

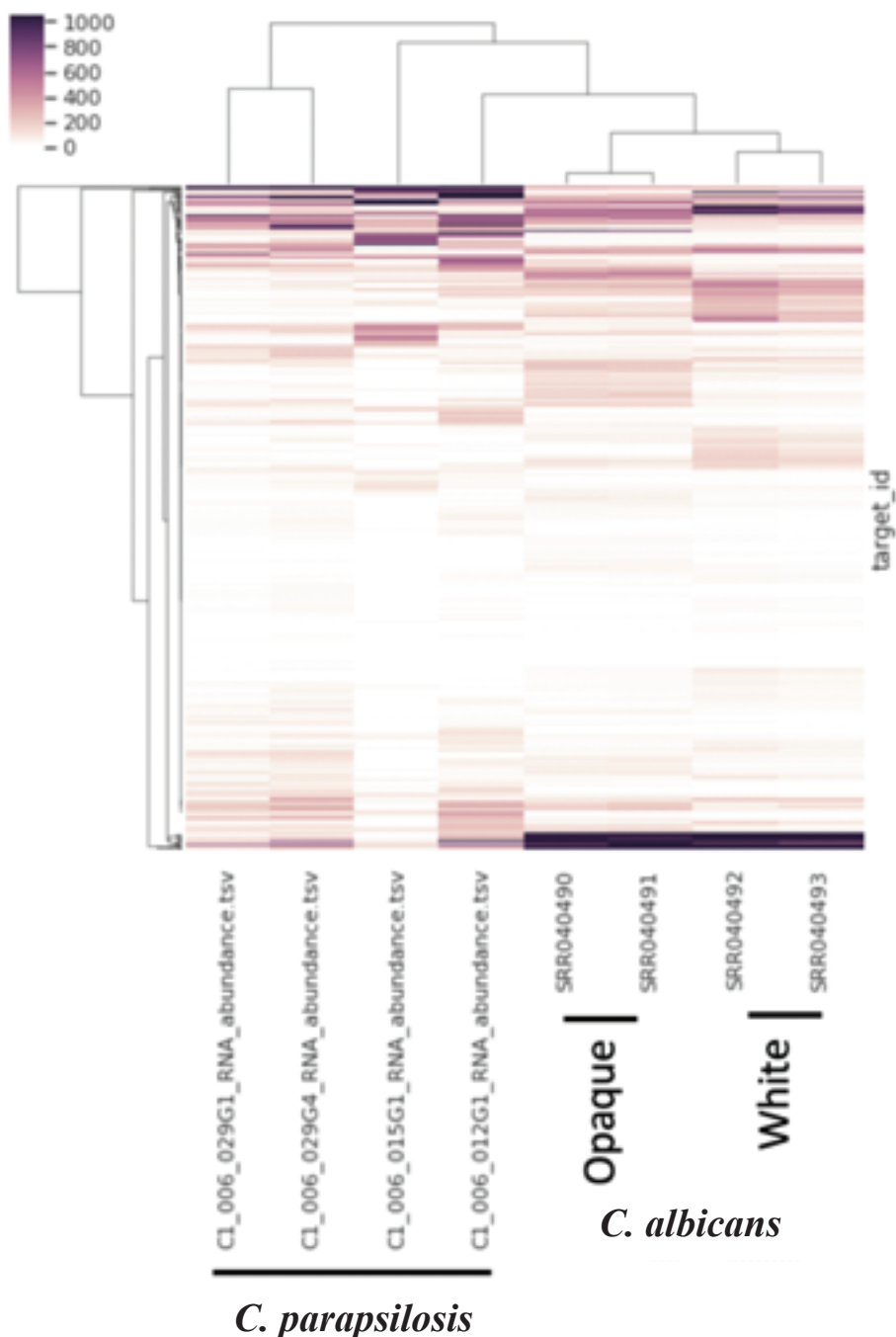


Figure S9: *C. parapsilosis* in situ transcriptomes show more variance than that observed between *C. albicans* white and opaque phenotypes. Samples are hierarchically clustered, with top bars reflecting how similar samples are to one another. Y axis represents only transcripts differentially expressed between white and opaque phenotypes identified in Tuch et al. 2010. *C. parapsilosis* orthologs for each *C. albicans* transcript were identified with orthofinder.