SUPPLEMENTAL MATERIALS

A. L. Dapper & B. A. Payseur. Molecular Evolution of the Meiotic Recombination Pathway in Mammals.

Table S1: Testes Expression Datasets (Barrett et al. 2012)

Species	**GEO Accession**	**Reference**
Bos taurus	GSM1020728 & GSM1020746	(Merkin et al. 2012)
Callithrix jacchus	GSM1227961, GSM1227962 & GSM1227963	(Cortez et al. 2014)
Canis lupus familiaris	GSM747469 & GSM1359286	(Derti et al. 2012; Vandewege et al. 2016)
Eptesicus fuscus	GSM1359287	(Vandewege et al. 2016)
Equus caballus	GSM1139276 & GSM1359288	(Coleman et al. 2013; Vandewege et al. 2016)
Gorilla gorilla	GSM752663	(Brawand et al. 2011)
Homo sapiens	GSM752707 & GSM752708	(Brawand et al. 2011)
Macaca mulatta	GSM752642 & GSM752643	(Brawand et al. 2011)
Mus musculus	GSM752629 & GSM752630	(Brawand et al. 2011)
Ovis aries	GSM1666944 & GSM1666936	(Guan et al. 2017)
Pan paniscus	GSM752690	(Brawand et al. 2011)
Pan troglodytes	GSM752678	(Brawand et al. 2011)
Pongo pygmaeus	GSM1858310 & GSM1858311	(Carelli et al. 2016)
Rattus norvegicus	GSM1278058	(Cortez et al. 2014)
Sus scrofa	GSM1902350, GSM2033157 & GSM2033163	(Li et al. 2016; Yang et al. 2017)
Tupaia chinensis	GSM957062	(Fan et al. 2013)

Table S2: NCBI Reference Genomes (O'Leary et al. 2015)

Species	**Assembly**	**RefSeq Accession**	**WGS Project Reference**
Bos taurus	Bos_taurus_UMD_3.1.1	GCF_000003055.6	(Zimin et al. 2009)
Callithrix jacchus	Callithrix_jacchus-3.2	GCF_000004665.1	-
Canis lupus familiaris	CanFam3.1	GCF_000002285.3	(Lindblad-Toh et al. 2005)
Eptesicus fuscus	EptFus1.0	GCF_000308155.1	-
Equus caballus	EquCab2.0	GCF_000002305.2	(Wade et al. 2009)
Gorilla gorilla	gorGor4	GCF_000151905.2	(Scally et al. 2012)
Homo sapiens	GRCh38.p10	GCF_000001405.36	-
Macaca mulatta	Mmul_8.0.1	GCF_000772875.2	(Zimin et al. 2014)
Mus musculus	GRCm38.p5	GCF_000001635.25	-
Ovis aries	Oar_v4.0	GCF_000298735.2	(International Sheep Genomics Consortium et al. 2010)
Pan paniscus	panpan1.1	GCF_000258655.2	(Prüfer et al. 2012)
Pan troglodytes	Pan_tro_3.0	GCF_000001515.7	(The Chimpanzee Sequencing Analysis Consortium et al. 2005)
Pongo abelii	P_pygmaeus_2.0.2	GCF_000001545.4	(Locke et al. 2011)
Rattus norvegicus	Rnor_6.0	GCF_000001895.5	(Rat Genome Sequencing Project Consortium et al. 2004)
Sus scrofa	Sscrofa11.1	GCF_000003025.6	-
Tupaia chinensis	TupChi_1.0	GCF_000334495.1	(Fan et al. 2013)

Table S3: Ensembl Reference Genomes (Zerbino et al. 2017)

