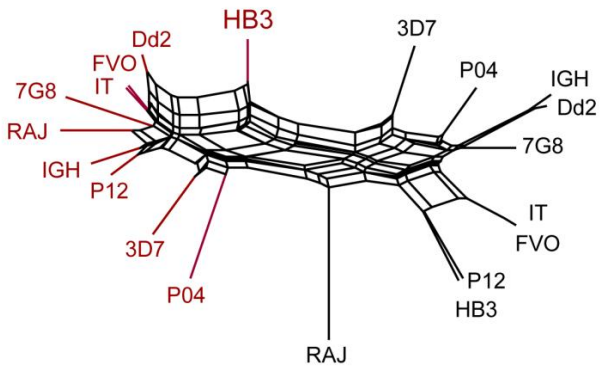
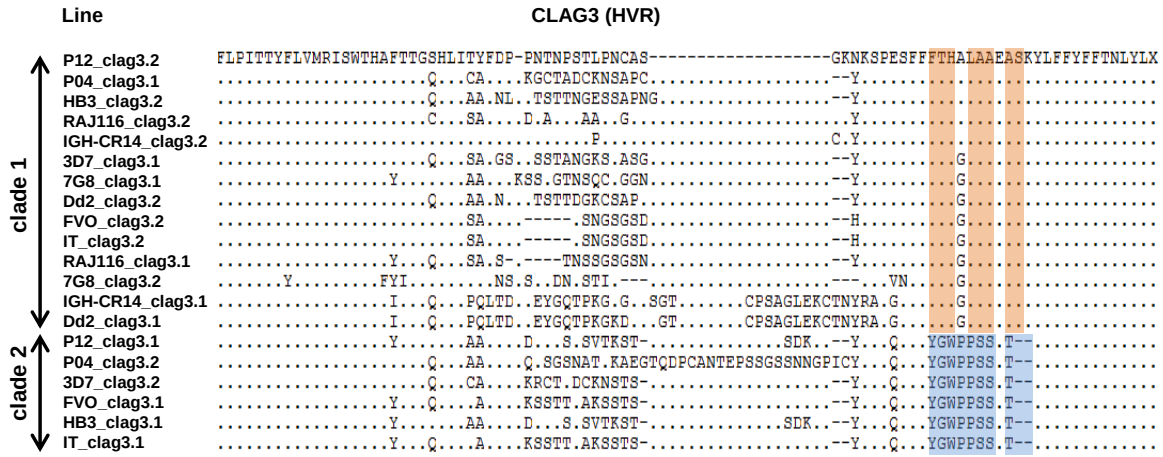
A



B



Supplemental Fig. S2. CLAG3 sequence analysis. (A) Split network of full CLAG3 sequences (publicly available sequences and new sequences from the P04 and P12 isolates). Connections between branches (parallel edges) represent recombination events. The distribution of these branches indicates that recombination events between the two paralog genes have likely occurred. CLAG3.1 and CLAG3.2 sequences are represented as black and red branches, respectively. **(B)** Alignment of a subset of CLAG3 hypervariable region (HVR) sequences (from the same parasite lines as in panel A) ordered according to the two separate clades observed in Fig. 3C. Dots indicate identity with the first sequence. This subset of sequences is representative of the full set of sequences analyzed (22 additional new sequences for each gene). Conserved sequence features specific for clades 1 or 2 are highlighted. These features are also conserved in all other clade 1 and clade 2 sequences analyzed. Each isolate had at least one *clag3* gene belonging to clade 1, which is suggestive of a non-random distribution of HVR sequences.