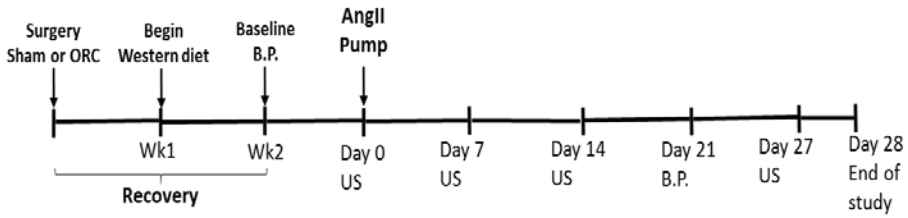
SUPPLEMENTAL MATERIAL

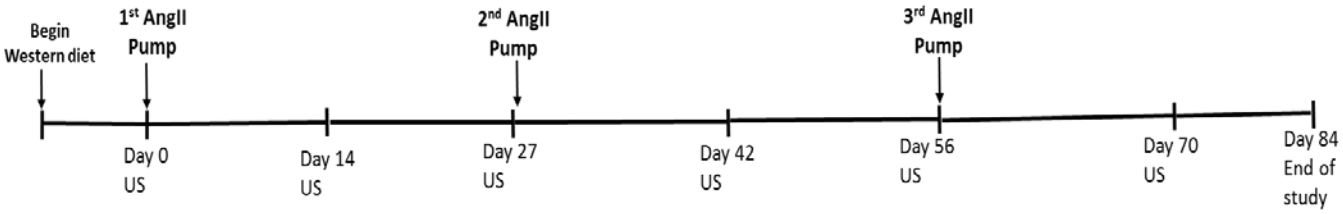
A. AAA formation study:

Groups:
1. XY males (sham) 2. XX males (sham)
3. XY males (ORC) 4. XX males (ORC)

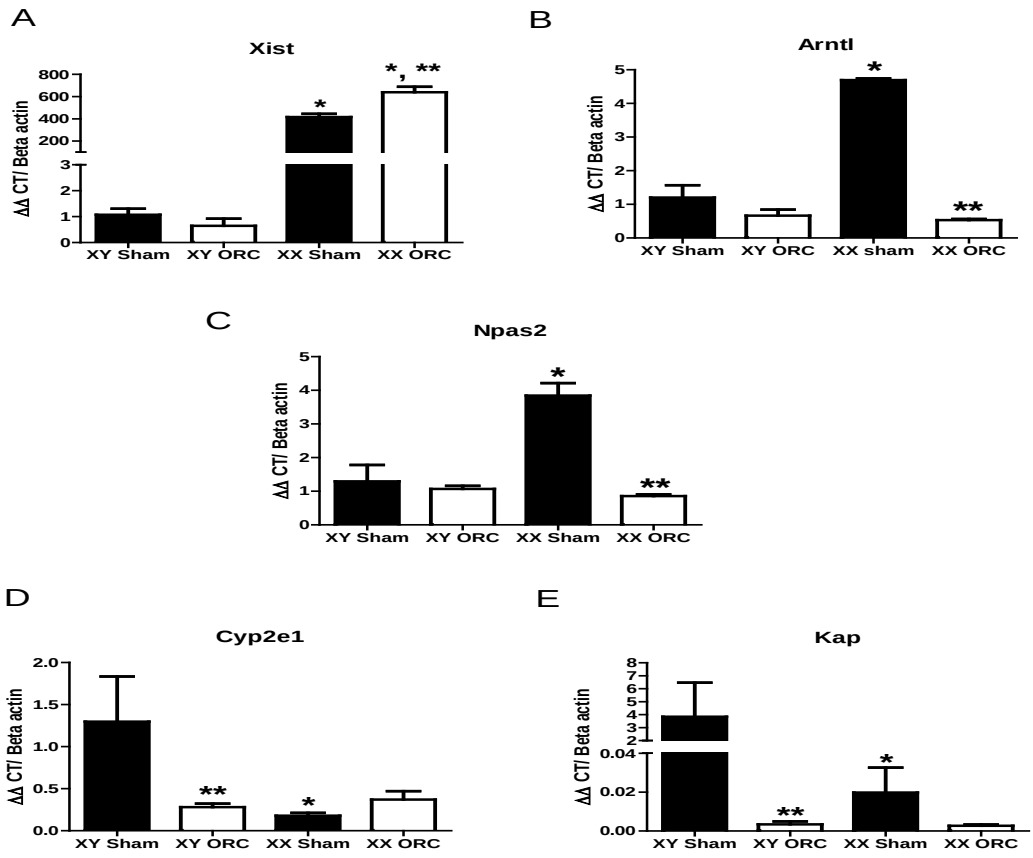


B. AAA Progression study:

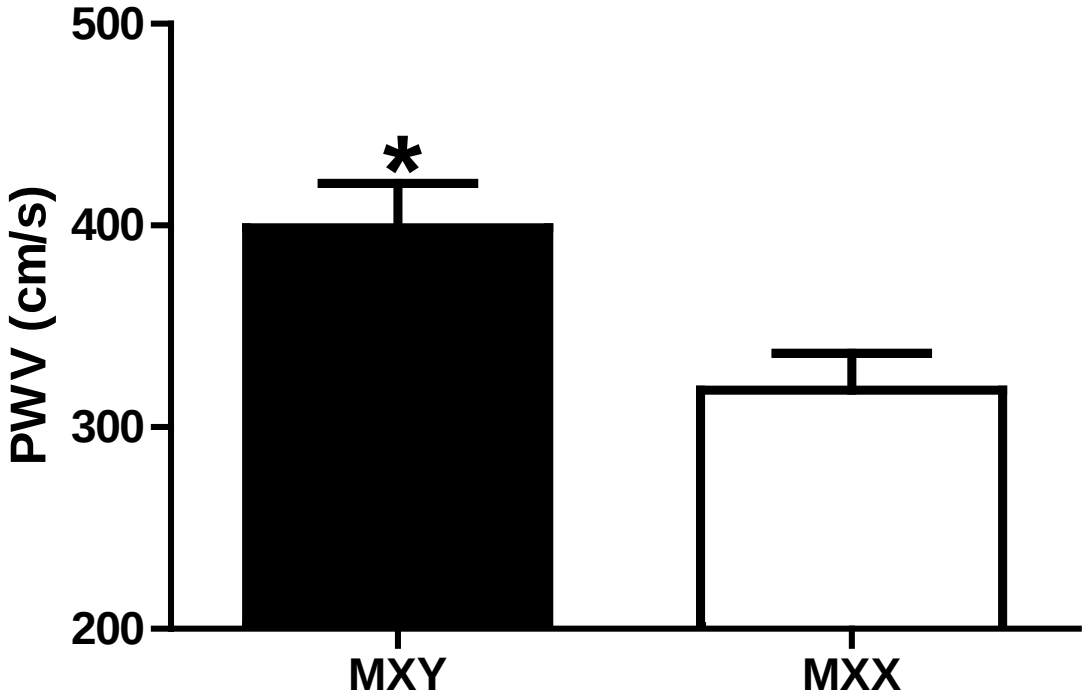
Groups:
1. XY males (intact) 2. XX males (intact)



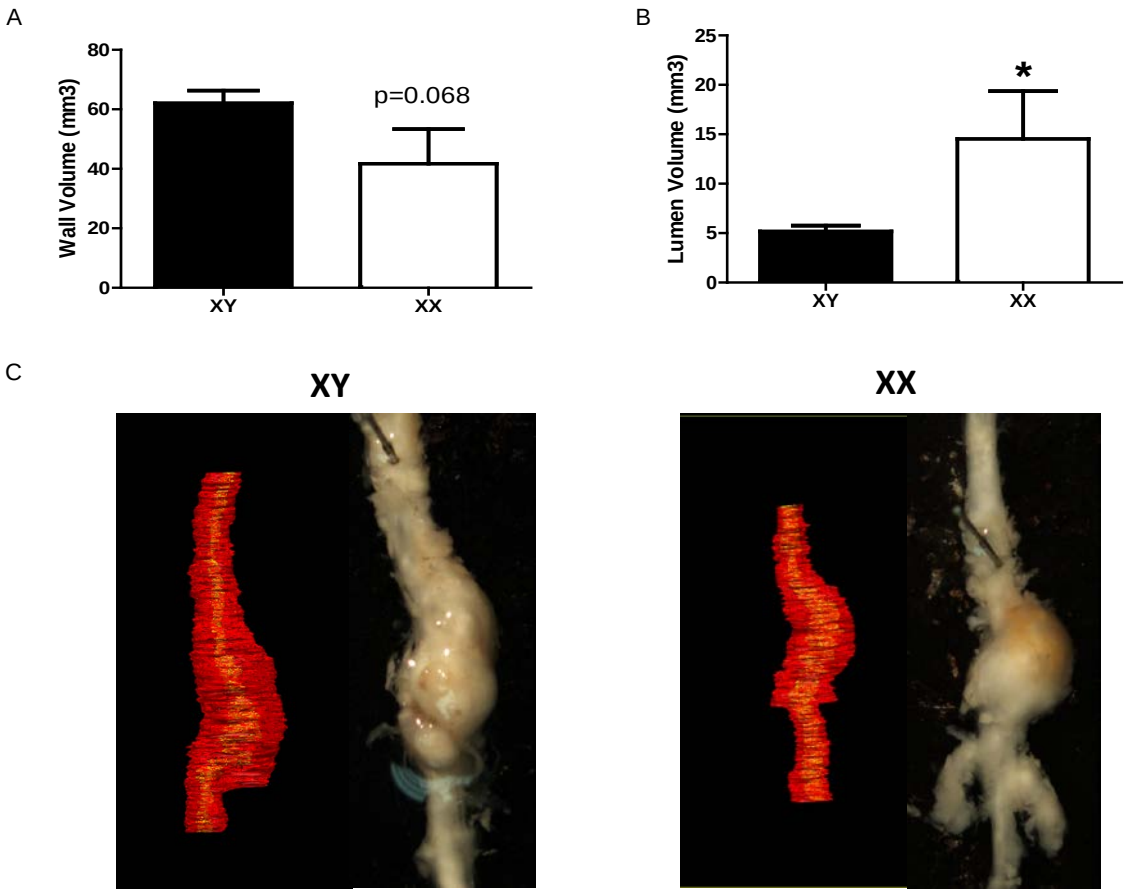
Supplemental Figure I. Graphic depiction of experimental design for studies focused on the formation (A) *versus* the progression (B) of AngII-induced AAAs.



Supplemental Figure II. RT-PCR analysis of mRNA abundance of key genes in abdominal aortas from male XY and XX mice (sham, orchiectomized, ORC). A-C, mRNA abundance of genes (A, *Xist*; B, *Arntl*; C, *Npas2*) exhibiting increased expression in gene arrays from abdominal aortas of XY compared to XX male mice. D,E, mRNA abundance of genes (D, *Cyp2e1*; E, *Kap*) exhibiting increased expression in gene arrays from abdominal aortas of XY compared to XX male mice. Data are mean ± SEM from n = 4-5 mice/group. *, P<0.05 compared to XY within surgical group as defined by two-way ANOVA with genotype and surgery as between group factors. **, P<0.05 compared to sham-operated within genotype as defined by two-way ANOVA with surgery and genotype as between group factors and Holm-Sidak post hoc analysis.



Supplemental Figure III. Pulse Wave Velocity (PWV) from male XY and XX *Ldlr*$^{-/-}$ mice. Data are mean ± SEM from n = 6 mice/group. *, P<0.05 compared to XY as defined by Student's t-test.



Supplemental Figure IV. Ex vivo ultrasound analysis of AAAs from XY and XX male mice infused with AngII for 3 months. A, Wall volume. B, Abdominal aortic lumen volume. C, Representative 3-D reconstructions of AAAs of mice from each genotype. Data are mean ± n = 5 mice/group that survived the study protocol. *, P<0.05 compared to XY as defined by Student's t-test.

