Supplemental Table 1. Composition of Datasets

	S. cerevisiae : C. glabrata			***S. cerevisiae : S. castellii***			***C. glabrata : S. castellii***				**Dataset**
Locus Type	**2:2**	**2:1**	**1:2**	**2:2**	**2:1**	**1:2**	**2:2**	**2:1**	**1:2**	**Total**	**Name**
YGOB Data	293	219	97	385	137	186	275	110	284	1986	**Set 0**
Synteny Filter PASS	204 (70%)	119 (54%)	41 (42%)	275 (71%)	70 (51%)	92 (50%)	161 (59%)	45 (41%)	125 (44%)	1132 (57%)	**Set 1**
Gene Conversion	*52 (25%)*	*63 (53%)*	*19 (46%)*	*96 (35%)*	*20 (29%)*	*46 (50%)*	*55 (34%)*	*12 (27%)*	*76 (61%)*	*439 (39%)*	GC
Phylogeny != Synteny	*4 (2%)*	-	-	*0 (0%)*	-	-	*3 (2%)*	-	-	*7 (1%)*	OPP
Other	*12 (6%)*	*16 (13%)*	*9 (22%)*	*13 (5%)*	*15 (21%)*	*16 (17%)*	*12 (7%)*	*13 (29%)*	*20 (16%)*	*126 (11%)*	OTH
Phylogeny Filter FAIL	68 (33%)	79 (66%)	28 (68%)	109 (40%)	35 (50%)	62 (67%)	70 (43%)	25 (56%)	96 (77%)	572 (51%)	
Phylogeny == Synteny	*68 (33%)*	*40 (34%)*	*13 (32%)*	*100 (36%)*	*35 (50%)*	*30 (33%)*	*38 (24%)*	*20 (44%)*	*29 (23%)*	*373 (33%)*	EQL
Phylogeny ~= Synteny	*68 (33%)*	-	-	*66 (24%)*	-	-	*53 (33%)*	-	-	*187 (17%)*	ONE
Phylogeny Filter PASS	136 (67%)	40 (34%)	13 (32%)	166 (60%)	35 (50%)	30 (33%)	91 (57%)	20 (44%)	29 (23%)	560 (49%)	**Set 2**
Significant Asymmetry	65 (48%)	20 (50%)	10 (77%)	62 (37%)	18 (51%)	17 (57%)	41 (45%)	13 (65%)	26 (90%)	272 (49%)	**Set 3**

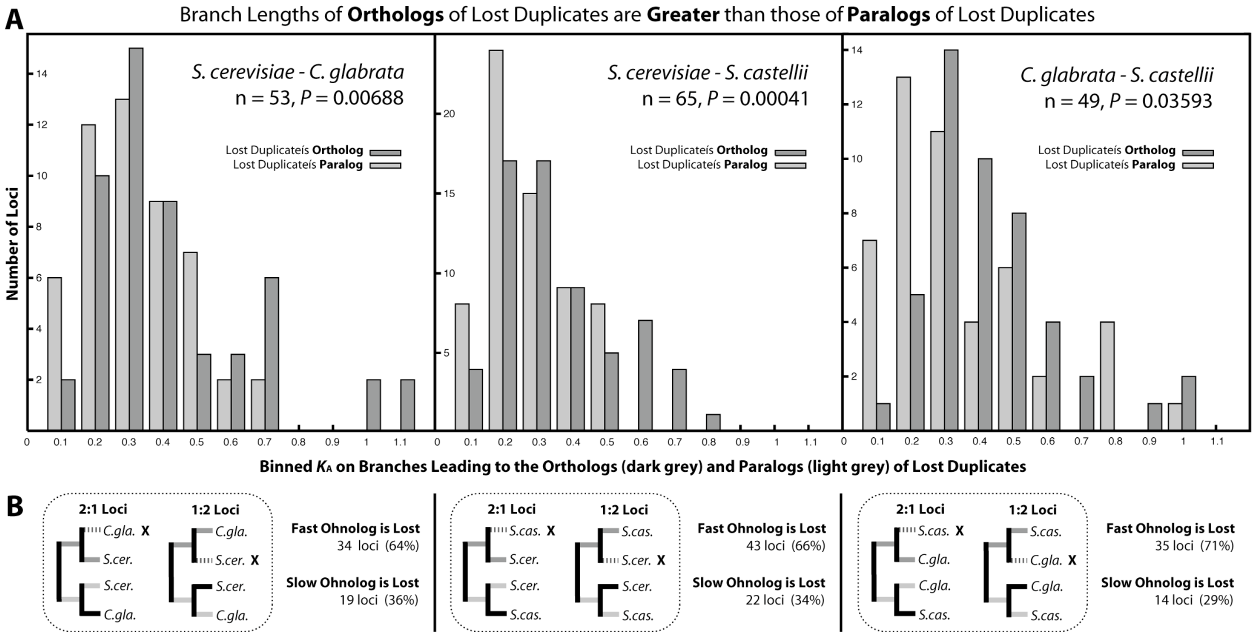
Numbers indicate the number of data-points in each category. Percentages are expressed relative to the previous Set in the same column.

