Supplemental Table 1 : The observation of asymmetry is not conditional on the inclusion of particular post-WGD lineages

	Post-WGD Sequences Excluded from Alignments			
	None	*S. bayanus* and *S. cerevisiae*	*C. glabrata*	*S. castellii*
Asymmetry* of Partitioned Dataset	180.4	88.13	92.0	145.0
Mean Asymmetry* of Randomized Datasets (100)	4	1	-3	6
Maximum of Randomized Datasets	190	76	148	90
Number of Randomized Datasets exceeding Partitioned Dataset	1	0	1	0
P-value (Empirical) §	< 0.02	< 0.01	< 0.02	< 0.01

* As described in the *Main Text*: The sum (%) of the differences in relative rates of protein sequence evolution between the "initially-fast" and "initially-slow" clades for all pairs of duplicate branches excluding the first branches after the WGD.

§ Calculated from the number of randomized datasets whose *Asymmetry* exceeds that of the partitioned dataset.

Supplemental Table 2 : The observation of asymmetry is not conditional on the inclusion of a particular subset of double-copy genes

	Percentage of Double-copy Genes Sampled without Replacement for Boostrap Replicates	
	100%	50%
Mean Asymmetry* of Partitioned Datasets (100)	180.4†	95.75
Mean Asymmetry* of Randomized Datasets (100)	4	-6
Maximum of Randomized Datasets	190	204
Number of Randomized Datasets exceeding Mean of Partitioned Datasets	1	13
P-value (Wilcoxon rank-sum test) ¶	NA	2.20E-16

* As described in the *Main Text*: The sum (%) of the differences in relative rates of protein sequence evolution between the "initially-fast" and "initially-slow" clades for all pairs of duplicate branches excluding the first branches after the WGD.

† A single dataset since when 100% of double-copy genes are sampled without replacement, only one unique partitioning into "Initially-fast" and "Initially-slow" clades exists.

¶ Calculated using the *Asymmetry* scores of 100 partitioned and 100 randomized bootstrap replicates.