Supplemental Table I

Annotations			Summary Statistics				2 way ANOVA p-values		
Probe Set ID	Symbol	Description	XY sh	XY Or	XX sh	XX Or	XY vs XX	Sh vs Or	Intrxn
TC0800001327.mm.1	Aars	alanyl-tRNA synthetase	7.49 ± 0.02	7.39 ± 0.02	7.38 ± 0.02	7.36 ± 0.02	0.00272	0.00377	0.05425
TC1100004000.mm.1	Abca9	ATP-binding cassette, sub-family A (ABC1), member 9	8.36 ± 0.07	8.06 ± 0.04	8.22 ± 0.06	7.93 ± 0.11	0.17682	0.00315	0.75664
TC0100002601.mm.1	Abcb6	ATP-binding cassette, sub-family B (MDR/TAP), member 6	6.24 ± 0.05	6.08 ± 0.05	6.04 ± 0.04	6.19 ± 0.03	0.25045	0.79884	0.00306
TC1400002714.mm.1	Abcc4	ATP-binding cassette, sub-family C (CFTR/MRP), member 4	7.14 ± 0.08	6.83 ± 0.06	6.92 ± 0.06	7.06 ± 0.02	0.7407	0.10789	0.00188
TC0500002085.mm.1	Abcf2	ATP-binding cassette, sub-family F (GCN20), member 2	8.55 ± 0.03	8.51 ± 0.04	8.37 ± 0.04	8.35 ± 0.05	0.00095	0.66706	0.97799
TC0800000073.mm.1	Abhd13	abhydrolase domain containing 13	7.34 ± 0.05	7.39 ± 0.04	7.33 ± 0	7.17 ± 0.03	0.00388	0.10663	0.02156
TC0900001348.mm.1	Abhd14b	abhydrolase domain containing 14b	7.92 ± 0.03	8.04 ± 0.07	8.17 ± 0.03	8.15 ± 0.02	0.00079	0.25826	0.11373
TC1100001127.mm.1	Abhd15	abhydrolase domain containing 15	7.08 ± 0.13	6.66 ± 0.15	6.54 ± 0.15	7.05 ± 0.05	0.35942	0.9749	0.00189
TC0900001638.mm.1	Abhd5	abhydrolase domain containing 5	8.66 ± 0.11	8.33 ± 0.09	8.01 ± 0.12	8.4 ± 0.05	0.01013	0.8602	0.00306
TC1900001711.mm.1	Ablim1	actin-binding LIM protein 1	7.43 ± 0.03	7.38 ± 0	7.3 ± 0.03	7.4 ± 0.01	0.0193	0.51627	0.00253
TC0600000572.mm.1	Abp1	amiloride binding protein 1 (amine oxidase, copper-containing	4.6 ± 0.03	4.75 ± 0.04	4.58 ± 0.04	4.73 ± 0.06	0.76206	0.00328	0.99043
TC1500001446.mm.1	Abra	actin-binding Rho activating protein	6.74 ± 0.19	7.45 ± 0.12	7.35 ± 0.21	6.81 ± 0.11	0.82783	0.72033	0.00317
TC0200001535.mm.1	Abtb2	ankyrin repeat and BTB (POZ) domain containing 2	7.48 ± 0.14	7.65 ± 0.04	7.99 ± 0.09	7.45 ± 0.05	0.14003	0.09297	0.0031
TC0900003334.mm.1	Acad11	acyl-Coenzyme A dehydrogenase family, member 11	8.3 ± 0.2	8.17 ± 0.21	7.64 ± 0.25	8.64 ± 0.1	0.36463	0.11266	0.00598
TC1100003073.mm.1	Acap1	ArfGAP with coiled-coil, ankyrin repeat and PH domains 1	5.23 ± 0.03	5.46 ± 0.03	5.35 ± 0.04	5.54 ± 0.08	0.08933	0.0008	0.81482
TC1100001767.mm.1	Ace	angiotensin I converting enzyme (peptidyl-dipeptidase A) 1	10.49 ± 0.13	10.1 ± 0.07	10.66 ± 0.07	9.84 ± 0.11	0.93978	0.00014	0.03487
TSUnmapped000000	Ache	acetylcholinesterase (Ache), transcript variant 1, mRNA.	8.2 ± 0.79	6.68 ± 0.47	5.59 ± 0.25	8.08 ± 0.33	0.42883	0.27989	0.00549
TC1200000798.mm.1	Acot1	acyl-CoA thioesterase 1	6.6 ± 0.09	6.74 ± 0.1	6.41 ± 0.11	7.04 ± 0.14	0.85238	0.0061	0.02299
TC1200000799.mm.1	Acot4	acyl-CoA thioesterase 4	5.04 ± 0.1	5.3 ± 0.11	4.88 ± 0.07	5.36 ± 0.08	0.36976	0.00457	0.14077
TC1100004107.mm.1	Acox1	acyl-Coenzyme A oxidase 1, palmitoyl	9.7 ± 0.13	9.47 ± 0.17	9.17 ± 0.19	9.9 ± 0.05	0.49443	0.21431	0.00277
TC0900001900.mm.1	Acp5	acid phosphatase 5, tartrate resistant	9.03 ± 0.12	8.78 ± 0.12	8.64 ± 0.12	9.11 ± 0.08	0.49532	0.57734	0.00345
TC0900002889.mm.1	Acpl2	acid phosphatase-like 2	5.84 ± 0.05	5.96 ± 0.02	6.03 ± 0.05	5.89 ± 0.01	0.09418	0.98064	0.00382
TC0800000538.mm.1	Acsl1	acyl-CoA synthetase long-chain family member 1	11.55 ± 0.12	11.29 ± 0.17	10.68 ± 0.25	11.61 ± 0.06	0.06472	0.09771	0.00149
TC1000002814.mm.1	Acss3	acyl-CoA synthetase short-chain family member 3	8.01 ± 0.24	7.34 ± 0.27	7.25 ± 0.26	7.85 ± 0.11	0.36745	0.60279	0.00803
TC0200003576.mm.1	Acvr1c	activin A receptor, type IC	7.79 ± 0.19	7.23 ± 0.2	7.01 ± 0.18	7.47 ± 0.03	0.08455	0.56857	0.00636
TC0200005097.mm.1	Ada	adenosine deaminase	6.28 ± 0.06	6.47 ± 0.06	6.54 ± 0.06	6.39 ± 0.05	0.12204	0.69859	0.00965
TC0700004431.mm.1	Adam12	a disintegrin and metallopeptidase domain 12 (meltrin alpha)	6.69 ± 0.12	6.47 ± 0.08	6.24 ± 0.11	6.69 ± 0.14	0.1952	0.58934	0.00589
TC0300002348.mm.1	Adam15	a disintegrin and metallopeptidase domain 15 (metargidin)	7.96 ± 0.04	7.85 ± 0.02	8 ± 0.04	7.83 ± 0.02	0.62531	0.00109	0.27884
TC1200001490.mm.1	Adam17	a disintegrin and metallopeptidase domain 17	7.9 ± 0.03	7.82 ± 0.06	7.89 ± 0.02	7.72 ± 0.04	0.14553	0.00644	0.31287
TC0800001901.mm.1	Adam9	a disintegrin and metallopeptidase domain 9 (meltrin gamma)	9.76 ± 0.07	9.63 ± 0.02	9.7 ± 0.04	9.37 ± 0.07	0.01443	0.00114	0.09377
TC1600001974.mm.1	Adamts1	a disintegrin-like and metallopeptidase (reprolysin type) with t	9.13 ± 0.2	9.6 ± 0.15	8.77 ± 0.12	8.69 ± 0.16	0.00329	0.21974	0.10093
TC1500000090.mm.1	Adamts12	a disintegrin-like and metallopeptidase (reprolysin type) with t	7.41 ± 0.07	6.93 ± 0.06	7.12 ± 0.04	6.83 ± 0.09	0.01294	7.1E-05	0.17517

Supplemental Table I

Annotations			Summary Statistics				2 way ANOVA p-values		
Probe Set ID	Symbol	Description	XY sh	XY Or	XX sh	XX Or	XY vs XX	Sh vs Or	Intrxn
TC0900001973.mm.1	Adamts15	a disintegrin-like and metallopeptidase (reprolysin type) with t	7.57 ± 0.15	7.41 ± 0.12	7.75 ± 0.11	6.98 ± 0.15	0.53718	0.00861	0.02614
TC1100000547.mm.1	Adamts2	a disintegrin-like and metallopeptidase (reprolysin type) with t	9.85 ± 0.11	9.58 ± 0.03	9.83 ± 0.07	9.22 ± 0.11	0.11031	0.00064	0.04492
TC1600001976.mm.1	Adamts5	a disintegrin-like and metallopeptidase (reprolysin type) with t	9.16 ± 0.1	8.85 ± 0.05	9.65 ± 0.08	8.83 ± 0.13	0.04451	3.8E-05	0.02943
TC0600002756.mm.1	Adamts9	a disintegrin-like and metallopeptidase (reprolysin type) with t	7.57 ± 0.06	7.56 ± 0.12	7.13 ± 0.04	7.29 ± 0.03	0.00015	0.43745	0.16705
TC1000002497.mm.1	Adamtsl5	ADAMTS-like 5	7.49 ± 0.08	7.77 ± 0.04	7.84 ± 0.08	7.64 ± 0.03	0.12609	0.5152	0.0034
TC1100001196.mm.1	Adap2	ArfGAP with dual PH domains 2	7.46 ± 0.09	7.02 ± 0.11	7.21 ± 0.04	7.01 ± 0.08	0.25757	0.00554	0.3019
TC0100000039.mm.1	Adhfe1	alcohol dehydrogenase, iron containing, 1	8.13 ± 0.16	7.79 ± 0.17	7.55 ± 0.19	8.24 ± 0.04	0.42315	0.51418	0.00234
TC1600000331.mm.1	Adipoq	adiponectin, C1Q and collagen domain containing	9.07 ± 0.12	8.65 ± 0.18	8.45 ± 0.18	9 ± 0.06	0.25456	0.77357	0.0028
TC0600003017.mm.1	Adipor2	adiponectin receptor 2	9.71 ± 0.13	9.38 ± 0.17	9.04 ± 0.19	9.59 ± 0.03	0.07335	0.68299	0.00453
TC0900000746.mm.1	Adpgk	ADP-dependent glucokinase	7.22 ± 0.06	7.33 ± 0.01	7.17 ± 0.06	7.06 ± 0.04	0.00996	0.81094	0.03493
TC0200004660.mm.1	Adra1d	adrenergic receptor, alpha 1d	8.16 ± 0.08	8.5 ± 0.07	8.41 ± 0.03	8.32 ± 0.02	0.66608	0.07652	0.00555
TC0800001955.mm.1	Adrb3	adrenergic receptor, beta 3	7.71 ± 0.14	7.21 ± 0.23	7.11 ± 0.22	7.74 ± 0.1	0.5986	0.98298	0.00396
TC1300001868.mm.1	Adtrp	androgen dependent TFPI regulating protein	7.27 ± 0.18	6.86 ± 0.21	6.38 ± 0.27	7.47 ± 0.13	0.31208	0.21738	0.00133
TC1000000903.mm.1	Aes	amino-terminal enhancer of split	10.99 ± 0.03	11.02 ± 0.02	11.11 ± 0.02	11.09 ± 0.03	0.00485	0.82482	0.46693
TC0500000303.mm.1	Agbl5	ATP/GTP binding protein-like 5	5.76 ± 0.01	5.89 ± 0.01	5.87 ± 0.01	5.93 ± 0.04	0.0072	0.00103	0.13473
TC1500001689.mm.1	Ago2	argonaute RISC catalytic subunit 2	8.93 ± 0.05	8.93 ± 0.02	8.82 ± 0.03	8.72 ± 0.07	0.00732	0.37346	0.28099
TC0800001883.mm.1	Agpat6	1-acylglycerol-3-phosphate O-acyltransferase 6 (lysophospha	8.75 ± 0.13	8.58 ± 0.14	8.18 ± 0.12	8.74 ± 0.1	0.06674	0.25133	0.0062
TC0500000987.mm.1	Agpat9	1-acylglycerol-3-phosphate O-acyltransferase 9	7.34 ± 0.08	6.99 ± 0.13	6.85 ± 0.05	7.06 ± 0.02	0.0157	0.33909	0.00281
TC0900000666.mm.1	Agphd1	aminoglycoside phosphotransferase domain containing 1	5.47 ± 0.04	5.29 ± 0.04	5.49 ± 0.05	5.25 ± 0.11	0.91289	0.00871	0.49501
TC1100002364.mm.1	Ahsa2	AHA1, activator of heat shock protein ATPase 2	7.22 ± 0.09	7.28 ± 0.09	6.98 ± 0.04	7.01 ± 0.03	0.00646	0.50009	0.74899
TC0300003147.mm.1	Ak5	adenylate kinase 5	5.57 ± 0.03	5.79 ± 0.04	5.65 ± 0.02	5.63 ± 0.04	0.31237	0.00486	0.00129
TC0300001154.mm.1	Aknad1	AKNA domain containing 1	6.04 ± 0.16	6.41 ± 0.07	6.61 ± 0.1	6.18 ± 0.1	0.22906	0.71271	0.00718
TC1300001377.mm.1	Akr1c18	aldo-keto reductase family 1, member C18	4.52 ± 0.08	4.77 ± 0.02	4.5 ± 0.06	4.9 ± 0.15	0.81685	0.00757	0.26377
TC1900000335.mm.1	Aldh1a1	aldehyde dehydrogenase family 1, subfamily A1	9.24 ± 0.16	8.6 ± 0.1	9.04 ± 0.05	8.47 ± 0.18	0.3102	0.00092	0.90029
TC0900000950.mm.1	Aldh1a2	aldehyde dehydrogenase family 1, subfamily A2	5.87 ± 0.05	5.82 ± 0.04	5.88 ± 0.05	5.59 ± 0.02	0.02939	0.00298	0.01998
TC1200002078.mm.1	Aldh6a1	aldehyde dehydrogenase family 6, subfamily A1	10 ± 0.15	9.79 ± 0.13	9.7 ± 0.14	10.16 ± 0.03	0.87046	0.59877	0.00814
TC1600001349.mm.1	Alg3	asparagine-linked glycosylation 3 (alpha-1,3-mannosyltransfe	7.41 ± 0.02	7.28 ± 0.04	7.24 ± 0.04	7.24 ± 0.04	0.00616	0.03622	0.04778
TC0500001599.mm.1	Alkbh4	alkB, alkylation repair homolog 4 (E. coli)	6.7 ± 0.01	6.8 ± 0.01	6.79 ± 0.01	6.81 ± 0.03	0.01148	0.00989	0.0496
TC0700000558.mm.1	Alkbh6	alkB, alkylation repair homolog 6 (E. coli)	6.19 ± 0.03	6.3 ± 0	6.35 ± 0.02	6.32 ± 0.01	0.00283	0.36273	0.01962
TC0600002975.mm.1	Alox5	arachidonate 5-lipoxygenase	6.05 ± 0.04	5.94 ± 0.03	6.03 ± 0.03	5.91 ± 0.03	0.66271	0.00786	0.67528
TC0500001844.mm.1	Alox5ap	arachidonate 5-lipoxygenase activating protein	8.54 ± 0.08	8.29 ± 0.1	8.39 ± 0.04	7.95 ± 0.08	0.01395	0.00097	0.14748
TC1500000087.mm.1	Amacr	alpha-methylacyl-CoA racemase	6.92 ± 0.08	6.81 ± 0.04	6.77 ± 0.06	7.02 ± 0.04	0.97915	0.54471	0.00398

