	MSH4	MSH5	MLH1	MLH3	ZIP1	ZIP2	ZIP3	ZIP4	MER3
V polysporus	10	15	16	10	33	30	1	13	15
L kluyveri	24	35	30	22	53		20	23	25
L thermotolerans			24	5					
L waltii			19	48	45				5
K lactis	13	20	26	12	45	8	8	45	19
E gossypii			4	6	9				
C glabrata	2	14	38	21	32	3	17	30	10
N castellii	31	21	34	14	63	18	49	30	9
S bayanus	24	30	23	46	43	38	18	51	32
S mikatae	15	46	26	38	44	47	5	39	34
S paradoxus	15	49	17	23	56	32	16	24	26
S cerevisiae	23	37	39	30	61	56	18	29	30
C tropicalis	7	12	9	2			5	9	5
C albicans	7	12	54	1			4	19	4
C dubliniensis	8	12	43	2				22	7
C lusitaniae			29						
C guilliermondii			10	15					
D hansenii			18	22					21

Figure S1 Several crossover proteins show low CAI ranks in *Candida glabrata*. We corrected for the genome-wide distribution of CAI in each species by reporting each gene's rank, shown here as percentile rank. In these data, *C. glabrata* has very low codon bias for *MSH4*, *MSH5*, *ZIP1*, *ZIP3*, and *MER3*, but bias at *MLH1*, *MLH3*, and *ZIP4* are not as extreme.

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