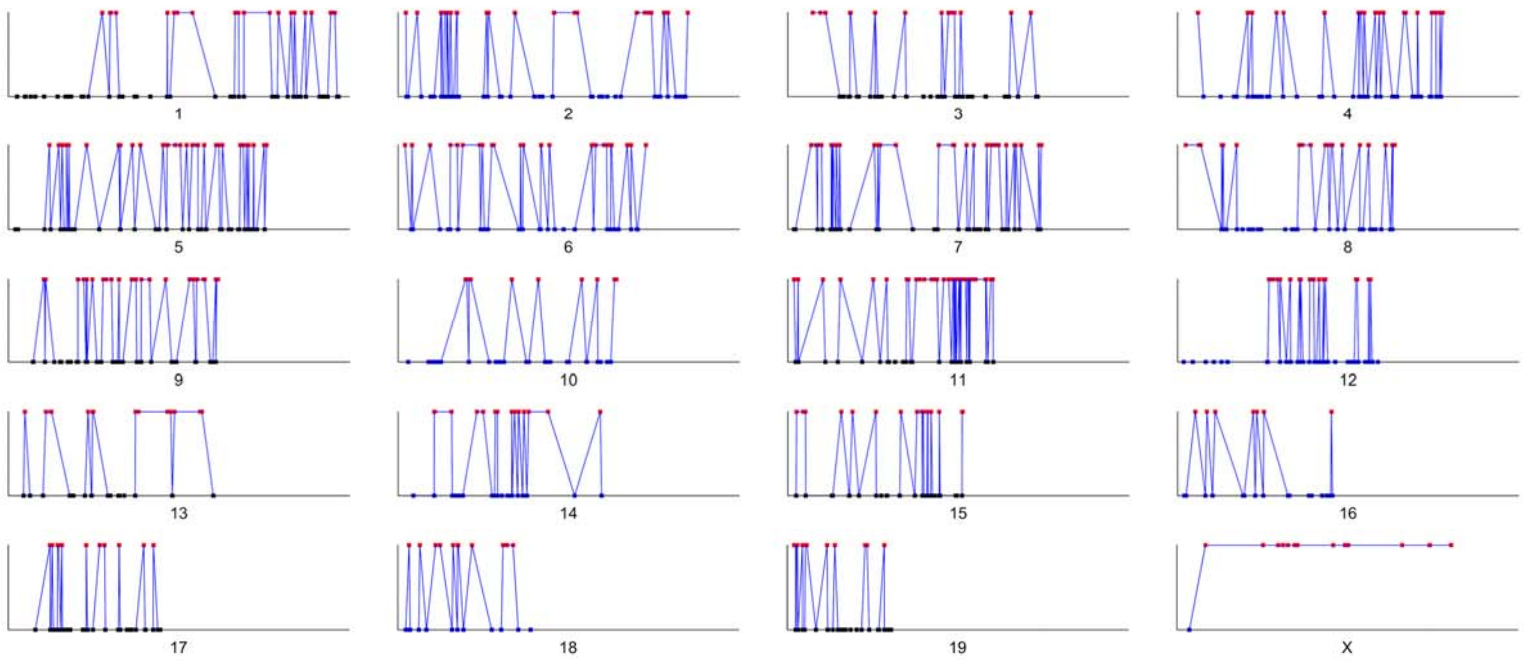
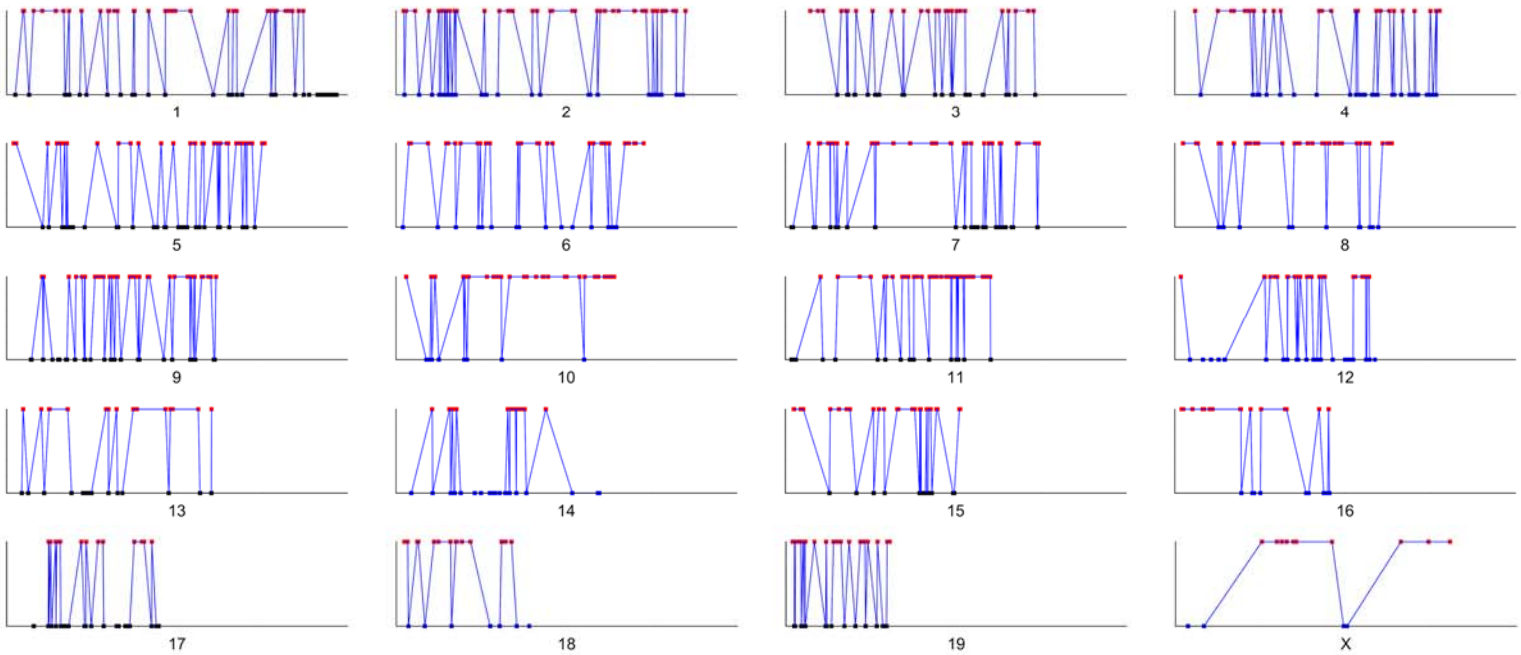
A



