Appendix

Table A1. Genes included in the training set.

Known Imprinted Genes		Non-Imprinted Genes		
Apoc2	*Osbpl5*	*Acvrl1*	*Fn1*	*Nog*
Asb4	*Peg10*	*Ada*	*Foxd1*	*Nte*
Calcr	*Peg12*	*Adcy3*	*Foxg1*	*Ntrk1*
Cd81	*Peg3*	*Adcy7*	*Fst*	*Ntrk2*
Cdkn1c	*Phlda2*	*Akp2*	*Gba*	*Ntrk3*
Commd1	*Plagl1*	*Apaf1*	*Gdf1*	*Otx1*
Copg2	*Pon2*	*Arnt*	*Gja1*	*Ppard*
Dcn	*Pon3*	*Ascl1*	*Hbb*	*Psen1*
Dlk1	*Ppp1r9a*	*Ass1*	*Hdh*	*Rela*
Gatm	*Rasgrf1*	*Atoh1*	*Hgs*	*Runx1*
Gnas	*Rb1*	*Bcl2*	*Inhba*	*Shh*
Grb10	*Sgce*	*Bdnf*	*Itga5*	*Slc4a1*
Gtl2	*Slc22a18*	*Cdh1*	*Itgav*	*Smo*
H19	*Slc22a2*	*Cdh2*	*Itgb1*	*Snap25*
Htr2a	*Slc22a3*	*Cdk5*	*Jun*	*Sp4*
Igf2	*Slc38a4*	*Chrna3*	*Jup*	*Tal1*
Igf2r	*Snrpn*	*Col3a1*	*Kcnj2*	*Tgfb1*
Impact	*Snurf*	*Csk*	*Klf1*	*Tgfbr1*
Ins2	*Tnfrsf23*	*Cxcr4*	*Kras*	*Tsc2*
Kcnq1	*Tspan32*	*Cycs*	*Lifr*	*Unc5c*
Magel2	*Tssc4*	*Dgat2*	*Mad2l1*	*Vcam1*
Mash2	*U2af1-rs1*	*Dnmt1*	*Maf*	*Vhlh*
Mcts2	*Ube3a*	*Edn3*	*Map2k4*	*Wnt3a*
Mest	*Zim1*	*Ednrb*	*Mdm2*	*Wnt5a*
Mkrn3		*Efemp2*	*Mgat1*	*Wnt7b*
Nap1l4		*En1*	*Myb*	*Wt1*
Nap1l5		*Epas1*	*Myf5*	
Ndn		*Evi1*	*Myf6*	
Nnat		*F5*	*Nf1*	

A total of 137 genes, including known imprinted and non-imprinted genes, were included in the training data set. Fifty-three genes fall within the known imprinted category, while 84 genes fall within the non-imprinted category. We compiled the 53 known imprinted genes from the Imprinted Gene Catalogue (http://igc.otago.ac.nz/Search.html). The non-imprinted genes were assumed to be non-imprinted based on the lethality of homozygous mutations and the viability of heterozygous mutations in mice as described in the Jackson Laboratories MGI database (http://www.informatics.jax.org/).

Table A2. Correlation coefficient p-values for features enriched in imprinted genes by gene region used to generate Figure 1.

Feature	100up	10up	1up	5'UTR	In Gene	Exons	Introns	3'UTR	1dn	10dn	100dn	Pos	Neg
%CG	0.912378	0.590616	0.043953	0.345161	0.287104	0.260332	0.813265	0.434307	0.294456	0.007114	0.200820	0	0
G-quartets	0.703111	0.133142	0.680119	0.001767	0.009755	0.968707	0.004456	0.768283	0.000098	0.757766	0.445824	1	0
miRNA	0.000000	0.050574	0.006366	0.859144	0.014490	0.003085	0.040250	0.818769	0.820586	0.003972	0.000000	2	0
CpG island	0.044549	0.773639	0.811157	0.042787	0.004542	0.704237	0.000046	0.000000	0.368262	0.044848	0.029007	2	0
Verified CTCF	0.000000	0.000000	0.859144	0.952835	0.000000	0.875636	0.000000	0.933337	0.933337	0.812930	0.000000	5	0
Predicted CTCF	0.013586	0.000000	0.026743	0.625201	0.683401	0.587129	0.681047	0.591622	0.064826	0.233170	0.077739	1	0
EF H3K4me3	0.548611	0.003186	0.548387	0.001679	0.058327	0.000727	0.034300	0.165958	0.220383	0.440995	0.868248	0	0
EF H3K9me3	0.006238	0.000002	0.000100	0.005080	0.372446	0.002976	0.171234	0.005558	0.139872	0.063811	0.053517	2	0
EF H3K27me3	0.000072	0.000000	0.007393	0.000062	0.003116	0.019873	0.002924	0.004269	0.101935	0.006277	0.003064	3	0
EF H3K36me3	0.001142	0.811425	0.714943	0.763260	0.621611	0.176142	0.766424	0.329263	0.006740	0.000020	0.018163	0	1
ES H4K20me3	0.000000	0.000000	0.000000	0.000000	0.000878	0.000001	0.000633	0.000000	0.000024	0.000000	0.000005	9	0
ES H3K4me3	0.336046	0.020766	0.254961	0.001146	0.005397	0.097354	0.005807	0.987056	0.227799	0.046610	0.146762	0	0
ES H3K9me3	0.000000	0.000000	0.000000	0.000000	0.001267	0.000001	0.001114	0.000000	0.000061	0.000000	0.000000	9	0
ES H3K27me3	0.000000	0.000000	0.000000	0.000000	0.000000	0.000006	0.000000	0.000096	0.000084	0.000070	0.000000	11	0
ES H3K36me3	0.005576	0.868870	0.595748	0.490950	0.424074	0.178215	0.633940	0.510597	0.004685	0.000147	0.102057	0	1
ES H3K4me3 (HMM)	0.171486	0.004015	0.000013	0.039469	0.000005	0.005329	0.000423	0.138784	0.388726	0.353818	0.251803	2	0
ES H3K9me3 (HMM)	0.000000	0.000000	0.000000	0.000000	0.000000	0.577023	0.000000	0.000000	0.000000	0.000794	0.000007	9	0
ES H3K27me3 (HMM)	0.000000	0.000000	0.002089	0.002150	0.000000	0.000000	0.000000	0.529679	0.366802	0.046649	0.017285	5	0
ES H3K36me3 (HMM)	0.007396	0.107181	0.039114	0.401464	0.073591	0.388030	0.041782	0.426347	0.100102	0.007915	0.013052	0	0
ES H4K20me3 (HMM)	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000006	11	0
ES H3K4me3 (WIN)	0.006011	0.341020	0.296925	0.161729	0.015081	0.062799	0.014067	0.565580	0.989288	0.216237	0.036394	0	0
ES H3K9me3 (WIN)	0.000047	0.000000	0.000000	0.000000	0.000000	0.000176	0.000000	0.006699	0.011259	0.000000	0.000197	7	0
ES H3K27me3 (WIN)	0.000000	0.000000	0.012421	0.002909	0.000000	0.504756	0.000000	0.000000	0.000000	0.000000	0.000001	8	0
EF H3K4me3 (WIN)	0.126426	0.341020	0.000000	0.042801	0.020089	0.866204	0.078138	0.114392	0.436092	0.443941	0.018221	1	0
EF H3K9me3 (WIN)	0.072684	0.000002	0.701288	0.824815	0.326421	0.220057	0.597690	0.762867	0.725864	0.254941	0.552456	1	0
EF H3K27me3 (WIN)	0.002882	0.000013	0.116783	0.003378	0.008004	0.297751	0.020161	0.983317	0.002083	0.018956	0.353656	1	0
NP H3K4me3 (WIN)	0.001221	0.061094	0.096342	0.045705	0.984355	0.834144	0.772224	0.881972	0.789637	0.552109	0.004411	1	0
NP H3K9me3 (WIN)	0.522721	0.646058	0.831093	0.884796	0.386553	0.771782	0.409352	0.771914	0.767341	0.690569	0.259141	0	0
NP H3K27me3 (WIN)	0.000000	0.000000	0.012421	0.000000	0.000007	0.000325	0.006452	0.004969	0.000000	0.000000	0.000000	7	0