Supplemental Table I

Annotations			Summary Statistics				2 way ANOVA p-values		
Probe Set ID	Symbol	Description	XY sh	XY Or	XX sh	XX Or	XY vs XX	Sh vs Or	Intrxn
TC1000002003.mm.1	Amd2	S-adenosylmethionine decarboxylase 2	6.8 ± 0.04	6.81 ± 0.04	6.71 ± 0.04	6.48 ± 0.12	0.00489	0.09896	0.12649
TC0600003482.mm.1	Amn1	antagonist of mitotic exit network 1	5.09 ± 0.03	5.02 ± 0.05	4.93 ± 0.04	4.93 ± 0.05	0.0085	0.36463	0.41694
TC0900001771.mm.1	Amotl1	angiomotin-like 1	8.36 ± 0.06	8.4 ± 0.01	8.54 ± 0.02	8.3 ± 0.05	0.44774	0.03479	0.00784
TC1100002036.mm.1	Anapc11	anaphase promoting complex subunit 11	7.28 ± 0.02	7.34 ± 0.01	7.41 ± 0.02	7.33 ± 0.01	0.00058	0.99577	0.00017
TC1400000578.mm.1	Ang	angiogenin, ribonuclease, RNase A family, 5	7.8 ± 0.08	7.52 ± 0.03	7.87 ± 0.05	7.42 ± 0.08	0.87193	0.00021	0.12464
TC0800001797.mm.1	Angpt2	angiopoietin 2	8.27 ± 0.08	8.62 ± 0.06	8.55 ± 0.05	8.38 ± 0.08	0.62402	0.16659	0.00194
TC0200002270.mm.1	Angpt4	angiopoietin 4	7.17 ± 0.05	7.22 ± 0.07	7.78 ± 0.16	7.05 ± 0.17	0.07504	0.01463	0.00525
TC0400004023.mm.1	Angptl7	angiopoietin-like 7	7.43 ± 0.18	6.97 ± 0.13	7.9 ± 0.28	6.62 ± 0.11	0.78089	0.00042	0.04904
TC1000000906.mm.1	Ankrd24	ankyrin repeat domain 24	6.39 ± 0.03	6.49 ± 0.02	6.41 ± 0.02	6.51 ± 0.06	0.44598	0.00857	0.80946
TC0300000955.mm.1	Ankrd35	ankyrin repeat domain 35	5.5 ± 0.04	5.57 ± 0.03	5.71 ± 0.05	5.55 ± 0.03	0.01273	0.41401	0.00596
TC0800002153.mm.1	Ankrd37	ankyrin repeat domain 37	4.38 ± 0.02	4.6 ± 0.05	4.43 ± 0.06	4.5 ± 0.03	0.67823	0.00299	0.08226
TC0700004608.mm.1	Ano1	anoctamin 1, calcium activated chloride channel	8.06 ± 0.11	8.48 ± 0.11	7.92 ± 0.05	8.21 ± 0.09	0.03715	0.00414	0.63101
TC0500002805.mm.1	Antxr2	anthrax toxin receptor 2	8.9 ± 0.03	8.63 ± 0.05	8.95 ± 0.03	8.58 ± 0.09	0.84769	7.6E-05	0.28898
TC0900000918.mm.1	Anxa2	annexin A2	9.93 ± 0.09	9.76 ± 0.06	9.92 ± 0.05	9.7 ± 0.04	0.41358	0.00722	0.89206
TC0100000428.mm.1	Aox3	aldehyde oxidase 3	5.57 ± 0.12	4.97 ± 0.07	5.29 ± 0.02	5.2 ± 0.06	0.97913	0.0025	0.02154
TC1100000058.mm.1	Ap1b1	adaptor protein complex AP-1, beta 1 subunit	8.2 ± 0.04	8.02 ± 0.04	8.06 ± 0.04	8.12 ± 0.02	0.60634	0.11445	0.00557
TC0700002057.mm.1	Ap2a2	adaptor-related protein complex 2, alpha 2 subunit	9.59 ± 0.09	9.19 ± 0.06	9.21 ± 0.05	9.31 ± 0.05	0.09879	0.05473	0.00426
TC0200004842.mm.1	Apmap	adipocyte plasma membrane associated protein	8.97 ± 0.13	8.87 ± 0.15	8.53 ± 0.13	9.14 ± 0.07	0.2844	0.15311	0.00629
TC0700002496.mm.1	Apoc1	apolipoprotein C-I	8.83 ± 0.2	8.3 ± 0.26	7.97 ± 0.27	8.77 ± 0.15	0.28081	0.74991	0.00702
TC1500000631.mm.1	Apol7e	apolipoprotein L 7e	4.26 ± 0.07	4.6 ± 0.07	4.35 ± 0.04	4.19 ± 0.08	0.01897	0.36497	0.00661
TC0700001431.mm.1	Arap1	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain	7.56 ± 0.05	7.64 ± 0.01	7.75 ± 0.03	7.67 ± 0.01	0.00691	0.77024	0.04628
TC1200002083.mm.1	Arel1	apoptosis resistant E3 ubiquitin protein ligase 1	8.41 ± 0.09	8.16 ± 0.05	8.1 ± 0.04	8.3 ± 0.03	0.22859	0.81233	0.00564
TC1100001722.mm.1	Arf2	ADP-ribosylation factor 2	7.76 ± 0.05	7.74 ± 0.04	7.79 ± 0.05	7.49 ± 0.05	0.08265	0.01454	0.00994
TC0200002575.mm.1	Arfgef2	ADP-ribosylation factor guanine nucleotide-exchange factor 2	8.61 ± 0.07	8.44 ± 0.06	8.38 ± 0.05	8.52 ± 0.03	0.08531	0.47328	0.00606
TC0700003985.mm.1	Arfip2	ADP-ribosylation factor interacting protein 2	6.85 ± 0.02	6.78 ± 0	6.75 ± 0.01	6.74 ± 0.01	0.00085	0.03951	0.05822
TC0800002497.mm.1	Arhgap10	Rho GTPase activating protein 10	8.17 ± 0.06	8.18 ± 0.02	8.35 ± 0.05	7.93 ± 0.1	0.74086	0.01231	0.00445
TC0900000621.mm.1	Arhgap20	Rho GTPase activating protein 20	6.86 ± 0.18	6.64 ± 0.08	7.98 ± 0.09	6.74 ± 0.16	0.00183	8.2E-05	0.00759
TC1100001538.mm.1	Arhgap23	Rho GTPase activating protein 23	7.96 ± 0.03	7.99 ± 0.01	8.09 ± 0.03	7.95 ± 0.02	0.08459	0.0989	0.00656
TC0500000997.mm.1	Arhgap24	Rho GTPase activating protein 24	7.23 ± 0.08	7.12 ± 0.03	7.24 ± 0.03	7.03 ± 0.03	0.32683	0.00682	0.45078
TC0X00003430.mm.1	Arhgap4	Rho GTPase activating protein 4	5.79 ± 0.02	5.91 ± 0.01	5.85 ± 0.04	5.96 ± 0.05	0.16898	0.00655	0.96131
TC0X00001700.mm.1	Arhgap6	Rho GTPase activating protein 6	6.28 ± 0.06	6.45 ± 0.05	6.61 ± 0.09	6.34 ± 0.05	0.12926	0.4597	0.0046
TC0400003862.mm.1	Arhgef10l	Rho guanine nucleotide exchange factor (GEF) 10-like	8.06 ± 0.11	8.3 ± 0.05	8.31 ± 0.05	8.1 ± 0.04	0.59526	0.64809	0.00827

Supplemental Table I

Annotations			Summary Statistics				2 way ANOVA p-values		
Probe Set ID	Symbol	Description	XY sh	XY Or	XX sh	XX Or	XY vs XX	Sh vs Or	Intrxn
TC0800000096.mm.1	Arhgef7	Rho guanine nucleotide exchange factor (GEF7)	8.25 ± 0.01	8.21 ± 0.03	8.23 ± 0.04	7.98 ± 0.09	0.02528	0.00994	0.04264
TC0900002382.mm.1	Arid3b	AT rich interactive domain 3B (BRIGHT-like)	5.4 ± 0.02	5.6 ± 0.03	5.54 ± 0.01	5.55 ± 0.02	0.10257	0.00063	0.00194
TC1800000490.mm.1	Arl14epl	ADP-ribosylation factor-like 14 effector protein-like	5.04 ± 0.04	5.24 ± 0.04	5.09 ± 0.06	5.19 ± 0.06	0.94528	0.00953	0.26431
TC0800001116.mm.1	Arl2bp	ADP-ribosylation factor-like 2 binding protein	8.59 ± 0.01	8.49 ± 0.04	8.65 ± 0.02	8.48 ± 0.07	0.61157	0.00587	0.36627
TC0700001660.mm.1	Arntl	aryl hydrocarbon receptor nuclear translocator-like	6.66 ± 0.22	6.33 ± 0.23	8.55 ± 0.1	6.37 ± 0.17	0.00052	1E-05	0.00072
TC0500001763.mm.1	Arpc1a	actin related protein 2/3 complex, subunit 1A	8.43 ± 0.05	8.28 ± 0.04	8.26 ± 0.02	8.37 ± 0.02	0.3463	0.60595	0.00585
TC0700001391.mm.1	Arrb1	arrestin, beta 1	8.64 ± 0.04	8.58 ± 0.03	8.85 ± 0.06	8.5 ± 0.09	0.21595	0.00297	0.01452
TC1800000619.mm.1	Arsi	arylsulfatase i	5.63 ± 0.04	5.84 ± 0.04	5.97 ± 0.03	5.87 ± 0.05	0.00148	0.45602	0.00656
TC0300001268.mm.1	Arsj	arylsulfatase J	5.8 ± 0.11	5.62 ± 0.04	5.76 ± 0.07	5.29 ± 0.07	0.09339	0.00439	0.04672
TC0500000871.mm.1	Art3	ADP-ribosyltransferase 3	8.01 ± 0.07	7.77 ± 0.04	7.64 ± 0.07	7.84 ± 0.07	0.04847	0.96266	0.00614
TC1200002263.mm.1	Asb2	ankyrin repeat and SOCS box-containing 2	7.85 ± 0.17	8.08 ± 0.06	8.15 ± 0.08	7.71 ± 0.05	0.86397	0.45537	0.0096
TC0600000025.mm.1	Asb4	ankyrin repeat and SOCS box-containing 4	4.14 ± 0.02	4.13 ± 0.02	4.22 ± 0.01	4.06 ± 0.05	0.51714	0.02293	0.00885
TC0800000588.mm.1	Asb5	ankyrin repeat and SOCs box-containing 5	4.72 ± 0.08	4.79 ± 0.06	5.21 ± 0.1	4.71 ± 0.05	0.02664	0.0151	0.00375
TC0800000937.mm.1	Asf1b	ASF1 anti-silencing function 1 homolog B (S. cerevisiae)	5.48 ± 0.06	5.67 ± 0.03	5.52 ± 0.03	5.74 ± 0.08	0.48234	0.00468	0.5393
TC0600001839.mm.1	Asns	asparagine synthetase	7.4 ± 0.2	7 ± 0.15	6.81 ± 0.16	7.43 ± 0.05	0.50254	0.59814	0.00454
TC1300000566.mm.1	Aspn	asporin	9.53 ± 0.06	9.1 ± 0.06	9.87 ± 0.12	9.01 ± 0.13	0.18107	1.7E-05	0.0355
TC0600000995.mm.1	Asprv1	aspartic peptidase, retroviral-like 1	4.25 ± 0.06	4.48 ± 0.08	4.29 ± 0.08	4.45 ± 0.08	0.65316	0.01	0.4378
TC0400002822.mm.1	Astn2	astrotactin 2	6.9 ± 0.11	6.9 ± 0.03	6.44 ± 0.02	6.76 ± 0.09	0.00696	0.02985	0.16484
TC0100003804.mm.1	Atf3	activating transcription factor 3	7.42 ± 0.1	7.97 ± 0.15	7.92 ± 0.11	7.53 ± 0.17	0.87407	0.81114	0.00699
TC1700000643.mm.1	Atf6b	activating transcription factor 6 beta	7.73 ± 0.04	7.81 ± 0.02	7.89 ± 0.04	7.72 ± 0.02	0.29249	0.18911	0.00195
TC0100000824.mm.1	Atg16l1	autophagy related 16-like 1 (S. cerevisiae)	6.66 ± 0.02	6.63 ± 0.01	6.55 ± 0.03	6.59 ± 0.02	0.00458	0.95207	0.10667
TC1200002311.mm.1	Atg2b	autophagy related 2B	7.33 ± 0.03	7.28 ± 0.01	7.19 ± 0.04	7.23 ± 0.03	0.00596	0.56866	0.12589
TC0800000111.mm.1	Atp11a	ATPase, class VI, type 11A	8.16 ± 0.06	7.89 ± 0.02	7.95 ± 0.04	7.72 ± 0.07	0.00837	0.00105	0.89987
TC0100003566.mm.1	Atp1a2	ATPase, Na+/K+ transporting, alpha 2 polypeptide	10.44 ± 0.13	10.39 ± 0.07	10.16 ± 0.1	10.71 ± 0.07	0.69923	0.08819	0.0038
TC0100003422.mm.1	Atp1b1	ATPase, Na+/K+ transporting, beta 1 polypeptide	9.42 ± 0.67	8.17 ± 0.28	7.16 ± 0.16	9.17 ± 0.27	0.27439	0.28785	0.00529
TC1000001198.mm.1	Atp2b1	ATPase, Ca++ transporting, plasma membrane 1	8.79 ± 0.07	8.59 ± 0.06	8.49 ± 0.02	8.37 ± 0.12	0.00945	0.09801	0.87954
TC0400003379.mm.1	Atp6v0b	ATPase, H+ transporting, lysosomal V0 subunit B	7.82 ± 0.08	7.62 ± 0.03	7.58 ± 0.05	7.74 ± 0.03	0.41028	0.82618	0.00822
TC0200001998.mm.1	Atrn	attractin	7.97 ± 0.03	7.9 ± 0.03	7.79 ± 0.02	7.83 ± 0.03	0.0007	0.52255	0.06483
TC0500003329.mm.1	Auts2	autism susceptibility candidate 2	6.65 ± 0.08	6.79 ± 0.02	6.91 ± 0.08	6.64 ± 0.03	0.36466	0.3588	0.00656
TC1000001506.mm.1	Avpr1a	arginine vasopressin receptor 1A	8.16 ± 0.12	7.09 ± 0.08	8.36 ± 0.04	6.83 ± 0.14	0.93719	2E-08	0.03206
TC1500001412.mm.1	Azin1	antizyme inhibitor 1	8.67 ± 0.07	8.59 ± 0.1	8.39 ± 0.03	8.2 ± 0.07	0.0009	0.14863	0.32388
TC1600000560.mm.1	B4galt4	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypep	6.88 ± 0.02	6.89 ± 0.04	6.85 ± 0	6.73 ± 0.04	0.00681	0.07826	0.03609

