

FIG S1 Violin plots of the \log_{10} Consistency Indexes of the genome, promoter, and attenuator SNP positions.

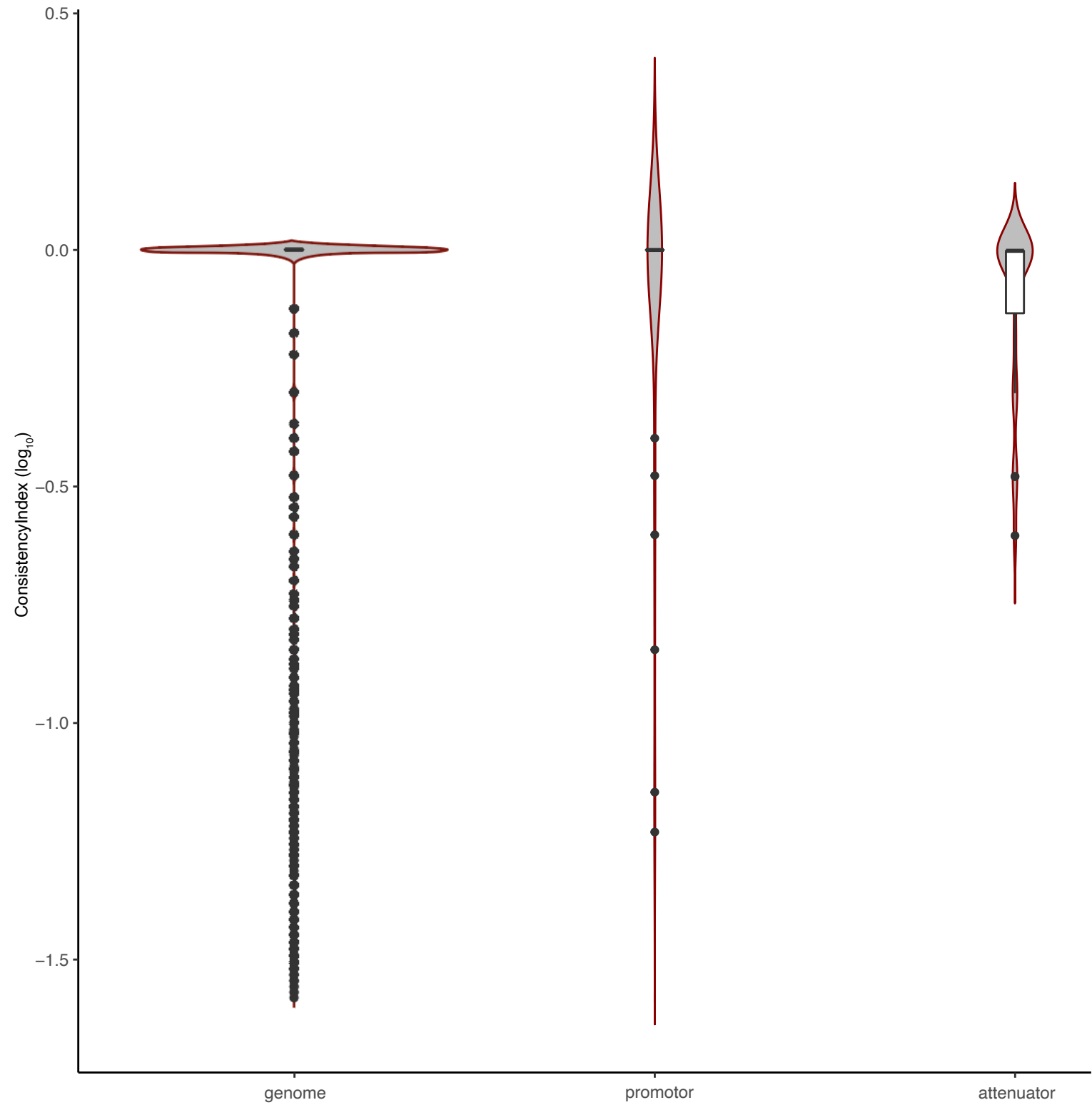
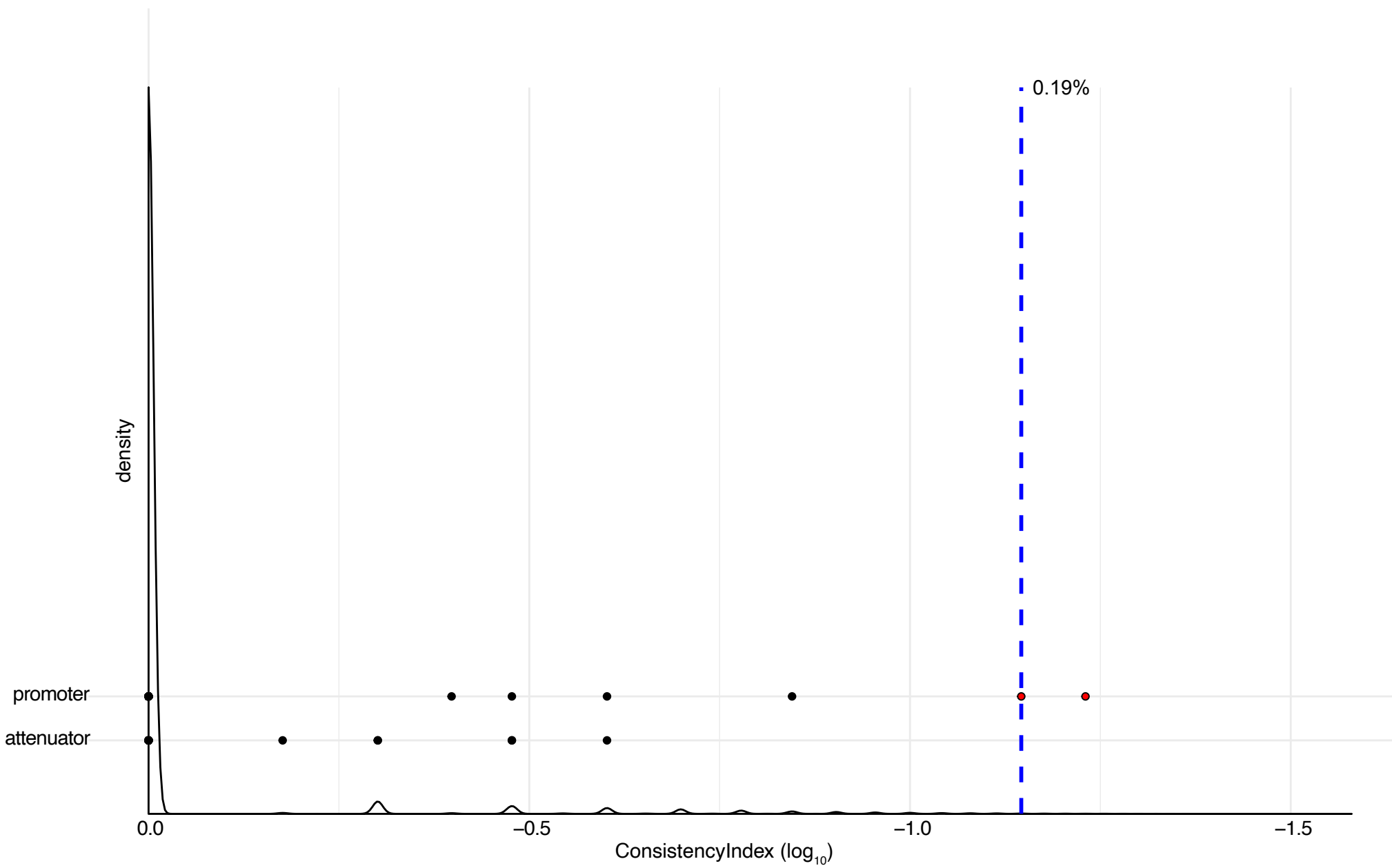


