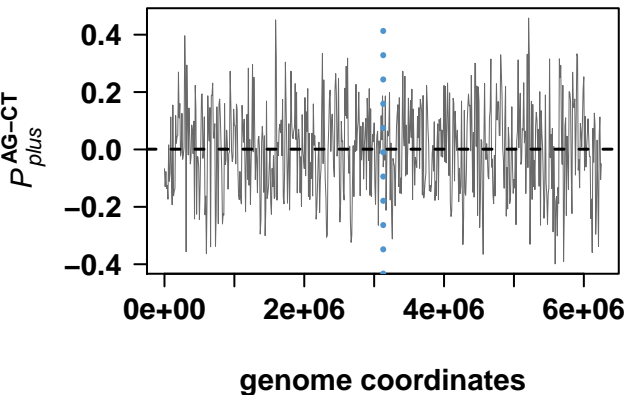
Vibrio cholerae O1 biovar El Tor str. N16961



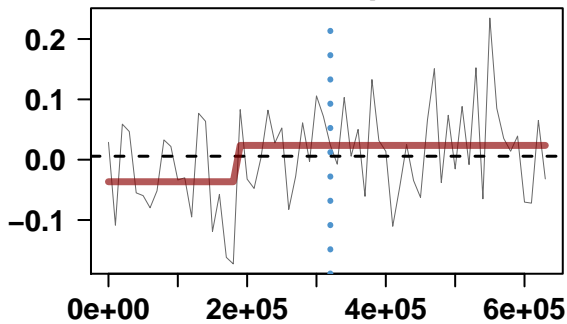
Vibrio cholerae O1 biovar El Tor str. N16961



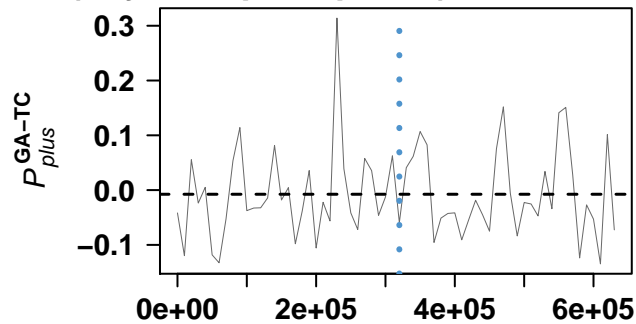
Pseudomonas aeruginosa PAO1



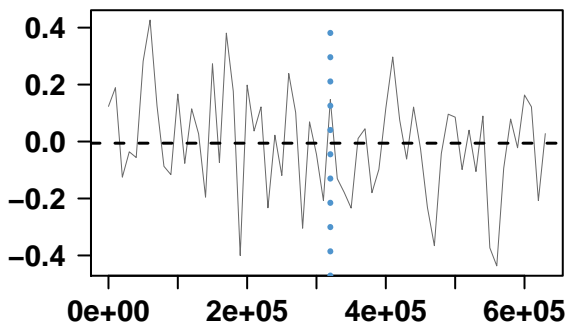
Buchnera aphidicola str. APS (Acyrthosiphon pisum)



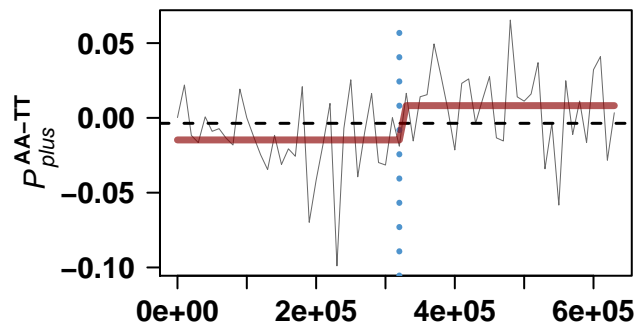
genome coordinates



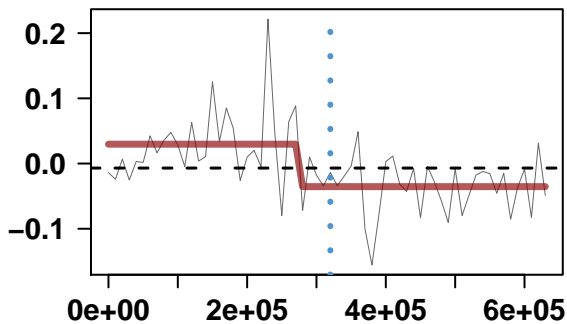
genome coordinates



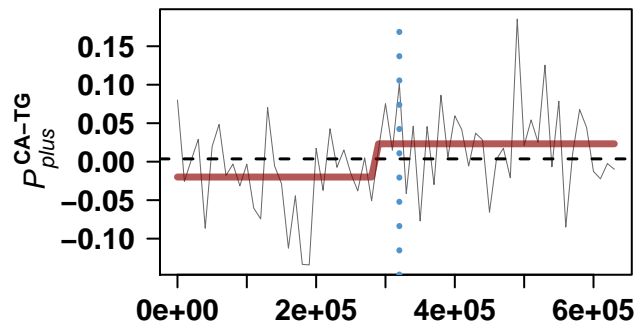
genome coordinates



genome coordinates

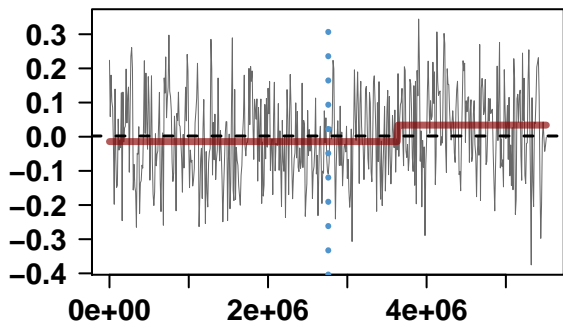


genome coordinates

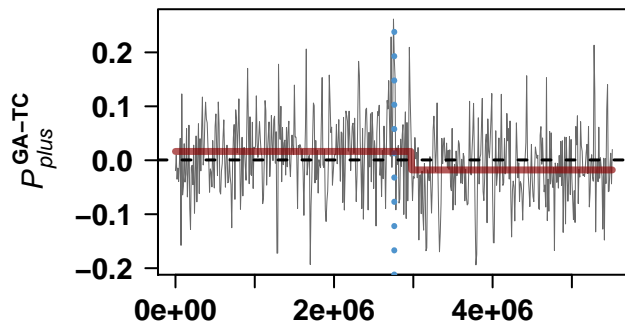


genome coordinates

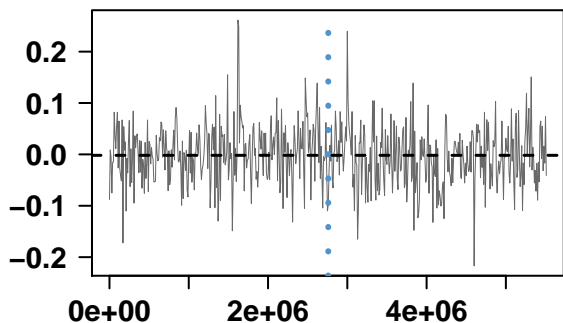
Escherichia coli O157:H7 str. EDL933



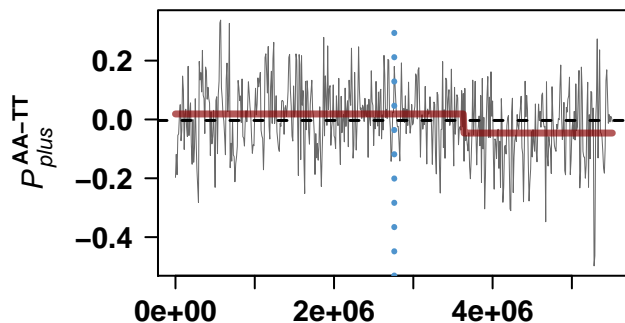
genome coordinates



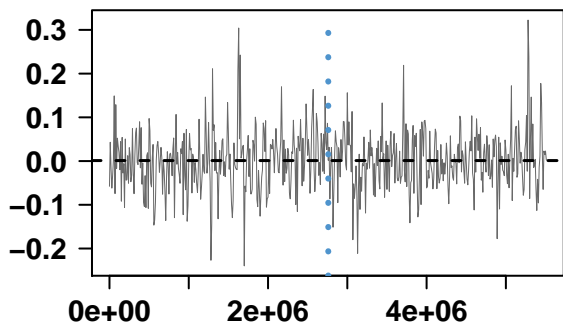
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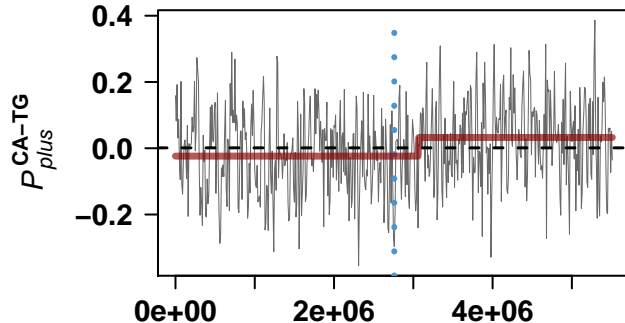
genome coordinates



genome coordinates

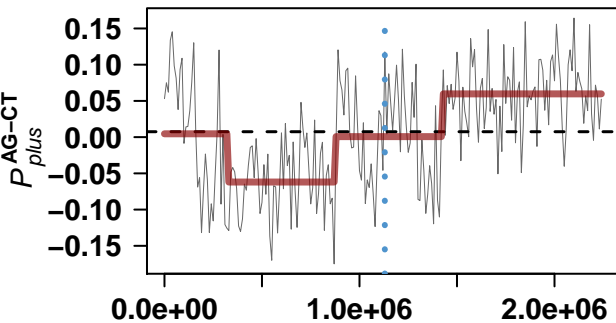


genome coordinates

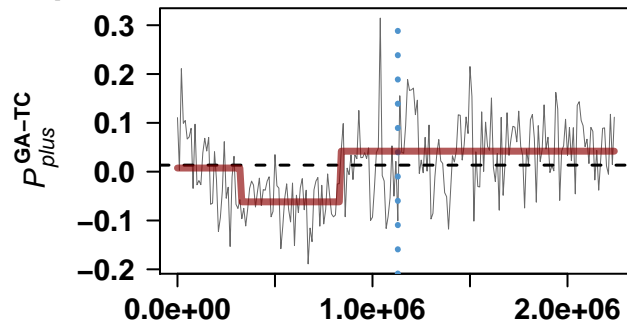


genome coordinates

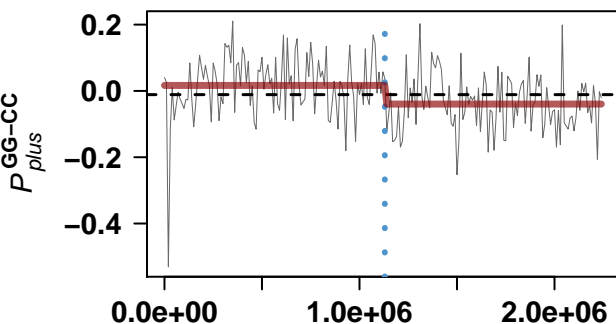
Pasteurella multocida subsp. *multocida* str. Pm70



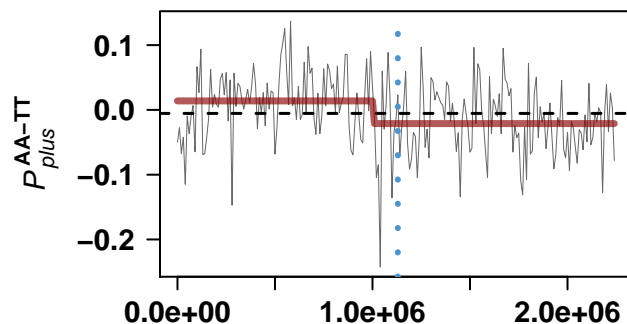
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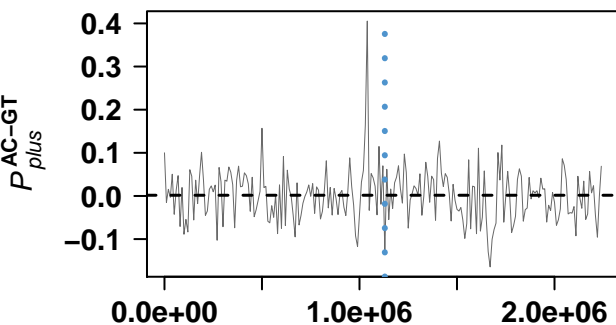
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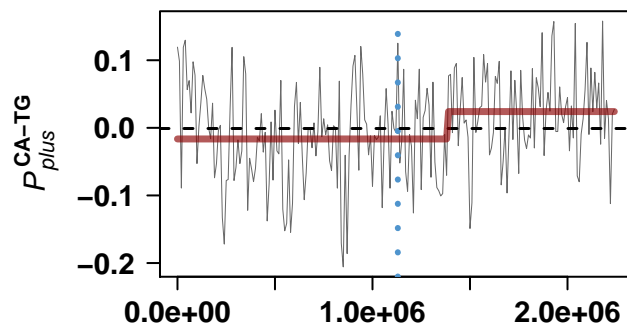
genome coordinates



genome coordinates

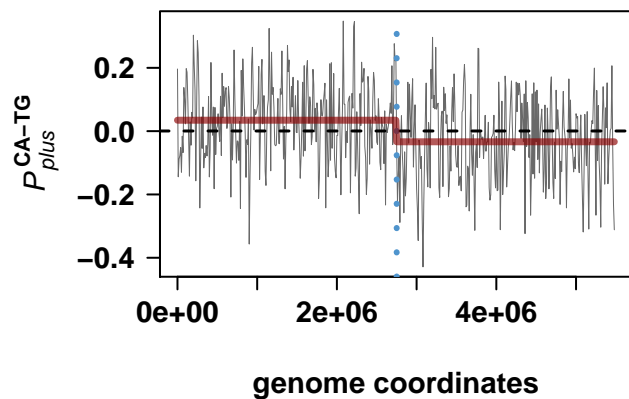
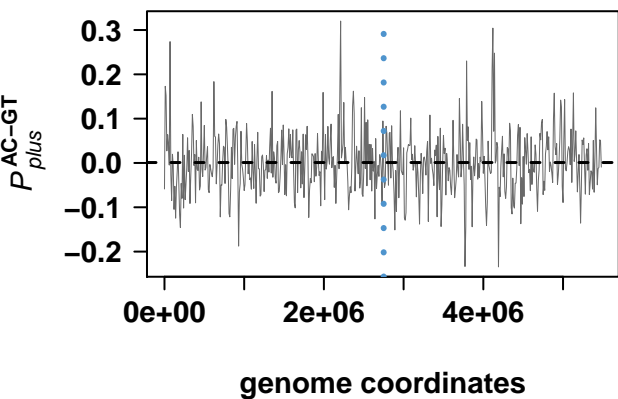
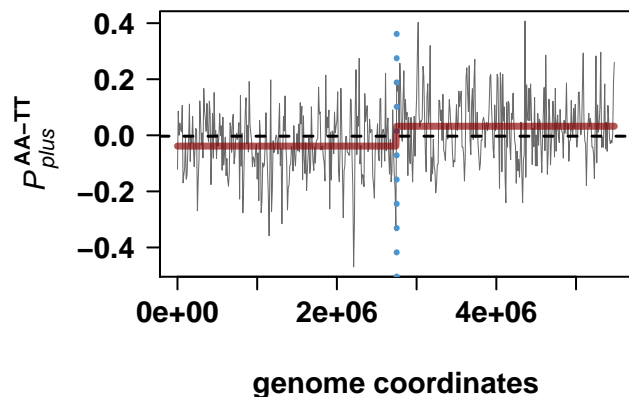
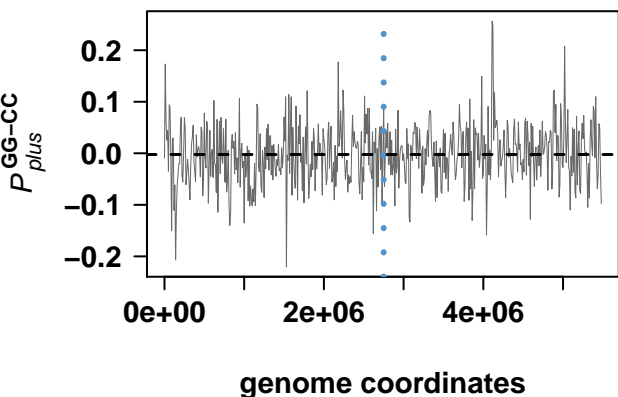
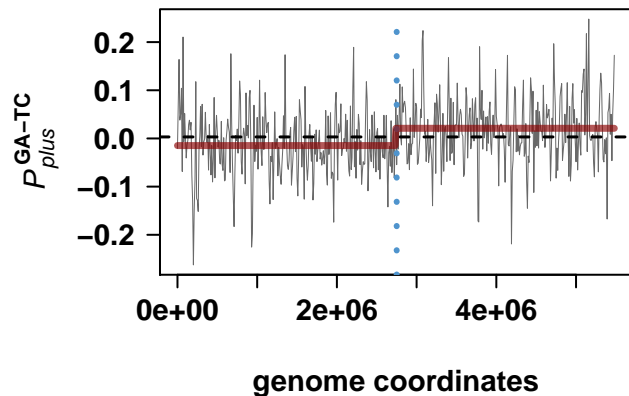
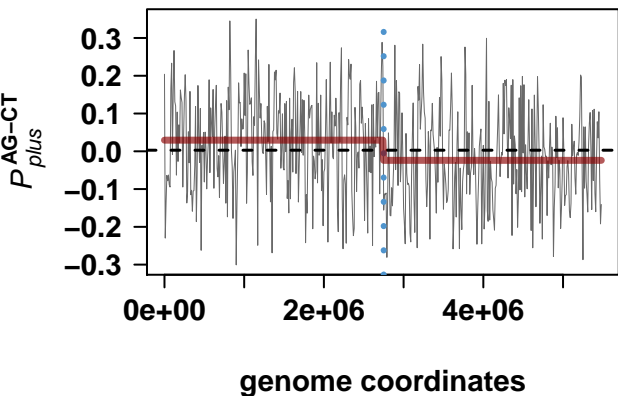


genome coordinates

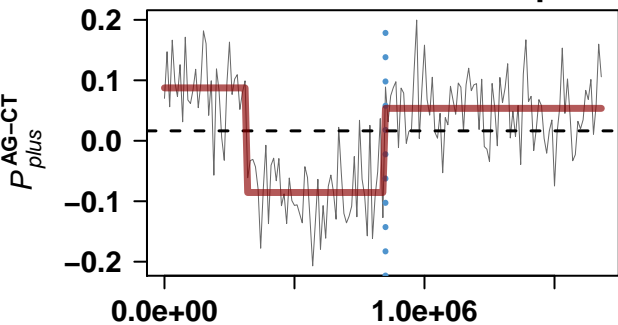


genome coordinates

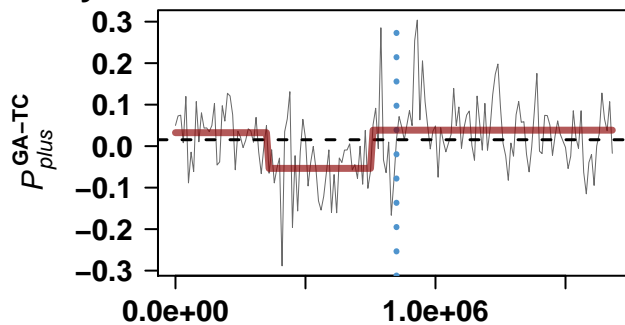
Escherichia coli O157:H7 str. Sakai



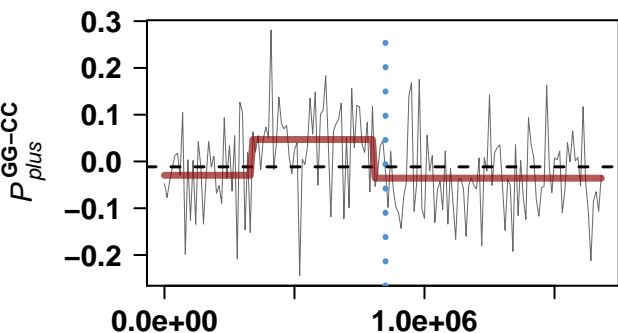
Haemophilus ducreyi 35000HP



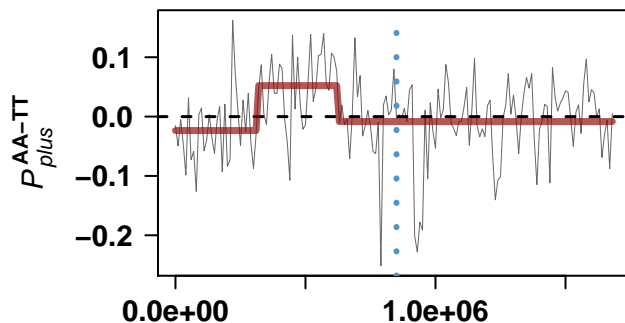
genome coordinates



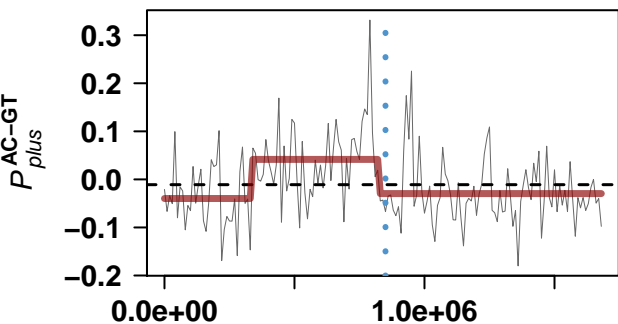
genome coordinates



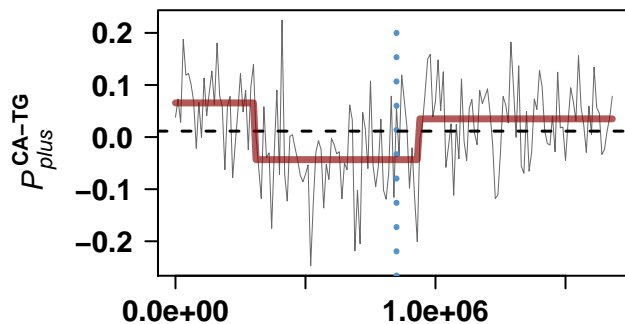
genome coordinates



genome coordinates

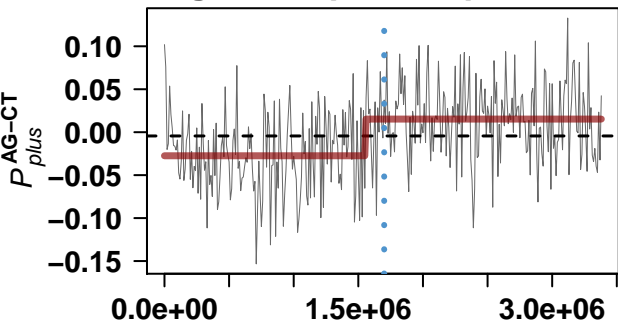


genome coordinates

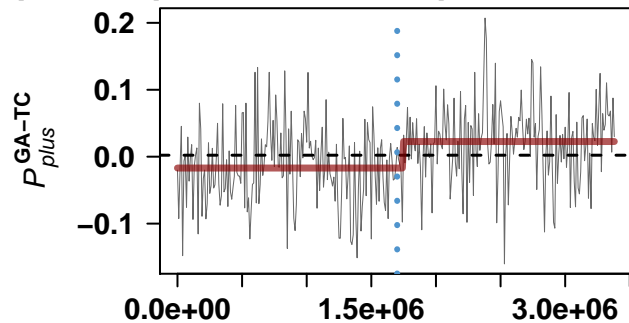


genome coordinates

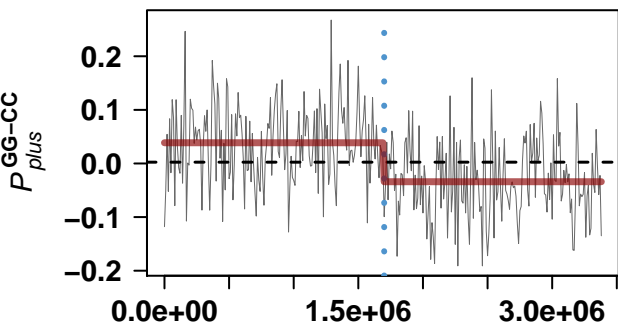
Legionella pneumophila subsp. pneumophila str. Philadelphia 1



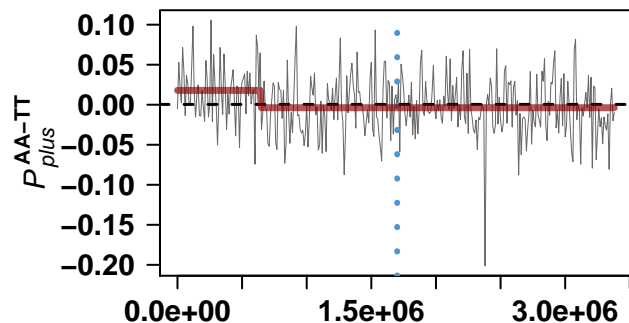
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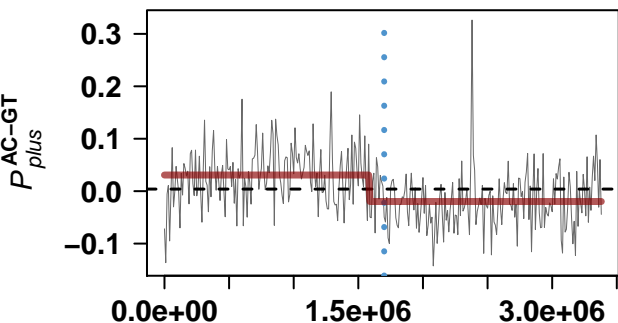
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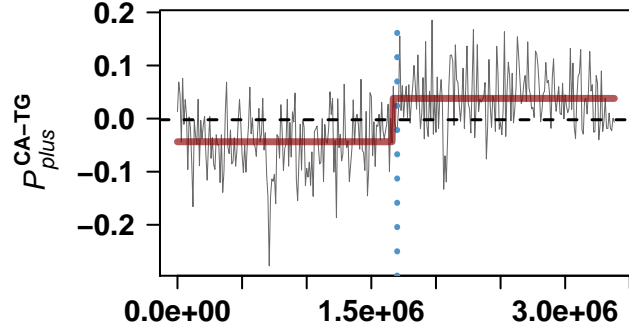
genome coordinates



genome coordinates

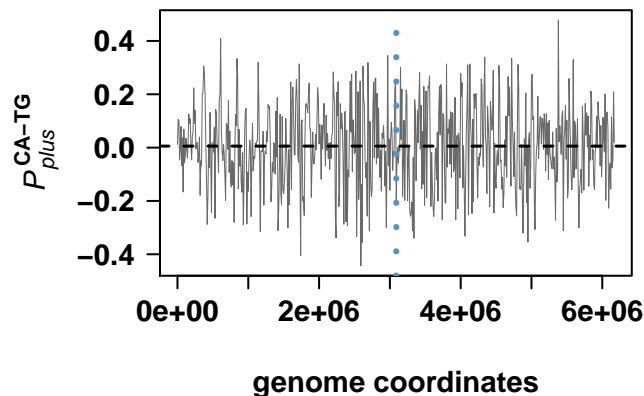
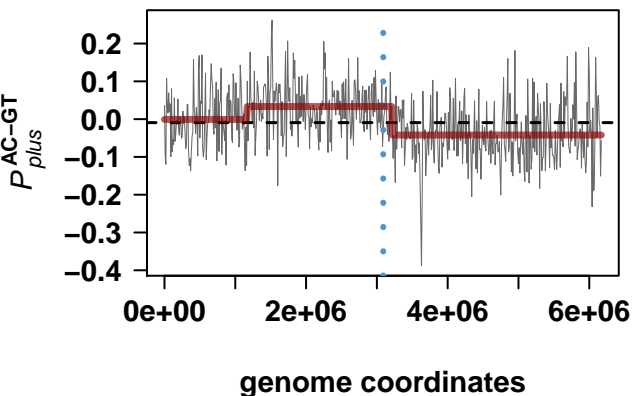
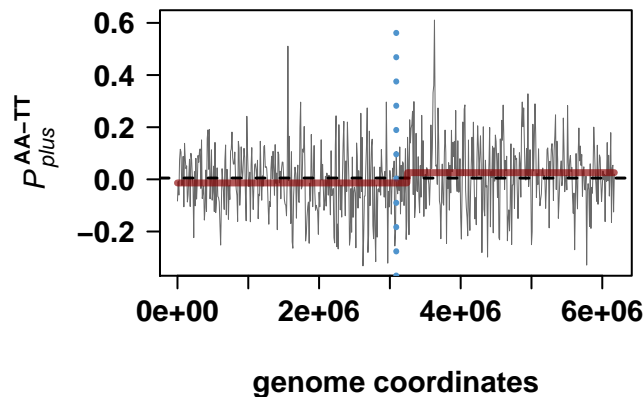
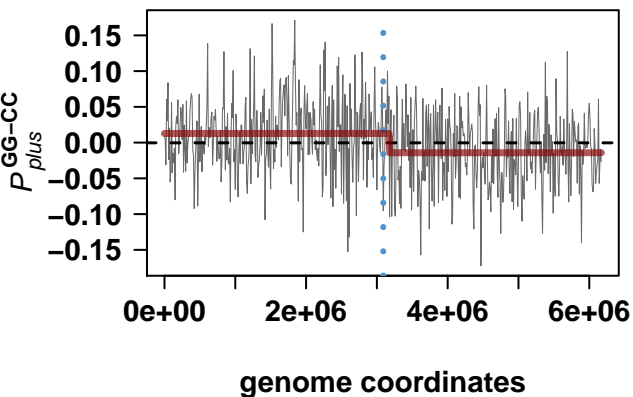
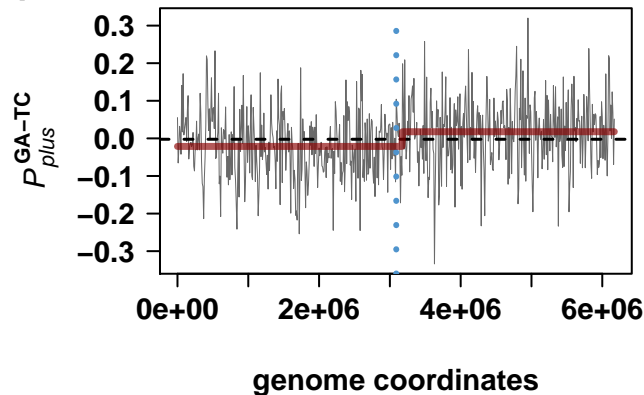
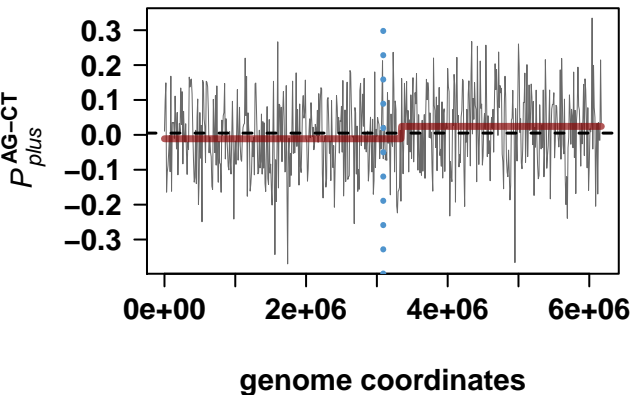


genome coordinates

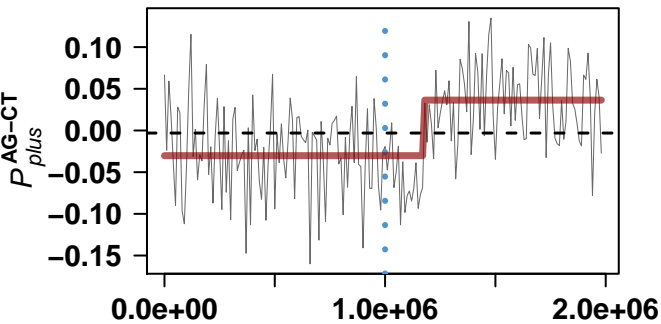


genome coordinates

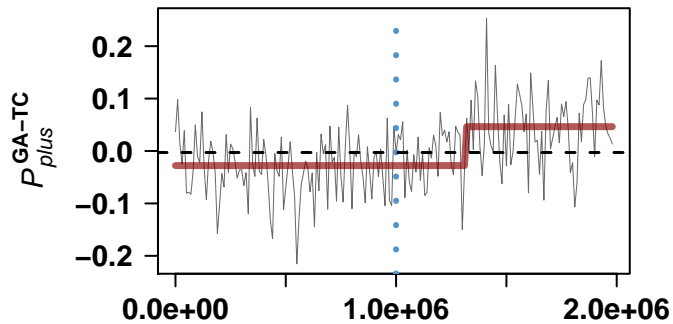
Pseudomonas putida KT2440



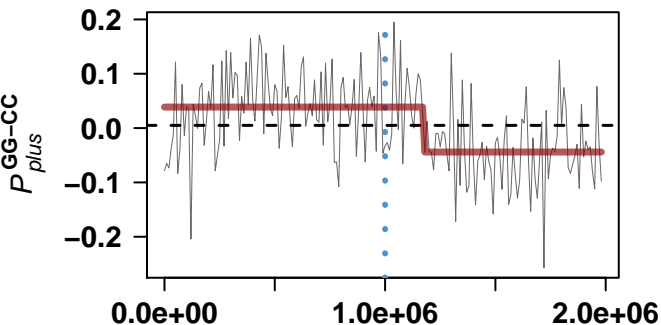
Coxiella burnetii RSA 493



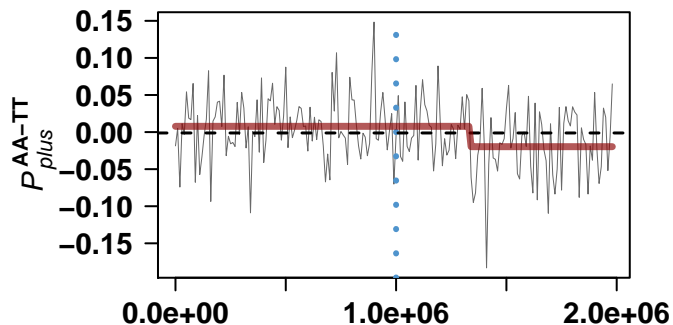
genome coordinates



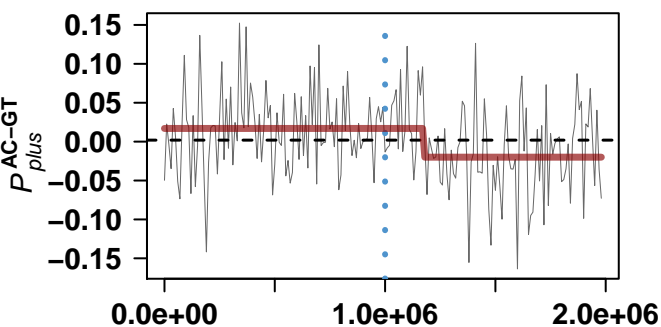
genome coordinates



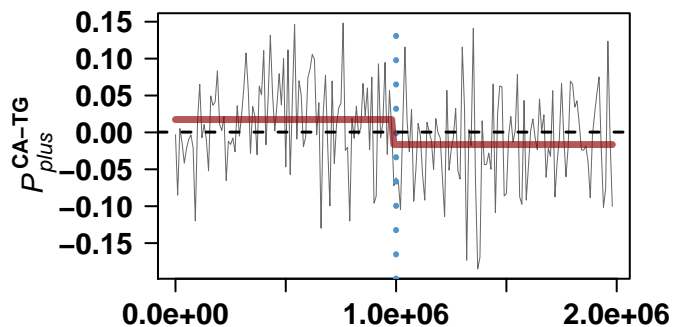
genome coordinates



genome coordinates

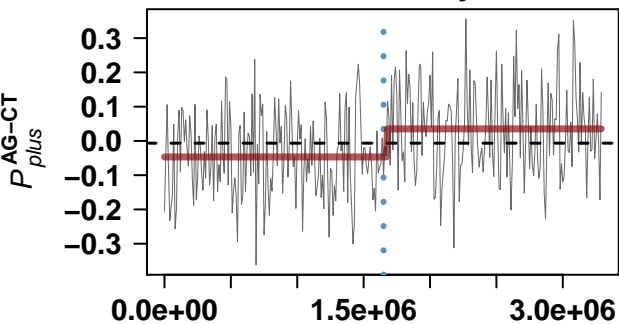


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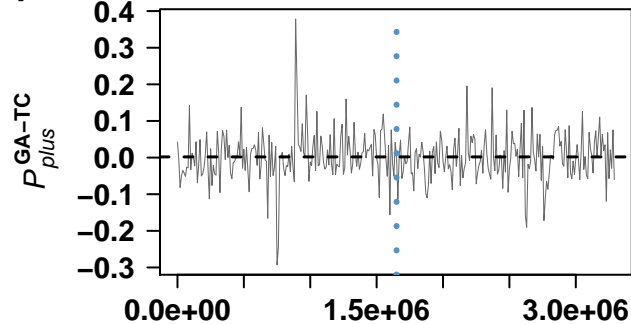


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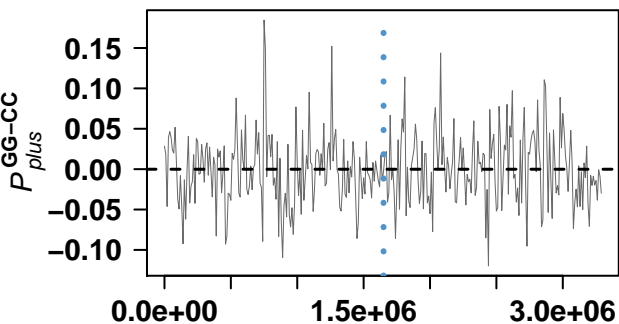
Methylococcus capsulatus str. Bath



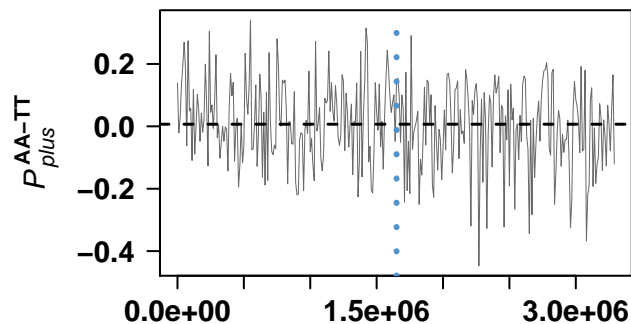
genome coordinates



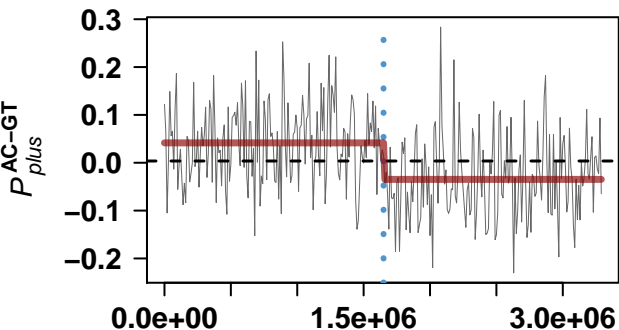
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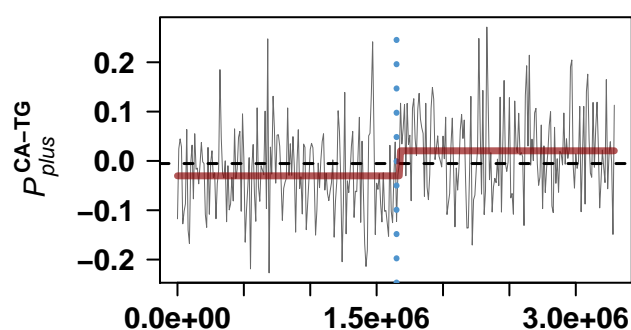
genome coordinates



genome coordinates

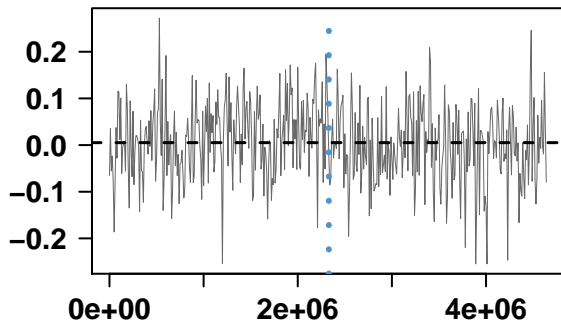


genome coordinates

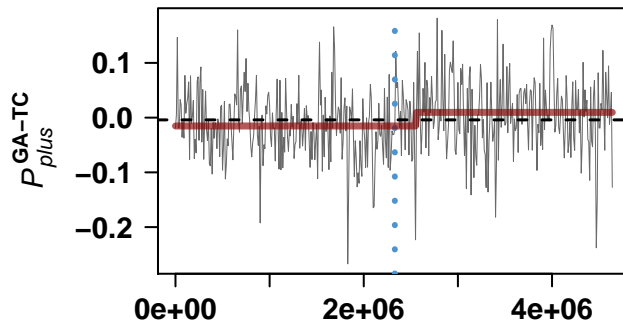


genome coordinates

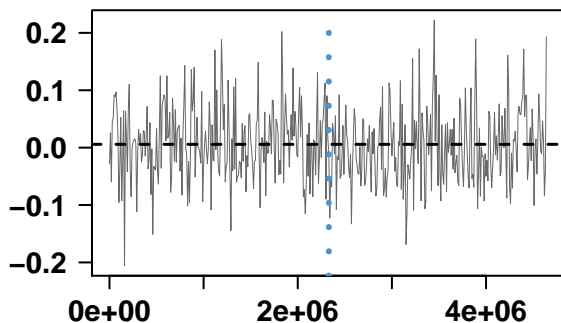
Yersinia pestis CO92



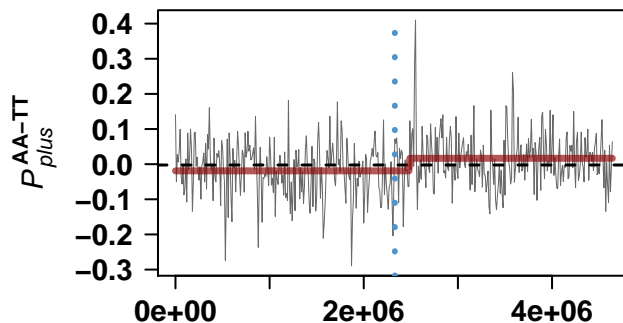
genome coordinates



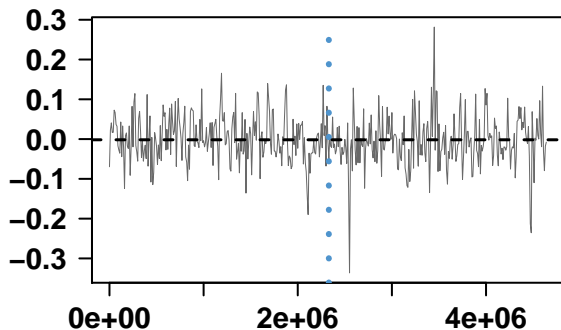
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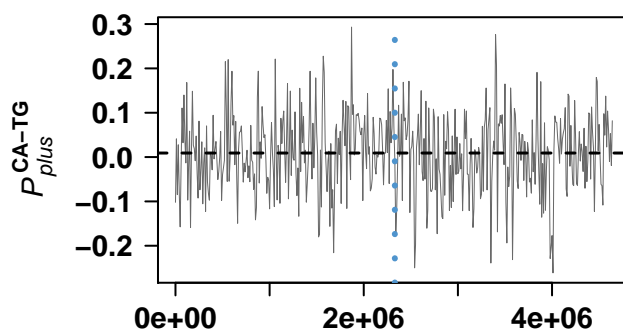
genome coordinates



genome coordinates

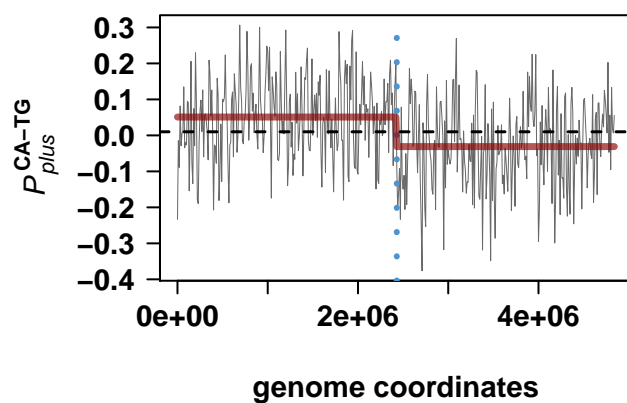
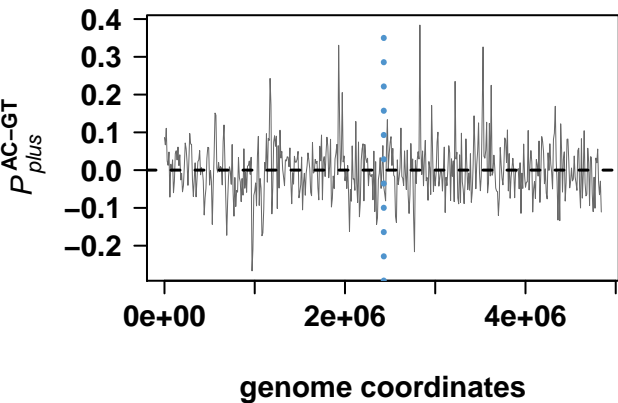
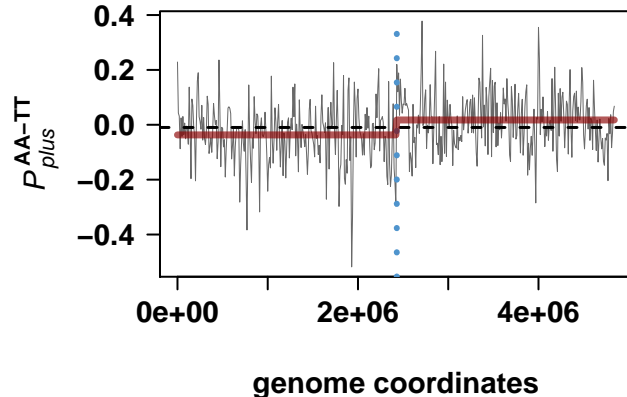
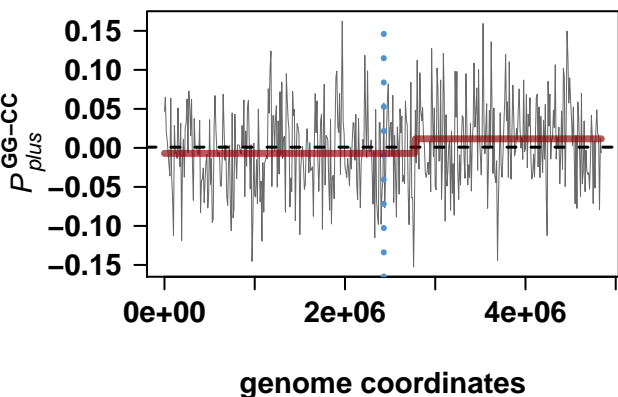
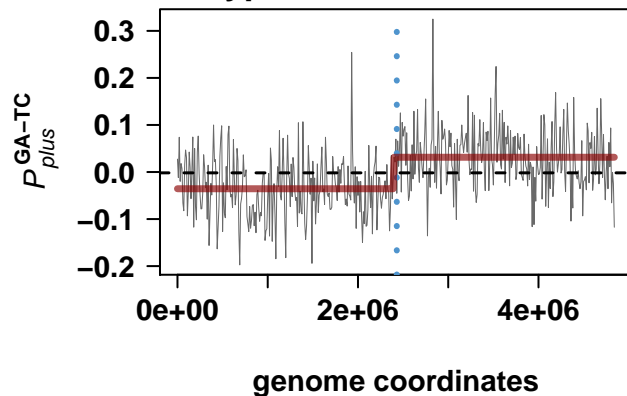
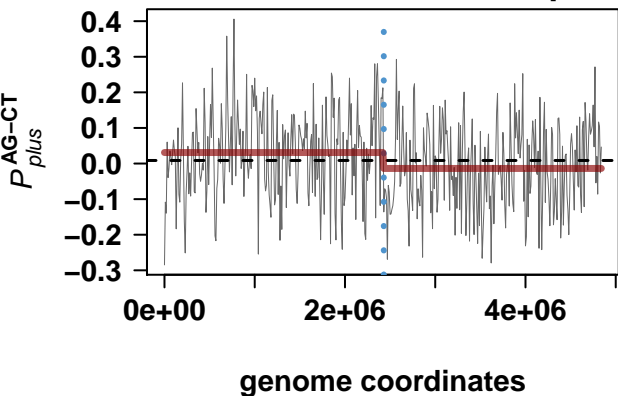


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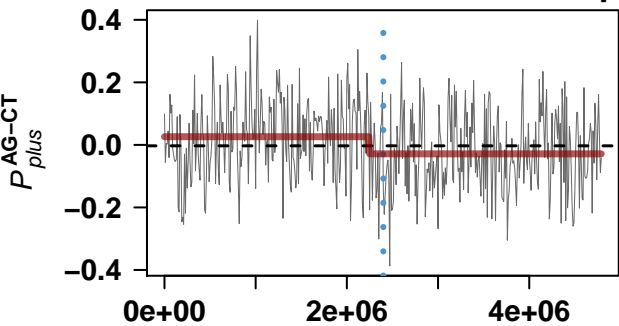


genome coordinates

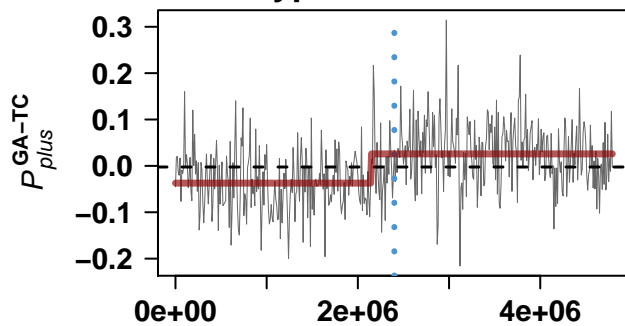
Salmonella enterica subsp. enterica serovar Typhimurium str. LT2



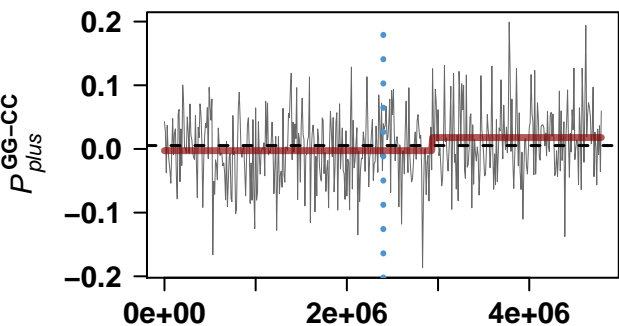
Salmonella enterica subsp. enterica serovar Typhi str. CT18



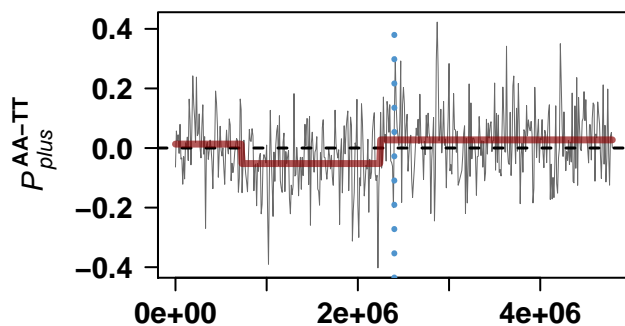
genome coordinates



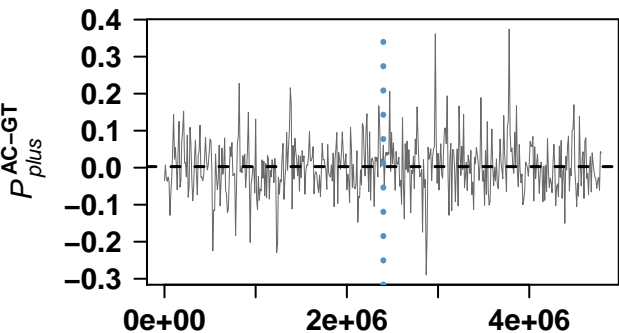
genome coordinates



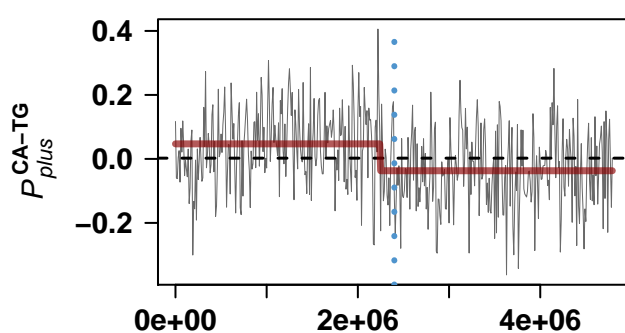
genome coordinates



genome coordinates

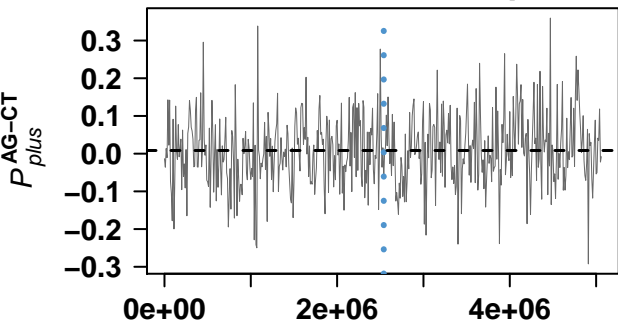


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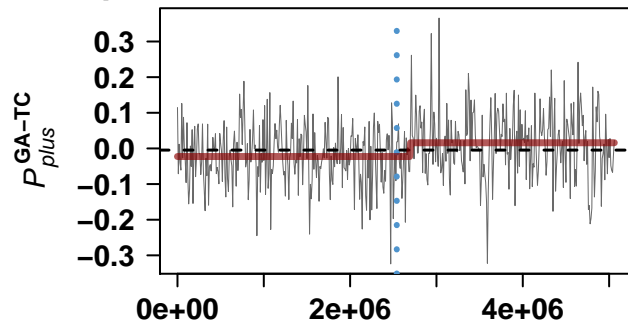


genome coordinates

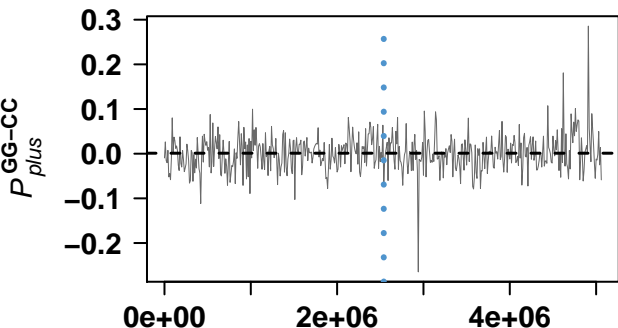
Xanthomonas campestris pv. *campestris* str. ATCC 33913