Supplemental Table I

Annotations			Summary Statistics				2 way ANOVA p-values		
Probe Set ID	Symbol	Description	XY sh	XY Or	XX sh	XX Or	XY vs XX	Sh vs Or	Intrxn
TC0200005186.mm.1	B4galt5	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypep	7.59 ± 0.05	7.56 ± 0.04	7.42 ± 0.04	7.43 ± 0.03	0.00734	0.92973	0.78814
TC0800000786.mm.1	Babam1	BRISC and BRCA1 A complex member 1	9.06 ± 0.05	9.08 ± 0.04	9.23 ± 0.03	9.26 ± 0.03	0.00335	0.85616	0.54758
TC0400000254.mm.1	Bach2	BTB and CNC homology 2	5.84 ± 0.02	5.98 ± 0.01	5.9 ± 0	5.98 ± 0.05	0.31005	0.00141	0.22373
TC0700001886.mm.1	Bag3	BCL2-associated athanogene 3	8.73 ± 0.05	8.77 ± 0.1	8.46 ± 0.08	8.5 ± 0.07	0.00374	0.4675	0.85558
TC0800001919.mm.1	Bag4	BCL2-associated athanogene 4	7.17 ± 0.08	6.88 ± 0.08	6.94 ± 0.08	7.06 ± 0.01	0.57524	0.17926	0.00941
TC1700000670.mm.1	Bag6	BCL2-associated athanogene 6	7.96 ± 0.02	8.01 ± 0.02	8.06 ± 0.01	8.07 ± 0.02	0.0033	0.17861	0.49154
TC1800000008.mm.1	Bambi	BMP and activin membrane-bound inhibitor	6.56 ± 0.05	6.96 ± 0.11	6.77 ± 0.04	6.74 ± 0.1	0.84241	0.02159	0.00978
TC0800001477.mm.1	Banp	BTG3 associated nuclear protein	7.11 ± 0.06	7.3 ± 0.06	7.05 ± 0.03	7.19 ± 0.03	0.16068	0.00758	0.61992
TC0500001578.mm.1	Baz1b	bromodomain adjacent to zinc finger domain, 1B	8.46 ± 0.03	8.52 ± 0.03	8.38 ± 0.02	8.38 ± 0.05	0.00853	0.36053	0.38536
TC1100000251.mm.1	Bcl11a	B cell CLL/lymphoma 11A (zinc finger protein)	4.39 ± 0.05	4.61 ± 0.03	4.55 ± 0.05	4.71 ± 0.08	0.06977	0.00836	0.88705
TC1200002339.mm.1	Bcl11b	B cell leukemia/lymphoma 11B	5.16 ± 0.08	5.7 ± 0.15	5.27 ± 0.05	5.6 ± 0.15	0.95866	0.00206	0.41861
TC0500001413.mm.1	Bcl7a	B cell CLL/lymphoma 7A	6.79 ± 0.02	6.88 ± 0.02	6.84 ± 0.02	6.87 ± 0.01	0.16847	0.0052	0.11325
TC1000000708.mm.1	Bcr	breakpoint cluster region	8.29 ± 0.03	8.26 ± 0.02	8.42 ± 0.05	8.21 ± 0.04	0.28109	0.00717	0.02934
TC0300001365.mm.1	Bdh2	3-hydroxybutyrate dehydrogenase, type 2	6.33 ± 0.03	6.28 ± 0.06	6.5 ± 0.02	6.36 ± 0.01	0.00287	0.04377	0.12627
TC0200000033.mm.1	Bend7	BEN domain containing 7	6.08 ± 0.03	6.06 ± 0.02	5.88 ± 0.03	6.11 ± 0.03	0.01379	0.00287	0.00053
TC1600000162.mm.1	Bfar	bifunctional apoptosis regulator	7.25 ± 0.03	7.23 ± 0.02	7.06 ± 0.05	7.22 ± 0.02	0.00489	0.10746	0.0095
TC0900002971.mm.1	Bfsp2	beaded filament structural protein 2, phakinin	5.12 ± 0.01	5.28 ± 0.02	5.21 ± 0.04	5.37 ± 0.1	0.09864	0.00763	0.97543
TC0600001203.mm.1	Bhlhe40	basic helix-loop-helix family, member e40	8.16 ± 0.08	8.09 ± 0.05	7.5 ± 0.1	8.27 ± 0.09	0.00658	0.00161	0.00011
TC0600003428.mm.1	Bhlhe41	basic helix-loop-helix family, member e41	7.5 ± 0.08	7.75 ± 0.11	6.52 ± 0.07	7.68 ± 0.15	0.00052	1.1E-05	0.00163
TC0900001722.mm.1	Birc3	baculoviral IAP repeat-containing 3	7.18 ± 0.04	7.12 ± 0.05	7.29 ± 0.04	6.97 ± 0.1	0.74608	0.00771	0.0401
TC1400002219.mm.1	Blk	B lymphoid kinase	5.23 ± 0.03	5.52 ± 0.06	5.41 ± 0.06	5.65 ± 0.09	0.03093	0.00102	0.79379
TC1400002343.mm.1	Bmp1	bone morphogenetic protein 1	8.68 ± 0.08	8.55 ± 0.04	8.64 ± 0.07	8.27 ± 0.05	0.04797	0.00409	0.04906
TC0900000226.mm.1	Bmper	BMP-binding endothelial regulator	6.74 ± 0.02	6.34 ± 0.03	6.64 ± 0.03	6.28 ± 0.04	0.01186	1.1E-08	0.37605
TC0700004474.mm.1	Bnip3	BCL2/adenovirus E1B interacting protein 3	8.87 ± 0.09	8.68 ± 0.11	8.12 ± 0.11	8.83 ± 0.06	0.00744	0.02361	0.0004
TC1600001643.mm.1	Boc	biregional cell adhesion molecule-related/down-regulated by	8.73 ± 0.09	8.67 ± 0.06	9.18 ± 0.1	8.6 ± 0.14	0.08186	0.00868	0.02289
TC1100003434.mm.1	Brip1	BRCA1 interacting protein C-terminal helicase 1	4.7 ± 0.05	4.78 ± 0.04	4.79 ± 0.04	4.6 ± 0.05	0.60903	0.47662	0.00778
TC1000000812.mm.1	Bsg	basigin	11.22 ± 0.03	11.13 ± 0.03	11.14 ± 0.01	11.25 ± 0.04	0.9002	0.93358	0.00199
TC1900000523.mm.1	Btaf1	BTAF1 RNA polymerase II, B-TFIID transcription factor-assoc	7.81 ± 0.08	7.8 ± 0.08	7.6 ± 0.05	7.46 ± 0.1	0.00307	0.28994	0.5361
TC1000002508.mm.1	Btbd2	BTB (POZ) domain containing 2	7.82 ± 0.03	7.81 ± 0.02	7.88 ± 0.01	7.9 ± 0.01	0.0048	0.81197	0.54103
TC0100003102.mm.1	Btg2	B cell translocation gene 2, anti-proliferative	8.56 ± 0.09	8.94 ± 0.13	8.86 ± 0.05	8.57 ± 0.11	0.61148	0.79894	0.00741
TC1100002654.mm.1	Btnl9	butyrophilin-like 9	6.96 ± 0.12	6.94 ± 0.16	6.71 ± 0.14	7.36 ± 0.01	0.82069	0.04935	0.00767
TC0X00003426.mm.1	C1galt1c1	C1GALT1-specific chaperone 1	7.25 ± 0.06	7.35 ± 0.04	7.21 ± 0.05	6.93 ± 0.09	0.00608	0.28714	0.00407

Supplemental Table I

Annotations			Summary Statistics				2 way ANOVA p-values		
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TC0400003794.mm.1	C1qa	complement component 1, q subcomponent, alpha polypeptic	8.18 ± 0.06	7.92 ± 0.08	8 ± 0.02	7.77 ± 0.06	0.01921	0.00147	0.93607
TC0400003792.mm.1	C1qb	complement component 1, q subcomponent, beta polypeptide	8.91 ± 0.08	8.43 ± 0.16	8.61 ± 0.09	8.16 ± 0.09	0.03903	0.00161	0.79765
TC0400003793.mm.1	C1qc	complement component 1, q subcomponent, C chain	7.89 ± 0.05	7.62 ± 0.08	7.8 ± 0.06	7.5 ± 0.05	0.19364	0.00066	0.51703
TC1100000427.mm.1	C1qtnf2	C1q and tumor necrosis factor related protein 2	7.62 ± 0.09	7.91 ± 0.05	8.04 ± 0.08	7.78 ± 0.05	0.05684	0.70844	0.00211
TC0900002156.mm.1	C2cd2l	C2 calcium-dependent domain containing 2-like	7.3 ± 0.05	7.21 ± 0.03	7.05 ± 0.03	7.2 ± 0.02	0.00778	0.2494	0.00984
TC0600003387.mm.1	C2cd5	C2 calcium-dependent domain containing 5	6.98 ± 0.03	6.88 ± 0.03	6.96 ± 0.02	6.84 ± 0.05	0.49846	0.00655	0.65532
TC1700002352.mm.1	C3	complement component 3	11.79 ± 0.03	11.31 ± 0.11	11.5 ± 0.02	11.45 ± 0.07	0.36841	0.00196	0.0073
TC0600003079.mm.1	C3ar1	complement component 3a receptor 1	6.69 ± 0.13	6.29 ± 0.11	6.46 ± 0.1	6.1 ± 0.07	0.13909	0.0078	0.91552
TC1700002815.mm.1	C4a	complement component 4A (Rodgers blood group)	7.91 ± 0.07	7.25 ± 0.07	7.67 ± 0.08	7.4 ± 0.03	0.62866	2.1E-05	0.02337
TC1700002814.mm.1	C4b	complement component 4B (Chido blood group)	9.17 ± 0.08	8.24 ± 0.1	8.82 ± 0.12	8.42 ± 0.03	0.44218	5.2E-06	0.01499
TC0700002422.mm.1	C5ar1	complement component 5a receptor 1	6.2 ± 0.07	5.83 ± 0.09	6.05 ± 0.07	5.89 ± 0.05	0.86453	0.005	0.28928
TC1500001151.mm.1	C7	complement component 7	12.42 ± 0.08	11 ± 0.03	12.43 ± 0.05	10.97 ± 0.24	0.88384	5E-08	0.70161
TC0400001020.mm.1	Cachd1	cache domain containing 1	7.54 ± 0.06	7.28 ± 0.03	7.31 ± 0.02	7.21 ± 0.06	0.01879	0.0075	0.24341
TC1100003562.mm.1	Cacna1g	calcium channel, voltage-dependent, T type, alpha 1G subun	6.57 ± 0.04	6.63 ± 0.04	6.77 ± 0.05	6.55 ± 0.02	0.10667	0.08788	0.00301
TC1500000699.mm.1	Cacna1i	calcium channel, voltage-dependent, alpha 1I subunit	5.8 ± 0.02	6 ± 0.04	5.9 ± 0.05	6.07 ± 0.08	0.14029	0.00399	0.84119
TC0700000007.mm.1	Cacng7	calcium channel, voltage-dependent, gamma subunit 7	8.45 ± 0.06	8.48 ± 0.04	8.72 ± 0.08	8.41 ± 0.04	0.046	0.09297	0.00568
TC1500002301.mm.1	Calcoco1	calcium binding and coiled coil domain 1	8.53 ± 0.04	8.71 ± 0.03	8.68 ± 0.04	8.58 ± 0.02	0.76765	0.36078	0.00306
TC1300000013.mm.1	Calm4	calmodulin 4	4.98 ± 0.05	5.3 ± 0.05	5.13 ± 0.01	5.09 ± 0.04	0.46629	0.00585	0.00153
TC0900000794.mm.1	Calml4	calmodulin-like 4	5.75 ± 0.03	5.68 ± 0.07	5.93 ± 0.03	5.65 ± 0.06	0.17728	0.00248	0.06691
TC0800002593.mm.1	Calr	calreticulin	10.76 ± 0.07	10.57 ± 0.02	10.67 ± 0.05	10.37 ± 0.05	0.03094	0.00081	0.1559
TC0200002876.mm.1	Camk1d	calcium/calmodulin-dependent protein kinase ID	6.29 ± 0.02	6.3 ± 0.01	6.33 ± 0.02	6.21 ± 0.02	0.11477	0.00695	0.00222
TC0400001728.mm.1	Camk2n1	calcium/calmodulin-dependent protein kinase II inhibitor 1	8.09 ± 0.08	8.33 ± 0.05	8.54 ± 0.06	8.26 ± 0.05	0.00723	0.93773	0.0008
TC0600001286.mm.1	Cand2	cullin-associated and neddylation-dissociated 2 (putative)	6.28 ± 0.04	6.42 ± 0.02	6.53 ± 0.04	6.42 ± 0.01	0.00213	0.61673	0.00182
TC1100002670.mm.1	Canx	calnexin	10.91 ± 0.05	10.72 ± 0.04	10.74 ± 0.02	10.62 ± 0.05	0.01924	0.0088	0.67005
TC1700002154.mm.1	Capn11	calpain 11	4.08 ± 0.03	4.25 ± 0.05	4.13 ± 0.01	4.23 ± 0.05	0.55836	0.00323	0.28161
TC0X00003114.mm.1	Capn6	calpain 6	5.49 ± 0.04	5.51 ± 0.06	5.83 ± 0.07	5.42 ± 0.08	0.03961	0.00944	0.00282
TC0700000860.mm.1	Car11	carbonic anhydrase 11	7.18 ± 0.03	7.26 ± 0.05	7.14 ± 0.03	7.28 ± 0.04	0.90925	0.00587	0.7457
TC0300000095.mm.1	Car3	carbonic anhydrase 3	12.71 ± 0.07	12.26 ± 0.1	12.17 ± 0.1	12.36 ± 0.12	0.03885	0.18705	0.00548
TC1100001285.mm.1	Car4	carbonic anhydrase 4	6.92 ± 0.07	6.77 ± 0.11	6.56 ± 0.11	6.98 ± 0.06	0.32913	0.18312	0.00482
TC0800003060.mm.1	Car5a	carbonic anhydrase 5a, mitochondrial	5.62 ± 0.03	5.78 ± 0.04	5.65 ± 0.03	5.74 ± 0.06	0.86742	0.00777	0.35322
TC0X00003327.mm.1	Car5b	carbonic anhydrase 5b, mitochondrial	8.92 ± 0.17	8.2 ± 0.16	8.23 ± 0.15	8.42 ± 0.09	0.1049	0.07866	0.00713
TC0500003518.mm.1	Card11	caspase recruitment domain family, member 11	5.59 ± 0.05	5.88 ± 0.02	5.67 ± 0.07	5.85 ± 0.06	0.77127	0.00088	0.34578