Species	**Assembly**	**RefSeq Accession**	**WGS Project Reference**
Bos taurus	Bos_taurus_UMD_3.1	GCF_000003055.3	(Zimin et al. 2009)
Callithrix jacchus	Callithrix_jacchus-3.2	GCF_000004665.1	-
Canis lupus familiaris	CanFam3.1	GCF_000002285.3	(Lindblad-Toh et al. 2005)
Eptesicus fuscus	-	-	-
Equus caballus	EquCab2.0	GCF_000002305.2	(Wade et al. 2009)
Gorilla gorilla	gorGor3.1	GCF_000151905.1	-
Homo sapiens	GRCh38.p10	GCF_000001405.36	-
Macaca mulatta	Mmul_8.0.1	GCF_000772875.2	(Zimin et al. 2014)
Mus musculus	GRCm38.p5	GCF_000001635.25	-
Ovis aries	Oar_v3.1	GCF_000298735.1	(International Sheep Genomics Consortium et al. 2010)
Pan paniscus	panpan1.1	GCF_000258655.2	(Prüfer et al. 2012)
Pan troglodytes	CHIMP2.1.4	GCF_000001515.6	(The Chimpanzee Sequencing Analysis Consortium et al. 2005)
Pongo abelii	PPYG2	GCF_000001545.4	(Locke et al. 2011)
Rattus norvegicus	Rnor_6.0	GCF_000001895.5	(Rat Genome Sequencing Project Consortium et al. 2004)
Sus scrofa	Sscrofa11.1	GCF_000003025.6	-
Tupaia chinensis	-	-	-

Table S4: Evolutionary rates and tests for positive selection across mammals at 32 recombination genes using the gene tree. Genes are organized by step in the pathway, as labeled in Figure 3. (Yang 2007).

Gene	***bp***	***N***	*ω*	***M***	***M1-M2***	***p-value***	***M7-M8***	***p-value***	***M8a-M8***	***p-value***
(A) DSB Formation										
HORMAD1	1212	16	0.3037	7	0	*1.000*	3.135	*0.2086*	—	—
MEI4	1170	16	0.4310	7	0	*1.000*	0.058	*0.9715*	—	—
REC114	870	15	0.4237	7	0	*1.000*	4.1874	*0.1232*	—	—
IHO1	1824	16	0.7099	**8**	13.384	***0.0012***	17.714	***0.0001***	14.707	***0.0001***
SPO11	1188	15	0.1701	7	0	*1.000*	4.697	*0.0955*	—	—
(B) DSB Processing										
HORMAD2	981	15	0.3290	1	0	*1.000*	3.881	*0.1436*	—	—
MRE11	2136	16	0.1686	**8**	0.636	*0.7277*	12.014	***0.0025***	4.822	***0.0281***
NBS1	2289	15	0.4185	**8**	0	*1.000*	12.899	***0.0016***	4.298	***0.0382***
RAD50	3936	16	0.0322	1	0	*1.000*	0.5615	*0.7552*	—	—-
BRCC3	954	15	0.0601	7	0	*1.000*	0.573	*0.7509*	—	—
(C) Homology Search & Strand Invasion										
DMC1	1020	15	0.0365	7	0	*1.000*	4.288	*0.1172*	—	—
RAD51	1017	16	0.0322	1	0	*1.000*	0.562	*0.7552*	—	—
SPATA22	1101	16	0.4932	7	0	*1.000*	0.200	*0.9049*	—	—
MEIOB	1425	16	0.2340	7	0	*1.000*	0.221	*0.8955*	—	—
MCMDC2	2052	16	0.2242	7	0	*1.000*	0.610	*0.7370*	—	—
(D) Synapsis										
REC8	1833	16	0.3698	**8**	0	*1.000*	14.690	***0.0006***	5.927	***0.0149***
RAD21L	1686	15	0.503	**8**	12.124	***0.0023***	32.050	***>0.0001***	12.049	***0.0005***
SYCP1	3015	16	0.4337	**8**	8.711	***0.0128***	26.860	***>0.0001***	9.243	***0.0024***
SYCP2	4650	16	0.5572	**8**	11.584	***0.0031***	37.200	***>0.0001***	15.838	***0.0001***
TEX12	369	14	0.2297	7	0.0565	*0.9721*	1.549	*0.4610*	—	—

Table S4: Cont.