B



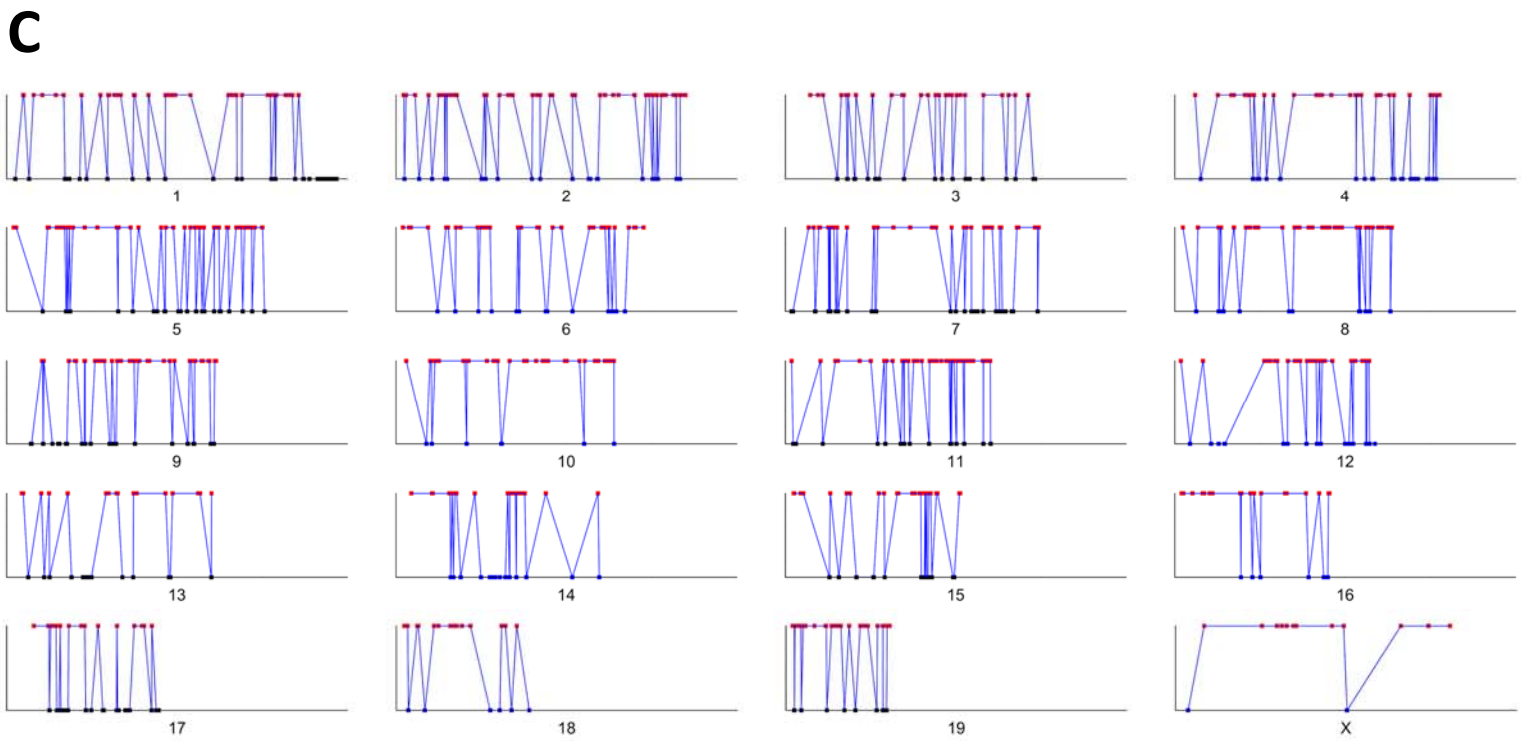
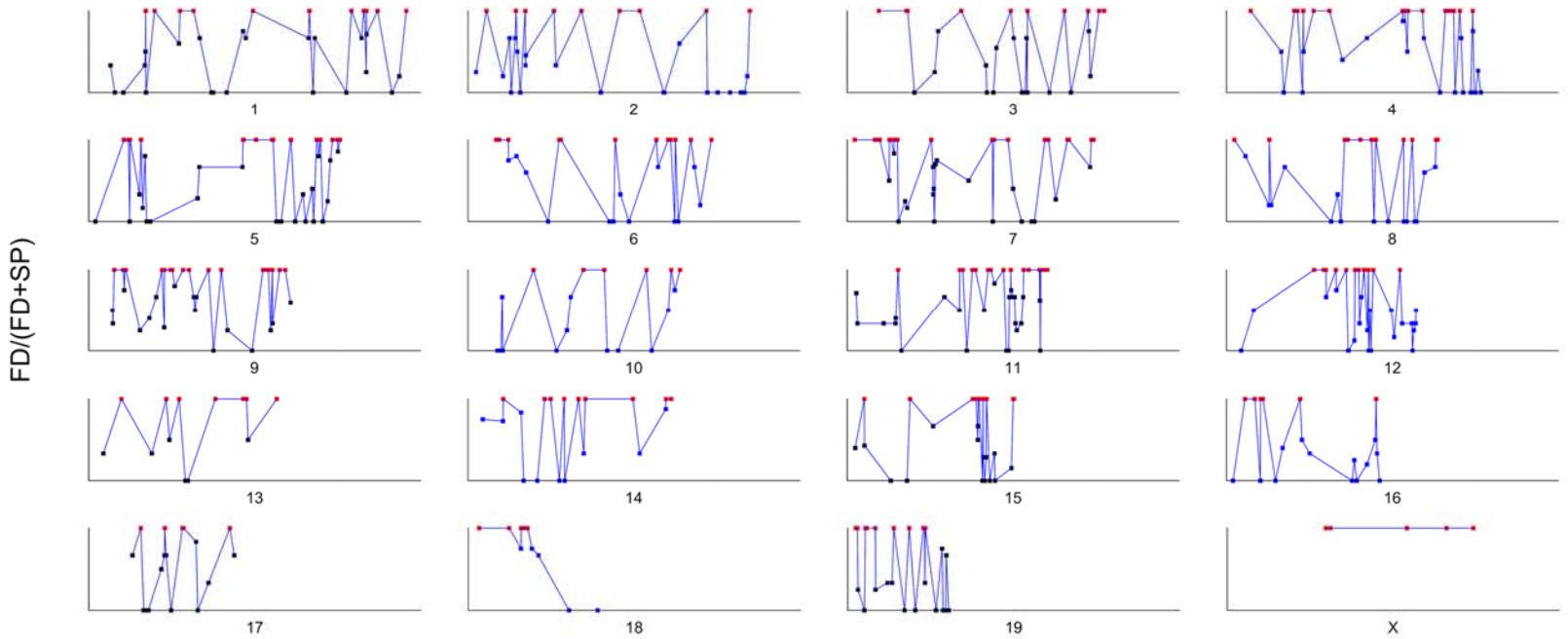
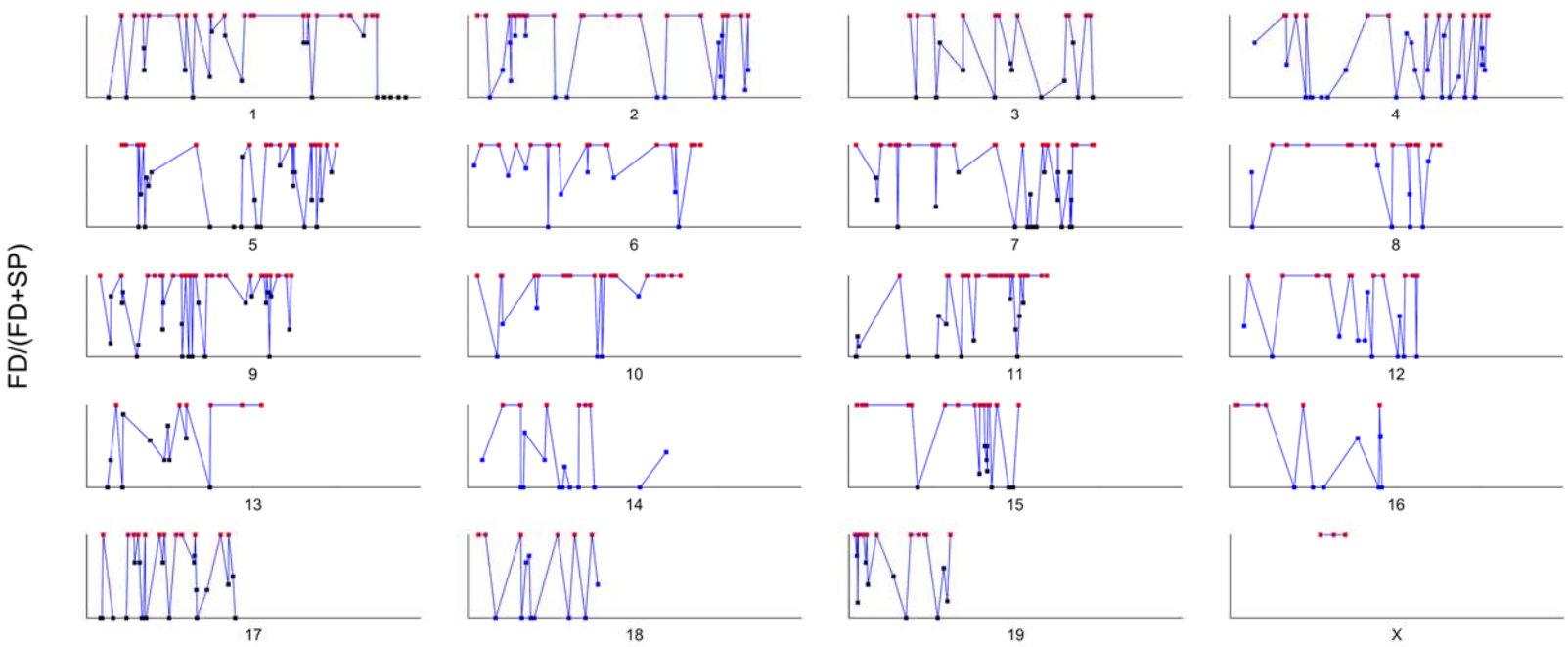


Figure S1 Fixed differences and shared polymorphisms across the genome for all pairwise comparisons of subspecies of *Mus*. Fixed differences are shown as red dots above the axis while shared polymorphisms are shown as dots on the x axis. (A) *M. m. castaneus* and *M. m. domesticus*. (B) *M. m. castaneus* and *M. m. musculus*. (C) *M. m. domesticus* and *M. m. musculus*.

A



B



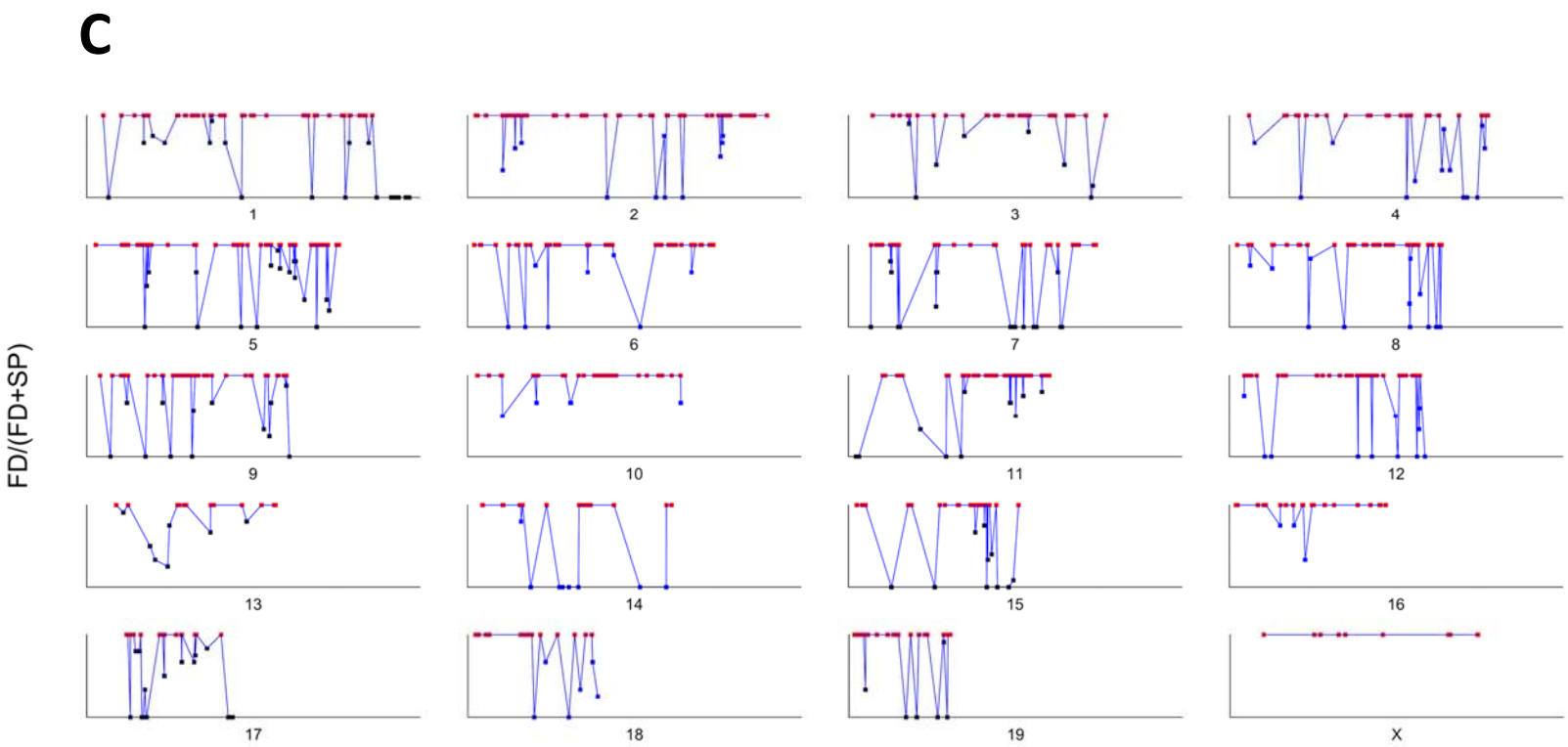


Figure S2 The ratio of fixed differences (FDs) to topologically informative sites, fixed differences and shared polymorphisms (SPs), across the genome for all pairwise comparisons of *Mus musculus* subspecies. Dots indicate the start of each region and red dots indicate fully sorted regions. (A) *M. m. castaneus* and *M. m. domesticus*. (B) *M. m. castaneus* and *M. m. musculus*. (C) *M. m. domesticus* and *M. m. musculus*.

