$_{\scriptscriptstyle 1}$ Table R1: 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	${\rm GSM1902350,GSM2033157\&GSM2033163}$	Li et al. (2016), Yang et al. (2017)
Tupaia chinensis	GSM957062	Fan et al. (2013)

$_{2}$ Table R2: NCBI Reference Genomes (O'Leary $\it et~\it al.~2015)$

Species	Assembly	RefSeq Accession	WGS Project Reference
Bos taurus	Bos_taurus_UMD_3.1.1	GCF_000003055.6	Zimin <i>et al.</i> (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 <i>et al.</i> (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	Consortium et al. (2010)
Pan paniscus	panpan1.1	GCF_000258655.2	Prüfer et al. (2012)
Pan troglodytes	Pan_tro_3.0	GCF_000001515.7	Consortium et al. (2005)
Pongo abelii	P_pygmaeus_2.0.2	GCF_000001545.4	Locke <i>et al.</i> (2011)
Rattus norvegicus	Rnor_6.0	GCF_000001895.5	Consortium and others (2004)
Sus scrofa	Sscrofa11.1	GCF_000003025.6	-
Tupaia chinensis	TupChi_1.0	GCF_000334495.1	Fan et al. (2013)

$_{\tt 3}$ **Table R3**: 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 <i>et al.</i> (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 <i>et al.</i> (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	Consortium et al. (2010)
Pan paniscus	panpan1.1	GCF_000258655.2	Prüfer et al. (2012)
Pan troglodytes	CHIMP2.1.4	GCF_000001515.6	Consortium et al. (2005)
Pongo abelii	PPYG2	GCF_000001545.4	Locke <i>et al.</i> (2011)
Rattus norvegicus	Rnor_6.0	GCF_000001895.5	Consortium and others (2004)
Sus scrofa	Sscrofa11.1	GCF_000003025.6	-
Tupaia chinensis	-	-	-

- 4 Table S1: Sequence divergence between Human ($Homo\ sapiens$) and Rhesus Macaque ($Macaca\ mulatta$)
- ⁵ (Yang and Nielsen 2000; Yang 2007).

Gene	bp	ω	$oldsymbol{S}$	$oldsymbol{N}$	t	κ	dN	dS
A)								
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)								
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)								
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)								
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
$\mathbf{E})$								
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

Gene	bp	ω	\boldsymbol{S}	N	t	κ	dN	dS
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)								
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

⁶ **Table S2**: PAML of 32 recombination genes using the gene tree (Yang 2007).

Gene	bp	N	ω	M	M1-M2	$p ext{-}value$	M7-M8	$p ext{-}value$	M8a- $M8$	$p ext{-}value$
A)										
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)										
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)										
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)										
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	_	_
$\mathbf{E})$										
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

Gene	bp	N	ω	M	M1-M2	$p ext{-}value$	M7-M8	$p ext{-}value$	M8a- $M8$	$p ext{-}value$
MSH5	2565	15	0.1642	7	0	1.000	4.214	0.1216	_	_
F)										
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	_	_

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