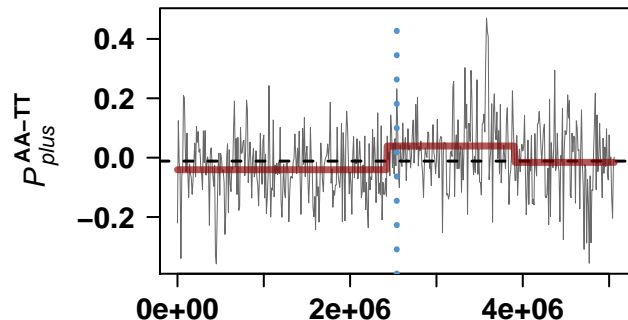
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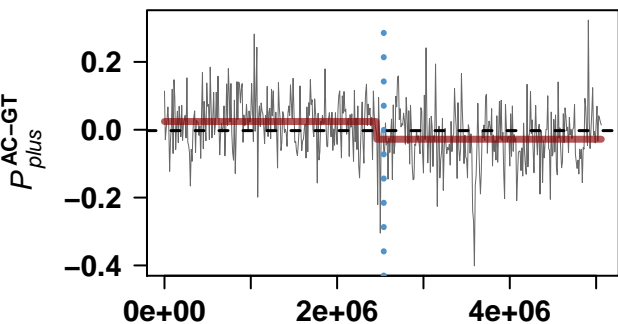
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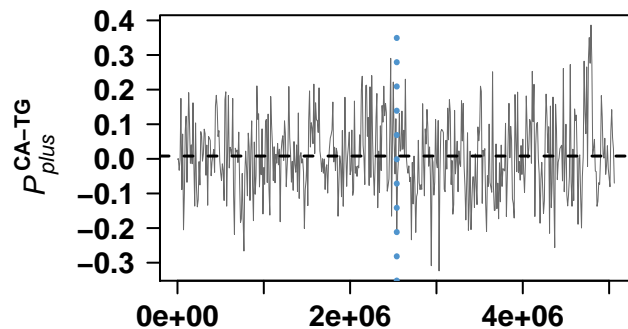
genome coordinates



genome coordinates

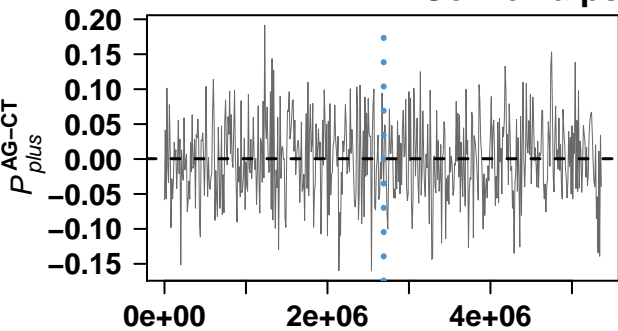


genome coordinates

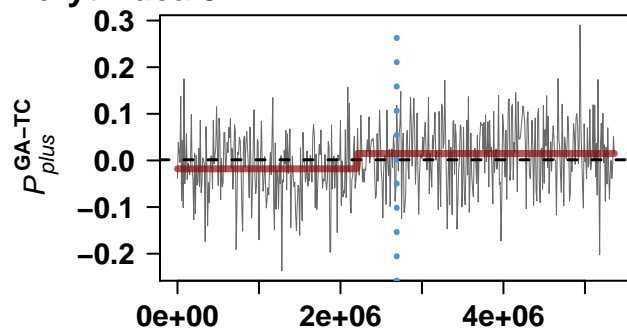


genome coordinates

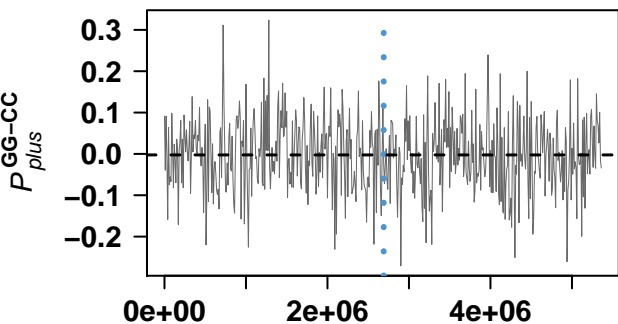
Colwellia psychrerythraea 34H



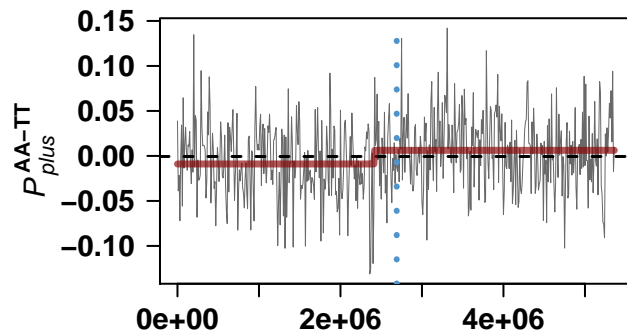
genome coordinates



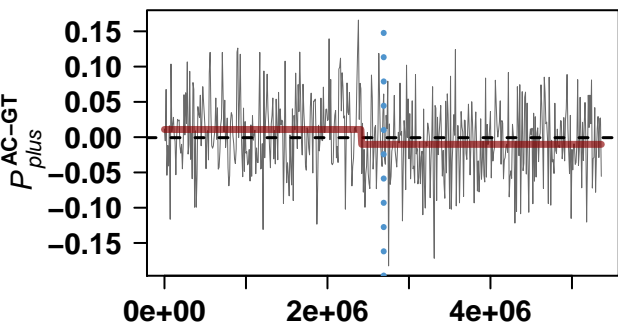
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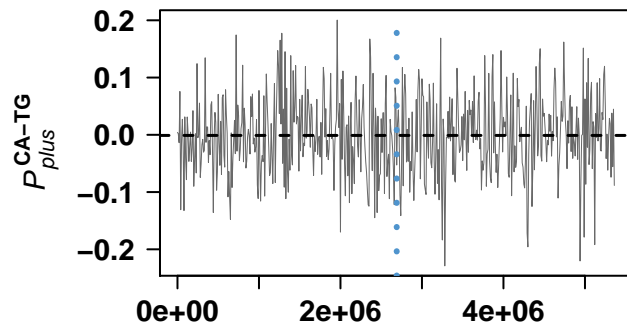
genome coordinates



genome coordinates

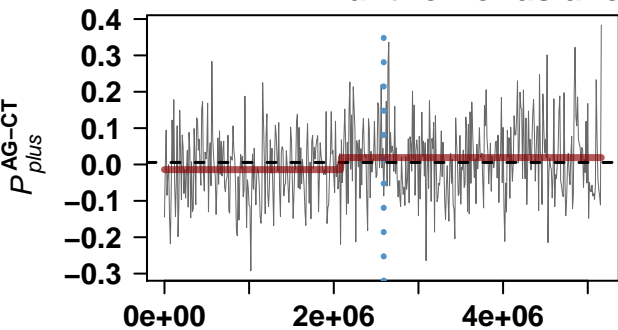


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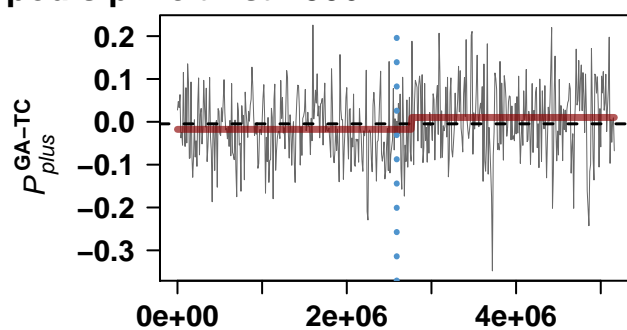


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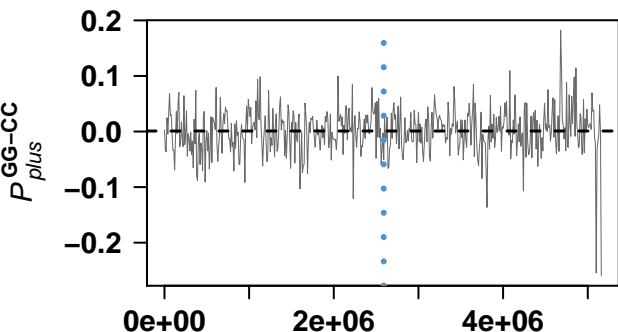
Xanthomonas axonopodis pv. citri str. 306



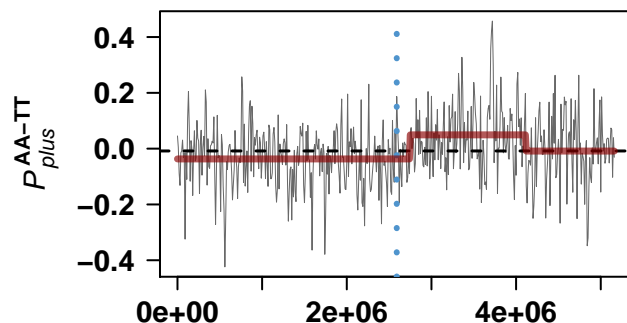
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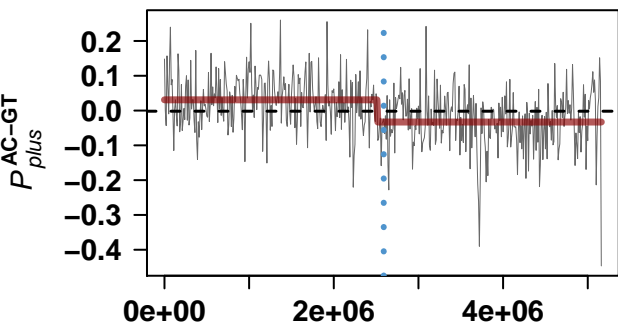
genome coordinates



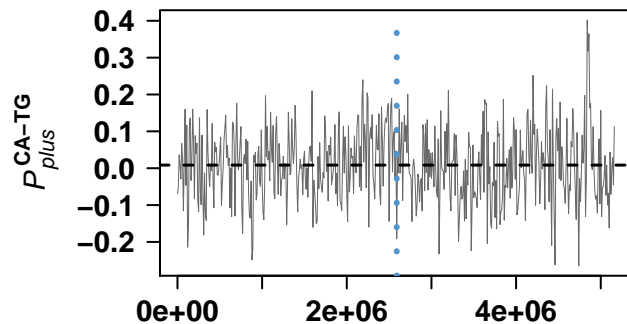
genome coordinates



genome coordinates

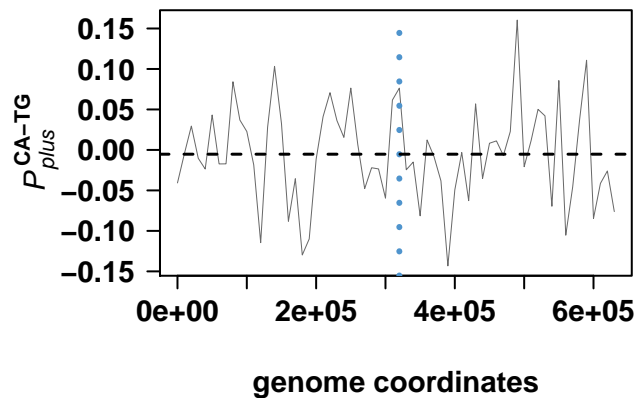
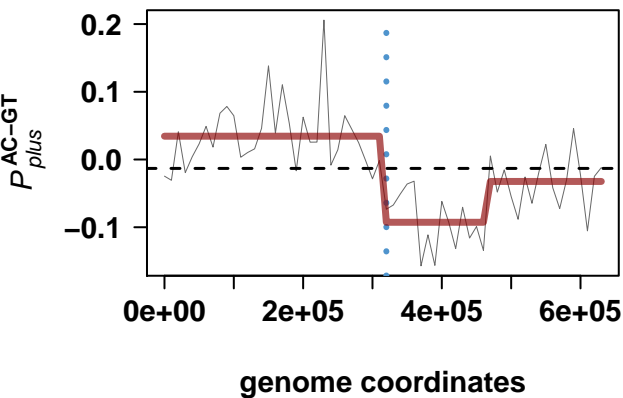
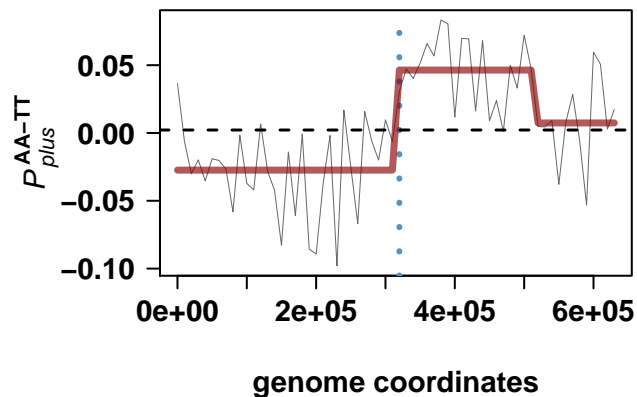
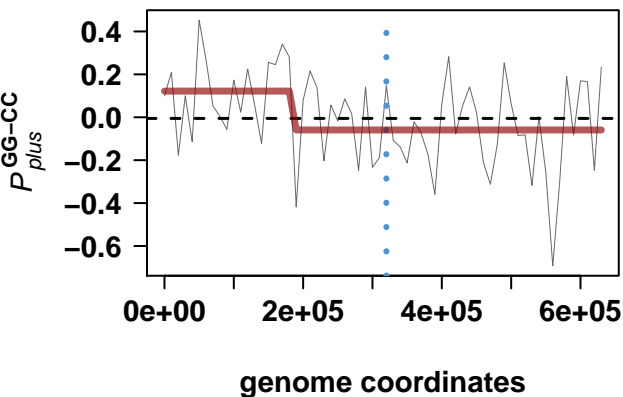
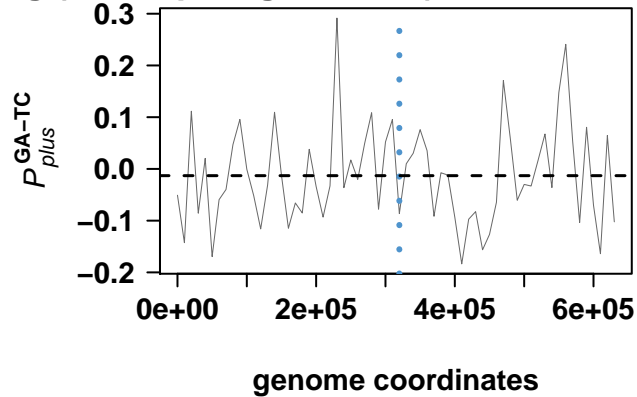
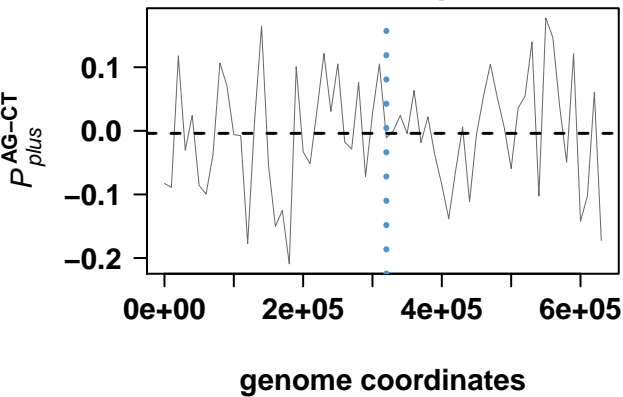


genome coordinates

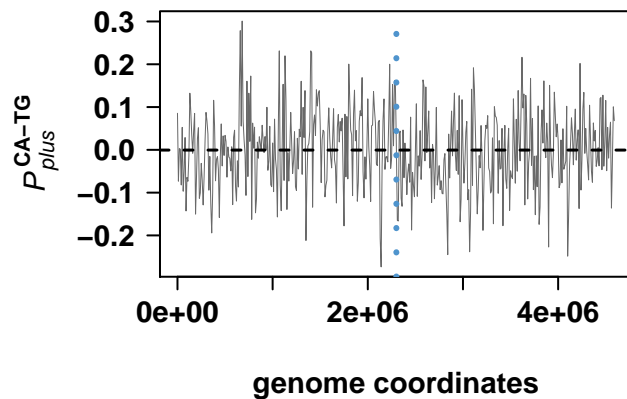
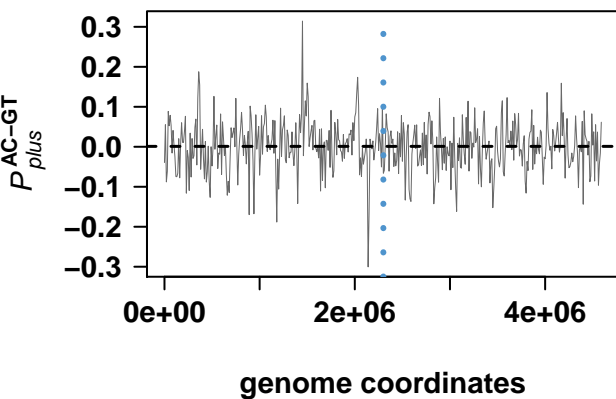
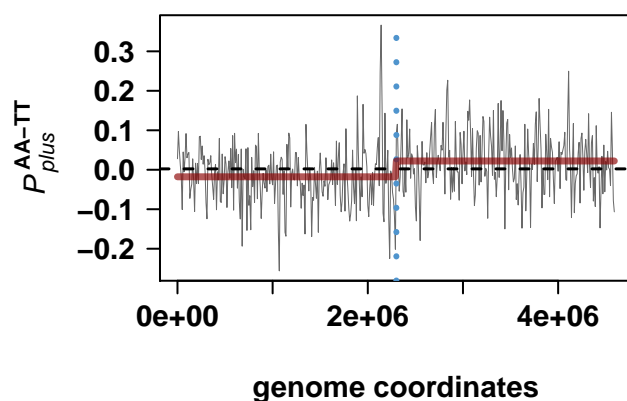
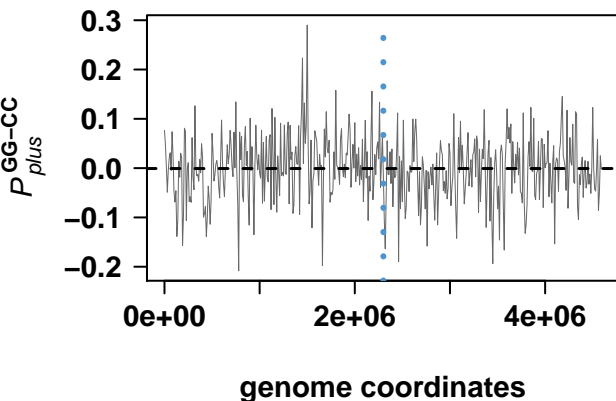
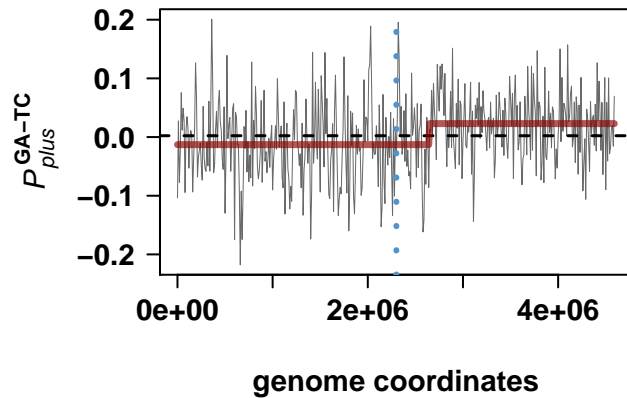
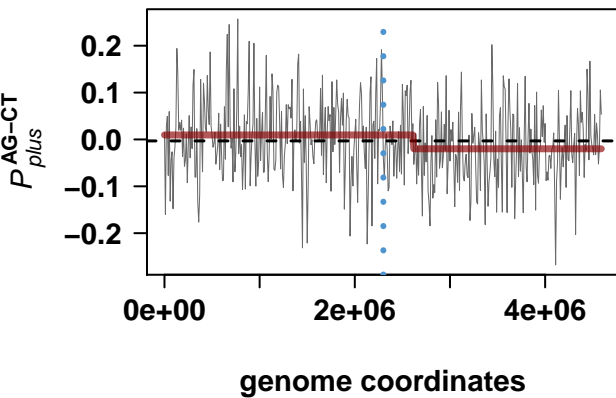


genome coordinates

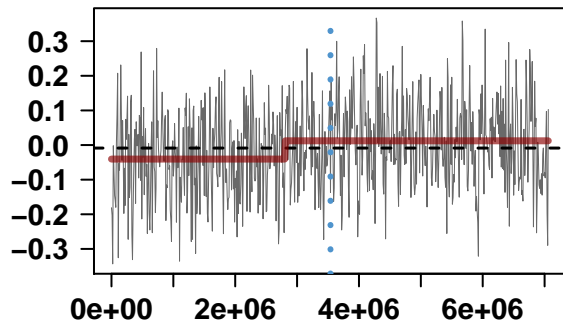
Buchnera aphidicola str. Sg (Schizaphis graminum)



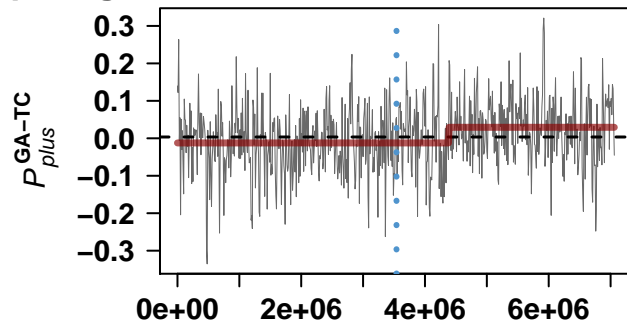
Yersinia pestis KIM10+



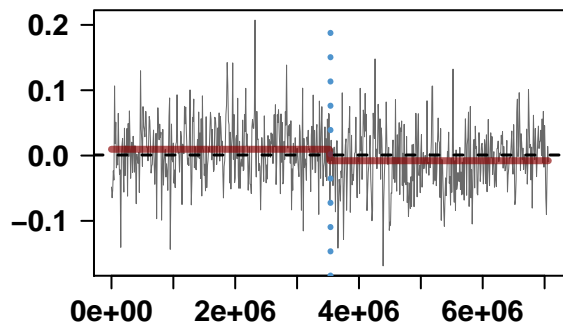
Pseudomonas protegens Pf-5



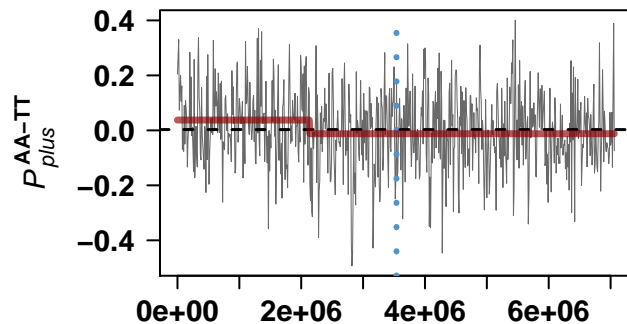
genome coordinates



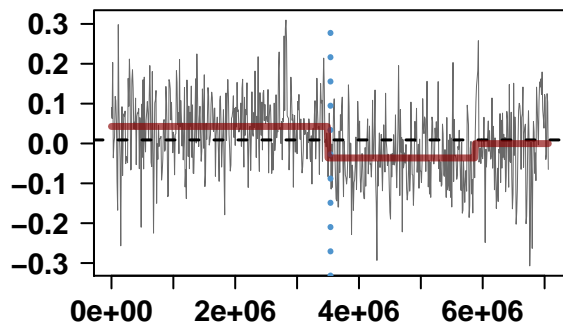
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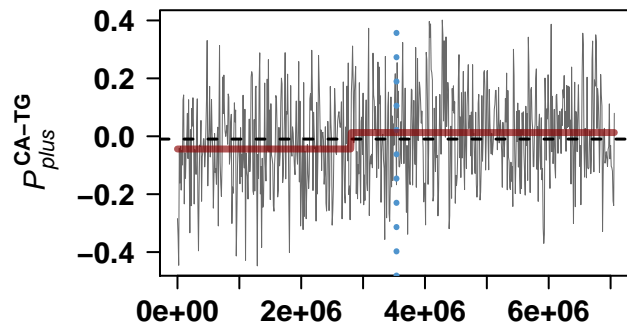
genome coordinates



genome coordinates

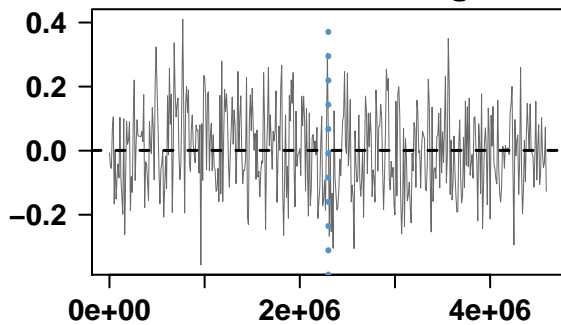


genome coordinates

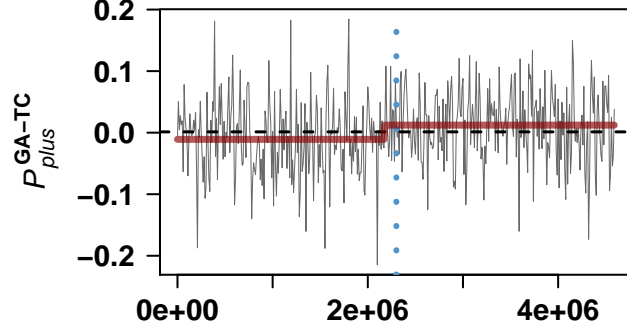


genome coordinates

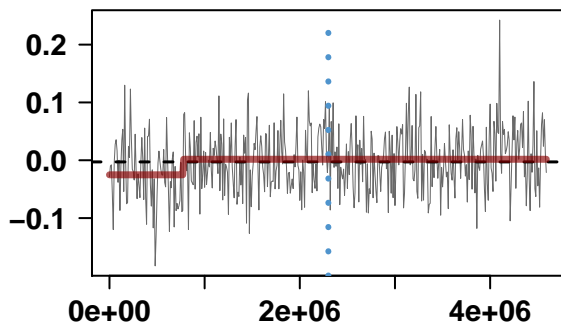
Shigella flexneri 2a str. 301



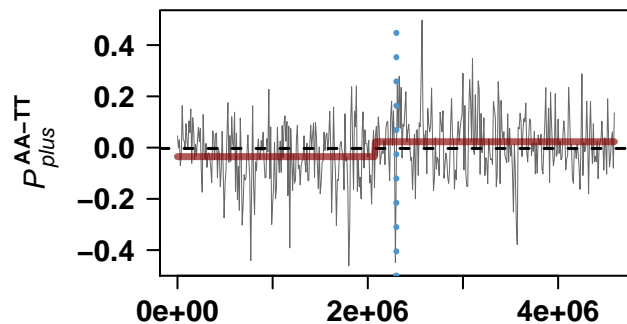
genome coordinates



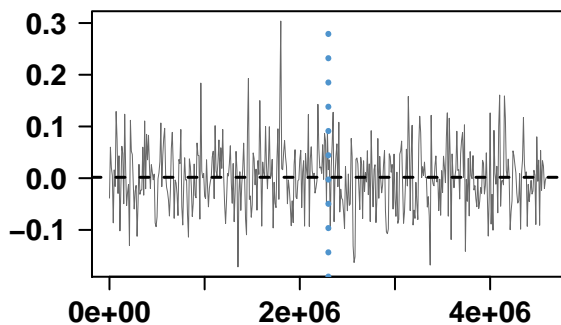
genome coordinates



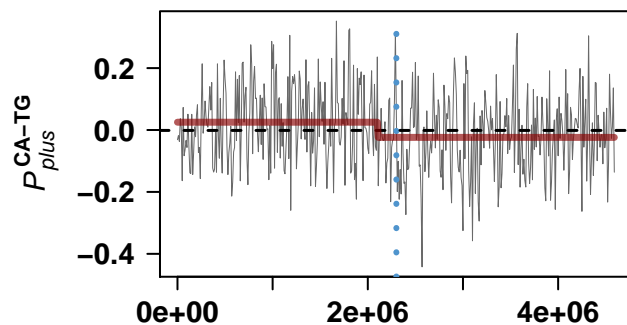
genome coordinates



genome coordinates

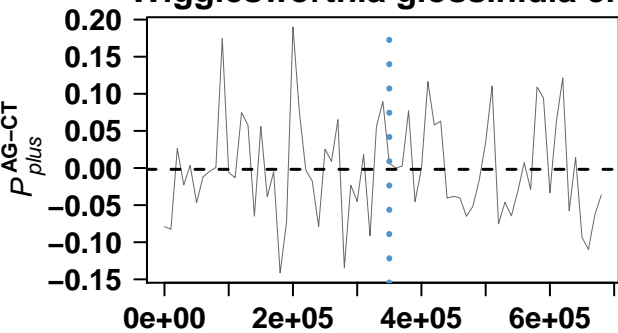


genome coordinates

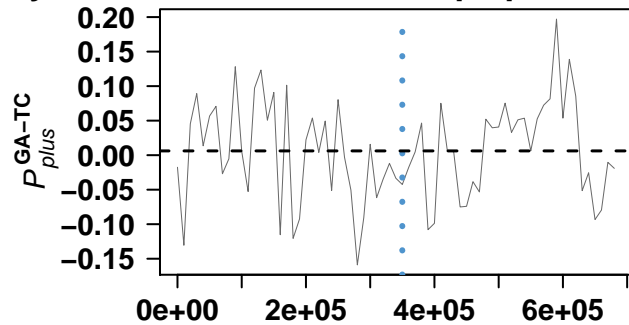


genome coordinates

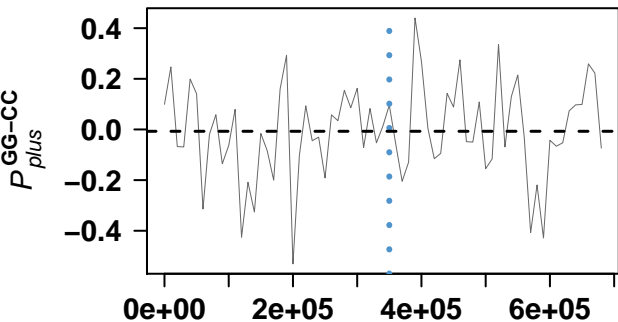
Wigglesworthia glossinidia endosymbiont of Glossina brevipalpis



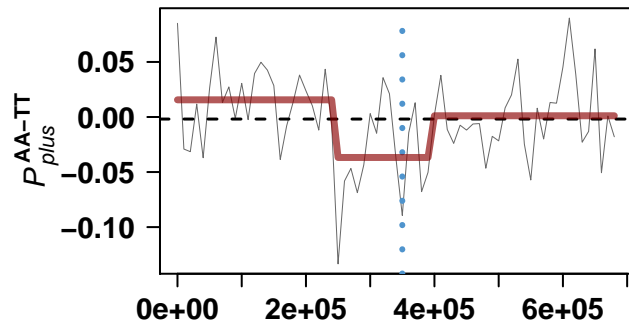
genome coordinates



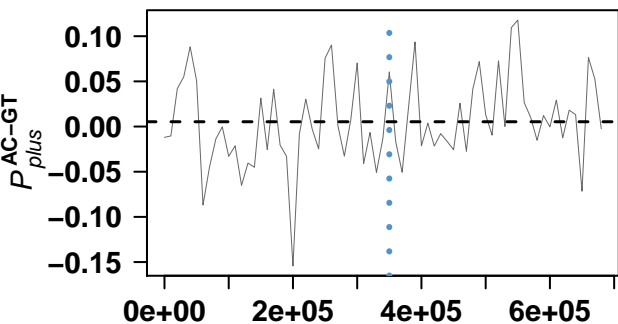
genome coordinates



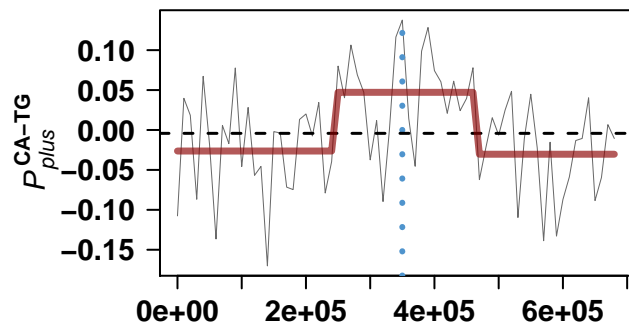
genome coordinates



genome coordinates

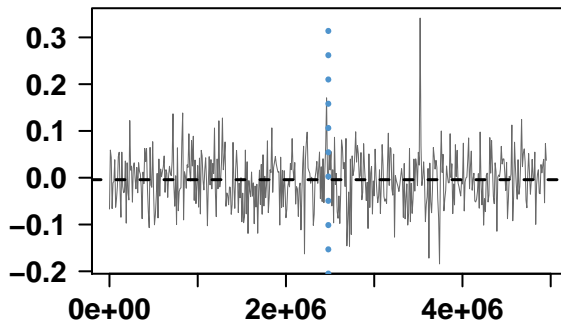


genome coordinates

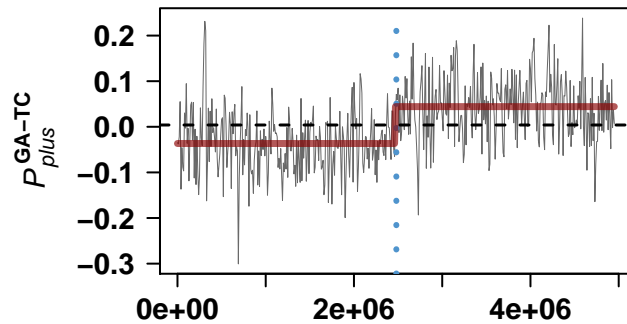


genome coordinates

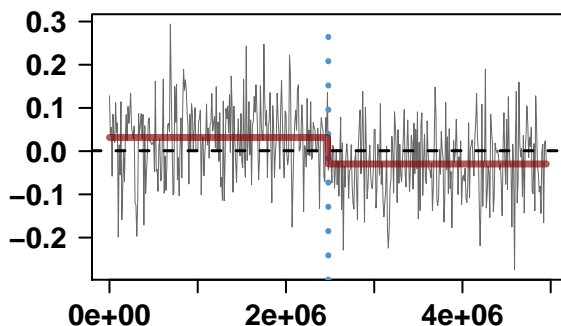
Shewanella oneidensis MR-1



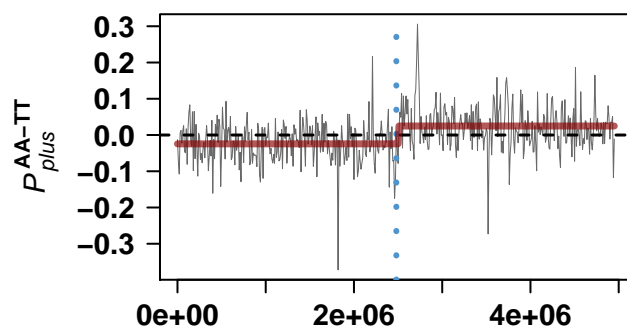
genome coordinates



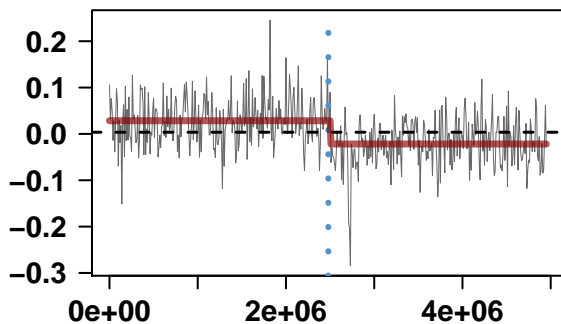
genome coordinates



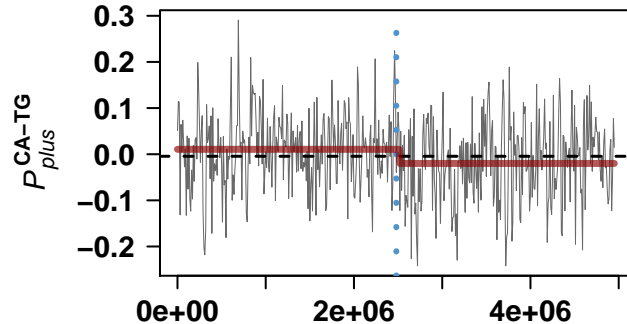
genome coordinates



genome coordinates

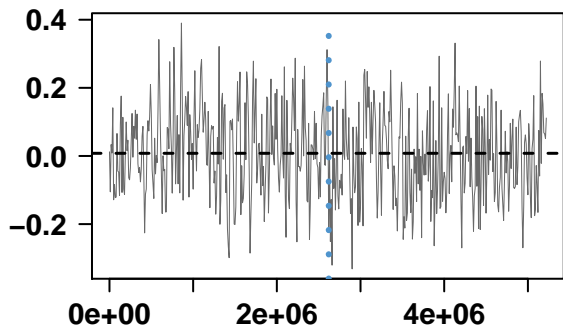


genome coordinates

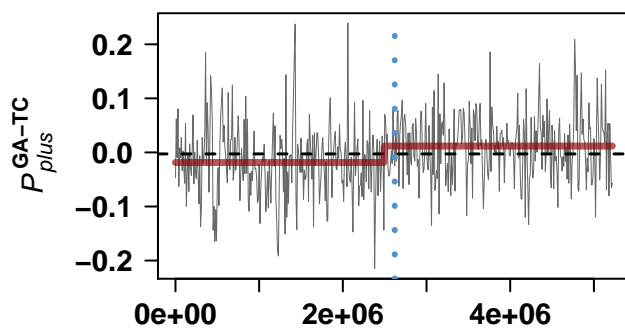


genome coordinates

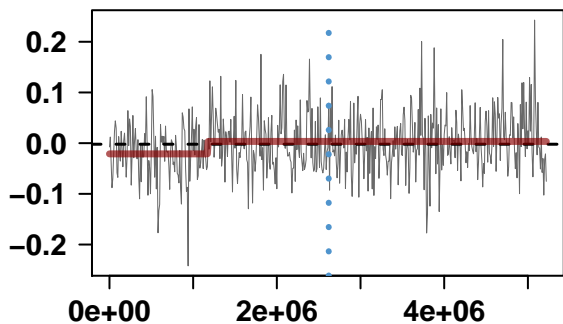
Escherichia coli CFT073



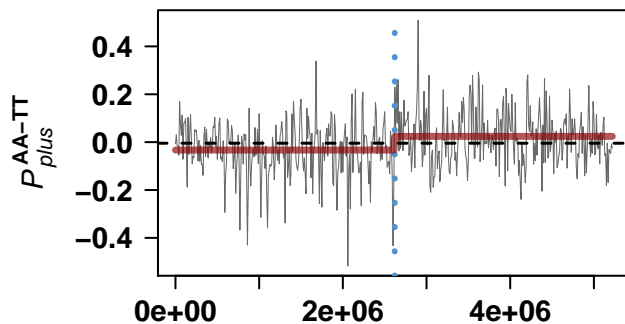
genome coordinates



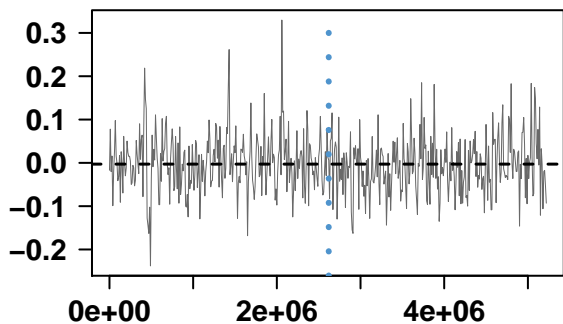
genome coordinates



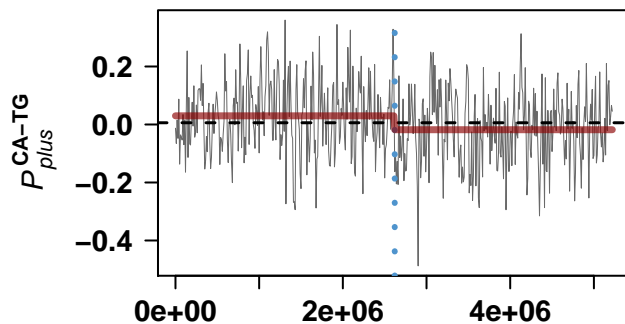
genome coordinates



genome coordinates

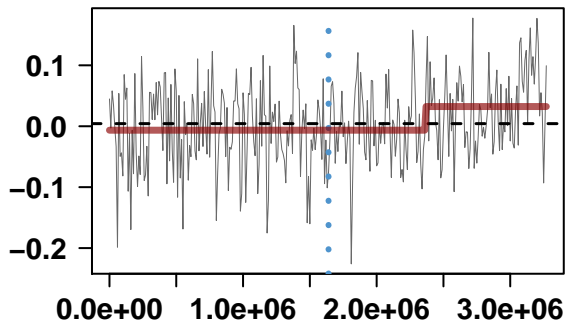


genome coordinates

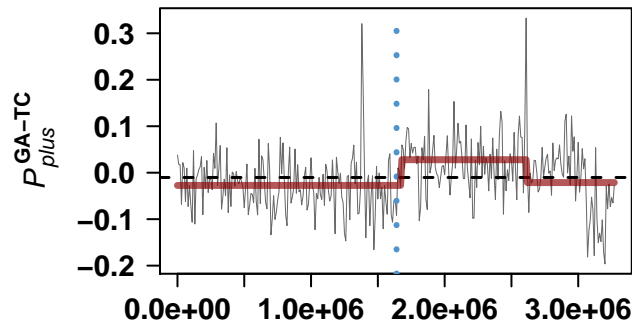


genome coordinates

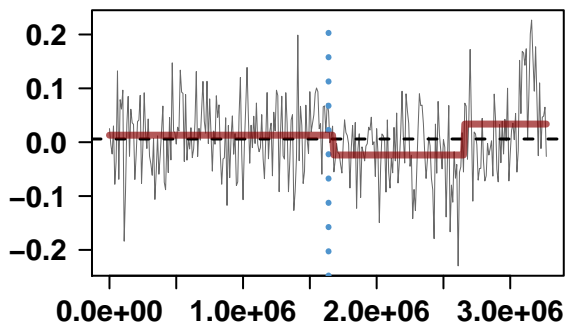
Vibrio vulnificus CMCP6



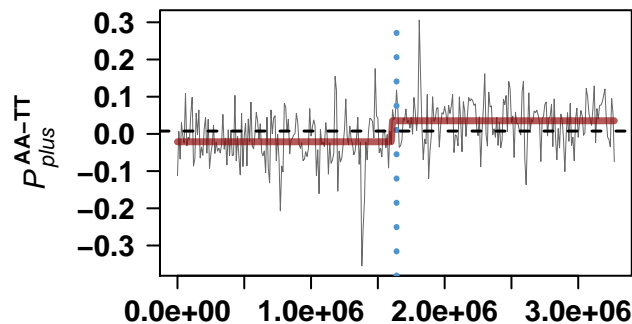
genome coordinates



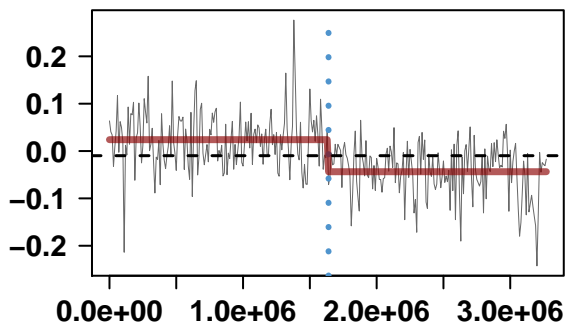
genome coordinates



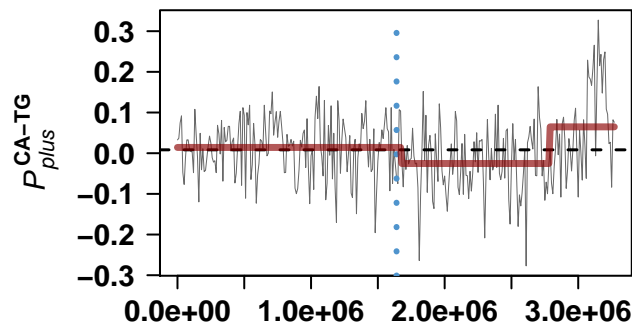
genome coordinates



genome coordinates

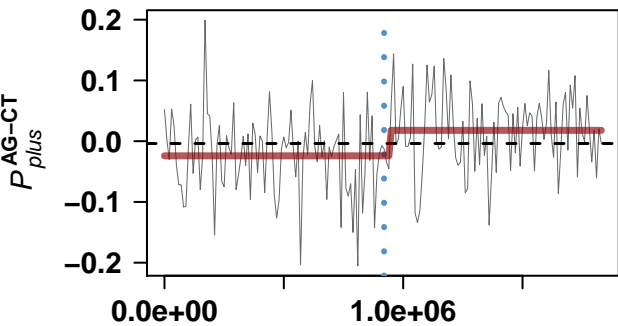


genome coordinates

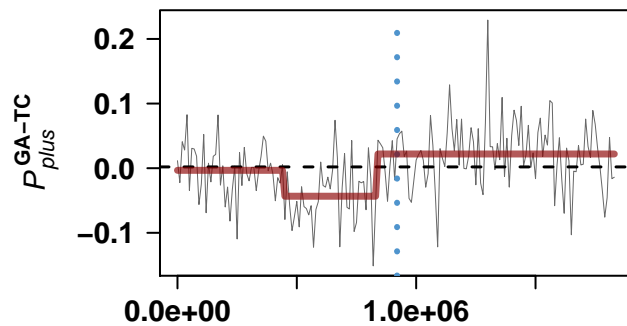


genome coordinates

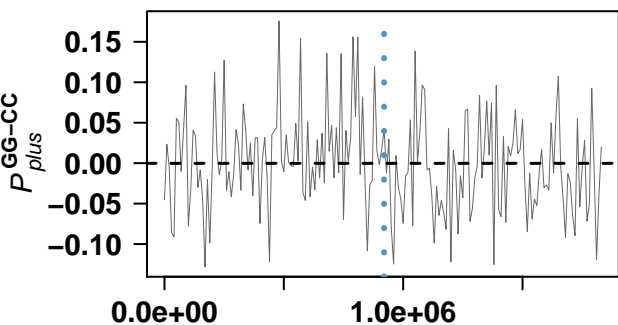
Vibrio vulnificus CMCP6



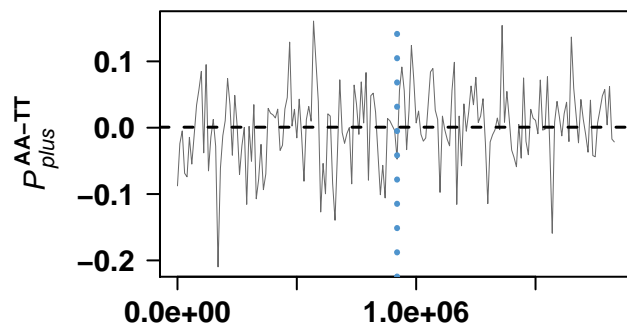
genome coordinates



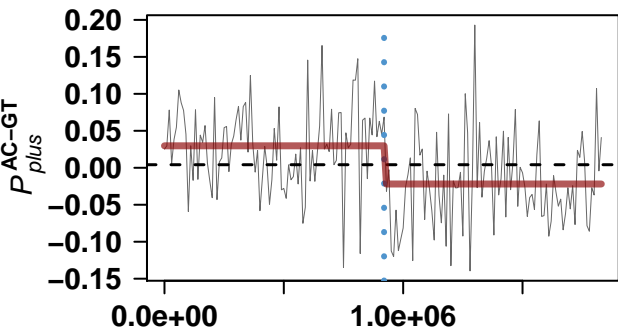
genome coordinates



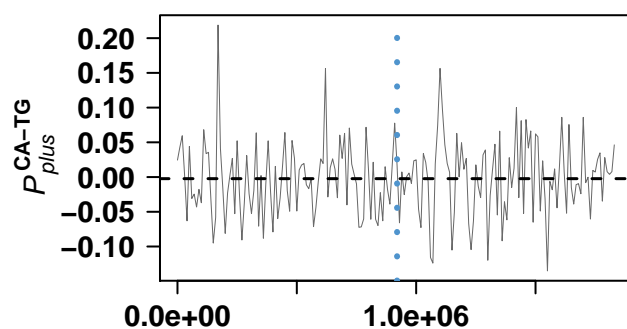
genome coordinates



genome coordinates

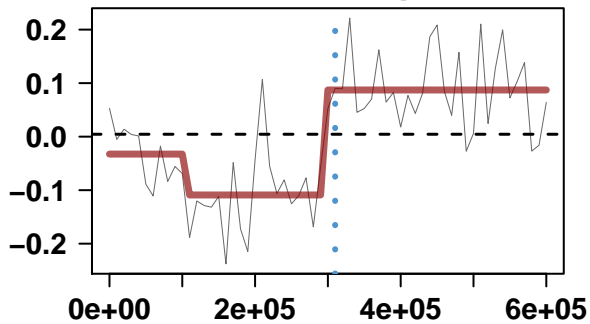


genome coordinates

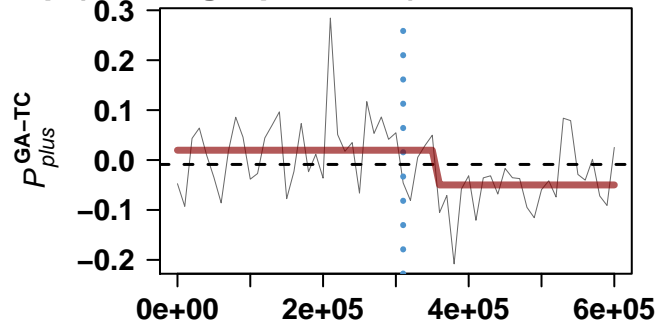


genome coordinates

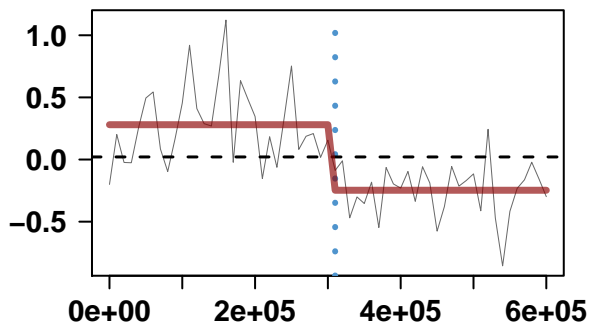
Buchnera aphidicola str. Bp (Baizongia pistaciae)



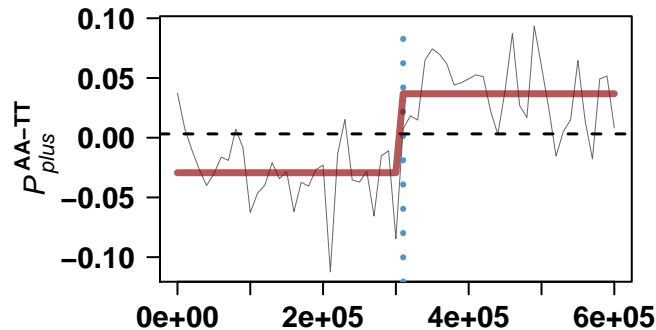
genome coordinates



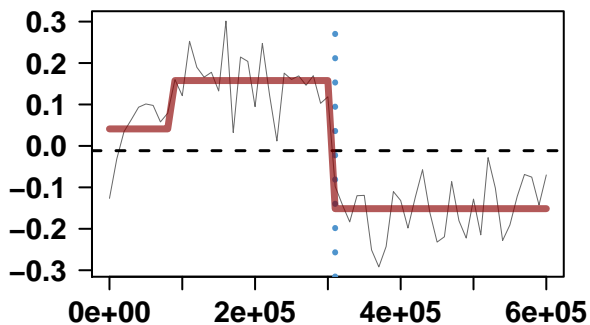
genome coordinates



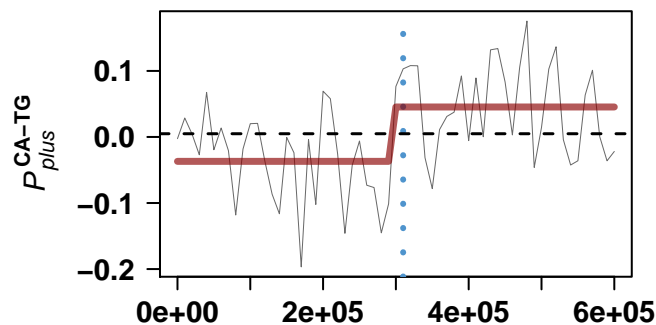
genome coordinates



genome coordinates

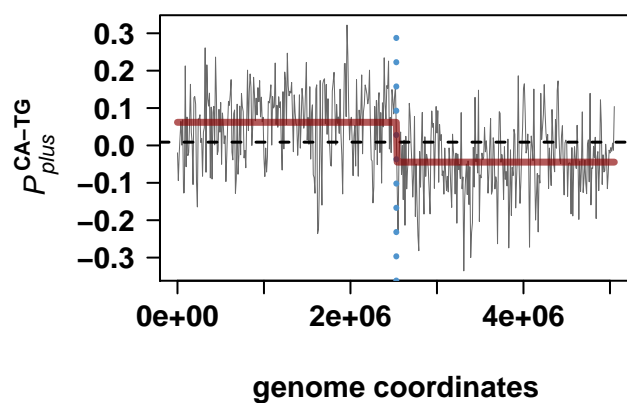
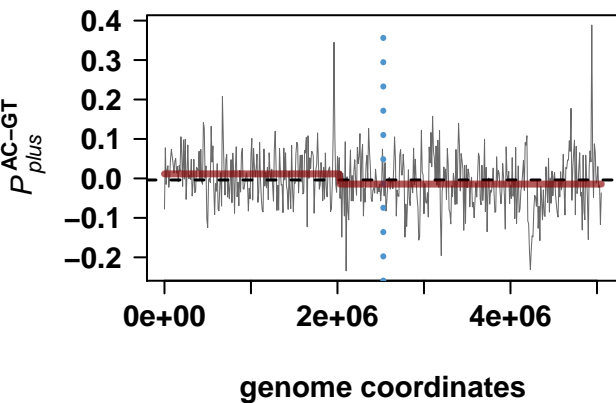
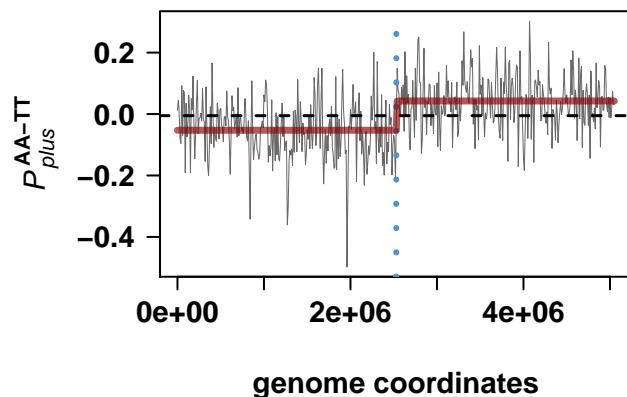
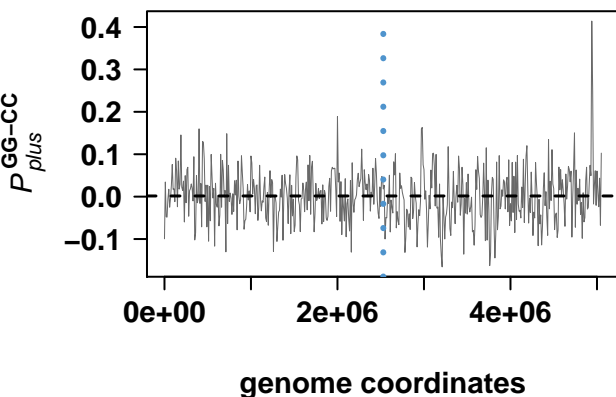
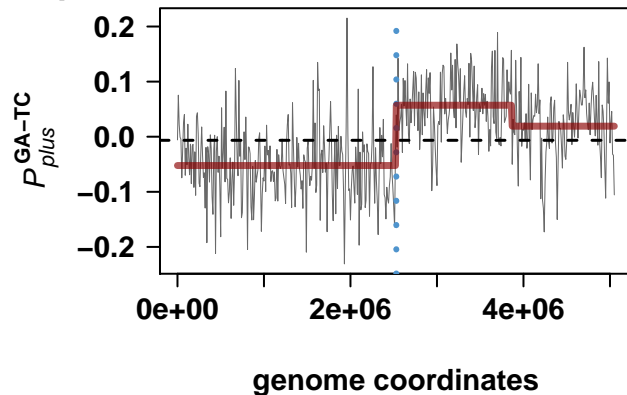
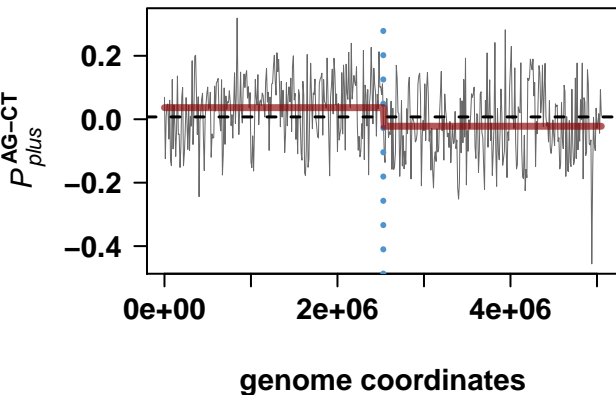


