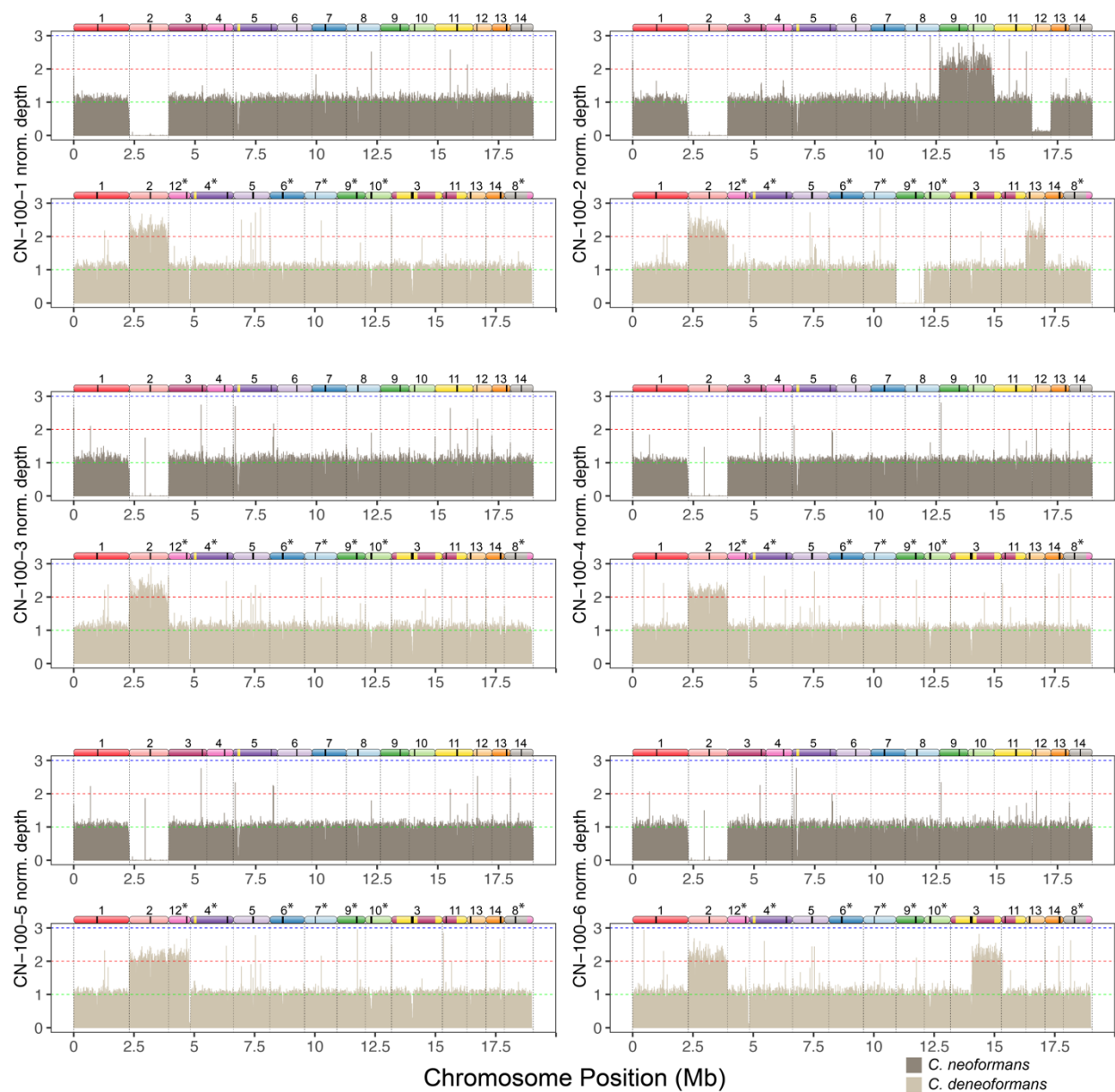
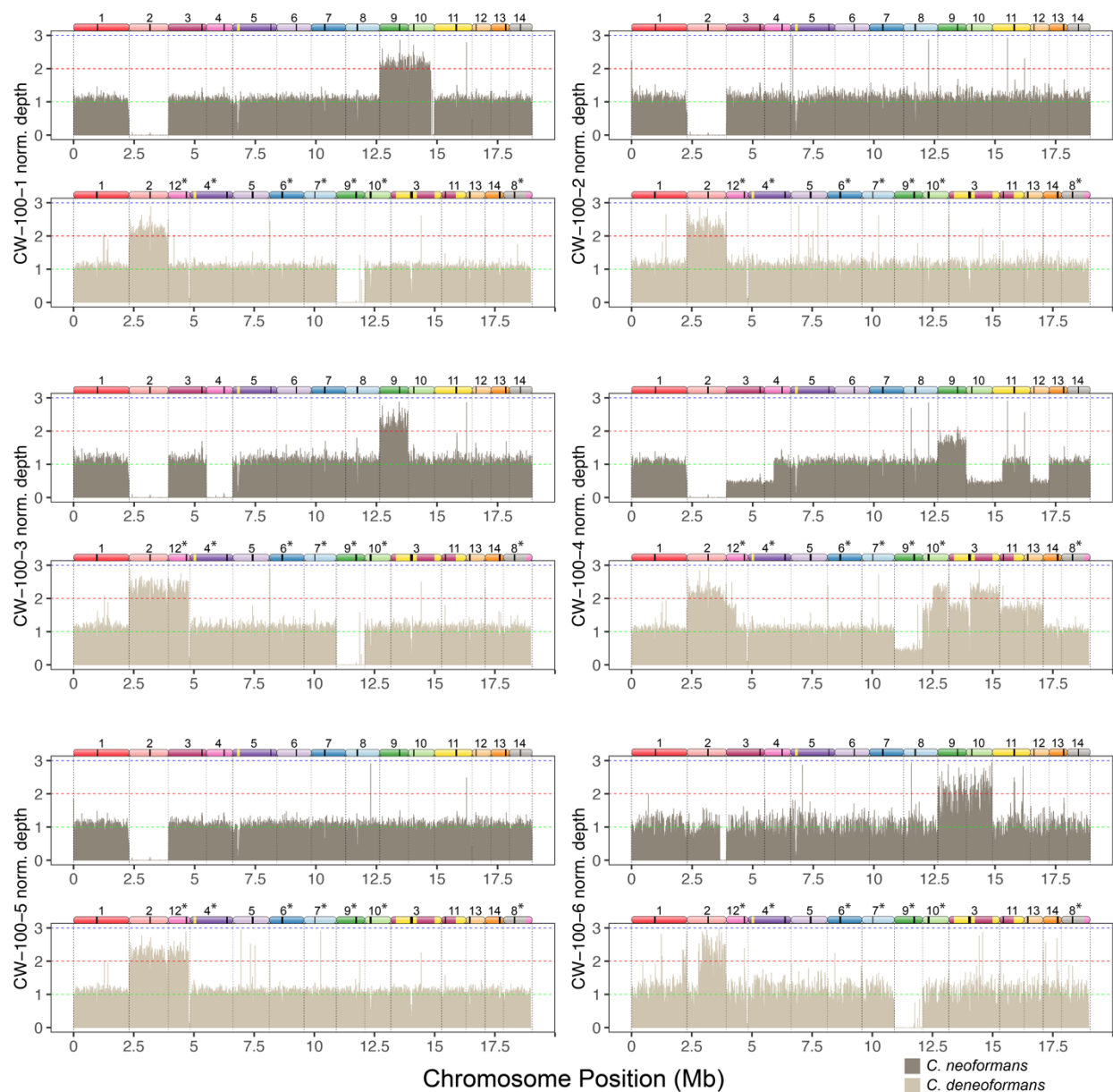


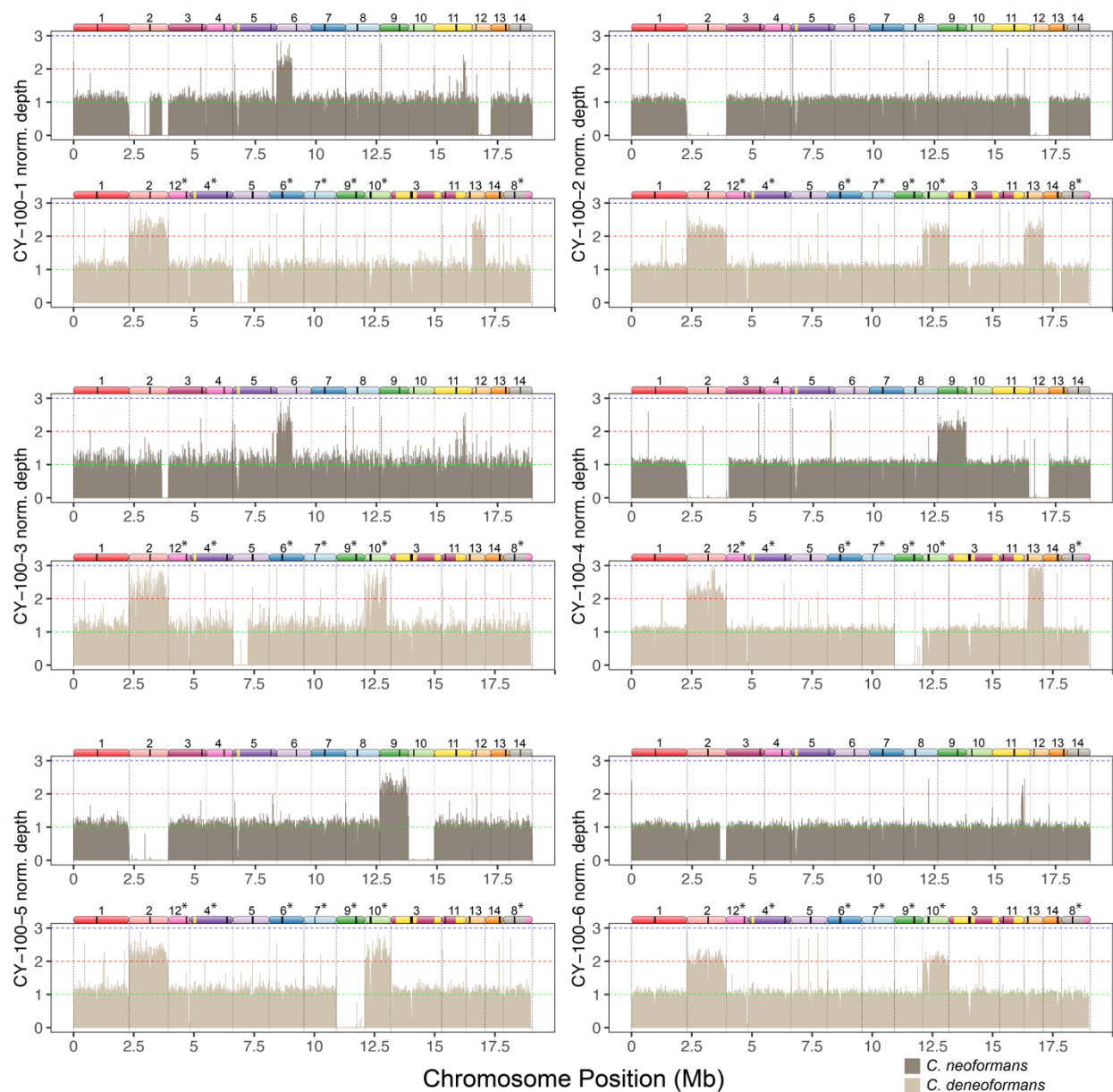
Suppl. Figure 1. Mapping of reads to a hybrid reference genome of strains evolved in beer wort. Bars show mean depth in 5 kb intervals that have been normalized by dividing the depth of each interval by the mean coverage for each strain. For each strain the top panel shows mapping to the *C. neoformans* reference genome, and the bottom panel shows mapping to the *C. deneoformans* reference genome. Diagrams of homeologous chromosomes are shown above each reference genome where colors reflect homology and black stripes indicate centromeres. *C. deneoformans* chromosomes were rearranged to better reflect homology, and asterisks indicate chromosomes that have been reverse-complemented.



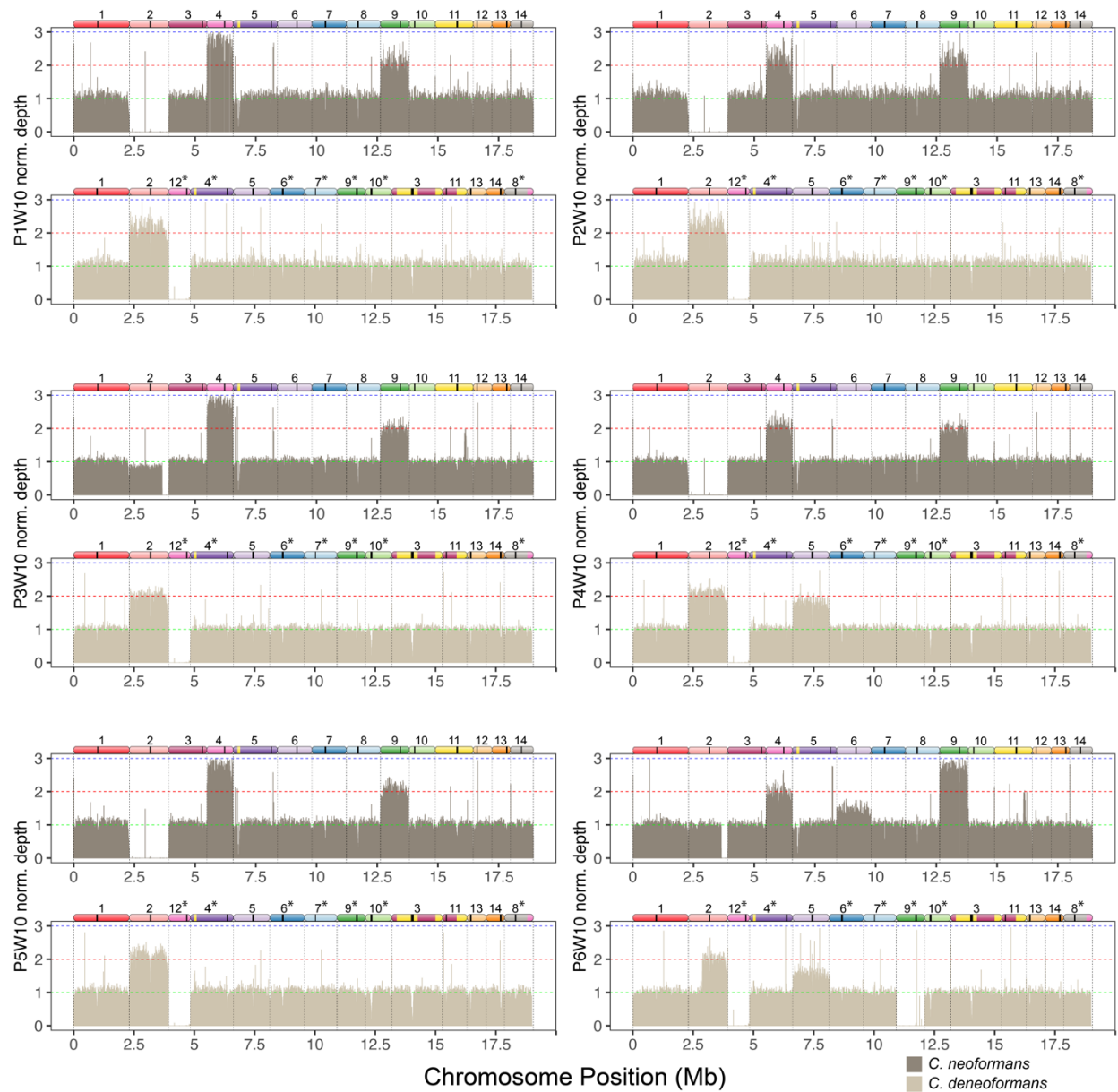