Gene	***bp***	***N***	ω	***M***	***M1-M2***	***p-value***	***M7-M8***	***p-value***	***M8a-M8***	***p-value***
(E) CO/NCO Decision										
TEX11	2844	15	0.8483	**8**	60.872	***>0.0001***	82.665	***>0.0001***	61.141	***>0.0001***
SHOC1	4644	16	0.6113	**8**	12.447	***0.0020***	30.561	***>0.0001***	15.645	***0.0001***
RNF212	948	16	0.5014	**8**	0	*1.000*	16.366	***0.0003***	5.202	***0.0226***
RNF212B	906	14	0.4066	7	0	*1.000*	0.500	*0.7788*	—	—
MSH4	2814	16	0.2132	**8**	16.608	***0.0002***	39.447	***>0.0001***	23.238	***>0.0001***
MSH5	2565	15	0.1642	7	0	*1.000*	4.214	*0.1216*	—	—
(F) Resolution										
MER3	4458	16	0.3633	8a	0	*1.000*	12.838	***0.0016***	3.109	*0.0779*
CNTD1	1026	15	0.2496	7	0	*1.000*	0.936	*0.6263*	—	—
HEI10	831	15	0.1226	7	0	*1.000*	0.250	*0.8826*	—	—
MLH1	2313	15	0.1652	8a	0	*1.000*	12.221	***0.0022***	0.280	*0.5970*
MLH3	4419	16	0.4444	7	0	*1.000*	3.757	*0.1528*	—	—
MUS81	1665	16	0.2124	7	0	*1.000*	0.628	*0.7304*	—	—

Table S5: Comparisons of polymorphism within humans (African/African-Amercian) to divergence between human and macaque at recombination genes.

Gene	Pn	Ps	Dn	Ds	MK Test	*NI*	*DoS*	Direction
(A) DSB Formation								
HORMAD1	17	5	5	12	***0.0040***	8.16	-0.4786	Neg.
MEI4	6	3	24	9	*0.6987*	**0.75**	**0.0606**	—
REC114	17	8	11	14	*0.1536*	2.705	-0.2400	—
IHO1	31	16	36	19	*1.000*	1.0226	-0.0050	—
SPO11	22	9	11	22	***0.0058***	4.8889	-0.3763	Neg.
(B) DSB Processing								
HORMAD2	24	5	7	9	***0.0164***	6.1714	-0.3901	Neg.
MRE11	43	16	5	35	<***0.0001***	18.8125	-0.6038	Neg.
NBS1	49	19	34	25	*0.0963*	1.8693	-0.1443	—
RAD50	57	24	8	43	<***0.0001***	12.7656	-0.5468	Neg.
BRCC3	6	4	2	6	*0.1880*	4.5000	-0.3500	—
(C) Homology Search & Strand Invasion								
DMC1	11	8	0	11	***0.0002***	—	-0.5789	Neg.
RAD51	9	8	0	13	***0.0033***	—	-0.5294	Neg.
SPATA22	26	10	21	10	*0.7900*	1.2381	-0.0448	—
MEIOB	23	11	20	22	*0.1000*	2.300	-0.2003	—.
MCMDC2	44	16	16	26	<***0.0001***	4.4688	-0.3524	Neg.
(D) Synapsis								
REC8	38	10	38	31	***0.0101***	3.1000	-0.2409	Neg.
RAD21L	18	9	27	13	*1.000*	**0.9630**	**0.0083**	—
SYCP1	36	27	33	27	textit0.8570	1.0909	-0.0214	—

Table S5: Cont.

Gene	Pn	Ps	Dn	Ds	MK Test	*NI*	*DoS*	Direction
(D) Synapsis Cont.								
SYCP2	108	33	74	53	***0.0016***	2.3440	-0.1833	Neg.
TEX12	6	6	2	4	*0.6380*	2.0000	-0.1667	—
(E) CO/NCO Decision								
TEX11	26	14	55	25	*0.6846*	**0.8442**	**0.0375**	—
SHOC1	79	39	85	37	*0.6788*	**0.8817**	**0.0272**	—
RNF212B	4	0	8	12	*0.0932*	4.1830	-0.3418	—
MSH4	44	23	24	29	***0.0279***	2.3116	-0.2039	Neg.
MSH5	49	22	19	33	***0.0005***	3.8684	-0.3248	Neg.
(F) Resolution								
MER3	80	34	54	44	***0.0319***	1.9172	-0.1507	Neg.
CNTD1	18	9	12	8	*0.7689*	1.2308	-0.0476	—
HEI10	17	13	4	5	*0.7062*	1.6346	-0.1222	—
MLH1	53	12	9	29	$<$***0.0001***	14.2315	-0.5785	Neg.
MLH3	106	40	77	57	***0.0085***	1.9617	-0.1514	Neg.
MUS81	48	27	17	40	***0.0001***	4.1830	-0.3418	Neg.