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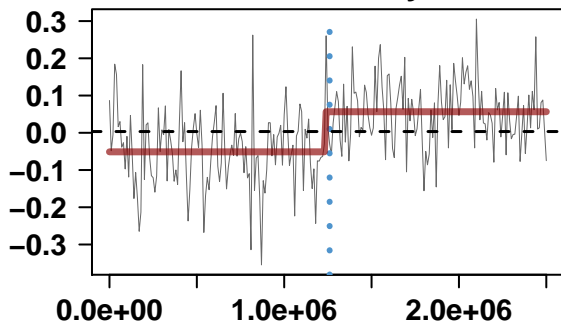


genome coordinates

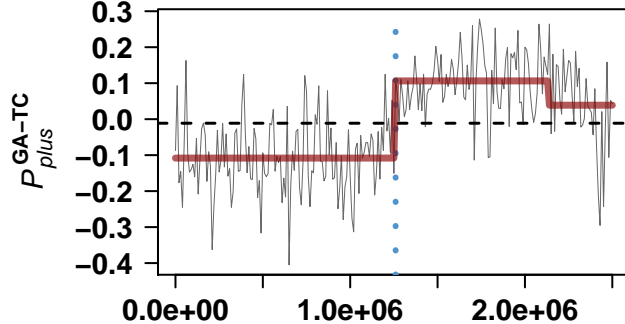
Pectobacterium atrosepticum SCRI1043



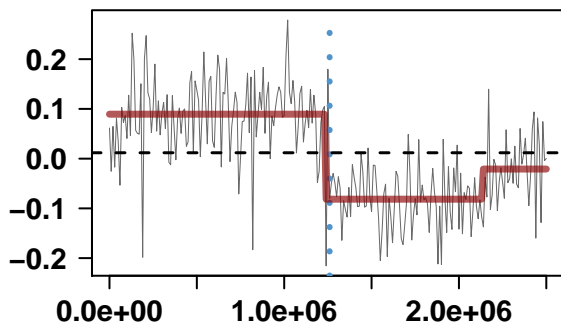
Xylella fastidiosa Temecula1



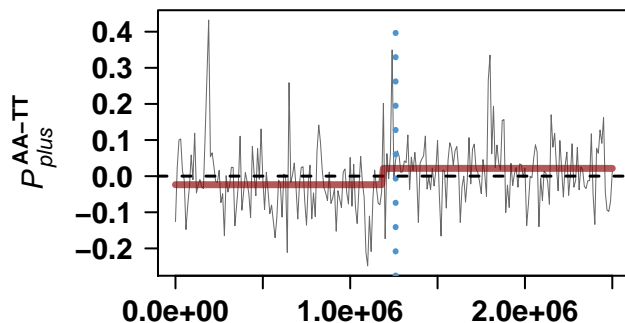
genome coordinates



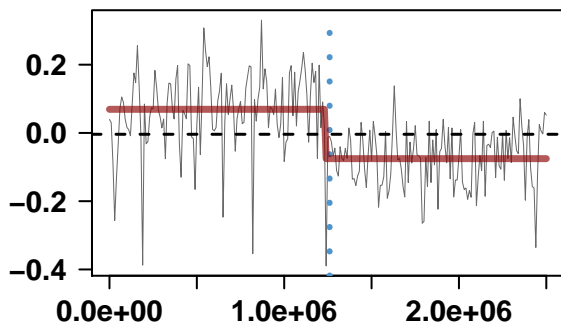
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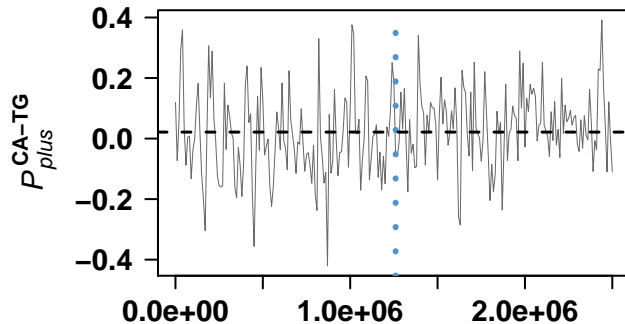
genome coordinates



genome coordinates

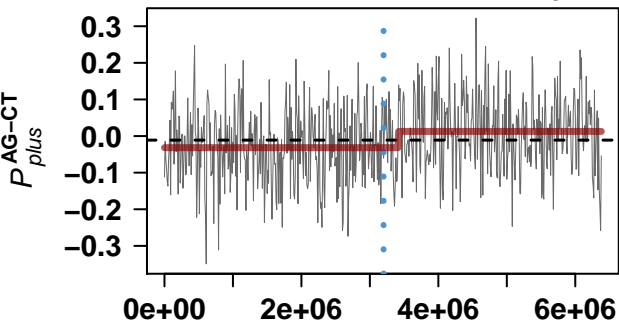


genome coordinates

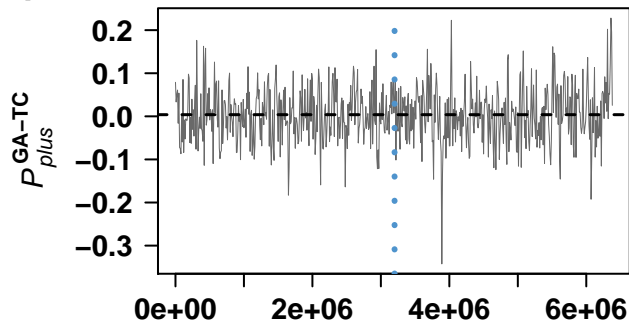


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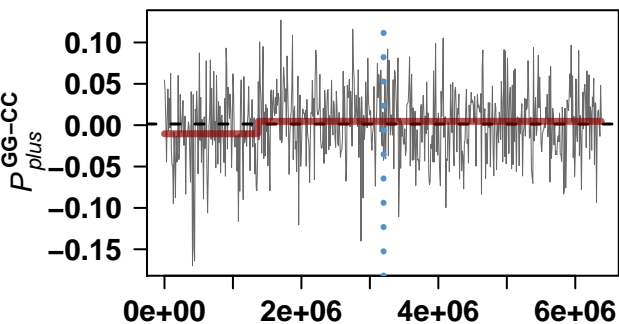
Pseudomonas syringae pv. *tomato* str. DC3000



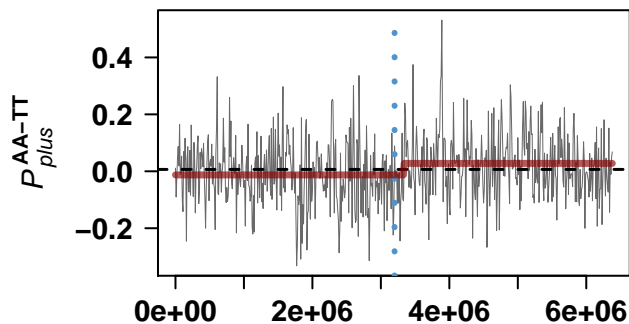
genome coordinates



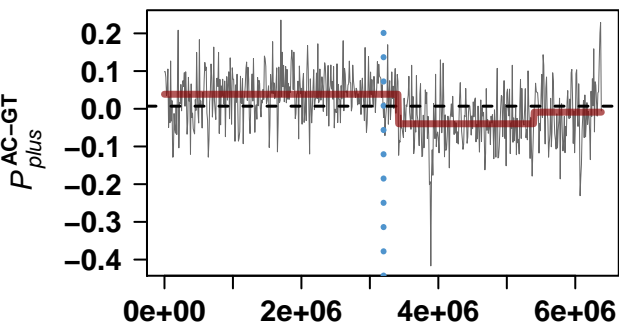
genome coordinates



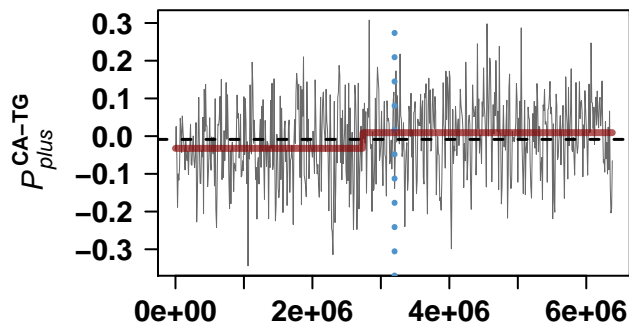
genome coordinates



genome coordinates

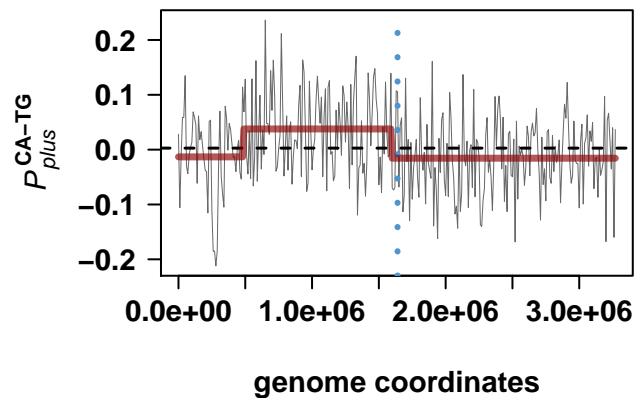
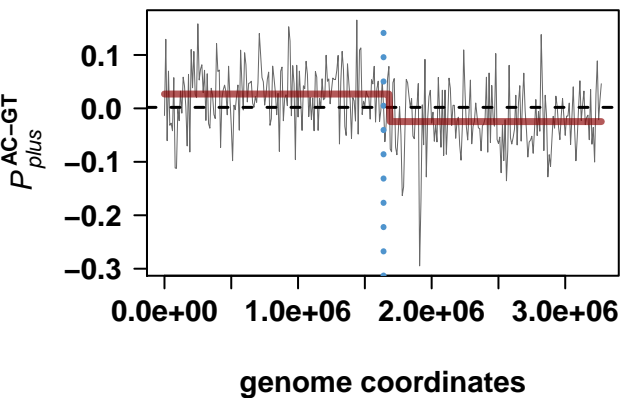
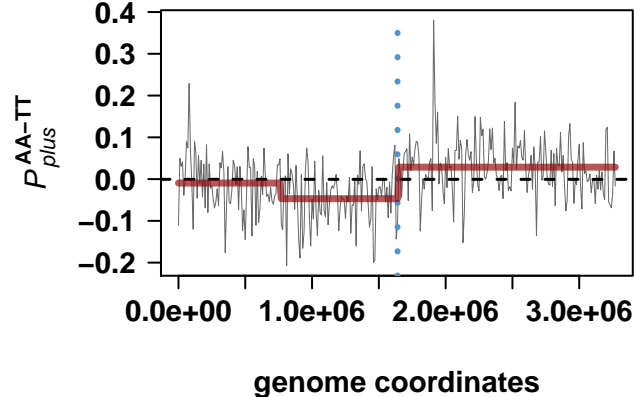
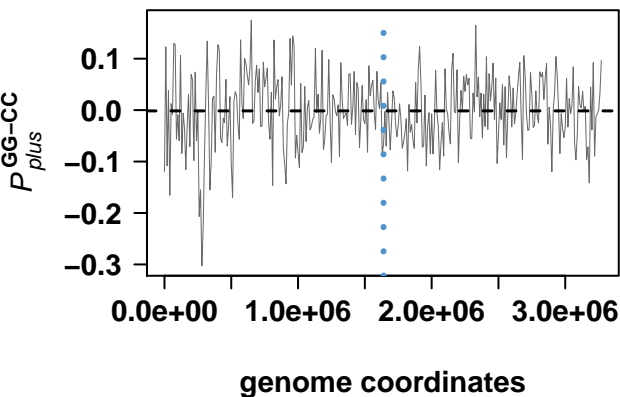
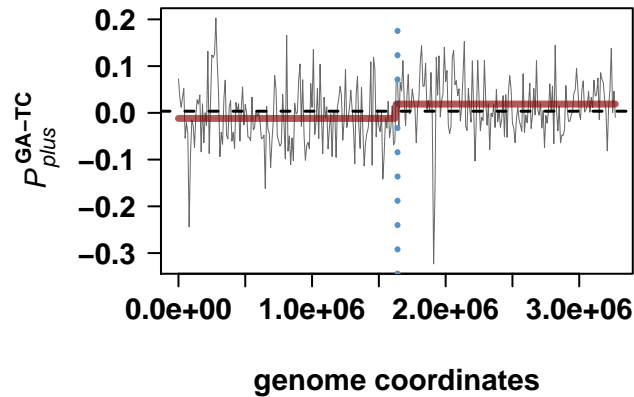
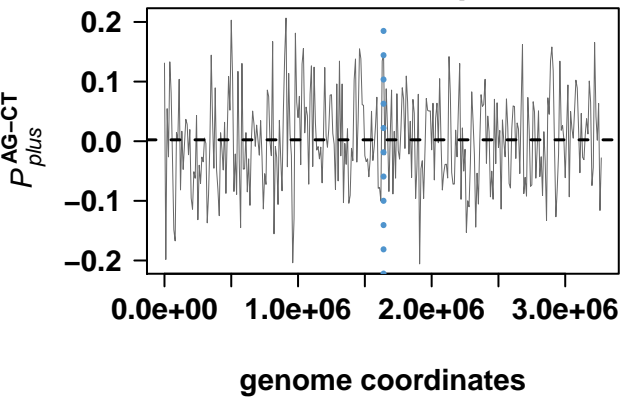


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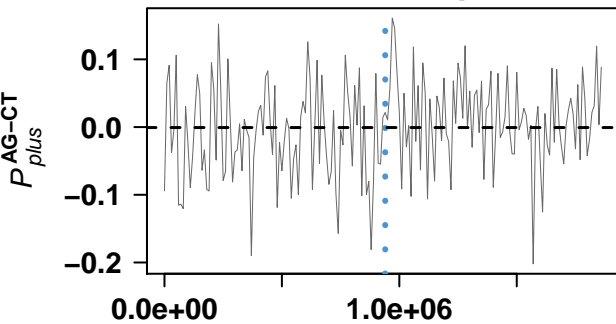


genome coordinates

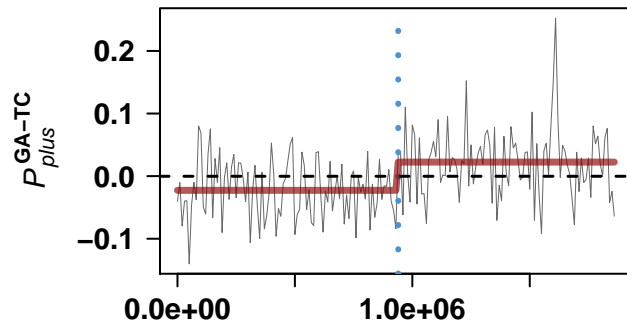
Vibrio parahaemolyticus RIMD 2210633



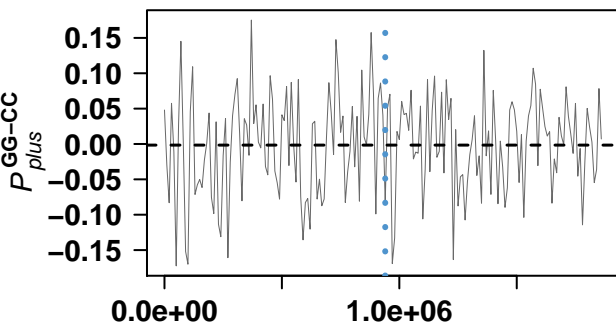
Vibrio parahaemolyticus RIMD 2210633



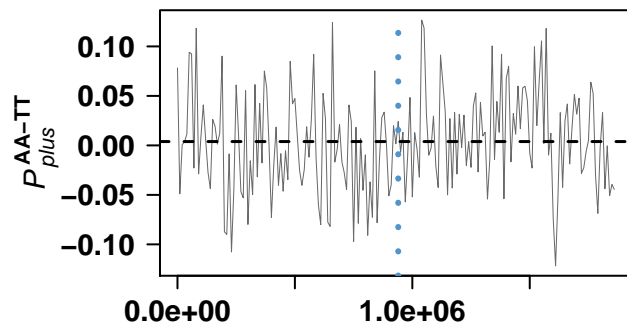
genome coordinates



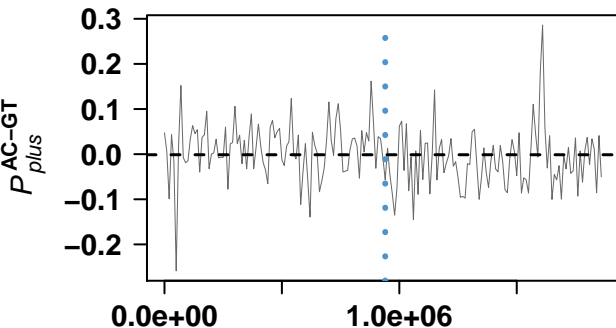
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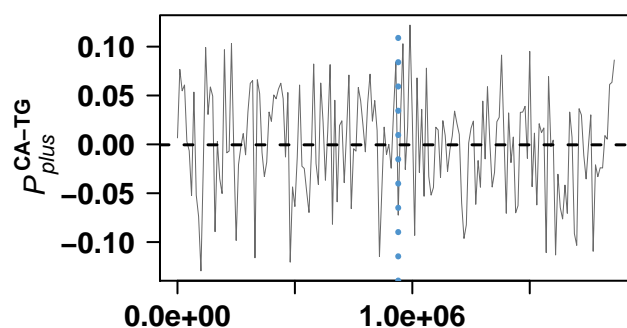
genome coordinates



genome coordinates

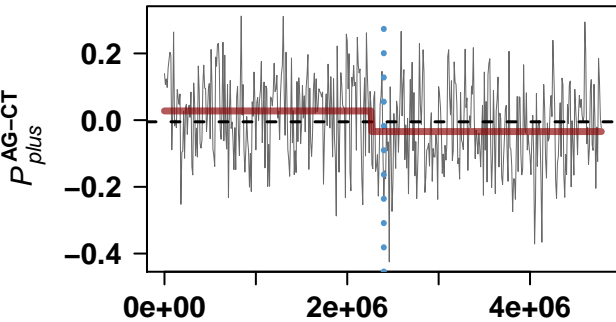


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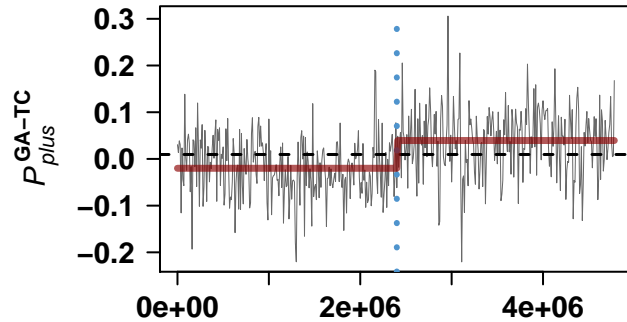


genome coordinates

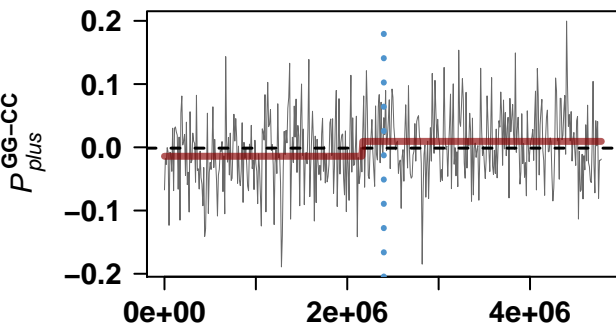
Salmonella enterica subsp. enterica serovar Typhi str. Ty2



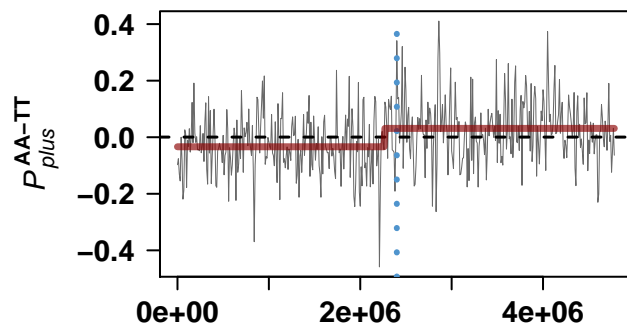
genome coordinates



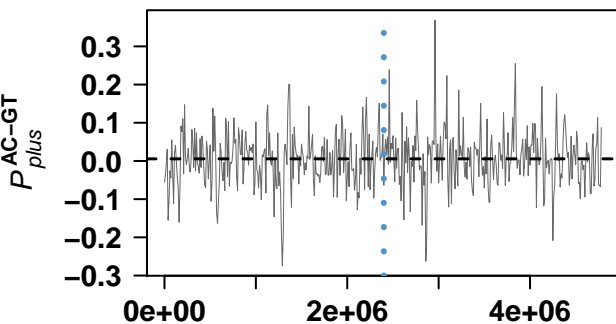
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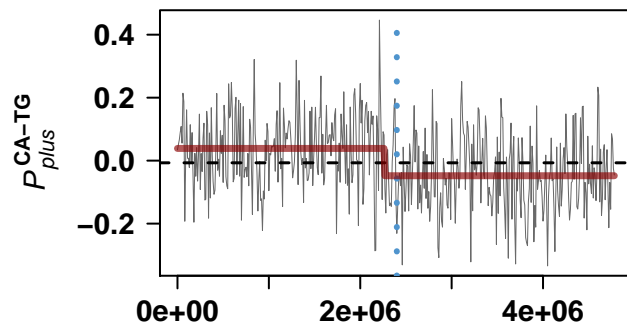
genome coordinates



genome coordinates

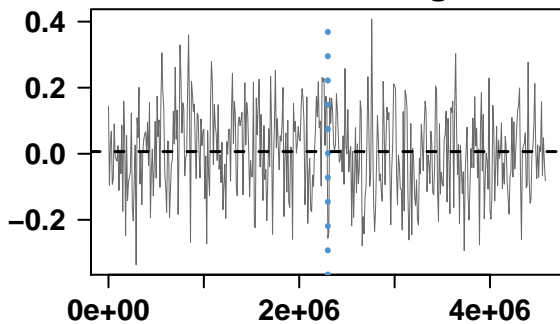


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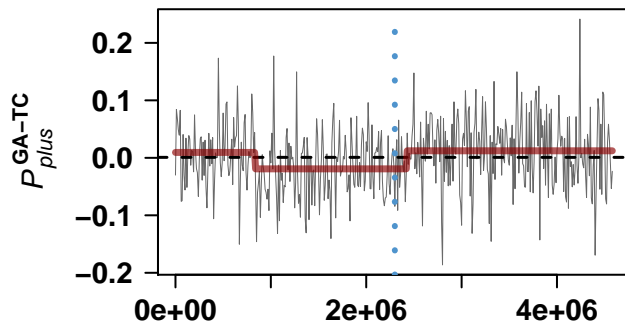


genome coordinates

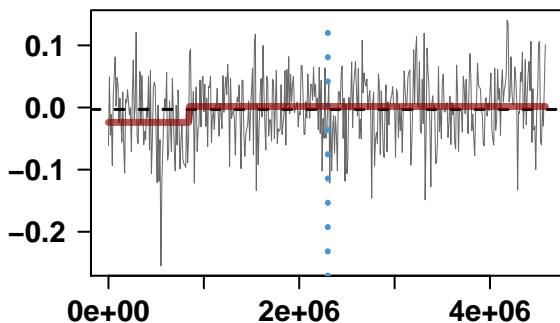
Shigella flexneri 2a str. 2457T



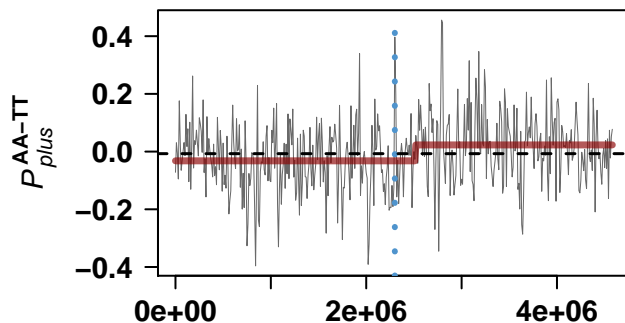
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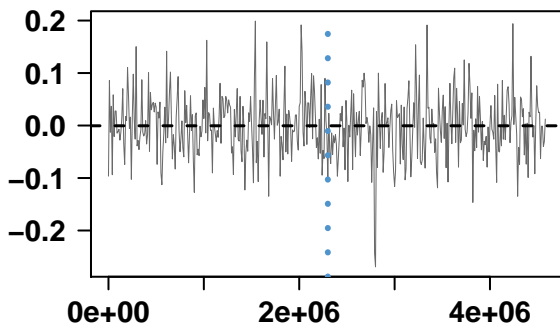
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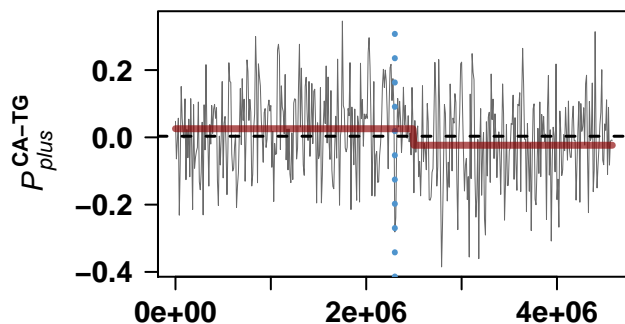
genome coordinates



genome coordinates

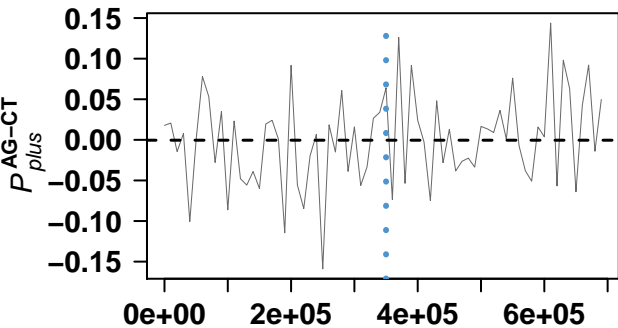


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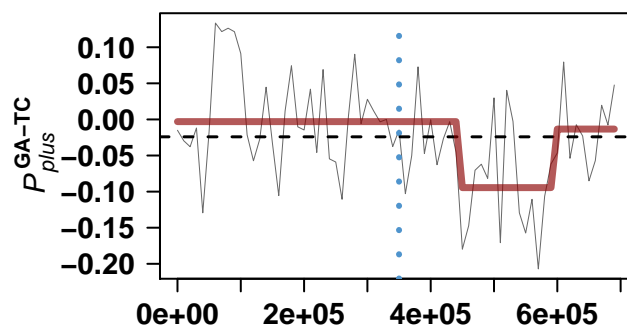


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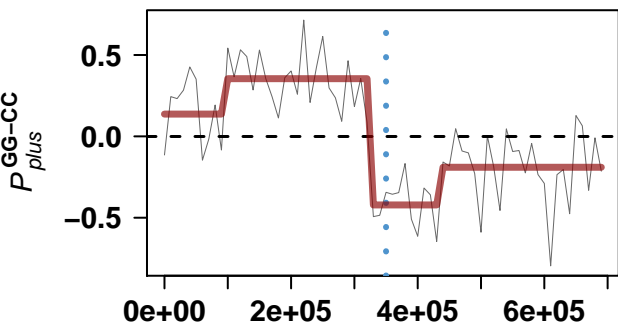
Candidatus Blochmannia floridanus



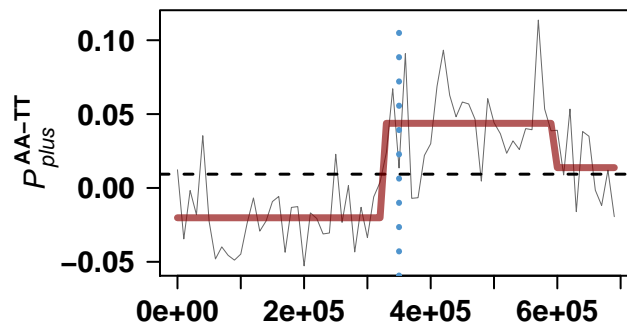
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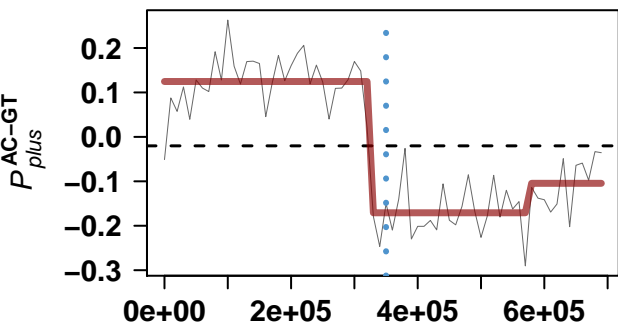
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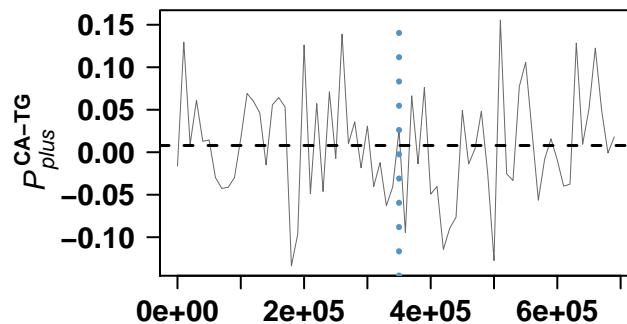
genome coordinates



genome coordinates

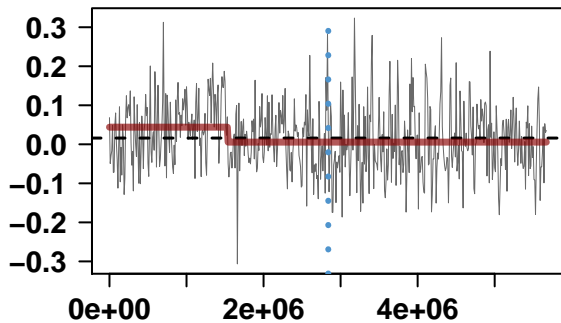


genome coordinates

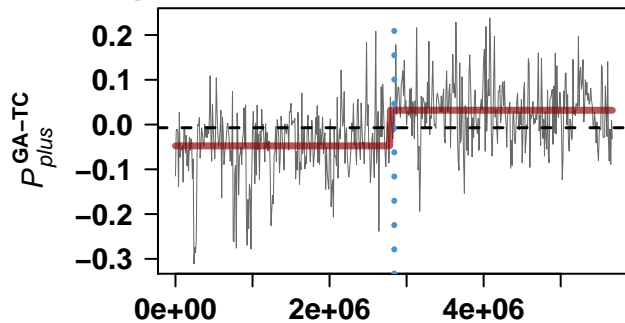


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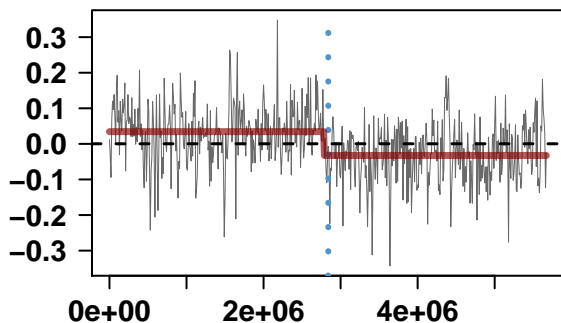
Photorhabdus luminescens subsp. laumondii TTO1



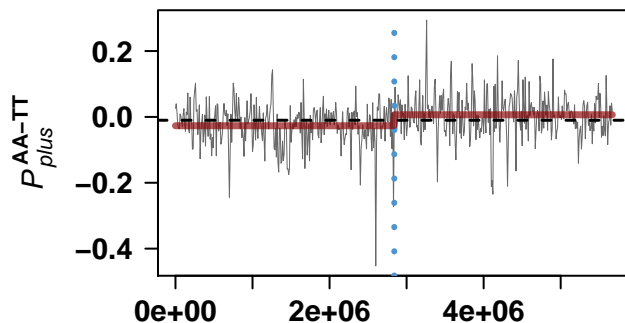
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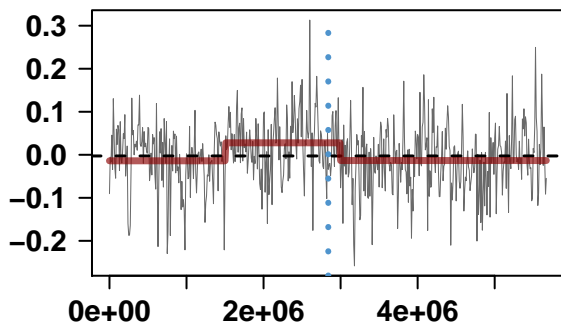
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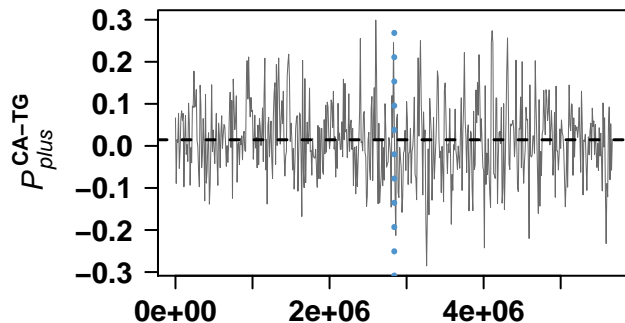
genome coordinates



genome coordinates

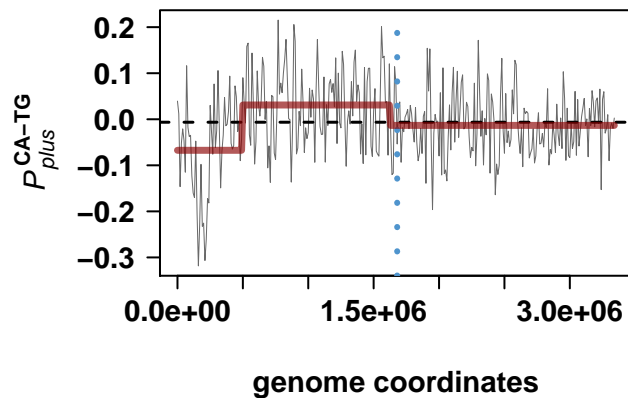
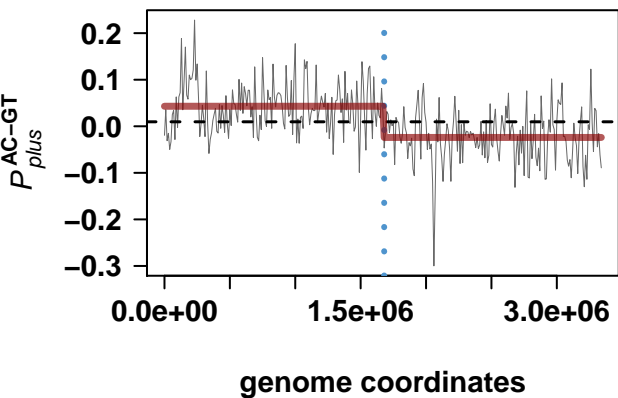
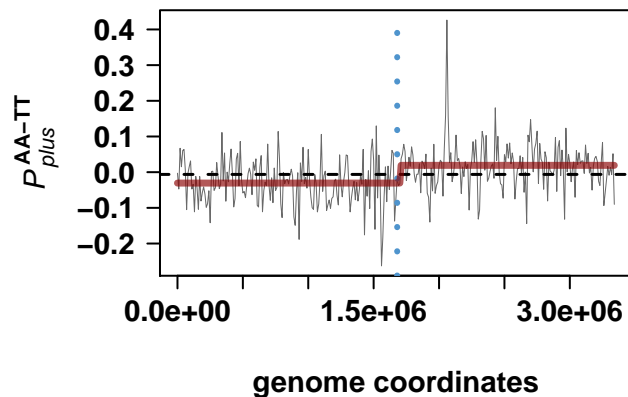
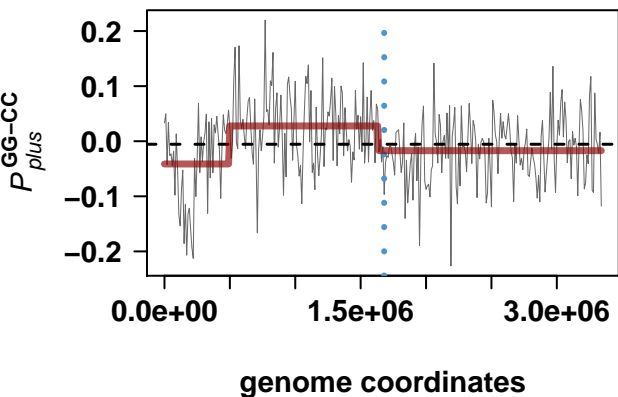
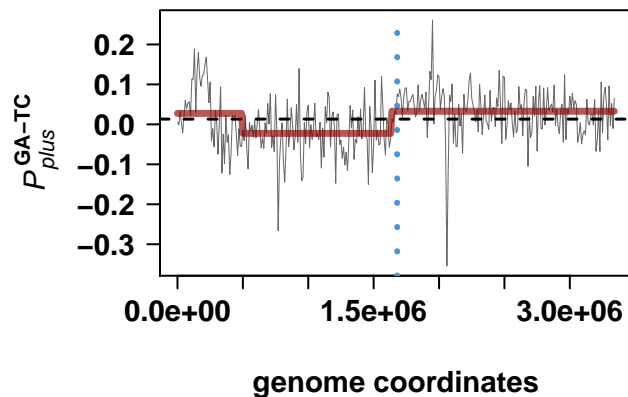
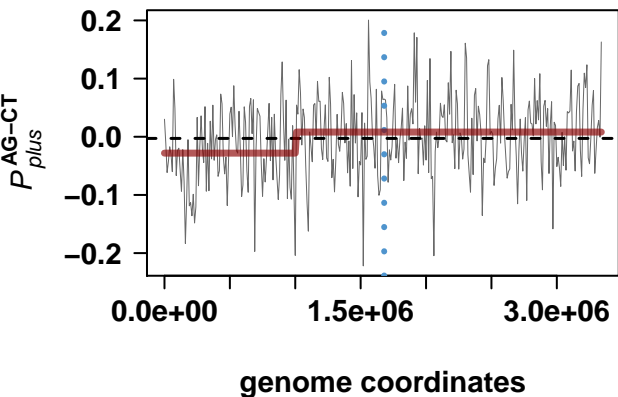


genome coordinates

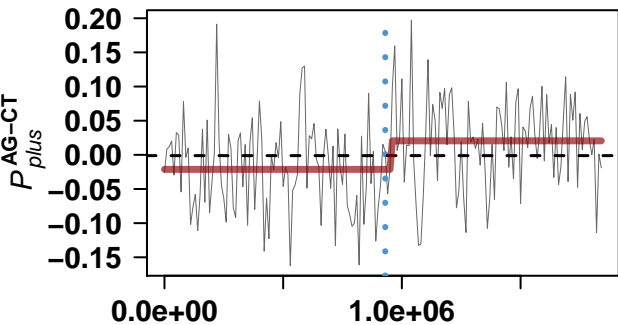


genome coordinates

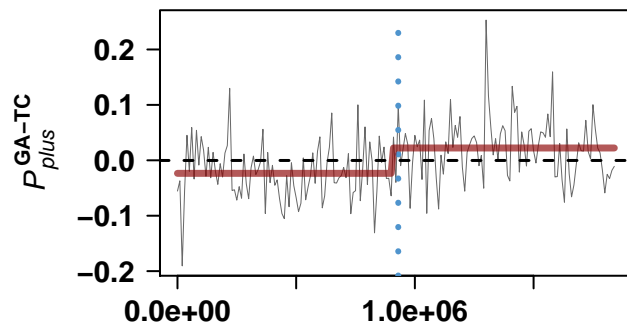
Vibrio vulnificus YJ016



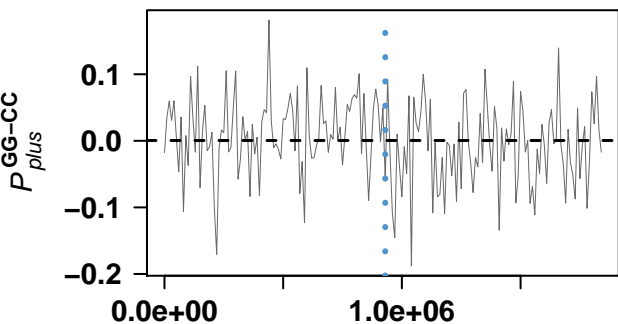
Vibrio vulnificus YJ016



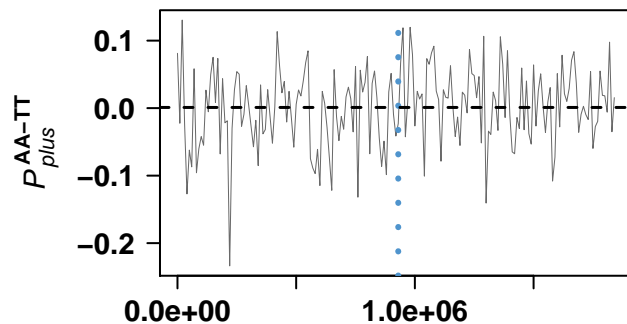
genome coordinates



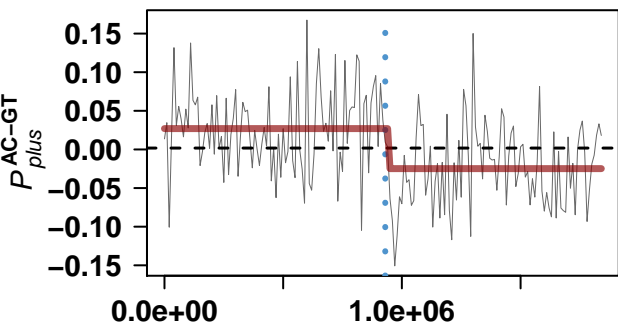
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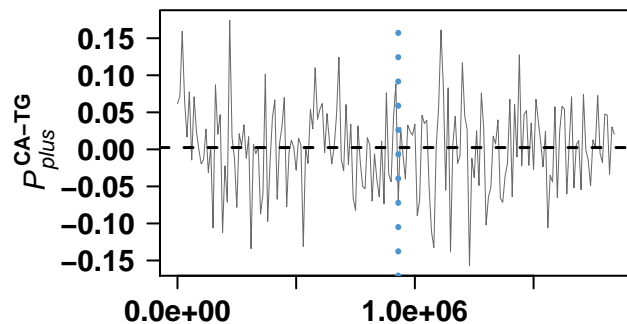
genome coordinates



genome coordinates

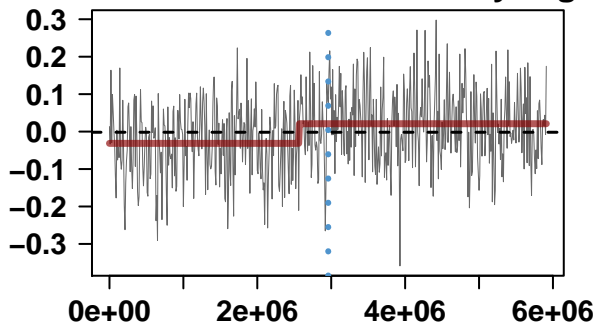


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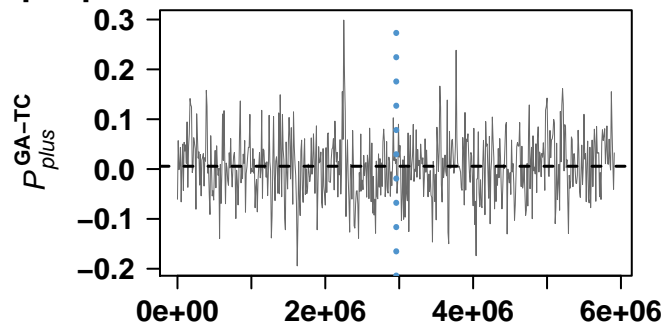


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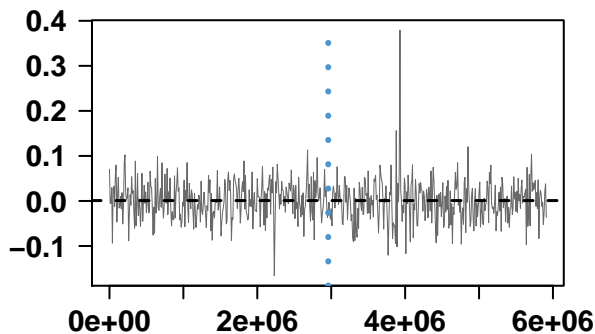
Pseudomonas syringae pv. *phaseolicola* 1448A



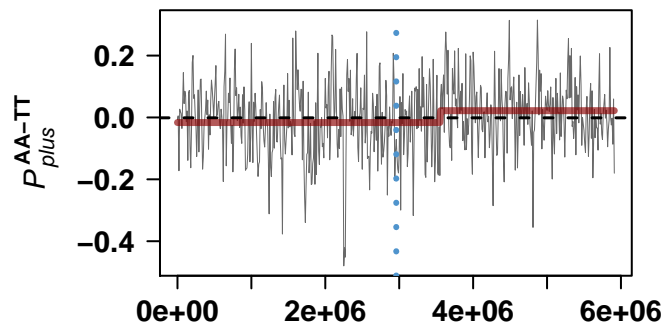
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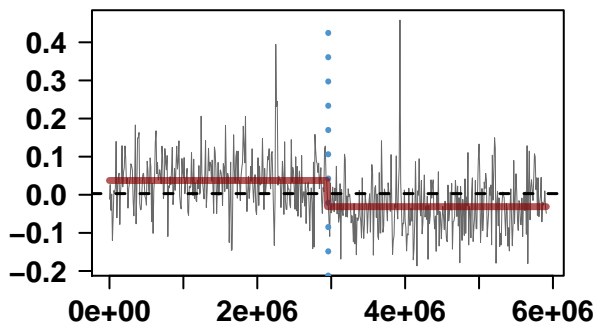
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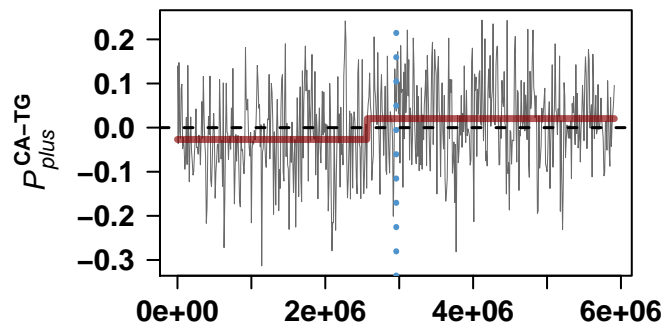
genome coordinates



genome coordinates

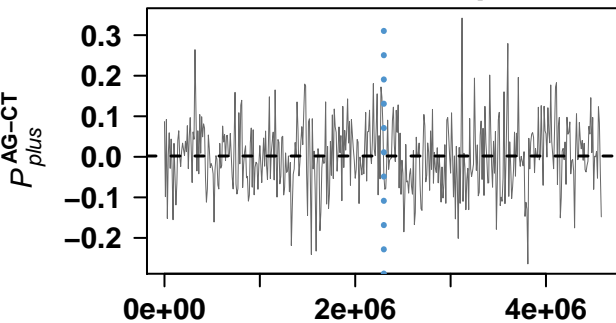


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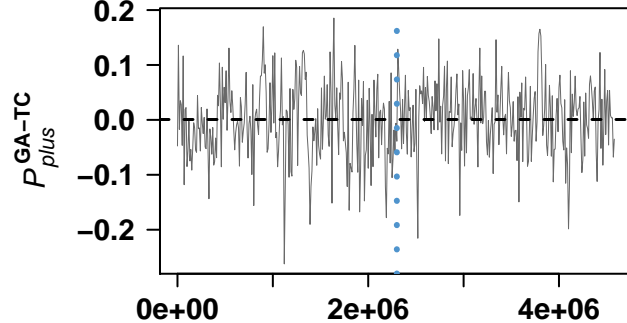


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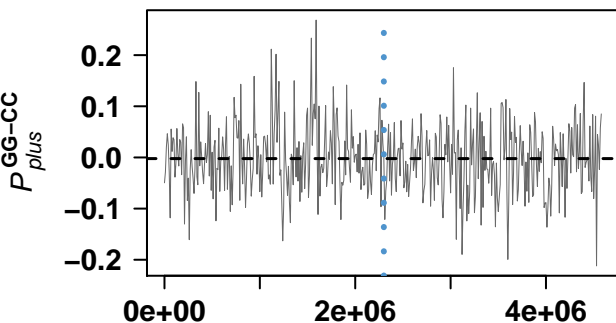
Yersinia pestis biovar *Microtus* str. 91001



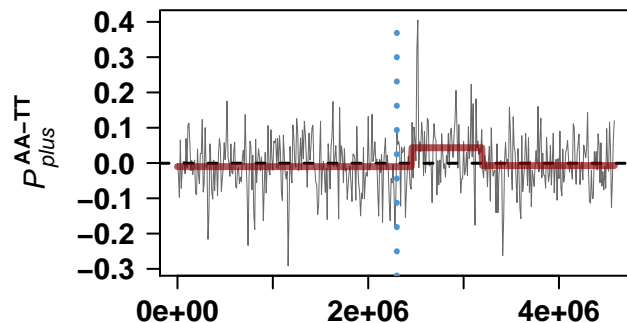
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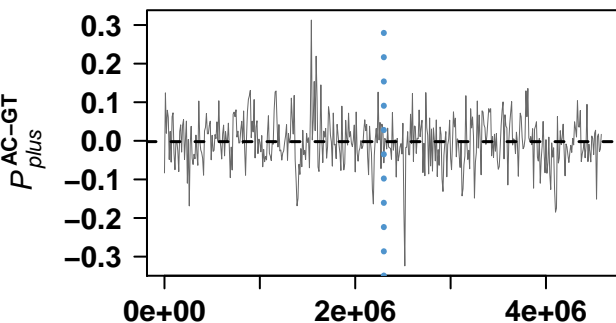
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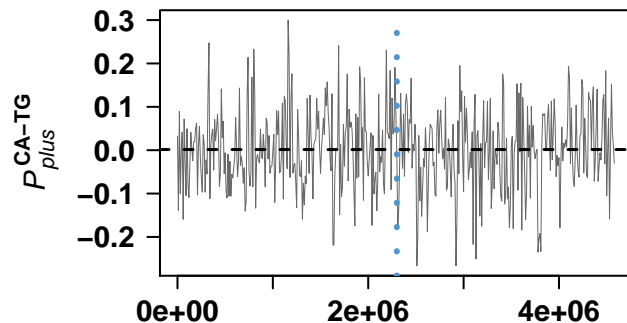
genome coordinates



genome coordinates

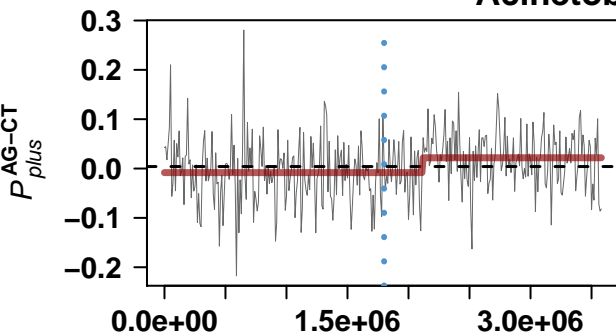


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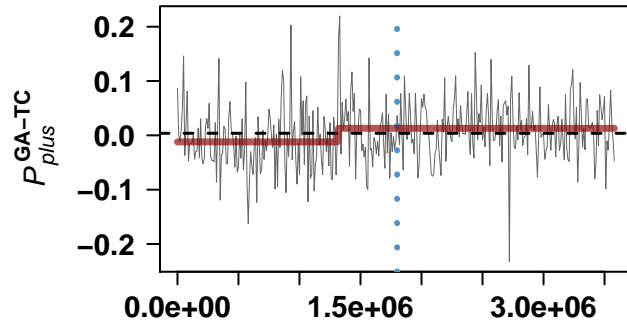


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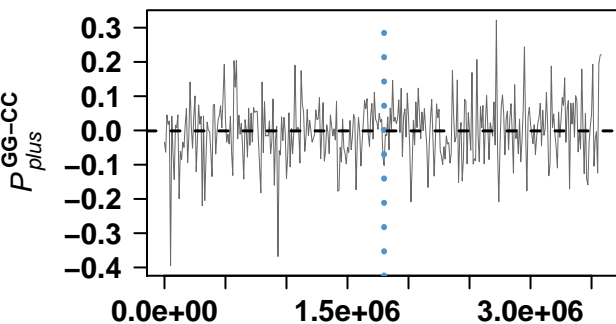
Acinetobacter sp. ADP1



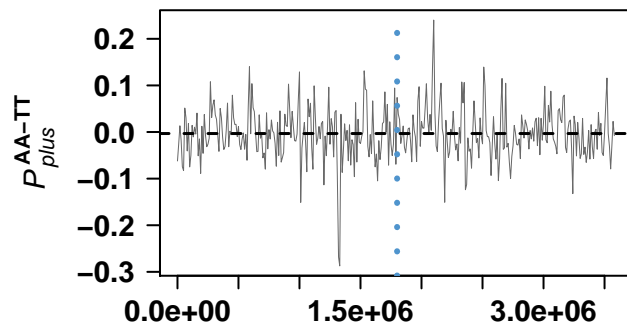
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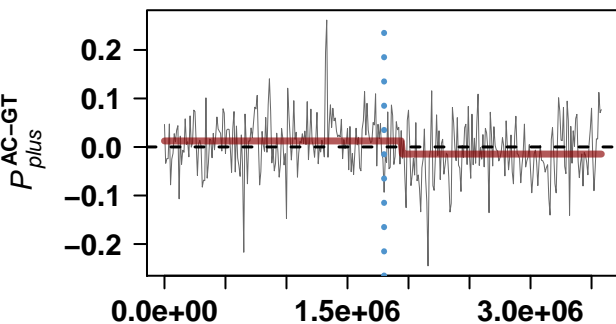
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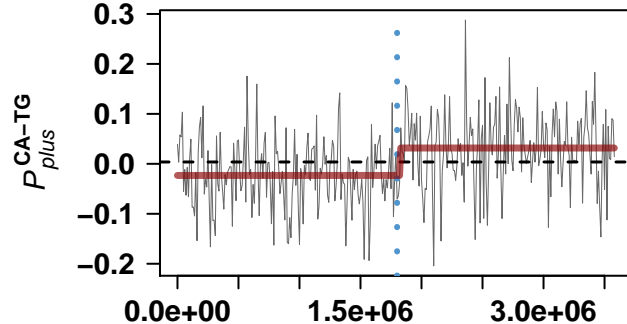
genome coordinates



genome coordinates

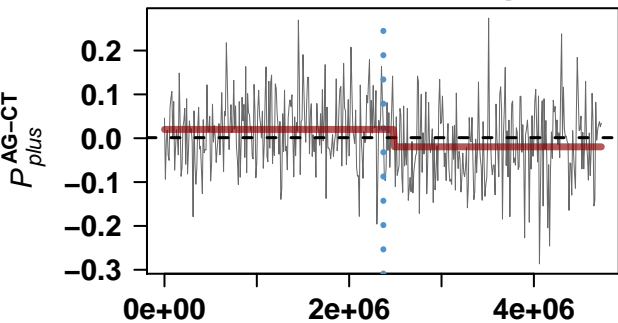


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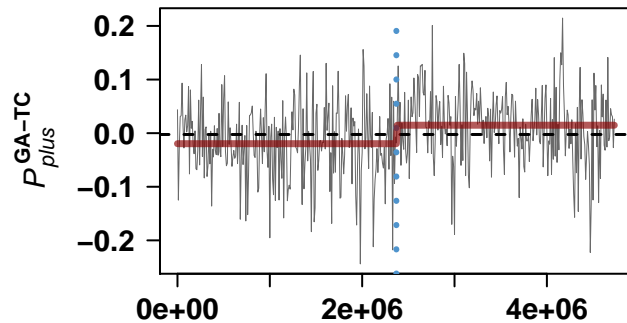