Supplemental Table I

Annotations			Summary Statistics				2 way ANOVA p-values		
Probe Set ID	Symbol	Description	XY sh	XY Or	XX sh	XX Or	XY vs XX	Sh vs Or	Intrxn
TC0700004589.mm.1	Cars	cysteinyl-tRNA synthetase	6.91 ± 0.04	6.8 ± 0.03	6.72 ± 0.02	6.73 ± 0	0.0026	0.3018	0.16235
TC0900000032.mm.1	Casp4	caspase 4, apoptosis-related cysteine peptidase	6.45 ± 0.1	6.13 ± 0.07	5.81 ± 0.07	5.51 ± 0.15	6.2E-05	0.01726	0.8269
TC0200004227.mm.1	Cat	catalase	11.67 ± 0.1	11.47 ± 0.1	11.34 ± 0.12	11.85 ± 0.03	0.86446	0.27167	0.00126
TC1500001890.mm.1	Cbx7	chromobox 7	7.23 ± 0.04	7.45 ± 0.03	7.51 ± 0.04	7.48 ± 0.03	0.0007	0.01574	0.00234
TC0400001152.mm.1	Cc2d1b	coiled-coil and C2 domain containing 1B	6.81 ± 0.01	6.84 ± 0.01	6.87 ± 0.02	6.84 ± 0	0.00428	0.90719	0.0022
TC1800001296.mm.1	Ccdc112	coiled-coil domain containing 112	6.08 ± 0.05	5.98 ± 0.09	6.66 ± 0.11	5.91 ± 0.13	0.01269	0.00131	0.00312
TC1700001791.mm.1	Ccdc167	coiled-coil domain containing 167	6.69 ± 0.07	6.8 ± 0.04	7.06 ± 0.07	6.76 ± 0.09	0.02466	0.25335	0.00803
TC0500003112.mm.1	Ccdc60	coiled-coil domain containing 60	6.03 ± 0.05	6.16 ± 0.03	6.32 ± 0.08	6.08 ± 0.04	0.04074	0.37799	0.00222
TC0700002462.mm.1	Ccdc61	coiled-coil domain containing 61	6.6 ± 0.02	6.77 ± 0.02	6.71 ± 0.02	6.79 ± 0.06	0.08153	0.00378	0.22948
TC1600000667.mm.1	Ccdc80	coiled-coil domain containing 80	9.86 ± 0.08	9.54 ± 0.04	9.66 ± 0.03	9.19 ± 0.08	0.00281	0.00012	0.16798
TC1100002406.mm.1	Ccdc85a	coiled-coil domain containing 85A	5.73 ± 0.02	5.81 ± 0.05	5.7 ± 0.02	5.84 ± 0.04	0.97549	0.00769	0.28722
TC1900000965.mm.1	Ccdc85b	coiled-coil domain containing 85B	7.75 ± 0.03	7.89 ± 0.02	7.72 ± 0.03	7.82 ± 0.02	0.25026	0.00049	0.24502
TC1200002237.mm.1	Ccdc88c	coiled-coil domain containing 88C	6.84 ± 0.04	7.03 ± 0.03	6.87 ± 0.04	6.94 ± 0.02	0.35144	0.00267	0.13436
TC4_JH584293_rand	Ccl27a	chemokine (C-C motif) ligand 27A	7.94 ± 0.03	8.06 ± 0.04	8.09 ± 0.01	8.12 ± 0.03	0.00763	0.03796	0.21202
TC1100003399.mm.1	Ccl6	chemokine (C-C motif) ligand 6	8.18 ± 0.12	7.43 ± 0.13	7.44 ± 0.08	7 ± 0.11	0.00052	0.0004	0.39803
TC1100001223.mm.1	Ccl8	chemokine (C-C motif) ligand 8	6.66 ± 0.22	5.63 ± 0.21	6.17 ± 0.08	5.28 ± 0.08	0.04739	0.00013	0.86269
TC1100003397.mm.1	Ccl9	chemokine (C-C motif) ligand 9	8.57 ± 0.18	7.72 ± 0.15	7.72 ± 0.11	7.06 ± 0.08	0.0005	0.0005	0.93167
TC0300001992.mm.1	Ccna1	cyclin A1	4.62 ± 0.03	4.72 ± 0.03	4.63 ± 0.05	4.78 ± 0.06	0.38379	0.00817	0.58124
TC0400000085.mm.1	Ccne2	cyclin E2	4.38 ± 0.05	4.41 ± 0.05	4.22 ± 0.05	4.28 ± 0.01	0.00943	0.25885	0.81547
TC0500002770.mm.1	Ccni	cyclin I	10.1 ± 0.05	10.18 ± 0.02	10.34 ± 0.02	10.19 ± 0.04	0.00452	0.39932	0.00779
TC0400002092.mm.1	Ccnl2	cyclin L2	7.39 ± 0.06	7.39 ± 0.04	7.2 ± 0.03	7.27 ± 0.02	0.00492	0.54302	0.36452
TC1100003796.mm.1	Ccr10	chemokine (C-C motif) receptor 10	4.8 ± 0.05	5.11 ± 0.12	4.91 ± 0.08	5.17 ± 0.1	0.34225	0.00459	0.75238
TC0900001675.mm.1	Ccr5	chemokine (C-C motif) receptor 5	4.83 ± 0.05	4.56 ± 0.08	4.73 ± 0.05	4.54 ± 0.05	0.26112	0.00122	0.37964
TC1700000084.mm.1	Ccr6	chemokine (C-C motif) receptor 6	4.27 ± 0.04	4.41 ± 0.01	4.37 ± 0.06	4.48 ± 0.04	0.04268	0.00885	0.61256
TC1100003696.mm.1	Ccr7	chemokine (C-C motif) receptor 7	6.61 ± 0.05	6.96 ± 0.11	6.72 ± 0.12	6.99 ± 0.03	0.47305	0.00306	0.71445
TC0900001670.mm.1	Ccr9	chemokine (C-C motif) receptor 9	3.82 ± 0.02	4.19 ± 0.1	3.92 ± 0.05	4.18 ± 0.07	0.50173	0.00022	0.42637
TC0900003125.mm.1	Ccrl2	chemokine (C-C motif) receptor-like 2	5.9 ± 0.08	6.02 ± 0.07	6.25 ± 0.1	5.84 ± 0.03	0.29139	0.08799	0.00488
TC1000002920.mm.1	Cct2	chaperonin containing Tcp1, subunit 2 (beta)	9.92 ± 0.04	9.86 ± 0.04	9.73 ± 0.02	9.72 ± 0.04	0.00174	0.48011	0.72043
TC0300000721.mm.1	Cct3	chaperonin containing Tcp1, subunit 3 (gamma)	9.06 ± 0.05	8.93 ± 0.09	8.76 ± 0.03	8.75 ± 0.06	0.00163	0.23672	0.30302
TC0600001418.mm.1	Cd163	CD163 antigen	8.77 ± 0.16	7.98 ± 0.09	8.08 ± 0.08	7.75 ± 0.06	0.00581	0.0012	0.18616
TC0300002277.mm.1	Cd1d1	CD1d1 antigen	7.71 ± 0.19	7.49 ± 0.17	7.14 ± 0.16	7.88 ± 0.04	0.32058	0.27069	0.00406
TC0300000689.mm.1	Cd1d2	CD1d2 antigen	7.46 ± 0.19	7.26 ± 0.17	6.89 ± 0.21	7.69 ± 0.03	0.40138	0.22594	0.00495

Supplemental Table I

Annotations			Summary Statistics				2 way ANOVA p-values		
Probe Set ID	Symbol	Description	XY sh	XY Or	XX sh	XX Or	XY vs XX	Sh vs Or	Intrxn
TC0800001624.mm.1	Cd209b	CD209b antigen	6.25 ± 0.08	5.68 ± 0.03	6.21 ± 0.11	6.12 ± 0.08	0.0177	0.00189	0.01468
TC0800001623.mm.1	Cd209d	CD209d antigen	5.82 ± 0.07	5.22 ± 0.1	5.76 ± 0.15	5.53 ± 0.05	0.22711	0.00091	0.0788
TC0800001627.mm.1	Cd209f	CD209f antigen	8.24 ± 0.06	7.92 ± 0.09	8.47 ± 0.07	8.06 ± 0.1	0.03975	0.00055	0.65051
TC0800000027.mm.1	Cd209g	CD209g antigen	8.44 ± 0.07	8.01 ± 0.09	8.65 ± 0.08	8.24 ± 0.12	0.03502	0.00047	0.87499
TC0100001527.mm.1	Cd247	CD247 antigen	5.24 ± 0.03	5.45 ± 0.03	5.3 ± 0.03	5.45 ± 0.06	0.61293	0.00087	0.60875
TC1900000055.mm.1	Cd248	CD248 antigen, endosialin	9.33 ± 0.1	9.13 ± 0.04	9.61 ± 0.11	9.07 ± 0.06	0.27353	0.00068	0.07373
TC0600003140.mm.1	Cd27	CD27 antigen	5.57 ± 0.06	6.18 ± 0.14	5.56 ± 0.1	6.12 ± 0.19	0.66443	0.00072	0.9704
TC0900002396.mm.1	Cd276	CD276 antigen	7.59 ± 0.07	7.76 ± 0.05	7.72 ± 0.03	7.58 ± 0.02	0.78779	0.69579	0.00742
TC0100000476.mm.1	Cd28	CD28 antigen	4.61 ± 0.03	4.83 ± 0.08	4.6 ± 0.05	4.79 ± 0.08	0.62745	0.00731	0.93106
TC1100004053.mm.1	Cd300ld	CD300 molecule-like family member d	7.34 ± 0.09	6.93 ± 0.06	7.21 ± 0.09	6.81 ± 0.12	0.30796	0.00122	0.88155
TC1100001677.mm.1	Cd300lg	CD300 antigen like family member G	7.84 ± 0.14	7.66 ± 0.12	7.39 ± 0.14	8.06 ± 0.04	0.60021	0.11851	0.00198
TC1100004058.mm.1	Cd300lh	CD300 antigen like family member H	7.88 ± 0.08	7.56 ± 0.1	7.83 ± 0.04	7.67 ± 0.04	0.55551	0.00736	0.35346
TC0700002950.mm.1	Cd33	CD33 antigen	6.99 ± 0.04	6.9 ± 0.05	7.11 ± 0.04	6.9 ± 0.05	0.19787	0.00353	0.19787
TC0100001882.mm.1	Cd34	CD34 antigen	10.16 ± 0.08	9.83 ± 0.05	10.29 ± 0.07	9.74 ± 0.06	0.56799	2.6E-05	0.07776
TC0900002189.mm.1	Cd3e	CD3 antigen, epsilon polypeptide	5.61 ± 0.06	5.99 ± 0.11	5.52 ± 0.08	6.02 ± 0.12	0.67908	0.00048	0.42825
TC0900002188.mm.1	Cd3g	CD3 antigen, gamma polypeptide	5.02 ± 0.05	5.61 ± 0.13	5 ± 0.08	5.53 ± 0.22	0.61454	0.00115	0.94104
TC0600003124.mm.1	Cd4	CD4 antigen	5.14 ± 0.03	5.76 ± 0.24	5.15 ± 0.03	5.65 ± 0.27	0.78198	0.00585	0.7109
TC0200004219.mm.1	Cd44	CD44 antigen	7.21 ± 0.05	7.18 ± 0.06	7.04 ± 0.07	6.86 ± 0.02	0.00089	0.15011	0.1036
TC1900001113.mm.1	Cd5	CD5 antigen	5.55 ± 0.05	5.79 ± 0.03	5.66 ± 0.07	5.83 ± 0.07	0.29826	0.00536	0.80215
TC1900001114.mm.1	Cd6	CD6 antigen	5.48 ± 0.03	5.74 ± 0.04	5.56 ± 0.03	5.72 ± 0.07	0.63002	0.00049	0.2886
TC1100003055.mm.1	Cd68	CD68 antigen	7.33 ± 0.15	6.94 ± 0.09	7.17 ± 0.05	6.82 ± 0.07	0.2611	0.00607	0.93
TC1100004240.mm.1	Cd7	CD7 antigen	4.84 ± 0.02	5 ± 0.04	4.94 ± 0.02	4.77 ± 0.07	0.11357	0.86579	0.00236
TC1600000553.mm.1	Cd80	CD80 antigen	5.23 ± 0.04	5.19 ± 0.03	5.56 ± 0.13	5.11 ± 0.05	0.14682	0.00302	0.01687
TC0600000827.mm.1	Cd8a	CD8 antigen, alpha chain	5.03 ± 0.07	6.06 ± 0.36	5.17 ± 0.05	5.99 ± 0.3	0.97853	0.00156	0.72349
TC0600000826.mm.1	Cd8b1	CD8 antigen, beta chain 1	5.76 ± 0.06	6.64 ± 0.3	5.84 ± 0.07	6.53 ± 0.39	0.88736	0.00644	0.74355
TC1900000112.mm.1	Cdc42bpg	CDC42 binding protein kinase gamma (DMPK-like)	6.78 ± 0.01	6.9 ± 0.01	6.91 ± 0.02	6.97 ± 0.04	0.00132	0.00382	0.33052
TC0300000894.mm.1	Cdc42se1	CDC42 small effector 1	7.95 ± 0.05	8.09 ± 0.01	8.04 ± 0.02	7.98 ± 0.01	0.86602	0.16796	0.00556
TC0200001056.mm.1	Cdca7	cell division cycle associated 7	5.14 ± 0.03	5.35 ± 0.08	5.25 ± 0.03	5.34 ± 0.05	0.26285	0.00817	0.2075
TC0800001414.mm.1	Cdh13	cadherin 13	9.49 ± 0.12	9.69 ± 0.07	9.66 ± 0.09	9.32 ± 0.06	0.42015	0.5747	0.00887
TC0100002916.mm.1	Cdh19	cadherin 19, type 2	8.22 ± 0.49	6.78 ± 0.25	6.53 ± 0.25	7.68 ± 0.3	0.53099	0.97265	0.0086
TC0800001253.mm.1	Cdh3	cadherin 3	6.68 ± 0.05	6.91 ± 0.02	6.94 ± 0.07	6.76 ± 0.04	0.27565	0.64171	0.00089
TC1300000781.mm.1	Cdk20	cyclin-dependent kinase 20	5.94 ± 0.04	5.96 ± 0.05	6.16 ± 0.04	6.07 ± 0.03	0.00237	0.31063	0.3557

