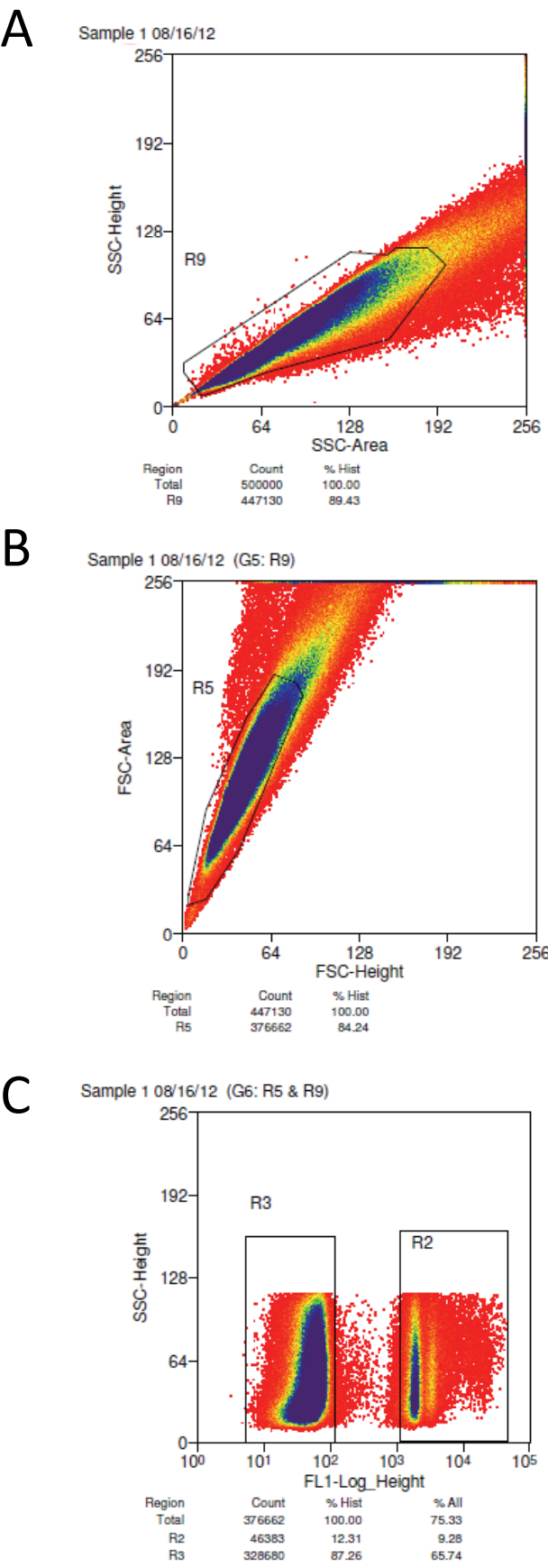
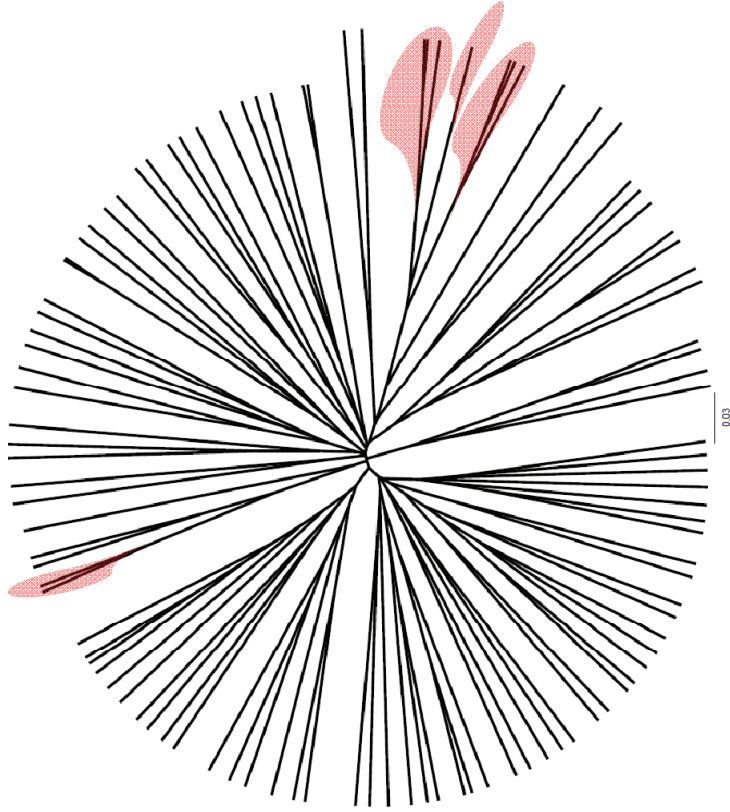


Supplementary Figure 1 | Flow sorting strategy for single cell experiments. Side-scatter (A) and forward scatter (B) doublet discriminate gates were used to identify single cell RBCs. iRBCs are then determined by selecting Vibrant Dye Cycle Green positive cells (C).