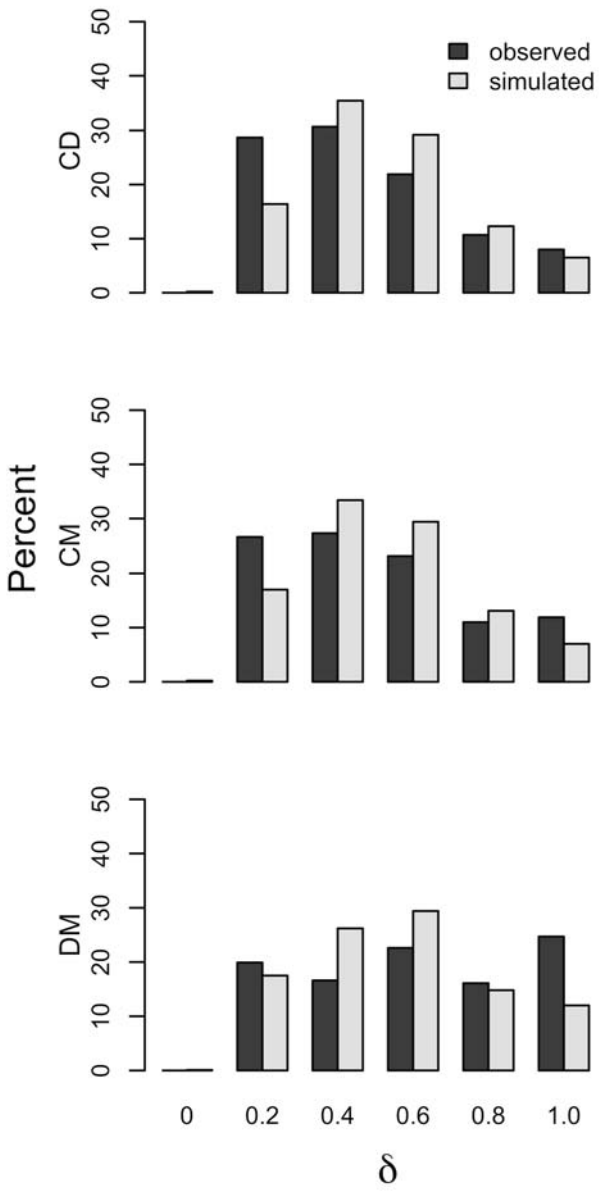


Figure S3 The distribution of values of δ in the observed data and in simulations based on demographic parameters from Supporting Information Table 7.

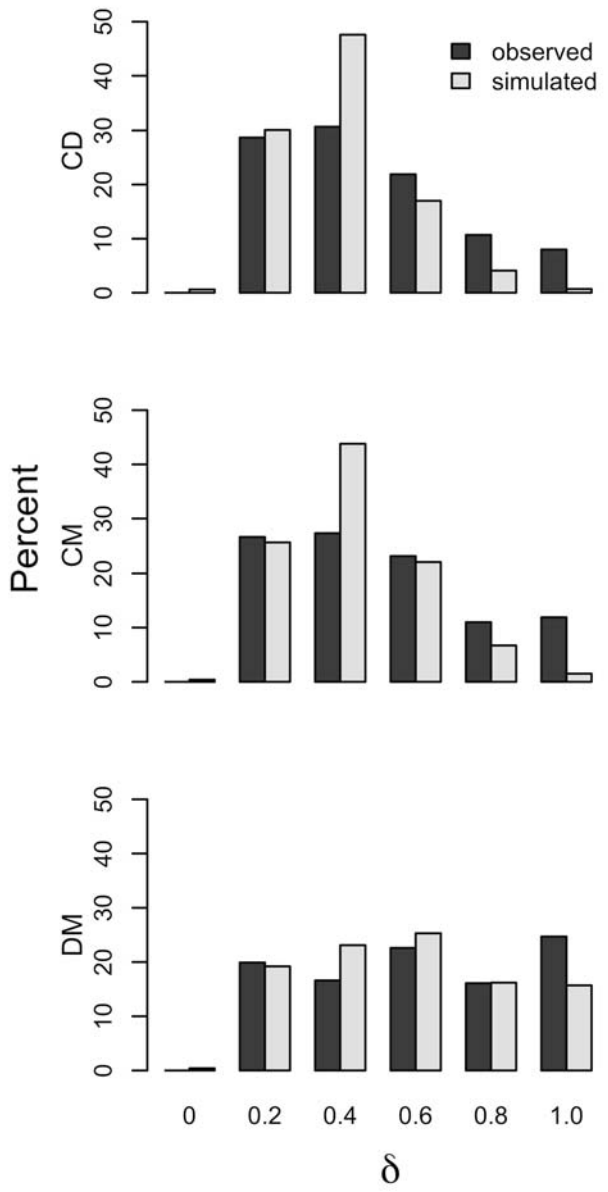


Figure S4 The distribution of values of δ in the observed data and in simulations based on demographic parameters from Supporting Information Table 9.

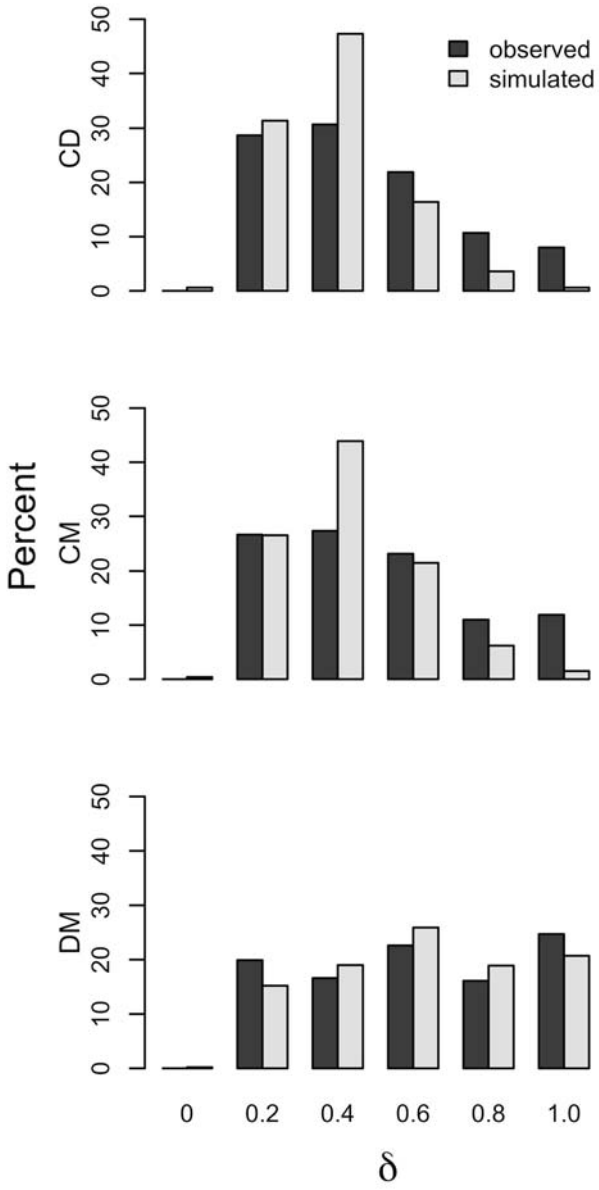


Figure S5 The distribution of values of δ in the observed data and in simulations based on demographic parameters from Supporting Information Table 7, but with a divergence time of 425 Kya.

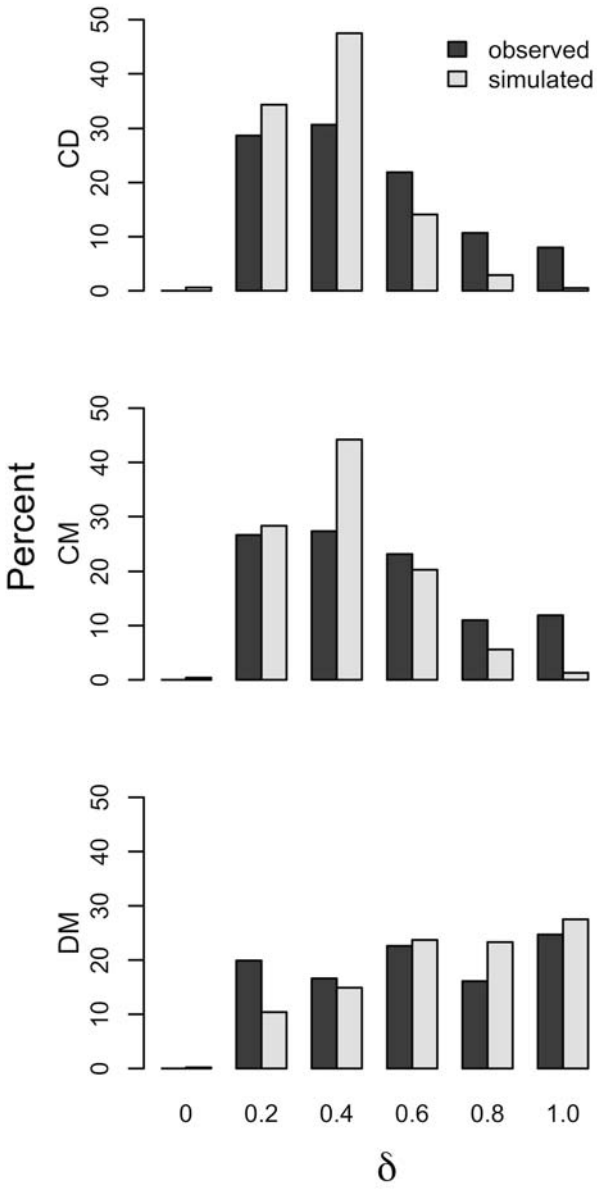


Figure S6 The distribution of values of δ in the observed data and in simulations based on demographic parameters from Supporting Information Table 7, but with a divergence time of 825 Kya.

