

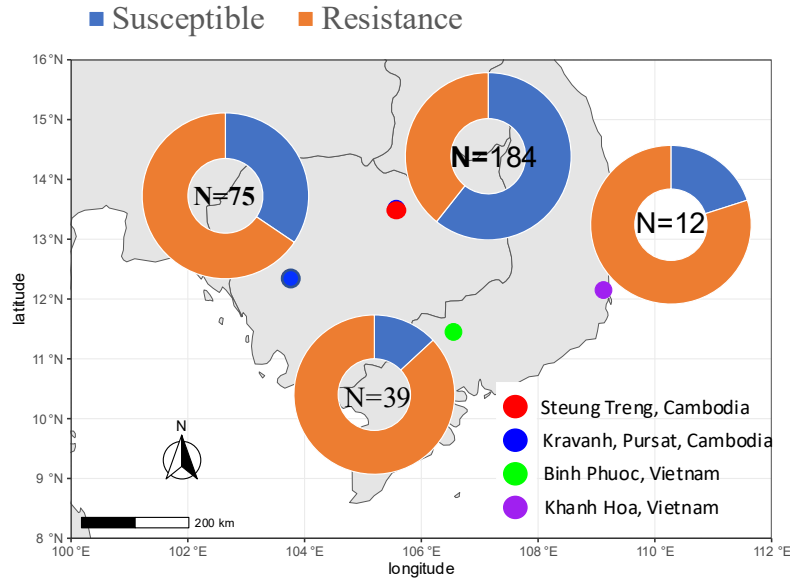


Figure S1: Geographic sample distribution of TACT-CV parasite isolates: This map shows four sample collection sites from two countries, Cambodia and Vietnam. Isolates were collected 2 sites in each country. Pie chart for each site reflects the distribution of resistant ($PC^{1/2} > 5$ hours) and susceptible ($PC^{1/2} < 5$ hours) parasites based on parasite clearance half-life.

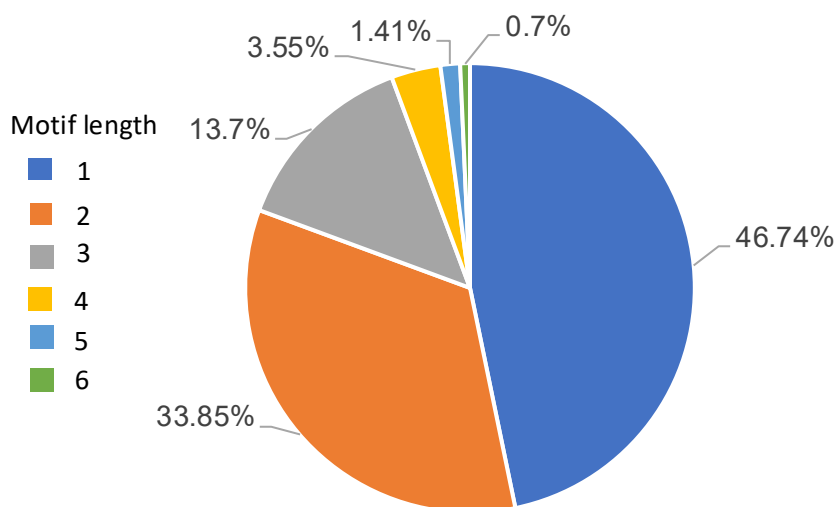


Figure S2: Short tandem repeats in *Plasmodium falciparum* 3D7 genome: This pie chart shows percentage of short tandem repeats according to their motif length distribution. This pie chart is drawn on the basis of 388,442 number of STR loci found in TR

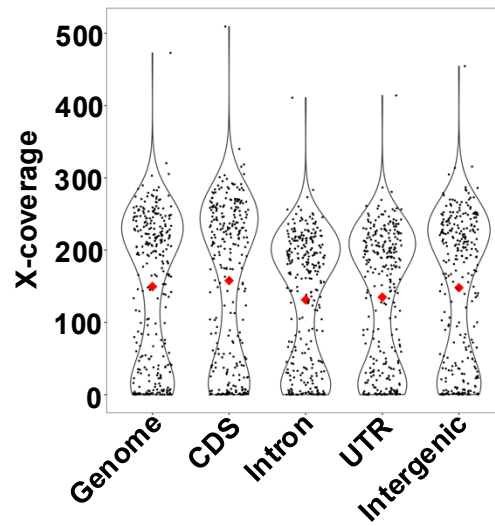


Figure S3: Coverage profile of each isolate for five different genomic regions. Overall, the plot shows no bias in coverage for genomic regions. A red diamond for each region denotes the mean coverage calculated for 300 isolates. Isolates with more than 10X genome coverage (n=239) were investigated further to detect the change in STR length.