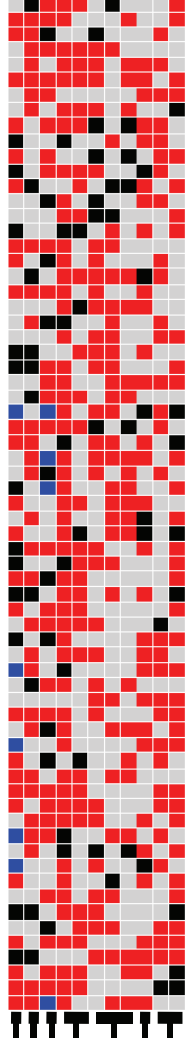


Supplementary Figure 2 | Single cell genotyping of a *P. falciparum* infection from the Thai-Burmese border. (a) UPGMA tree of 1-pair-wise allele sharing of a single *P. falciparum* infection (in red) and 101 unique single clone infections (randomly selected from the genotyping in ⁹). (b) Haplotype plots from the single cell genotyping, haplotypes are shown by black boxes on the left of the plot. (c) Rarefaction and extrapolation curve of haplotype abundance.

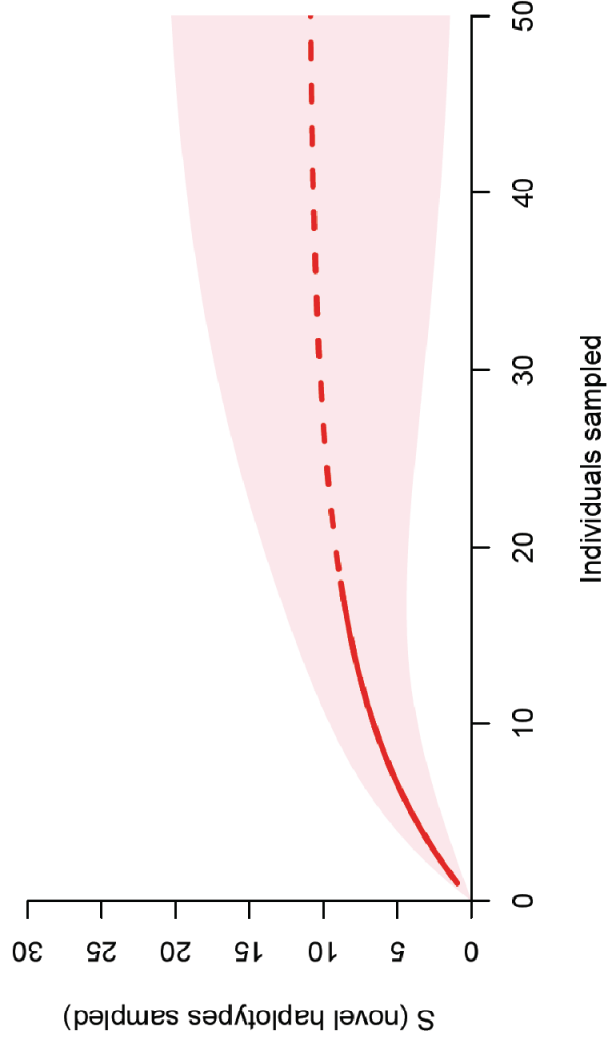
A



B

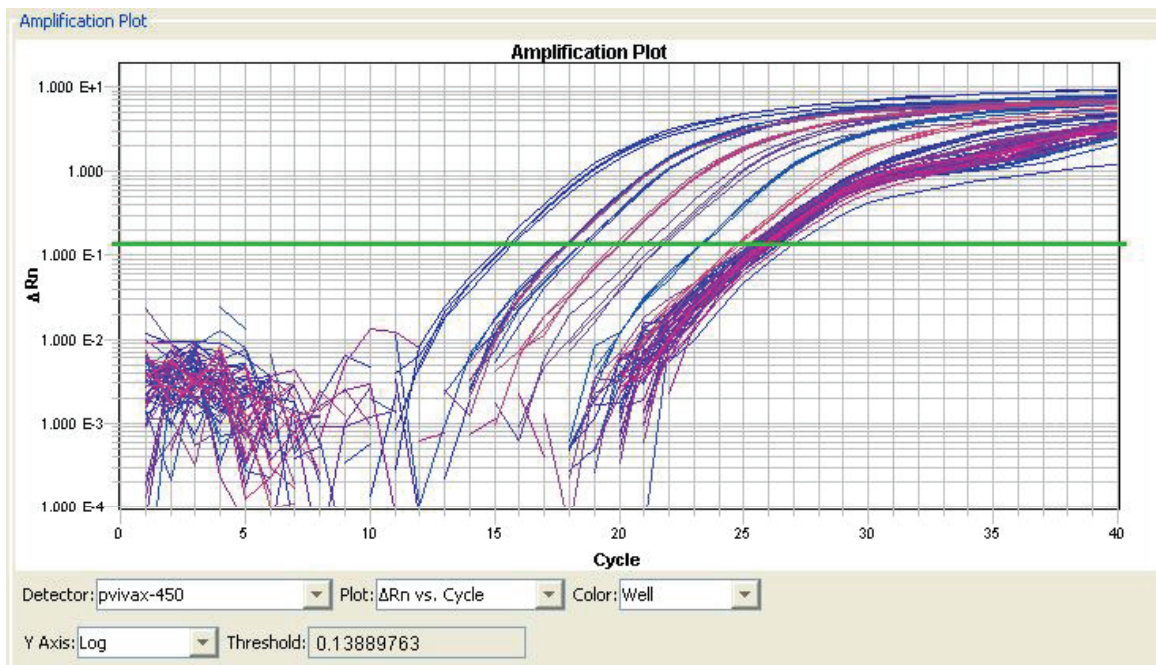