File S1

SNP Table

Available for download as a .txt file at http://www.genetics.org/lookup/suppl/doi:10.1534/genetics.114.166827/-/DC1

File S2

Supplementary Methods and Results

Measures of differentiation measured on a per SNP basis

δ is the absolute value of the difference in minor allele frequency among populations.

$$\delta = |\text{ Minor Allele Frequency}_{\text{pop1}} - \text{Minor Allele Frequency}_{\text{pop2}}|$$

D_{xy} can be thought of as the number of mismatches between two sets divided by the total number of comparisons between two sets.

$$D_{XY} = \frac{\left(\text{Minor Allele Count}_{\text{pop1}} * \text{Major Allele Count}_{\text{pop2}}\right) + \left(\text{Major Allele Count}_{\text{pop1}} * \text{Minor Allele Count}_{\text{pop2}}\right)}{\text{Number of Alleles}_{\text{pop1}} * \text{Number of Alleles}_{\text{pop2}}}$$

F_{st} is the portion of the variance in the data that lies between two populations.

$$F_{st} = \frac{Pi_{total} - \overline{Pi}_{within}}{Pi_{total}}$$

$$Pi_{total} = \frac{\text{Minor Allele Count}_{\text{total}} * \text{Major Allele Count}_{\text{total}}}{\binom{\text{Total number of Alleles}}{2}}$$

$$Pi_{within\ for\ popk} = \frac{\text{Minor Allele Count}_{\text{popk}} * \text{Major Allele Count}_{\text{popk}}}{\binom{\text{Number of Alleles in popk}}{2}}$$

Runs of fixed differences Another approach to evaluating differentiation across the genome is to consider runs of fixed differences. When sampling is adequate, runs of fixed differences uninterrupted by shared polymorphisms, can also identify fully sorted gene genealogies. For this analysis, we only included genes that contained at least one fixed difference or shared polymorphism from each pairwise comparison. We sampled a single SNP from each gene included in the analysis. Because we were interested in identifying highly differentiated regions, to be conservative, if a gene contained fixed differences and shared polymorphisms, the SNP included in the analysis was selected from among the shared polymorphisms. On average, "pruned" SNPs included in these analyses were ~2.19 Mbs apart. Using publicly available source code, we amended the program SLIDER (McDonald 1996) to generate a distribution of runs of fixed differences based on 10,000 Monte Carlo simulations of coalescence and recombination for each pairwise comparison. In each simulation, the observed number of polymorphisms and fixed differences were distributed randomly among sites such that the number of polymorphisms and fixed differences matched the observed data. These simulations assumed a constant N_e, uniform recombination rates among adjacent sites,

random union of gametes, point mutation, and silent site neutrality. We used data from chromosome two for these simulations as it had, on average, the largest number of topologically informative markers and is the second largest autosome (~182 Mb). We replicated 10,000 simulations over ten recombination parameters ranging from one to ten.

We identified many runs of fixed differences in all pairwise comparisons (Supporting Information Figures 1a, b, c). Consistent with the window analyses, we found that there were more runs of fixed differences in the DM comparison and that those runs were, on average, larger both in terms of number of SNPs and distance covered (Supporting Information Table 5). However, SLIDER analysis failed to reject the null model. Regardless of recombination rate, summary statistics for the distribution of runs did not fall in the extreme tails of results from simulations of coalescence and recombination (Supporting Information Table 6). The X chromosome was characterized by long runs of fixed differences in all three pairwise comparisons (Supporting Information Figures 1a, b, c).

References

McDonald J. H., 1996 Detecting non-neutral heterogeneity across a region of DNA sequence in the ratio of polymorphism to divergence. Mol Biol Evol 13: 253–260.

Files S3-S4

Available for download at http://www.genetics.org/lookup/suppl/doi:10.1534/genetics.114.166827/-/DC1

File S3 Testis Specific Expression Table

File S4 Genes identified as significantly differentially expressed in each pairwise comparison among subspecies of *M. musculus*

Table S1 Sampling localities for all wild-derived inbred laboratory strains used in this study.

Subspecies	Wild Derived Inbred Line ID	Country	Locality
M. m. castaneus	CAST/EiJ[a]	Thailand	Thonburi
	CIM/MPL	India	Masinagudi
	CKN/MPL	Kenya	Nairobi
	CKS/MPL	Kenya	Shanzu
	CTP/MPL[b]	Thailand	Pathumthani
	DKN/MPL	Kenya	Nairobi
	MDG/MPL	Madagascar	Manakasina
	MPR/MPL[b]	Pakistan	Rawalpindi
M. m. domesticus	BIK/MPL	Israel	Kefar Galim
	BZ0/MPL	Algeria	Oran
	DCP/MPL	Cyprus	Paphos
	DJO/MPL	Italy	Orcetto
	DMZ/MPL	Morrocco	Azemmour
	LEWES/EiJ	USA	Delaware
	WLA/MPL	France	Toulouse
	WSB/EiJ[a]	USA	Maryland
M. m. musculus	BID/MPL[b]	Iran	Birdjand
	CZECHII/EiJ	Czechoslovakia	
	MBK/MPL	Bulgaria	Kranevo
	MBT/MPL	Bulgaria	Général Toshevo
	MCZ/MPL	Czech Republic	Bialowieza
	MDH/MPL	Denmark	Hov
	MPB/MPL	Poland	Prague
	PWK/PhJ[c]	Czech Republic	Lhotka
M. caroli	CAROLI/EiJ	Thailand	
M. spretus	SPRET/EiJ[c]	Spain	Cadiz

[a]Data were taken from the Wellcome Trust Mouse Genomes Project.
[b]Data were excluded from further analyses due to admixture.
[c]Data from transcriptome sequencing was combined with data from the Wellcome Trust Mouse Genomes Project.

Table S2 Short read transcriptome sequencing yields in megabases for all wild-derived inbred lines included in the study.

Subspecies	Line	Sequenced	Mapped	Mapped Uniquely	6X high quality sequence
M. m. castaneus	CIM	1,330.84	712	377	16.63
	CKN	1,122.00	631	324	14.13
	CKS	869.97	453	273	12.01
	CTP	968.65	533	302	13.76
	DKN	1,189.87	671	341	14.85
	MDG	1,113.24	596	319	14.03
	MPR	1,190.66	621	334	15.41
M. m. domesticus	BIK/MPL	998.97	543	296	13.42
	BZ0/MPL	1,014.07	588	333	15.02
	DCP/MPL	1,489.47	799	380	16.55
	DJO/MPL	1,169.41	631	324	14.39
	DMZ/MPL	1,397.35	776	376	16.85
	LEWES/EiJ	3,640.53	1,585	573	22.69
	WLA/MPL	1,241.30	652	324	14.25
M. m. musculus	BID/MPL	863.31	486	288	13.3
	CZECHII/EiJ	1,237.15	716	375	16.93
	MBK/MPL	1,005.21	546	295	13.01
	MBT/MPL	1,651.32	931	444	19.16
	MCZ/MPL	1,574.79	977	474	19.86
	MDH/MPL	1,127.44	663	355	15.53
	MPB/MPL	801.8	488	287	12.85
	PWK/PhJ	1,675.66	1,048	496	21.25
M. caroli	CAROLI/EiJ	3,063.49	1,442	596	21.68
M. spretus	SPRET/EiJ	1,921.25	1,092	513	21.85

Table S3 Summary data from comparisons of genotype data in coding regions collected by this study and data collected by the Wellcome Trust.

Inbred Line	Bases in common	Mismatches	% mismatch
PWK	13,019,770	40	0.0003
SPRET	13,547,788	32	0.0002

Table S4 The results of a STRUCTURE analysis to determine the probability of different numbers of populations (K) within wild-derived inbred lines sampled from the three subspecies of *M. musculus* after the removal of lines found to be highly admixed in previous runs of STRUCTURE.

Model	K	Average ln Pr(X|K)	Pr(K)
Admixture	1	-15937.8	<0.001
Admixture	2	-12492.3	<0.001
Admixture	3[a]	-8918.2	>0.999
Admixture	4	-9648.40	<0.001
Admixture	5	-9603.07	<0.001
No admixture	1	-15932.5	<0.001
No admixture	2	-11890.1	<0.001
No admixture	3[a]	-8879.2	>0.999
No admixture	4	-10641.9	<0.001
No admixture	5	-9059.4	<0.001

[a]In these runs, the lines assigned to the three clusters were consistent with our subspecies assignment as shown in Supporting Information Table 1.

Table S5 Summary statistics describing runs of fixed differences in pairwise comparisons among subspecies of *Mus musculus*.

Subspecies 1	Subspecies 2	Chr Type	n	Avg. # SNPs/run (SD)	Max # of SNPs/run	Avg. Mb covered (SD)	Max Mb covered (SD)
M. m. castaneus	*M. m. domesticus*	Autosomes	98	3.07 (1.82)	17	3.22 (4.14)	20.71
		X	1	14 (-)	(-)	144.19	(-)
M. m. castaneus	*M. m. musculus*	Autosomes	138	4.09 (2.59)	19	5.87 (7.59)	44.23
		X	2	5.5 (2.12)	41.5	34.96 (8.75)	41.5
M. m. domesticus	*M. m. musculus*	Autosomes	144	4.55 (2.75)	19	7.17 (8.29)	40.99
		X	2	6.5 (2.54)	9	55.30 (37.51)	81.83

Table S6 Summary statistics describing runs of fixed differences on chromosome 2 in all pairwise comparisons of the subspecies of *Mus musculus* as well as the percentile rank of those statistics in 10,000 coalescent and recombination simulations.

Subspecies	Subspecies	# of runs	Perc. Rank	Avg. # of SNPs/run (SD)	Perc. Rank	Max # of SNPs/run	Perc. Rank
M. m. castaneus	*M. m. domesticus*	9	75%	2.89 (1.54)	67%	6	73%
M. m. castaneus	*M. m. musculus*	11	30%	3.91 (2.07)	66%	8	39%
M. m. domesticus	*M. m. musculus*	12	49%	4.67 (3.31)	50%	12	52%

Table S7 Demographic parameters used in ms (Hudson 2002) simulations. All values are based on averages of estimates from Geraldes *et al.* (2011) and assume a generation length of 1 year.