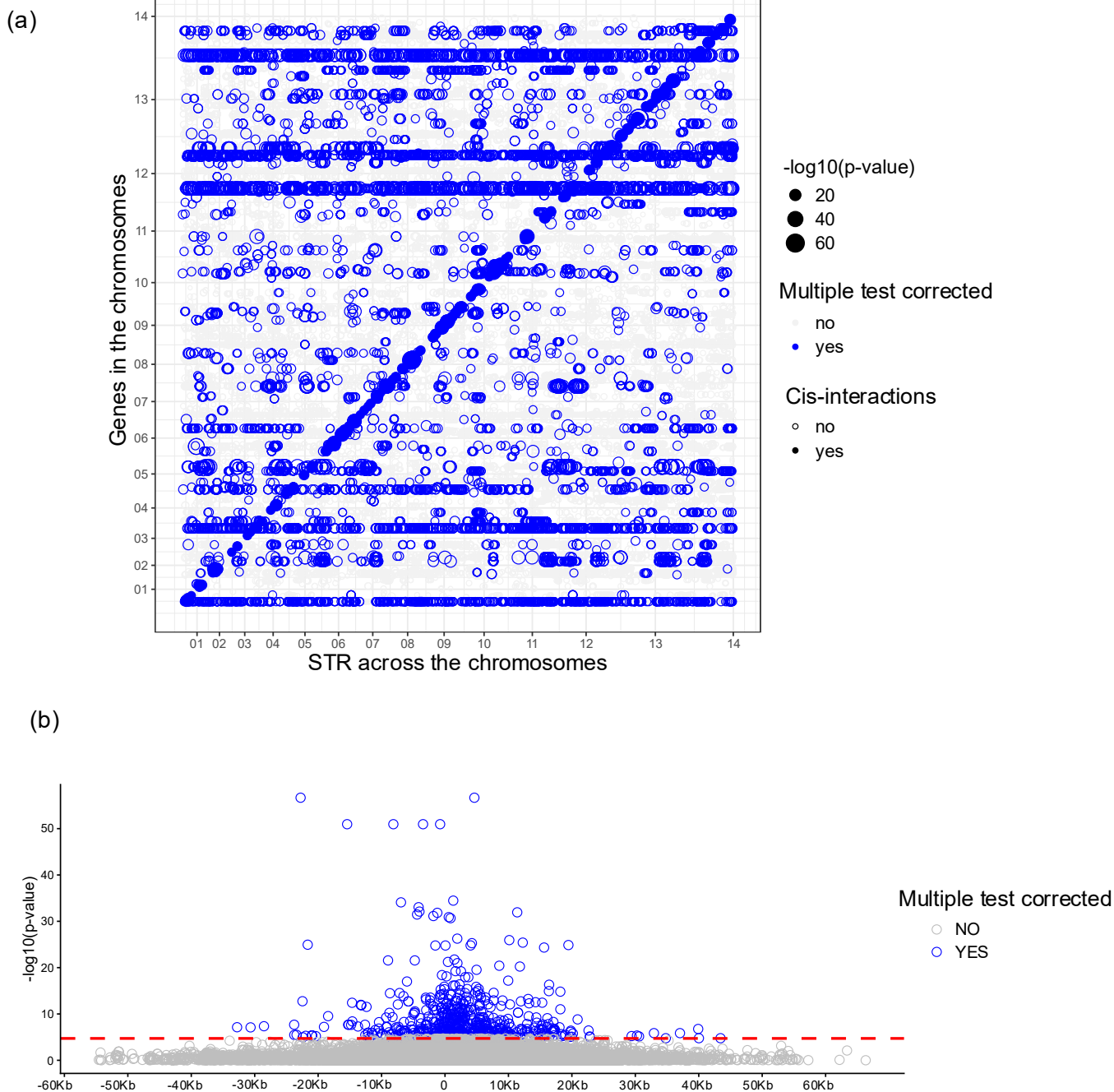


Figure S4: eQTL analysis of TACT-CV cohort. (a) Cis-trans plot showing SNP association with gene expression. In this plot, the X-axis represents the genomic coordinates of SNPs, and the y-axis represents the transcription start site of the genes. Here, the blue colored circles denote the multiple-test corrected associations, and the grey-colored circles denote association with $p\text{-value} < 1\text{e-}05$. Filled circles are SNPs associated through local interactions, while hollow circles are trans-eQTLs. The size of the circles increases with higher association. (b) All cis-eQTLs tested are shown here. The red horizontal line shows genome wide significant p-value ($p\text{-value} < 1.7\text{e-}05$).