Supplemental Table I

Annotations			Summary Statistics				2 way ANOVA p-values		
Probe Set ID	Symbol	Description	XY sh	XY Or	XX sh	XX Or	XY vs XX	Sh vs Or	Intrxn
TC0400002847.mm.1	Cdk5rap2	CDK5 regulatory subunit associated protein 2	6.84 ± 0.03	6.93 ± 0.02	7.02 ± 0.03	6.88 ± 0.04	0.0656	0.3803	0.00333
TC0500000008.mm.1	Cdk6	cyclin-dependent kinase 6	7.22 ± 0.07	7.32 ± 0.04	7.09 ± 0.07	7.08 ± 0.05	0.00902	0.48219	0.41566
TC0700004585.mm.1	Cdkn1c	cyclin-dependent kinase inhibitor 1C (P57)	7.74 ± 0.04	7.86 ± 0	7.96 ± 0.02	7.87 ± 0.01	0.00078	0.67282	0.00209
TC0400000917.mm.1	CDKN2B-AS	CDKN2B antisense RNA 1 intronic convserved region	5.42 ± 0.04	5.65 ± 0.09	5.4 ± 0.03	5.66 ± 0.1	0.79293	0.00448	0.7175
TC1300000405.mm.1	Cdyl	chromodomain protein, Y chromosome-like	6.48 ± 0.04	6.63 ± 0.02	6.57 ± 0.01	6.53 ± 0.02	0.9091	0.04999	0.00489
TC0700000652.mm.1	Cebpa	CCAAT/enhancer binding protein (C/EBP), alpha	8.98 ± 0.2	8.64 ± 0.16	8.57 ± 0.23	9.2 ± 0.04	0.96147	0.76915	0.00648
TC0600003042.mm.1	Cecr5	cat eye syndrome chromosome region, candidate 5	6.29 ± 0.02	6.34 ± 0.01	6.28 ± 0.03	6.42 ± 0.05	0.34665	0.00605	0.09855
TC1100001816.mm.1	Cep112	centrosomal protein 112	6.29 ± 0.04	6.41 ± 0.03	6.49 ± 0.05	6.33 ± 0.05	0.13595	0.80385	0.00363
TC1200002150.mm.1	Cep128	centrosomal protein 128	5.96 ± 0.05	6.09 ± 0.04	6.12 ± 0.05	5.99 ± 0.05	0.36452	0.87654	0.00869
TC0800002698.mm.1	Ces1a	carboxylesterase 1A	5.31 ± 0.05	5.45 ± 0.03	5.33 ± 0.05	5.58 ± 0.06	0.3189	0.00418	0.16735
TC0800002702.mm.1	Ces1d	carboxylesterase 1D	9.03 ± 0.23	8.87 ± 0.26	8.5 ± 0.24	9.53 ± 0.06	0.89326	0.13846	0.00729
TC1700002816.mm.1	Cfb	complement factor B	8.68 ± 0.04	8.45 ± 0.11	8.49 ± 0.06	8.13 ± 0.09	0.00435	0.00155	0.4804
TC1200001757.mm.1	Cfl2	cofilin 2, muscle	9.36 ± 0.04	9.41 ± 0.04	9.32 ± 0.01	9.22 ± 0.04	0.00837	0.61154	0.04299
TC0X00001934.mm.1	Cfp	complement factor properdin	7.64 ± 0.03	7.27 ± 0.1	7.47 ± 0.03	7.25 ± 0.07	0.22665	0.00058	0.35255
TC0800000133.mm.1	Champ1	chromosome alignment maintaining phosphoprotein 1	7.1 ± 0.02	7.17 ± 0.02	7.18 ± 0.02	7.14 ± 0.01	0.17027	0.68437	0.01
TC0600001171.mm.1	Chl1	cell adhesion molecule with homology to L1CAM	7.8 ± 0.58	6.46 ± 0.32	6.01 ± 0.16	7.47 ± 0.23	0.52955	0.64459	0.00797
TC0200001773.mm.1	Chp1	calcineurin-like EF hand protein 1	8.97 ± 0.06	8.78 ± 0.06	8.76 ± 0.04	8.87 ± 0.03	0.15771	0.31169	0.00642
TC0500000219.mm.1	Chpf2	chondroitin polymerizing factor 2	6.99 ± 0.02	7.02 ± 0.01	7.07 ± 0.02	7.01 ± 0.01	0.02344	0.57673	0.00409
TC0X00003113.mm.1	Chrdl1	chordin-like 1	9.16 ± 0.16	8.65 ± 0.03	9.27 ± 0.13	8.64 ± 0.16	0.48045	0.00226	0.42429
TC1400000944.mm.1	Chrna2	cholinergic receptor, nicotinic, alpha polypeptide 2 (neuronal)	4.47 ± 0.05	4.63 ± 0.02	4.59 ± 0.02	4.89 ± 0.11	0.01806	0.00672	0.17616
TC0500000630.mm.1	Chrna9	cholinergic receptor, nicotinic, alpha polypeptide 9	4 ± 0.02	4.11 ± 0.04	4.05 ± 0.01	4.19 ± 0.06	0.10618	0.00438	0.57301
TC0200001441.mm.1	Chst1	carbohydrate (keratan sulfate Gal-6) sulfotransferase 1	7.13 ± 0.18	6.38 ± 0.07	6.18 ± 0.09	6.5 ± 0.08	0.0113	0.19362	0.00207
TC0100002229.mm.1	Chst10	carbohydrate sulfotransferase 10	5.59 ± 0.03	5.68 ± 0.02	5.6 ± 0.02	5.62 ± 0.02	0.6501	0.00994	0.07928
TC0200001751.mm.1	Chst14	carbohydrate (N-acetylgalactosamine 4-0) sulfotransferase 1	7.24 ± 0.03	7.36 ± 0.02	7.41 ± 0.06	7.28 ± 0.02	0.195	0.81619	0.00315
TC1800000599.mm.1	Chsy3	chondroitin sulfate synthase 3	5.36 ± 0.08	5.65 ± 0.05	5.54 ± 0.03	5.4 ± 0.01	0.59306	0.20141	0.00194
TC0600002920.mm.1	Cidec	cell death-inducing DFFA-like effector c	10.46 ± 0.14	9.83 ± 0.19	9.42 ± 0.22	10.26 ± 0.02	0.04953	0.71503	0.00032
TC0900000834.mm.1	Cilp	cartilage intermediate layer protein, nucleotide pyrophosphoh	6.49 ± 0.04	6.31 ± 0.07	6.5 ± 0.07	6.26 ± 0.06	0.97643	0.00408	0.4736
TC0800002374.mm.1	Cilp2	cartilage intermediate layer protein 2	6.3 ± 0.01	6.51 ± 0.02	6.42 ± 0.04	6.56 ± 0.09	0.08462	0.00247	0.39186
TC1200002396.mm.1	Cinp	cyclin-dependent kinase 2 interacting protein	6.49 ± 0.03	6.49 ± 0.03	6.42 ± 0.02	6.39 ± 0.02	0.00866	0.4384	0.88636
TC0200000577.mm.1	Ciz1	CDKN1A interacting zinc finger protein 1	7.6 ± 0.03	7.67 ± 0.01	7.71 ± 0.02	7.65 ± 0.01	0.052	0.80081	0.00398
TC0300002352.mm.1	Cks1b	CDC28 protein kinase 1b	6.8 ± 0.04	7.02 ± 0.03	6.95 ± 0.04	6.93 ± 0.04	0.3953	0.0191	0.00448
TC0700002489.mm.1	Clasrp	CLK4-associating serine/arginine rich protein	6.78 ± 0.02	6.9 ± 0.02	6.87 ± 0.01	6.92 ± 0.04	0.05347	0.00572	0.31499

Supplemental Table I

Annotations			Summary Statistics				2 way ANOVA p-values		
Probe Set ID	Symbol	Description	XY sh	XY Or	XX sh	XX Or	XY vs XX	Sh vs Or	Intrxn
TC1400001288.mm.1	Cldn10	claudin 10	5.48 ± 0.04	5.28 ± 0.05	5.57 ± 0.08	5.26 ± 0.05	0.49029	0.00071	0.25109
TC0400001330.mm.1	Cldn19	claudin 19	5.82 ± 0.09	5.65 ± 0.05	5.48 ± 0.09	6 ± 0.14	0.72415	0.05226	0.0051
TC1600001168.mm.1	Cldn26	claudin 26	6.11 ± 0.02	6.22 ± 0.02	6.29 ± 0.04	6.3 ± 0.03	0.00098	0.05784	0.15857
TC1100000942.mm.1	Clec10a	C-type lectin domain family 10, member A	7.29 ± 0.02	7.09 ± 0.06	7.19 ± 0.01	7.01 ± 0.06	0.0291	0.00029	0.7414
TC0900001658.mm.1	Clec3b	C-type lectin domain family 3, member b	9.13 ± 0.1	8.84 ± 0.04	9.14 ± 0.06	8.73 ± 0.11	0.88895	0.00351	0.27835
TC0600001397.mm.1	Clec4a1	C-type lectin domain family 4, member a1	6.82 ± 0.05	6.5 ± 0.06	6.62 ± 0.04	6.22 ± 0.09	0.0015	5.3E-05	0.54584
TC0600001401.mm.1	Clec4a2	C-type lectin domain family 4, member a2	4.77 ± 0.06	4.59 ± 0.09	4.71 ± 0.05	4.43 ± 0.08	0.21205	0.00843	0.37628
TC0600001398.mm.1	Clec4a3	C-type lectin domain family 4, member a3	6.41 ± 0.07	6.1 ± 0.13	6.37 ± 0.11	5.79 ± 0.19	0.19316	0.00416	0.3185
TC0600001400.mm.1	Clec4b1	C-type lectin domain family 4, member b1	4.74 ± 0.07	4.46 ± 0.08	4.6 ± 0.05	4.4 ± 0.12	0.2199	0.00927	0.60192
TC0600002142.mm.1	Clec5a	C-type lectin domain family 5, member a	4.78 ± 0.08	4.55 ± 0.06	4.76 ± 0.13	4.29 ± 0.03	0.15846	0.00142	0.12067
TC1200002296.mm.1	Clmn	calmin	6.53 ± 0.08	6.27 ± 0.07	6.26 ± 0.06	6.41 ± 0.02	0.33323	0.42471	0.00898
TC0500002628.mm.1	Clock	circadian locomotor output cycles kaput	9.59 ± 0.11	9.42 ± 0.09	9.95 ± 0.04	9.31 ± 0.11	0.30049	0.00079	0.05494
TC1700000482.mm.1	Clpsl2	colipase-like 2	5.82 ± 0.05	5.99 ± 0.05	5.87 ± 0.07	6.09 ± 0.08	0.29489	0.00956	0.61393
TC0700002492.mm.1	Clptm1	cleft lip and palate associated transmembrane protein 1	9.49 ± 0.06	9.4 ± 0.04	9.38 ± 0.04	9.53 ± 0.02	0.7104	0.88789	0.00531
TC1300000884.mm.1	Clptm1l	CLPTM1-like	9.22 ± 0.01	9.11 ± 0.03	9.21 ± 0.03	9.05 ± 0.07	0.38604	0.00382	0.54878
TC1100003455.mm.1	Cltc	clathrin, heavy polypeptide (Hc)	10.81 ± 0.04	10.64 ± 0.03	10.68 ± 0.03	10.49 ± 0.08	0.02554	0.0052	0.61619
TC1500000207.mm.1	Cmbl	carboxymethylenebutenolidase-like (Pseudomonas)	8.49 ± 0.23	7.89 ± 0.23	7.58 ± 0.18	8.3 ± 0.14	0.18827	0.93297	0.00461
TC0600003598.mm.1	Cml3	camello-like 3	5.66 ± 0.05	5.9 ± 0.04	5.7 ± 0.06	5.83 ± 0.08	0.79063	0.00628	0.35056
TC0800001181.mm.1	Cmtm2b	CKLF-like MARVEL transmembrane domain containing 2B	4.5 ± 0.06	4.75 ± 0.02	4.61 ± 0.02	4.68 ± 0.07	0.61899	0.0054	0.06998
TC1300002429.mm.1	Cmya5	cardiomyopathy associated 5	5.61 ± 0.04	5.73 ± 0.02	5.76 ± 0.03	5.66 ± 0.05	0.18594	0.69672	0.00921
TC0100000247.mm.1	Cnnm3	cyclin M3	6.73 ± 0.02	6.69 ± 0.03	6.79 ± 0.03	6.69 ± 0.02	0.24812	0.00916	0.2687
TC0600001176.mm.1	Cntn6	contactin 6	4.75 ± 0.05	4.97 ± 0.03	5.27 ± 0.05	4.62 ± 0.05	0.08596	0.00062	6.6E-07
TC0800001323.mm.1	Cog4	component of oligomeric golgi complex 4	8.39 ± 0.07	8.22 ± 0.06	8.11 ± 0.07	8.28 ± 0.02	0.03126	0.68501	0.00579
TC0900002735.mm.1	Col12a1	collagen, type XII, alpha 1	6.71 ± 0.07	6.66 ± 0.03	6.85 ± 0.12	6.38 ± 0.05	0.2958	0.00291	0.02294
TC1500000395.mm.1	Col14a1	collagen, type XIV, alpha 1	9.85 ± 0.06	10.33 ± 0.04	9.82 ± 0.08	9.99 ± 0.07	0.02273	8.9E-05	0.01479
TC0400000518.mm.1	Col15a1	collagen, type XV, alpha 1	8.8 ± 0.07	8.88 ± 0.08	8.64 ± 0.04	8.38 ± 0.05	0.00039	0.28867	0.00977
TC0100002073.mm.1	Col19a1	collagen, type XIX, alpha 1	6.61 ± 0.06	6.69 ± 0.02	6.89 ± 0.08	6.58 ± 0.06	0.14826	0.09834	0.00469
TC1100001448.mm.1	Col1a1	collagen, type I, alpha 1	11.09 ± 0.11	10.8 ± 0.09	10.63 ± 0.07	10.08 ± 0.07	5.9E-05	0.00151	0.08205
TC0600000010.mm.1	Col1a2	collagen, type I, alpha 2	11.39 ± 0.11	11.22 ± 0.07	11.13 ± 0.08	10.61 ± 0.09	0.00094	0.00611	0.03257
TC1100000566.mm.1	Col23a1	collagen, type XXIII, alpha 1	6.93 ± 0.03	7.13 ± 0.03	7.06 ± 0.03	7.13 ± 0.05	0.0759	0.00198	0.0654
TC0100000343.mm.1	Col3a1	collagen, type III, alpha 1	11.41 ± 0.1	11.23 ± 0.04	11.11 ± 0.07	10.44 ± 0.13	0.00019	0.00192	0.00942
TC0800001696.mm.1	Col4a1	collagen, type IV, alpha 1	9.65 ± 0.08	9.43 ± 0.02	9.57 ± 0.05	9.08 ± 0.04	0.00552	8.6E-05	0.02157

