

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

Figure S2

Available for download as a PDF file at <http://www.genetics.org/lookup/suppl/doi:10.1534/genetics.112.145979/-/DC1>.

This pairwise matrix shows empirical P-values for the set of 129 meiosis proteins in yeasts. Each value corresponds to the P-value for the column protein within all values of the row protein. Hence, values above and below the diagonal are similar but can differ. Empirical P-values in the main manuscript are the mean of these two values. There are a number of clusters of elevated ERC within this large set of proteins.

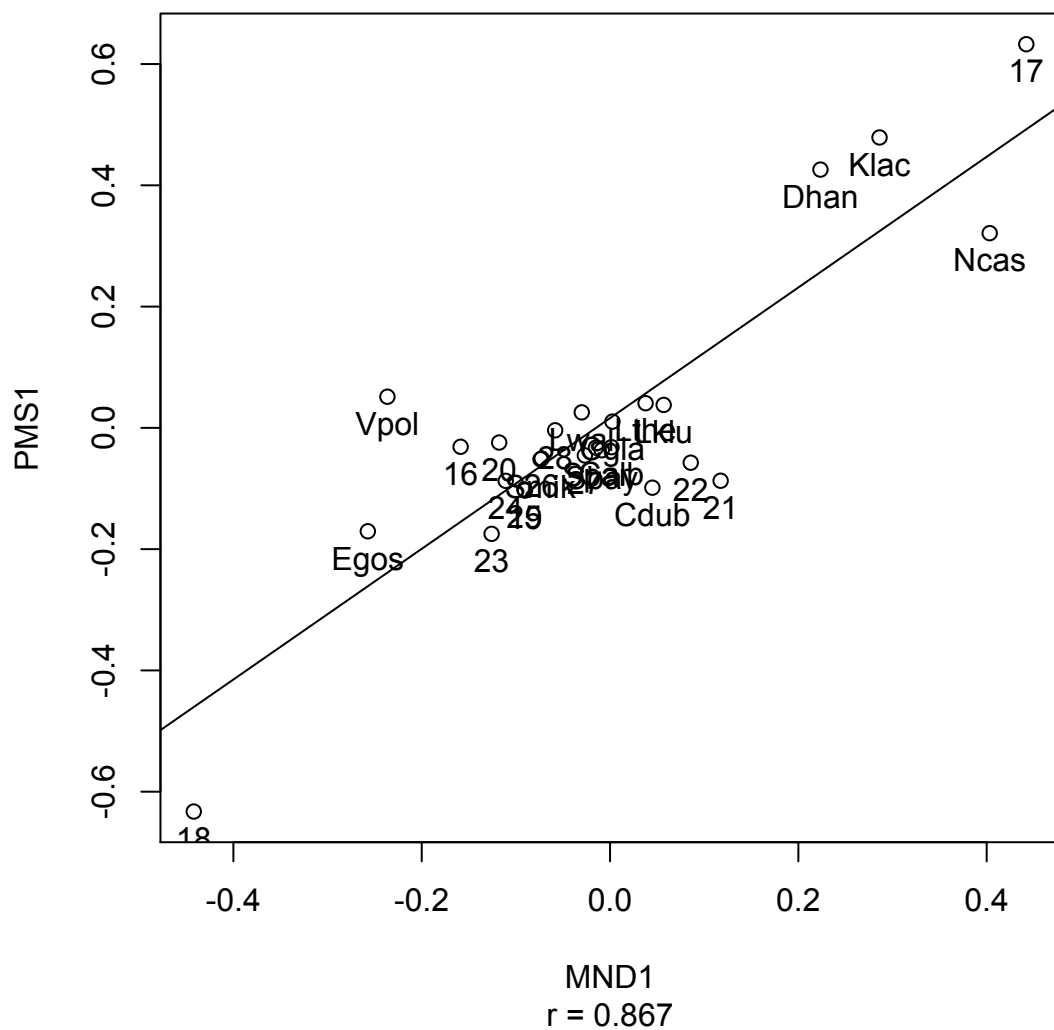


Figure S3 The relative rates of the Mnd1 and Pms1 proteins correlate very well in yeasts ($r = 0.867$), and their relationship involves several branches from the phylogenetic tree. Three species (*N. castelii*, *K. lactis*, and *D. hansenii*) and one internal branch had particularly rapid rates of evolution for these two DNA repair proteins.

Figure S4

Available for download as a PDF file at <http://www.genetics.org/lookup/suppl/doi:10.1534/genetics.112.145979/-/DC1>.

This pairwise matrix shows empirical P-values for a set of 91 mammalian meiotic proteins. Each value corresponds to the P-value for the column protein within all values of the row protein. Hence, values above and below the diagonal are similar but can differ. Empirical P-values in the main manuscript are the mean of these two values. There are a number of notable clusters of high ERC in this matrix. In particular there were two clusters involving piRNA production and metabolism (see main text).

Table S1 Species-specific patterns of meiotic gene loss

	missing Meiotic genes (of 128)	proportion missing: Meiosis	proportion missing: Genome	missing proportion ratio: Meiosis to Genome	meiosis- specific expression: P- value
<i>V polysporus</i>	1	0.008	0.124	0.063	0.43239
<i>L kluyveri</i>	5	0.039	0.174	0.225	0.90304
<i>L thermotolerans</i>	15	0.117	0.194	0.606	0.00895
<i>L waltii</i>	17	0.133	0.176	0.754	0.12492
<i>K lactis</i>	1	0.008	0.105	0.074	0.88704
<i>E gossypii</i>	8	0.063	0.147	0.424	0.00884
<i>C glabrata</i>	1	0.008	0.155	0.050	0.43496
<i>N castellii</i>	8	0.063	0.222	0.282	0.25790
<i>S bayanus</i>	1	0.008	0.062	0.126	0.63988
<i>S mikitae</i>	3	0.023	0.088	0.266	0.86970
<i>S paradoxus</i>	1	0.008	0.046	0.168	0.53128
<i>S cerevisiae</i>	0	0.000	0.000	NA	NA
<i>C tropicalis</i>	31	0.242	0.220	1.102	0.15643
<i>C albicans</i>	24	0.188	0.178	1.052	0.29070
<i>C dubliniensis</i>	27	0.211	0.214	0.987	0.01059
<i>C lusitanae</i>	45	0.352	0.270	1.302	0.00001
<i>C guilliermondii</i>	44	0.344	0.280	1.230	0.00001
<i>D hansenii</i>	26	0.203	0.162	1.251	0.03978