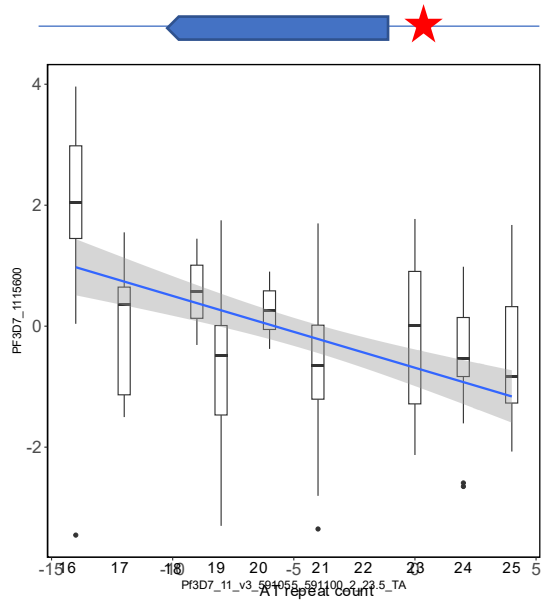


Figure S5: Expression of CYP19B (Pf3D7_1115600) gene is negatively correlated with the increase of STR length (with p-value 0.058). In this plot x-axis denotes length change of an AT repeat count and y-axis shows the expression values. On top, the approximate position of the STR (marked with red star) with respect to the gene.

