**Figure S2. No evidence for gene flow from/to *Saccharomyces* species or *S. paradoxus*.** Coverage depth of Jean-Talon reads mapped to concatenated genomes of eight *Saccharomyces* species (top) and concatenated genomes of *S. cerevisiae* and six *S. paradoxus* lineages (bottom). Reads map exclusively to the *S. cerevisiae* genome. Coverage depth in the plot was averaged across 10 kb non-overlapping windows. Statistically significant positive residuals of a $\chi^2$ test of randomness of read counts across all genomes (p-value <2.2E-16) are produced only by *S. cerevisiae.*