Supplemental Table I

Annotations			Summary Statistics				2 way ANOVA p-values		
Probe Set ID	Symbol	Description	XY sh	XY Or	XX sh	XX Or	XY vs XX	Sh vs Or	Intrxn
TC0800000088.mm.1	Col4a2	collagen, type IV, alpha 2	9.83 ± 0.08	9.65 ± 0.01	9.75 ± 0.06	9.32 ± 0.05	0.01081	0.00061	0.04518
TC0X00001394.mm.1	Col4a5	collagen, type IV, alpha 5	8.05 ± 0.14	8.17 ± 0.07	8.13 ± 0.09	7.58 ± 0.1	0.06103	0.10846	0.00559
TC0X00003083.mm.1	Col4a6	collagen, type IV, alpha 6	7.31 ± 0.14	7.58 ± 0.08	7.48 ± 0.07	7.08 ± 0.07	0.15806	0.61406	0.0052
TC0100002278.mm.1	Col5a2	collagen, type V, alpha 2	8.41 ± 0.11	8.3 ± 0.03	8.23 ± 0.07	7.72 ± 0.05	0.00078	0.00465	0.01324
TC1000002406.mm.1	Col6a1	collagen, type VI, alpha 1	9.91 ± 0.09	9.77 ± 0.05	9.8 ± 0.06	9.36 ± 0.07	0.00729	0.00306	0.02607
TC1000002405.mm.1	Col6a2	collagen, type VI, alpha 2	9.53 ± 0.1	9.42 ± 0.06	9.46 ± 0.07	8.99 ± 0.06	0.01621	0.00605	0.01439
TC0100002789.mm.1	Col6a3	collagen, type VI, alpha 3	9.37 ± 0.1	9.35 ± 0.06	9.19 ± 0.07	8.87 ± 0.06	0.00246	0.09988	0.03633
TC0100000393.mm.1	Coq10b	coenzyme Q10 homolog B (S. cerevisiae)	7.98 ± 0.08	8.28 ± 0.03	7.5 ± 0.09	8 ± 0.12	0.00064	0.00029	0.31344
TC0300000137.mm.1	Cp	ceruloplasmin	9.19 ± 0.08	8.69 ± 0.11	9 ± 0.04	8.6 ± 0.19	0.37584	0.00274	0.84823
TC0300001707.mm.1	Cpb1	carboxypeptidase B1 (tissue)	5.93 ± 0.11	5.93 ± 0.05	6.37 ± 0.13	5.67 ± 0.17	0.34704	0.02383	0.00913
TC0700003608.mm.1	Cpeb1	cytoplasmic polyadenylation element binding protein 1	6.71 ± 0.11	6.5 ± 0.01	6.3 ± 0.04	6.64 ± 0.03	0.13311	0.23354	0.00371
TC0800001112.mm.1	Cpne2	copine II	9.02 ± 0.06	8.92 ± 0.02	9.1 ± 0.03	8.81 ± 0.09	0.79158	0.00883	0.04695
TC0400000439.mm.1	Creb3	cAMP responsive element binding protein 3	8.13 ± 0.04	8.1 ± 0.02	8.03 ± 0.02	7.96 ± 0.03	0.00706	0.33276	0.21679
TC0200004133.mm.1	Creb3l1	cAMP responsive element binding protein 3-like 1	8.87 ± 0.11	8.72 ± 0.07	9.02 ± 0.08	8.45 ± 0.1	0.71523	0.0035	0.03012
TC0600002325.mm.1	Crhr2	corticotropin releasing hormone receptor 2	6.65 ± 0.04	6.89 ± 0.03	7.03 ± 0.05	6.91 ± 0.04	0.00037	0.18756	0.00093
TC1200001282.mm.1	Crip1	cysteine-rich protein 1 (intestinal)	10.03 ± 0.06	10.19 ± 0.05	10.29 ± 0.09	9.96 ± 0.1	0.59702	0.45146	0.0039
TC1100003339.mm.1	Crlf3	cytokine receptor-like factor 3	7 ± 0.02	7.09 ± 0.02	7.01 ± 0.01	7.07 ± 0.03	0.90152	0.00164	0.52929
TC0900003168.mm.1	Crtap	cartilage associated protein	9.46 ± 0.07	9.61 ± 0.03	9.68 ± 0.05	9.42 ± 0.1	0.85571	0.41185	0.00798
TC1000002605.mm.1	Cry1	cryptochrome 1 (photolyase-like)	6.33 ± 0.05	6.7 ± 0.05	6.68 ± 0.12	6.51 ± 0.01	0.30881	0.2109	0.00184
TC0200004140.mm.1	Cry2	cryptochrome 2 (photolyase-like)	7.48 ± 0.04	7.6 ± 0.06	7.32 ± 0.05	7.58 ± 0.04	0.10318	0.00058	0.17066
TC0900000605.mm.1	Cryab	crystallin, alpha B	9.18 ± 0.1	9.23 ± 0.06	9.31 ± 0.06	8.94 ± 0.03	0.44147	0.08068	0.00515
TC1600001805.mm.1	Crybg3	beta-gamma crystallin domain containing 3	7.97 ± 0.12	7.69 ± 0.08	8.08 ± 0.04	7.48 ± 0.13	0.58478	0.00073	0.14687
TC1500002285.mm.1	Csad	cysteine sulfinic acid decarboxylase	8.1 ± 0.11	7.99 ± 0.11	7.97 ± 0.06	8.36 ± 0.03	0.49743	0.35682	0.00491
TC1800000625.mm.1	Csf1r	colony stimulating factor 1 receptor	8.89 ± 0.05	8.66 ± 0.07	9 ± 0.07	8.62 ± 0.07	0.52993	0.00042	0.19233
TC0500002214.mm.1	Ctbp1	C-terminal binding protein 1	9.13 ± 0.02	9.06 ± 0.03	9.1 ± 0.02	8.98 ± 0.05	0.10942	0.00884	0.54546
TC1000000215.mm.1	Ctgf	connective tissue growth factor	10.71 ± 0.2	11.19 ± 0.08	11.14 ± 0.13	10.57 ± 0.11	0.46434	0.7291	0.00385
TC0400003437.mm.1	Ctps	cytidine 5-triphosphate synthase	7.97 ± 0.1	7.94 ± 0.1	7.78 ± 0.08	7.43 ± 0.1	0.00707	0.14267	0.06854
TC0700001258.mm.1	Ctsc	cathepsin C	9.16 ± 0.06	8.75 ± 0.07	9.07 ± 0.05	8.55 ± 0.17	0.19882	0.00036	0.43432
TC0300000635.mm.1	Ctso	cathepsin O	7.81 ± 0.05	7.58 ± 0.09	7.76 ± 0.05	7.45 ± 0.13	0.34328	0.0099	0.5882
TC0300000903.mm.1	Ctss	cathepsin S	9.29 ± 0.15	9.13 ± 0.18	8.85 ± 0.08	8.49 ± 0.15	0.00283	0.1011	0.5242
TC1100003653.mm.1	Cwc25	CWC25 spliceosome-associated protein homolog (S. cerevisi	6.39 ± 0.03	6.48 ± 0.02	6.45 ± 0.02	6.42 ± 0.01	0.46784	0.07496	0.00529
TC0800001119.mm.1	Cx3cl1	chemokine (C-X3-C motif) ligand 1	6.48 ± 0.06	6.55 ± 0.01	6.73 ± 0.02	6.53 ± 0.02	0.00819	0.17815	0.00267

Supplemental Table I

Annotations			Summary Statistics				2 way ANOVA p-values		
Probe Set ID	Symbol	Description	XY sh	XY Or	XX sh	XX Or	XY vs XX	Sh vs Or	Intrxn
TC0500000922.mm.1	Cxcl13	chemokine (C-X-C motif) ligand 13	9.21 ± 0.24	6.86 ± 0.24	8.08 ± 0.17	6.65 ± 0.37	0.03977	1.2E-05	0.15663
TC0X00002242.mm.1	Cxx1b	CAAX box 1B	8.67 ± 0.06	8.3 ± 0.08	8.63 ± 0.04	8.37 ± 0.06	0.74714	0.00026	0.42947
TC1500001967.mm.1	Cyb5r3	cytochrome b5 reductase 3	8.76 ± 0.05	8.83 ± 0.01	8.88 ± 0.05	8.71 ± 0.03	0.6885	0.39845	0.00662
TC0800003068.mm.1	Cyba	cytochrome b-245, alpha polypeptide	7.59 ± 0.05	7.64 ± 0.02	7.66 ± 0.02	7.45 ± 0.05	0.32067	0.15732	0.00291
TC0700000933.mm.1	Cyfip1	cytoplasmic FMR1 interacting protein 1	8.63 ± 0.05	8.54 ± 0.02	8.61 ± 0.03	8.38 ± 0.07	0.09899	0.00481	0.12129
TC1700002571.mm.1	Cyp1b1	cytochrome P450, family 1, subfamily b, polypeptide 1	9.52 ± 0.14	9.32 ± 0.1	9.79 ± 0.08	9.01 ± 0.16	0.85878	0.00363	0.0207
TC0600002592.mm.1	Cyp26b1	cytochrome P450, family 26, subfamily b, polypeptide 1	6.14 ± 0.09	6.53 ± 0.08	6.44 ± 0.09	6.58 ± 0.07	0.0374	0.00492	0.11351
TC0700000430.mm.1	Cyp2b10	cytochrome P450, family 2, subfamily b, polypeptide 10	5.75 ± 0.2	4.92 ± 0.09	5.23 ± 0.04	4.96 ± 0.05	0.22451	0.00376	0.1427
TC0700002023.mm.1	Cyp2e1	cytochrome P450, family 2, subfamily e, polypeptide 1	12.04 ± 0.25	10.44 ± 0.17	10.34 ± 0.14	10.69 ± 0.27	0.01091	0.0274	0.00137
TC0400003097.mm.1	Cyp2j6	cytochrome P450, family 2, subfamily j, polypeptide 6	7.52 ± 0.15	6.95 ± 0.13	7.1 ± 0.09	7.41 ± 0.1	0.88263	0.31847	0.00366
TC1700001856.mm.1	Cyp4f14	cytochrome P450, family 4, subfamily f, polypeptide 14	4.96 ± 0.04	5 ± 0.01	5.17 ± 0.04	5.01 ± 0.01	0.00717	0.09372	0.0125
TC0300003087.mm.1	Cyr61	cysteine rich protein 61	10.88 ± 0.15	11.63 ± 0.3	11.64 ± 0.13	11.18 ± 0.12	0.51827	0.58817	0.00883
TC1200001536.mm.1	Cys1	cystin 1	6.88 ± 0.08	7.37 ± 0.11	6.93 ± 0.04	7.03 ± 0.02	0.14076	0.00062	0.00905
TC1600001971.mm.1	Cyyr1	cysteine and tyrosine-rich protein 1	7.38 ± 0.06	7.26 ± 0.1	7.04 ± 0.1	7.41 ± 0.02	0.17353	0.22202	0.00537
TC1700002317.mm.1	D17Wsu104e	DNA segment, Chr 17, Wayne State University 104, expresse	7.66 ± 0.02	7.62 ± 0.01	7.62 ± 0.02	7.51 ± 0.01	0.00281	0.00138	0.03503
TC1500000031.mm.1	Dab2	disabled 2, mitogen-responsive phosphoprotein	8.39 ± 0.06	7.97 ± 0.07	8.33 ± 0.05	8.04 ± 0.09	0.84013	0.0003	0.4928
TC0700000240.mm.1	Dact3	dapper homolog 3, antagonist of beta-catenin (xenopus)	8.51 ± 0.13	8.8 ± 0.08	9.01 ± 0.13	8.64 ± 0.07	0.13225	0.78318	0.0093
TC1300000735.mm.1	Dapk1	death associated protein kinase 1	8.49 ± 0.07	8.16 ± 0.12	8.56 ± 0.01	8.09 ± 0.14	0.91657	0.00128	0.42762
TC0900000865.mm.1	Dapk2	death-associated protein kinase 2	7.24 ± 0.06	7.45 ± 0.03	7.57 ± 0.07	7.33 ± 0.04	0.06525	0.85671	0.00099
TC0200000894.mm.1	Dapl1	death associated protein-like 1	4.19 ± 0.04	4.43 ± 0.05	4.24 ± 0.04	4.16 ± 0.03	0.0087	0.14523	0.00421
TC0200000467.mm.1	Dbh	dopamine beta hydroxylase	9.84 ± 0.84	8.06 ± 0.62	6.34 ± 0.52	9.88 ± 0.29	0.31064	0.13275	0.00201
TC0700000861.mm.1	Dbp	D site albumin promoter binding protein	8.94 ± 0.19	9.16 ± 0.16	6.98 ± 0.05	9.05 ± 0.1	2.5E-05	1.3E-06	8.1E-05
TC1000000465.mm.1	Dcbld1	discoidin, CUB and LCCL domain containing 1	4.6 ± 0.03	4.58 ± 0.04	4.41 ± 0.05	4.55 ± 0.01	0.00734	0.12793	0.03322
TC0200000006.mm.1	Dclre1c	DNA cross-link repair 1C, PSO2 homolog (S. cerevisiae)	5.75 ± 0.03	5.55 ± 0.01	5.63 ± 0.03	5.44 ± 0.07	0.02852	0.00101	0.94211
TC0300000761.mm.1	Dcst2	DC-STAMP domain containing 2	5.43 ± 0.02	5.48 ± 0.03	5.37 ± 0.04	5.54 ± 0.05	0.94723	0.00535	0.10788
TC0400002477.mm.1	Dctn3	dynactin 3	8.65 ± 0.1	8.29 ± 0.07	8.26 ± 0.09	8.47 ± 0.04	0.22412	0.38189	0.00345
TC1100004228.mm.1	Dcxr	dicarbonyl L-xylulose reductase	6.61 ± 0.04	6.66 ± 0.03	6.81 ± 0.04	6.69 ± 0.01	0.00521	0.3525	0.01933
TC1700000663.mm.1	Ddah2	dimethylarginine dimethylaminohydrolase 2	6.93 ± 0.04	7.03 ± 0.03	7.22 ± 0.05	7.1 ± 0.01	0.00022	0.91292	0.0088
TC1100002225.mm.1	Ddc	dopa decarboxylase	7.96 ± 0.68	6.59 ± 0.31	5.86 ± 0.16	7.72 ± 0.25	0.44906	0.42454	0.00617
TC1400001906.mm.1	Ddhd1	DDHD domain containing 1	6.73 ± 0.08	6.43 ± 0.06	6.38 ± 0.06	6.58 ± 0.06	0.15335	0.43509	0.00265
TSUnmapped000000	Ddit3	DNA-damage inducible transcript 3 (Ddit3), transcript variant	7.74 ± 0.04	8.02 ± 0.04	7.78 ± 0.06	7.87 ± 0.03	0.19253	0.0007	0.03858
TC0300001394.mm.1	Ddit4l	DNA-damage-inducible transcript 4-like	5.19 ± 0.05	5.26 ± 0.04	5.42 ± 0.03	5.44 ± 0.07	0.0021	0.4892	0.75846