Table S6: Sequence divergence between human (*Homo sapiens*) and macaque (*Macaca mulatta*) for 32 recombination genes (Yang and Nielsen 2000; Yang 2007).

Gene	***bp***	ω	***S***	***N***	***t***	κ	***dN***	***dS***
(A) DSB Formation								
HORMAD1	1182	**0.0901**	273.9	908.1	0.0443	3.8819	0.0044 +- 0.0022	0.0490 +- 0.0137
MEI4	1167	**0.7252**	331	824	0.0822	4.6295	0.0247 +/- 0.0056	0.0341 +/- 0.0104
REC114	864	**0.3239**	237.2	557.8	0.0974	2.9455	0.0200 +/- 0.0061	0.0618 +/- 0.0168
IHO1	1797	**0.6608**	509	1273	0.0951	3.6035	0.0276 +- 0.0047	0.0418 +- 0.0094
SPO11	1188	**0.1434**	291.2	896.8	0.0872	2.5317	0.0118 +/- 0.0036	0.0823 +/- 0.0178
(B) DSB Processing								
HORMAD2	921	**0.295**	256.7	664.3	0.0531	4.2164	0.0106 +- 0.0040	0.0360 +- 0.0121
MRE11	2124	**0.0392**	479.4	1644.6	0.0597	2.6154	0.0030 +- 0.0014	0.0778 +- 0.0135
NBS1	2265	**0.4155**	553.7	1705.3	0.0804	5.0955	0.0199 +- 0.0035	0.0480 +- 0.0097
RAD50	3969	**0.0714**	1118.7	2817.3	0.0401	5.0903	0.0028 +- 0.0010	0.0399 +- 0.0062
BRCC3	951	**0.0979**	264	609	0.028	4.6	0.0025 +- 0.0020	0.0252 +- 0.0100
(C) Homology Search & Strand Invasion								
DMC1	1020	**0.0000**	273.7	746.3	0.0335	5.1279	0.0000 +- 0.0000	0.0416 +- 0.0127
RAD51	1017	**0.0000**	306.5	710.5	0.0398	6.7467	0.0000 +- 0.0000	0.0441 +- 0.0124
SPATA22	1089	**0.4523**	247.8	841.2	0.0879	3.6505	0.0230 +- 0.0053	0.0508 +- 0.0150
MEIOB	1413	**0.2462**	348.9	1064.1	0.0927	4.3887	0.0176 +- 0.0041	0.0715 +- 0.0151
MCMDC2	2043	**0.2108**	534	1509	0.0635	7.8547	0.0107 +- 0.0027	0.0507 +- 0.0101
(D) Synapsis								
REC8	1701	**0.477**	497	1138	0.1293	2.8869	0.0323 +- 0.0054	0.0678 +- 0.0122
RAD21L	1680	**0.6334**	427.5	1237.5	0.0735	5.6876	0.0213 +- 0.0042	0.0337 +- 0.0091
SYCP1	2928	**0.3676**	761.6	2166.4	0.0628	4.8307	0.0145 +- 0.0026	0.0393 +- 0.0074
SYCP2	4590	**0.3873**	1070.7	3519.3	0.0854	5.994	0.0208 +- 0.0025	0.0537 +- 0.0074
TEX12	369	**0.1349**	80.2	288.8	0.05	1.9678	0.0070 +- 0.0049	0.0516 +- 0.0260

Table S6: Cont.