For each gene region examined, the correlation coefficient p-value (indicating the significance of correlation with imprinting status) for each of the features of interest included in our analysis is shown. Correlation coefficients were calculated using the cor() function in [R]. P-values for the correlation coefficients were calculated using a two-tailed t-test and were considered significant if less than 0.000157 (0.05 p-value/319 comparisons) after Bonferroni correcting for multiple comparisons. Features with significant p-values are highlighted in either green, to signify a correlation in the positive direction, or red, to signify a correlation in the negative direction. The columns labelled “Pos” and “Neg” tally the number of regions in which each feature correlates with imprinted genes in a positive and a negative direction, respectively. ES stands for embryonic stem cells, EF stands for embryonic fibroblast cells, and NP stands for neural progenitor cells. HMM stands for

enrichment as determined using a Hidden Markov Model, while WIN stands for enrichment as determined using a sliding window model (30).

Table A3. Correlation coefficients for features enriched in imprinted genes by gene region used to generate Figure 1.

Feature	100up	10up	1up	5'UTR	In Gene	Exons	Introns	3'UTR	1dn	10dn	100dn
%CG	-0.0006	0.0031	0.0117	0.0055	0.0062	0.0065	-0.0014	-0.0045	-0.0061	-0.0157	-0.0074
G-quartets	0.0022	0.0087	-0.0024	0.0182	0.0150	-0.0002	0.0165	-0.0017	0.0227	0.0018	0.0044
miRNA	0.0472	0.0114	0.0159	-0.0010	0.0142	0.0172	0.0119	-0.0013	-0.0013	0.0168	0.0311
CpG island	-0.0117	0.0017	0.0014	0.0118	0.0165	0.0022	0.0237	0.0380	-0.0052	-0.0117	-0.0127
Verified CTCF	0.0795	0.0928	-0.0010	-0.0003	0.0342	-0.0009	0.0339	-0.0005	-0.0005	-0.0014	0.0778
Predicted CTCF	0.0144	0.0314	0.0129	-0.0028	-0.0024	-0.0032	-0.0024	-0.0031	0.0107	0.0069	0.0103
EF H3K4me3	-0.0035	0.0172	0.0035	0.0183	0.0110	0.0197	0.0123	0.0081	0.0071	-0.0045	-0.0010
EF H3K9me3	0.0159	0.0276	0.0226	0.0163	0.0052	0.0173	0.0080	0.0161	-0.0086	0.0108	0.0112
EF H3K27me3	0.0231	0.0294	0.0156	0.0233	0.0172	0.0135	0.0173	0.0166	0.0095	0.0159	0.0172
EF H3K36me3	-0.0189	-0.0014	0.0021	-0.0018	-0.0029	-0.0079	-0.0017	-0.0057	-0.0158	-0.0248	-0.0137
ES H4K20me3	0.0457	0.1074	0.0949	0.0325	0.0194	0.0282	0.0199	0.0327	0.0246	0.0351	0.0266
ES H3K4me3	-0.0056	0.0135	0.0066	0.0189	0.0162	0.0096	0.0160	0.0001	-0.0070	-0.0116	-0.0084
ES H3K9me3	0.0452	0.0902	0.0929	0.0443	0.0188	0.0292	0.0190	0.0337	0.0233	0.0305	0.0298
ES H3K27me3	0.0448	0.0405	0.0466	0.0344	0.0338	0.0263	0.0326	0.0227	0.0229	0.0231	0.0395
ES H3K36me3	-0.0161	-0.0010	-0.0031	-0.0040	0.0047	-0.0078	0.0028	0.0038	-0.0165	-0.0221	-0.0095
ES H3K4me3 (HMM)	-0.0080	0.0167	0.0254	0.0120	0.0266	0.0162	0.0205	-0.0086	-0.0050	-0.0054	-0.0067
ES H3K9me3 (HMM)	0.0373	0.0939	0.1475	0.0395	0.0864	-0.0032	0.0766	0.0715	0.0424	0.0195	0.0261
ES H3K27me3 (HMM)	0.0408	0.0385	0.0179	0.0179	0.0474	0.0323	0.0367	0.0037	-0.0053	0.0116	0.0138
ES H3K36me3 (HMM)	-0.0156	-0.0094	0.0120	-0.0049	-0.0104	-0.0050	-0.0118	-0.0046	-0.0096	-0.0155	-0.0144
ES H4K20me3 (HMM)	0.0476	0.0864	0.1825	0.0584	0.0869	0.0370	0.0747	0.0342	0.0459	0.0483	0.0263
ES H3K4me3 (WIN)	-0.0160	0.0055	0.0061	0.0081	0.0141	-0.0108	0.0143	-0.0033	0.0001	-0.0072	-0.0122
ES H3K9me3 (WIN)	0.0237	0.0649	0.1111	0.0301	0.0607	0.0218	0.0465	0.0158	0.0147	0.0318	0.0217
ES H3K27me3 (WIN)	0.0498	0.0364	0.0145	0.0173	0.0733	0.0039	0.0646	0.0301	0.0331	0.0294	0.0283
EF H3K4me3 (WIN)	-0.0089	0.0055	0.0434	0.0118	0.0135	0.0010	0.0102	0.0092	0.0045	-0.0045	-0.0137
EF H3K9me3 (WIN)	0.0104	0.0276	-0.0022	-0.0013	0.0057	0.0071	0.0031	-0.0018	-0.0020	0.0066	0.0035
EF H3K27me3 (WIN)	0.0173	0.0253	0.0091	0.0171	0.0154	0.0061	0.0135	-0.0001	0.0179	0.0137	0.0054
NP H3K4me3 (WIN)	-0.0188	-0.0109	0.0097	0.0116	-0.0001	0.0012	-0.0017	0.0009	0.0016	-0.0035	-0.0166
NP H3K9me3 (WIN)	-0.0037	-0.0027	-0.0012	-0.0008	-0.0050	-0.0017	-0.0048	-0.0017	-0.0017	-0.0023	-0.0066
NP H3K27me3 (WIN)	0.0440	0.0452	0.0145	0.0393	0.0261	0.0209	0.0158	0.0163	0.0481	0.0495	0.0374

For each gene region examined, the correlation coefficient (indicating the degree of correlation with imprinting status) for each of the features of interest included in our analysis is shown. Features that show positive correlation with imprinting are highlighted in green, while features that show negative correlation with imprinting are highlighted in red. ES stands for embryonic stem cells, EF stands for embryonic fibroblast cells, and NP stands for neural progenitor cells. HMM stands for enrichment as determined using a Hidden Markov Model, while WIN stands for enrichment as determined using a sliding window model (30).

