Supporting Information

Yang and Stiller 10.1073/pnas.1323616111

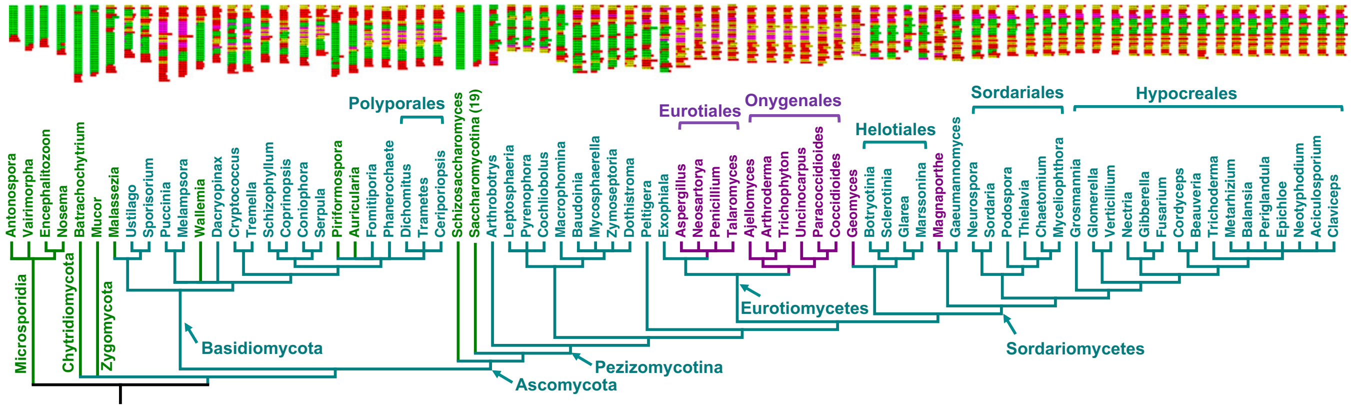

Fig. S1. C-terminal domain (CTD) evolution in fungi. The tree shows consensus relationships of all fungal genera used in this study. Branch colors are based on the conventions described for Fig. 1. The annotated CTD structure for each genus is shown above the tree (CTD N-termini are at the top of each sequence). Each bracket contains all genera belonging to the taxonomic order named above.

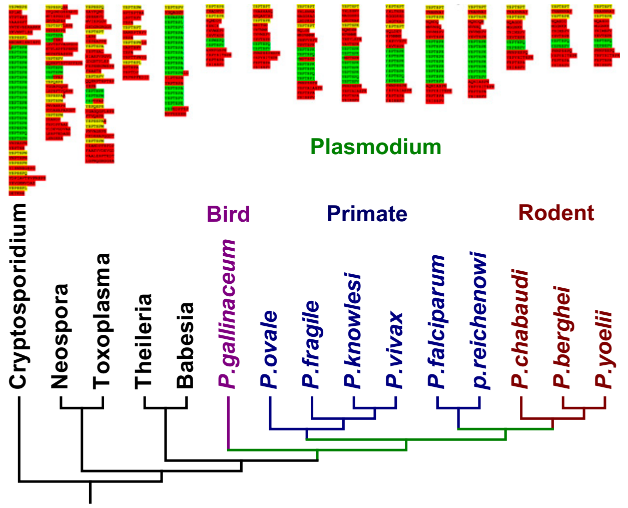

Fig. S2. CTD evolution in the Apicomplexa. The tree shows the evolutionary relationships of apicomplexans. The 10 *Plasmodium* species are divided into three groups (shown in different colors) according to their hosts: bird, primate, and rodent. CTD N-termini are at the top of each sequence.

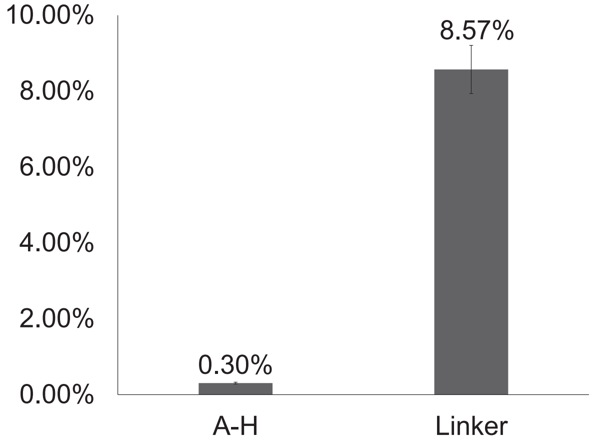

Fig. S3. Submotif SP content comparison. To avoid biases based on imbalances of available RPB1 sequences across eukaryotic taxa, and similarities within closely related genera, we chose 20 RPB1 sequences (n = 6 from metazoa, n = 6 from fungi, n = 4 from green plants, n = 3 from Apicomplexa, and n = 1 from Excavata) from distantly related genera across eukaryotic taxa for a submotif comparison of Ser–Pro pair content between RPB1 domains A–H and the CTD linker region. Each bar represents the mean percentage (SEs are shown on each bar) of SP submotifs for the main body of RPB1 and the CTD linker, respectively.