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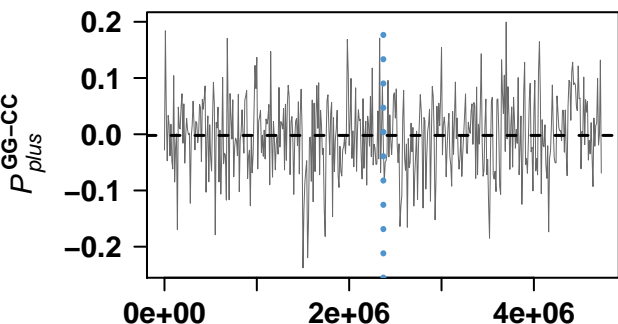
Yersinia pseudotuberculosis IP 32953



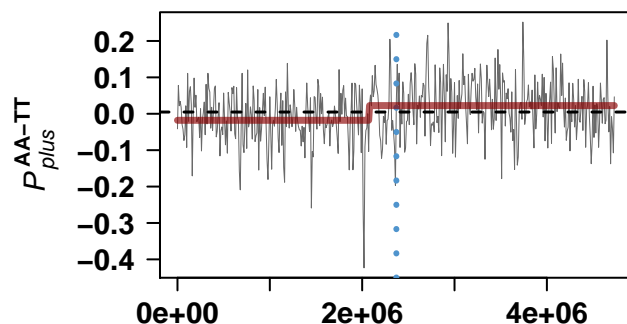
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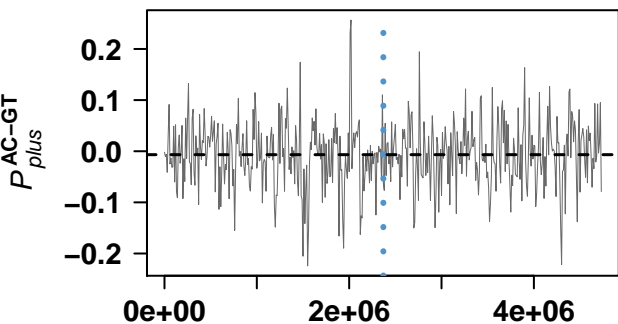
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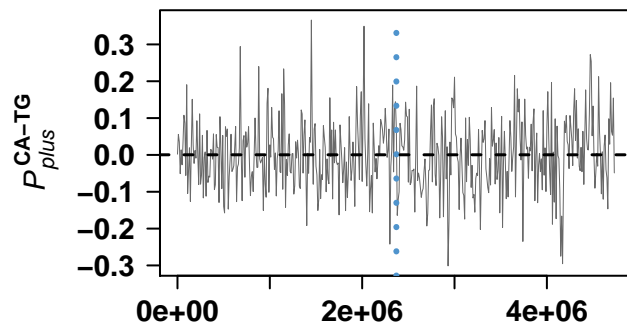
genome coordinates



genome coordinates

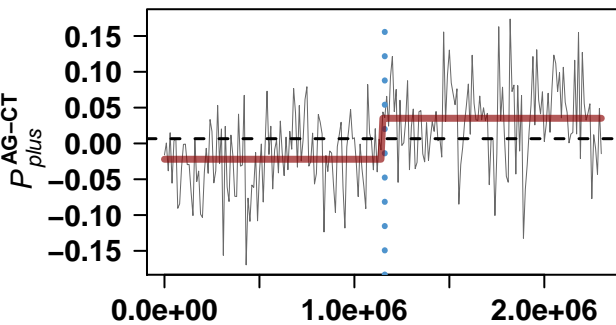


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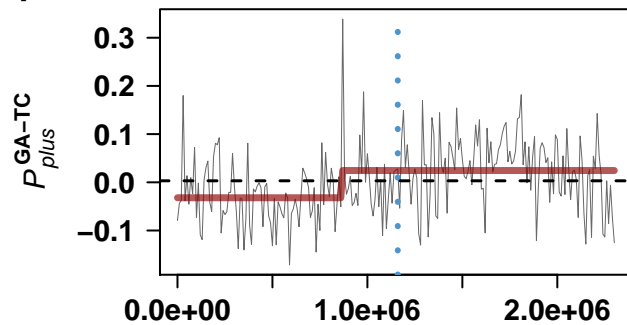


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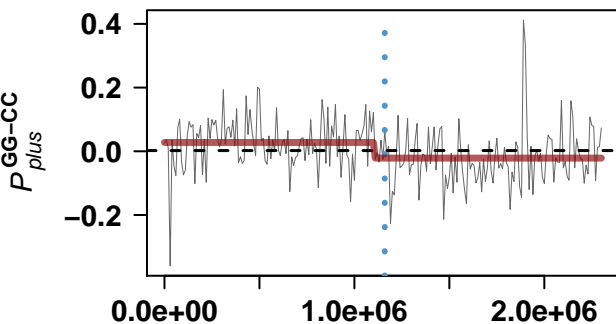
Mannheimia succiniciproducens MBEL55E



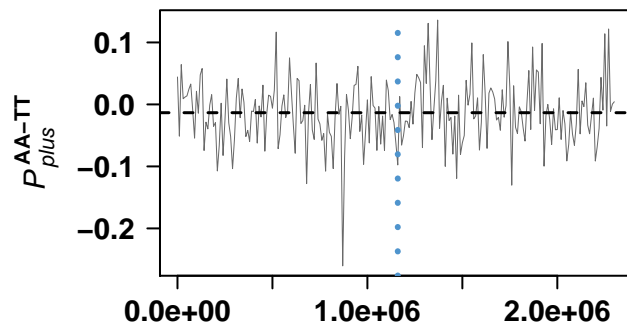
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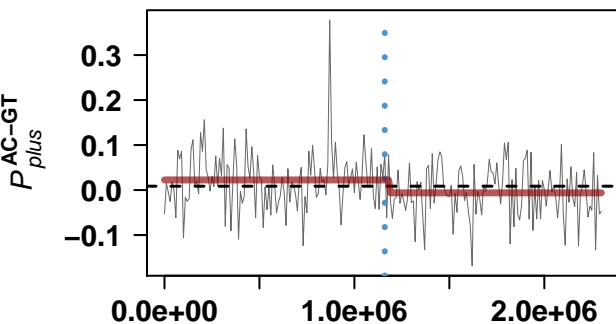
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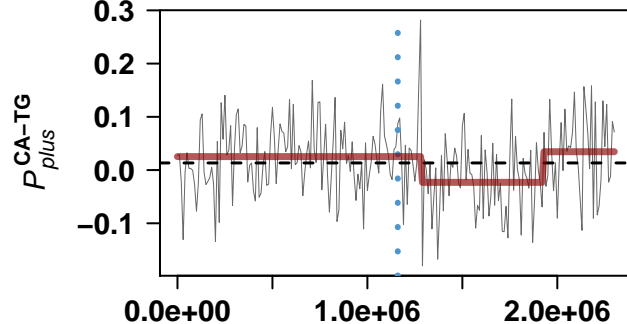
genome coordinates



genome coordinates

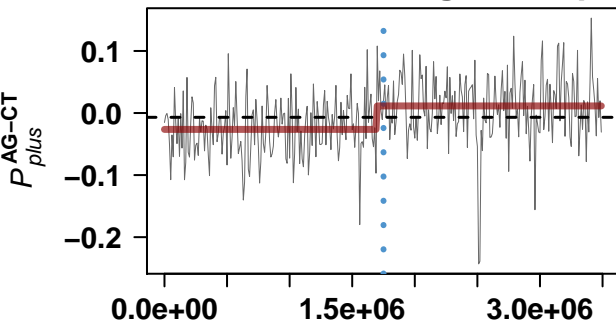


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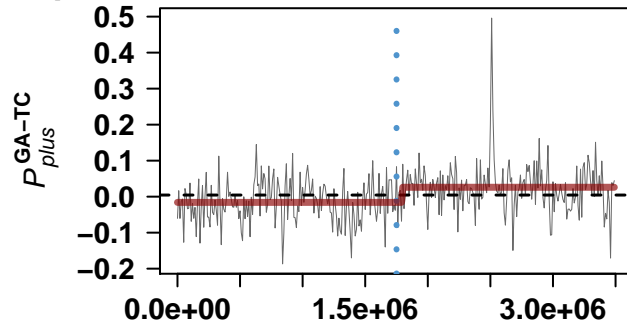


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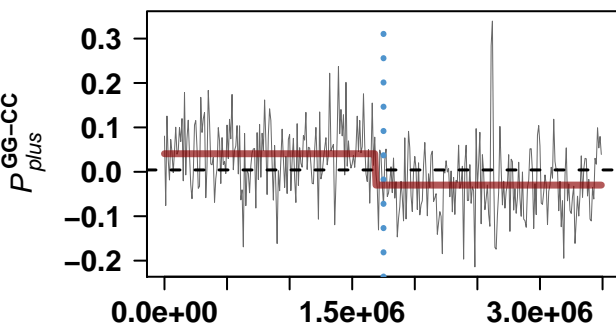
Legionella pneumophila str. Paris



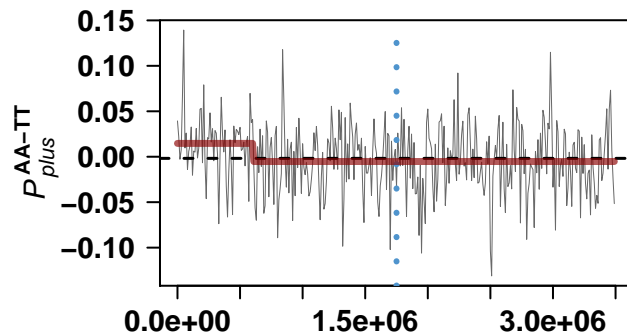
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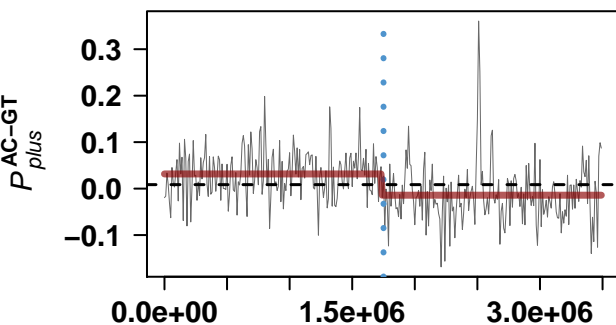
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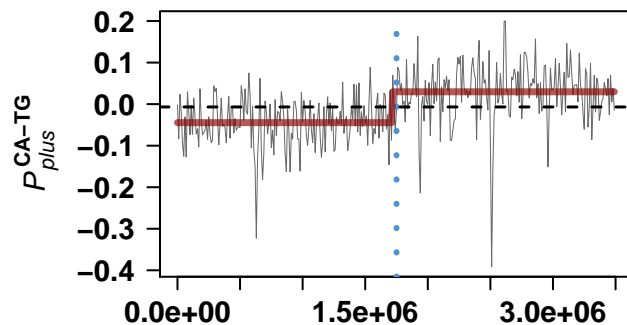
genome coordinates



genome coordinates

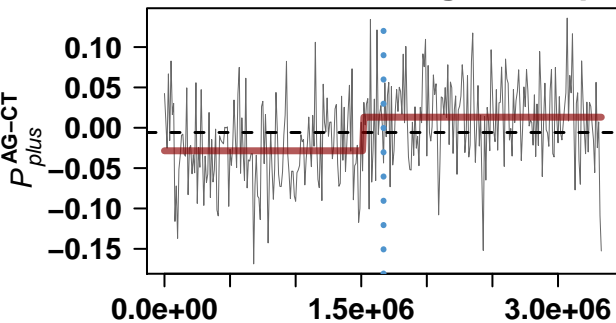


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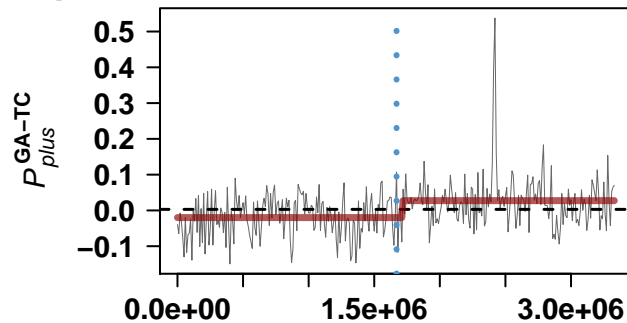


genome coordinates

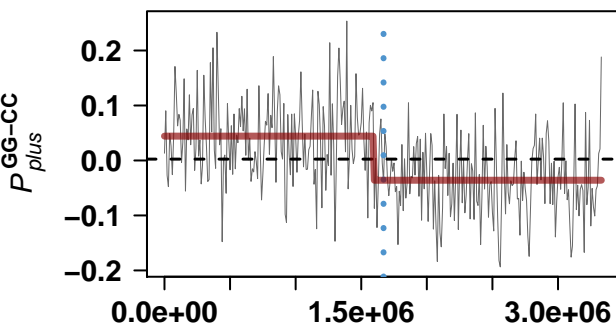
Legionella pneumophila str. Lens



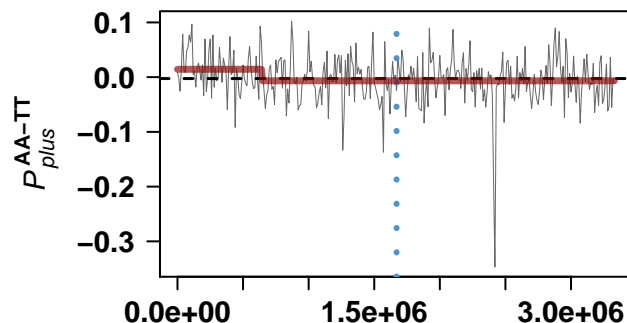
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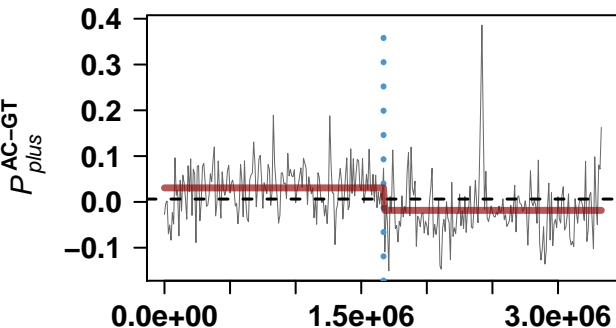
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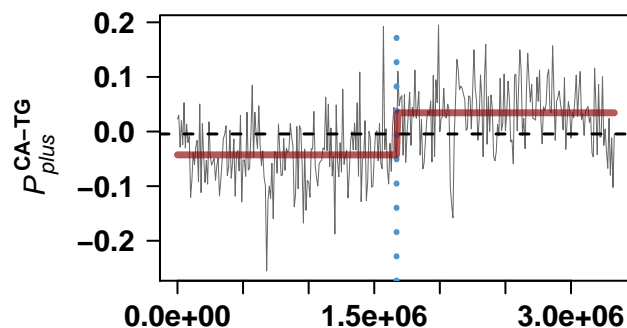
genome coordinates



genome coordinates

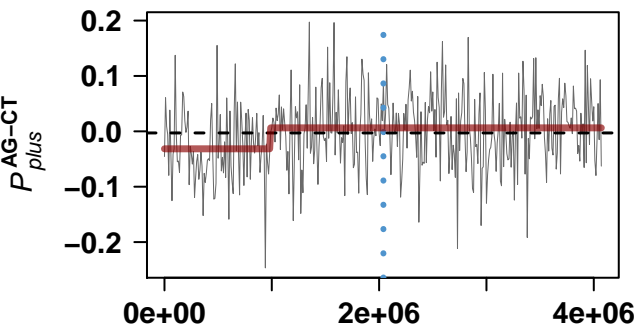


genome coordinates

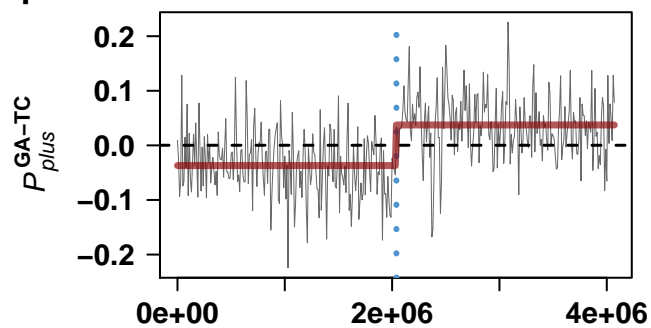


genome coordinates

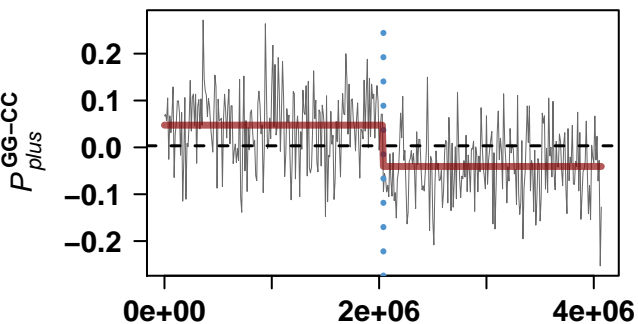
Photobacterium profundum SS9



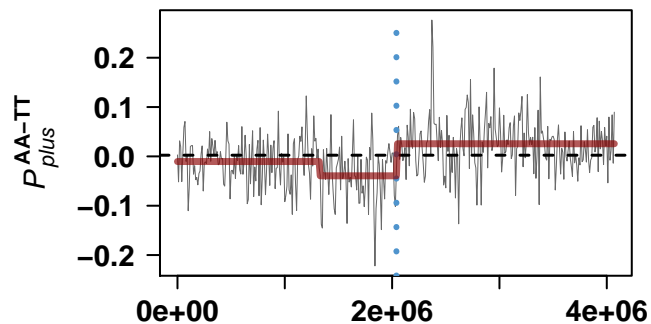
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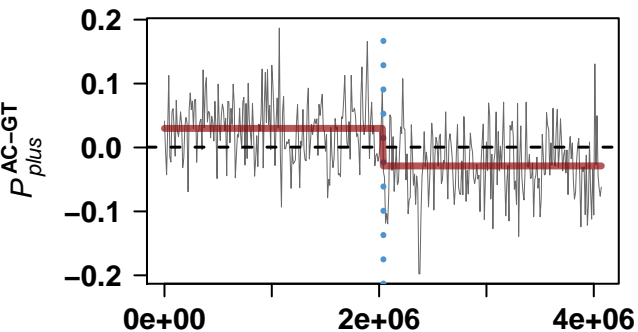
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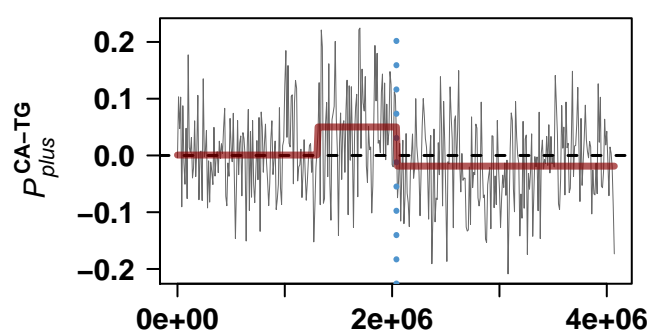
genome coordinates



genome coordinates

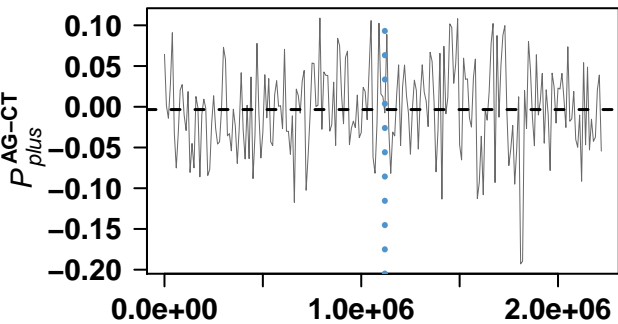


genome coordinates

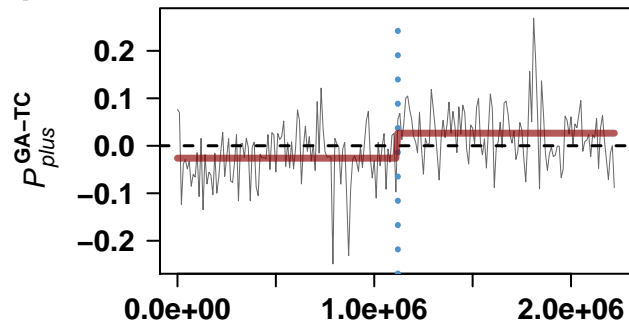


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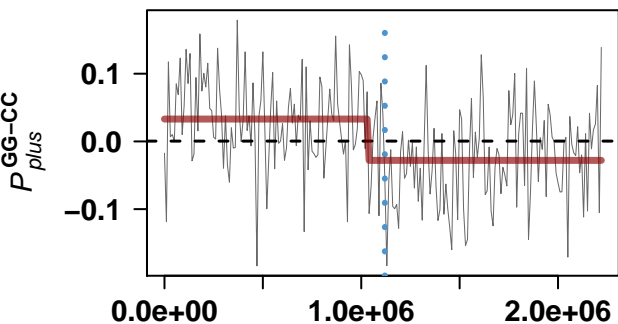
Photobacterium profundum SS9



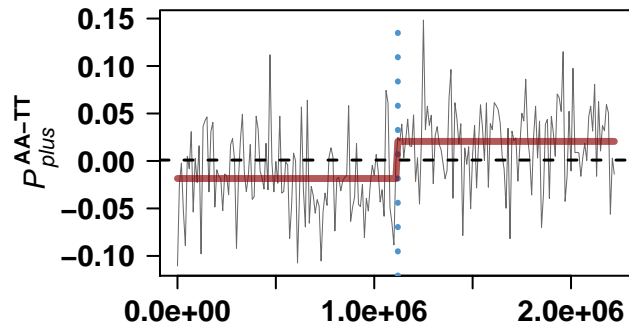
genome coordinates



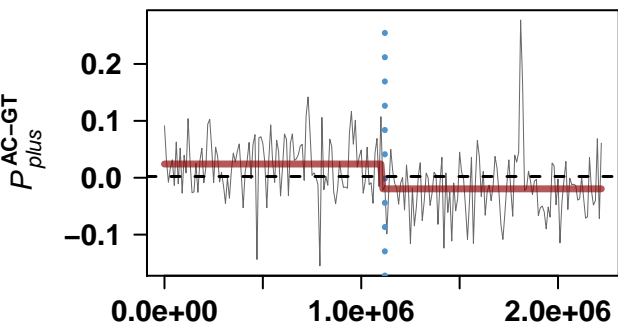
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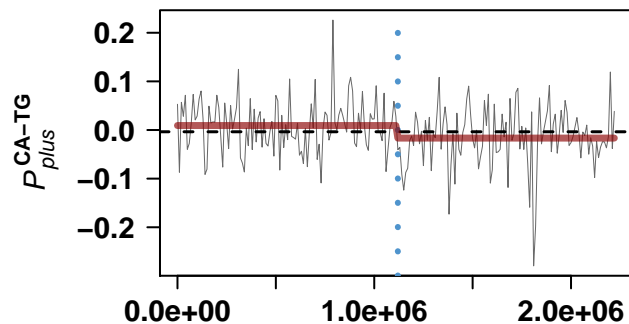
genome coordinates



genome coordinates

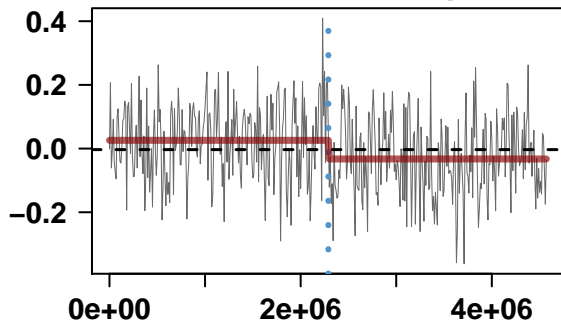


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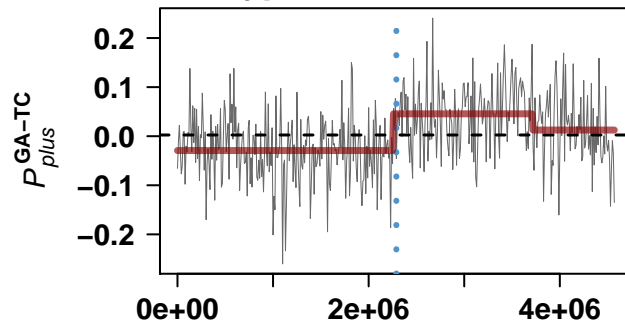


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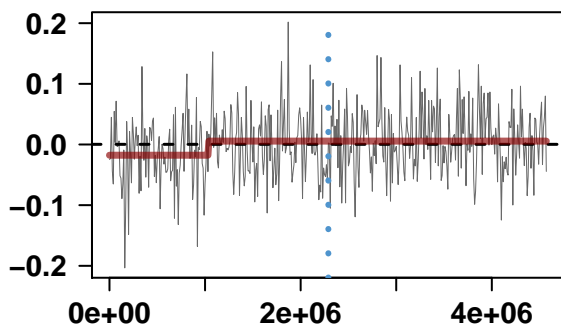
Salmonella enterica subsp. enterica serovar Paratyphi A str. ATCC 9150



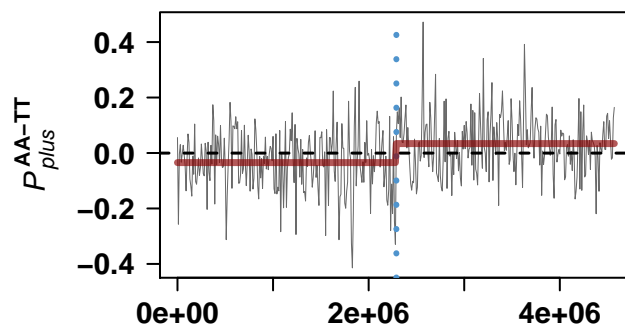
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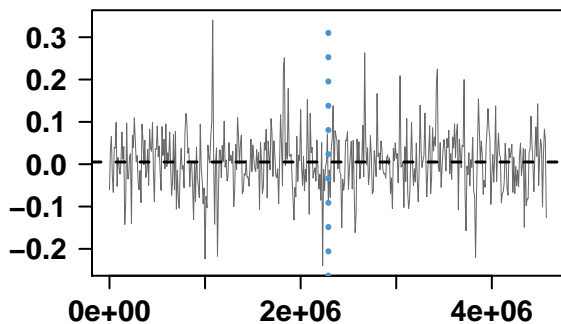
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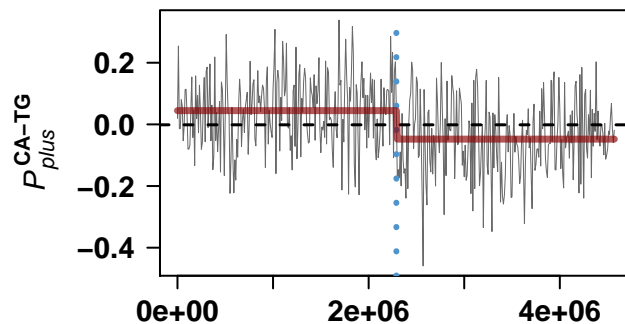
genome coordinates



genome coordinates

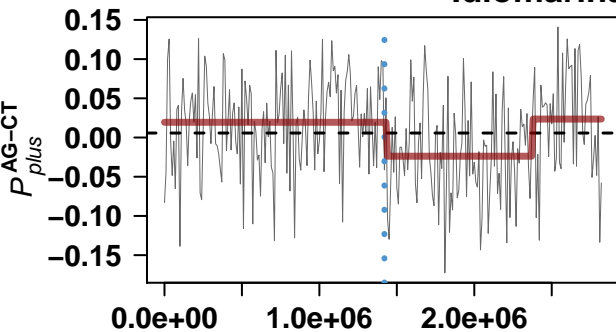


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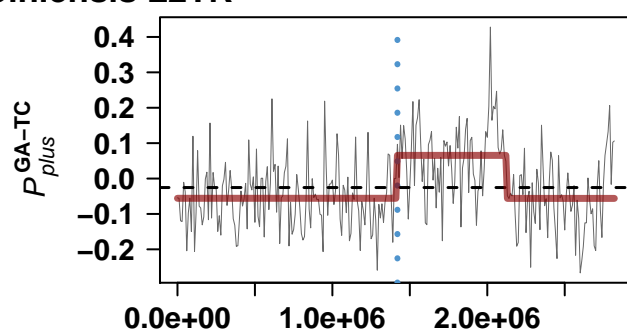


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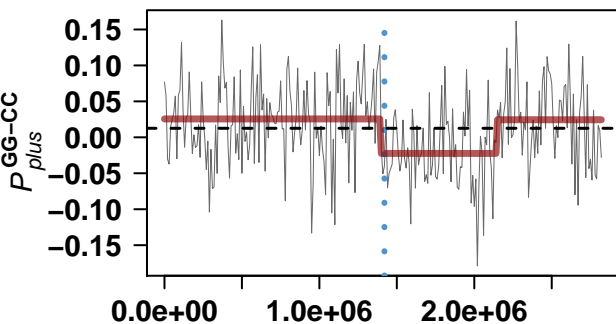
Idiomarina loihiensis L2TR



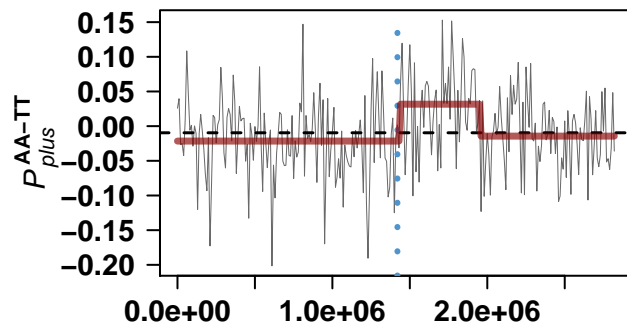
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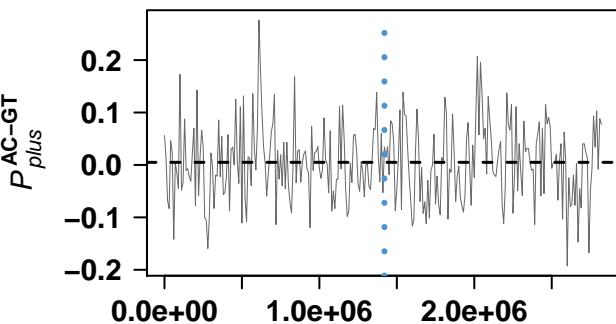
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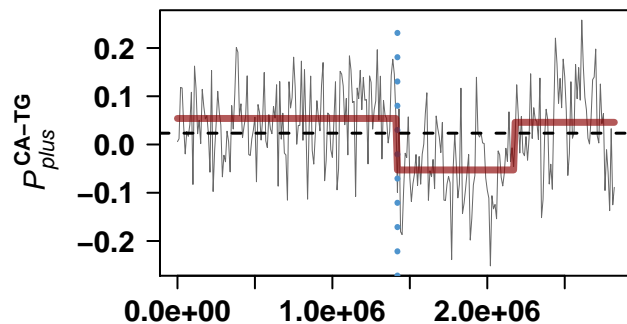
genome coordinates



genome coordinates

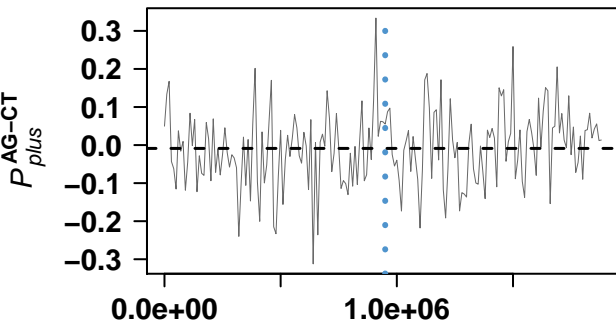


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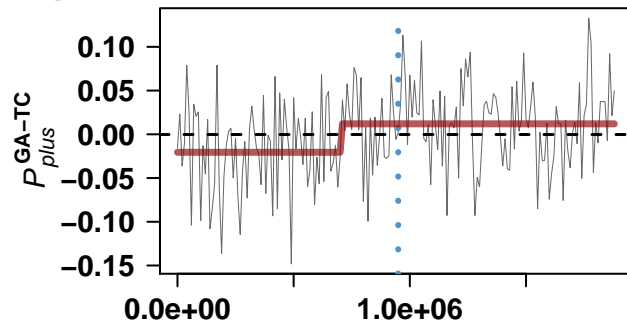


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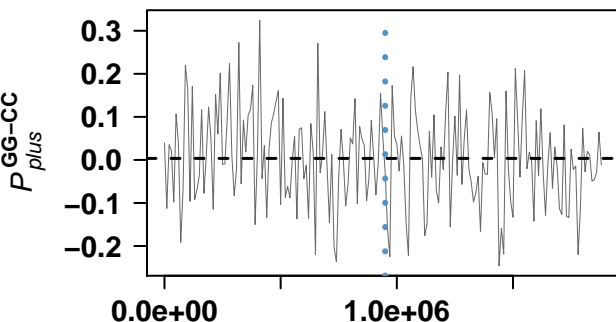
Francisella tularensis subsp. tularensis SCHU S4



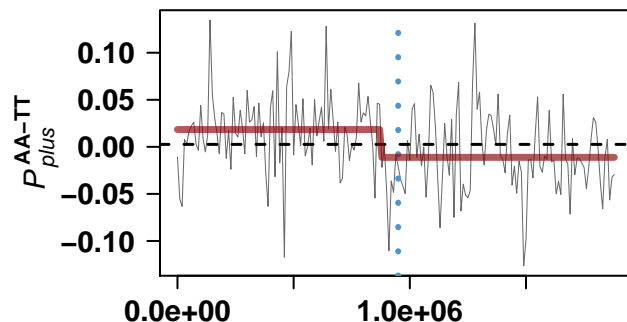
genome coordinates



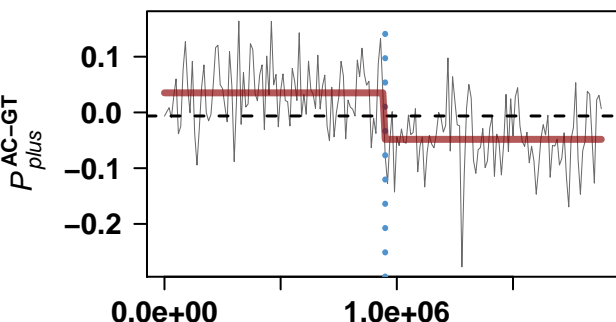
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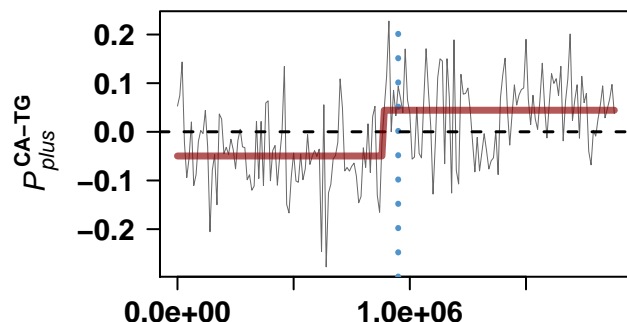
genome coordinates



genome coordinates

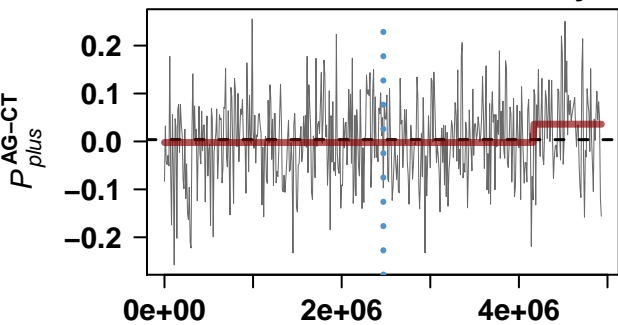


genome coordinates

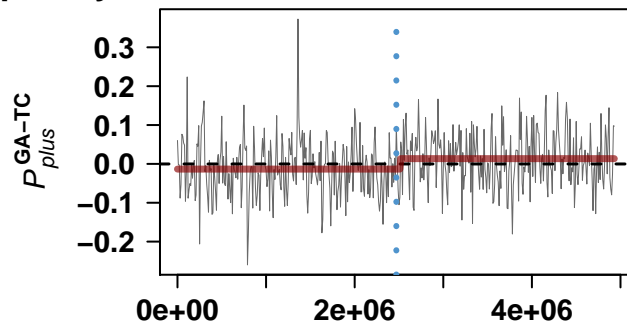


genome coordinates

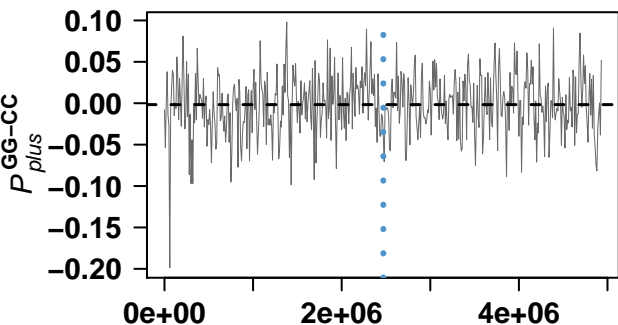
Xanthomonas oryzae pv. oryzae KACC 10331



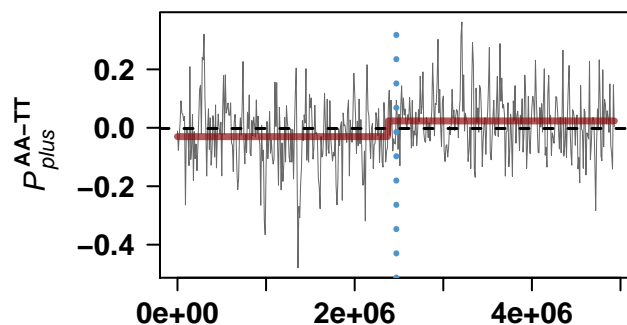
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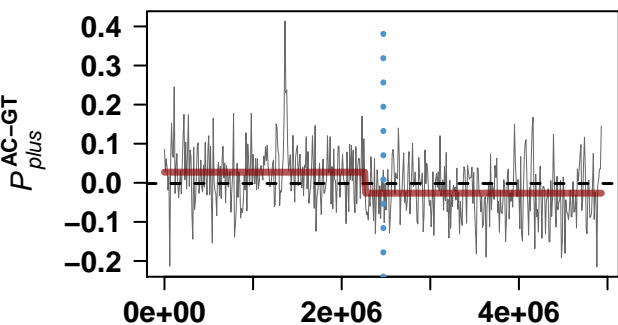
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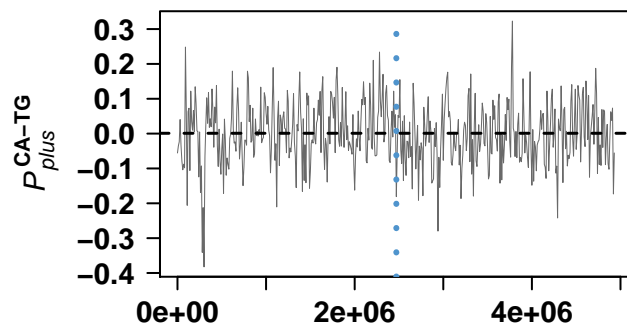
genome coordinates



genome coordinates

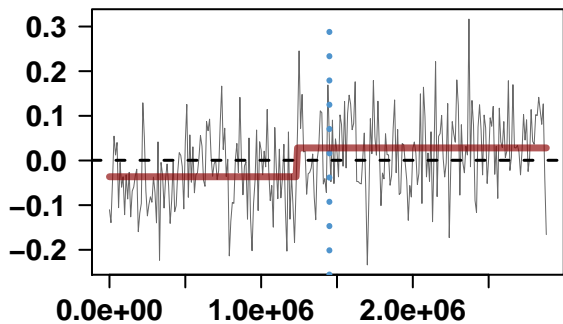


genome coordinates

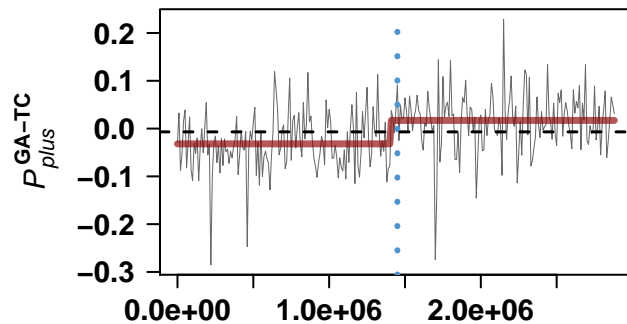


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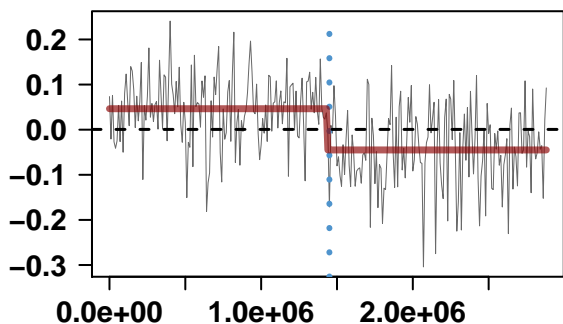
Vibrio fischeri ES114



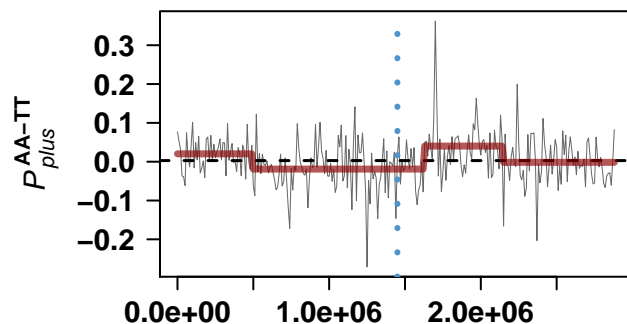
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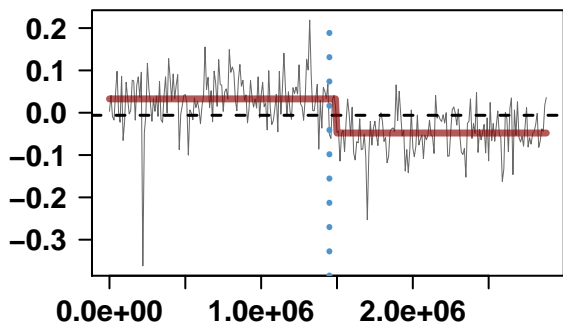
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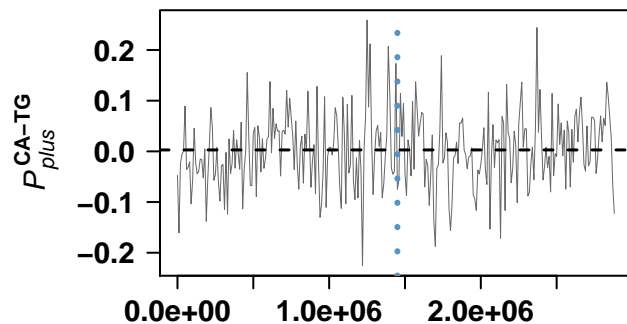
genome coordinates



genome coordinates

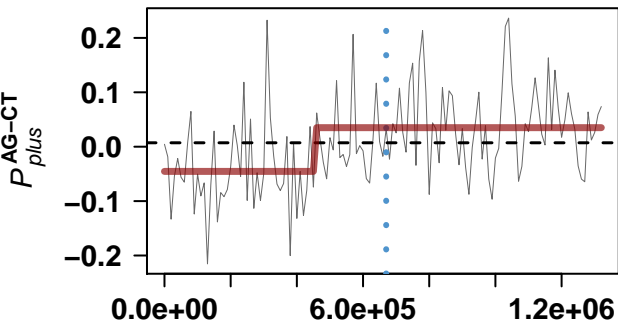


genome coordinates

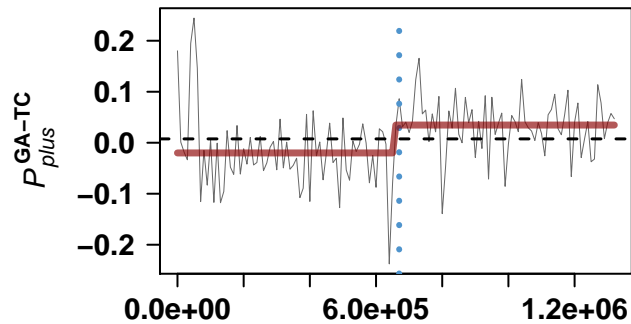


genome coordinates

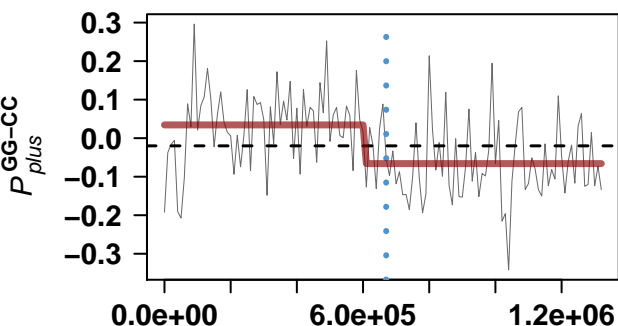
Vibrio fischeri ES114



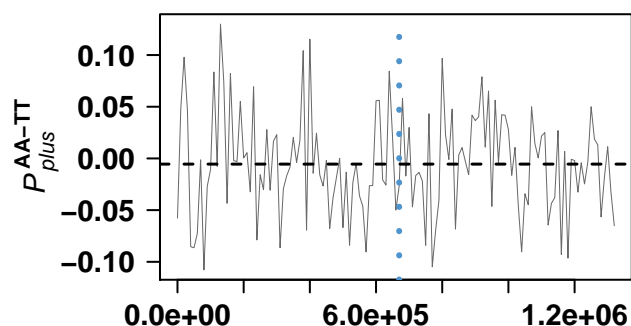
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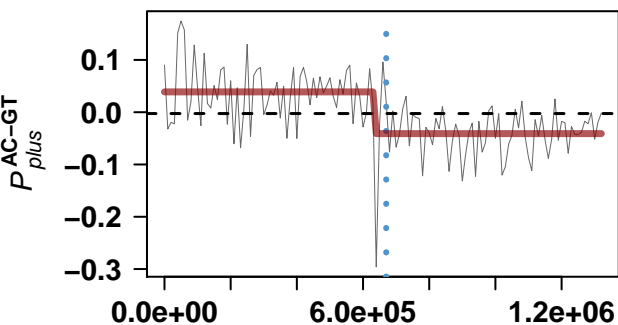
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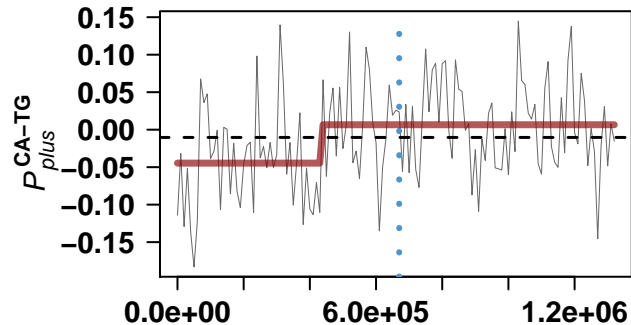
genome coordinates



genome coordinates

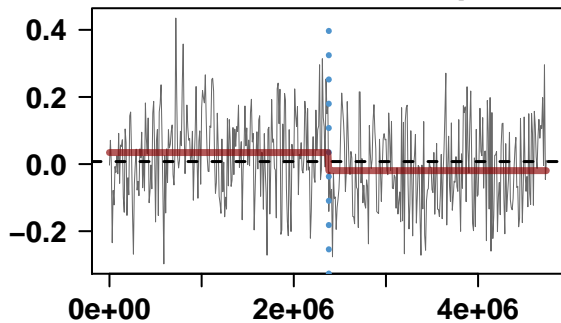


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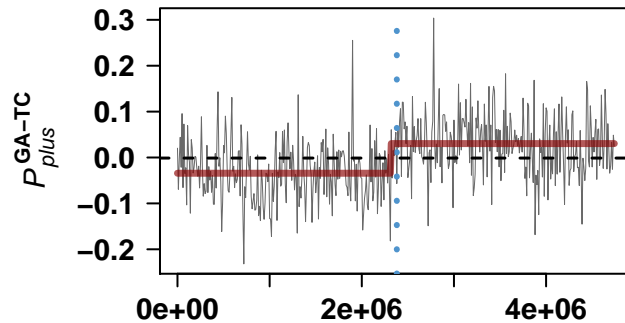


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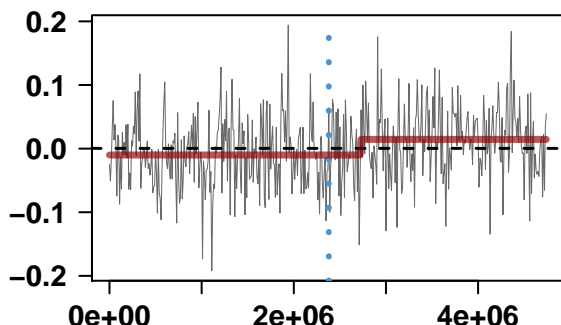
Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67



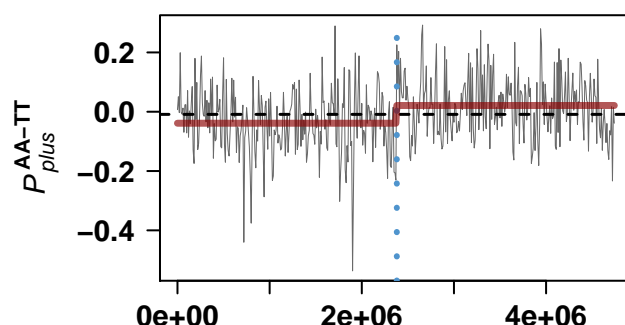
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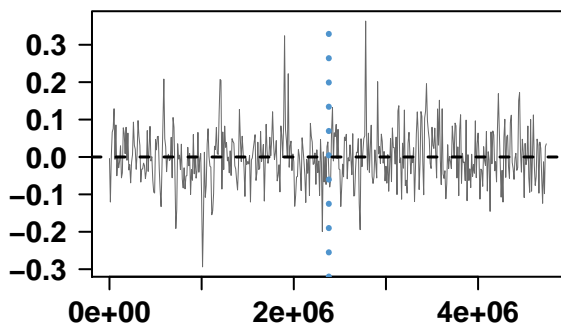
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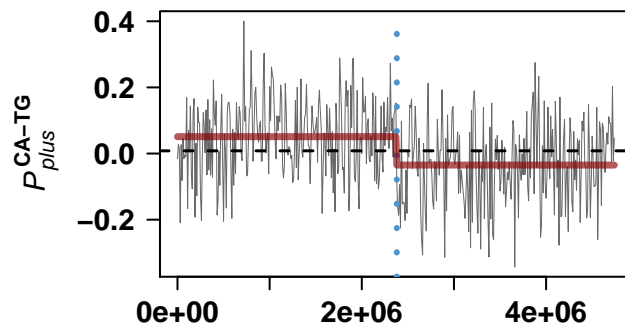
genome coordinates



genome coordinates

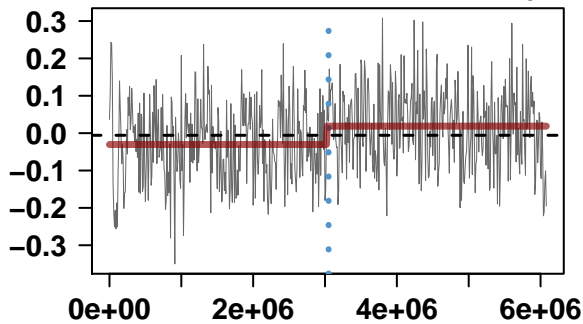


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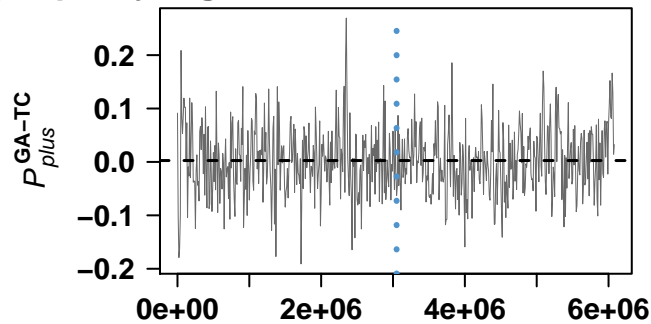


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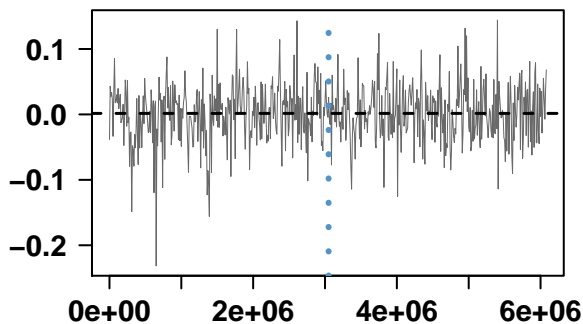
Pseudomonas syringae pv. *syringae* B728a