Table A4. Genes included in the test data set.

Known Imprinted	Non-Imprinted	
Air	*Alx4*	*Ntf3*
Atp10a	*Bub1*	*Phoxa2*
Ddc	*Casr*	*Rxrn*
Dhcr7	*Cpt1a*	*Sall2*
Peg10	*Eln*	*Ski1*
Inpp5f_v2	*Gja5*	*Sod2*
Sfmbt2	*Hoxc13*	*Tbx4*
Tfpi2	*Inppl1*	*Trp35b2*
Th	*Kcna2*	*Vcl*
	Myh6	*Wrn*

A total of 29 genes, including known imprinted genes and non-imprinted genes, were included in the test data set. Nine genes fall within the known imprinted category, while 20 genes fall within the non-imprinted category. Genes in bold were called as imprinted at the stringency levels indicated in the text.

Table A5. Summary of microimprinted genes and hosts.

Microimprinted Gene	Microimprinted Gene Prediction	Host Gene	Host Gene Status	Host Gene Prediction
Inpp5f_v2	Imprinted	*Inpp5f*	Non-imprinted	Non-imprinted
Nap1l5	Imprinted	*Herc3*	Non-imprinted	Non-imprinted
Nnat1	Imprinted	*Blcap*	Imprinted	Non-imprinted
Peg13	Non-imprinted	*1810044AZ24Rik*	Imprinted	Non-imprinted
U2af1rs1	Imprinted	*Commd1*	Imprinted	Imprinted

Each of the five known microimprinted genes and their host genes is listed, along with the expression status of each host gene. Also indicated is the expression status predicted by our models for each gene and its host.

Table A6. Primers used for allele-specific expression assays.