Subspecies 1	Subspecies 2	$N_{e\ species\ 1}$	$N_{e\ species\ 2}$	$N_{e\ Ancestral}$	t	2Nm (species1)[a]	2Nm (species2)[b]	Avg. # SNPs surveyed in observed loci (SD)	Avg. # SNPs in simulated loci (SD)
M. m. castaneus	*M. m. domesticus*	366,700	82,600	277,800	313,800	0.193	0.000	2.61 (2.39)	5.28 (3.05)
M. m. castaneus	*M. m. musculus*	366,700	36,600	277,800	345,800	0.190	0.058	2.59 (2.36)	4.90 (2.93)
M. m. domesticus	*M. m. musculus*	82,600	36,600	277,800	320,800	0.003	0.057	2.38 (2.08)	2.24 (1.29)

[a]The effective rate at which genes enter subspecies 1 from subspecies 2.
[b]The effective rate at which genes enter subspecies 2 from subspecies 1.

Table S8 Average values of δ for different classes of sites in all pairwise comparisons between subspecies of *M. musculus*.

Subspecies 1	Subspecies 2	$\overline{\delta}_{non-synonymous}$ (SD)	$n_{non\text{-}synonymous}$	$\overline{\delta}_{synonymous}$ SD	$n_{synonymous}$	P^a
M. m. castaneus	*M. m. domesticus*	0.39 (0.30)	7,118	0.40 (0.29)	16,772	<0.001
M. m. castaneus	*M. m. musculus*	0.42 (0.31)	6,965	0.43 (0.30)	16,503	<0.0001
M. m. domesticus	*M. m. musculus*	0.48 (0.35)	6,740	0.54 (0.35)	14,687	<0.0001

[a]Results of *t*-tests comparing average measures of differentiation for non-synonymous and synonymous sites

Table S9 Demographic parameters used in ms (Hudson 2002) simulations intended to more closely match the number of SNPs surveyed in the observed data.

Subspecies 1	Subspecies 2	$N_{e\ species\ 1}$	$N_{e\ species\ 2}$	$N_{e\ Ancestral}$	t	2Nm (species1)[a]	2Nm (species2)[b]	Avg. # SNPs surveyed in observed loci (SD)	Avg. # SNPs in simulated loci (SD)
M. m. castaneus	*M. m. domesticus*	167,000	101,000	280,000	325,000	0.193	0.000	2.61 (2.39)	3.34 (1.93)
M. m. castaneus	*M. m. musculus*	167,000	89,000	280,000	325,000	0.190	0.058	2.59 (2.36)	3.28 (1.90)
M. m. domesticus	*M. m. musculus*	101,000	89,000	280,000	325,000	0.003	0.057	2.38 (2.08)	2.65 (1.52)

[a]The effective rate at which genes enter subspecies 1 from subspecies 2.
[b]The effective rate at which genes enter subspecies 2 from subspecies 1.

Table S10 Demographic parameters used in ms (Hudson 2002) simulations. Population size estimates are based on averages of estimates from Geraldes *et al.* (2011) and assume a generation length of 1 year. Gene flow was increased until the proportion of simulated loci with low average values of differentiation matched observed proportions.

Subspecies 1	Subspecies 2	$N_{e\ species\ 1}$	$N_{e\ species\ 2}$	$N_{e\ Ancestral}$	t	2Nm (species1)[a]	2Nm (species2)[b]
M. m. castaneus	*M. m. domesticus*	366,700	82,600	277,800	325,000	1.930	0.000
M. m. castaneus	*M. m. musculus*	366,700	36,600	277,800	325,000	1.330	0.406
M. m. domesticus	*M. m. musculus*	82,600	36,600	277,800	325,000	0.045	0.855

[a]The effective rate at which genes enter subspecies 1 from subspecies 2
[b]The effective rate at which genes enter subspecies 2 from subspecies 1

Table S11 Overlap between inversions and runs of fixed differences identified between each pair of subspecies of *Mus musculus.*

Subspecies	Subspecies	# of runs of fixed differences	Observed overlap with inversions	Perc. Rank
M. m. castaneus	*M. m. domesticus*	99	36	35%
M. m. castaneus	*M. m. musculus*	140	70	54%
M. m. domesticus	*M. m. musculus*	146	80	98.5%

Table S12 Average measures of differentiation in regions containing testis specific genes and all other regions for all pairwise comparisons of *Mus musculus* subspecies.

Subspecies	Subspecies	Regions	n	$\overline{F}_{st}$ (SD)	*t*	$\overline{D}_{xy}$ (SD)	*t*	$\overline{\delta}$ (SD)	*t*
M. m. castaneus	*M. m. domesticus*	Contain testis specific genes	520	0.24 (0.16)	0.41	0.42 (0.14)	0.29	0.41 (0.14)	0.16
		All Others	1226	0.24 (0.19)		0.42 (0.16)		0.41 (0.16)	
M. m. castaneus	*M. m. musculus*	Contain testis specific genes	515	0.29 (0.19)	1.73*	0.47 (0.15)	1.47	0.46 (0.16)	1.64*
		All Others	1247	0.27 (0.20)		0.45 (0.16)		0.44 (0.17)	
M. m. domesticus	*M. m. musculus*	Contain testis specific genes	518	0.43 (0.22)	2.15*	0.56 (0.18)	1.81*	0.56 (0.18)	1.93*
		All Others	1364	0.41 (0.24)		0.55 (0.19)		0.54 (0.20)	

*P<=0.05 in 1-sided *t*-tests comparing measures from regions containing testis specific regions and all others.

Table S13 Genes identified in regions of overlap between the results of QTL mapping and our study in comparisons between *M. m. castaneus* and *M. m. domesticus.*

Ensembl Gene ID	Chr	Gene Start (bp)	Gene End (bp)	Associated Gene Name
ENSMUSG00000005510	2	90734791	90744984	*Ndufs3*
ENSMUSG00000005505	2	90744897	90751783	*Kbtbd4*
ENSMUSG00000005506	2	90780539	90859654	*Celf1*
ENSMUSG00000002104	2	90875777	90885886	*Rapsn*
ENSMUSG00000002102 [a]	2	90894166	90906526	*Psmc3*
ENSMUSG00000002105	2	90901948	90910574	*Slc39a13*
ENSMUSG00000002111	2	90922547	90955913	*Spi1*
ENSMUSG00000002100	2	90958301	90976673	*Mybpc3*
ENSMUSG00000040687	2	90977517	91023994	*Madd*
ENSMUSG00000002108	2	91024218	91042991	*Nr1h3*
ENSMUSG00000002103	2	91043042	91054255	*Acp2*
ENSMUSG00000002109	2	91051729	91077139	*Ddb2*
ENSMUSG00000027257	2	91096111	91104836	*Pacsin3*
ENSMUSG00000027255	2	91105131	91117088	*Arfgap2*
ENSMUSG00000027253	2	91297668	91354058	*Lrp4*
ENSMUSG00000040549	2	91366919	91460821	*Ckap5*
ENSMUSG00000027249	2	91465477	91476571	*F2*
ENSMUSG00000075040	2	91483826	91489948	*Zfp408*
ENSMUSG00000027247	2	91490017	91512483	*Arhgap1*
ENSMUSG00000040591	2	91275068	91444704	*1110051M20Rik*
ENSMUSG00000027244	2	91514775	91550733	*Atg13*
ENSMUSG00000027243	2	91551009	91561702	*Harbi1*
ENSMUSG00000040506	2	91570291	91759006	*Ambra1*
ENSMUSG00000040495	2	91762346	91769986	*Chrm4*
ENSMUSG00000027239	2	91769962	91772454	*Mdk*
ENSMUSG00000040479	2	91772981	91816021	*Dgkz*
ENSMUSG00000095332	2	91785862	91786173	*Gm9821*
ENSMUSG00000027230	2	91815044	91864659	*Creb3l1*
ENSMUSG00000058318	2	91933274	92204823	*Phf21a*
ENSMUSG00000027293	2	119914911	119980342	*Ehd4*
ENSMUSG00000050211	2	119992148	120071071	*Pla2g4e*
ENSMUSG00000070719	2	120091331	120114933	*Pla2g4d*
ENSMUSG00000046971	2	120125693	120139901	*Pla2g4f*
ENSMUSG00000027291	2	120142197	120178873	*Vps39*
ENSMUSG00000033808	2	120181045	120229852	*Tmem87a*
ENSMUSG00000062646	2	120229632	120287436	*Ganc*
ENSMUSG00000079110	2	120281755	120330649	*Capn3*
ENSMUSG00000027288	2	120332556	120389579	*Zfp106*
ENSMUSG00000027287	2	120393407	120426991	*Snap23*
ENSMUSG00000027286 [a]	2	120429974	120435256	*Lrrc57*
ENSMUSG00000027285	2	120435119	120447296	*Haus2*
ENSMUSG00000033705	2	120454862	120557633	*Stard9*
ENSMUSG00000027284	2	120541890	120675864	*Cdan1*
ENSMUSG00000090100 [a]	2	120558552	120676340	*Ttbk2*
ENSMUSG00000027272	2	120686005	120796451	*Ubr1*
ENSMUSG00000054484	2	120802753	120833588	*Tmem62*
ENSMUSG00000023572	2	120834139	120842640	*Ccndbp1*
ENSMUSG00000023216	2	120843627	120862808	*Epb4.2*
ENSMUSG00000053675	2	120871847	120911577	*Tgm5*
ENSMUSG00000079103	2	120919301	120935531	*Tgm7*

[a]indicates genes that are testis-specific.

Table S13. cont'd.

