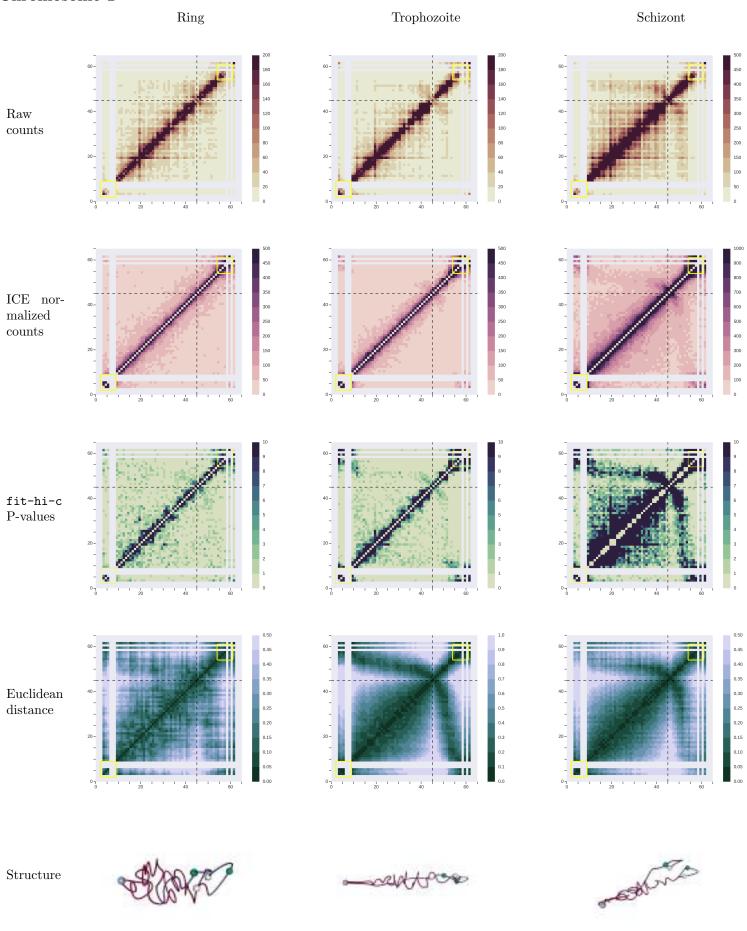
Supplementary Data 1: Chromosome visualizations for P. falciparum stages. For each chromosome, we generated three pages of figures for the various stages and parasite strains assessed. On the first page are the ring, trophozoite, and schizont stage from our previous study re-analyzed using the same pipeline as the new stages. On the second page are stage II/III gametocytes, stage IV/V gametocytes and sporozoites. On the third page are the wild-type ring stage (same as on the first page, but repeated here to facilitate the comparison with the HP1 strains), the ring stage of the HP1-tagged strain, and the ring stage of the HP1-knockdown strain. Within each page, the top row shows the raw contact count matrices at 10 kb resolution, the second row shows the ICE-normalized contact count matrices at 10 kb resolution, and the third row shows matrices of the fit-hi-c P-values assigned to the contacts. In these three matrices, the location of the centromere is indicated by a dashed black line and the location of the virulence gene clusters in indicated by a yellow box. Unmappable regions are colored in grey. The fourth row shows the pairwise Euclidean distance matrices derived from the 3D model, and the bottom row shows the inferred configuration in 3D with light blue spheres indicating centromeres, white spheres indicating telomeres and purple regions indicating the location of virulence gene clusters. Of note, we obtained zero mapped sequence reads for chr4:1-40,000 and chr5:1,310,000-1,343,557 in stage II/III gametocytes, suggesting that these regions are deleted in the *P. falciparum* NF54^{Pfs16} reporter gene line used for this experiment.



${\bf Chromosome}~1$