Gene	-RT	Tissue Tested	MGI SNP ID	RE	Cross Needed	PCR (bp)	Expected AKR Bands (bp)	Expected PWK Bands (bp)	Forward (5' - 3')	Reverse (5' - 3')
6330405A18Rik	YES	P	rs30523543	ClaI	AKR/PWD	226	74/152	226	CCCGAATGACAAGTCAACCT	TTAGTGGGGATGCCTCTTTT
9430015G10Rik	YES	P	rs33232729	AluI	AKR/PWD	315	152/163	315	GCCACTGGCAGTTTATGGAT	CCATCCCCAGAGACACACCT
A830018L16Rik	YES	P	rs32537969	n/a	AKR/PWD	278	SEQUENCED	SEQUENCED	CAACTGCCCCGATTTGATTA	TTCATTAAAGCCCACCAAAAA
Arhgap18	YES	P	rs39149866	Tsp45I	AKR/PWD	396	396	175/221	CCATCGTCAAGACCCAGACT	CAAAAAGCCCTGGGGATAAT
Arhgef3	YES	P	rs6214108	n/a	AKR/PWD	317	SEQUENCED	SEQUENCED	TCGGCCACTCCTCTTTTCTA	TTTGAACCCATCCTTGCTCT
Ccr9	YES	P	rs48048570	n/a	AKR/PWD	386	SEQUENCED	SEQUENCED	GGATCTGGTGAAGACCCTGA	AGCATCCTCCTCAGAACTGC
Cflar	YES	P	rs13468974	n/a	AKR/PWD	296	SEQUENCED	SEQUENCED	GTTGTGTTTGCAGGGCCTAT	TGTAATGACTCCTTAAAATGAAACAGA
Cpm	YES	P	rs48284033	n/a	AKR/PWD	291	SEQUENCED	SEQUENCED	GACTTCATGCGGGTTTTTGT	AAGCTCAGAGGTAGTCATGGTC
Dlk1 (c)	YES	P	rs50424874	n/a	AKR/PWD	385	SEQUENCED	SEQUENCED	CCATCTGCTTCACCATCCTG	CGTTCACTCGATTCCACACA
Eif2b5	NO	P	rs48607872	HpyCH4III	AKR/PWD	390	145/245	70/75/245	GCTGGTTCAGCCAAAGAGAC	AGGGAAAGCTGGAACACAAA
Entpd1	YES	P	rs49894562	n/a	AKR/PWD	243	SEQUENCED	SEQUENCED	GGCCCTCTGCTCTTAACCTC	CTGCCTCCCCTCACTAAACA
Entpd1	YES	P	rs47465876	n/a	AKR/PWD	220	SEQUENCED	SEQUENCED	ATGTGCTCGTGAGCTAATG	TTTTTCCAATTCTGGGTGGT
Hmgcs2	YES	P	rs36506234	n/a	AKR/PWD	337	SEQUENCED	SEQUENCED	TGTTGAACCTTGAGGGAAGC	CCAACAATGGGACACAGAAA
Hs6st1	YES	P	rs31399915	n/a	AKR/PWD	351	SEQUENCED	SEQUENCED	ATGGGGACTTTCCCATTCTC	AGACAGAGGCAGGGAGTGTG
Isx	YES	P	rs13479838	RsaI	AKR/PWD	372	47/325	47/94/231	ATGACCCACAGTCCAGGAAG	TCAGCTAACCTGGGCAGAAT
Itsn1	YES	P	rs33601143	BstUI	AKR/PWD	393	393	75/318	CTGAGAAGGGAAAACCCACA	GTGGAATGTTGCAGAGCAGA
Kcnj15	YES	P	rs47548183	PleI	AKR/PWD	228	228	40/188	AGACAGCTTTCTGATGGCAAC	TCAGAGGTGCGTCTCTCCTT
Kdr	YES	P	rs33606899	n/a	AKR/PWD	365	SEQUENCED	SEQUENCED	TGTGTTGAGGATGGGTGAGA	AGCAAGCTGCATCATTTCCT
Laptm4b	YES	P	rs13460434	BsrGI	AKR/PWD	303	35/86/182	86/217	TCACACTCCCTTTTCCTTGG	TGCAGACAAACTTTAATTGCAAAG
Nefm	YES	P	rs31130948	AluI	AKR/PWD	616	81/82/127/134/192	81/82/85/107/127/134	AGTGGTGGTCACCAAGAAGG	TGTGCAGATCAGCAAGGTTC
Nlgn1	YES	P	rs33775315	BsoBI	AKR/PWD	616	616	173/443	CAGCTGGAGGGTTTGTCTTT	TCTTGAAAAAGGGTAGCTGGA
Pcdh21	YES	P	rs51706664	n/a	AKR/PWD	320	SEQUENCED	SEQUENCED	ATGATGAGGTTGGGAACAGC	AAATCCTCTGCTTTGCAGGA
Peg3 (c)	YES	P	rs45778768	HinFI	AKR/PWD	429	11/22/26/43/75/84/168	11/22/26/75/84/211	GGATGCACTGATGGGAAACT	GCTGGCAAGCTATGGATGAT
Ptpm2	NO	P	rs51240328	Sau96I	AKR/PWD	238	32/60/146	32/60/63/83	AGCACTTGAGGGACAGAGA	CTAGCCACTGCACTGACTG
Stk4	YES	P	rs27300226	n/a	AKR/PWD	399	SEQUENCED	SEQUENCED	GCAGTGGACTCTCTGCTTCC	TGCAGGATCTGCAGTGATGT
Tinagl	NO	P	rs27517674	HpaII	AKR/PWD	397	134/263	88/134/175	AGTACCGCAGACATGGGACT	AGCCTGGTGCATCTTTGTCT
Tmem169	YES	P	rs36357460	StyI	AKR/PWD	318	151/167	318	AGGAAGGGGAACAGGGATTA	CTGACCTCTTGGGACTCAGC
Tnpppc9	NO	P	rs31410905	NdeI	AKR/PWD	342	75/267	342	CGGTGTGCACAACTATGACC	AATAGGCCAGAAGCAAAGCA
Ubxd2	YES	P	rs13464870	RsaI	AKR/PWD	241	17/224	17/105/119	CTCAGGTCCAGGCTCAAGTC	GCCCAGCTCCATGTGTACTT
A530088H08Rik	NO	B/P	rs26891226	n/a	AKR/PWD	329	SEQUENCED	SEQUENCED	GATTGGCAGCACACTGATGT	TGGGCTTGTGGTAGATTTCC
Ankrd55	NO	B/P	rs47406379	DdeI	AKR/PWD	589	21/39/250/279	21/39/121/158/250	GCAGAAAGCCCATCAGAAAG	GTTTGGGGAGAGATGCTGAA
Art5	NO	B/P	rs31839713	n/a	AKR/PWD	374	SEQUENCED	SEQUENCED	AGCCACTTTAACTGCGCCTA	GCCATCCAGTTCTTTACCTTGC
Ccdc108	NO	B/P	rs49059569	Hpy188III	AKR/PWD	455	104/351	455	ACCAGCCGAATCCTGTAGTG	GCCCACCAGGTCTTCCTTAT
Cdh13	NO	B/P	rs37221381	Tsp45I	AKR/PWD	416	9/407	9/112/295	GTGCTCCTGGTCACGTCTG	GGCTGTCTCTGGTTCTCTGG
Cdh15	NO	B/P	rs36272769	Fnu4HI	AKR/PWD	294	5/289	5/83/206	CCCGAAATGTCTTCTCCATC	GGGCTGCATTGTCTGTCTCT
Cmah	NO	B/P	rs29888988	TaqaI	AKR/PWD	307	307	100/207	AACACAGTGGACTGCACCAG	TGTTGAGCTGATTTGGGTCA
Cntn3	NO	B/P	rs13478935	PciI	AKR/PWD	365	365	160/204	GGATGAGAAGCACTGTGTCG	TTCCAACCTCACAGTTGAACC
Ddo	NO	B/P	rs29357341	PmlI	AKR/PWD	332	199/133	332	CGGTGGATACCAGACTGCTT	AAGCCTGGCCAAACACATAC
Dennd1a	NO	B/P	rs27167794	n/a	AKR/PWD	793	SEQUENCED	SEQUENCED	ACCTTCTGGGCTGTCTGATT	CCCTTTGATGACCTCCAGA
Drd1a	YES	B/P	rs48196064	Cac8I	AKR/PWD	303	119/184	31/119/153	AAATAATTGGCCCTCCCTGT	CGATGAGGCACAGCTCATTA
Dusp27	NO	B/P	rs31389162	BstUI	AKR/PWD	458	458	167/291	AACCGAAAGCATCTTCATGG	TCCACCTCTGGGAAGTCATC
Enpp3	NO	B/P	rs50802743	Hpy99I	AKR/PWD	367	367	170/197	CAGGAAATGTCCCCATTTTG	GCTGGCACTGATGTCCCTAT
Etl4	NO	B/P	rs13476371	n/a	AKR/PWD	598	SEQUENCED	SEQUENCED	AGCGTGTGAGGAGCATGAC	ATGATGTTGGCCTGAGCTTC
Fbxo40	NO	B/P	rs46567644	BsaJI	AKR/PWD	413	1/60/149/203	1/149/263	TCAGGTGCTCAGACATGGAG	CCCTGGACAAAAAGCAAAAG
