

**Table S2 YGOB-HMM families detected in representative strains of five *Saccharomyces* species.** Families with two members displaying conserved synteny to the ancestral gene order (Gordon *et al.* 2009) were inferred to be descended from the ancient whole-genome duplication (“Ohnologs”; see Methods).

	YGOB-HMM Hits	YGOB-HMM Families (of 4,704)		
		Detected	Not Detected	Ohnologs
<i>S. cerevisiae</i>	5,490	4,605	99	527
<i>S. paradoxus</i>	5,440	4,547	157	542
<i>S. mikatae</i>	5,454	4,604	100	528
<i>S. kudriavzevii</i>	5,450	4,606	98	529
<i>S. bayanus</i>	5,559	4,611	93	522
Shared (excluding <i>S. paradoxus</i> )	-	4,589	90	520