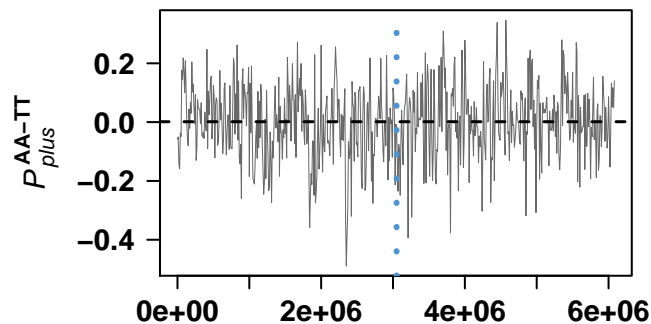
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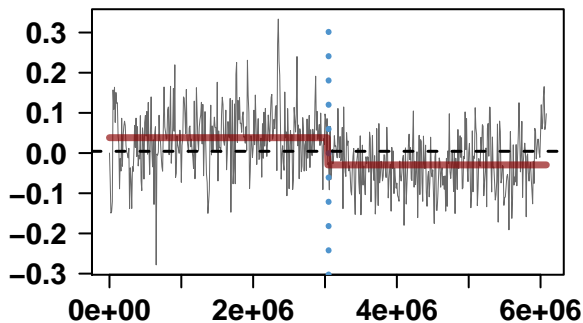
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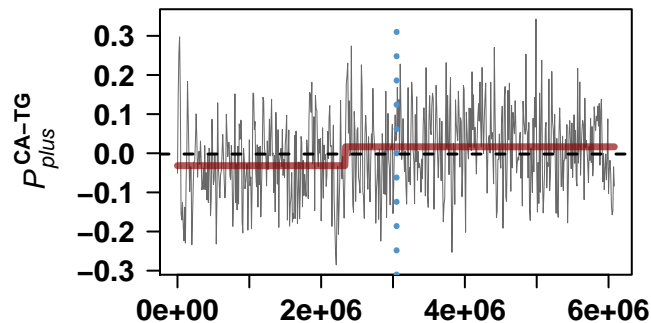
genome coordinates



genome coordinates

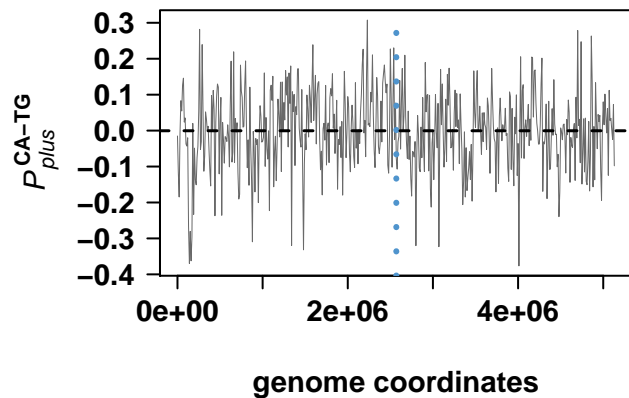
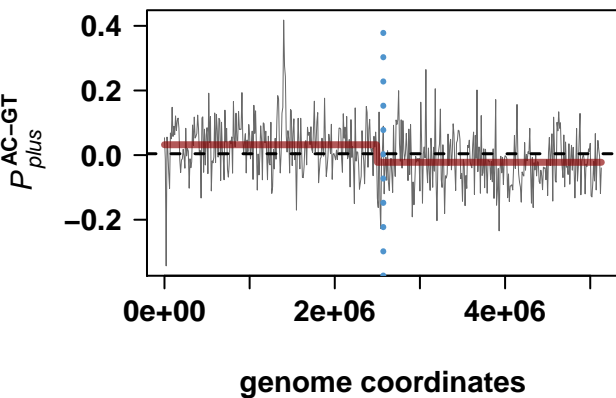
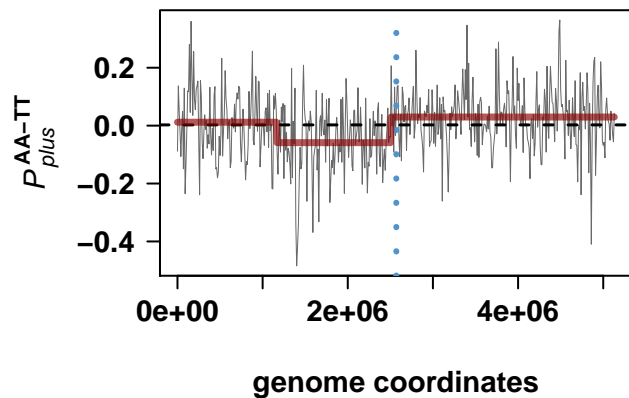
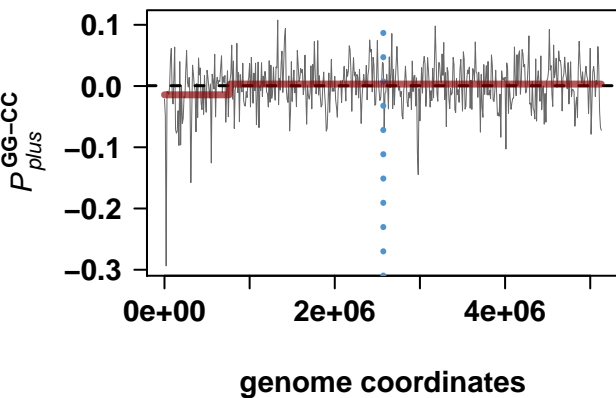
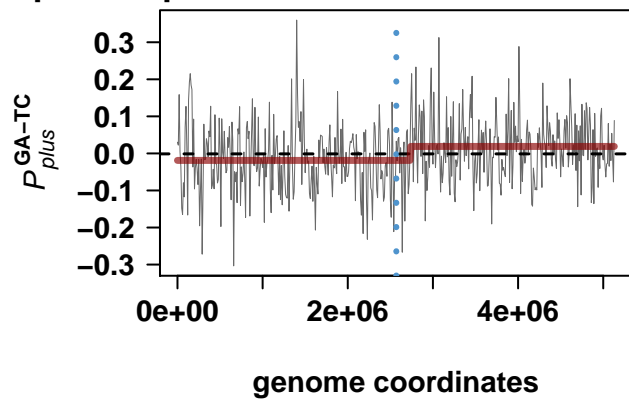
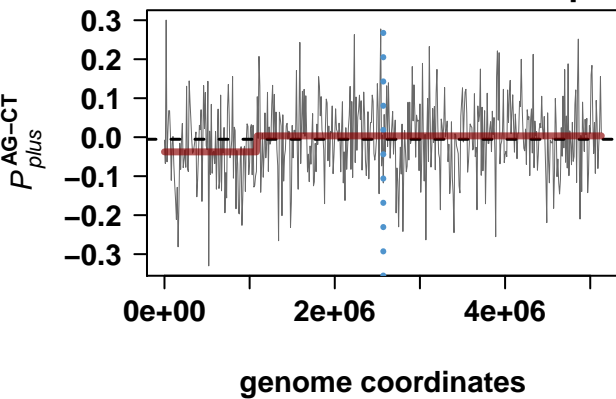


genome coordinates

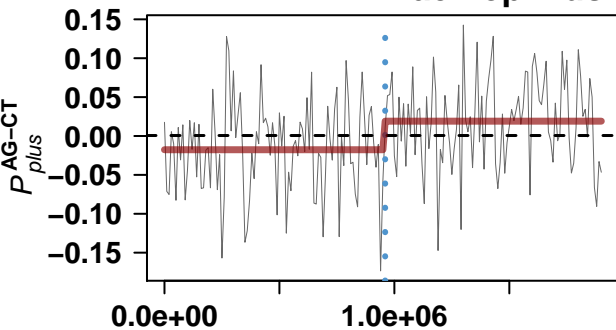


genome coordinates

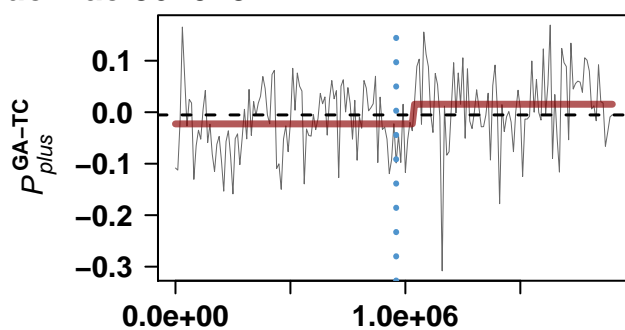
Xanthomonas campestris pv. *campestris* str. 8004



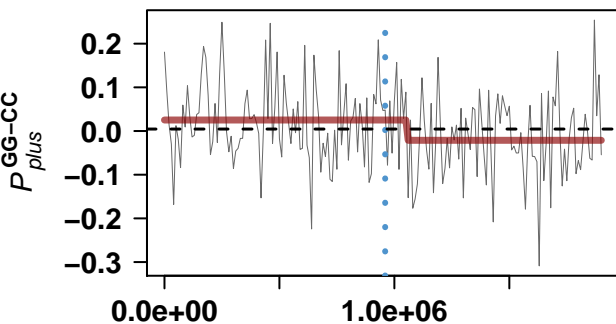
Haemophilus influenzae 86-028NP



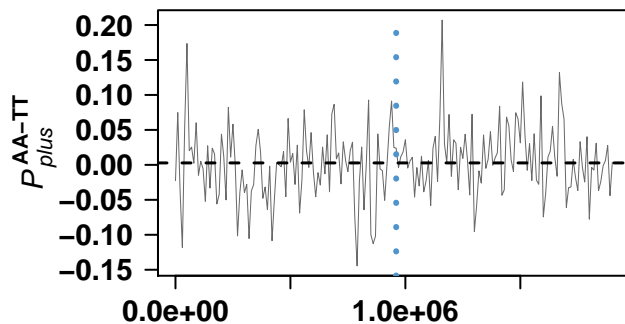
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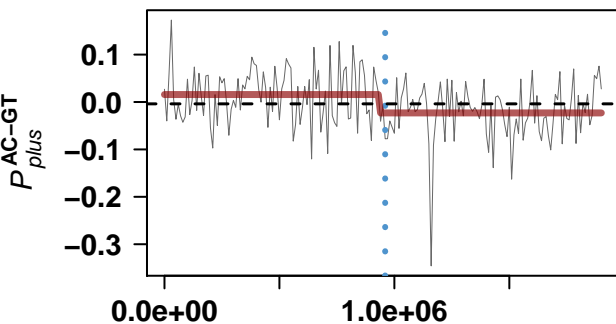
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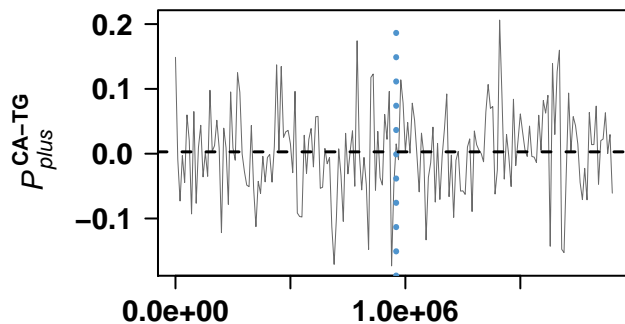
genome coordinates



genome coordinates

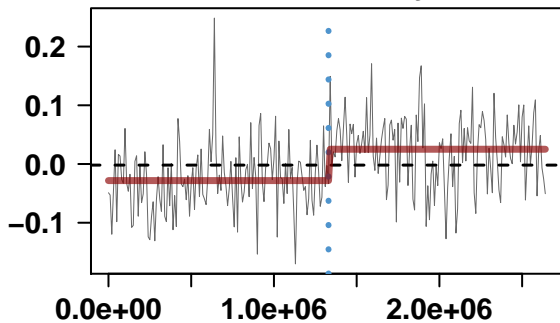


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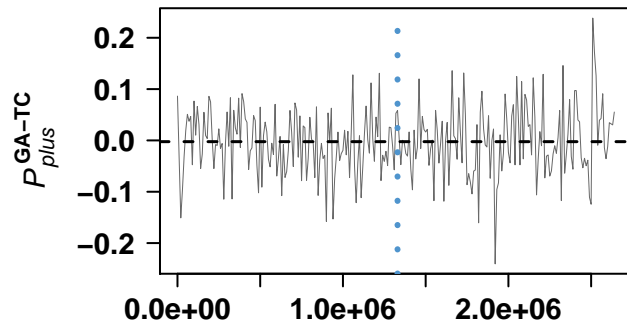


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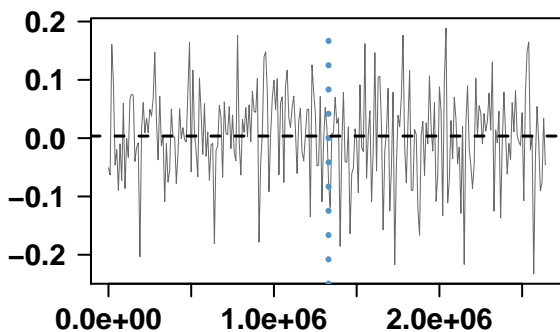
Psychrobacter arcticus 273-4



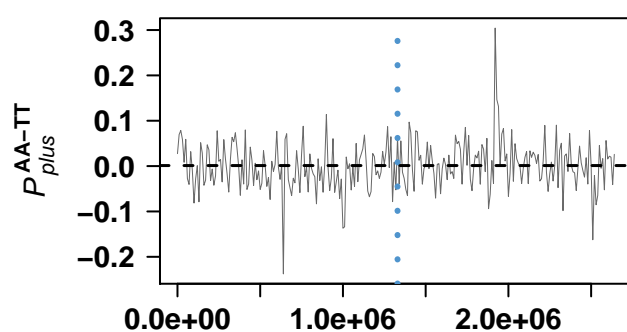
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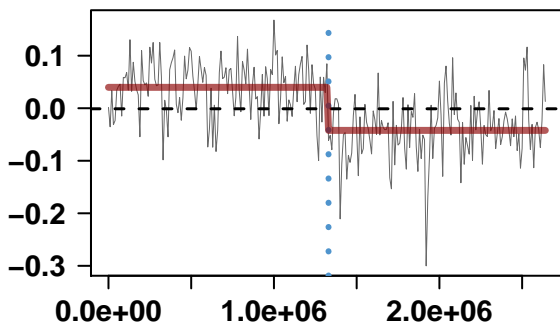
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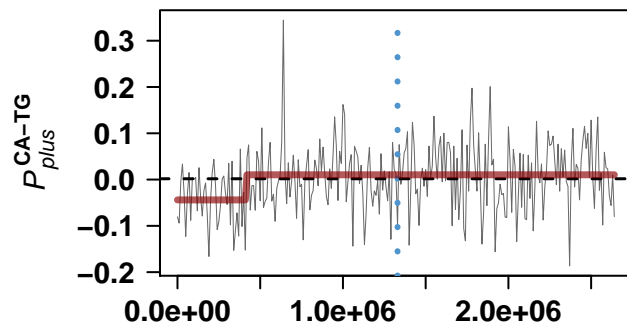
genome coordinates



genome coordinates

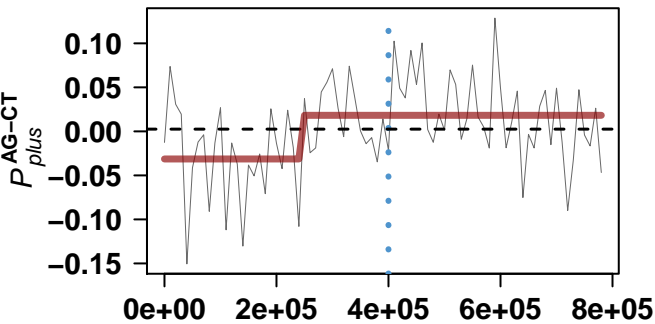


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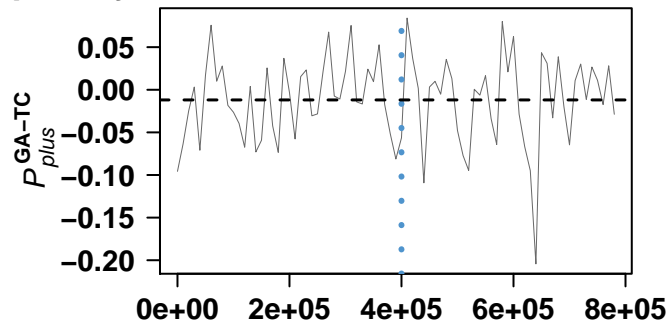


genome coordinates

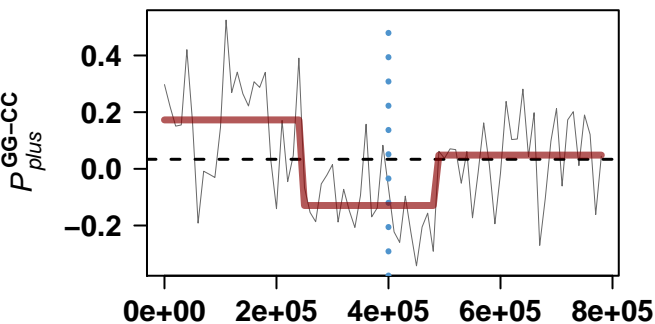
Candidatus Blochmannia pennsylvanicus str. BPEN



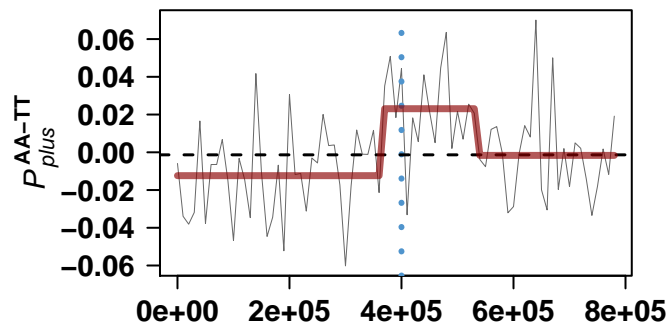
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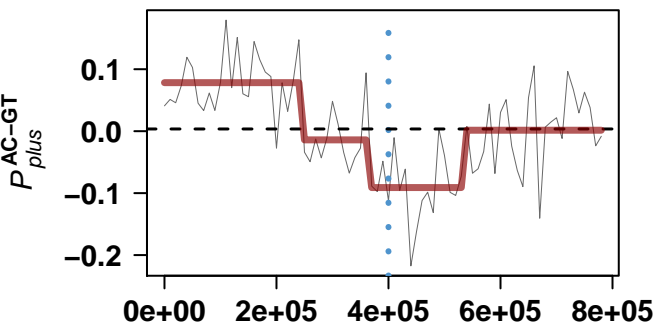
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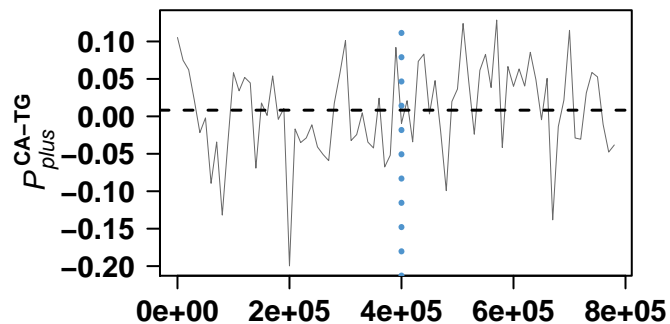
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genome coordinates

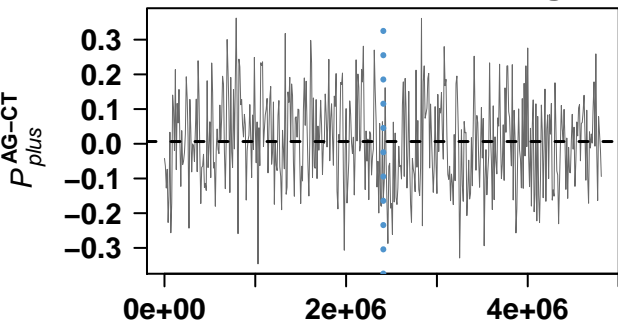


genome coordinates

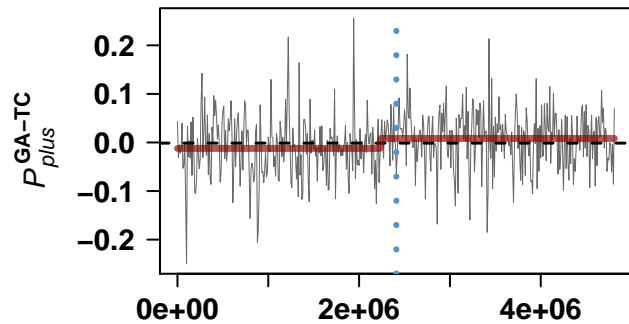


genome coordinates

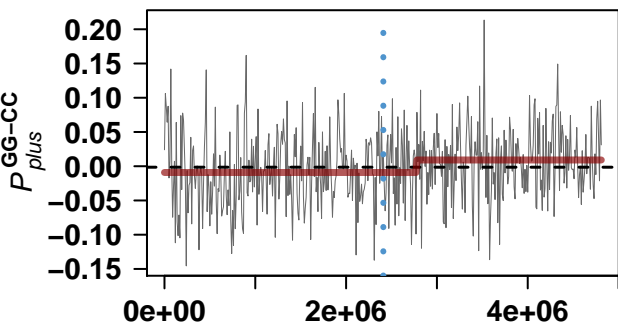
Shigella sonnei Ss046



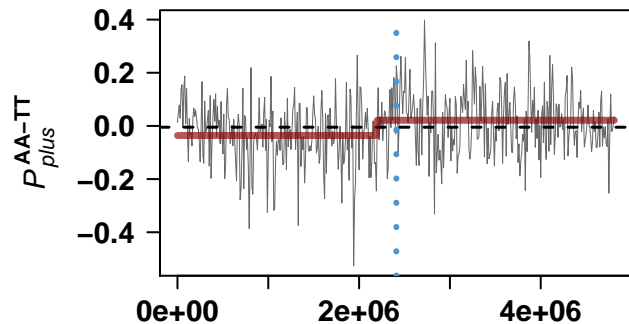
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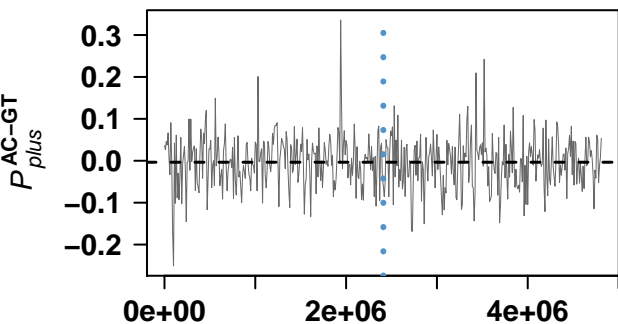
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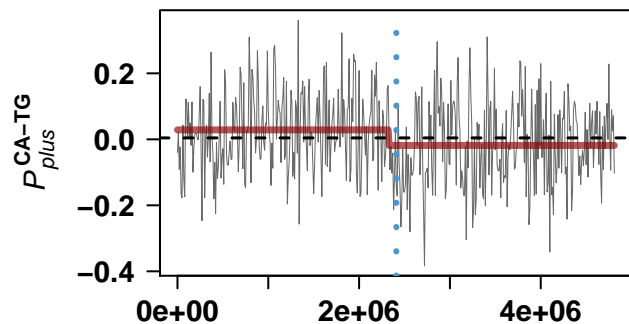
genome coordinates



genome coordinates

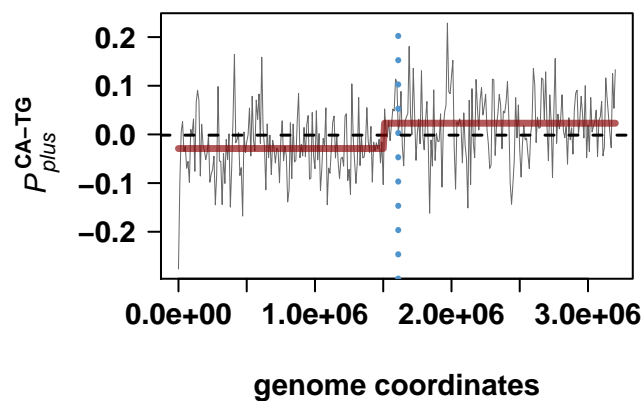
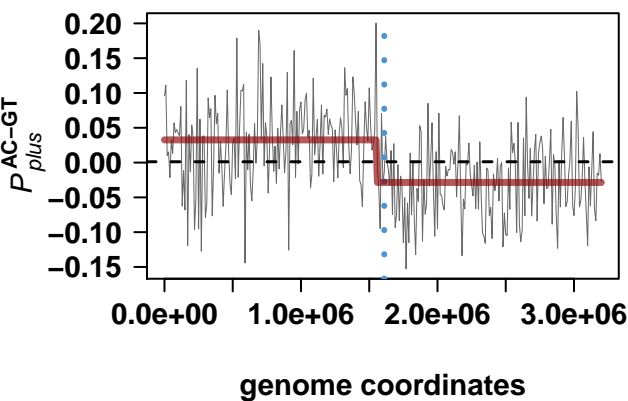
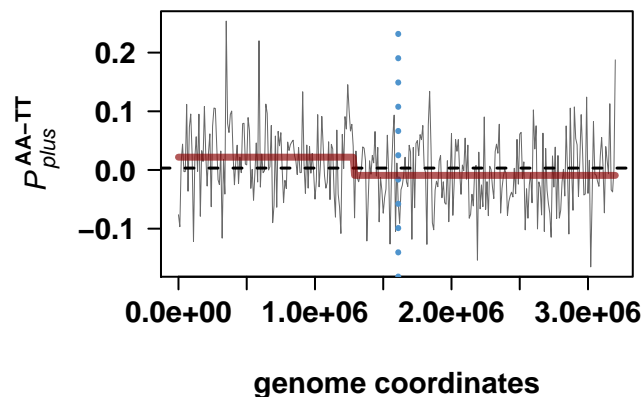
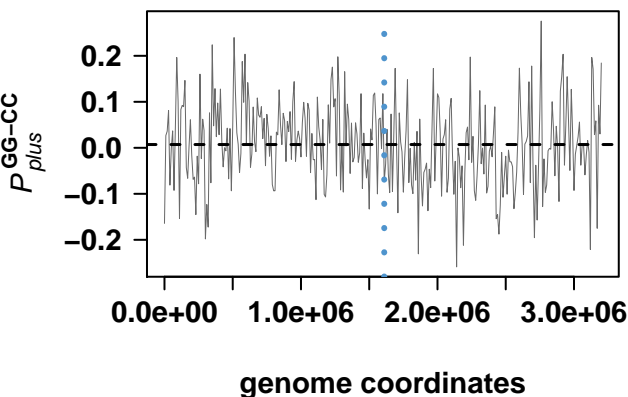
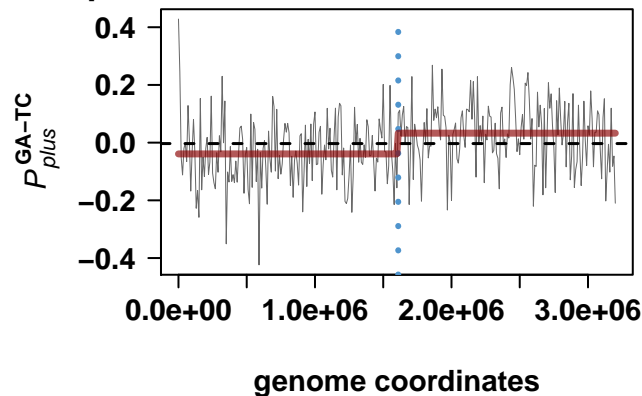
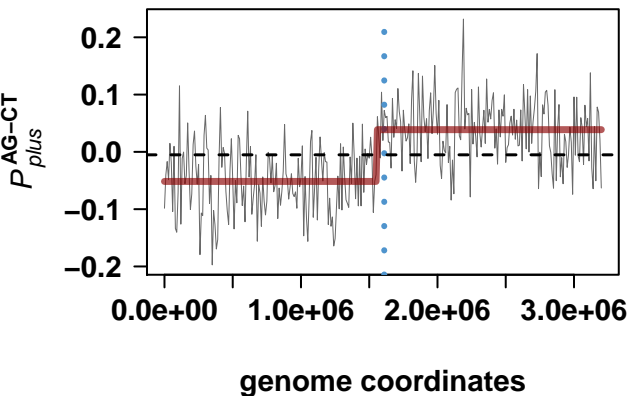


genome coordinates

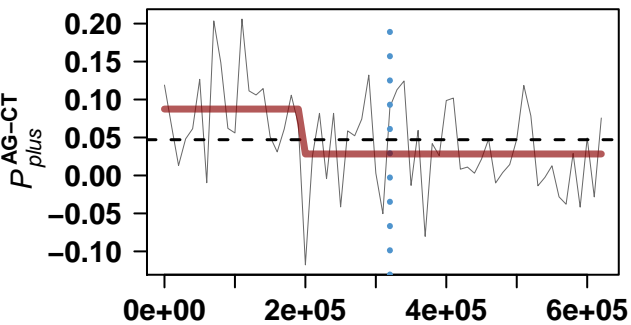


genome coordinates

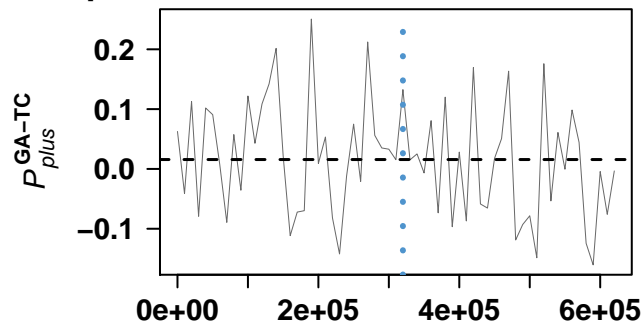
Pseudoalteromonas haloplanktis TAC125



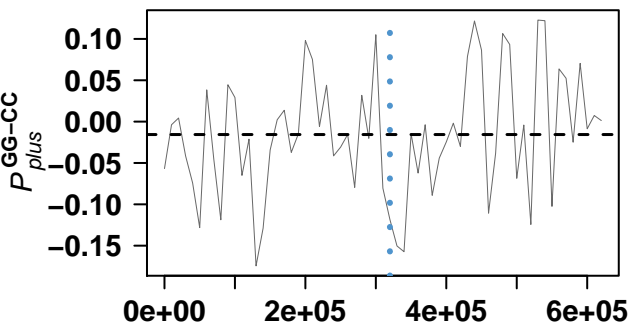
Pseudoalteromonas haloplanktis TAC125



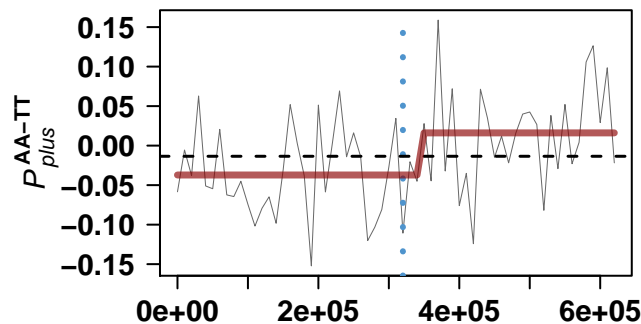
genome coordinates



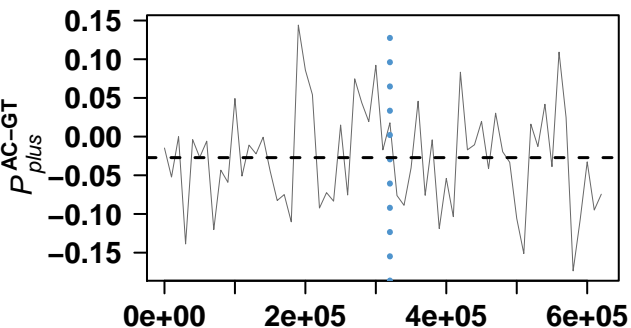
genome coordinates



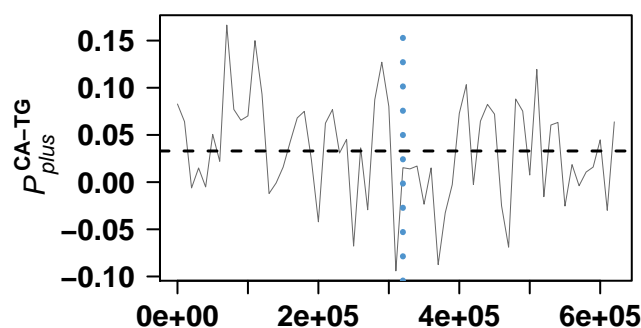
genome coordinates



genome coordinates

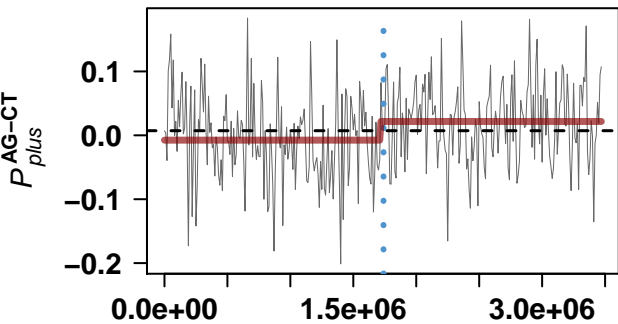


genome coordinates

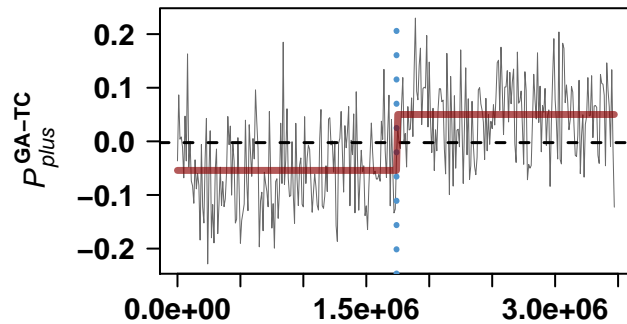


genome coordinates

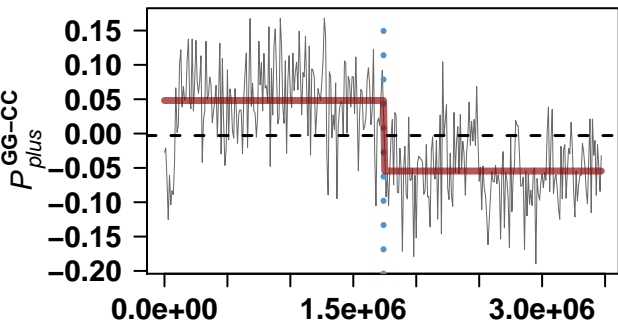
Nitrosococcus oceani ATCC 19707



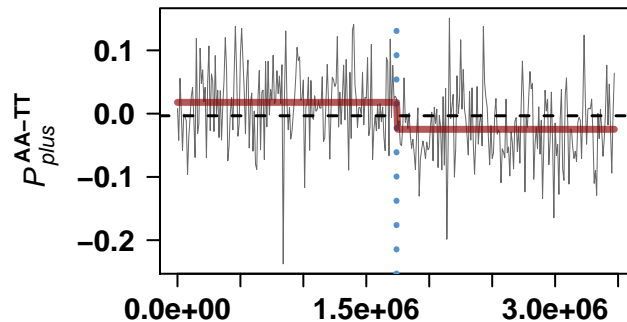
genome coordinates



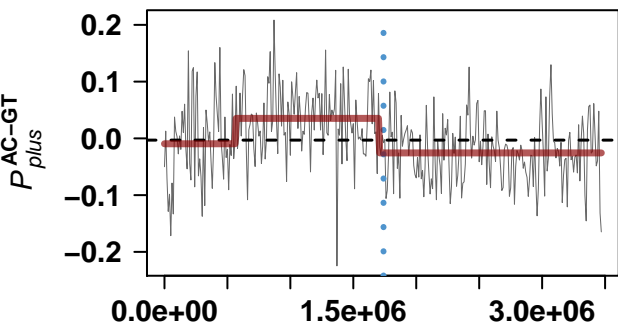
genome coordinates



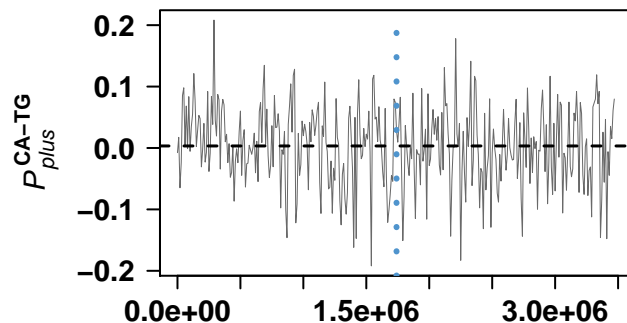
genome coordinates



genome coordinates

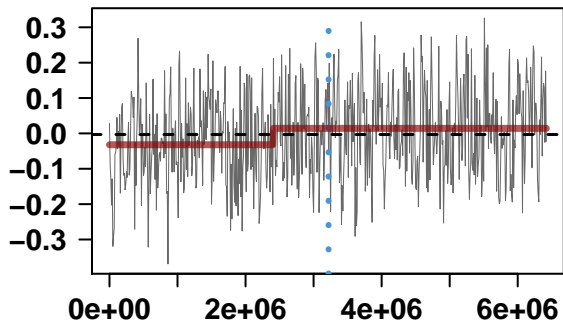


genome coordinates

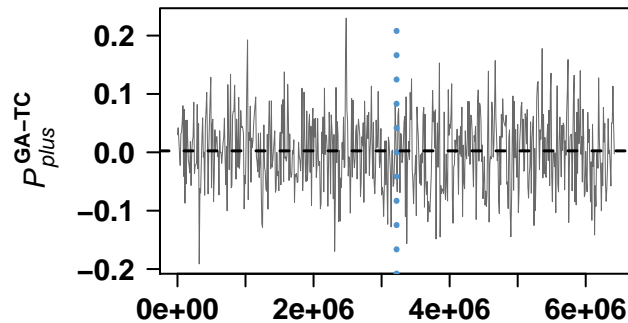


genome coordinates

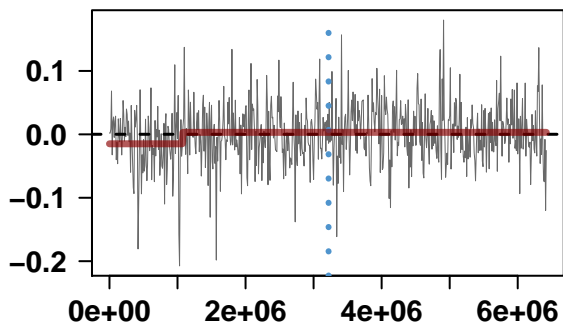
Pseudomonas fluorescens Pf0-1



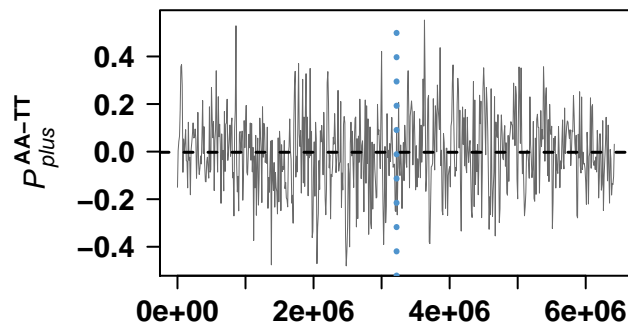
genome coordinates



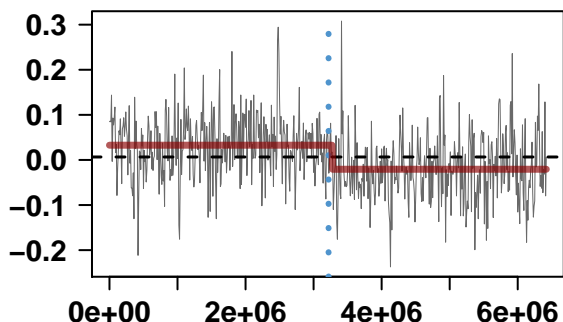
genome coordinates



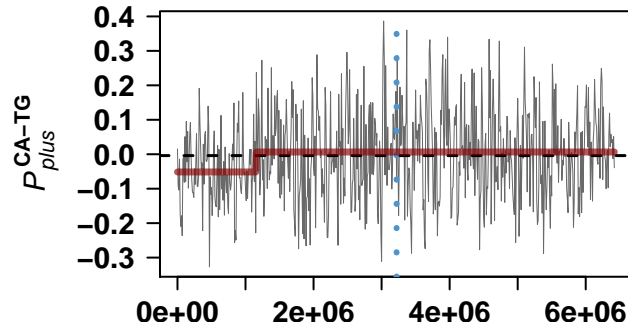
genome coordinates



genome coordinates

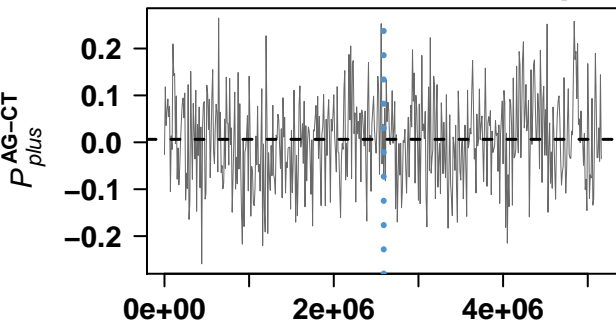


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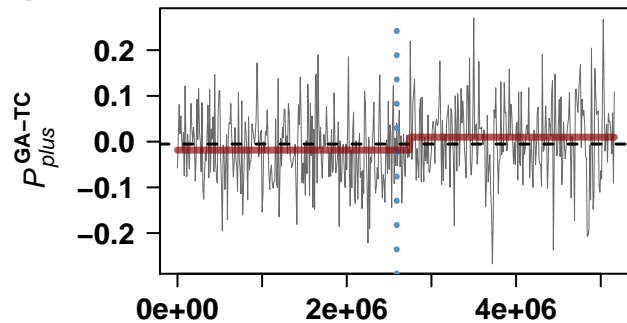


genome coordinates

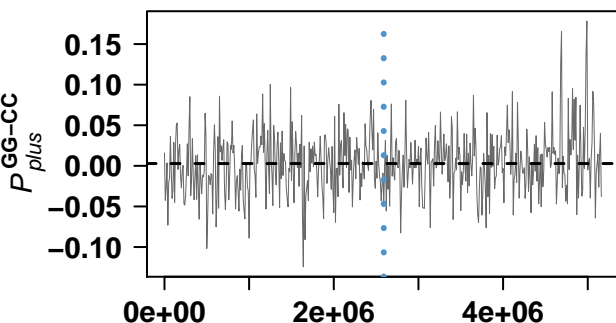
Xanthomonas campestris pv. *vesicatoria* str. 85-10



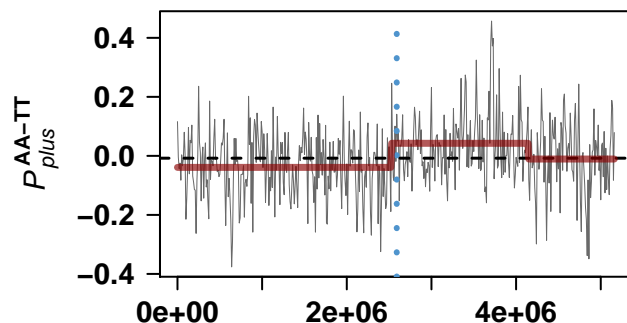
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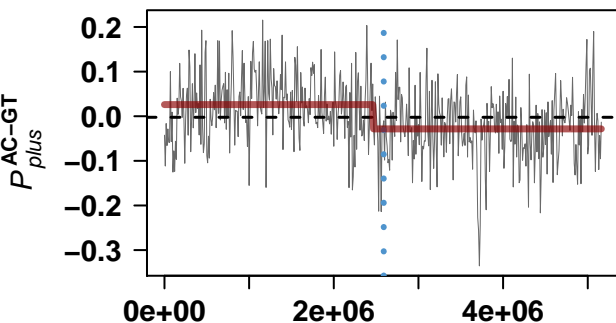
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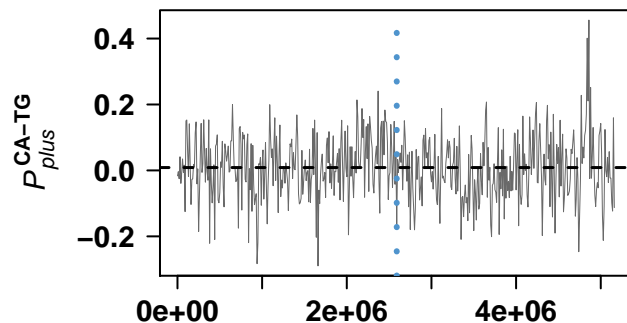
genome coordinates



genome coordinates

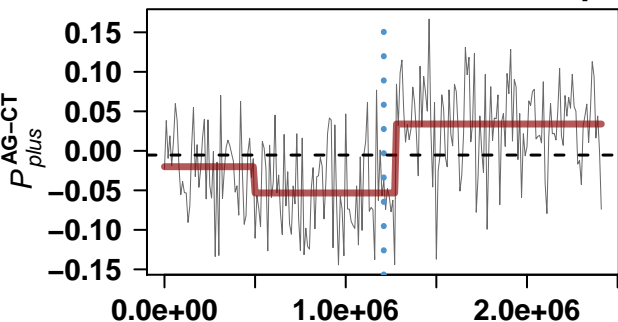


genome coordinates

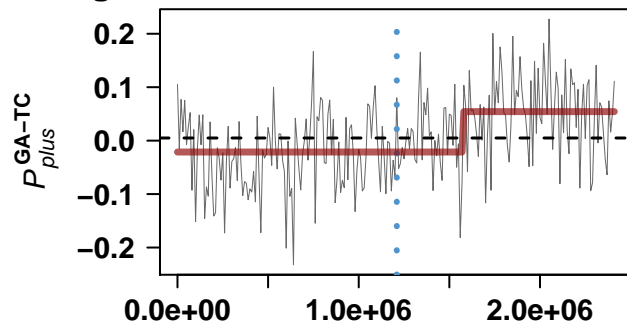


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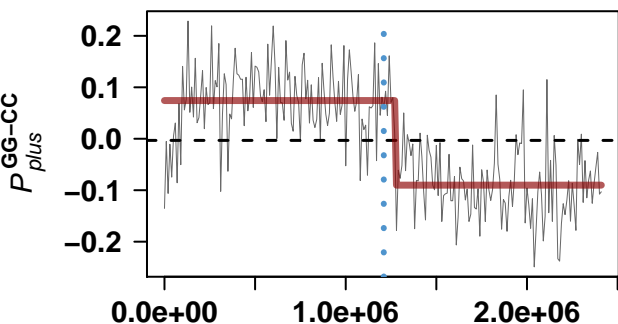
Thiomicrospira crunogena XCL-2



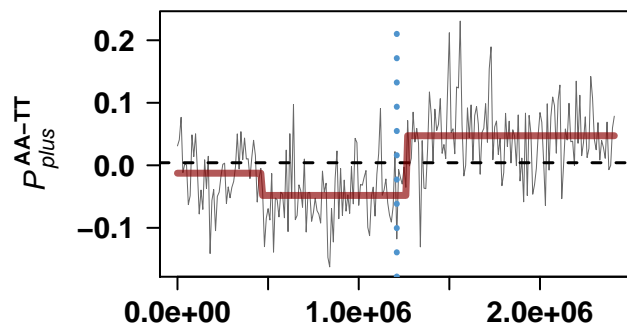
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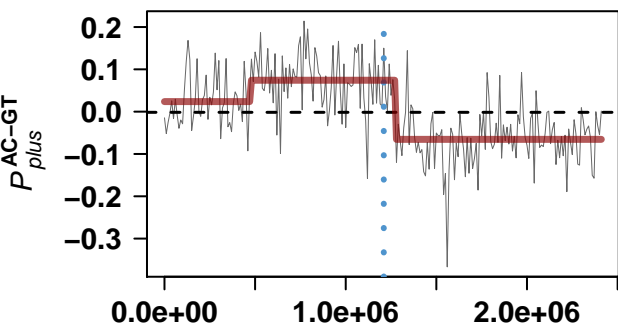
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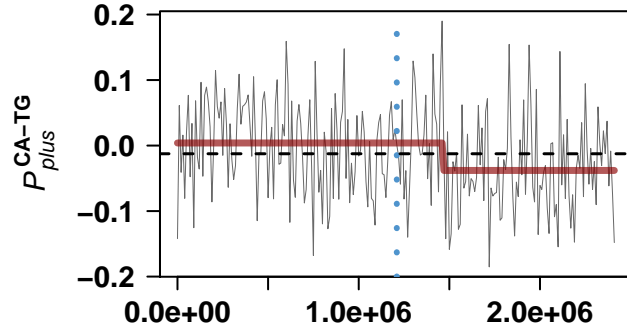
genome coordinates



genome coordinates

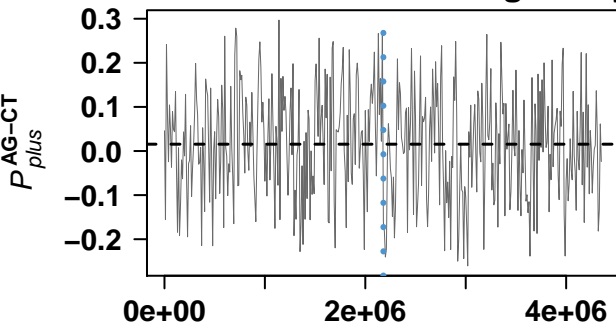


genome coordinates

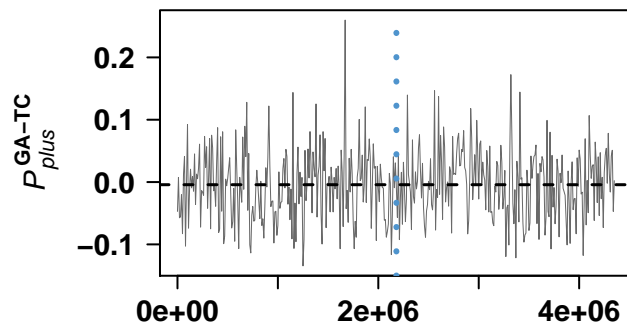


genome coordinates

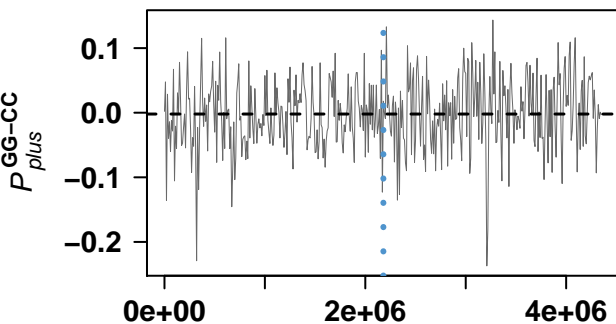
Shigella dysenteriae Sd197



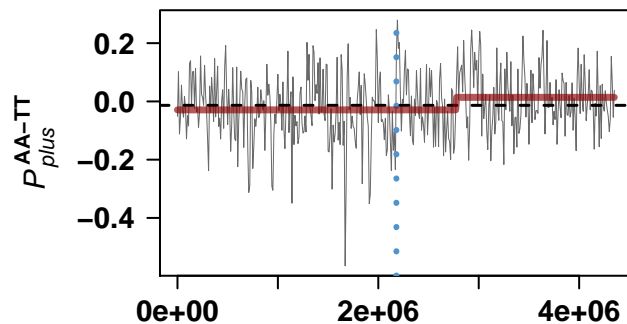
genome coordinates



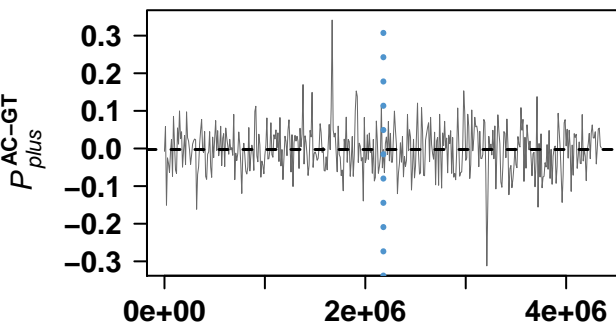
genome coordinates



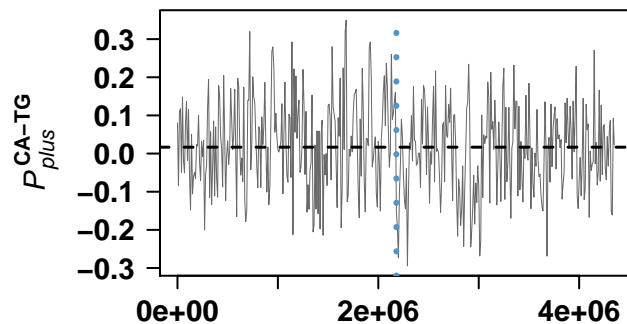
genome coordinates



genome coordinates

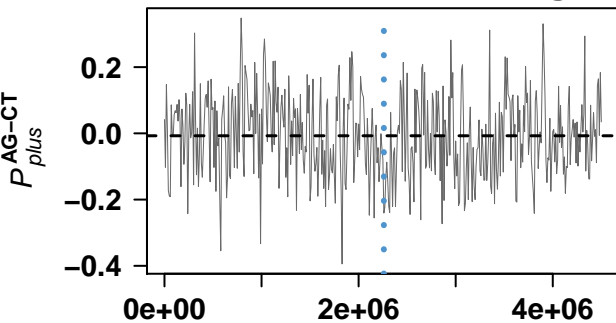


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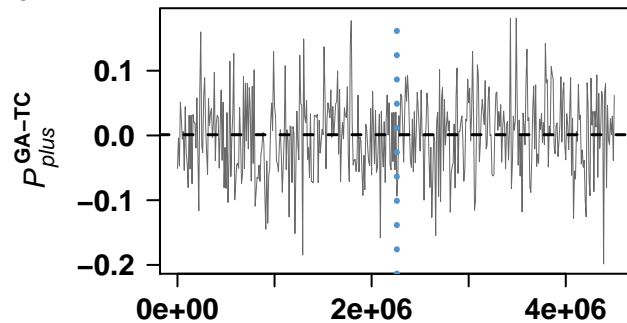


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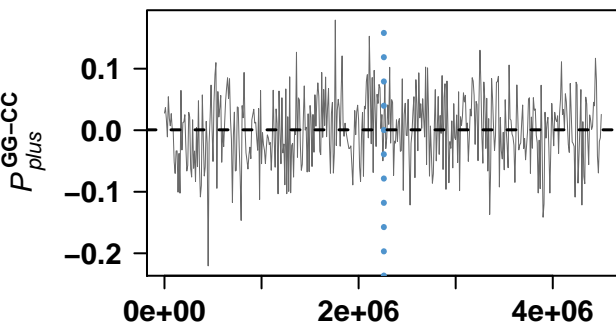
Shigella boydii Sb227