Ensembl Gene ID	Chr	Gene Start (bp)	Gene End (bp)	Associated Gene Name
ENSMUSG00000074890	2	120954043	120966434	*Lcmt2*
ENSMUSG00000027259	2	120966164	120982416	*Adal*
ENSMUSG00000050619	2	120984009	120996861	*Zscan29*
ENSMUSG00000027263	2	120996390	121024506	*Tubgcp4*
ENSMUSG00000043909	2	121019017	121097143	*Trp53bp1*
ENSMUSG00000027254	2	121115336	121136568	*Map1a*
ENSMUSG00000033526	2	121136297	121181132	*Ppip5k1*
ENSMUSG00000000308	2	121183450	121189473	*Ckmt1*
ENSMUSG00000033498	2	121189464	121212904	*Strc*
ENSMUSG00000033486 [a]	2	121218367	121240317	*Catsper2*
ENSMUSG00000027248	2	121239511	121264423	*Pdia3*
ENSMUSG00000027246	2	121264746	121270014	*Ell3*
ENSMUSG00000046110	2	121264795	121282517	*Serinc4*
ENSMUSG00000074884	2	121274931	121284049	*Serf2*
ENSMUSG00000027245	2	121279026	121284408	*Hypk*
ENSMUSG00000048222	2	121285971	121299803	*Mfap1b*
ENSMUSG00000068479	2	121317647	121332401	*Mfap1a*
ENSMUSG00000027242	2	121332459	121370596	*Wdr76*
ENSMUSG00000027238	2	121371265	121632823	*Frmd5*
ENSMUSG00000060227	2	121692706	121761956	*Casc4*
ENSMUSG00000074881	2	121779488	121781096	*Mageb3*
ENSMUSG00000033411	2	121781737	121839378	*Ctdspl2*
ENSMUSG00000027236 [a]	2	121854282	121882334	*Eif3j1*
ENSMUSG00000033396	2	121879256	121944122	*Spg11*
ENSMUSG00000027233	2	121945844	122011925	*Patl2*
ENSMUSG00000060802	2	121973422	121978819	*B2m*
ENSMUSG00000033368 [a]	2	121986436	122004763	*Trim69*
ENSMUSG00000027229	2	122012008	122032133	*4933406J08Rik*
ENSMUSG00000027227 [a]	2	122060485	122091076	*Sord*
ENSMUSG00000068452	2	122104983	122124185	*Duox2*
ENSMUSG00000027225	2	122124636	122128621	*Duoxa2*
ENSMUSG00000027224	2	122127927	122139466	*Duoxa1*
ENSMUSG00000033268	2	122141408	122173708	*Duox1*
ENSMUSG00000033256	2	122174628	122194898	*Shf*
ENSMUSG00000027219	2	122251126	122286873	*Slc28a2*
ENSMUSG00000079071	2	122310677	122353776	*Gm14085*
ENSMUSG00000073889	4	41647021	41716347	*Il11ra1*
ENSMUSG00000028447	4	41661830	41670202	*Dctn3*
ENSMUSG00000066224	4	41670868	41678174	*Arid3c*
ENSMUSG00000036078	4	41685366	41703030	*Sigmar1*
ENSMUSG00000036073	4	41702101	41705998	*Galt*
ENSMUSG00000073888 [a]	4	41716340	41721120	*Ccl27a*
ENSMUSG00000073884	4	41774204	41775337	*Ccl21b*
ENSMUSG00000096543	4	41870187	41870612	*Gm21966*
ENSMUSG00000094065	4	41903610	41904743	*Gm21541*
ENSMUSG00000078747	4	41941572	41943124	*Gm20878*
ENSMUSG00000078746	4	41966058	41971856	*Gm20938*
ENSMUSG00000096256	4	42033017	42034726	*Gm21093*
ENSMUSG00000095611	4	42035113	42035538	*Gm10597*
ENSMUSG00000095881	4	42083899	42084291	*Gm21968*
ENSMUSG00000094293	4	42091207	42092287	*Gm3893*
ENSMUSG00000073878	4	42114817	42115917	*Gm13304*
ENSMUSG00000073877 [a]	4	42153436	42158839	*Gm13306*

[a]indicates genes that are testis-specific.

Table S13. cont'd.

Ensembl Gene ID	Chr	Gene Start (bp)	Gene End (bp)	Associated Gene Name
ENSMUSG00000073876	4	42158842	42168603	*Gm13305*
ENSMUSG00000096609	4	42170845	42171335	*1700045I11Rik*
ENSMUSG00000094984	4	42219428	42219853	*Gm10595*
ENSMUSG00000083929	4	42240639	42242685	*Gm10600*
ENSMUSG00000095675	4	42255767	42256432	*Ccl21b*
ENSMUSG00000094695	4	42294267	42294855	*Gm21953*
ENSMUSG00000093996	4	42318334	42323929	*Gm21598*
ENSMUSG00000095234	4	42439378	42439966	*Gm21586*
ENSMUSG00000096892	4	42458751	42459176	*Gm10597*
ENSMUSG00000093909	4	42459563	42461272	*Gm3883*
ENSMUSG00000095779	4	42466752	42589938	*Gm2163*
ENSMUSG00000094066	4	42522580	42528175	*Gm13298*
ENSMUSG00000096260	4	42581229	42581621	*Gm10592*
ENSMUSG00000096596	4	42612195	42612860	*Gm10591*
ENSMUSG00000091938	4	42629719	42631714	*Gm2564*
ENSMUSG00000096826 [a]	4	42655251	42656005	*Ccl27b*
ENSMUSG00000078735	4	42656355	42661893	*Il11ra2*
ENSMUSG00000094731	4	42668043	42668438	*Gm9969*
ENSMUSG00000095375	4	42714926	42719893	*Gm21955*
ENSMUSG00000054885	4	42735545	42846248	*4930578G10Rik*
ENSMUSG00000071005	4	42754525	42756577	*Ccl19*
ENSMUSG00000094686	4	42772860	42773993	*Ccl21a*
ENSMUSG00000078722	4	42781928	42856771	*Gm12394*
ENSMUSG00000078721	4	42848071	42853888	*Gm12429*
ENSMUSG00000050141 [a]	4	42868004	42874234	*BC049635*
ENSMUSG00000036062	4	42916660	42944752	*N28178*
ENSMUSG00000028551	4	109660876	109667189	*Cdkn2c*
ENSMUSG00000010517 [a]	4	109676588	109963960	*Faf1*
ENSMUSG00000029722	5	137650483	137684726	*Agfg2*
ENSMUSG00000045348	5	137730883	137741607	*Nyap1*
ENSMUSG00000029723 [a]	5	137745730	137768450	*Tsc22d4*
ENSMUSG00000029659	5	149411749	149431723	*Medag*
ENSMUSG00000029660 [a]	5	149439706	149470620	*Tex26*
ENSMUSG00000029658	5	149528679	149611894	*Wdr95*
ENSMUSG00000033174	6	88724412	88828360	*Mgll*
ENSMUSG00000030083	6	88835915	88841935	*Abtb1*
ENSMUSG00000033152	6	88842558	88875044	*Podxl2*
ENSMUSG00000030314	6	114643097	114860614	*Atg7*
ENSMUSG00000030315	6	114860628	114969994	*Vgll4*
ENSMUSG00000030316	6	115004381	115037876	*Tamm41*
ENSMUSG00000009394	6	115134902	115282626	*Syn2*
ENSMUSG00000092004	6	115227343	115259294	*Gm17482*
ENSMUSG00000030317	6	115245616	115251849	*Timp4*
ENSMUSG00000000440	6	115361221	115490401	*Pparg*
ENSMUSG00000042389	6	115544664	115578350	*Tsen2*
ENSMUSG00000068011	6	115583544	115592576	*2510049J12Rik*
ENSMUSG00000000439	6	115601938	115618670	*Mkrn2*
ENSMUSG00000000441	6	115618067	115676635	*Raf1*
ENSMUSG00000055396	6	115675995	115677136	*D830050J10Rik*
ENSMUSG00000059900	6	115729131	115762466	*Tmem40*
ENSMUSG00000030319	6	115774538	115804893	*Cand2*
ENSMUSG00000071226	6	120666369	120771190	*Cecr2*
ENSMUSG00000004902	6	120773768	120793982	*Slc25a18*
ENSMUSG00000019210	6	120795245	120822685	*Atp6v1e1*

[a]indicates genes that are testis-specific.

Table S13. cont'd.

Ensembl Gene ID	Chr	Gene Start (bp)	Gene End (bp)	Associated Gene Name
ENSMUSG00000009112	6	120836230	120892842	*Bcl2l13*
ENSMUSG00000004446	6	120891930	120916853	*Bid*
ENSMUSG00000051586	6	120931707	121003153	*Mical3*
ENSMUSG00000003178	6	121007241	121081609	*Mical3*
ENSMUSG00000030143	6	132361041	132364134	*Gm8882*
ENSMUSG00000059934	6	132569809	132572941	*Prh1*
ENSMUSG00000058295	6	132595913	132601236	*Prp2*
ENSMUSG00000067541	6	132625111	132627511	*A630073D07Rik*
ENSMUSG00000059382	6	132656957	132657844	*Tas2r120*
ENSMUSG00000071150	6	132700090	132701007	*Tas2r121*
ENSMUSG00000078280	6	132710999	132711928	*Tas2r122*
ENSMUSG00000071149	6	132737010	132738035	*Tas2r115*
ENSMUSG00000060412	6	132754730	132755659	*Tas2r124*
ENSMUSG00000056901	6	132762131	132763174	*Tas2r102*
ENSMUSG00000053217	6	132777179	132778162	*Tas2r136*
ENSMUSG00000058349	6	132802818	132803975	*Tas2r117*
ENSMUSG00000057381	6	132847142	132848143	*Tas2r123*
ENSMUSG00000030194	6	132855438	132856355	*Tas2r116*
ENSMUSG00000062952	6	132868008	132869009	*Tas2r110*
ENSMUSG00000056926	6	132893011	132893940	*Tas2r113*
ENSMUSG00000059410	6	132909651	132910587	*Tas2r125*
ENSMUSG00000063762	6	132951102	132952064	*Tas2r129*
ENSMUSG00000057699	6	132956884	132957919	*Tas2r131*
ENSMUSG00000062528	6	132980015	132980965	*Tas2r109*
ENSMUSG00000030196	6	133036163	133037101	*Tas2r103*
ENSMUSG00000071147	6	133054817	133055816	*Tas2r140*
ENSMUSG00000072704	6	133105239	133107747	*2700089E24Rik*
ENSMUSG00000055594	6	133292216	133295790	*5530400C23Rik*
ENSMUSG00000095412	6	133529189	133532762	*Gm5885*
ENSMUSG00000032758	6	133849855	133853667	*Kap*
ENSMUSG00000030199	6	134035700	134270158	*Etv6*
ENSMUSG00000030200	6	134396318	134438736	*Bcl2l14*
ENSMUSG00000035919 [a]	9	22475715	22888280	*Bbs9*
ENSMUSG00000020052	10	87490819	87493660	*Ascl1*
ENSMUSG00000020051	10	87521795	87584136	*Pah*
ENSMUSG00000020053	10	87858265	87937042	*Igf1*
ENSMUSG00000035383	10	88091072	88092375	*Pmch*
ENSMUSG00000035365 [a]	10	88091432	88146941	*Parpbp*
ENSMUSG00000035351 [a]	10	88146992	88178388	*Nup37*
ENSMUSG00000020056 [a]	10	88201093	88246158	*Ccdc53*
ENSMUSG00000020057	10	88322804	88379080	*Dram1*
ENSMUSG00000035311	10	88379132	88447329	*Gnptab*
ENSMUSG00000060002	10	88452745	88504073	*Chpt1*
ENSMUSG00000020059 [a]	10	88459569	88473236	*Sycp3*
ENSMUSG00000020061	10	88518279	88605152	*Mybpc1*
ENSMUSG00000004359	10	88674772	88685015	*Spic*
ENSMUSG00000060904	10	88730858	88744094	*Arl1*
ENSMUSG00000004356	10	88746607	88826814	*Utp20*
ENSMUSG00000020062	10	88885992	88929505	*Slc5a8*
ENSMUSG00000035189	10	88948994	89344762	*Ano4*
ENSMUSG00000074802	10	89408823	89443967	*Gas2l3*
ENSMUSG00000047638	10	89454234	89533585	*Nr1h4*
ENSMUSG00000019935	10	89574020	89621253	*Slc17a8*
ENSMUSG00000019906 [a]	10	107271843	107425143	*Lin7a*

[a]indicates genes that are testis-specific.