Gnao1	YES	B/P	rs32048898	DdeI	AKR/PWD	555	57/197/301	197/358	GTTTTCCTGGGACAGCACAT	TTCTAGCCTGGTCTGCCAGT
Hjurp	NO	B/P	rs47242786	BsmAI	AKR/PWD	359	359	155/204	CACGTAGCCATGGAGTCTA	GCTGCCTAGGATCACCAGAG
Hjurp	NO	B/P	rs47242786	BsmAI	AKR/PWD	431	119/312	119/155/157	CACGTAGCCATGGAGTCTA	ACGGCCTACCCATGATTGTC
Hlcs	NO	B/P	rs46075810	BsaHI	AKR/PWD	783	310/473	159/310/314	TCCGTAGCACATCTCTCCTG	ACAGGCTCCAGATGGACAAC
Kcnq2	NO	B/P	rs27665342	HinFI	AKR/PWD	663	15/20/71/118/178/261	15/20/118/178/439	CTGGAGCTGCTGAGGAATCT	GCGGTCCTTATCCGTTATTG
Klrb1f	YES	B/P	rs36918569	TaqaI	AKR/PWD	326	148/178	326	TTGACCCTATCCCCACTTCA	AGGACATCCCACTTTCATGC
Magel2 (c)	YES	B/P	rs33055130	n/a	AKR/PWD	330	SEQUENCED	SEQUENCED	GGGACATTGTGCTTTCTGGT	TTTTCTCCAGACGATATTTTACCG
Mamld3	NO	B/P	rs46281300/	Hpy99I	AKR/PWD	269	269	84/185	CAGCAGGTCAACCAGTTTCA	CTCTGATTGGAATGCTGCAA
Metaplt1	NO	B/P	rs28296173	n/a	AKR/PWD	363	SEQUENCED	SEQUENCED	CTCGTCCGTGGAGGTTGT	CCAATGAACAAGGGCATCTA
Mst1r	YES	B/P	rs33282822	BstNI	AKR/PWD	362	7/21/42/42/68/182	7/21/68/84/182	GTGAGGTGATCGTGCCATT	GGGGACCACGTACTTGACAC
Nefm	YES	B/P	rs30748232	BstNI	AKR/PWD	480	221/259	480	AAATCCCCTATGCCCAAATC	AGTGACCACCCCTTTCTCCT
Oxsm	NO	B/P	rs13482075	EagI	AKR/PWD	492	219/273	492	GGTGATACGCCTGCATCTTT	CAGCCCATTCTTTGTCCCTA
Parva	NO	B/P	rs32338767	AccI	AKR/PWD	468	468	222/246	ACGAGAAGGGATCCTCCAGT	CCAGGGTCTCACTCCACATT
Pigl	NO	B/P	rs26924902	Tsp45I	AKR/PWD	244	99/145	244	AGGAGGGAAGCTGCCTAAAG	CCGCAGTGAGTTGATTCTCA
Qpct	YES	B/P	rs52229296	n/a	AKR/PWD	320	SEQUENCED	SEQUENCED	TGATGCCTTCACTAATTTTCCTC	CATGAAAATAAATTCACAATATGCAA
Rasgrf1 (c)	NO	B/P	rs29947965	HinFI	AKR/PWD	355	59/134/162	59/296	GGCTCATGATGAATGCCTTT	TACAGAAGCTGGCGTTGTG
Scin	NO	B/P	rs49691441	AluI	AKR/PWD	485	124/361	106/124/255	TGAATTTGCATCAACGTCAAC	TTGATGCCTCAAAACTGCAC
Sfi1	NO	B/P	rs26899985	BaeGI	AKR/PWD	430	168/262	430	GTTCTGCTTGGTGGTTTGGT	GAGGTCCCCAGAGTGGTACA
Shcbp1	NO	B/P	rs51765774	PleI	AKR/PWD	471	67/406	67/149/257	TCACCATCATAGCAGGCATT	TGTGTTGAACCTCGACTGAGA
Slc38a1	NO	B/P	rs49654319	MspA1I	AKR/PWD	416	416	192/224	ATGAGAAGCTGGGAGAGCAA	AAGGTGACATACTTTGGTGTGC
Syt9	NO	B/P	rs49223695	Hpy188III	AKR/PWD	624	16/301/307	16/66/241/301	CACAGAGCCAACACCATCAG	GCCGTTGGAAGATAGCAGAG
Tlrm25	YES	B/P	rs27099824	n/a	AKR/PWD	293	SEQUENCED	SEQUENCED	ATTCATTGTACAGGGCAAGG	AGCAGGCTTATCCCTCATCA
Tnpc2	NO	B/P	rs31840788	Fnu4HI	AKR/PWD	246	159/57	246	AGAGAGTGCAGAGCCCAGAG	TGCTGGGGAAGAGTCTCAAT
Vil2	NO	B/P	rs13474581	SexAI	AKR/PWD	415	415	315/100	GAGCTTGTGTTGGTCCATGA	CGGGAAGCAGCTCTTTGAT
Wt1	YES	B/P	rs27444810	n/a	AKR/PWD	336	SEQUENCED	SEQUENCED	TGAAATTCCTCCCACTCACC	ACACATGCCCTGGCCTATAA
Wt1	YES	B/P	rs27444811	n/a	AKR/PWD	336	SEQUENCED	SEQUENCED	TGAAATTCCTCCCACTCACC	ACACATGCCCTGGCCTATAA
Zfp629	YES	B/P	rs33162562	HaeII	AKR/PWD	697	132/270/295	270/427	GGCAAGAGCTTTAGCCAGTG	TGGCACTCAGTGTGAAGGTC
Zfp810	NO	B/P	rs48701411	MspA1I	AKR/PWD	339	159/180	339	TCTATTCCCTGGAAGCTGGA	CCAGGCTGCTGTAAGTCTCC
Adam18	NO	B	rs36490947	SspI	AKR/PWD	594	SEQUENCED	SEQUENCED	TTGGTTGCAATACATGCACA	TGGGGAAATTTTTGTTTGACT
Bcmo1	NO	B	rs45757813	NciI	AKR/PWD	561	185/188/188	188/373	CAGGAAGACAGGAGGCTTTG	CCGGTAATCAACCTTCTCCA
Cyba2	NO	B	rs50671503	n/a	AKR/PWD	492	SEQUENCED	SEQUENCED	GGACTCTTCGAATGGACTGC	ACTGTGCCAACGTCTGTGAG
Hjurp	YES	B	rs30298180	n/a	AKR/PWD	336	SEQUENCED	SEQUENCED	CCCATGGCTAGAAATCTGGA	CACCCTTTGGCCTCTAAGTG
Hoxc4	NO	B	rs32322072	MspI	AKR/PWD	594	251	38/213	GTTAGCACGGGAGCGACTCT	GCAAGGGGCTTGTTTGTTTA
Mpv17l	YES	B	rs37484918	n/a	AKR/PWD	520	SEQUENCED	SEQUENCED	CCTCCTGCCTCTGCATTCTA	GCTGAAATGATCCTCCTCCA
Mrs2l	YES	B	rs37484918	HaeII	AKR/PWD	371	520	410/110	CCTTGGAAGACAGCTGGAAG	GCGAGGAAGTGAGGTCTGTG
Neurod2	YES	B	rs27071146	Cac8I	AKR/PWD	336	SEQUENCED	SEQUENCED	AACCCAAGTTTGGGAATGTG	AGCTCAACGCATTTTTCCAT
Rpo1-4	NO	B	rs30703724	BsmAI	AKR/PWD	553	63/475	63/115/360	GCCTGCACTGATCAGCAGTAT	GCTGGAGGTAGGCAGTGAAG
Tbl1xr1	YES	B	rs36665902	n/a	AKR/PWD	326	SEQUENCED	SEQUENCED	AGAACATCCCCAAGGCACATC	ATAACCTCCCTGCAATGGTG
Th	NO	B	rs33824309	Hpy99I	AKR/PWD	634	132/502	132/159/343	TGAAGCCAAAATCCACCACT	GGCATGACGGATGTACTGTG
Tmed4	NO	B	rs26899778	AclI	AKR/PWD	369	369	181/188	GGTTCTCCAAGAAGCAGACG	GTCTGGACTGGTGGTTTTCG
9530015I07Rik	NO	n/a	rs50181318	HpyCH4III	AKR/PWD	435	196/249	435	GGAAAATTGGCAAGACCAGA	GTGTGCATCCTCATGTGTCC
AK016821	NO	n/a	rs37897697	NlaIII	AKR/PWD	408	147/261	408	TGAGAAACCCCAGACTTGGA	TCTCGCTTGCACAAGACTGT
AK046026	YES	n/a	rs49964787	BsoBI	AKR/PWD	521	132/389	521	CCCAACACAATAGCTGCTGA	AAGGTGAAAAGGGCAGGACT
Rasd2	YES	n/a	rs31959150	n/a	AKR/PWD	326	SEQUENCED	SEQUENCED	CAGGAAAGGTTGGAAGGACA	GACCTGGGCCTTGAGAGAAT
Rnf36	NO	n/a	rs27425655	MspA1I	AKR/PWD	419	178/241	419	CAAAGCCAAGTTGCCTGACT	AGGTTCTCTCCATGCTCTGG
Ugt1a1	YES	n/a	rs30305269	BsrDI	AKR/PWD	411	411	180/231	TGAAAGTCAAAAGGGATTCCA	GGCTCAGAAGATCCTGGACA

