Supplemental Table 1. Gene sets, homology, tandem repeats and ohnologs

Genome	**Genes**	**Homologs** [a]	**Singletons** [b]	**Tandems** [c]	**Ohnologs** [d]
S. cerevisiae	5616	93.7%	6.3%	81 (1.4%)	551 (19.6%)
S. castellii	5596	91.8%	8.2%	77 (1.4%)	599 (21.4%)
C. glabrata	5181	93.8%	6.2%	84 (1.6%)	404 (15.6%)
A. gossypii	4716	96.0%	4.0%	67 (1.4%)	N/A
K. lactis	5327	89.0%	11.0%	67 (1.3%)	N/A
K. waltii	5230	89.2%	10.8%	65 (1.2%)	N/A
S. kluyveri	2970	89.1%	10.9%	43 (1.5%)	N/A

[a] Percentage of genes that are in a pillar with at least one other gene.

[b] Percentage of genes in singleton pillars.

[c] Number and percentage of genes that are in tandem repeats. A tandem repeat is defined as adjacent genes with BLASTP of E < 1e-100, or with E < 1e-10 provided that the HSP is more than half the length of the shorter sequence, which is in turn at least half the length of the longer sequence.

[d] Number of ohnolog pairs (paralogs arising from a WGD) in the genome, and the percentage of the genome these genes represent.