C

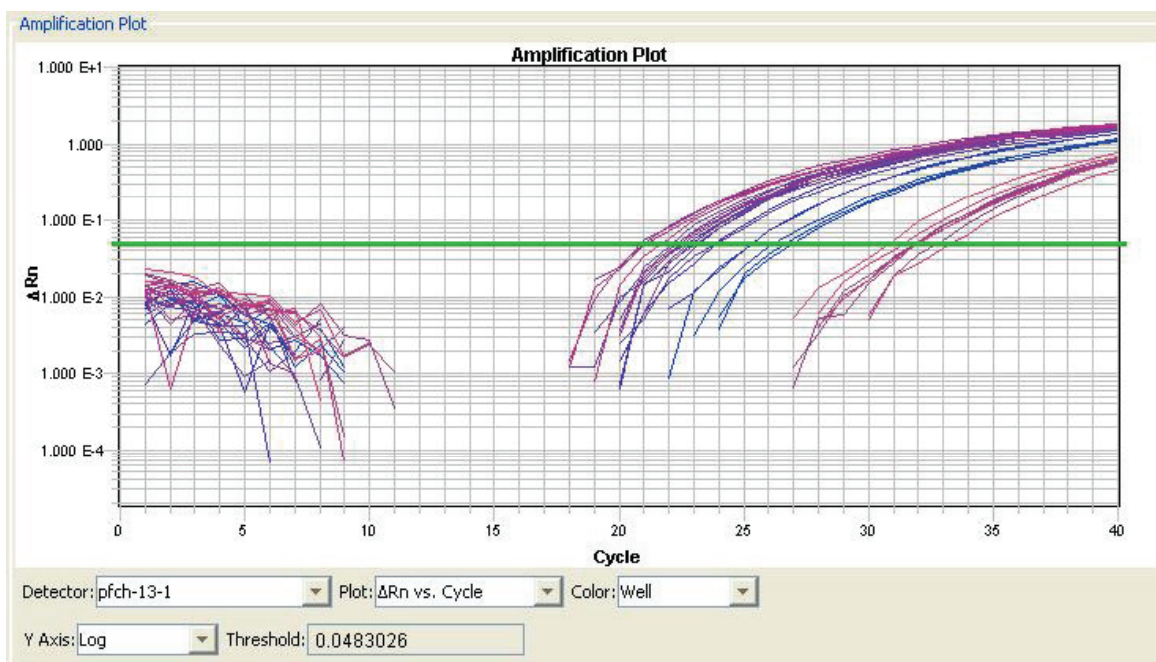


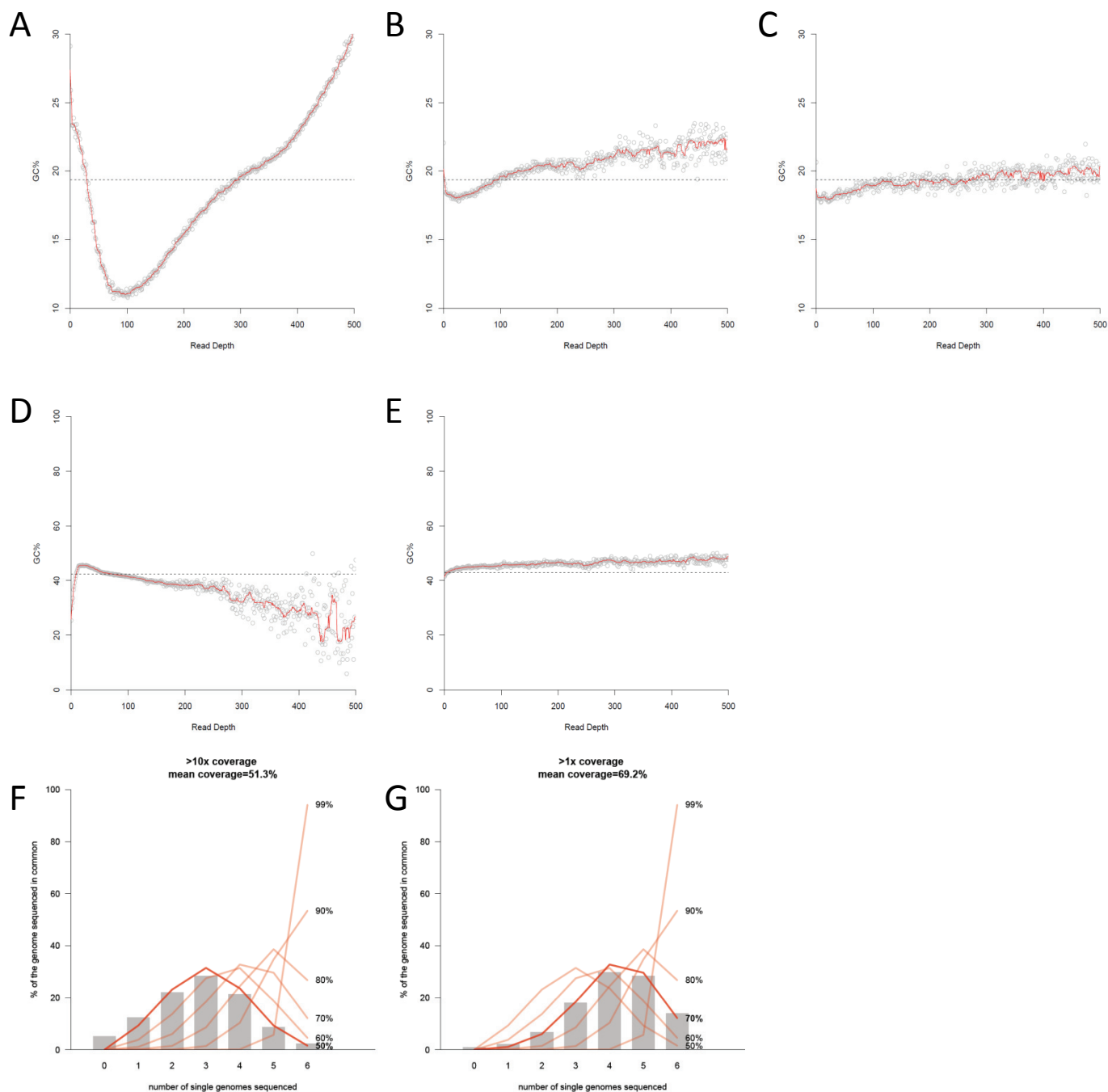
Supplementary Figure 3 | qPCR of *P. vivax* (A) and *P. falciparum* (B) whole genome amplifications efficiently identifies reactions with low level contamination with endogenous DNA.