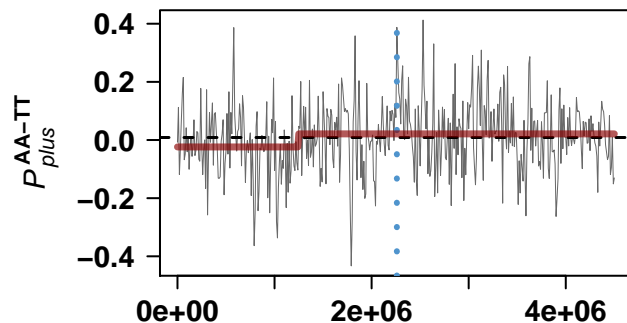
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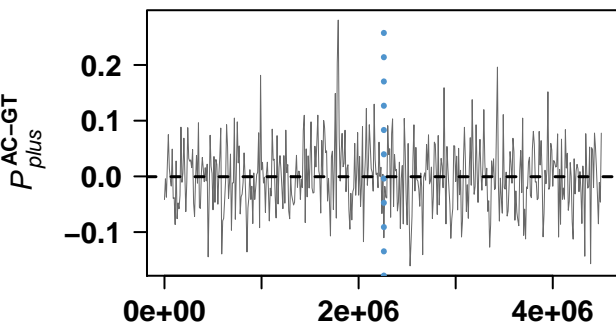
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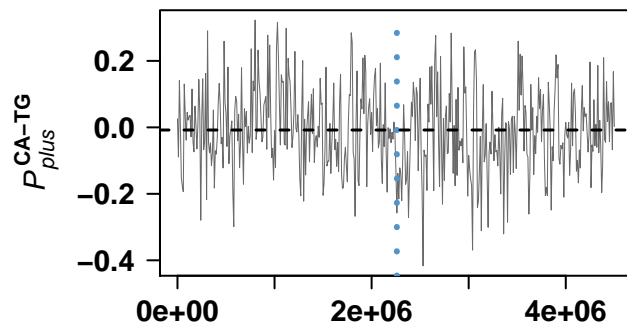
genome coordinates



genome coordinates

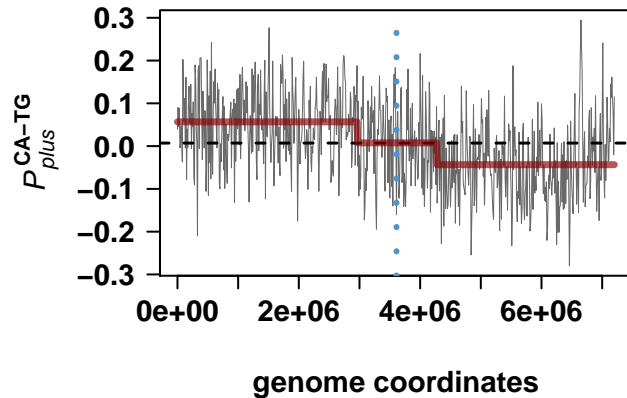
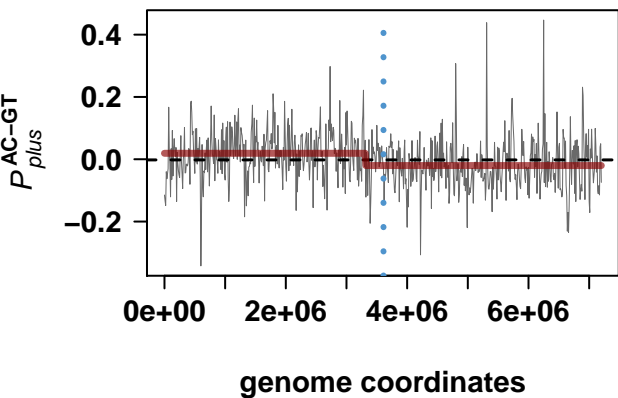
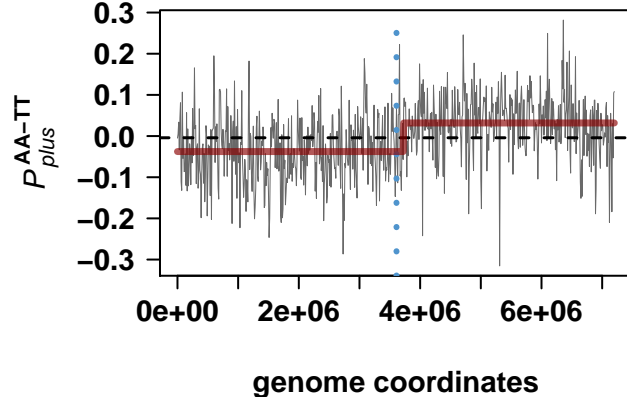
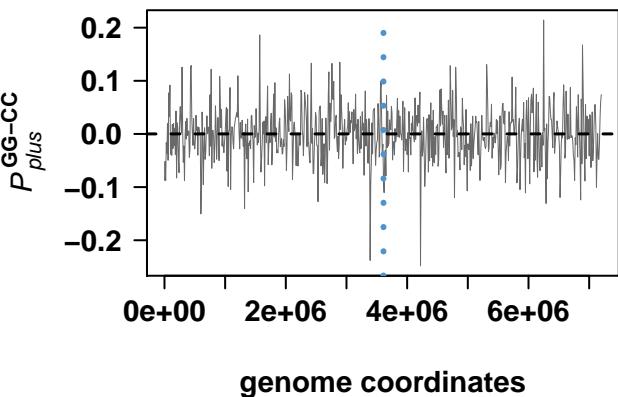
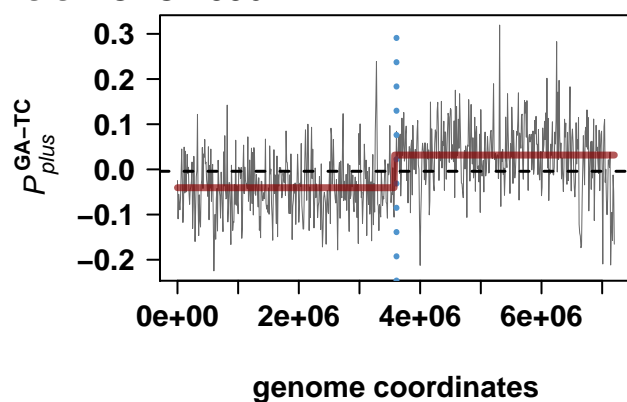
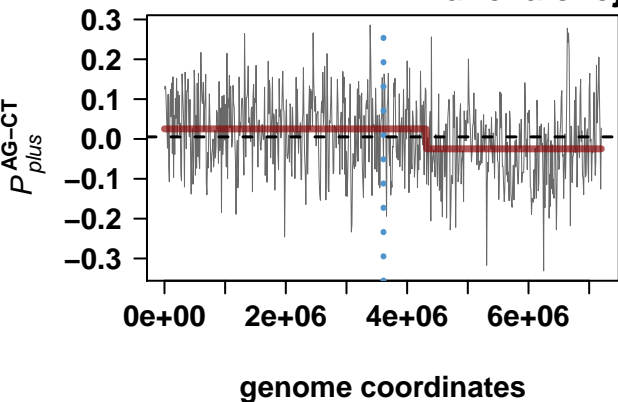


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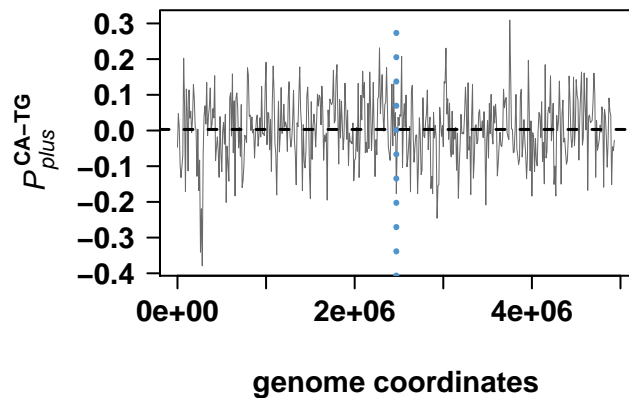
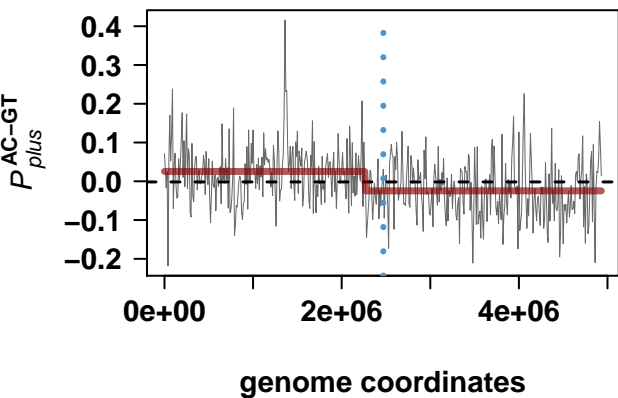
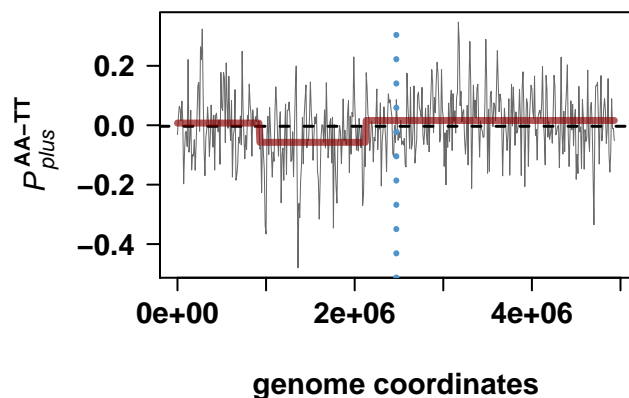
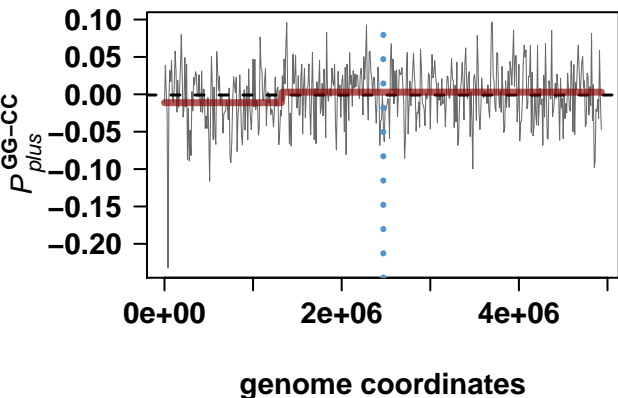
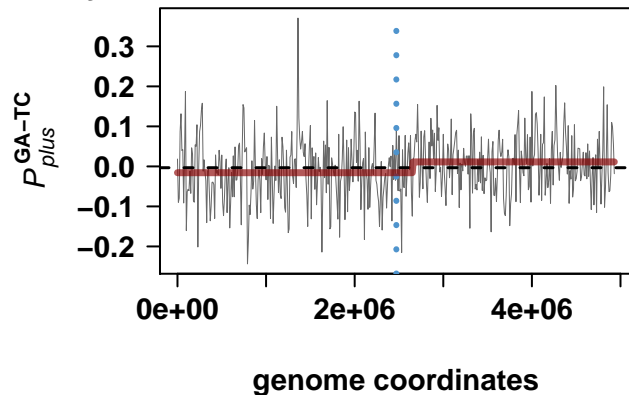
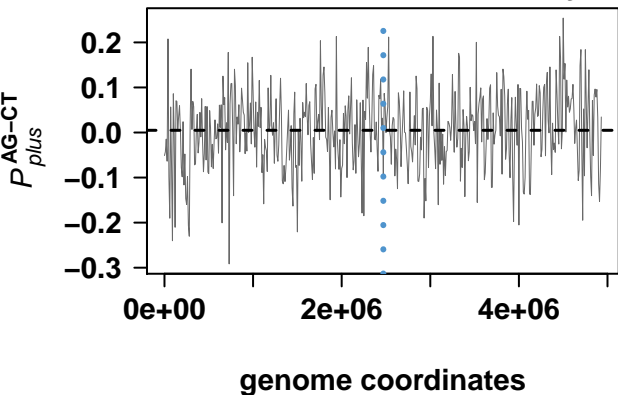


genome coordinates

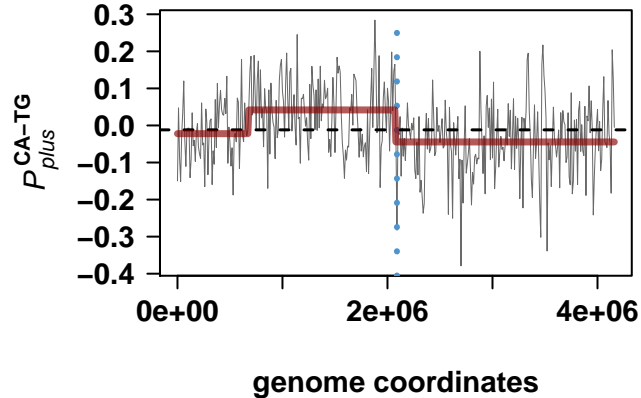
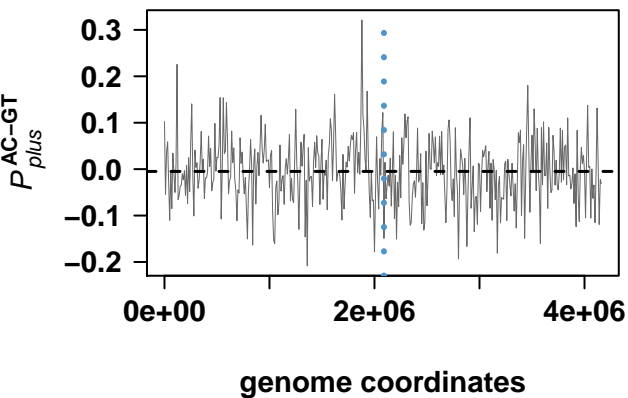
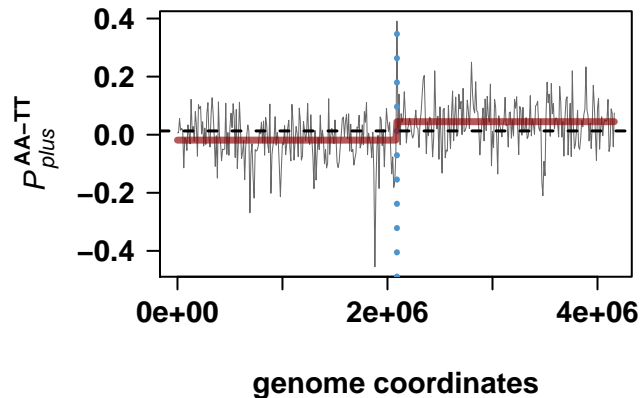
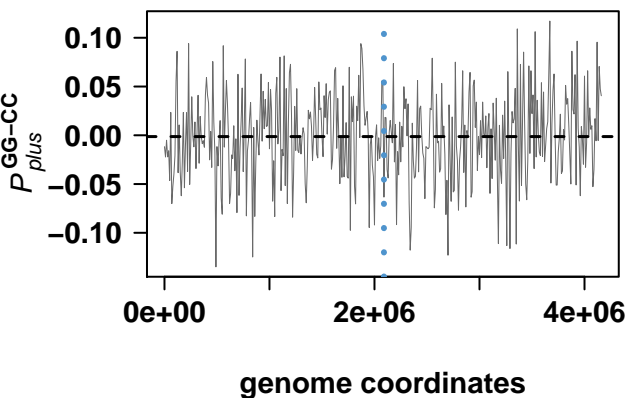
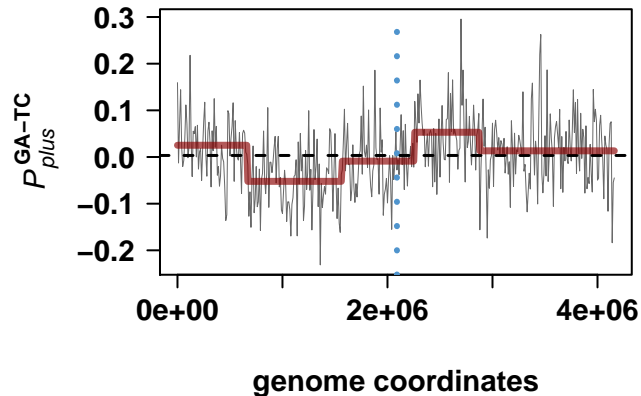
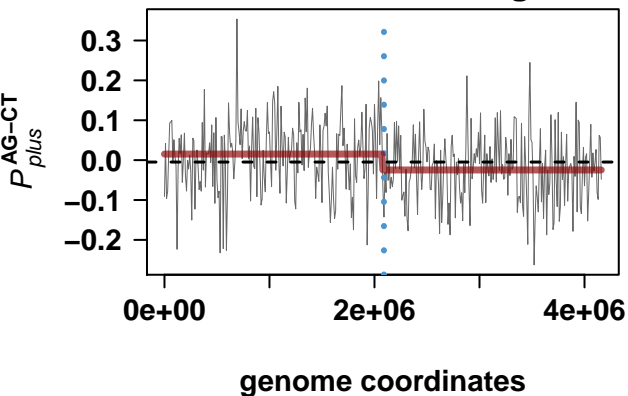
Hahella chejuensis KCTC 2396



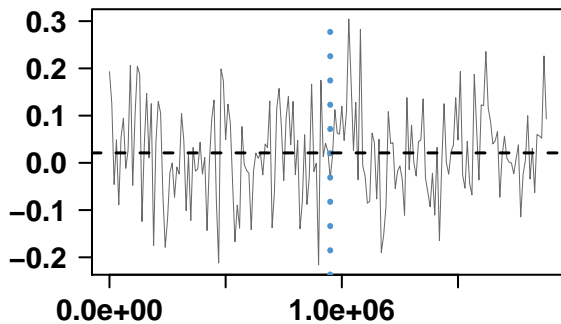
Xanthomonas oryzae pv. oryzae MAFF 311018



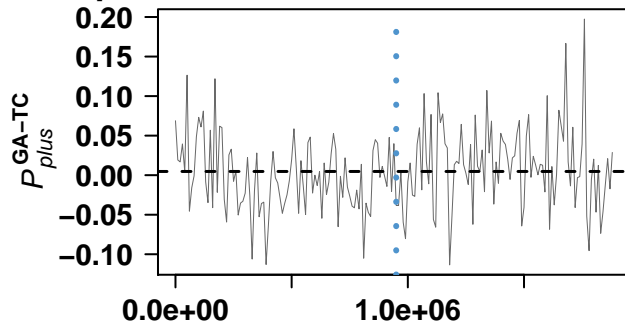
Sodalis glossinidius str. 'morsitans'



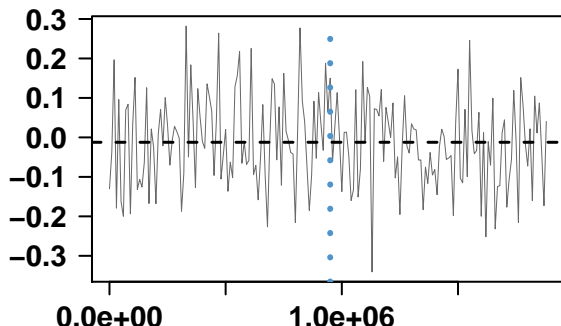
Francisella tularensis subsp. holarctica LVS



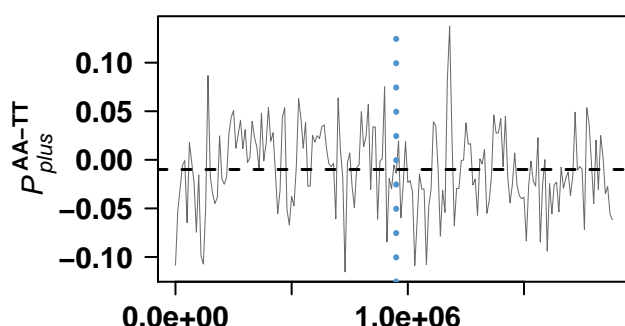
genome coordinates



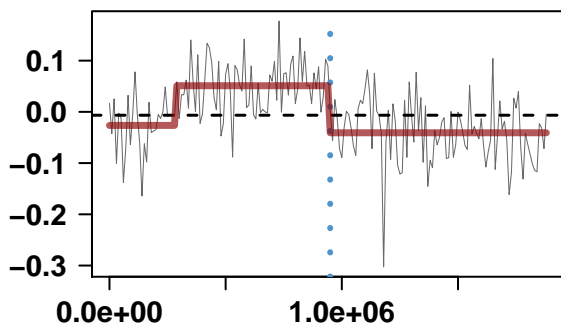
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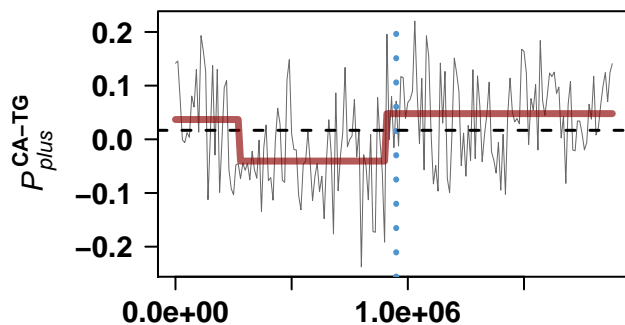
genome coordinates



genome coordinates

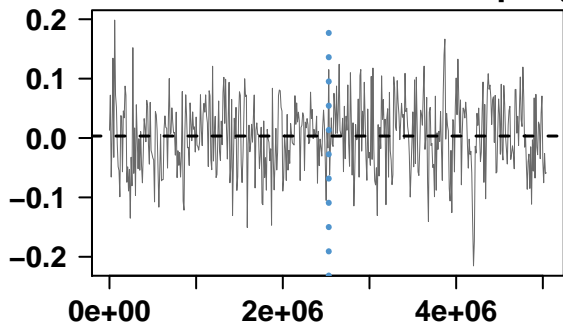


genome coordinates

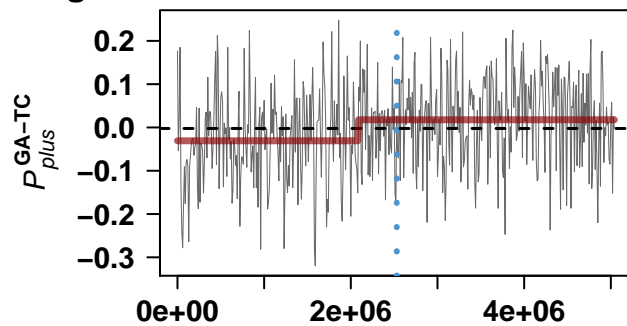


genome coordinates

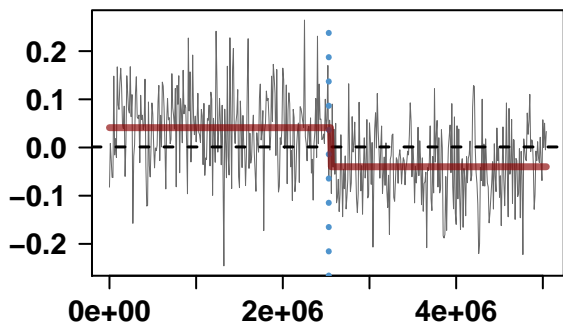
Saccharophagus degradans 2-40



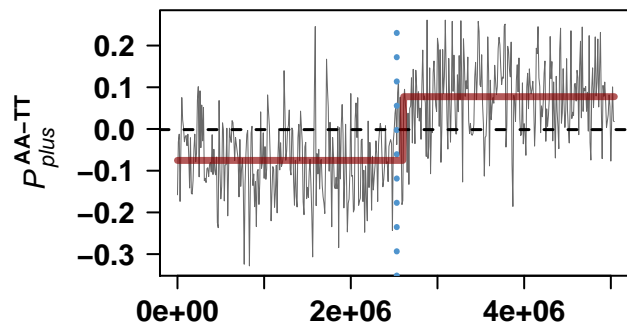
genome coordinates



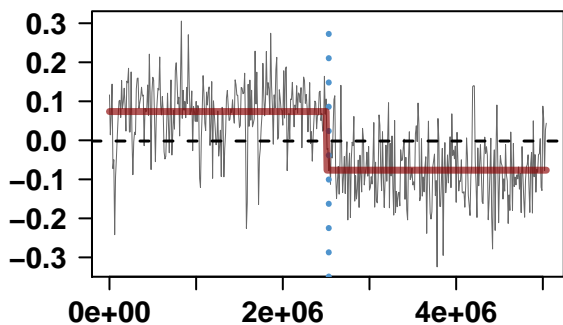
genome coordinates



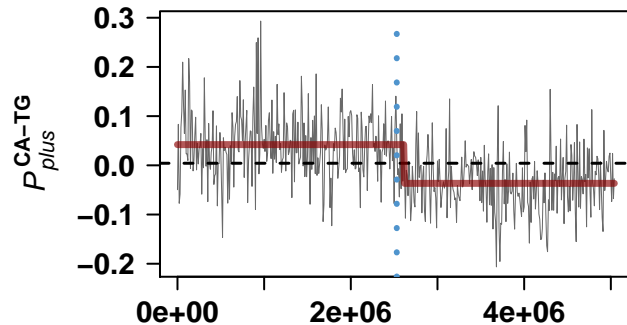
genome coordinates



genome coordinates

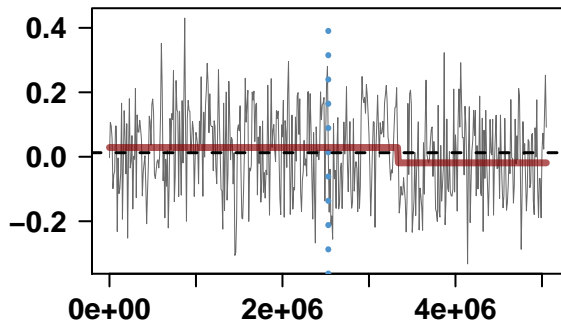


genome coordinates

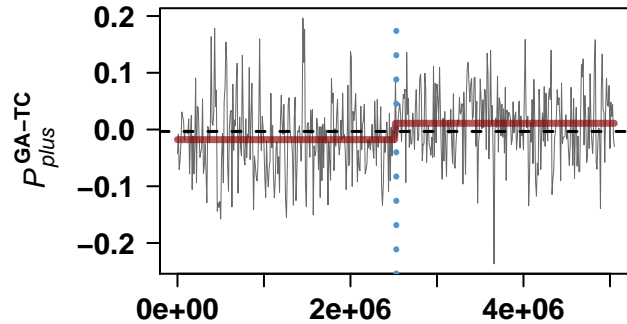


genome coordinates

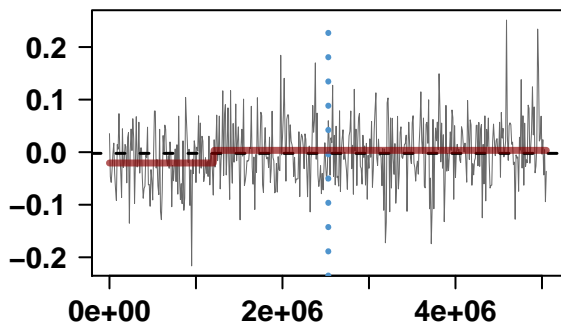
Escherichia coli UTI89



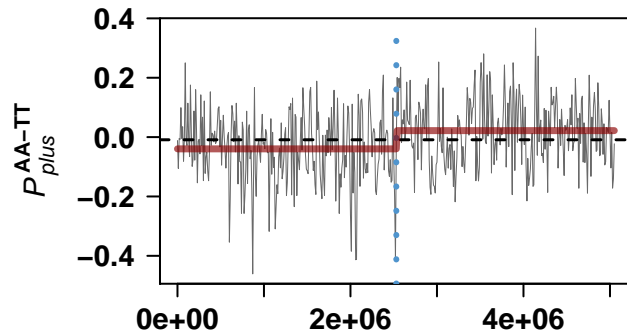
genome coordinates



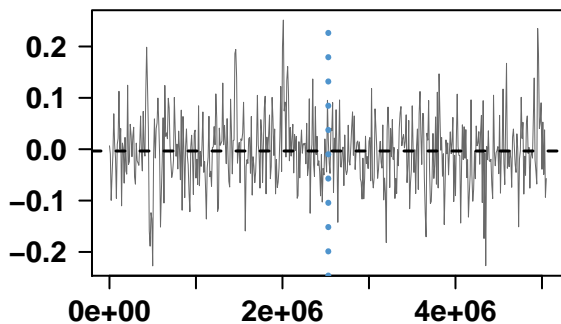
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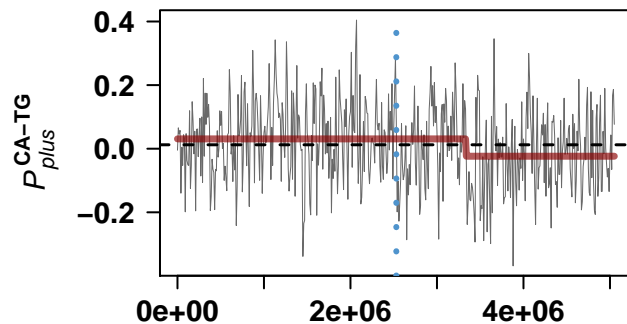
genome coordinates



genome coordinates

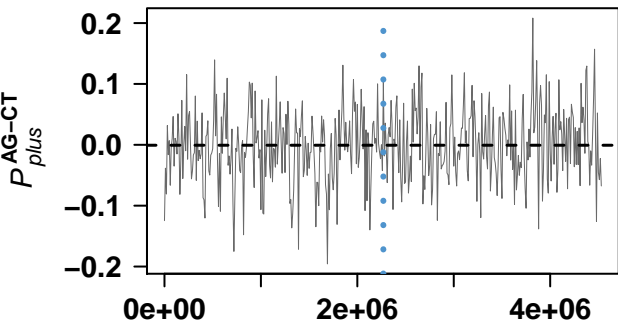


genome coordinates

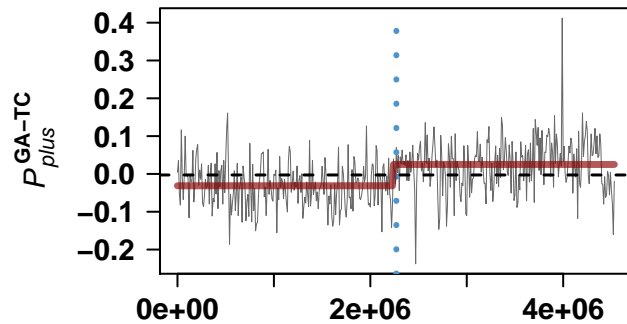


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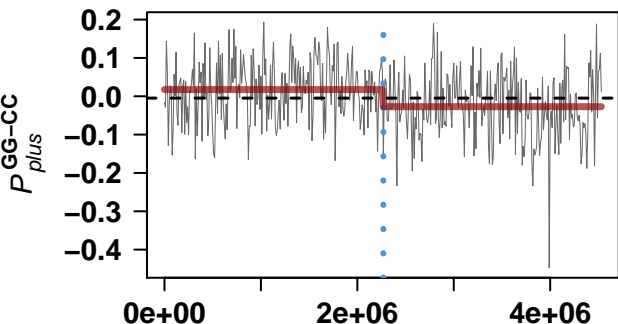
Shewanella denitrificans OS217



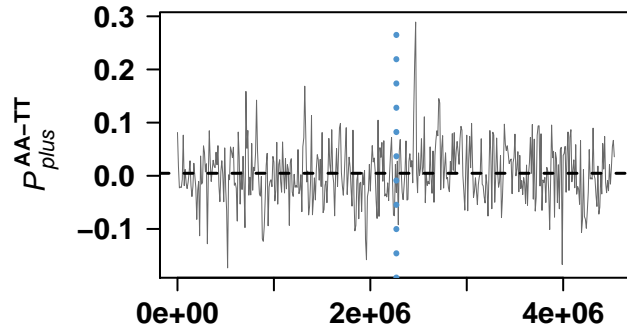
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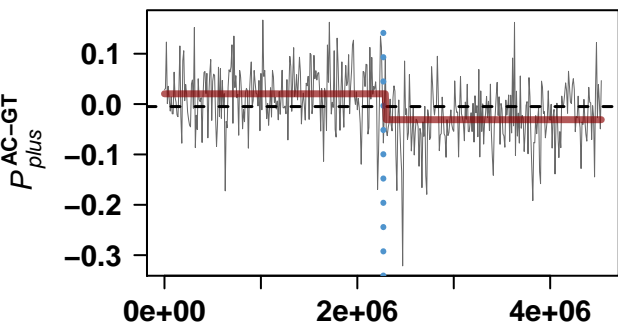
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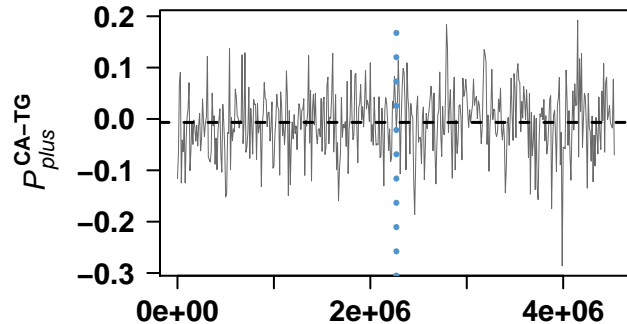
genome coordinates



genome coordinates

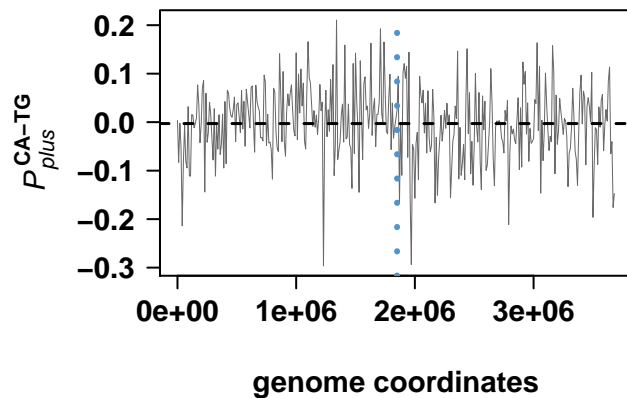
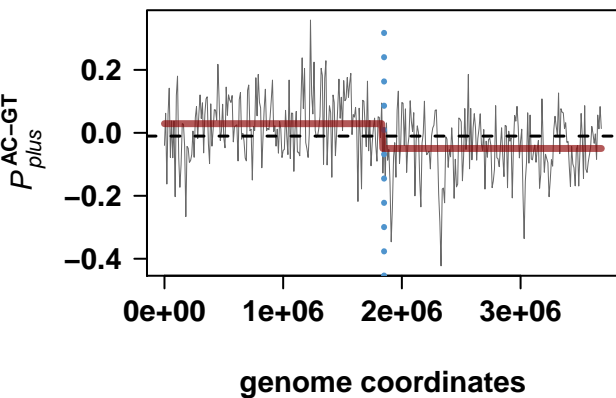
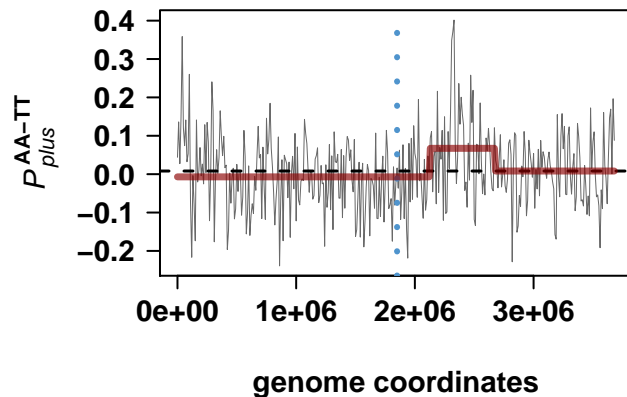
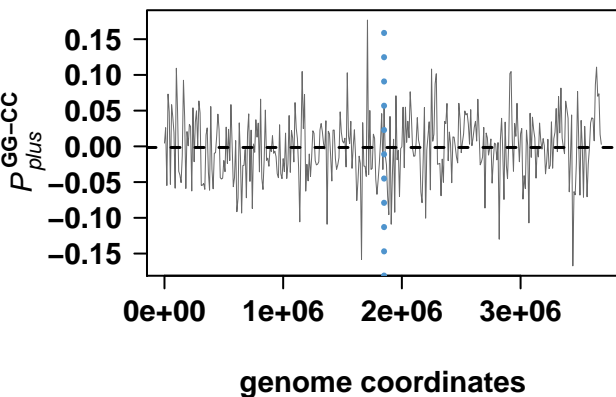
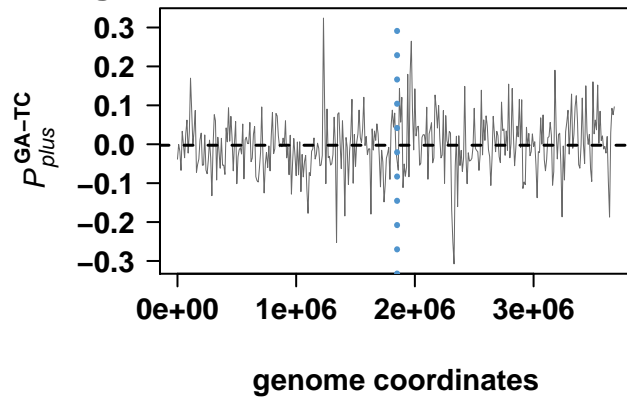
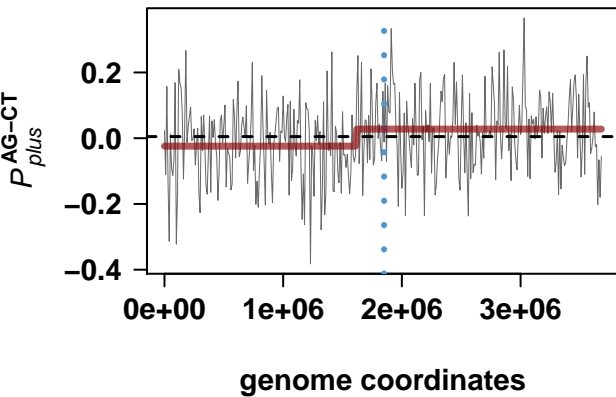


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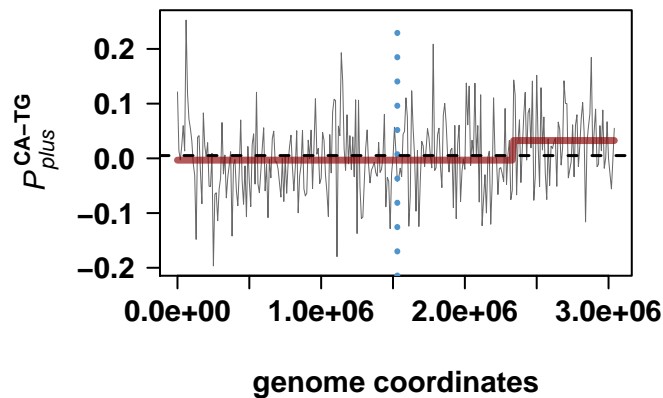
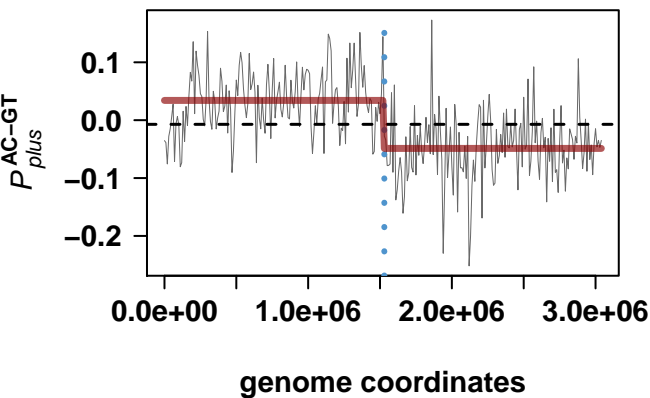
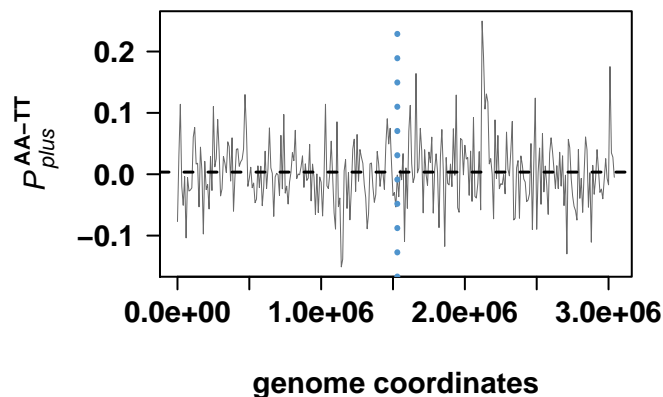
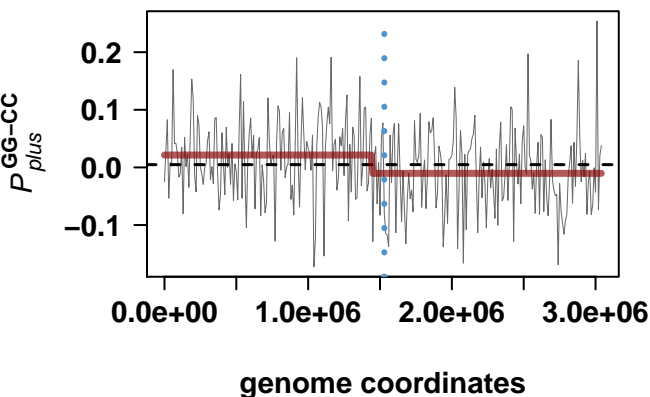
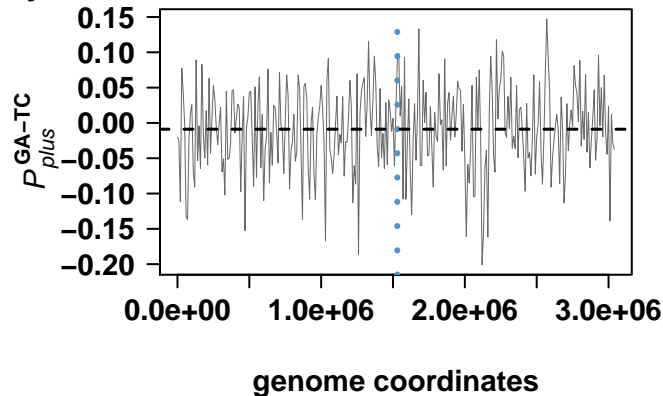
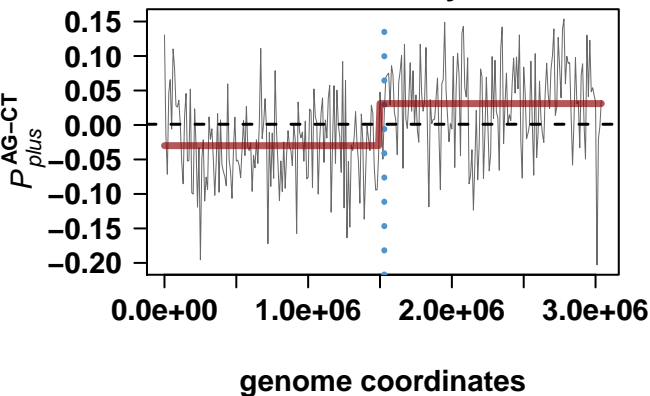


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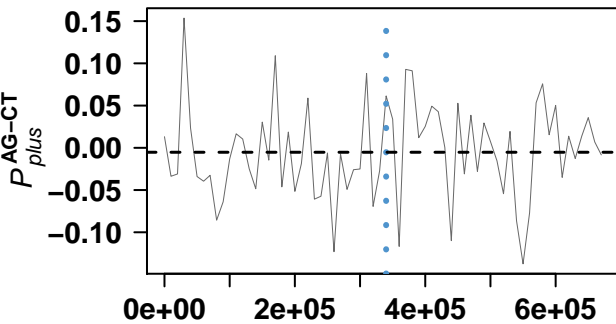
Chromohalobacter salexigens DSM 3043



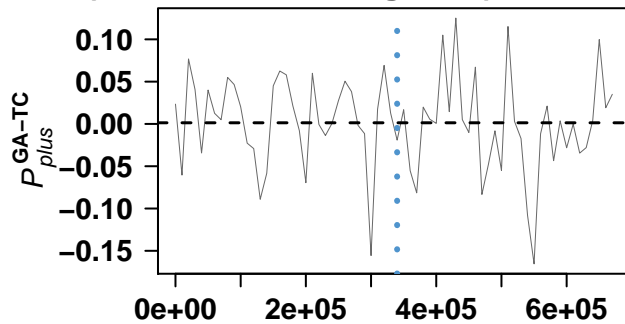
Psychrobacter cryohalientis K5



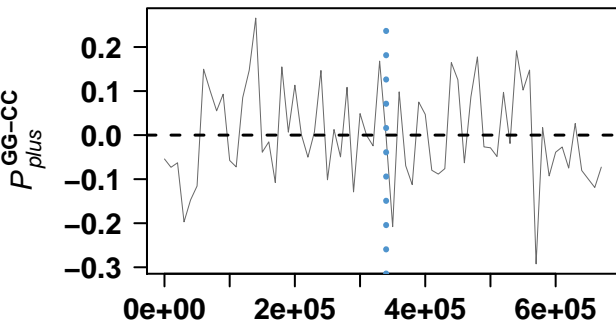
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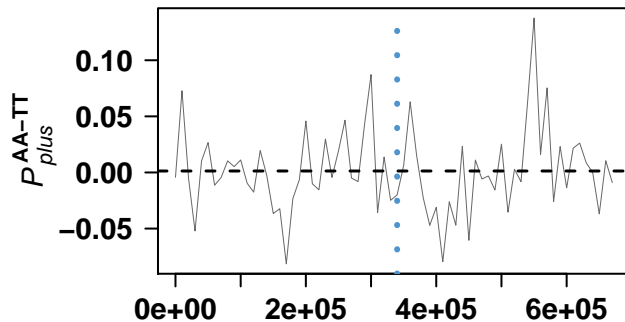
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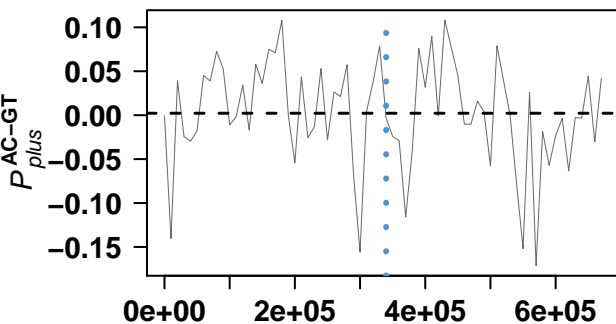
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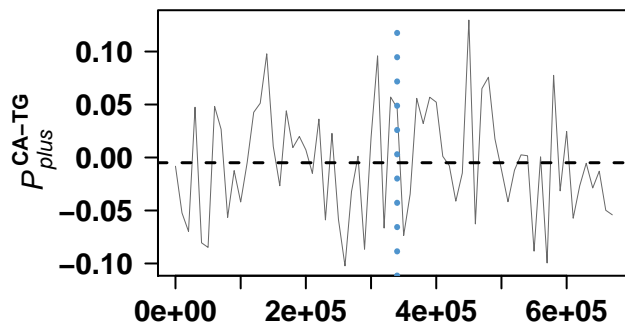
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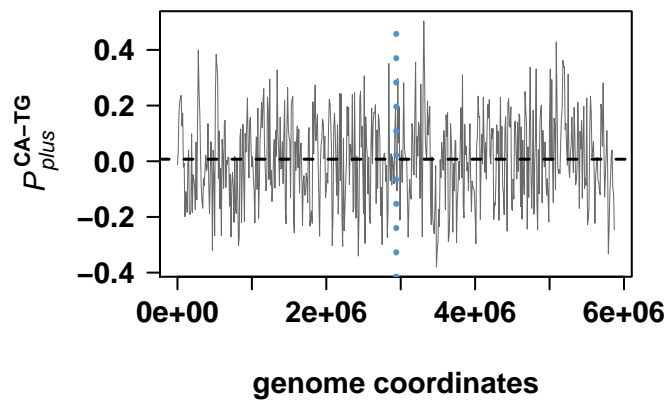
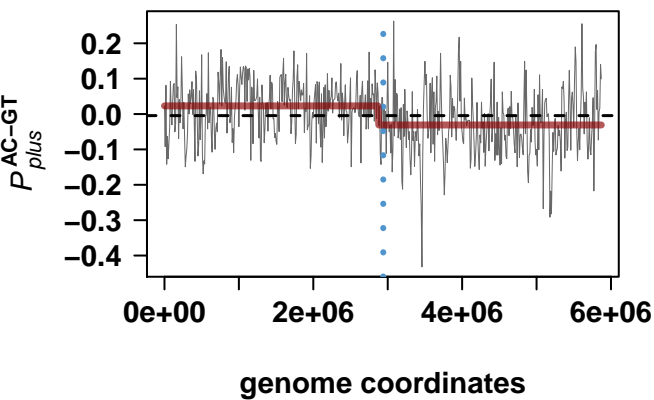
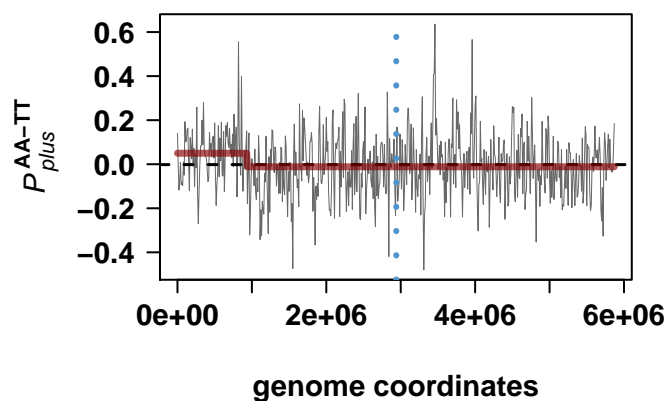
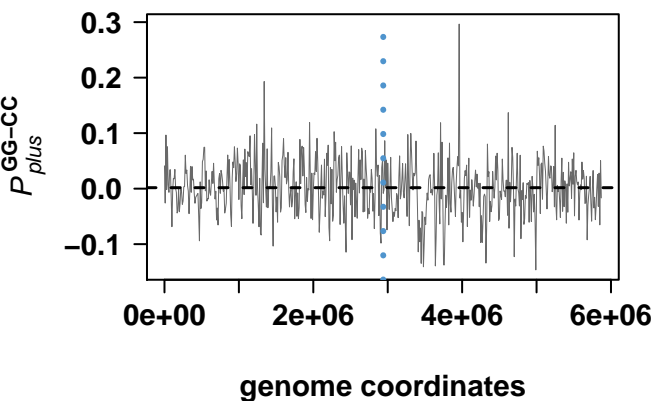
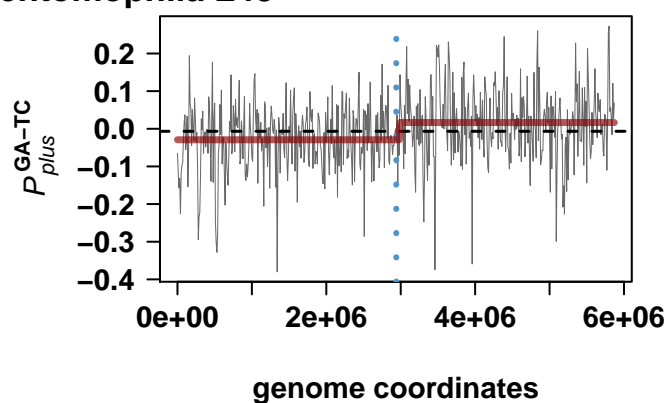
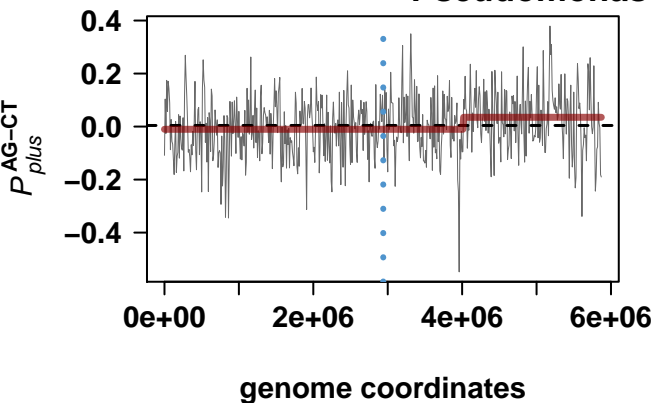


genome coordinates

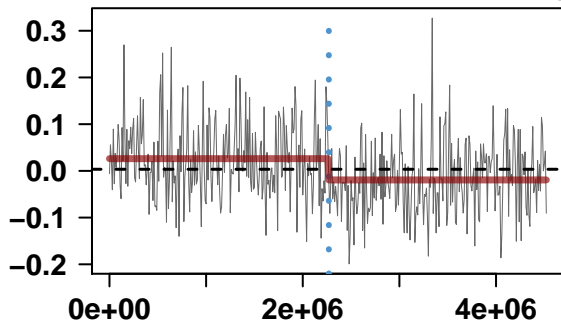


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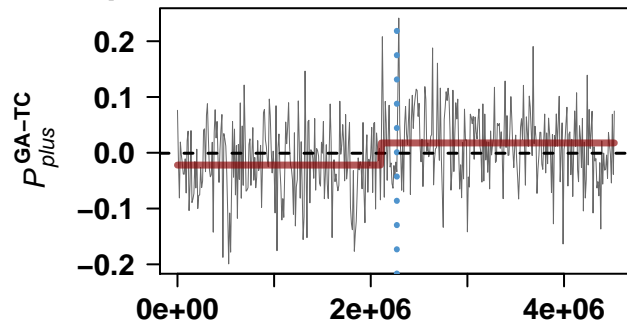
Pseudomonas entomophila L48



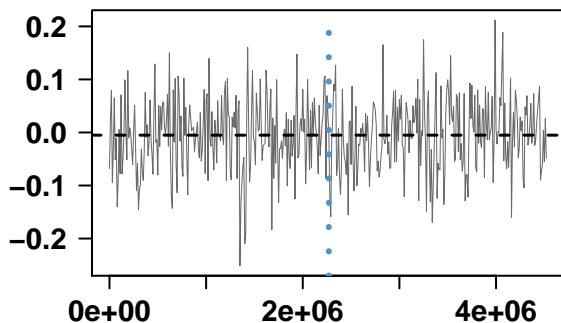
Yersinia pestis Nepal516



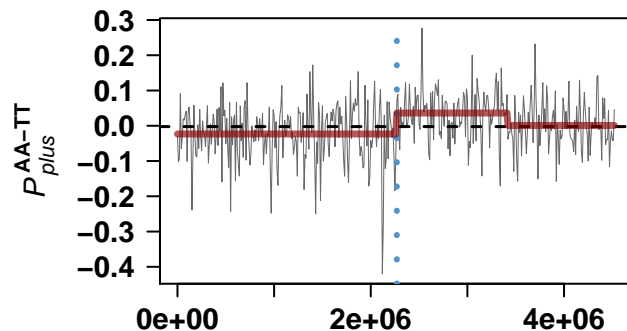
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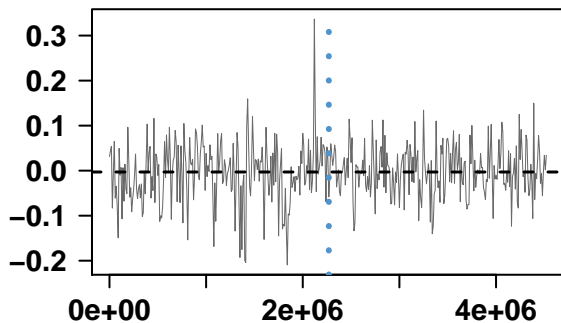
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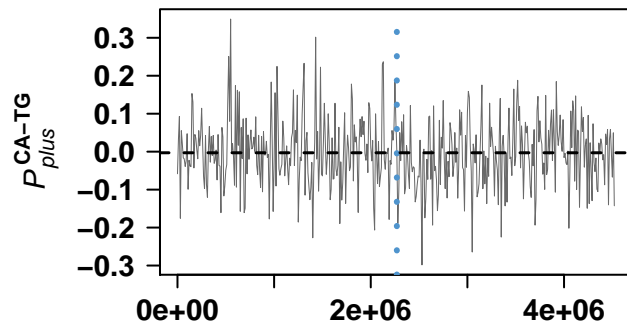
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genome coordinates

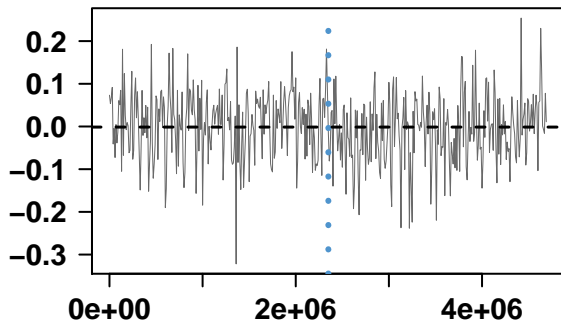


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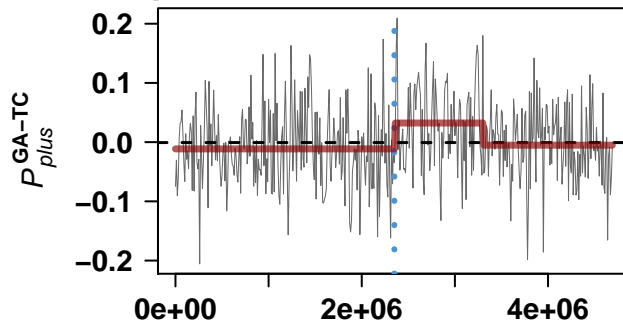


