Supplementary Figure S5. Phylogeny of protection-related proteins



The amino acid sequences of CAHS, SAHS, MAHS, RvLEAM and Dsup genes in *H. dujardini* and *R. varieornatus* were aligned with ClustalW2, and a phylogenetic tree was inferred with FastTree with 1,000 bootstraps. Each clade was annotated with the corresponding subtype as defined in *R. varieornatus* (CAHS1:g673, CAHS2:g675, CAHS3:g884, SAHS1:g1671, SAHS2:g1676, MAHS:g6834, RvLEAM:g2978, Dsup:g4591).