Table S13. cont'd.

Ensembl Gene ID	Chr	Gene Start (bp)	Gene End (bp)	Associated Gene Name
ENSMUSG00000000435	10	107482908	107486134	*Myf5*
ENSMUSG00000035923	10	107492860	107494729	*Myf6*
ENSMUSG00000035916	10	107517360	107720027	*Ptprq*
ENSMUSG00000091455	10	107762223	107912134	*Otogl*
ENSMUSG00000019907	10	108162400	108277575	*Ppp1r12a*
ENSMUSG00000035873	10	108332189	108414391	*Pawr*
ENSMUSG00000035864	10	108497650	109010982	*Syt1*
ENSMUSG00000020181	10	109682660	110000219	*Nav3*

[a]indicates genes that are testis-specific.

Table S14 Genes identified in regions of overlap between the results of QTL mapping, a study of the hybrid zone, and our study in comparisons between *M. m. musculus* and *M. m. domesticus.*

Ensembl Gene ID	Chr	Gene Start (bp)	Gene End (bp)	Associated Gene Name
ENSMUSG00000040152	2	118111876	118127133	*Thbs1*
ENSMUSG00000027344 [a]	2	118204888	118256966	*Fsip1*
ENSMUSG00000040133	2	118277110	118373419	*Gpr176*
ENSMUSG00000005102	2	118388618	118475234	*Eif2ak4*
ENSMUSG00000009549 [a]	2	118475850	118479711	*Srp14*
ENSMUSG00000040093	2	118528757	118549687	*Bmf*
ENSMUSG00000040084	2	118598211	118641591	*Bub1b*
ENSMUSG00000074923	2	118663303	118698020	*Pak6*
ENSMUSG00000078137	2	118699103	118703963	*Ankrd63*
ENSMUSG00000040061	2	118707517	118728438	*Plcb2*
ENSMUSG00000045838	2	118754158	118762661	*A430105I19Rik*
ENSMUSG00000046804	2	118772769	118778165	*Phgr1*
ENSMUSG00000040035	2	118779719	118811293	*Disp2*
ENSMUSG00000027331	2	118814003	118853957	*Knstrn*
ENSMUSG00000027332	2	118861954	118882909	*Ivd*
ENSMUSG00000040007	2	118900377	118924528	*Bahd1*
ENSMUSG00000074916	2	118926497	118928585	*Chst14*
ENSMUSG00000039983	2	119017779	119029393	*Ccdc32*
ENSMUSG00000027324	2	119034790	119039769	*Rpusd2*
ENSMUSG00000027326 [a]	2	119047119	119105501	*Casc5*
ENSMUSG00000027323 [a]	2	119112793	119147445	*Rad51*
ENSMUSG00000070730	2	119137001	119157034	*Rmdn3*
ENSMUSG00000046814	2	119167773	119172390	*Gchfr*
ENSMUSG00000034278	2	119172500	119208795	*Dnajc17*
ENSMUSG00000055926	2	119174509	119177575	*Gm14137*
ENSMUSG00000068580 [a]	2	119208617	119217049	*Zfyve19*
ENSMUSG00000027317	2	119218119	119229906	*Ppp1r14d*
ENSMUSG00000027315	2	119237362	119249527	*Spint1*
ENSMUSG00000034226 [a]	2	119269201	119271272	*Rhov*
ENSMUSG00000034216	2	119288740	119298453	*Vps18*
ENSMUSG00000027314	2	119325784	119335962	*Dll4*
ENSMUSG00000027313	2	119351229	119354381	*Chac1*
ENSMUSG00000034154	2	119373042	119477687	*Ino80*
ENSMUSG00000048647	2	119516505	119547627	*Exd1*
ENSMUSG00000014077	2	119547697	119587027	*Chp1*
ENSMUSG00000072980	2	119609512	119618469	*Oip5*
ENSMUSG00000027306	2	119618298	119651244	*Nusap1*
ENSMUSG00000027305	2	119655446	119662827	*Ndufaf1*
ENSMUSG00000027304	2	119675068	119735407	*Rtf1*
ENSMUSG00000027296	2	119742337	119751263	*Itpka*
ENSMUSG00000027297	2	119751320	119760431	*Ltk*
ENSMUSG00000034032	2	119763304	119787537	*Rpap1*
ENSMUSG00000027298	2	119797733	119818104	*Tyro3*
ENSMUSG00000028524	4	102741297	102973628	*Sgip1*
ENSMUSG00000028523 [a]	4	102986379	103005594	*Tctex1d1*
ENSMUSG00000066090	4	103017872	103026842	*Insl5*
ENSMUSG00000035126 [a]	4	103038065	103114555	*Wdr78*
ENSMUSG00000028522 [a]	4	103114390	103165754	*Mier1*
ENSMUSG00000028521	4	103170649	103215164	*Slc35d1*

[a]indicates genes that are testis-specific.

Table S14. cont'd.

Ensembl Gene ID	Chr	Gene Start (bp)	Gene End (bp)	Associated Gene Name
ENSMUSG00000028520 [a]	4	103230445	103290863	*4921539E11Rik*
ENSMUSG00000035069	4	103313812	103371868	*Oma1*
ENSMUSG00000028519	4	103619359	104744844	*Dab1*
ENSMUSG00000070886	4	104328252	104330557	*Gm10304*
ENSMUSG00000029656	4	104766317	104804548	*C8b*
ENSMUSG00000035031	4	104815679	104876398	*C8a*
ENSMUSG00000095386	4	104857329	104859137	*Gm17662*
ENSMUSG00000078612	4	104913456	105016863	*1700024P16Rik*
ENSMUSG00000028518	4	105029874	105109890	*Prkaa2*
ENSMUSG00000028517	4	105157347	105232764	*Ppap2b*
ENSMUSG00000029705	5	136248135	136567490	*Cux1*
ENSMUSG00000046548	5	136613702	136615328	*4731417B20Rik*
ENSMUSG00000005474 [a]	5	136693146	136701094	*Myl10*
ENSMUSG00000004415	5	136741759	136883209	*Col26a1*
ENSMUSG00000007987 [a]	5	136908150	136913244	*Rabl5*
ENSMUSG00000019054	5	136953275	136966234	*Fis1*
ENSMUSG00000001739	5	136966616	136975858	*Cldn15*
ENSMUSG00000059518 [a]	5	136982164	136988021	*Znhit1*
ENSMUSG00000004846	5	136987019	136996648	*Plod3*
ENSMUSG00000037428	5	137030295	137033351	*Vgf*
ENSMUSG00000004849	5	137034993	137046135	*Ap1s1*
ENSMUSG00000037411	5	137061504	137072272	*Serpine1*
ENSMUSG00000043279	5	137105644	137116209	*Trim56*
ENSMUSG00000037390 [a]	5	137134924	137149320	*Muc3*
ENSMUSG00000079174	5	137154030	137166001	*Gm3054*
ENSMUSG00000094840	5	137208813	137212389	*A630081J09Rik*
ENSMUSG00000023328	5	137287519	137294466	*Ache*
ENSMUSG00000051502	5	137294669	137295664	*Ufsp1*
ENSMUSG00000037364 [a]	5	137295704	137307674	*Srrt*
ENSMUSG00000023348	5	137309899	137314241	*Trip6*
ENSMUSG00000037344	5	137314558	137333597	*Slc12a9*
ENSMUSG00000029710	5	137350109	137378669	*Ephb4*
ENSMUSG00000079173	5	137378637	137477064	*Zan*
ENSMUSG00000029711	5	137483020	137533242	*Epo*
ENSMUSG00000029715	5	137501438	137502518	*Pop7*
ENSMUSG00000029714	5	137518880	137527934	*Gigyf1*
ENSMUSG00000029713	5	137528127	137533510	*Gnb2*
ENSMUSG00000029712	5	137553517	137569582	*Actl6b*
ENSMUSG00000029716	5	137569851	137587481	*Tfr2*
ENSMUSG00000037221	5	137596645	137601058	*Mospd3*
ENSMUSG00000029718	5	137605103	137613784	*Pcolce*
ENSMUSG00000089984 [a]	5	137612503	137629002	*Fbxo24*
ENSMUSG00000093445	5	137629121	137641099	*Lrch4*
ENSMUSG00000029720	5	137629175	137642899	*Gm20605*
ENSMUSG00000079165	5	137641334	137642902	*Sap25*
ENSMUSG00000047182	5	137643032	137645714	*Irs3*
ENSMUSG00000029722	5	137650483	137684726	*Agfg2*
ENSMUSG00000045348	5	137730883	137741607	*Nyap1*
ENSMUSG00000029723 [a]	5	137745730	137768450	*Tsc22d4*
ENSMUSG00000029725 [a]	5	137778849	137780110	*Ppp1r35*
ENSMUSG00000029726 [a]	5	137781906	137786715	*Mepce*
ENSMUSG00000037108	5	137787798	137822621	*Zcwpw1*
ENSMUSG00000046245	5	137821952	137836268	*Pilra*

[a]indicates genes that are testis-specific.

Table S14. cont'd.