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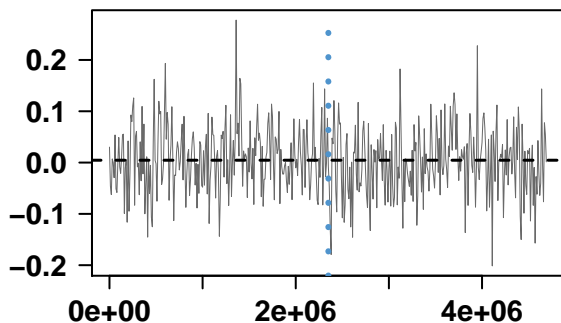
Yersinia pestis Antiqua



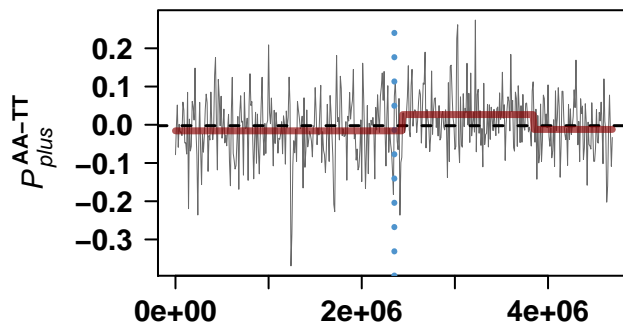
genome coordinates



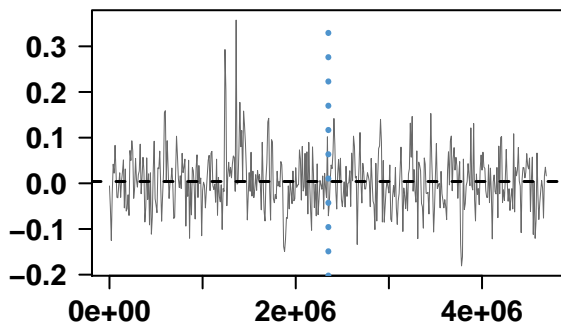
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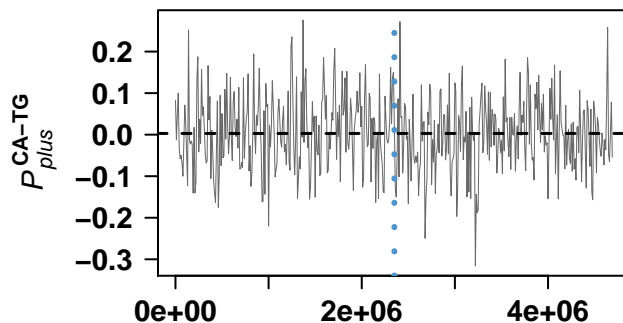
genome coordinates



genome coordinates

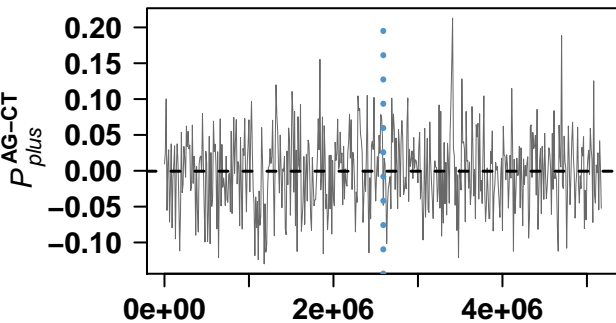


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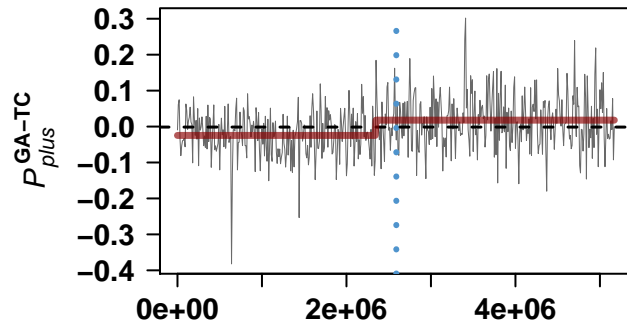


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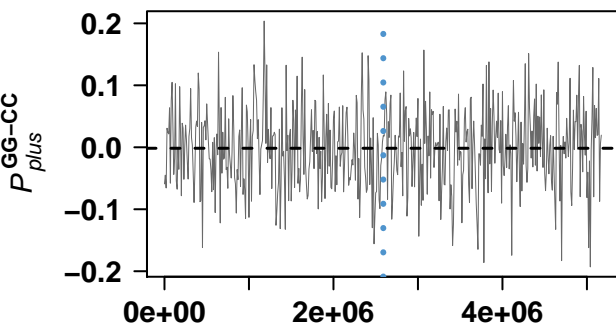
Pseudoalteromonas atlantica T6c



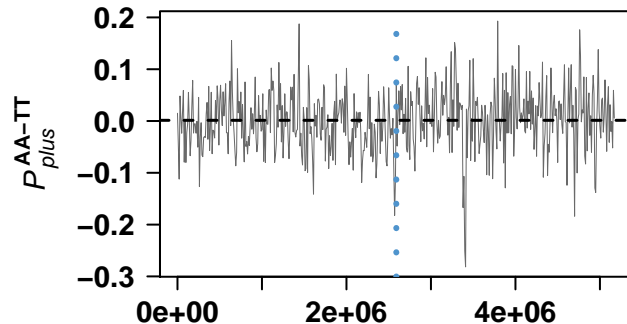
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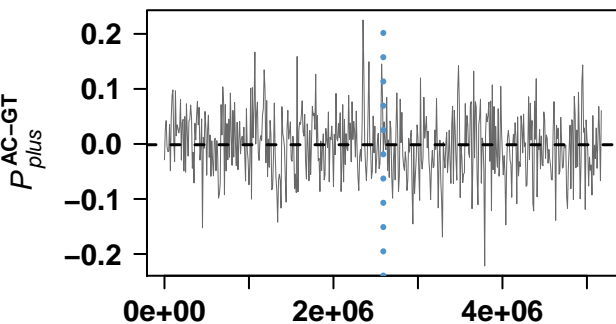
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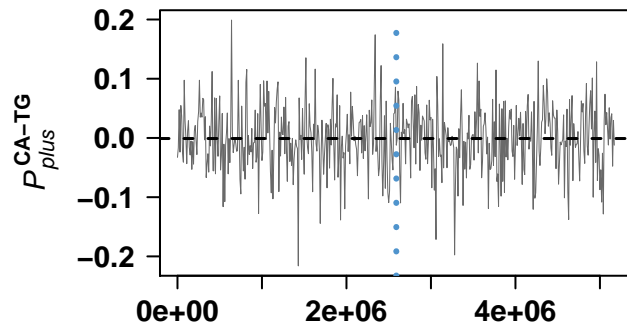
genome coordinates



genome coordinates

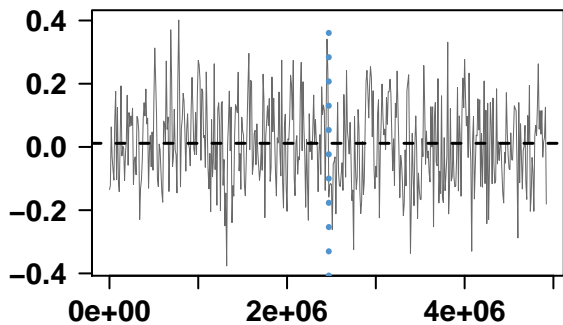


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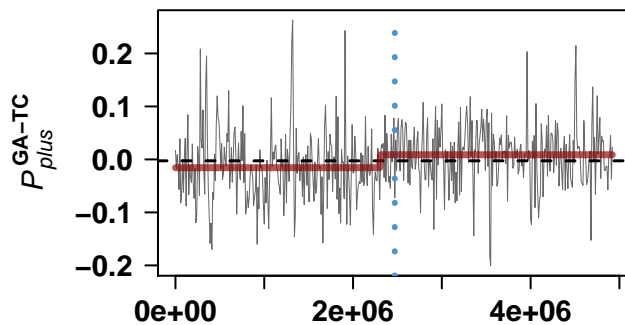


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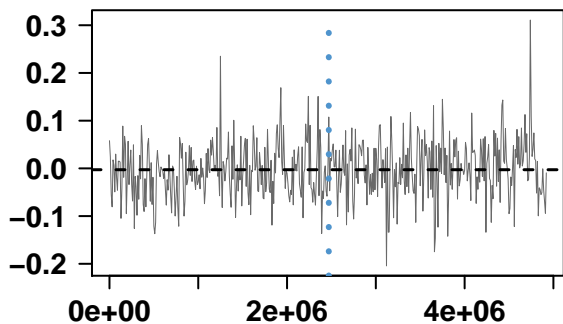
Escherichia coli 536



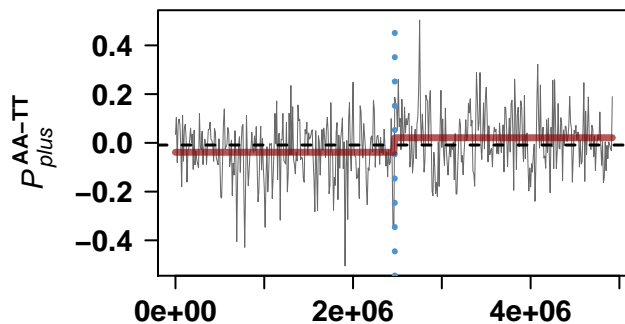
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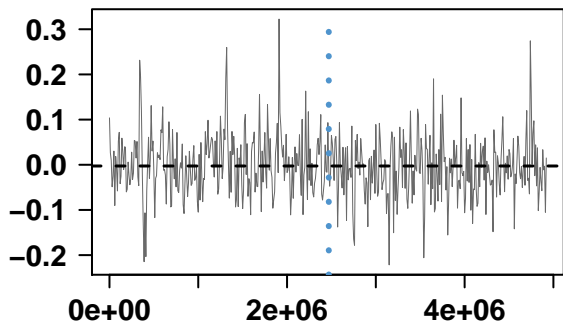
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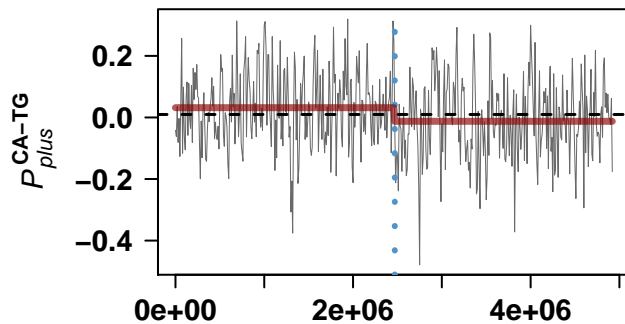
genome coordinates



genome coordinates

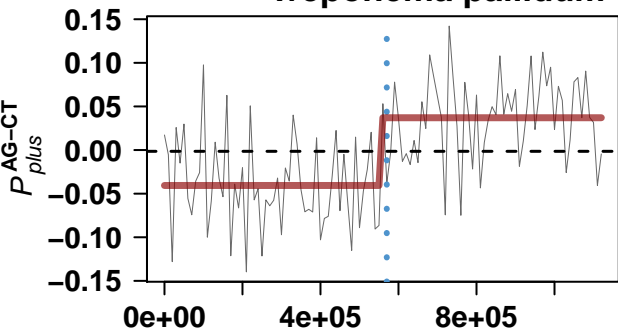


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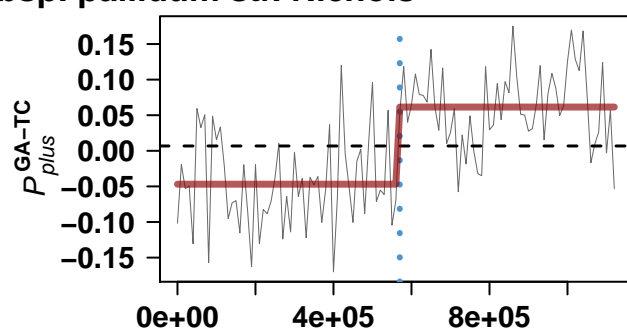


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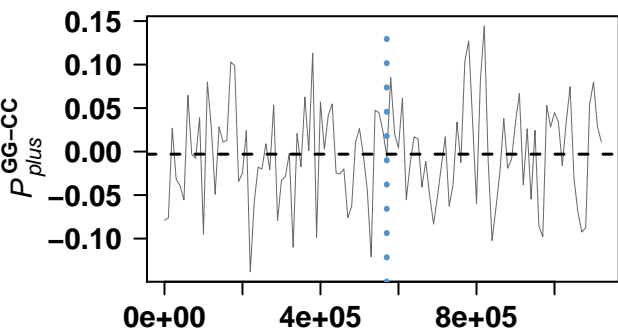
Treponema pallidum subsp. pallidum str. Nichols



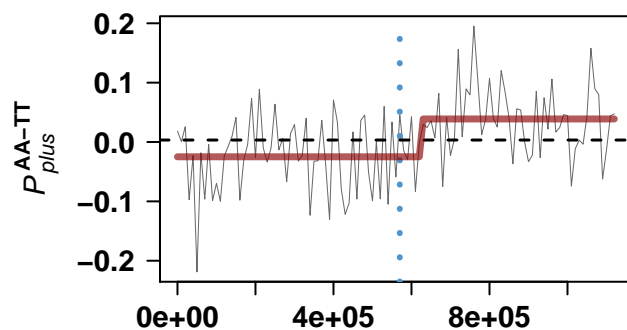
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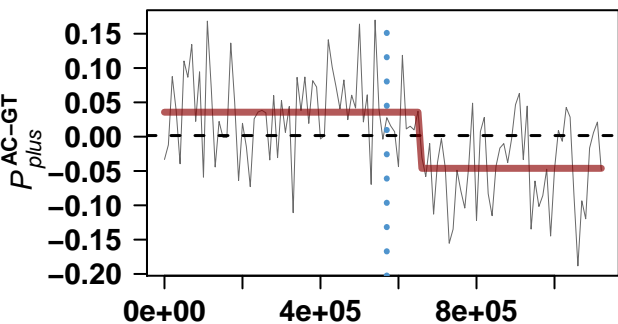
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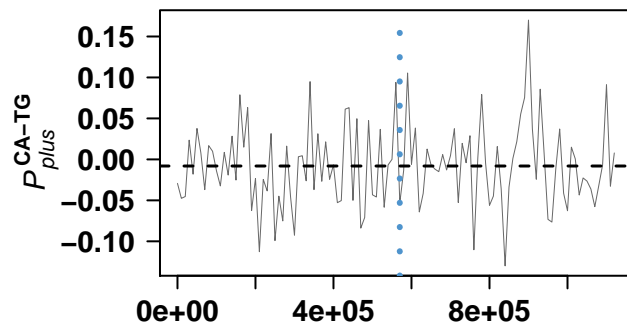
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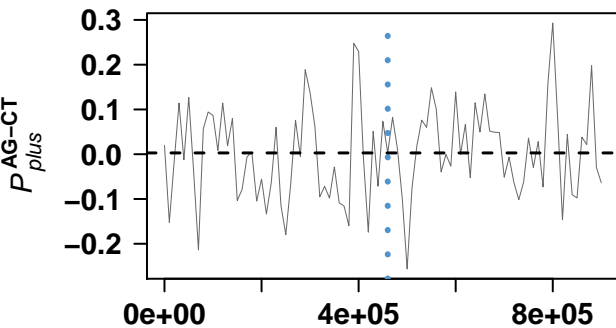


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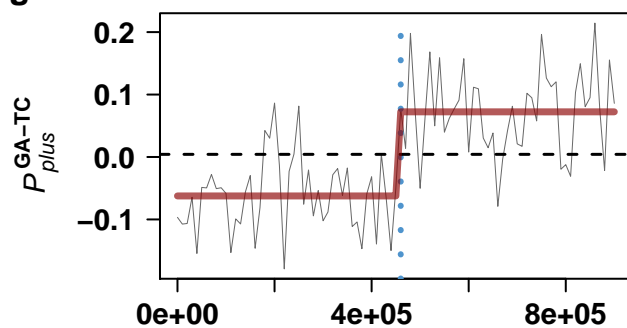


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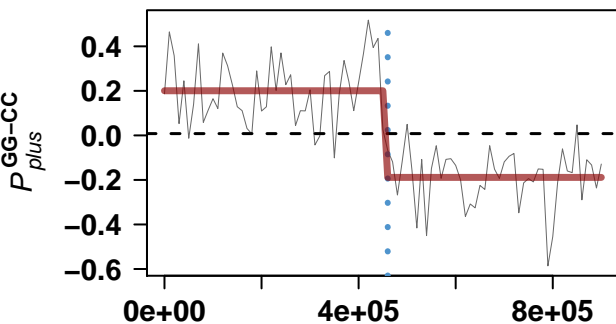
Borrelia burgdorferi B31



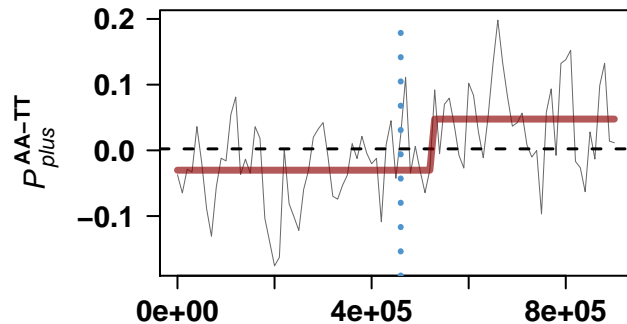
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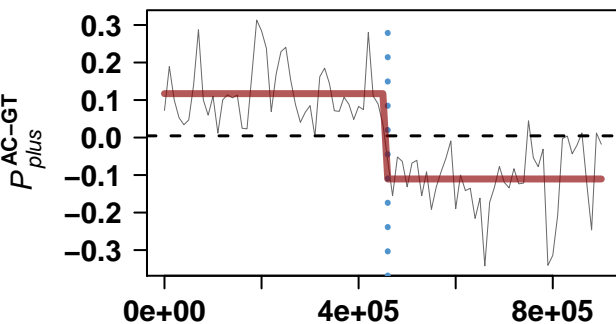
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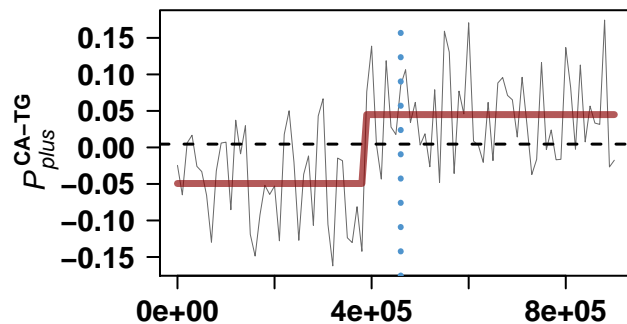
genome coordinates



genome coordinates

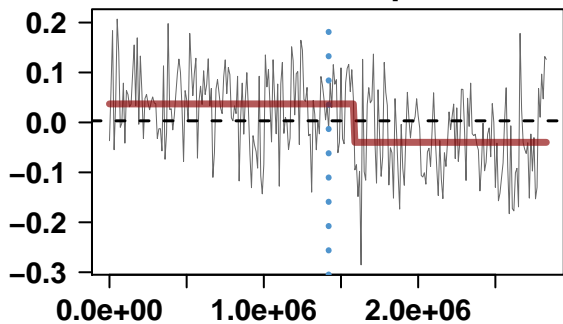


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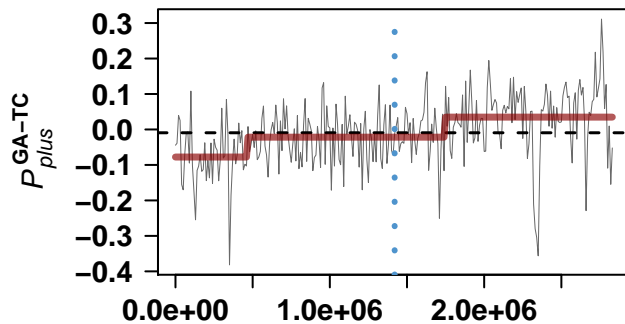


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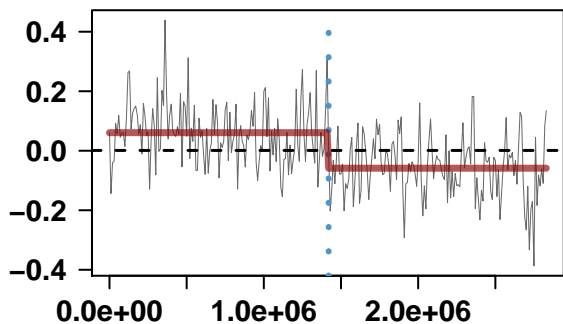
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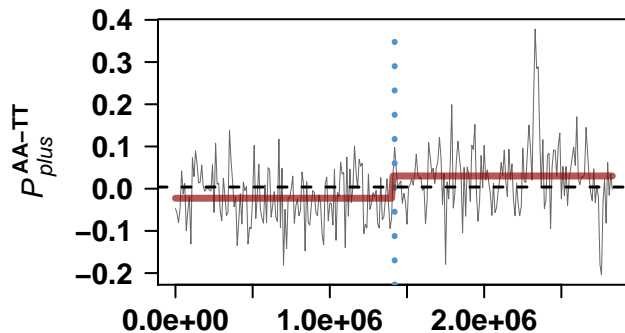
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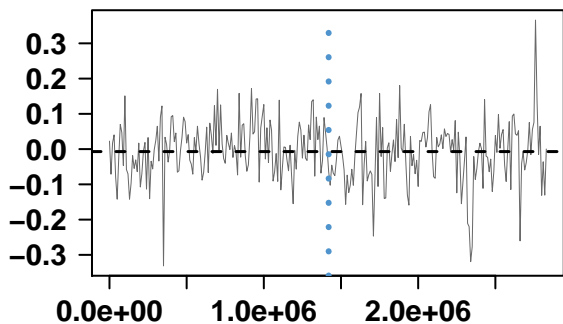
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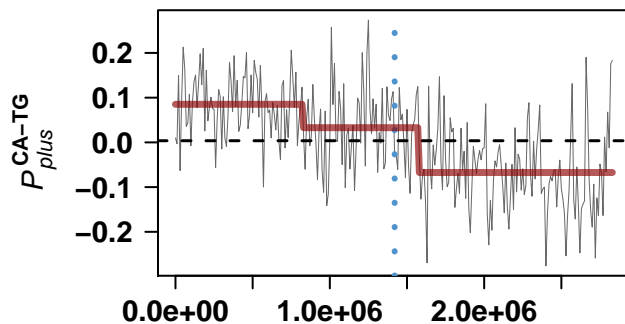
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genome coordinates

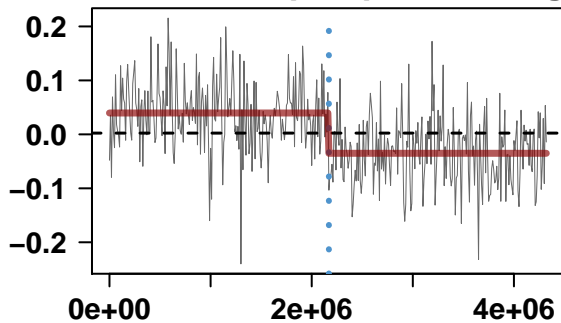


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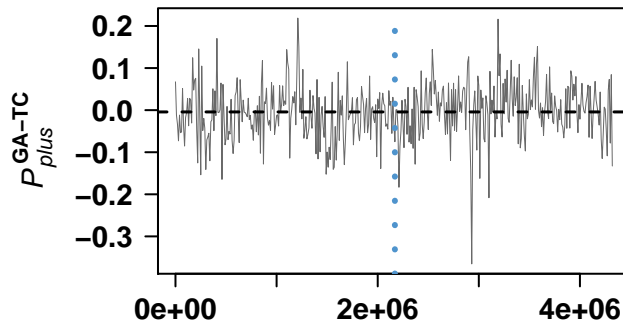


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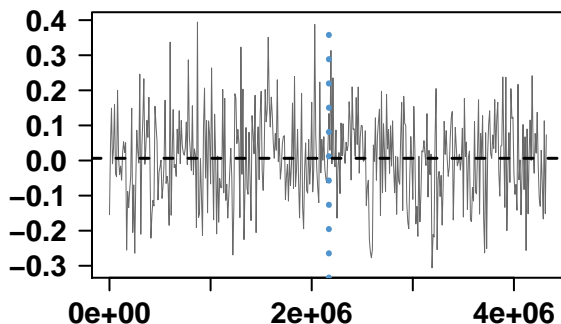
Leptospira interrogans serovar Lai str. 56601



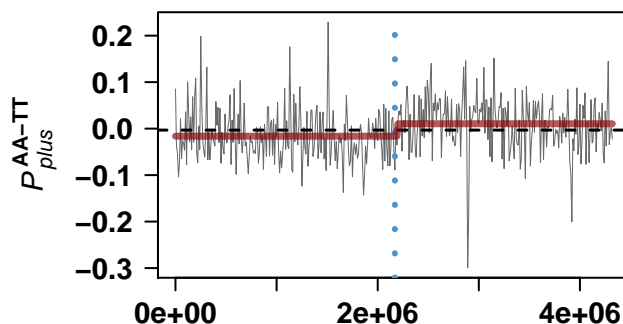
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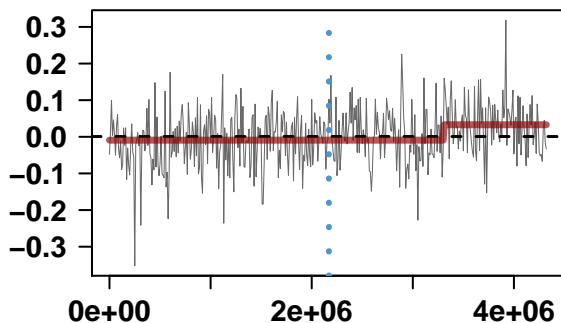
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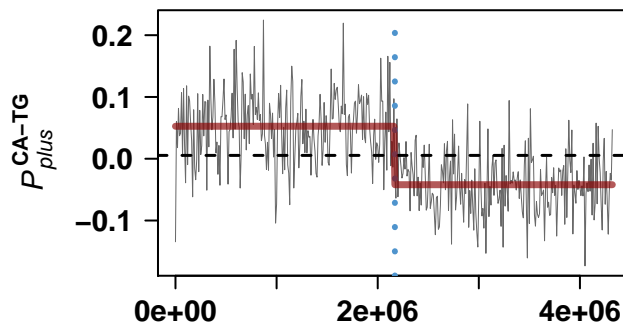
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genome coordinates

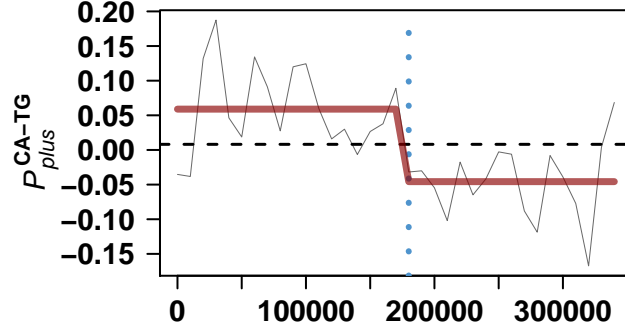
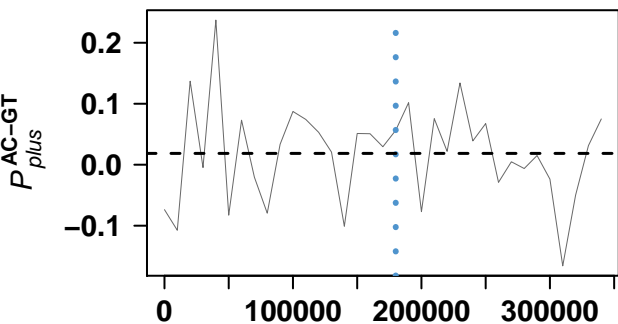
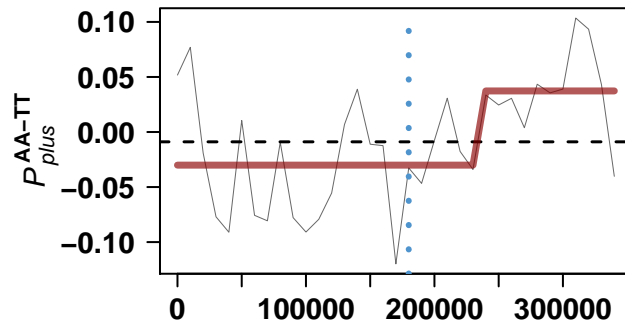
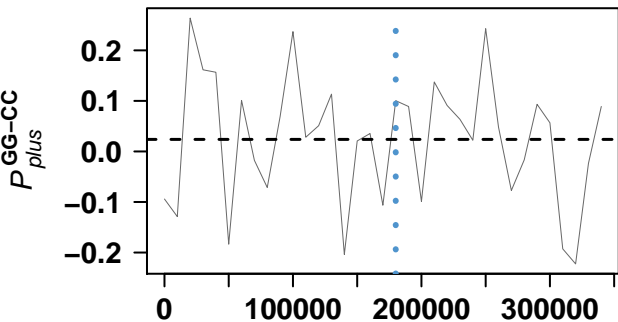
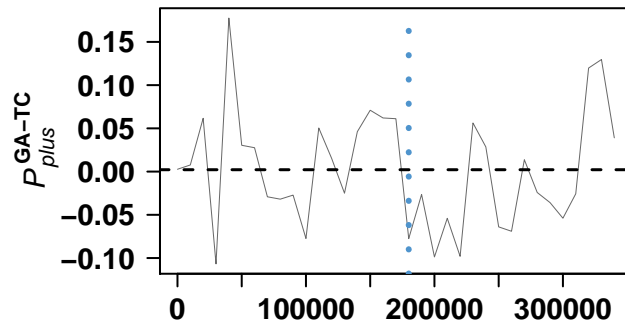
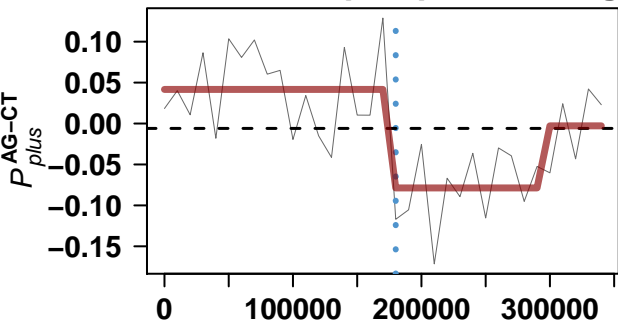


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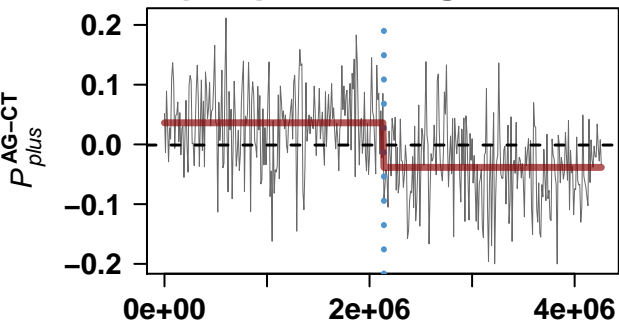


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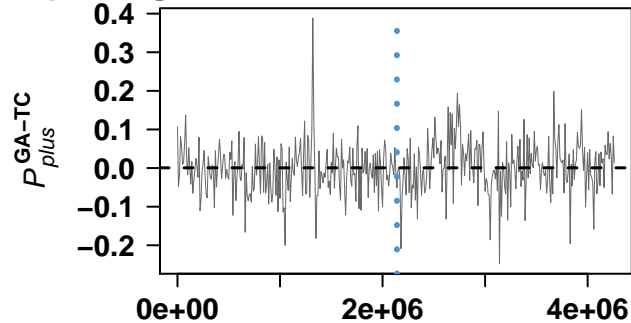
Leptospira interrogans serovar Lai str. 56601



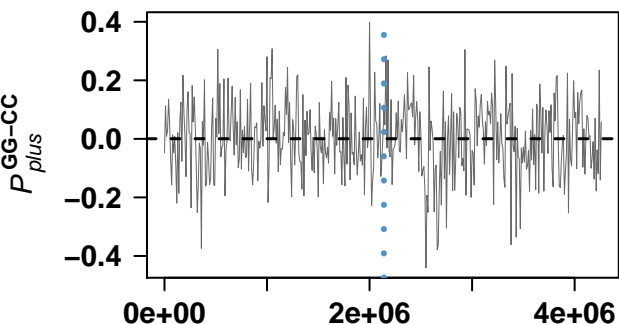
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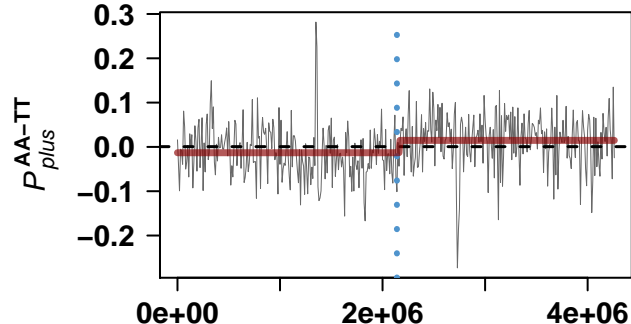
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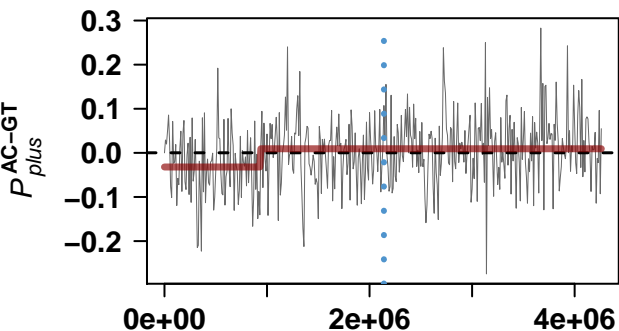
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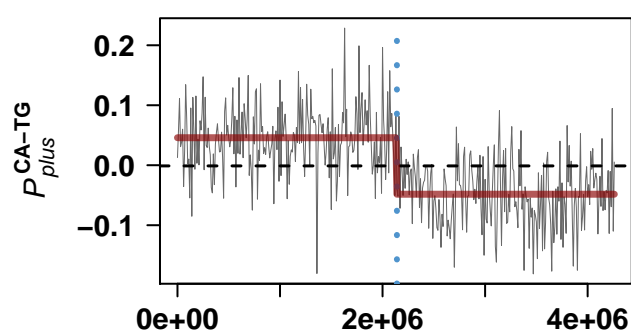
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genome coordinates

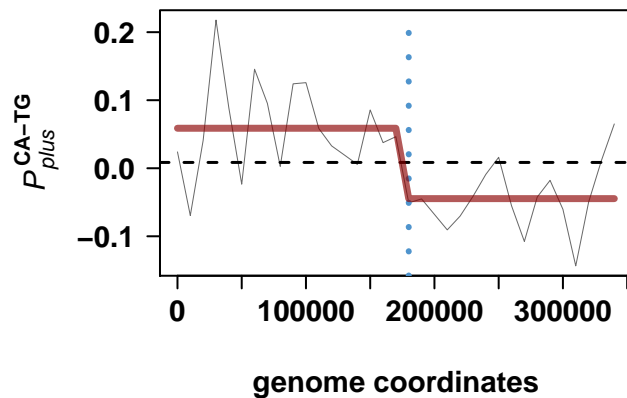
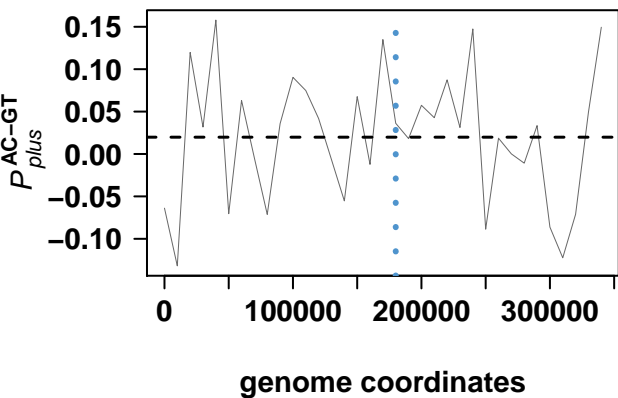
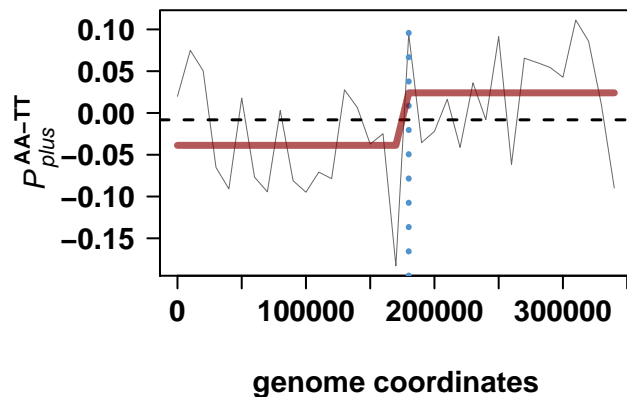
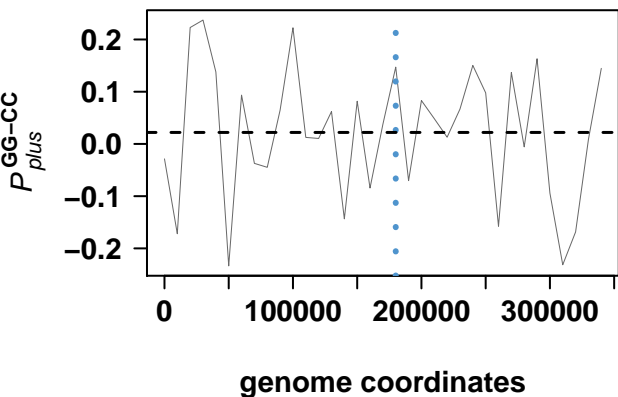
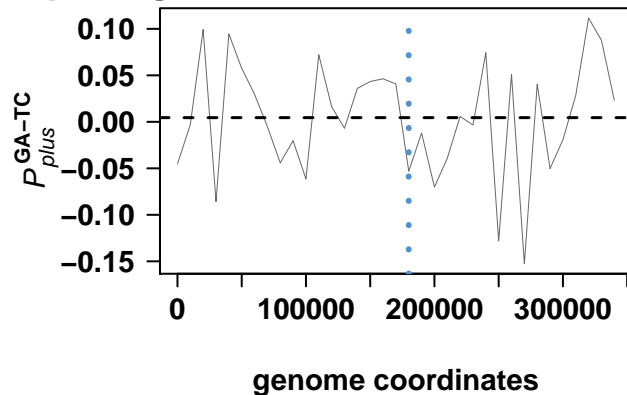
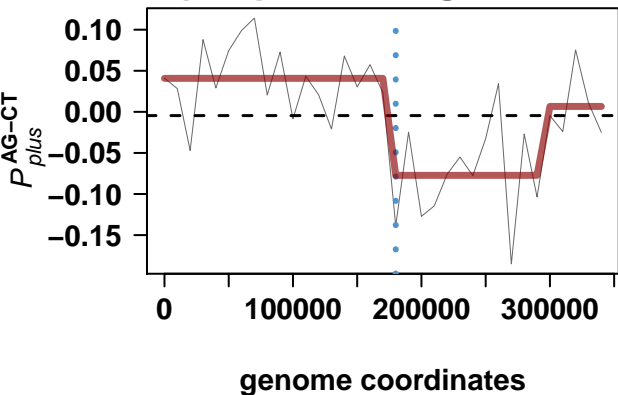


genome coordinates

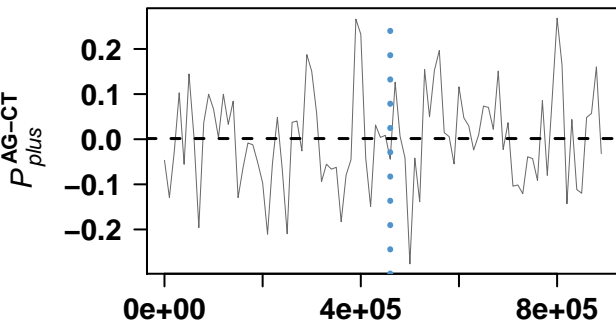


genome coordinates

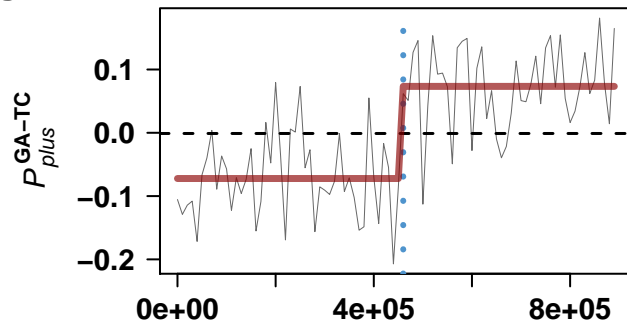
Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130



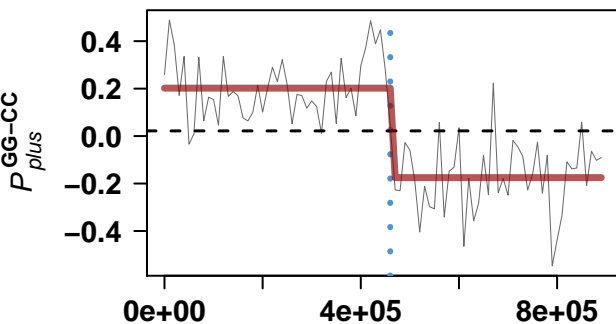
Borrelia garinii PBI



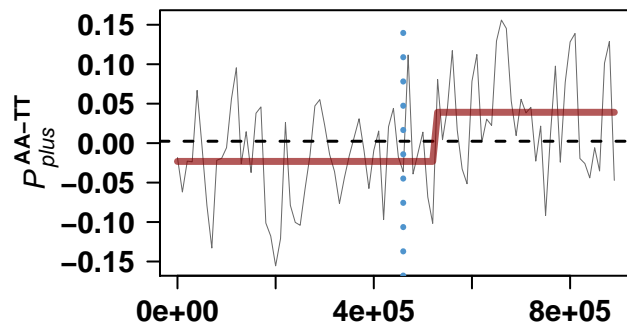
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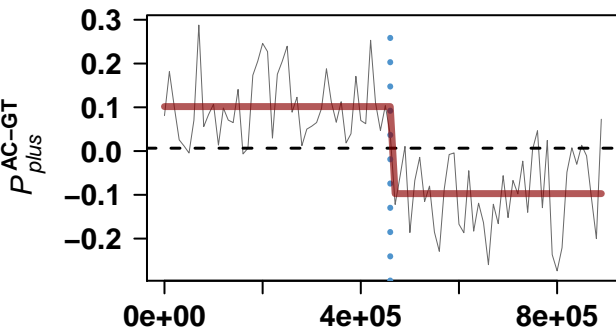
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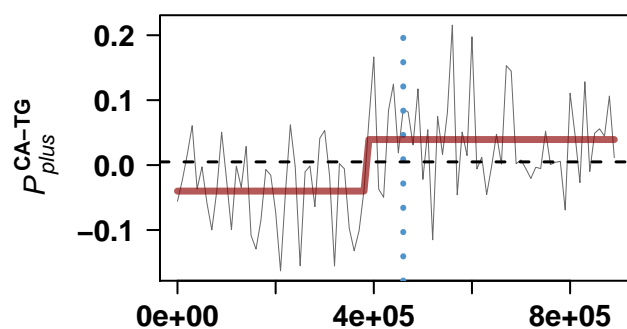
genome coordinates



genome coordinates

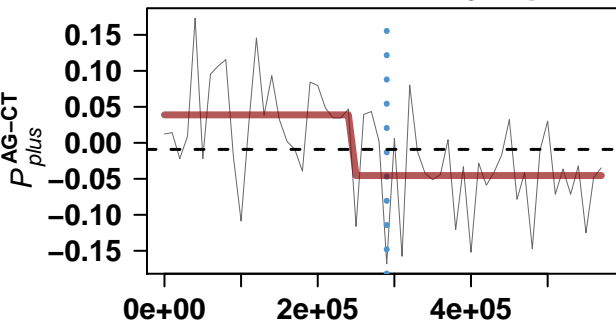


genome coordinates

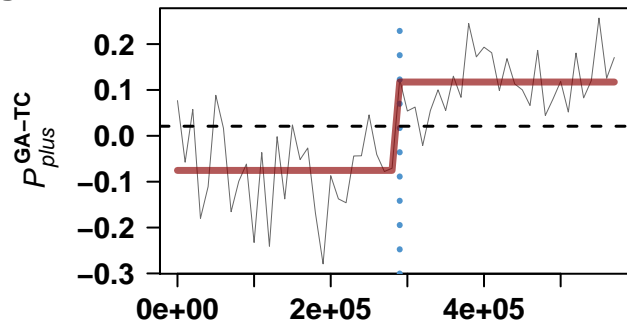


genome coordinates

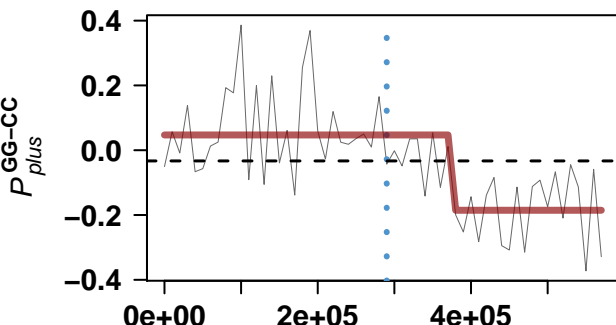
Mycoplasma genitalium G37



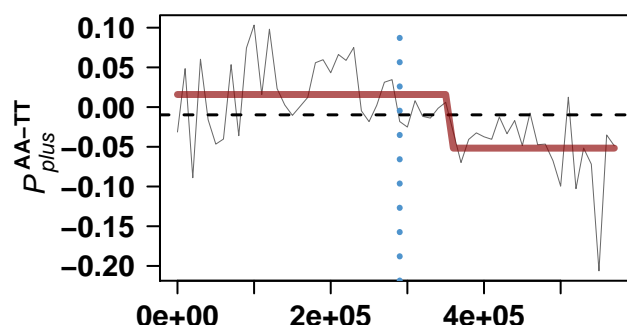
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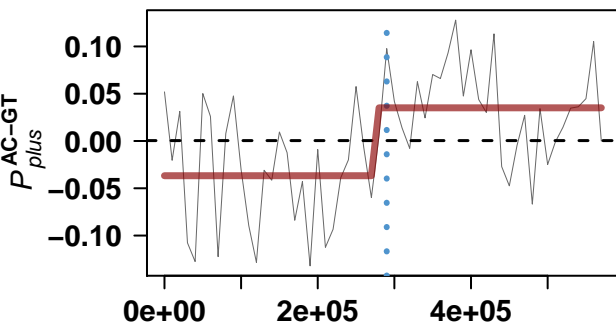
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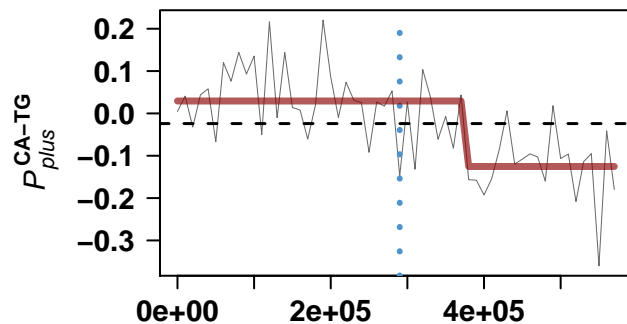
genome coordinates



genome coordinates

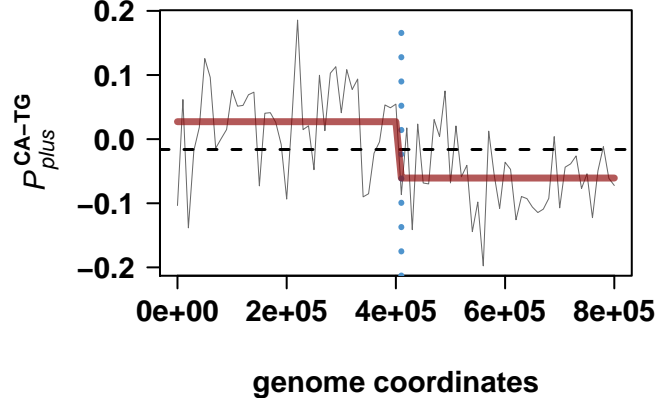
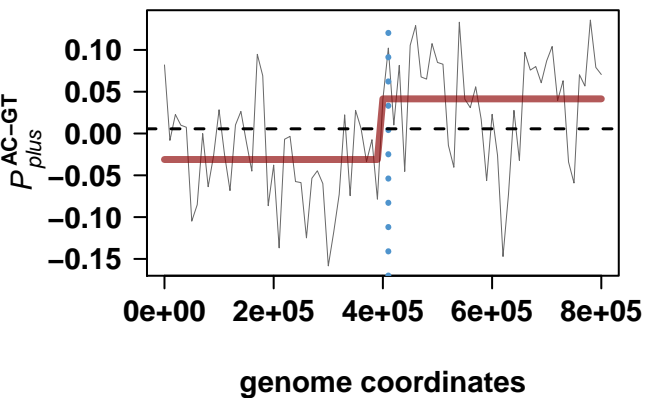
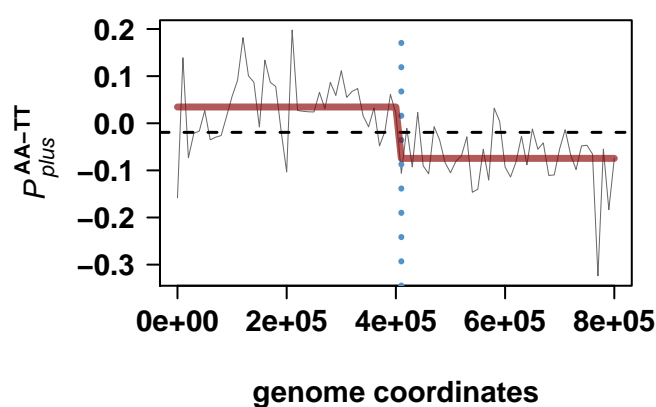
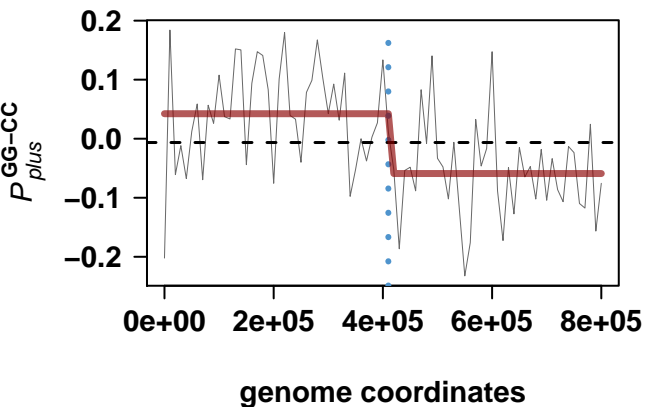
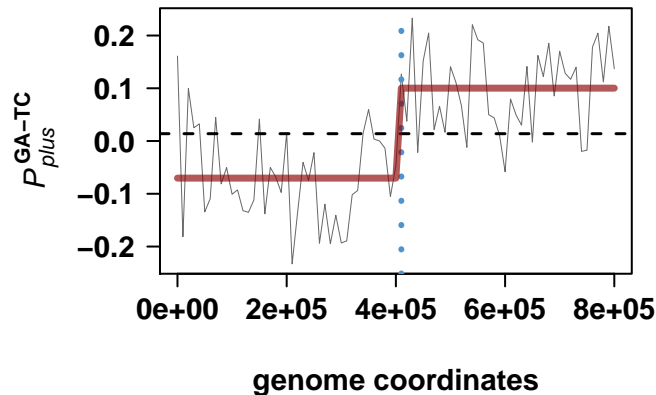
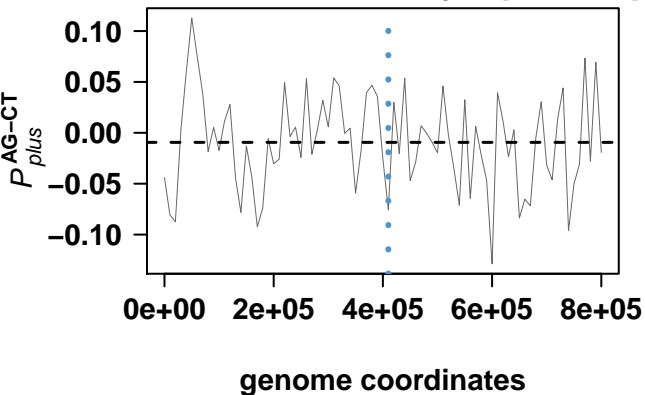


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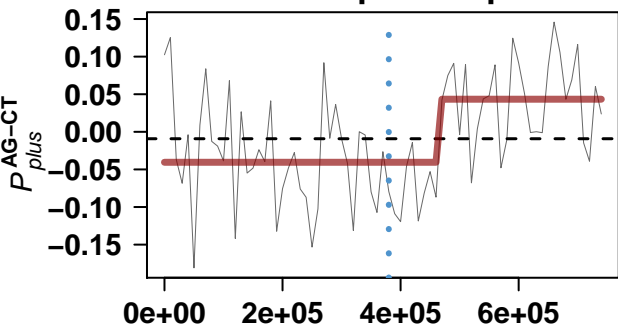


genome coordinates

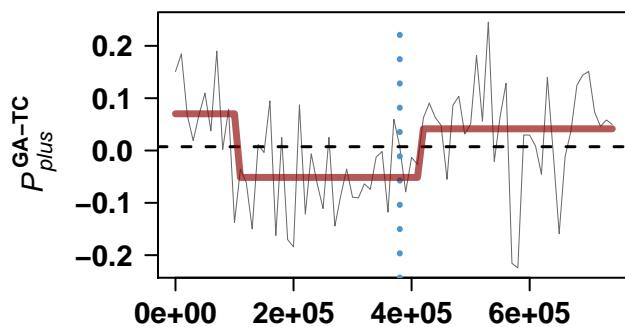
Mycoplasma pneumoniae M129



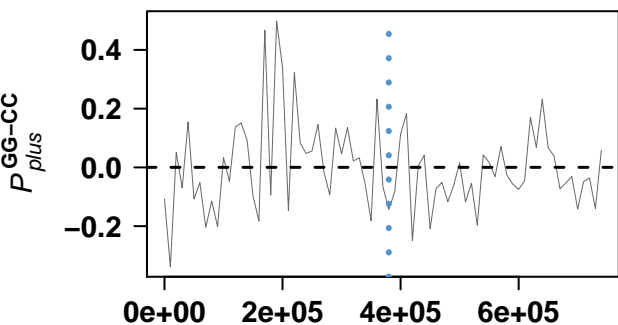
Ureaplasma parvum serovar 3 str. ATCC 700970



