

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

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

<sup>a</sup> Percentage of genes that are in a pillar with at least one other gene.

<sup>b</sup> Percentage of genes in singleton pillars.

<sup>c</sup> 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.

<sup>d</sup> Number of ohnolog pairs (paralogs arising from a WGD) in the genome, and the percentage of the genome these genes represent.