Gene	***bp***	ω	***S***	***N***	***t***	κ	***dN***	***dS***
(E) CO/NCO Decision								
TEX11	2775	**0.9068**	805.9	1933.1	0.0897	7.8022	0.0290 +- 0.0040	0.0320 +- 0.0064
SHOC1	4332	**0.7225**	1203	3129	0.0865	9.5737	0.0261 +- 0.0029	0.0361 +- 0.0057
RNF212	816	**0.387**	243.2	572.8	0.1342	4.996	0.0304 +- 0.0074	0.0785 +- 0.0189
RNF212B	900	**0.2566**	255.6	644.4	0.0685	3.4122	0.0125 +- 0.0044	0.0488 +- 0.0143
MSH4	2808	**0.2635**	731.3	2073.7	0.058	7.5194	0.0112 +- 0.0023	0.0425 +- 0.0079
MSH5	2502	**0.2106**	728.7	1770.3	0.0643	3.9993	0.0102 +- 0.0024	0.0486 +- 0.0085
(F) Resolution								
MER3	4305	**0.3247**	987.6	3317.4	0.0703	7.0099	0.0159 +- 0.0022	0.0488 +- 0.0074
CNTD1	990	**0.6803**	335.3	651.7	0.065	8.0721	0.0187 +- 0.0054	0.0274 +- 0.0092
HEI10	1059	**0.3235**	241.5	589.5	0.0329	5.9591	0.0068 +- 0.0034	0.0211 +- 0.0095
MLH1	2268	**0.0924**	602.3	1665.7	0.0522	2.4752	0.0048 +- 0.0017	0.0521 +- 0.0097
MLH3	4368	**0.4919**	1209.8	3149.2	0.0949	6.4296	0.0246 +- 0.0028	0.0500 +- 0.0067
MUS81	1653	**0.1299**	465.8	1187.2	0.1106	5.7915	0.0128 +- 0.0033	0.0983 +- 0.0158

Table S7 – Recombination rate data used for comparative analysis, including: species, sex, autosomal fundamental number (aFN), autosomal haploid chromosome number (aHCN), estimate of the average number of *MLH1* foci per cell, and the reference.

Species	***Sex***	***aFN***	***aHCN***	***MLH1 foci / cell***	***Reference***
Bos taurus	M	58	29	47.53	(Fröhlich et al. 2015)
Canis lupus familiaris	M	76	38	38.89	(Fröhlich et al. 2015)
Equus caballus	M	88	31	50.12	(Al-Jaru et al. 2014)
Homo sapiens	M	78	22	49.8	(Hassold et al. 2004)
Macaca mulatta	M	80	20	39	(Hassold et al. 2009)
Mus musculus	M	38	19	28.5	(Dumont and Payseur 2011)
Ovis aries	M	58	26	62.9	(Fröhlich et al. 2015)
Rattus norvegicus	M	62	20	34.46	(Dumont and Payseur 2011)
Sus scrofa	M	60	18	32	(Mary et al. 2014)