Suppl. Figure 2. Mapping of reads to a hybrid reference genome of strains evolved in high salt. Bars show mean depth in 5 kb intervals that have been normalized by dividing the depth of each interval by the mean coverage for each strain. For each strain the top panel shows mapping to the *C. neoformans* reference genome, and the bottom panel shows mapping to the *C. deneoformans* reference genome. Diagrams of homeologous chromosomes are shown above each reference genome where colors reflect homology and black stripes indicate centromeres. *C. deneoformans* chromosomes were rearranged to better reflect homology, and asterisks indicate chromosomes that have been reverse-complemented.



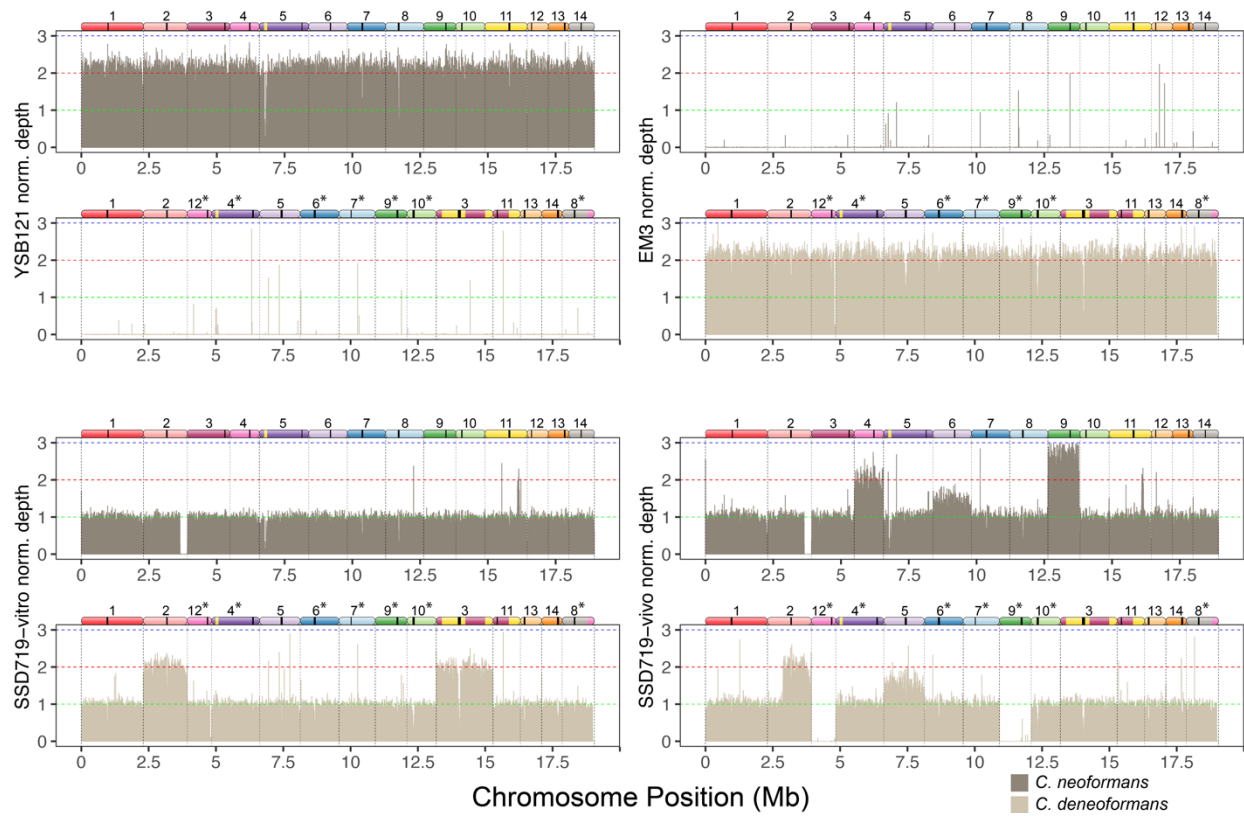
Suppl. Figure 3. Mapping of reads to a hybrid reference genome of strains evolved in wine must. Bars show mean depth in 5 kb intervals that have been normalized by dividing the depth of each interval by the mean coverage for each strain. For each