Ensembl Gene ID	Chr	Gene Start (bp)	Gene End (bp)	Associated Gene Name
ENSMUSG00000066684	5	137852147	137858049	*Pilrb1*
ENSMUSG00000066682	5	137865829	137871758	*Pilrb2*
ENSMUSG00000029727	5	137892932	137921619	*Cyp3a13*
ENSMUSG00000056966	5	137953809	137962959	*Gjc3*
ENSMUSG00000037053	5	137981521	137990233	*Azgp1*
ENSMUSG00000075599	5	138021276	138034665	*Smok3a*
ENSMUSG00000079156	5	138021429	138050636	*Smok3b*
ENSMUSG00000029729	5	138085084	138107822	*Zkscan1*
ENSMUSG00000037017 [a]	5	138116903	138134265	*Zscan21*
ENSMUSG00000037007	5	138139702	138155744	*Zfp113*
ENSMUSG00000019494	5	138161071	138164646	*Cops6*
ENSMUSG00000029730 [a]	5	138164583	138172422	*Mcm7*
ENSMUSG00000019518	5	138172002	138178708	*Ap4m1*
ENSMUSG00000036980 [a]	5	138178617	138187451	*Taf6*
ENSMUSG00000036968	5	138187485	138193918	*Cnpy4*
ENSMUSG00000049285	5	138194314	138195621	*Mblac1*
ENSMUSG00000089783	5	138203609	138207308	*Gm454*
ENSMUSG00000047592	5	138225898	138253363	*Nxpe5*
ENSMUSG00000050552	5	138255608	138259398	*Lamtor4*
ENSMUSG00000036948	5	138259656	138264046	*BC037034*
ENSMUSG00000091964	5	138259658	138264046	*BC037034*
ENSMUSG00000075593	5	138264921	138272840	*Gal3st4*
ENSMUSG00000029510	5	138264952	138280005	*Gpc2*
ENSMUSG00000036928 [a]	5	138280240	138312393	*Stag3*
ENSMUSG00000075591	5	138363719	138388287	*Gm10874*
ENSMUSG00000036898	5	138441468	138460694	*Zfp157*
ENSMUSG00000029526	5	138561840	138564694	*1700123K08Rik*
ENSMUSG00000058291	5	138604616	138619761	*Zfp68*
ENSMUSG00000056014	5	138622859	138648903	*A430033K04Rik*
ENSMUSG00000025854	5	138754514	138810077	*Fam20c*
ENSMUSG00000094504	5	138820080	138821619	*Gm5294*
ENSMUSG00000025856	5	138976014	138997370	*Pdgfa*
ENSMUSG00000075585	5	138995056	139000576	*6330403L08Rik*
ENSMUSG00000025855	5	139017306	139150001	*Prkar1b*
ENSMUSG00000025857	5	139150223	139186510	*Heatr2*
ENSMUSG00000036817	5	139200637	139249840	*Sun1*
ENSMUSG00000025858	5	139252324	139270051	*Get4*
ENSMUSG00000056413	5	139271876	139325622	*Adap1*
ENSMUSG00000045438	5	139336189	139345233	*Cox19*
ENSMUSG00000029541	5	139352617	139357033	*Cyp2w1*
ENSMUSG00000053553	5	139359739	139460502	*3110082I17Rik*
ENSMUSG00000044197	5	139377742	139396415	*Gpr146*
ENSMUSG00000021206	5	139378220	139379259	*D830046C22Rik*
ENSMUSG00000044092	5	139405280	139415623	*C130050O18Rik*
ENSMUSG00000053647	5	139423151	139427800	*Gper1*
ENSMUSG00000053581	5	139471211	139484549	*Zfand2a*
ENSMUSG00000029546	5	139543494	139548179	*Uncx*
ENSMUSG00000036718	5	139706693	139736336	*Micall2*
ENSMUSG00000029547	5	139751282	139775678	*Ints1*
ENSMUSG00000018143	5	139791513	139802653	*Mafk*
ENSMUSG00000036687 [a]	5	139802485	139819917	*Tmem184a*
ENSMUSG00000098140	5	139807978	139826407	*Gm26938*
ENSMUSG00000029551	5	139823592	139826885	*Psmg3*

[a]indicates genes that are testis-specific.

Table S14. cont'd.

Ensembl Gene ID	Chr	Gene Start (bp)	Gene End (bp)	Associated Gene Name
ENSMUSG00000048988	5	139907943	139974711	*Elfn1*
ENSMUSG00000031737	8	92357796	92361456	*Irx5*
ENSMUSG00000031738	8	92674289	92680956	*Irx6*
ENSMUSG00000031740	8	92827328	92853417	*Mmp2*
ENSMUSG00000033192	8	92855350	92919279	*Lpcat2*
ENSMUSG00000078144	8	92901395	92902409	*Capns2*
ENSMUSG00000055368	8	92960079	93001667	*Slc6a2*
ENSMUSG00000071047	8	93020214	93048192	*Ces1a*
ENSMUSG00000078964	8	93056727	93080017	*Ces1b*
ENSMUSG00000057400	8	93099015	93131283	*Ces1c*
ENSMUSG00000056973	8	93166068	93197838	*Ces1d*
ENSMUSG00000061959	8	93201218	93229619	*Ces1e*
ENSMUSG00000031725	8	93256236	93279747	*Ces1f*
ENSMUSG00000057074	8	93302369	93337308	*Ces1g*
ENSMUSG00000074156	8	93351843	93363676	*Ces1h*
ENSMUSG00000058019	8	93499213	93535707	*Ces5a*
ENSMUSG00000031748	8	93809966	93969388	*Gnao1*
ENSMUSG00000031751	8	93971588	94012663	*Amfr*
ENSMUSG00000031754 [a]	8	94017770	94037021	*Nudt21*
ENSMUSG00000033009	8	94037198	94067921	*Ogfod1*
ENSMUSG00000031755	8	94067954	94098811	*Bbs2*
ENSMUSG00000031757	8	94137204	94139031	*Mt4*
ENSMUSG00000031760	8	94152607	94154148	*Mt3*
ENSMUSG00000031762	8	94172618	94173567	*Mt2*
ENSMUSG00000031765	8	94179089	94180325	*Mt1*
ENSMUSG00000032939	8	94214597	94315066	*Nup93*
ENSMUSG00000031766	8	94329192	94366213	*Slc12a3*
ENSMUSG00000031770	8	94386438	94395377	*Herpud1*
ENSMUSG00000074151	8	94472763	94527272	*Nlrc5*
ENSMUSG00000034361	8	94532990	94570529	*Cpne2*
ENSMUSG00000031774	8	94574943	94601726	*Fam192a*
ENSMUSG00000050079 [a]	8	94601955	94660275	*Rspry1*
ENSMUSG00000031776 [a]	8	94666755	94674417	*Arl2bp*
ENSMUSG00000031775	8	94674895	94696242	*Pllp*
ENSMUSG00000031779	8	94745590	94751699	*Ccl22*
ENSMUSG00000031778	8	94772009	94782423	*Cx3cl1*
ENSMUSG00000031780	8	94810453	94812035	*Ccl17*
ENSMUSG00000031781	8	94819818	94838358	*Ciapin1*
ENSMUSG00000031782	8	94838321	94854895	*Coq9*
ENSMUSG00000031783	8	94857450	94864242	*Polr2c*
ENSMUSG00000040631	8	94863828	94876312	*Dok4*
ENSMUSG00000063605	8	94902869	94918098	*Ccdc102a*
ENSMUSG00000061577	8	94923694	94943290	*Gpr114*
ENSMUSG00000031785	8	94977109	95014208	*Gpr56*
ENSMUSG00000022295	15	38661904	38692443	*Atp6v1c1*
ENSMUSG00000022296	15	38933142	38949405	*Baalc*
ENSMUSG00000022297	15	39006280	39038186	*Fzd6*
ENSMUSG00000054196	15	39076932	39087121	*Cthrc1*
ENSMUSG00000022299	15	39094191	39112716	*Slc25a32*
ENSMUSG00000022300	15	39112874	39146856	*Dcaf13*
ENSMUSG00000037386	15	39198332	39681940	*Rims2*
ENSMUSG00000022303	15	39745932	39760934	*Dcstamp*
ENSMUSG00000022304	15	39768485	39857470	*Dpys*
ENSMUSG00000022305	15	39870603	39943994	*Lrp12*

[a]indicates genes that are testis-specific.

Table S14. cont'd.

Ensembl Gene ID	Chr	Gene Start (bp)	Gene End (bp)	Associated Gene Name
ENSMUSG00000094112	15	40142188	40148689	*9330182O14Rik*
ENSMUSG00000022306	15	40655042	41104592	*Zfpm2*
ENSMUSG00000022307	15	41447482	41861048	*Oxr1*
ENSMUSG00000042895	15	41865293	41869720	*Abra*
ENSMUSG00000022309	15	42424727	42676977	*Angpt1*
ENSMUSG00000051920	15	43020811	43170818	*Rspo2*
ENSMUSG00000022336	15	43250040	43282736	*Eif3e*
ENSMUSG00000072592	15	43430943	43477036	*Gm10373*
ENSMUSG00000022337	15	43477229	43527777	*Emc2*
ENSMUSG00000054409	15	43866695	43870029	*Tmem74*
ENSMUSG00000048915	17	62604184	62881317	*Efna5*
ENSMUSG00000090425	17	62604292	62606707	*Efna5*
ENSMUSG00000023965 [a]	17	63057452	63500017	*Fbxl17*
ENSMUSG00000045506	17	63863300	63863791	*A930002H24Rik*
ENSMUSG00000000127	17	63896018	64139494	*Fer*
ENSMUSG00000024083	17	64281005	64331916	*Pja2*
ENSMUSG00000073377	17	64514081	64555660	*AU016765*
ENSMUSG00000024085	17	64600736	64755110	*Man2a1*
ENSMUSG00000024088	17	64832523	64836071	*4930583I09Rik*
ENSMUSG00000045036 [a]	17	65256005	65540782	*Tmem232*
ENSMUSG00000024091	17	65580056	65613555	*Vapa*
ENSMUSG00000050612 [a]	17	65637505	65642204	*Txndc2*
ENSMUSG00000056515	17	65651726	65772752	*Rab31*
ENSMUSG00000061950 [a]	17	65782573	65841926	*Ppp4r1*
ENSMUSG00000024096	17	65848433	65885755	*Ralbp1*
ENSMUSG00000024098	17	65923066	65951187	*Twsg1*
ENSMUSG00000034647	17	65967501	66077089	*Ankrd12*
ENSMUSG00000024099 [a]	17	66078795	66101559	*Ndufv2*
ENSMUSG00000024101	17	66111546	66120503	*Wash*
ENSMUSG00000035842 [a]	17	66123520	66152167	*Ddx11*
ENSMUSG00000052105	17	66336982	66449750	*Soga2*
ENSMUSG00000023460	17	66494512	66519717	*Rab12*
ENSMUSG00000024105	17	66555252	66594621	*Themis3*

[a]indicates genes that are testis-specific.