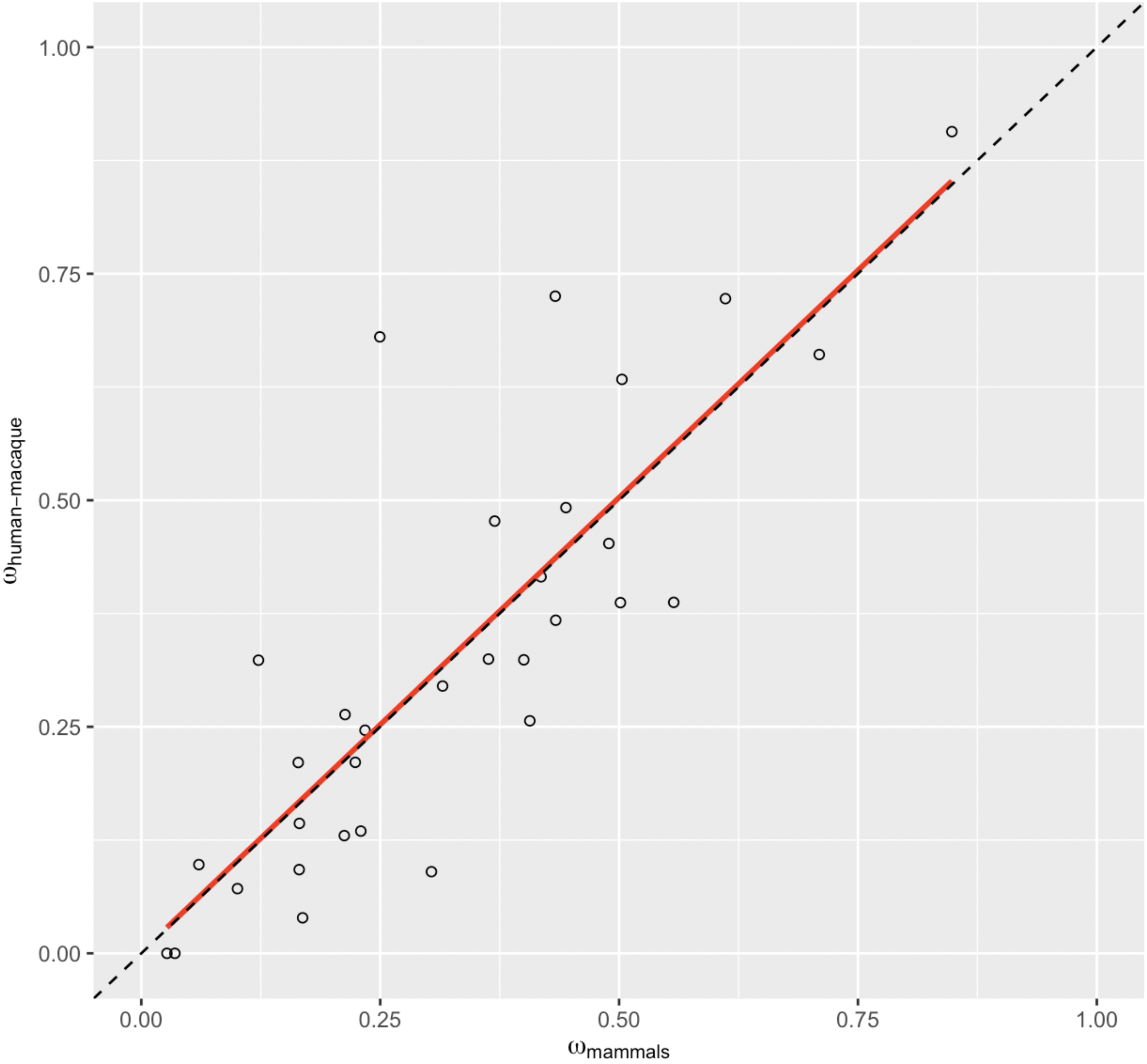
Table S8: Correlations between substitution rate and recombination rate, measured as the average number of *MLH1* foci per cell divided by the autosomal haploid chromosome number (aHCN), across nine species of mammals for 31 recombination genes. The posterior probability (1 − posterior probability for negative correlations) is given in parentheses.

	Correlation Coefficient			Partial Correlation Coefficient		
Gene	dS - ω	dS - MLH1	ω - MLH1	dS - ω	dS - MLH1	ω - MLH1
(A) DSB Formation						
HORMAD1	0.812(**0.95**)	0.492(0.85)	0.341(0.73)	0.804(**0.96**)	0.272(0.68)	-0.0849(0.56)
MEI4	-0.828(**0.97**)	0.392(0.83)	-0.407(0.80)	-0.826(**0.96**)	-0.0236(0.52)	-0.184(0.62)
REC114	-0.491(0.81)	-0.0628(0.52)	-0.125(0.58)	-0.499(0.80)	-0.148(0.61)	-0.186(0.62)
IHO1	0.483(0.82)	0.094(0.59)	0.0451(0.53)	0.551(0.85)	-0.0291(0.53)	0.0124(0.50)
SPO11	0.505(0.82)	-0.0492(0.54)	-0.0867(0.56)	0.592(0.86)	0.0144(0.51)	-0.0861(0.45)
(B) DSB Processing						
HORMAD2	0.187(0.63)	0.361(0.78)	0.308(0.69)	0.13(0.59)	0.197(0.65)	0.255(0.66)
MRE11	-0.448(0.83)	0.431(0.85)	-0.292(0.71)	-0.346(0.78)	-0.272(0.74)	-0.129(0.60)
NBS1	-0.727(0.94)	-0.198(0.65)	0.18(0.62)	-0.741(0.94)	-0.0171(0.56)	0.04(0.53)
RAD50	-0.38(0.77)	-0.0902(0.58)	0.165(0.62)	-0.398(0.76)	0.0103(0.51)	0.146(0.60)
BRCC3	0.0833(0.56)	0.196(0.70)	0.0644(0.55)	0.0795(0.55)	0.082(0.57)	0.0646(0.54)
(C) Homology Search & Strand Invasion						
DMC1	0.302(0.69)	-0.0885(0.59)	-0.0647(0.55)	0.322(0.69)	-0.0377(0.54)	-0.0296(0.52)
RAD51	-0.31(0.52)	-0.348(0.78)	0.00623(0.50)	-0.0216(0.51)	-0.17(0.64)	-0.0073(0.49)
SPATA22	-0.17(0.61)	0.219(0.72)	-0.0861(0.57)	-0.151(0.60)	0.104(0.59)	-0.0585(0.54)
MEIOB	0.147(0.59)	-0.402(0.85)	0.0146(0.49)	0.204(0.62)	-0.262(0.71)	0.105(0.57)
MCMDC2	-0.469(0.83)	0.179(0.64)	-0.584(0.86)	-0.492(0.83)	-0.235(0.68)	-0.574(0.85)