FIG S2 Distribution of the \log_{10} Consistency Indexes of all genomic SNP positions based on the *E. coli* ampC_0069 reference chromosome, compared to the \log_{10} Consistency Indexes of the promoter and attenuator region.



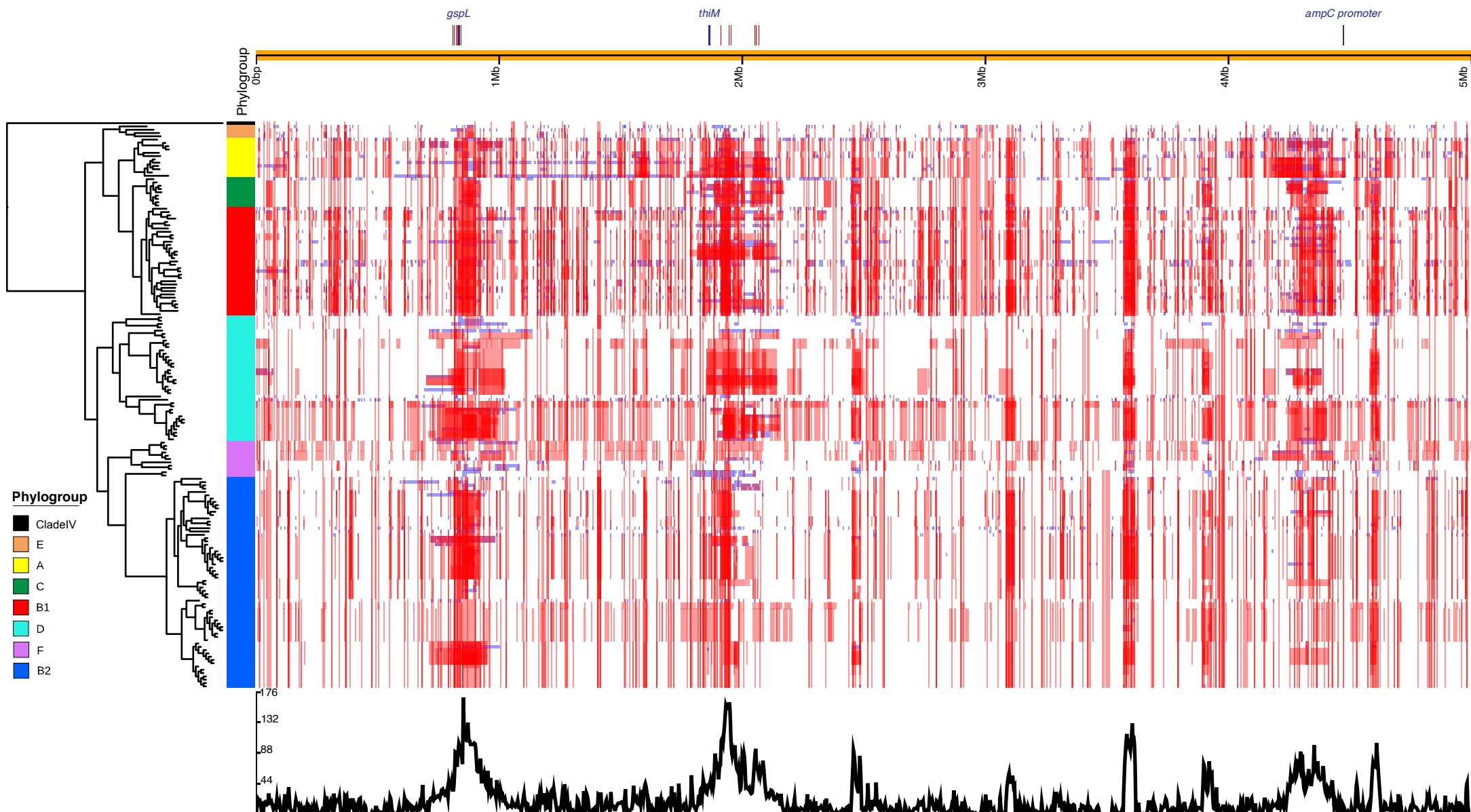


FIG S3 Recombination events inferred from all 172 *E. coli* isolates by Gubbins displayed along the approximately maximum-likelihood phylogenetic tree based on the coreSNP alignment. Phylogroups are depicted as in FIG 2. Gubbins blocks are coloured red if they are ancestral, and blue if they only affect one isolate. The line graph represents the recombination prevalence along the sequence. The 24 positions with a significant association with cefotaxime resistance ($FDR \leq 0.05$) and a consistency index ≤ 0.05882353 are indicated on the top of the figure. The two missense mutations and *ampC* promoter region are displayed in blue.