A

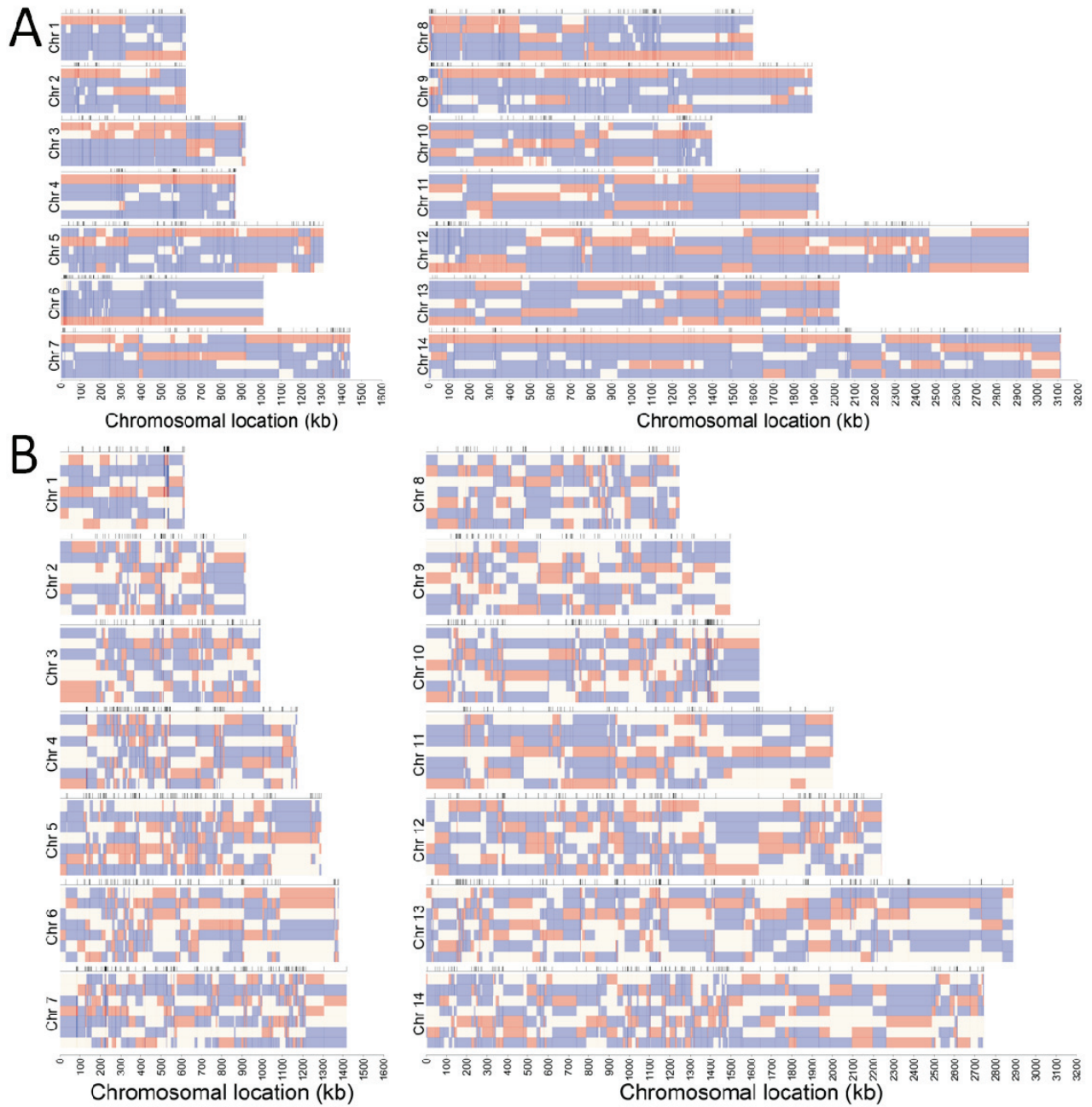


B





Supplemental Figure 4 | Bias in single cell sequence coverage. The relationship between GC% and read depth was explored for (A) unamplified *P. falciparum* DNA, (B/C) *P. falciparum* single cells, (D) unamplified *P. vivax* and (E) *P. vivax* single cells. For clarity only a subset of *P. vivax* and *P. falciparum* single cells are shown. In contrast to the characteristic GC skew seen in standard NGS library preparations of *P. falciparum* where GC content is a strong predictor of read depth only minimal correlation was seen in single cell sequences. To a lesser extent this was also observed in the more GC neutral genome of *P. vivax*. (F) Observed sharing of genomic fragments in *P. falciparum* single cells (black bars) follows the expected distribution where 50% of the genome was randomly selected for each single cell sequence (red lines). (G) After relaxing the minimum coverage to 1X (a mean coverage of 69.2%) the shared proportion of the genome changes with expectations.



Supplemental Figure 5 | Haplotype sharing in malaria infections. (A) Genome-wide patterns of haplotype sharing in *P. vivax* MGI WPP1494 using 1,562 SNPs sequenced in ≥ 4 single cells. (B) Genome-wide patterns of haplotype sharing in *P. falciparum* MGI MKK2664 using 1,917 SNPs sequenced in ≥ 4 single cells. Major alleles are shown in blue, minor alleles in red and missing data in white.