Table S8: Cont.

	Correlation Coefficient			Partial Correlation Coefficient		
Gene	dS - ω	dS - MLH1	ω - MLH1	dS - ω	dS - MLH1	ω - MLH1
(D) Synapsis						
REC8	-0.537(0.84)	-0.0298(0.51)	0.238(0.65)	-0.572(0.85)	0.136(0.61)	0.284(0.68)
RAD21L	-0.517(0.84)	-0.0528(0.55)	0.447(0.78)	-0.566(0.85)	0.279(0.71)	0.54(0.82)
SYCP1	-0.0366(0.53)	0.135(0.65)	0.152(0.60)	-0.0375(0.53)	0.0785(0.58)	0.178(0.61)
SYCP2	0.286(0.69)	-0.257(0.74)	-0.0292(0.52)	0.344(0.74)	-0.181(0.66)	0.0549(0.53)
TEX12	0.207(0.62)	0.263(0.67)	0.0829(0.54)	0.221(0.64)	0.156(0.62)	0.0158(0.50)
(E) CO/NCO Decision						
TEX11	0.168(0.64)	-0.449(0.90)	0.577(0.9)	0.736(**0.97**)	-0.752(**0.97**)	0.813(**0.97**)
SHOC1	-0.683(0.94)	0.0205(0.52)	0.19(0.64)	-0.748(**0.95**)	0.217(0.67)	0.287(0.70)
RNF212	0.0404(0.52)	0.0305(0.53)	-0.11(0.57)	0.0479(0.52)	0.0213(0.52)	-0.102(0.44)
MSH4	-0.792(**0.97**)	0.0886(0.60)	0.163(0.61)	-0.88(**0.99**)	0.336(0.74)	0.376(0.74)
MSH5	0.0407(0.53)	-0.176(0.69)	0.0243(0.51)	0.069(0.55)	-0.122(0.61)	0.0347(0.52)
(F) Resolution						
MER3	-0.493(0.82)	-0.133(0.64)	0.0393(0.54)	-0.542(0.85)	-0.0901(0.59)	-0.0296(0.52)
CNTD1	-0.836(**0.97**)	-0.401(0.78)	0.501(0.82)	-0.78(**0.96**)	0.0968(0.57)	0.334(0.72)
HEI10	-0.284(0.69)	-0.594(0.93)	0.326(0.69)	-0.164(0.60)	-0.27(0.70)	0.276(0.67)
MLH1	0.146(0.60)	0.00648(0.51)	0.14(0.59)	0.184(0.63)	-0.0267(0.52)	0.151(0.59)
MLH3	-0.108(0.58)	-0.0165(0.51)	-0.294(0.69)	-0.12(0.41)	-0.0762(0.57)	-0.319(0.70)
MUS81	0.307(0.72)	-0.167(0.65)	-0.0922(0.57)	0.343(0.72)	-0.097(0.58)	-0.0469(0.54)
Average	-0.137	-0.007	0.068	-0.115	-0.019	0.058
SD	0.465	0.261	0.252	0.486	0.212	0.260

Figure S1: High concordance in evolutionary rate compute across mammals and between humans and macaque. The best-fit regression line is shown in red and the 1:1 line is shown as a dashed line.



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