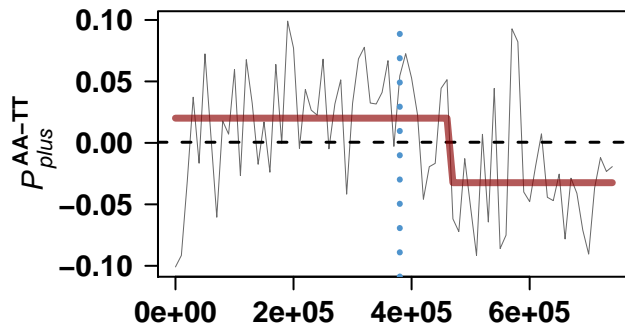
genome coordinates



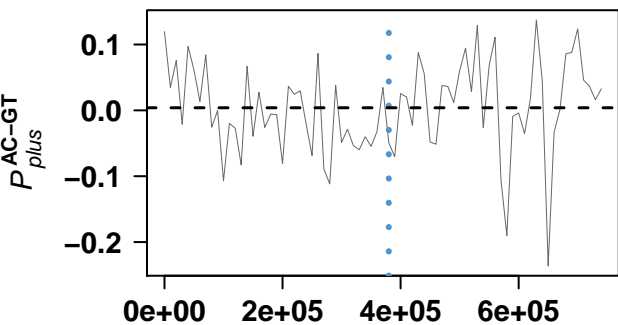
genome coordinates



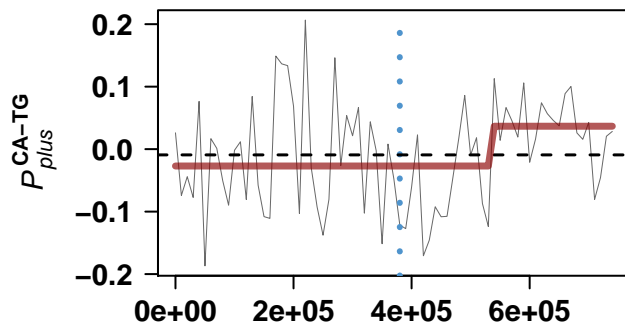
genome coordinates



genome coordinates

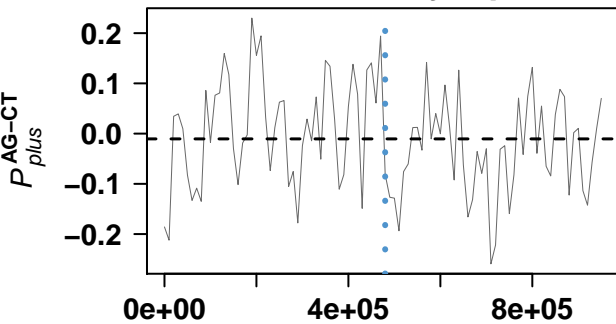


genome coordinates

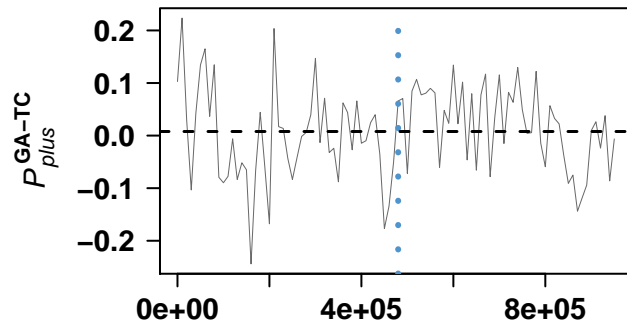


genome coordinates

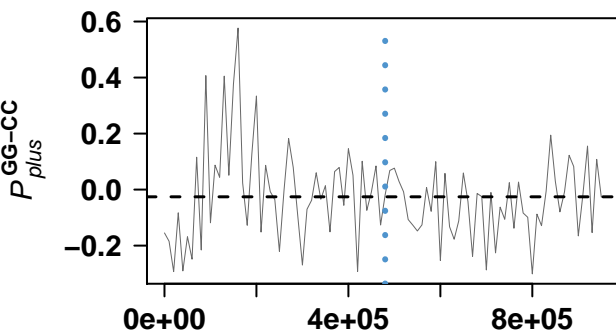
Mycoplasma pulmonis UAB CTIP



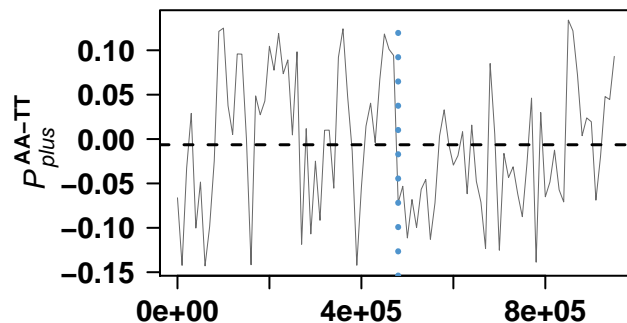
genome coordinates



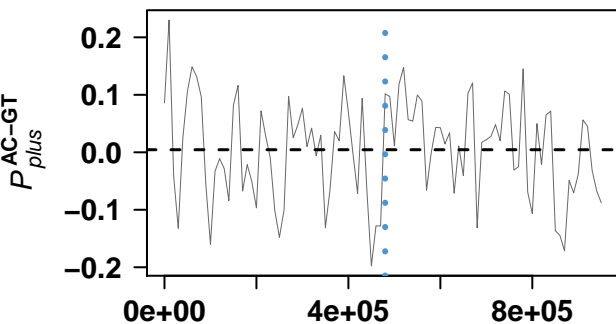
genome coordinates



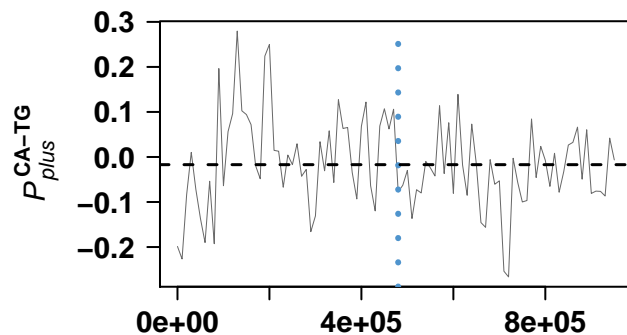
genome coordinates



genome coordinates

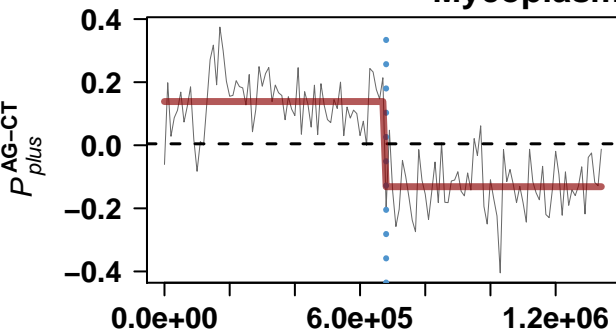


genome coordinates

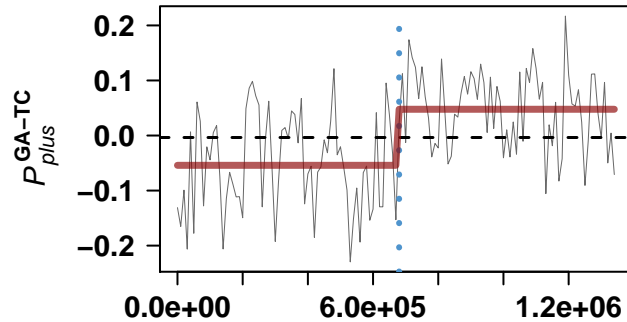


genome coordinates

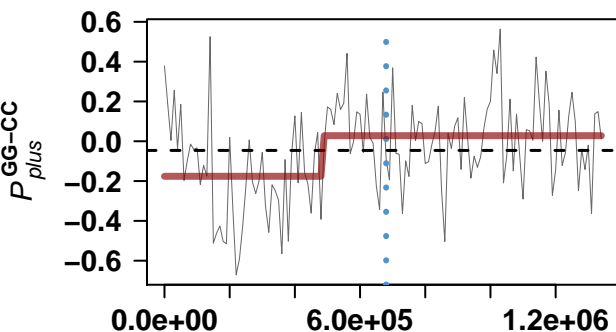
Mycoplasma penetrans HF-2



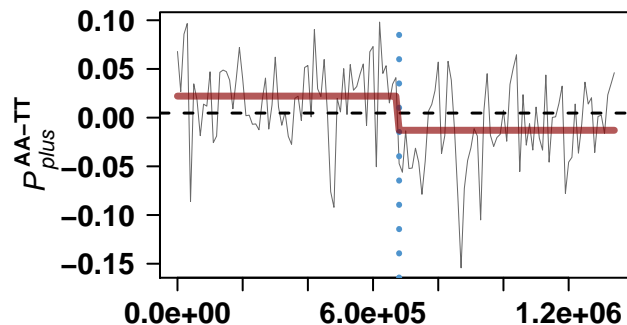
genome coordinates



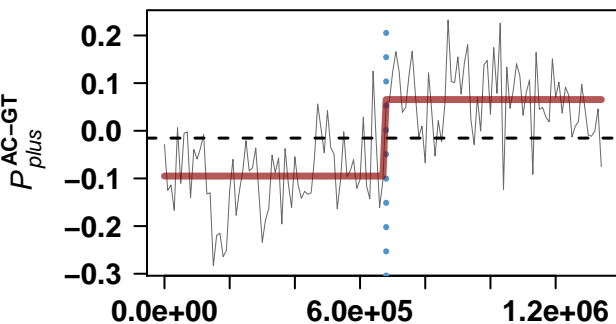
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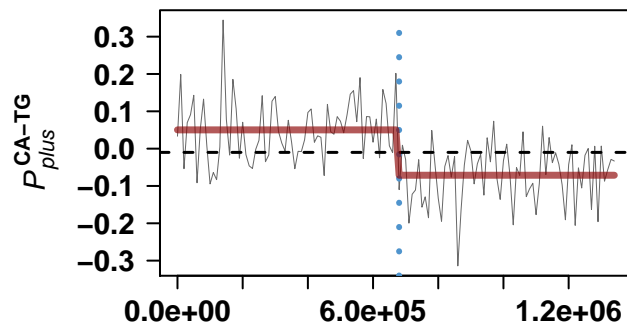
genome coordinates



genome coordinates

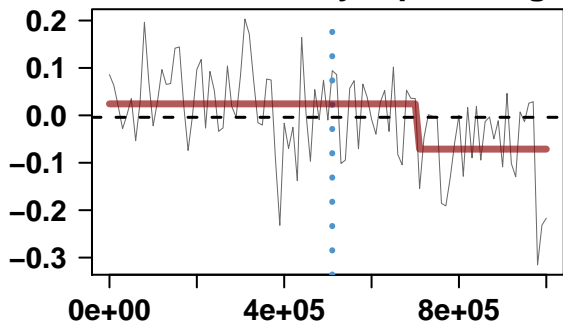


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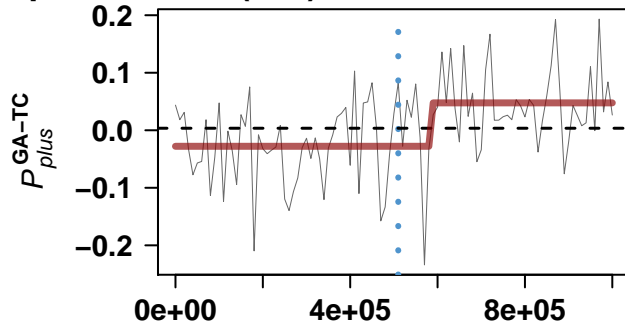


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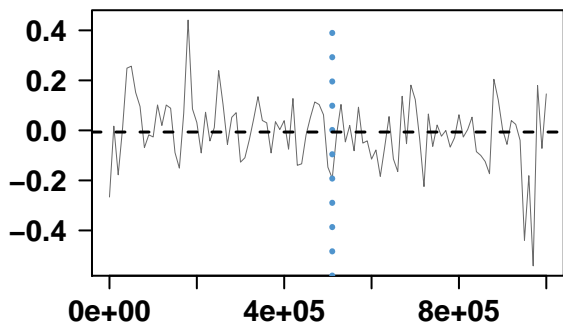
Mycoplasma gallisepticum str. R(low)



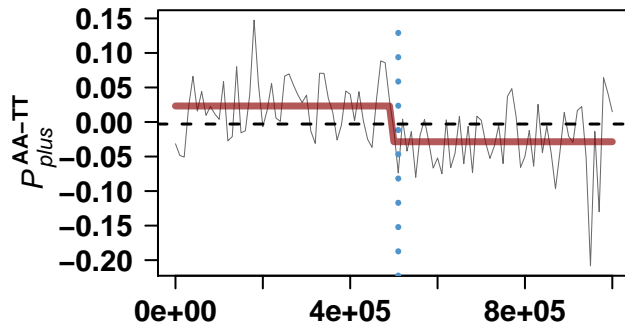
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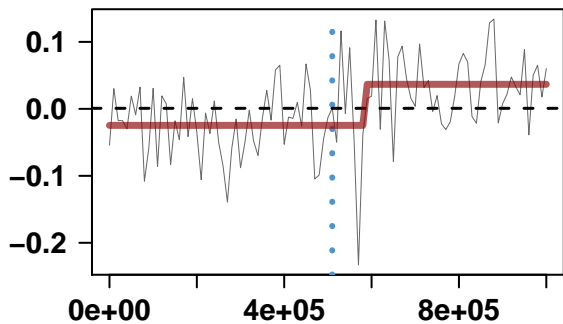
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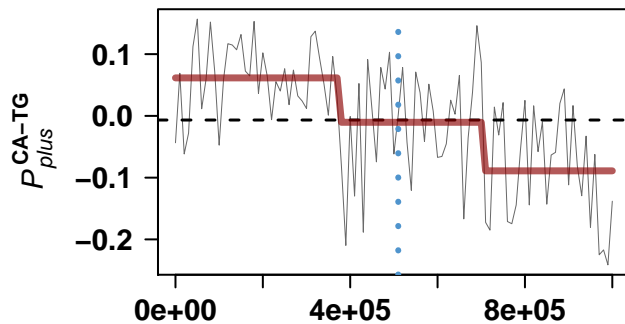
genome coordinates



genome coordinates

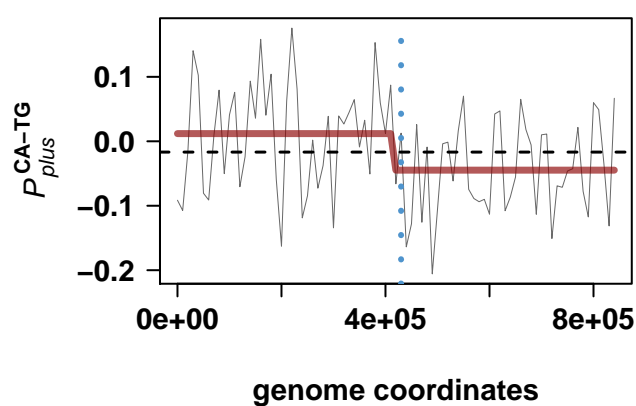
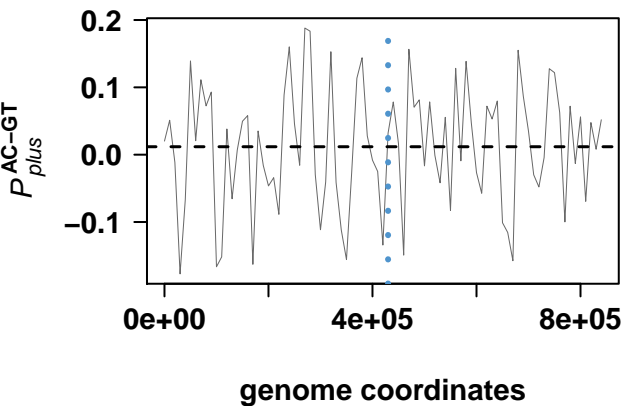
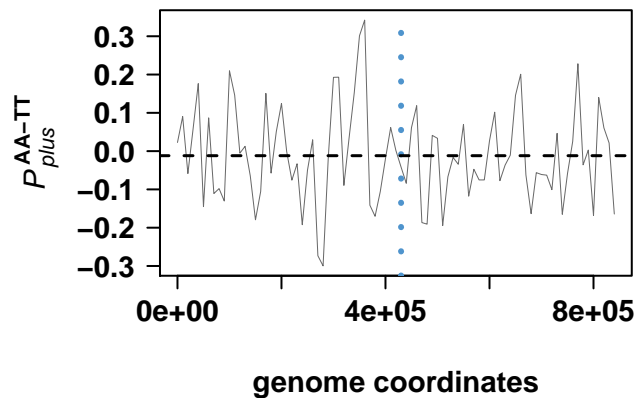
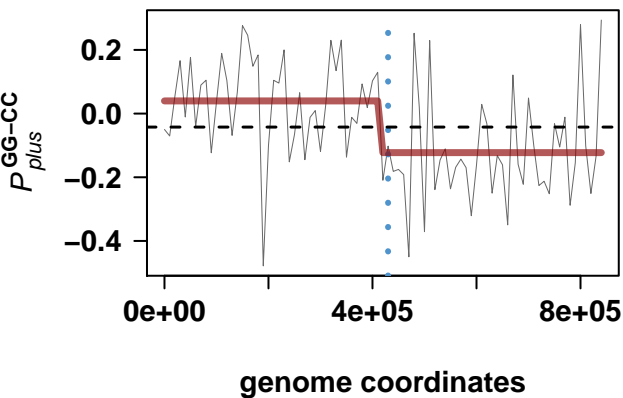
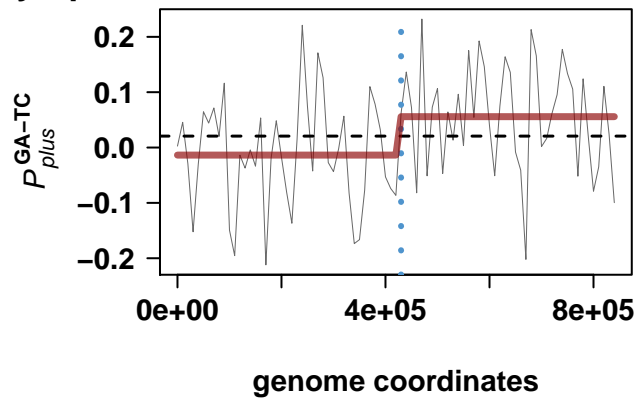
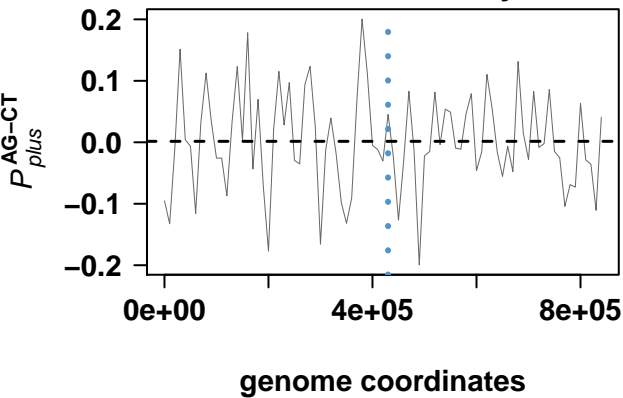


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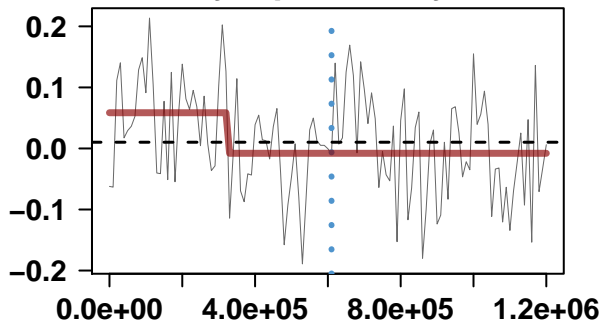


genome coordinates

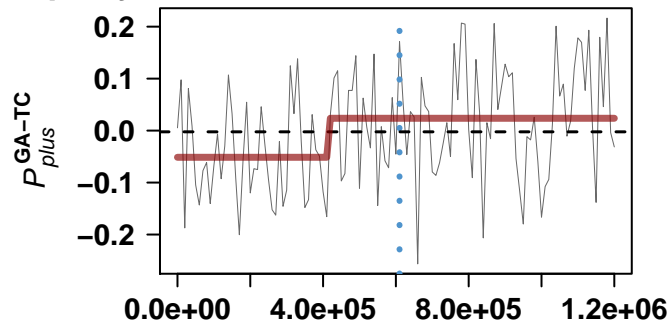
Onion yellows phytoplasma OY-M



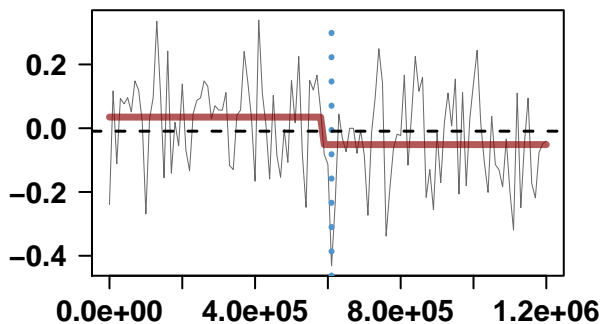
Mycoplasma mycoides subsp. *mycoides* SC str. PG1



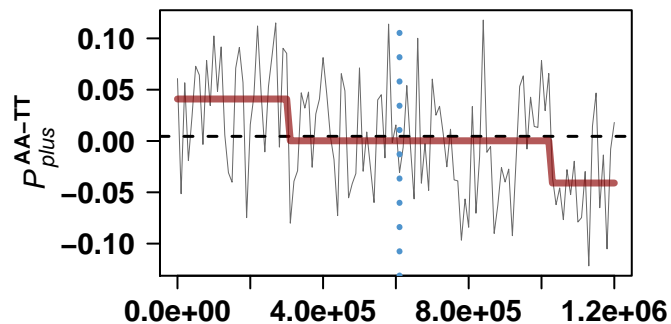
genome coordinates



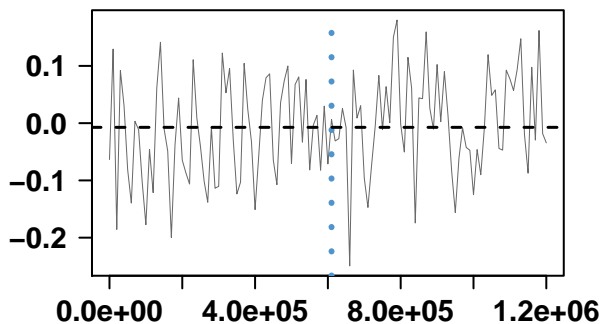
genome coordinates



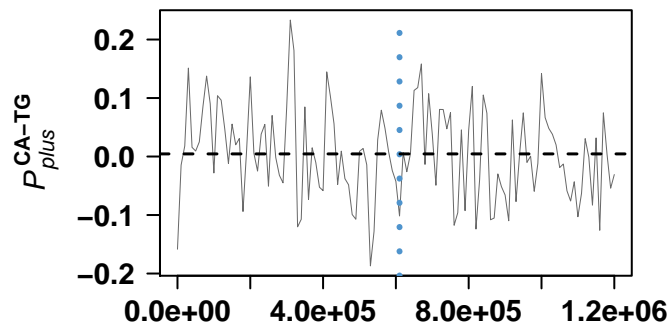
genome coordinates



genome coordinates

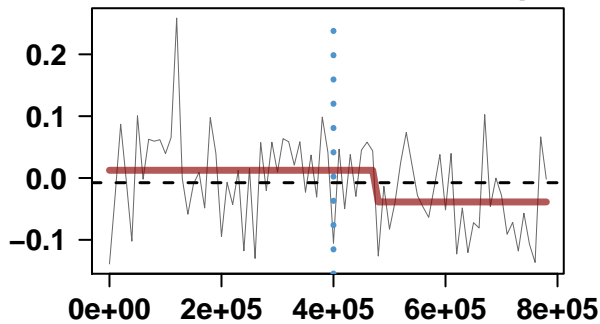


genome coordinates

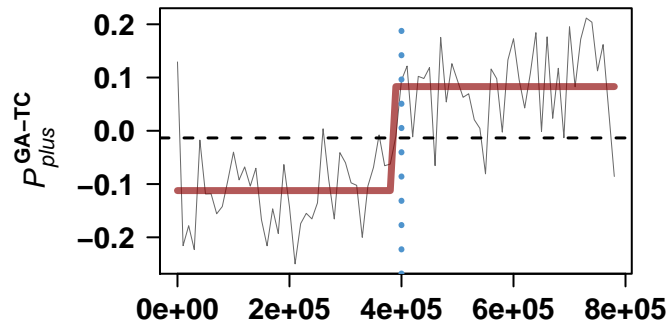


genome coordinates

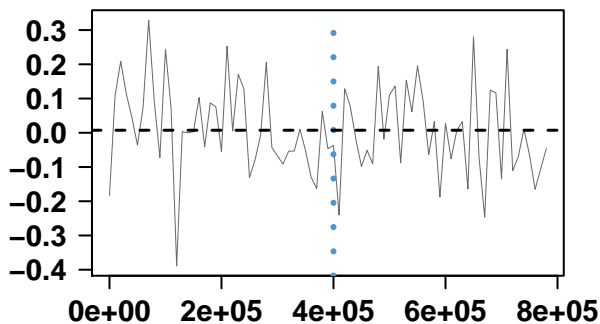
Mesoplasma florum L1



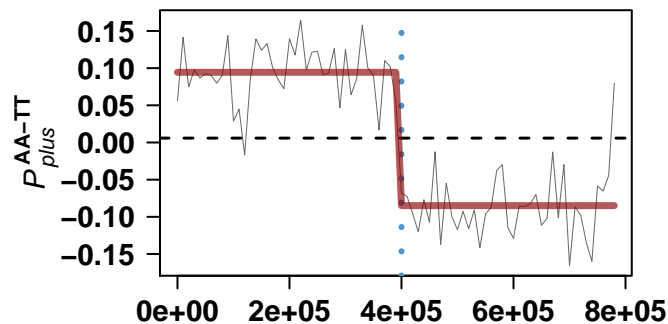
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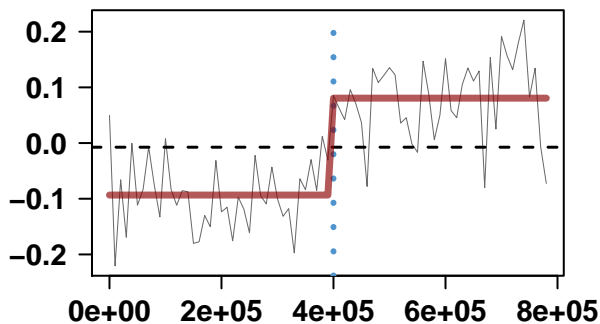
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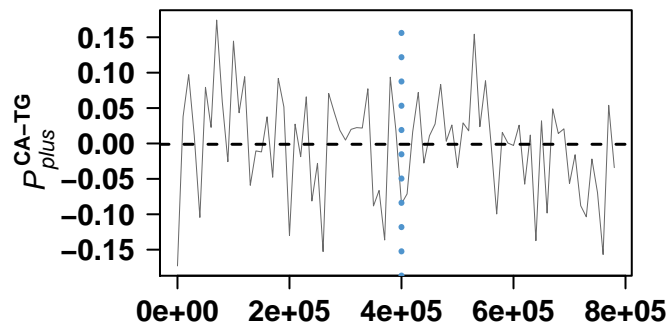
genome coordinates



genome coordinates

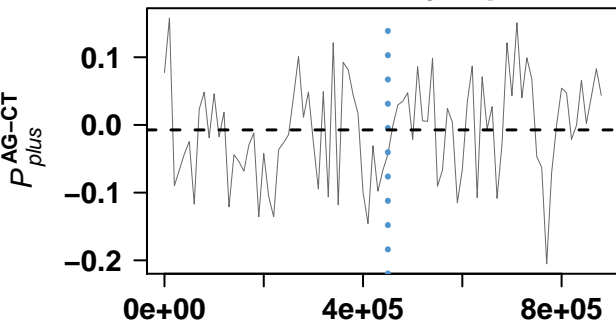


genome coordinates

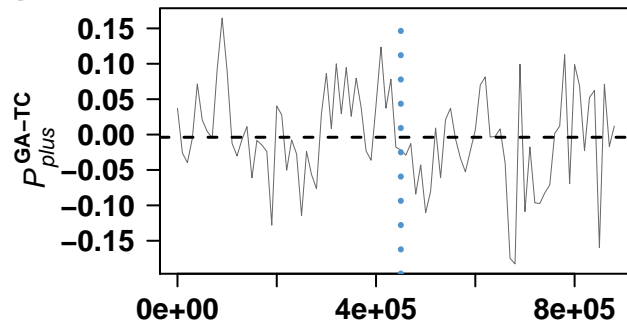


genome coordinates

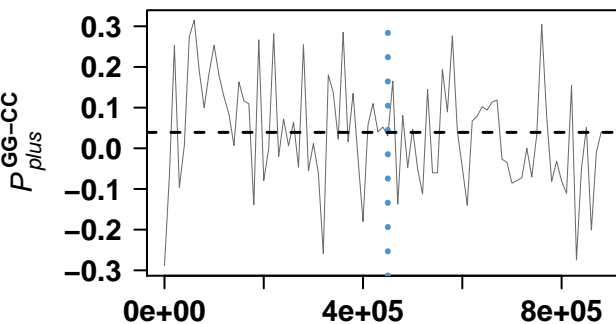
Mycoplasma hyopneumoniae 232



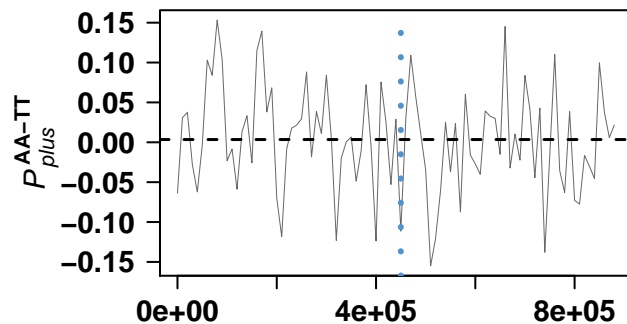
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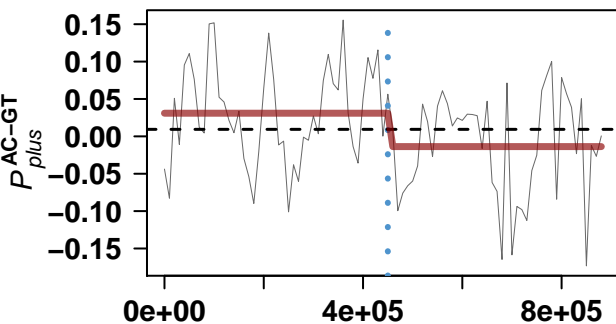
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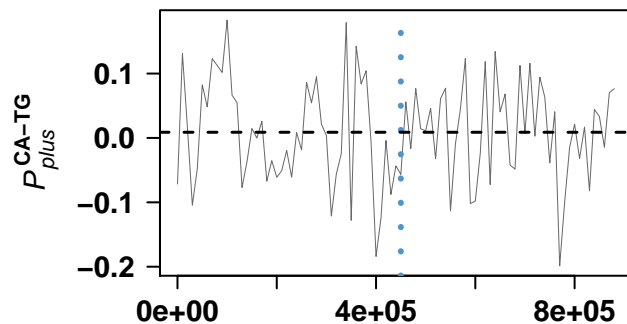
genome coordinates



genome coordinates

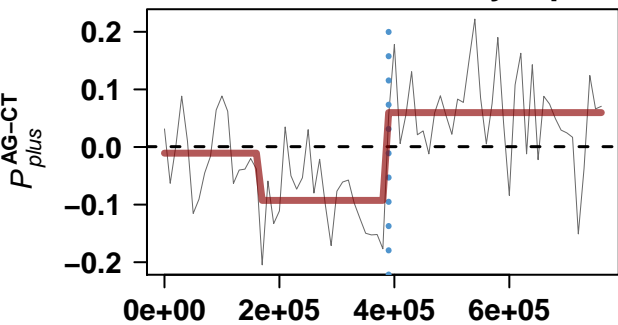


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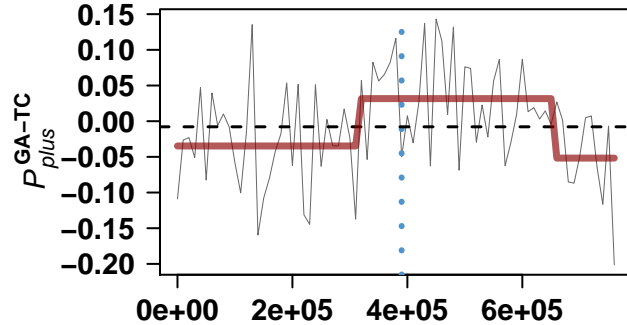


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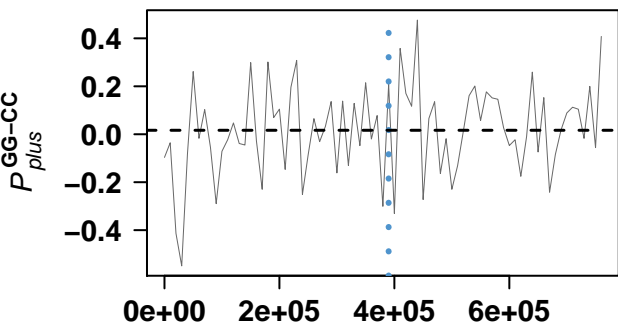
Mycoplasma mobile 163K



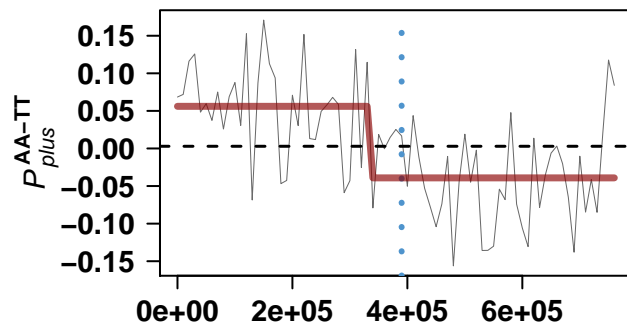
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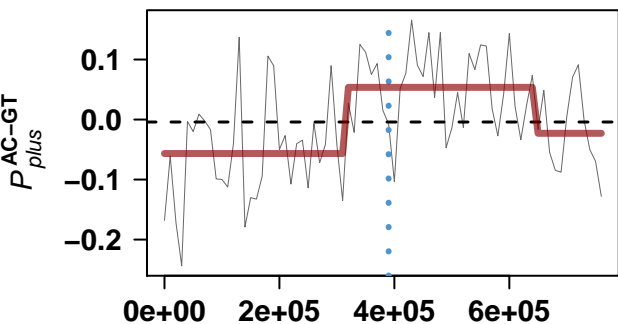
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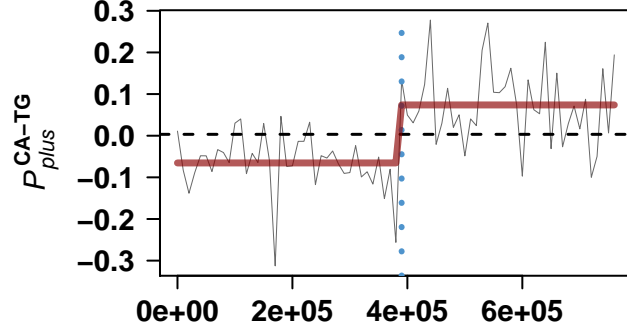
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genome coordinates

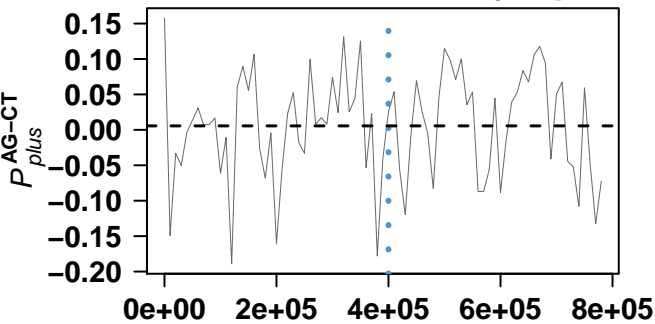


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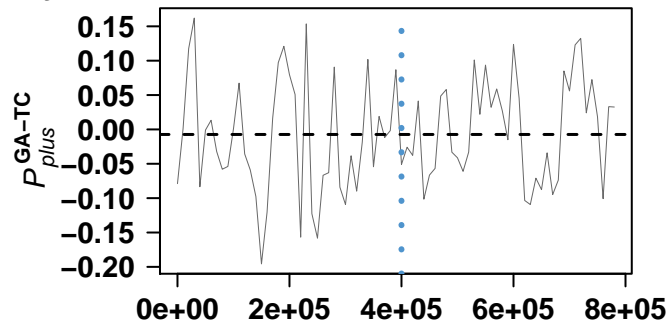


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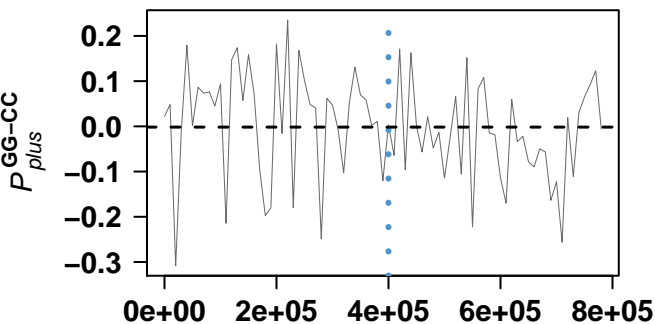
Mycoplasma synoviae 53



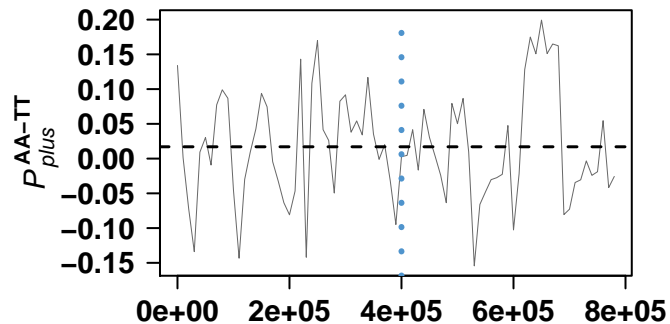
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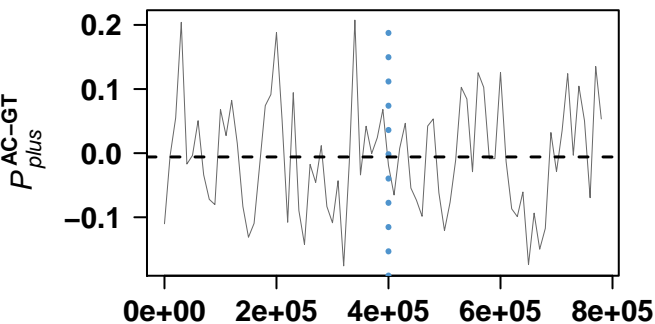
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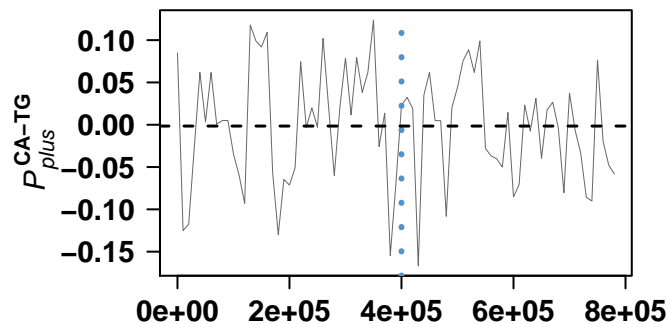
genome coordinates



genome coordinates

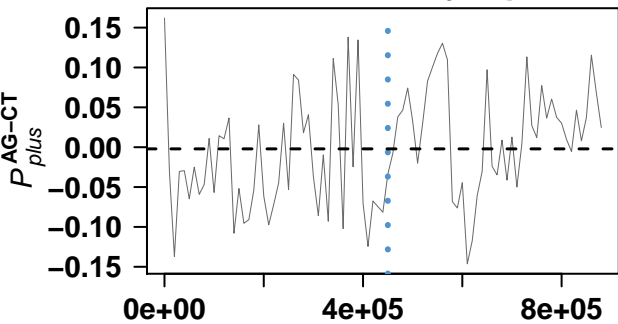


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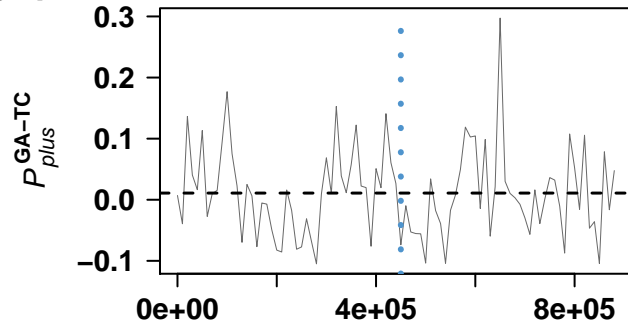


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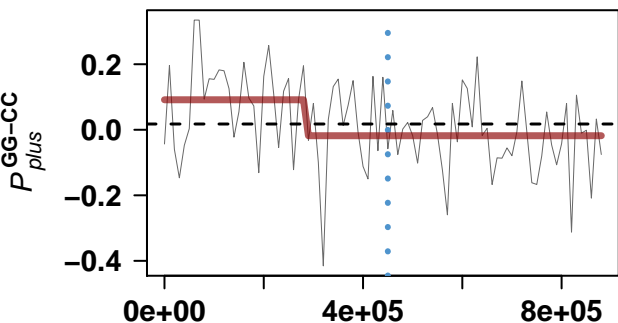
Mycoplasma hyopneumoniae J



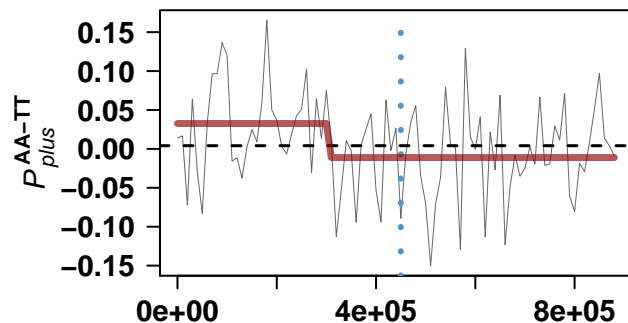
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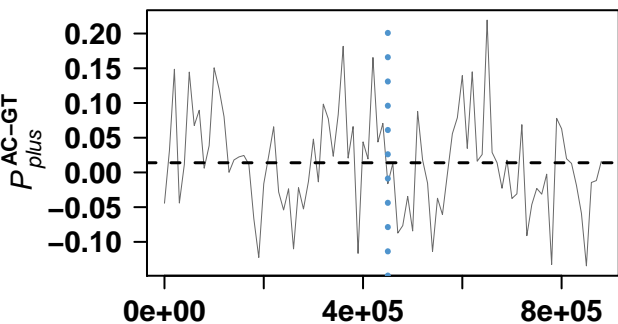
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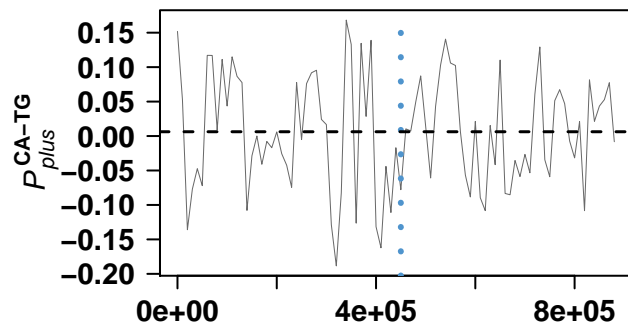
genome coordinates



genome coordinates

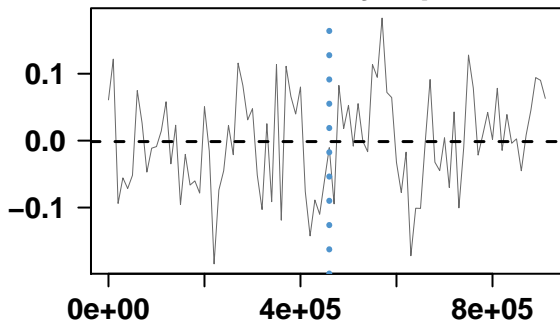


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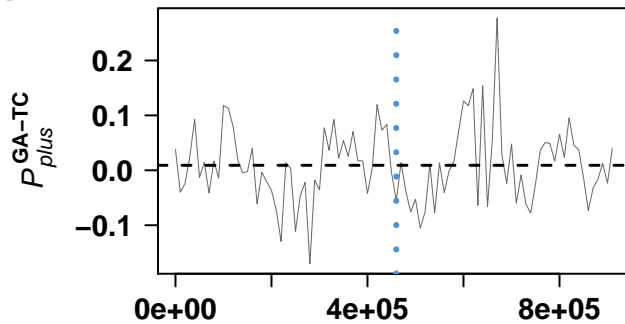


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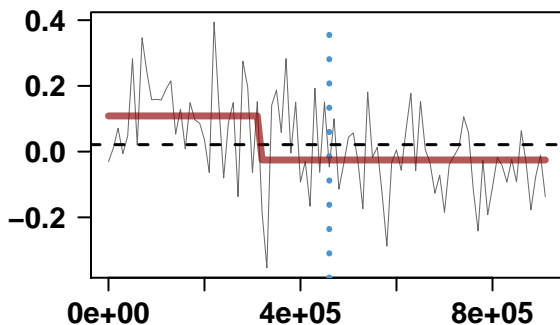
Mycoplasma hyopneumoniae 7448



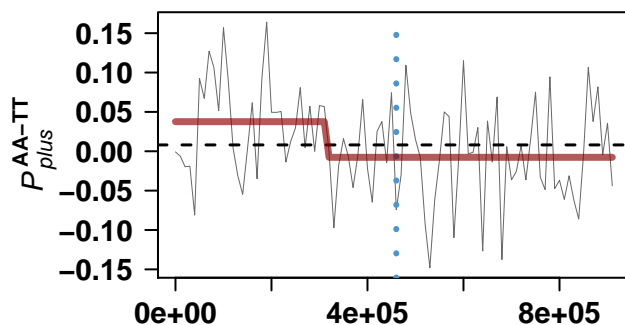
genome coordinates



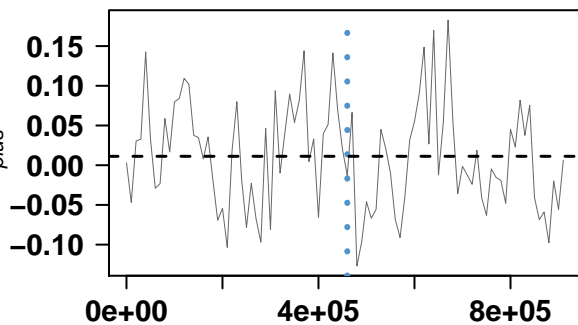
genome coordinates



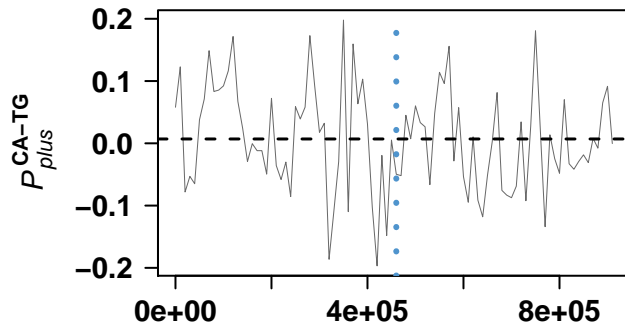
genome coordinates



genome coordinates

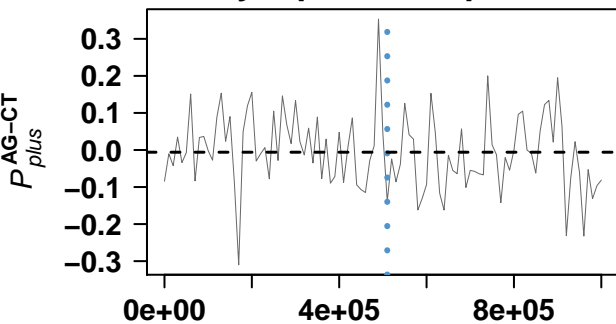


genome coordinates

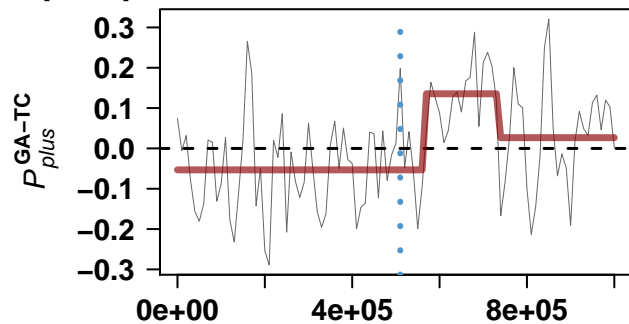


genome coordinates

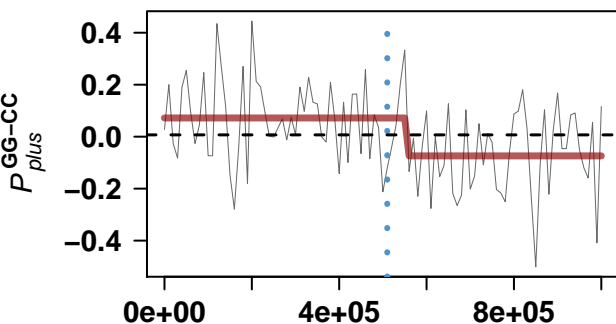
Mycoplasma capricolum subsp. *capricolum* ATCC 27343



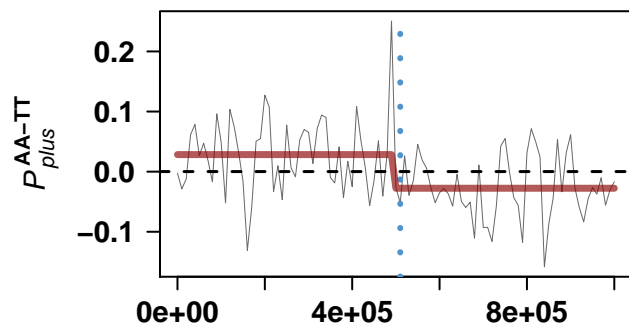
genome coordinates



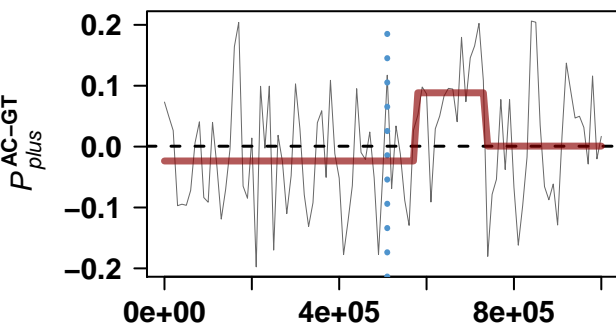
genome coordinates



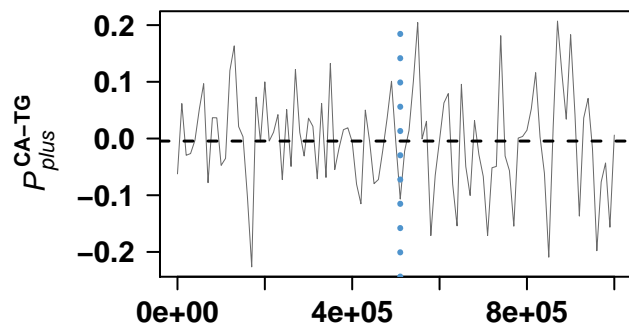
genome coordinates



genome coordinates

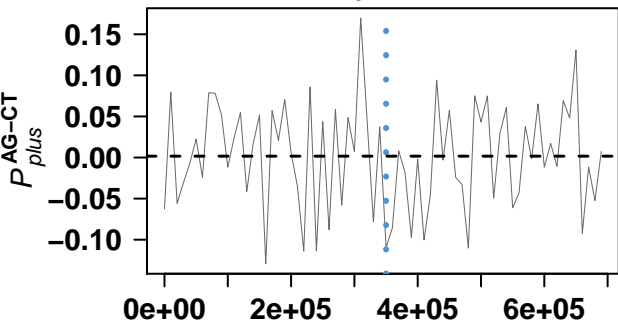


genome coordinates

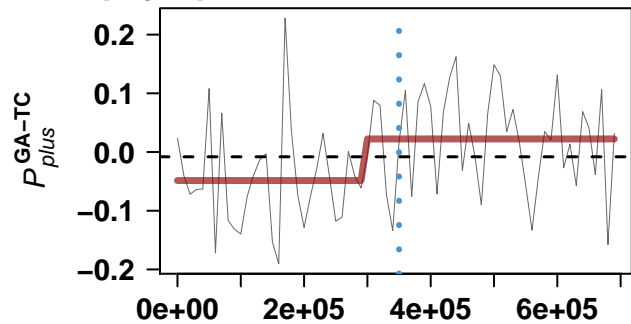


genome coordinates

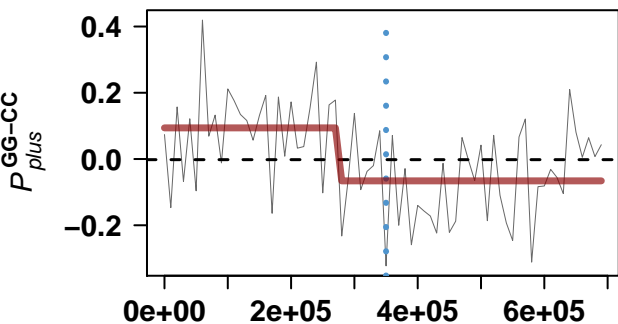
Aster yellows witches'-broom phytoplasma AYWB



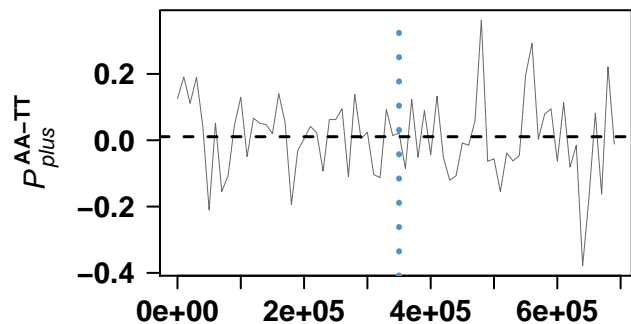
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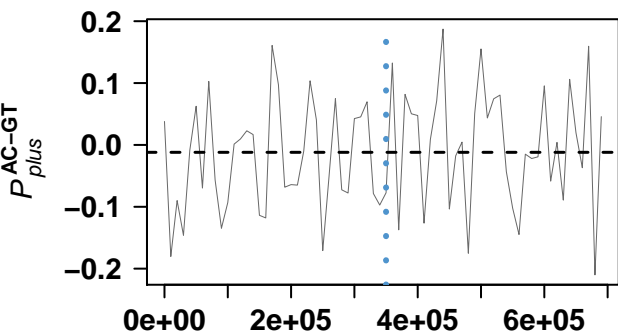
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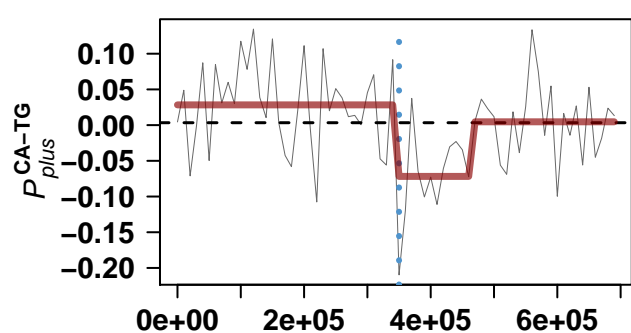
genome coordinates



genome coordinates



genome coordinates



genome coordinates