* n/a in "Tissue Tested" column= either primer pairs that did not amplify or genes that, upon experimental testing, did not actually contain a SNP between the two mouse stains used. (c) = known imprinted genes used as expression controls.

Figure Legends

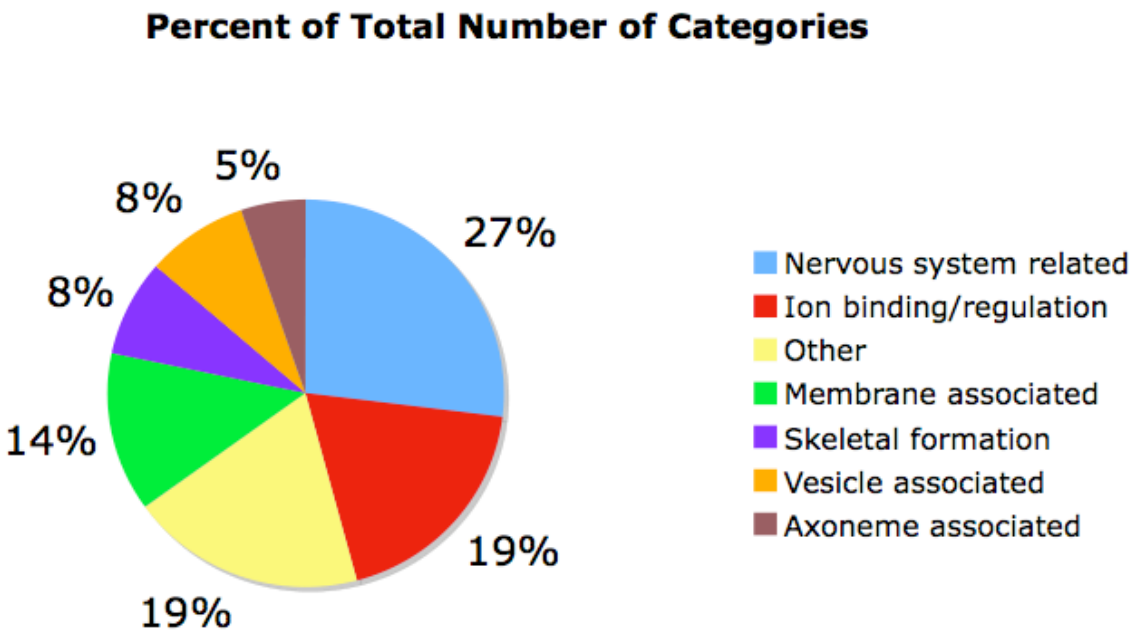
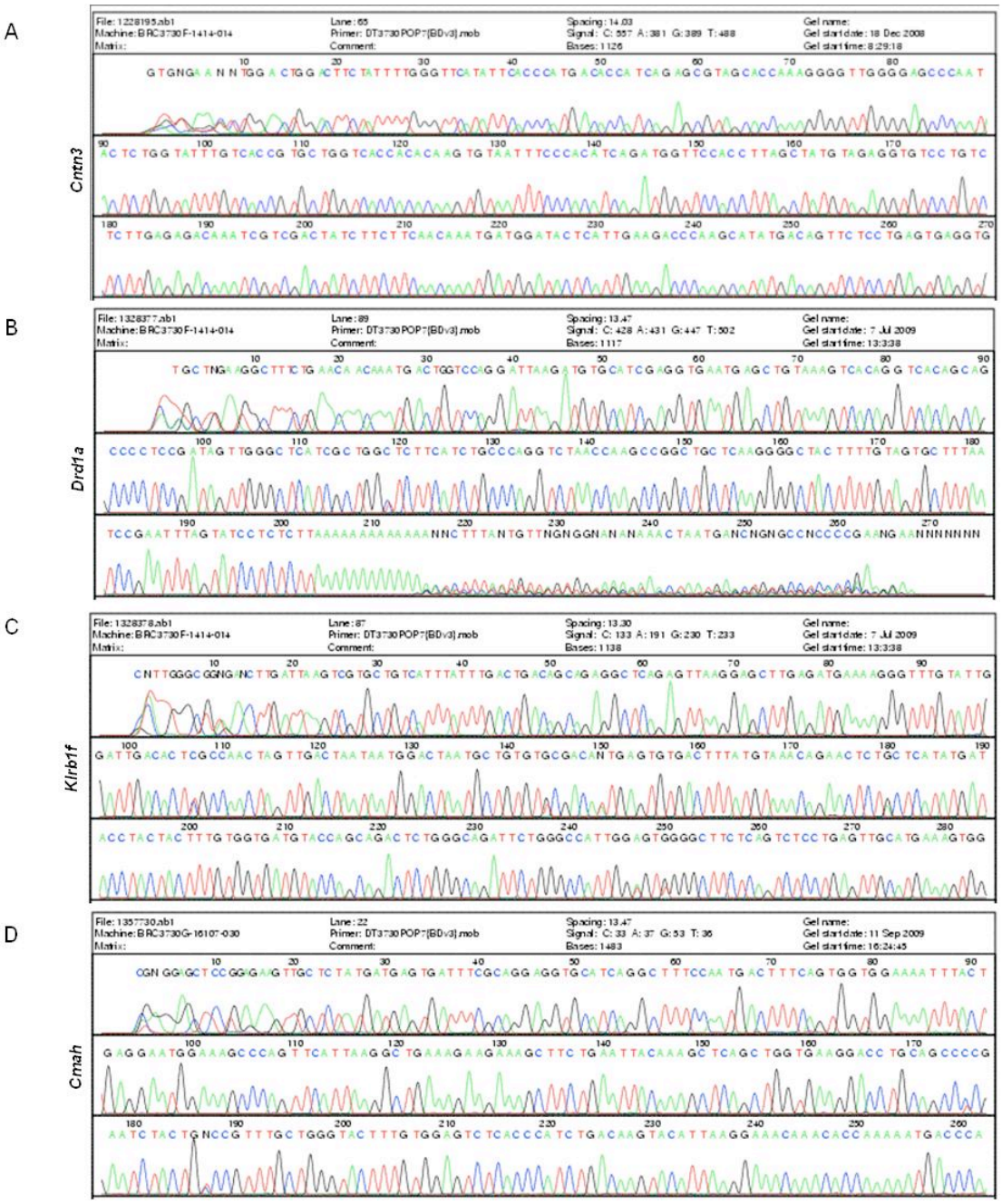


Figure A1. Gene ontology categories overrepresented in both known imprinted genes and predicted imprinted genes. To identify any trends in function among imprinted genes, known imprinted genes included in the training array, as well as our initial list of 155 candidate imprinted genes, were analyzed with GOEAST (http://omicslab.genetics.ac.cn/GOEAST/php/batch_genes.php), which identified gene ontology (GO) classes that are statistically overrepresented in imprinted genes. 209 GO classes are overrepresented in known imprinted genes ($p<0.05$) and 103 GO classes are overrepresented in the candidate imprinted genes ($p<0.05$). 37 categories that are overrepresented in the candidates gene set are similar to categories overrepresented in the known imprinted gene set. Within the 37 similar GO categories, several trends appear: 27.0% of the 37 similar GO categories are

nervous system related, 18.9% are implicated in ion binding/regulation, and 13.5% are membrane related.