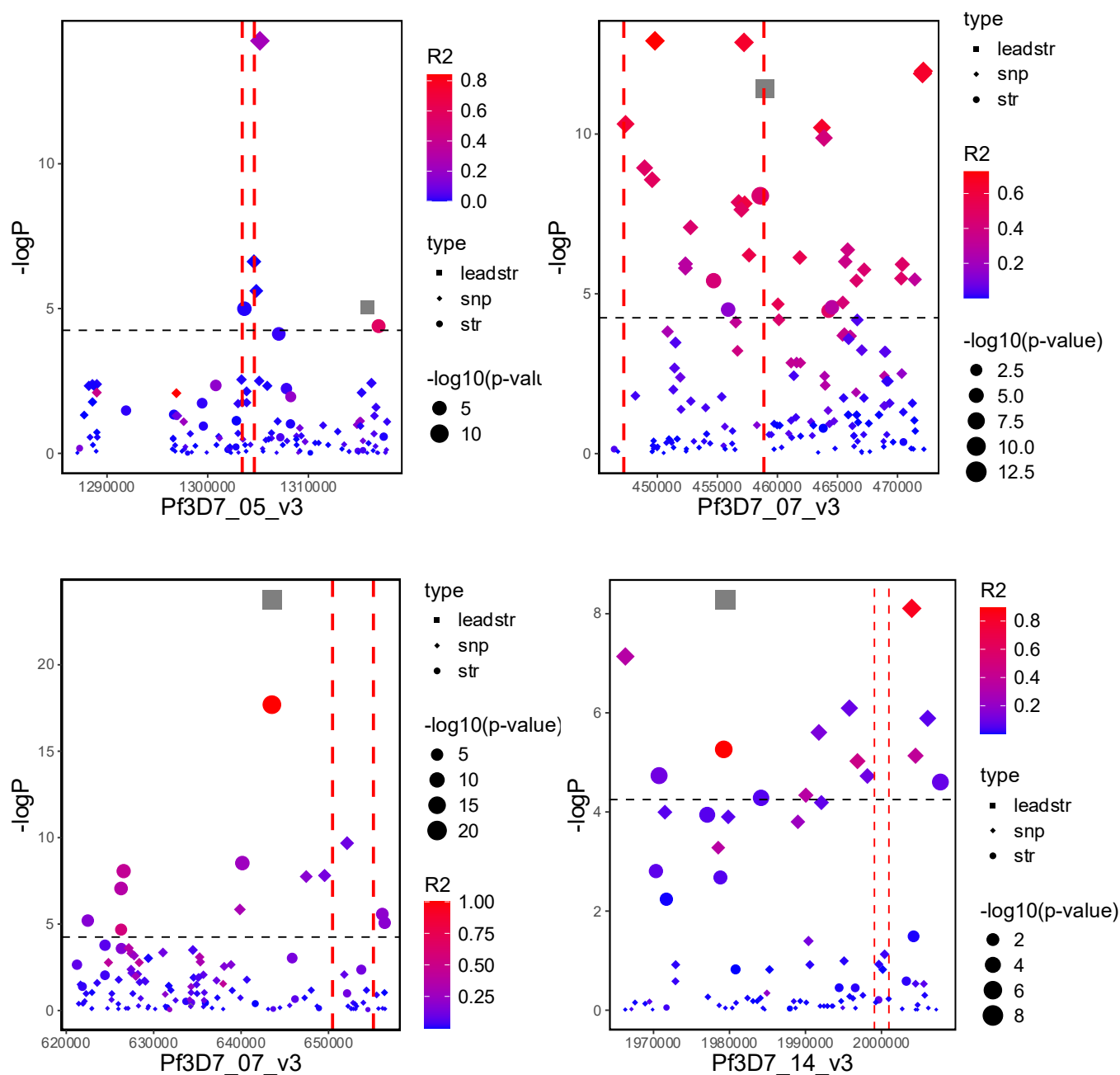


Figure S6: Four more examples of local eSTR-eQTL associated genes. Each plot shows locations of all the SNPs and STRs within their gene boundary with their p-values of association and linkage disequilibrium (R^2) values calculated with lead STR. Gene body are marked by the vertical red lines.

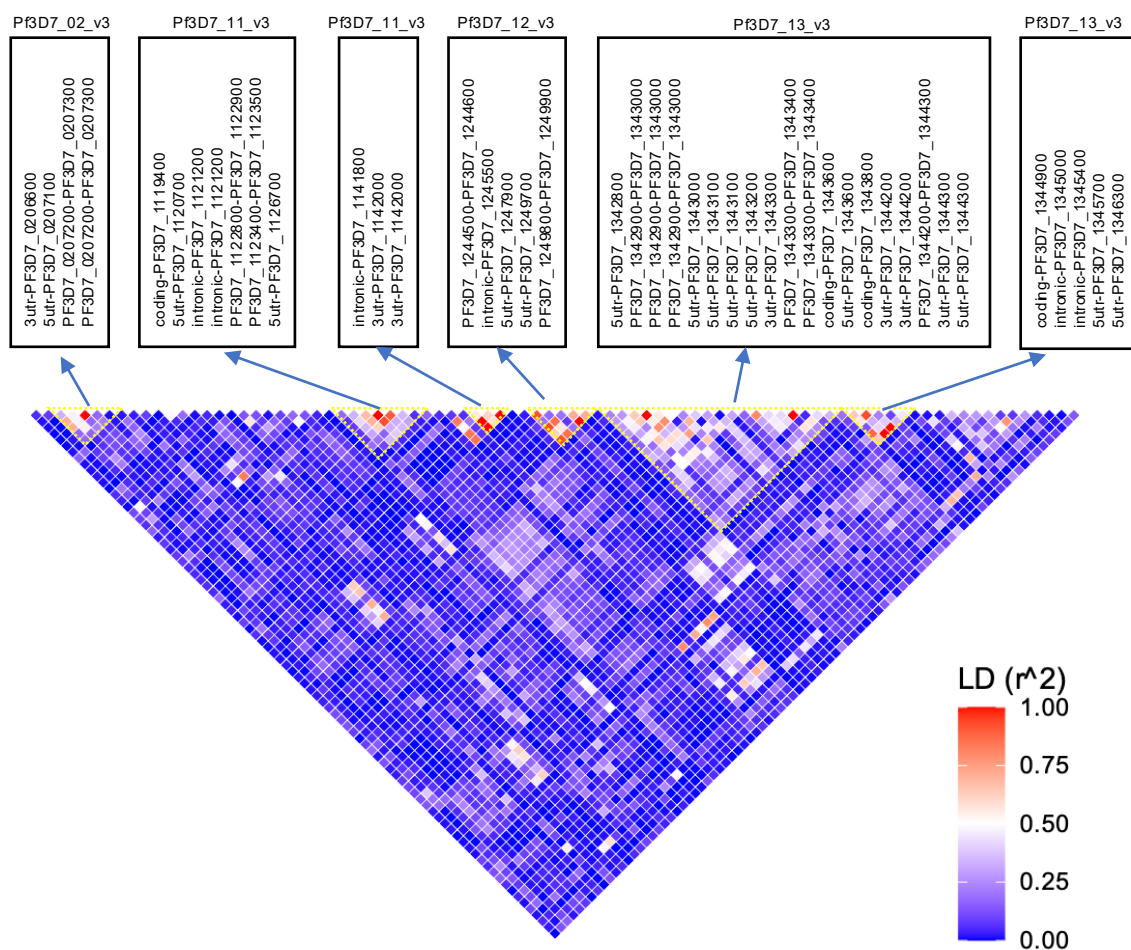


Figure S7: Linkage disequilibrium plot: LD heatmap showing R^2 values for all isolates (both resistant and susceptible) involving STRs found significantly associated with PC1/2. Several chromosomal regions showed stronger LD patterns indicating putative selection pattern. Annotation of these STRs were shown on the top with respect to gene features.