Supplemental Table 2. Consistency of Asymmetric Evolution across Species (examining amino acid divergence on terminal branches at 2:2 loci from alternative datasets to that used Table 1A)

	S. cerevisiae*: *C. glabrata		***S. cerevisiae*: *S. castellii***		***C. glabrata*: *S. castellii***	
Supplemental Table 2A	All loci, including those with non-significant asymmetry (Set 2)					
Locus status [a]	**Loci**	**Percentage**	**Loci**	**Percentage**	**Loci**	**Percentage**
Fast (sp. 1) is Fast (sp. 2)	**105**	**77%**	**121**	**73%**	**69**	**76%**
Fast (sp. 1) is Slow (sp. 2)	**31**	**23%**	**45**	**27%**	**22**	**24%**
Total Number of Loci	**136**	**100%**	**166**	**100%**	**91**	**100%**
		***P* = 4.78e-6**		***P* = 2.75e-5**		***P* = 3.87e-4**
Supplemental Table 2B	Only including loci with R' > 1.25 and ΔK_A > 0.1 (Set 2 with cut-offs)					
Locus status [a]	**Loci**	**Percentage**	**Loci**	**Percentage**	**Loci**	**Percentage**
Fast (sp. 1) is Fast (sp. 2)	**45**	**33%**	**40**	**24%**	**34**	**37%**
Fast (sp. 1) is Slow (sp. 2)	**1**	**1%**	**5**	**3%**	**2**	**2%**
Excluded Loci	**90**	**66%**	**121**	**73%**	**55**	**60%**
Total Number of Loci	**136**	**100%**	**166**	**100%**	**91**	**100%**
		***P* = 9.57e-8**		***P* = 7.28e-5**		***P* = 3.87e-5**
Supplemental Table 2C	Only including loci where synteny and phylogeny agree perfectly (Dataset "EQL")					
Locus status [a]	**Loci**	**Percentage**	**Loci**	**Percentage**	**Loci**	**Percentage**
Fast (sp. 1) is Fast (sp. 2)	**58**	**85%**	**74**	**74%**	**29**	**76%**
Fast (sp. 1) is Slow (sp. 2)	**10**	**15%**	**26**	**26%**	**9**	**24%**
Total Number of Loci	**68**	**100%**	**100**	**100%**	**38**	**100%**
		***P* = 1.77e-5**		***P* = 0.00076**		***P* = 0.032**

P-values are from Fisher's Exact Two-Tail Tests against neutral expectation.

[a] "Fast (sp. 1) is Fast (sp. 2)" means that the same ohnolog is the faster evolving one in both species. "Fast (sp. 1) is Slow (sp. 2)" means that the faster copy in one species is the slower evolving copy in the other. "Excluded Loci" are those that did not meet the cut-off criteria.



Supplemental Figure 1. Association across species of fast-evolving and lost ohnologs (Figure 5 analysis repeated on Set 2 dataset). See Figure 5 of main text for details.