A
Cntn3
B
Drd1a
C
Klrb1f
D
Cmah

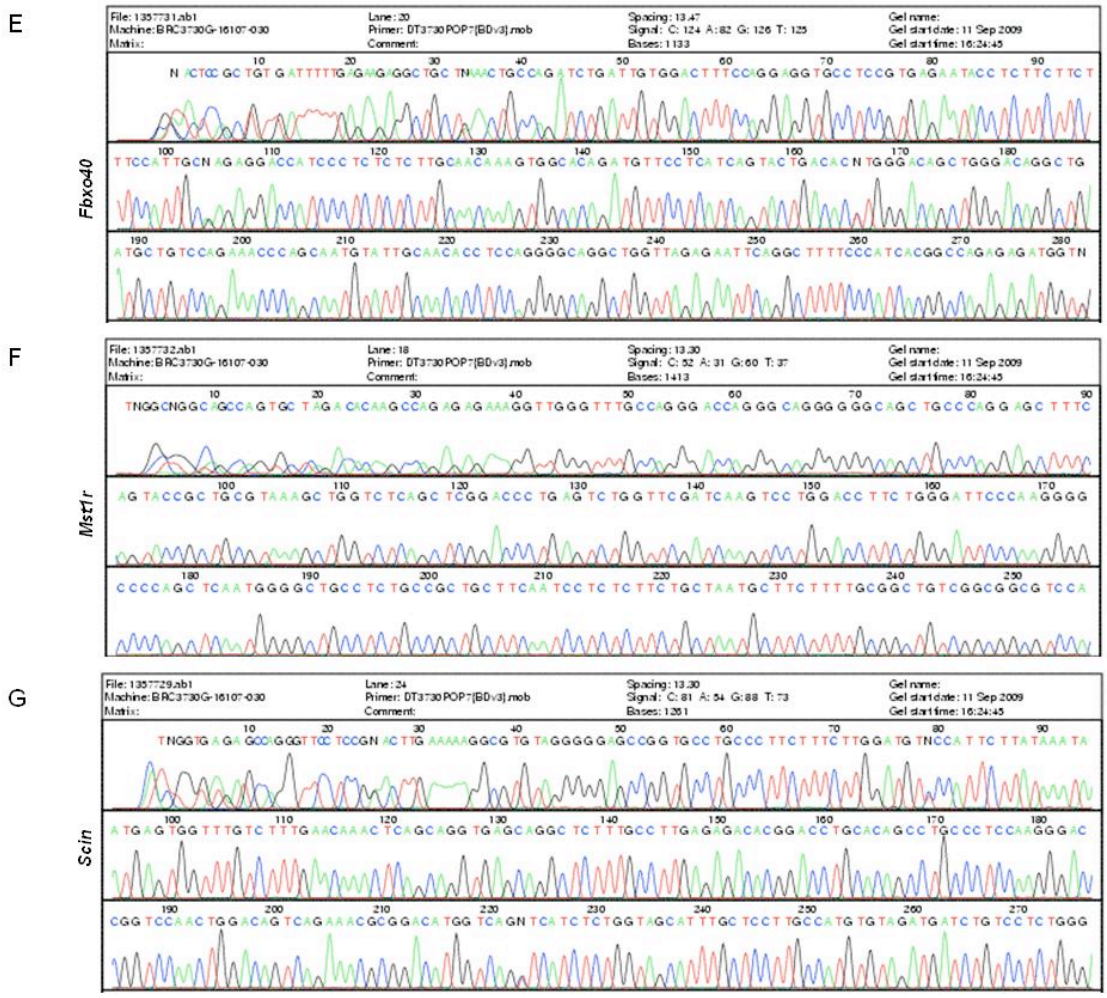


Figure A2. Sequence trace files of *Cntn3, Drd1a, Klrb1f*, *Cmah*, *Fbxo40*, *Mst1r*, and *Scin* PCR products. Sequence trace files of gel-purified PCR products from primers amplifying *Cntn3* (panel A), *Drd1a* (panel B), *Klrb1f* (panel C) *Cmah* (panel D), *Fbxo40* (panel E), *Mst1r* (panel F), and *Scin* (panel G). Sequencing results confirm that the expected products were amplified and that products are specific to the genes indicated.

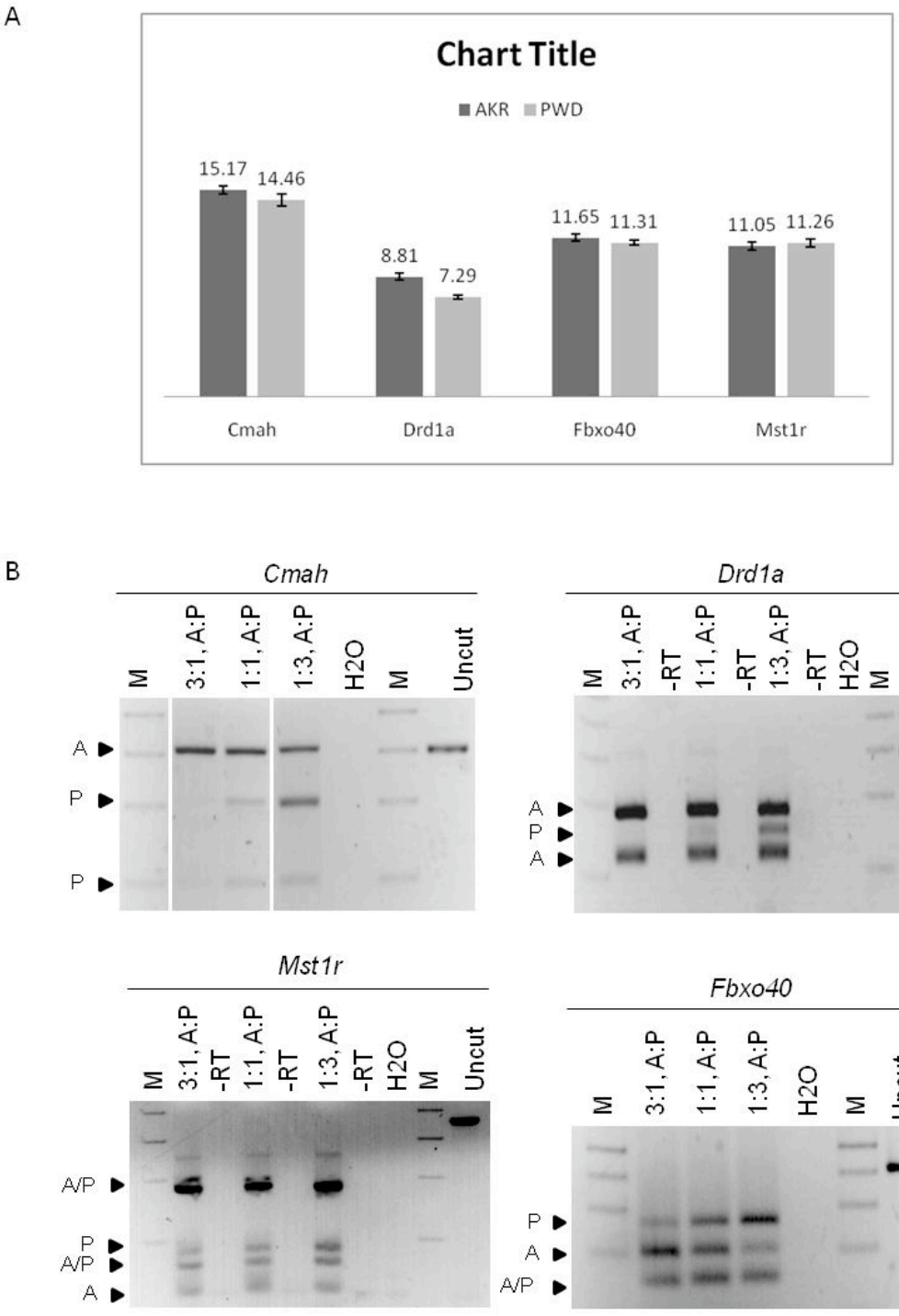


Figure A3. Expression and amplification bias of *Cmah, Drd1a, Fbxo40* and *Mst1r.* In panel A, cDNA prepared from the AKR and PWD pure inbred strains was subjected to quantitative real-time PCR (qRT). Amplification for each gene was done in triplicate, and results were normalized to *Rpl32* and *Tuba2* internal

controls. Normalized Ct values for AKR (dark grey bars) and PWD (light grey bars) are shown for each of the four genes analyzed. A lower Ct value indicates higher levels of expression. The expression in the AKR and PWD strain backgrounds is roughly equal for *Cmah, Fbxo40*, and *Mst1r.* The expression of *Drd1a* is higher in the PWD strain background. Error bars show standard error. In panel B, the same cDNAs were mixed in 3:1 (AKR:PWD), 1:1 (AKR:PWD), and 1:3 (AKR:PWD) ratios and PCR amplified with the same primer pairs used for the imprinting analysis. After PCR amplification, PCR products were digested with the same restriction enzyme used for imprinting analysis. *Cmah* and *Drd1a* show an amplification bias for the AKR allele, while *Fbxo40* and *Mst1r* show no amplification bias. M = 1kb+ DNA marker. A:P = AKR:PWD. A = AKR. P = PWD.