strain the top panel shows mapping to the *C. neoformans* reference genome, and the bottom panel shows mapping to the *C. deneoformans* reference genome. Diagrams of homeologous chromosomes are shown above each reference genome where colors reflect homology and black stripes indicate centromeres. *C. deneoformans* chromosomes were rearranged to better reflect homology, and asterisks indicate chromosomes that have been reverse-complemented.



Suppl. Figure 4. Mapping of reads to a hybrid reference genome of strains evolved in complete media (YPD). Bars show mean depth in 5 kb intervals that have been normalized by dividing the depth of each interval by the mean coverage for each strain. For each strain the top panel shows mapping to the *C. neoformans* reference genome, and the bottom panel shows mapping to the *C. deneoformans* reference genome. Diagrams of homeologous chromosomes are shown above each reference genome where colors reflect homology and black stripes indicate centromeres. *C. deneoformans* chromosomes were rearranged to better reflect homology, and asterisks indicate chromosomes that have been reverse-complemented.



Suppl. Figure 5. Mapping of reads to a hybrid reference genome of strains evolved in larvae. Bars show mean depth in 5 kb intervals that have been normalized by dividing the depth of each interval by the mean coverage for each strain. For each strain the top panel shows mapping to the *C. neoformans* reference genome, and the bottom panel shows mapping to the *C. deneoformans* reference genome. Diagrams of homeologous chromosomes are shown above each reference genome where colors reflect homology and black stripes indicate centromeres. *C. deneoformans* chromosomes were rearranged to better reflect homology, and asterisks indicate chromosomes that have been reverse-complemented.



Suppl. Figure 6. Mapping of reads to a hybrid reference genome of ancestral strains. Strains YSB121 and EM3 are haploid *C. neoformans* and *C. deneoformans* parents, respectively. Strain SSD719-in vitro was used to initiate the in vitro evolution populations and strain SSD719-in vivo was used to initiate the passages in larvae. Bars show mean depth in 5 kb intervals that have been normalized by dividing the depth of each interval by the mean coverage for each strain. For each strain the top panel shows mapping to the *C. neoformans* reference genome, and the bottom panel shows mapping to the *C. deneoformans* reference genome. Diagrams of homeologous chromosomes are shown above each reference genome where colors reflect homology and black stripes indicate centromeres. *C. deneoformans* chromosomes were rearranged to better reflect homology, and asterisks indicate chromosomes that have been reverse-complemented.