

Supplementary Information for

Plasmodium falciparum genomic surveillance reveals spatial and temporal trends, association of genetic and physical distance, and household clustering

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Year	Point Estimate	68% CI	90% CI
2015	0.054	(0.029, 0.076)	(0.022, 0.099)
2016	0.138	(0.088, 0.187)	(0.064, 0.231)
2017	0.197	(0.095, 0.286)	(0.067, 0.400)

Table S1. Fraction of Related Pairs by Year

Point estimates of the fraction of related pairs by year were calculated by sub-sampling with 1000 iterations per year. We have performed this analysis for the 3 years with sufficiently large sample sizes, namely 2015, 2016, and 2017 and have compiled 68% confidence intervals, (representing the mean +/- 1 standard deviation (1 sigma)), and 90% confidence intervals.

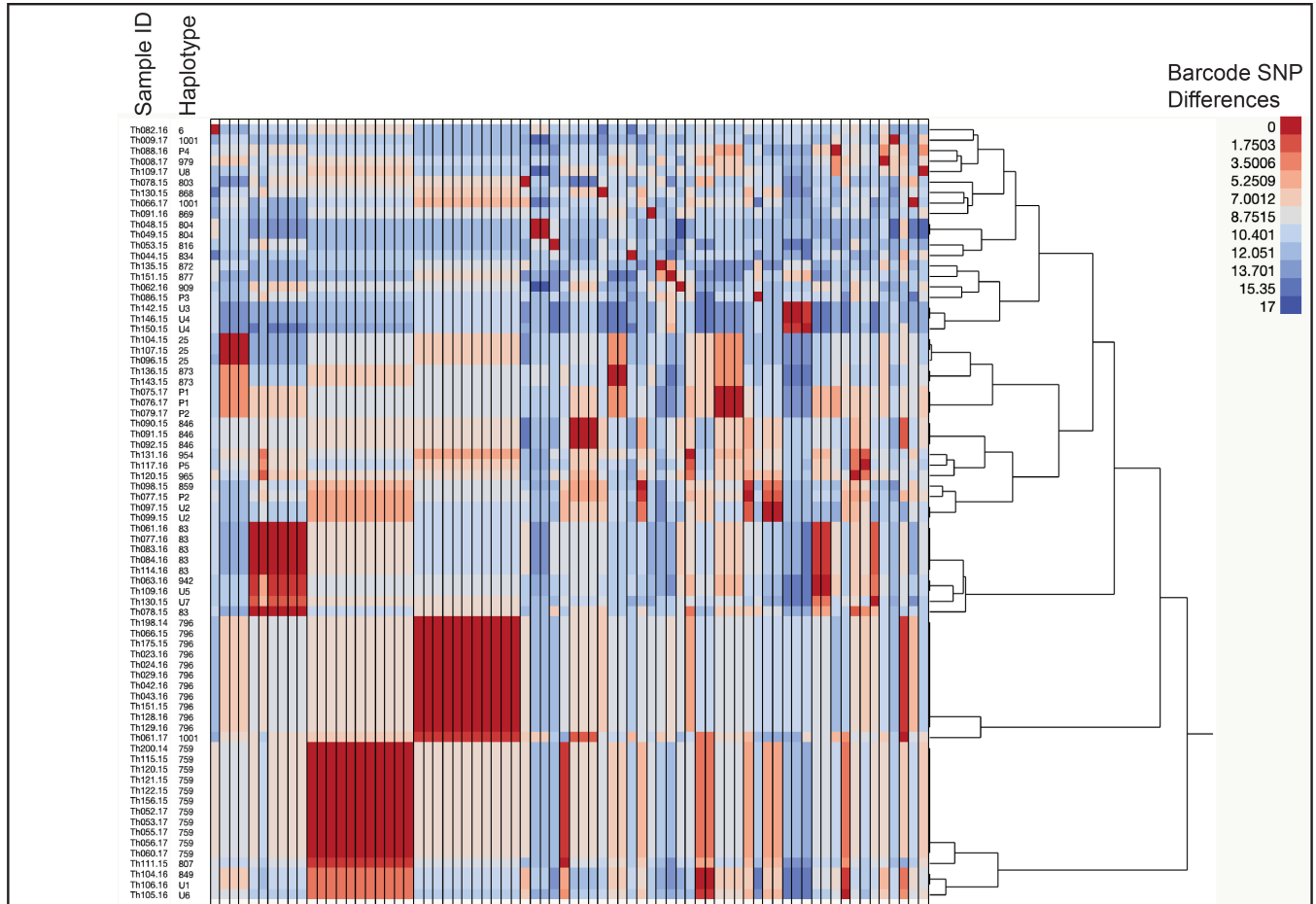


Fig. S1. Hierarchical clustering of Haplotypes according to IBS difference

Barcode SNP differences (IBS differences) were used to perform hierarchical clustering using Ward's method to identify clusters of barcode haplotypes by similarity. Hierarchical clustering was performed using JMP pro (version 15.0.0).