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	GSM1902350, GSM2033157 & GSM2033163	Li et al. (2016), Yang et al. (2017)
Tupaia chinensis	GSM957062	Fan et al. (2013)

Table R2: 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	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 et al. (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)

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 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	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 et al. (2011)
Rattus norvegicus	Rnor_6.0	GCF_000001895.5	Consortium and others (2004)
Sus scrofa	Sscrofa11.1	GCF_000003025.6	-
Tupaia chinensis	-	-	-

Table S1: Sequence divergence between Human (*Homo sapiens*) and Rhesus Macaque (*Macaca mulatta*) (Yang and Nielsen 2000; Yang 2007).

Gene	***bp***	ω	***S***	***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
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	***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

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

Gene	***bp***	***N***	ω	***M***	***M1-M2***	***p-value***	***M7-M8***	***p-value***	***M8a-M8***	***p-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*	—	—
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-value***	***M7-M8***	***p-value***	***M8a-M8***	***p-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*	—	—

References

Barrett T, Wilhite SE, Ledoux P, Evangelista C, Kim IF, Tomashevsky M, Marshall KA, Phillippy KH, Sherman PM, Holko M, et al. 2012. NCBI geo: Archive for functional genomics data sets—update. Nucleic acids research 41:D991–D995.

Brawand D, Soumillon M, Necsulea A, Julien P, Csárdi G, Harrigan P, Weier M, Liechti A, Aximu-Petri A, Kircher M, et al. 2011. The evolution of gene expression levels in mammalian organs. Nature 478:343.

Carelli FN, Hayakawa T, Go Y, Imai H, Warnefors M, Kaessmann H. 2016. The life history of retrocopies illuminates the evolution of new mammalian genes. Genome research:gr–198473.

Coleman SJ, Zeng Z, Hestand MS, Liu J, Macleod JN. 2013. Analysis of unannotated equine transcripts identified by mRNA sequencing. PLoS One 8:e70125.

Consortium ISG, Archibald A, Cockett N, Dalrymple B, Faraut T, Kijas J, Maddox J, McEwan J, Hutton Oddy V, Raadsma H, et al. 2010. The sheep genome reference sequence: A work in progress. Animal genetics 41:449–453.

Consortium RGSP, others. 2004. Genome sequence of the brown norway rat yields insights into mammalian evolution. Nature 428:493.

Consortium TCSA, Waterson RH, Lander ES, Wilson RK. 2005. Initial sequence of the chimpanzee genome and comparison with the human genome. Nature 437:69.

Cortez D, Marin R, Toledo-Flores D, Froidevaux L, Liechti A, Waters PD, Gruetzner F, Kaessmann H. 2014. Origins and functional evolution of y chromosomes across mammals. Nature 508:488.

Derti A, Garrett-Engele P, MacIsaac KD, Stevens RC, Sriram S, Chen R, Rohl CA, Johnson JM, Babak T. 2012. A quantitative atlas of polyadenylation in five mammals. Genome research:gr–132563.

Fan Y, Huang Z-Y, Cao C-C, Chen C-S, Chen Y-X, Fan D-D, He J, Hou H-L, Hu L, Hu X-T, et al. 2013. Genome of the chinese tree shrew. Nature communications 4:1426.

Guan Y, Liang G, Martin GB, others. 2017. Functional changes in mRNA expression and alternative pre-mRNA splicing associated with the effects of nutrition on apoptosis and spermatogenesis in the adult testis. BMC genomics 18:64.

Li Y, Li J, Fang C, Shi L, Tan J, Xiong Y, Fan B, Li C. 2016. Genome-wide differential expression of genes and small rnas in testis of two different porcine breeds and at two different ages. Scientific reports 6:26852.

Lindblad-Toh K, Wade CM, Mikkelsen TS, Karlsson EK, Jaffe DB, Kamal M, Clamp M, Chang JL, Kulbokas III EJ, Zody MC, et al. 2005. Genome sequence, comparative analysis and haplotype structure of the domestic dog. Nature 438:803.

Locke DP, Hillier LW, Warren WC, Worley KC, Nazareth LV, Muzny DM, Yang S-P, Wang Z, Chinwalla AT, Minx P, et al. 2011. Comparative and demographic analysis of orang-utan genomes. Nature 469:529.

Merkin J, Russell C, Chen P, Burge CB. 2012. Evolutionary dynamics of gene and isoform regulation in mammalian tissues. Science 338:1593–1599.

O'Leary NA, Wright MW, Brister JR, Ciufo S, Haddad D, McVeigh R, Rajput B, Robbertse B, Smith-White B, Ako-Adjei D, et al. 2015. Reference sequence (refseq) database at ncbi: Current status, taxonomic expansion, and functional annotation. Nucleic acids research 44:D733–D745.

Prüfer K, Munch K, Hellmann I, Akagi K, Miller JR, Walenz B, Koren S, Sutton G, Kodira C, Winer R, et al. 2012. The bonobo genome compared with the chimpanzee and human genomes. Nature 486:527.

Scally A, Dutheil JY, Hillier LW, Jordan GE, Goodhead I, Herrero J, Hobolth A, Lappalainen T, Mailund T, Marques-Bonet T, et al. 2012. Insights into hominid evolution from the gorilla genome sequence. Nature 483:169.

Vandewege MW, Platt RN, Ray DA, Hoffmann FG. 2016. Transposable element targeting by piRNAs in laurasiatherians with distinct transposable element histories. Genome biology and evolution 8:1327–1337.

Wade C, Giulotto E, Sigurdsson S, Zoli M, Gnerre S, Imsland F, Lear T, Adelson D, Bailey E, Bellone R, et al. 2009. Genome sequence, comparative analysis, and population genetics of the domestic horse. Science 326:865–867.

Yang Y, Liang G, Niu G, Zhang Y, Zhou R, Wang Y, Mu Y, Tang Z, Li K. 2017. Comparative analysis of dna methylome and transcriptome of skeletal muscle in lean-, obese-, and mini-type pigs. Scientific reports 7:39883.

Yang Z. 2007. PAML 4: Phylogenetic analysis by maximum likelihood. Molecular Biology and Evolution 24:1586–1591.

Yang Z, Nielsen R. 2000. Estimating synonymous and nonsynonymous substitution rates under realistic evolutionary models. Molecular Biology and Evolution 17:32–43.

Zerbino DR, Achuthan P, Akanni W, Amode MR, Barrell D, Bhai J, Billis K, Cummins C, Gall A, Girón CG, et al. 2017. Ensembl 2018. Nucleic acids research 46:D754–D761.

Zimin AV, Cornish AS, Maudhoo MD, Gibbs RM, Zhang X, Pandey S, Meehan DT, Wipfler K, Bosinger SE, Johnson ZP, et al. 2014. A new rhesus macaque assembly and annotation for next-generation sequencing analyses. Biology direct 9:20.

Zimin AV, Delcher AL, Florea L, Kelley DR, Schatz MC, Puiu D, Hanrahan F, Pertea G, Van Tassell CP, Sonstegard TS, et al. 2009. A whole-genome assembly of the domestic cow, bos taurus. Genome biology 10:R42.