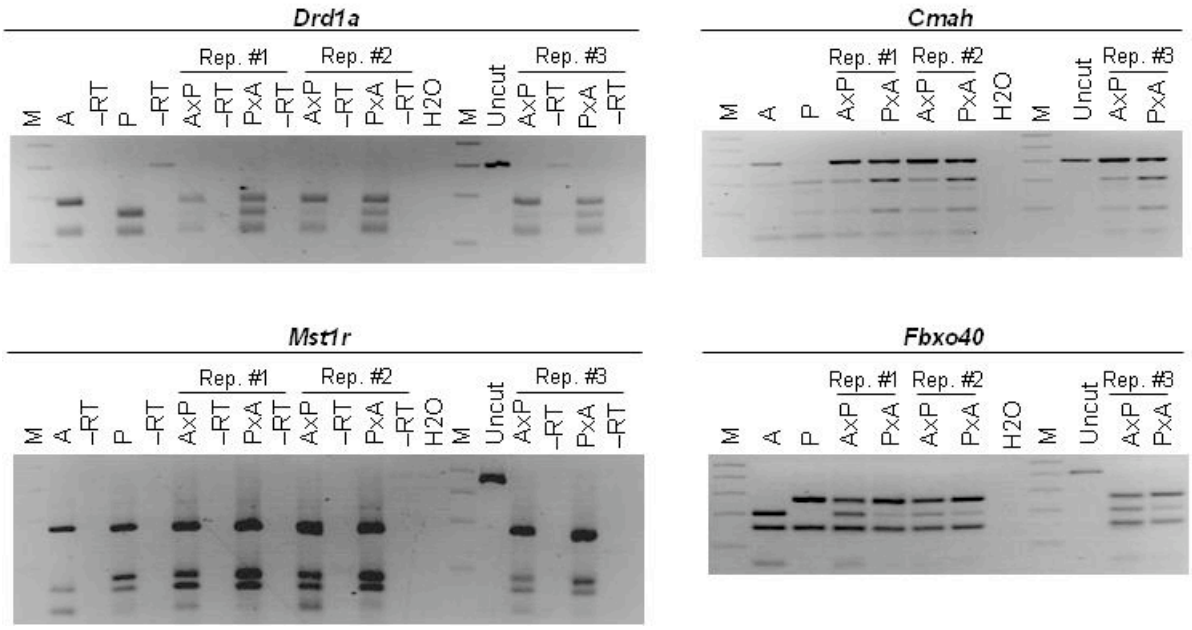


Figure A4. Additional biological replicate confirms maternal expression of *Drd1a, Cmah, Mst1r,* and *Fbxo40.* We PCR amplified placental cDNA from e17.5 embryos prepared using reciprocal crosses between AKR/J (A) and PWD/PhJ (P) mice, as well as from the parental strains. In the figure labels, the maternal strain is written first. PCR primers were specific *Drd1a, Cmah, Mst1r, and Fbxo40*. PCR products were digested overnight with restriction enzymes specific for one parental allele and run on 3% agarose gels. All 4 genes reproducibly show expression patterns consistent with maternal allele expression, as seen in Figure 2. The addition of a third biological replicate for each gene, shown on the far right-hand side of each gel under the heading Rep. #3, further confirms the results seen in Figure 2. M = 1kb+ DNA marker. A = AKR. P = PWD. Rep. # = biological replicate number.

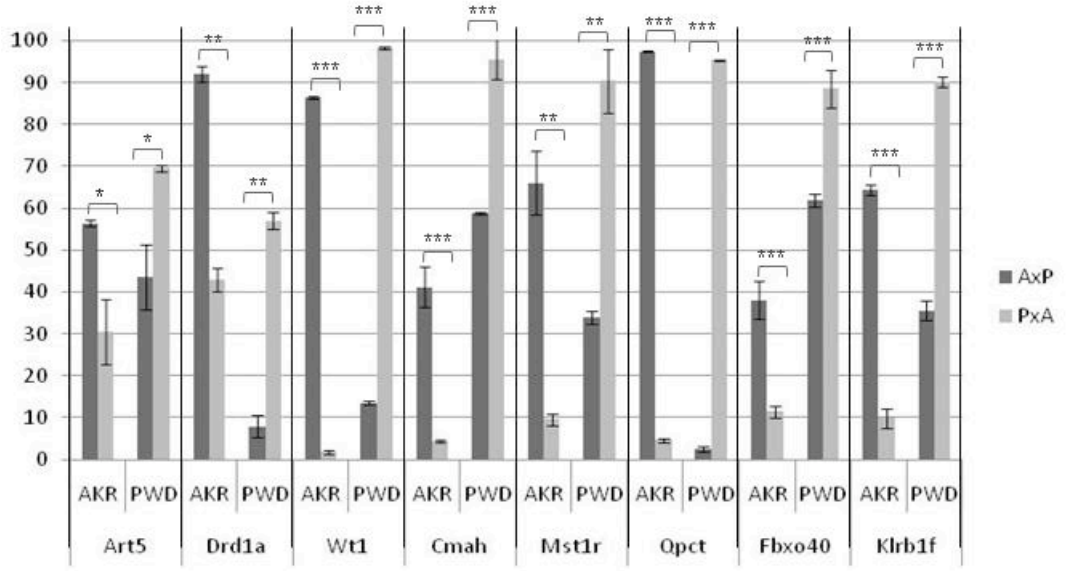


Figure A5. Quantitation of AKR and PWD allele-specific expression. The expression level of the AKR and PWD alleles was determined as previously described using Sanger sequencing and the Peak Picker2 software (10 and 35). Briefly, F1 genomic DNA and two to three cDNA biological replicates from both the AKRxPWD and the PWDxAKR crosses were amplified by standard PCR using the primers in Table A6. PCR products were gel-purified (Qiaex Quick Spin, Qiagen) then Sanger sequenced. The sequence trace files were analyzed using the PeakPicker2 software. For each gene, the expression level for each allele is reported as a percentage out of 100. Error bars represent standard error. Each gene was queried by at least one SNP and, whenever possible, data from multiple SNPs were used. For *Wt, Cmah,* and *Fbxo40,* two SNPs were available. Three and six SNPs were available for *Qpct* and *Klrb1f*, respectively. Data reported represent combined results from all available SNPs. Differences in allelic expression levels between the two reciprocal crosses were significant in every case, as determined by a one-tailed T-test.

AxP = AKR mother crossed to PWD father. PxA = PWD mother crossed to AKR father. * = p-value < 0.05. ** = p-value<0.005. *** = p-value<0.001.