Supplemental Table I

Annotations			Summary Statistics				2 way ANOVA p-values		
Probe Set ID	Symbol	Description	XY sh	XY Or	XX sh	XX Or	XY vs XX	Sh vs Or	Intrxn
TC1000002264.mm.1	Ddx21	DEAD (Asp-Glu-Ala-Asp) box polypeptide 21	8.52 ± 0.06	8.49 ± 0.05	8.42 ± 0.02	8.28 ± 0.06	0.00951	0.10611	0.30847
TC0X00000166.mm.1	Ddx3x	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 3, X-linked	10.67 ± 0.05	10.71 ± 0.07	10.98 ± 0.05	10.82 ± 0.05	0.00295	0.30439	0.10246
TC0Y00000235.mm.1	Ddx3y	DEAD (Asp-Glu-Ala-Asp) box polypeptide 3, Y-linked	8.71 ± 0.1	8.64 ± 0.12	4.13 ± 0.02	4.07 ± 0.04	1.1E-16	0.31083	0.74463
TC0800000261.mm.1	Defb2	defensin beta 2	4.01 ± 0.04	4.31 ± 0.05	4.17 ± 0.07	4.18 ± 0.04	0.83292	0.00951	0.01408
TC0200002287.mm.1	Defb20	defensin beta 20	5.29 ± 0.04	5.64 ± 0.03	5.35 ± 0.05	5.48 ± 0.07	0.25528	0.00046	0.06947
TC0800000209.mm.1	Defb33	defensin beta 33	4.04 ± 0.01	4.26 ± 0.05	4.15 ± 0.02	4.24 ± 0.06	0.30044	0.00182	0.1033
TC0100003709.mm.1	Degs1	degenerative spermatocyte homolog 1 (Drosophila)	8.35 ± 0.04	8.35 ± 0.02	8.24 ± 0.04	8.22 ± 0.03	0.00868	0.78072	0.45578
TC1200002354.mm.1	Degs2	degenerative spermatocyte homolog 2 (Drosophila), lipid des	5.06 ± 0.01	5.19 ± 0.02	5.22 ± 0.07	5.33 ± 0.06	0.0057	0.01777	0.7202
TC1300001928.mm.1	Dek	DEK oncogene (DNA binding)	8.76 ± 0.08	8.96 ± 0.06	9.06 ± 0.06	8.8 ± 0.1	0.2793	0.84656	0.00975
TC1700002347.mm.1	Dennd1c	DENN/MADD domain containing 1C	5.36 ± 0.02	5.49 ± 0.03	5.43 ± 0.04	5.5 ± 0.03	0.16646	0.00435	0.43296
TC0300000787.mm.1	Dennd4b	DENN/MADD domain containing 4B	6.7 ± 0.01	6.8 ± 0.02	6.77 ± 0.01	6.8 ± 0.01	0.01683	0.00036	0.0417
TC1500001777.mm.1	Dgat1	diacylglycerol O-acyltransferase 1	7.75 ± 0.16	7.69 ± 0.14	7.35 ± 0.19	8.11 ± 0.08	0.66183	0.08763	0.00691
TC1600001301.mm.1	Dgcr14	DiGeorge syndrome critical region gene 14	7.61 ± 0.03	7.75 ± 0.03	7.73 ± 0.02	7.71 ± 0.02	0.11894	0.03502	0.00467
TC1600001380.mm.1	Dgkg	diacylglycerol kinase, gamma	8.12 ± 0.16	7.99 ± 0.1	7.56 ± 0.04	7.54 ± 0.09	0.00285	0.9916	0.84323
TC1400002476.mm.1	Dgkh	diacylglycerol kinase, eta	6.75 ± 0.05	6.69 ± 0.03	6.42 ± 0.05	6.55 ± 0.05	0.00036	0.30138	0.10459
TC0400001856.mm.1	Dhrs3	dehydrogenase/reductase (SDR family) member 3	9.31 ± 0.08	9.39 ± 0.03	9.76 ± 0.03	9.23 ± 0.13	0.12532	0.01187	0.00331
TC0100003834.mm.1	Diexf	digestive organ expansion factor homolog (zebrafish)	6.26 ± 0.01	6.34 ± 0.04	6.28 ± 0.01	6.2 ± 0.03	0.02615	0.99027	0.00488
TC0300001342.mm.1	Dkk2	dickkopf homolog 2 (Xenopus laevis)	5.82 ± 0.26	5.14 ± 0.03	5.19 ± 0.09	5.64 ± 0.1	0.84624	0.62025	0.00739
TC0X00000963.mm.1	Dlg3	discs, large homolog 3 (Drosophila)	6.71 ± 0.05	6.8 ± 0.03	6.92 ± 0.07	6.68 ± 0.05	0.29941	0.28395	0.00447
TC1700001497.mm.1	Dll1	delta-like 1 (Drosophila)	6.98 ± 0.05	7.14 ± 0.09	7.31 ± 0.05	7.02 ± 0.05	0.18798	0.25092	0.00539
TC1500001878.mm.1	Dmc1	DMC1 dosage suppressor of mck1 homolog, meiosis-specific	4.43 ± 0.02	4.55 ± 0.02	4.58 ± 0.03	4.52 ± 0.01	0.00555	0.13009	0.00068
TC0800002617.mm.1	Dnaja2	DnaJ (Hsp40) homolog, subfamily A, member 2	9.26 ± 0.02	9.23 ± 0.06	9.11 ± 0.03	9.13 ± 0.05	0.00833	0.96744	0.51684
TC1600000322.mm.1	Dnajb11	DnaJ (Hsp40) homolog, subfamily B, member 11	7.59 ± 0.05	7.41 ± 0.06	7.45 ± 0.06	7.15 ± 0.08	0.01111	0.00386	0.2669
TC1100003776.mm.1	Dnajc7	DnaJ (Hsp40) homolog, subfamily C, member 7	7.8 ± 0.06	7.74 ± 0.06	7.62 ± 0.03	7.85 ± 0.03	0.31872	0.25672	0.00549
TC1500001886.mm.1	Dnal4	dynein, axonemal, light chain 4	5.82 ± 0.02	5.89 ± 0.01	5.9 ± 0.01	5.85 ± 0.03	0.44132	0.55551	0.00846
TC1400001432.mm.1	Dnase1l3	deoxyribonuclease 1-like 3	4.1 ± 0.05	4.26 ± 0.07	4.09 ± 0.03	4.29 ± 0.07	0.9772	0.0086	0.59521
TC1900000583.mm.1	Dntt	deoxynucleotidyltransferase, terminal	3.5 ± 0.05	4.39 ± 0.45	3.67 ± 0.03	4.66 ± 0.43	0.51116	0.00801	0.81549
TC0600002554.mm.1	Dok1	docking protein 1	7.2 ± 0.07	7.35 ± 0.05	7.41 ± 0.05	7.04 ± 0.04	0.52113	0.14149	0.00062
TC1300002062.mm.1	Dok3	docking protein 3	5.98 ± 0.02	6.17 ± 0.05	6.09 ± 0.02	6.14 ± 0.03	0.48014	0.00536	0.0993
TC0800002735.mm.1	Dok4	docking protein 4	6.77 ± 0.02	6.83 ± 0.02	6.87 ± 0.01	6.8 ± 0.01	0.11503	0.62568	0.00465
TC0900000504.mm.1	Dpagt1	dolichyl-phosphate (UDP-N-acetylglucosamine) acetylglucosa	7.26 ± 0.03	7.12 ± 0.03	7.19 ± 0.05	6.99 ± 0.07	0.04676	0.00233	0.4706
TC0800001511.mm.1	Dpep1	dipeptidase 1 (renal)	10.05 ± 0.11	8.84 ± 0.07	10.15 ± 0.08	8.81 ± 0.21	0.56865	2.9E-07	0.44213

Supplemental Table I

Annotations			Summary Statistics				2 way ANOVA p-values		
Probe Set ID	Symbol	Description	XY sh	XY Or	XX sh	XX Or	XY vs XX	Sh vs Or	Intrxn
TC0100001510.mm.1	Dpt	dermatopontin	12.25 ± 0.05	12.07 ± 0.03	12.31 ± 0.02	11.95 ± 0.13	0.66228	0.00244	0.24275
TC0600000917.mm.1	Dqx1	DEAQ RNA-dependent ATPase	5.14 ± 0.03	5.25 ± 0.02	5.17 ± 0.03	5.32 ± 0.07	0.18708	0.00397	0.82294
TC1000002642.mm.1	Dram1	DNA-damage regulated autophagy modulator 1	8.57 ± 0.08	8.27 ± 0.09	8.37 ± 0.04	8.18 ± 0.08	0.0595	0.00455	0.38094
TC0900000593.mm.1	Drd2	dopamine receptor D2	6.84 ± 0.66	5.51 ± 0.22	4.98 ± 0.08	6.57 ± 0.26	0.52072	0.57438	0.00826
TC0X00001277.mm.1	Drp2	dystrophin related protein 2	5.96 ± 0.15	5.65 ± 0.08	5.54 ± 0.07	6.01 ± 0.11	0.8537	0.30605	0.00971
TC0X00001888.mm.1	Drr1	developmentally regulated repeat element-containing transcri	10.59 ± 0.09	10.59 ± 0.03	10.33 ± 0.05	10.43 ± 0.04	0.00813	0.41787	0.50158
TC1900001163.mm.1	Dtx4	deltex 4 homolog (Drosophila)	7.65 ± 0.05	7.39 ± 0.06	7.88 ± 0.06	7.49 ± 0.04	0.00915	4.1E-05	0.24594
TC0200001913.mm.1	Dusp2	dual specificity phosphatase 2	5.38 ± 0.04	5.71 ± 0.06	5.57 ± 0.06	5.71 ± 0.02	0.09165	0.00043	0.07718
TC0200001881.mm.1	Dut	deoxyuridine triphosphatase	6.74 ± 0.02	6.83 ± 0.01	6.82 ± 0.03	6.78 ± 0.01	0.33302	0.11076	0.00221
TC1100000936.mm.1	Dvl2	dishevelled 2, dsh homolog (Drosophila)	6.62 ± 0.04	6.83 ± 0.02	6.78 ± 0	6.85 ± 0.04	0.02835	0.00173	0.11639
TC1700001264.mm.1	Dync2li1	dynein cytoplasmic 2 light intermediate chain 1	6.79 ± 0.03	6.73 ± 0.05	7.01 ± 0.05	6.66 ± 0.09	0.14323	0.00473	0.01347
TC1700001381.mm.1	Dynlt1a	dynein light chain Tctex-type 1A	7.36 ± 0.05	7.27 ± 0.04	7.53 ± 0.03	7.42 ± 0.03	0.0009	0.04105	0.61615
TC1700000060.mm.1	Dynlt1b	dynein light chain Tctex-type 1B	8.14 ± 0.07	7.99 ± 0.03	8.33 ± 0.04	8.23 ± 0.04	0.00067	0.03182	0.65268
TC1700000061.mm.1	Dynlt1c	dynein light chain Tctex-type 1C	6.32 ± 0.03	6.19 ± 0.03	6.43 ± 0.04	6.34 ± 0.04	0.00215	0.00735	0.57462
TC1700001388.mm.1	Dynlt1f	dynein light chain Tctex-type 1F	6.53 ± 0.04	6.44 ± 0.03	6.7 ± 0.05	6.57 ± 0.02	0.00133	0.01138	0.6885
TC0600003319.mm.1	Dynlt1-ps1	dynein light chain Tctex-type 1, pseudogene 1	8.97 ± 0.05	8.84 ± 0.05	9.23 ± 0.03	9.15 ± 0.06	6.9E-05	0.0772	0.74107
TC0600000948.mm.1	Dysf	dysferlin	7.48 ± 0.03	7.4 ± 0.01	7.33 ± 0.01	7.5 ± 0.05	0.51788	0.22727	0.00197
TC0900003325.mm.1	Dyx1c1	dyslexia susceptibility 1 candidate 1 homolog (human)	5.16 ± 0.04	5.29 ± 0.03	5.37 ± 0.03	5.32 ± 0.05	0.00538	0.24955	0.02658
TC1400002719.mm.1	Dzip1	DAZ interacting protein 1	6.35 ± 0.07	6.52 ± 0.01	6.64 ± 0.06	6.48 ± 0.06	0.036	0.88313	0.00861
TC0300002482.mm.1	Ecm1	extracellular matrix protein 1	9.1 ± 0.09	9.02 ± 0.07	9.26 ± 0.08	8.77 ± 0.03	0.80753	0.00371	0.01023
TC1300000565.mm.1	Ecm2	extracellular matrix protein 2, female organ and adipocyte spe	9.66 ± 0.1	9.95 ± 0.09	9.95 ± 0.05	9.63 ± 0.13	0.99234	0.99234	0.00761
TC1000002205.mm.1	Edar	ectodysplasin-A receptor	5.35 ± 0.03	5.54 ± 0.04	5.43 ± 0.05	5.52 ± 0.05	0.60396	0.00642	0.28903
TC0200004970.mm.1	Edem2	ER degradation enhancer, mannosidase alpha-like 2	7.13 ± 0.01	7.07 ± 0.02	7.13 ± 0.02	7.09 ± 0.01	0.38076	0.0087	0.55399
TC1300000998.mm.1	Edil3	EGF-like repeats and discoidin I-like domains 3	5.23 ± 0.15	4.85 ± 0.06	4.8 ± 0.03	5.15 ± 0.09	0.80028	0.89282	0.00824
TC1400002641.mm.1	Ednrb	endothelin receptor type B	8.47 ± 0.07	7.98 ± 0.17	8.1 ± 0.11	8.31 ± 0.03	0.85624	0.2053	0.00438
TC1500001750.mm.1	Eef1d	eukaryotic translation elongation factor 1 delta (guanine nucle	7.33 ± 0.03	7.47 ± 0.02	7.45 ± 0.03	7.42 ± 0.03	0.17228	0.04072	0.00553
TC0400003894.mm.1	Efhd2	EF hand domain containing 2	8.67 ± 0.04	8.72 ± 0.05	8.75 ± 0.04	8.54 ± 0.06	0.5207	0.23656	0.00829
TC1100000161.mm.1	Egfr	epidermal growth factor receptor	8.85 ± 0.1	8.29 ± 0.09	8.76 ± 0.07	8.03 ± 0.14	0.18458	5.2E-05	0.31441
TC0700002417.mm.1	Ehd2	EH-domain containing 2	10.48 ± 0.06	10.34 ± 0.02	10.5 ± 0.03	10.11 ± 0.07	0.05979	0.00018	0.04092
TC1600001368.mm.1	Ehhadh	enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coenzyme A de	8.68 ± 0.18	8.15 ± 0.24	7.26 ± 0.31	8.56 ± 0.21	0.04287	0.14708	0.00157
TC1700000650.mm.1	Ehmt2	euchromatic histone lysine N-methyltransferase 2	8.29 ± 0.01	8.35 ± 0.01	8.34 ± 0.01	8.36 ± 0.02	0.06403	0.00474	0.16336
TC0X00002643.mm.1	Eif2s3x	eukaryotic translation initiation factor 2, subunit 3, structural g	9.55 ± 0.02	9.62 ± 0.05	10.08 ± 0.05	10 ± 0.07	2.5E-07	0.85098	0.13539

Supplemental Table I

Annotations			Summary Statistics				2 way ANOVA p-values		
Probe Set ID	Symbol	Description	XY sh	XY Or	XX sh	XX Or	XY vs XX	Sh vs Or	Intrxn
TC0Y00000006.mm.1	Eif2s3y	eukaryotic translation initiation factor 2, subunit 3, structural g	6.64 ± 0.12	6.71 ± 0.1	4.51 ± 0.03	4.56 ± 0.03	2.4E-12	0.85942	0.66076
TC0500001692.mm.1	Eif3b	eukaryotic translation initiation factor 3, subunit B	9.32 ± 0.02	9.2 ± 0.05	9.17 ± 0.01	9.09 ± 0.04	0.00152	0.00586	0.52517
TC1500001504.mm.1	Eif3h	eukaryotic translation initiation factor 3, subunit H	10.71 ± 0.05	10.89 ± 0.03	10.87 ± 0.02	10.75 ± 0.08	0.73247	0.42607	0.00792
TC1100003056.mm.1	Eif4a1	eukaryotic translation initiation factor 4A1	8.89 ± 0.02	8.83 ± 0.04	8.72 ± 0.02	8.77 ± 0.03	0.00051	0.66451	0.03689
TC1600000288.mm.1	Eif4g1	eukaryotic translation initiation factor 4, gamma 1	9.43 ± 0.02	9.3 ± 0.02	9.24 ± 0.04	9.32 ± 0.03	0.00585	0.24888	0.00176
TC0400001715.mm.1	Eif4g3	eukaryotic translation initiation factor 4 gamma, 3	8.12 ± 0.02	7.97 ± 0.03	8.08 ± 0.03	7.9 ± 0.05	0.19635	0.00041	0.50431
TC0200004973.mm.1	Eif6	eukaryotic translation initiation factor 6	8.12 ± 0.03	8.19 ± 0.01	8.22 ± 0.01	8.27 ± 0.03	0.00563	0.04864	0.77167
TC0400003043.mm.1	Elavl2	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (	5.66 ± 0.21	5.33 ± 0.14	5.08 ± 0.04	5.77 ± 0.09	0.82268	0.16234	0.00771
TC0500003379.mm.1	Eln	elastin	11.13 ± 0.14	11.1 ± 0.06	11.32 ± 0.1	10.43 ± 0.15	0.10226	0.00325	0.00268
TC0900001899.mm.1	Elof1	elongation factor 1 homolog (ELF1, S. cerevisiae)	7.6 ± 0.03	7.75 ± 0.05	7.68 ± 0.04	7.84 ± 0.06	0.12965	0.00683	0.70817
TC0300001521.mm.1	Eltd1	EGF, latrophilin seven transmembrane domain containing 1	8.62 ± 0.13	8.27 ± 0.15	8.1 ± 0.17	8.62 ± 0.03	0.37274	0.72995	0.00402
TC0800003249.mm.1	Emc8	ER membrane protein complex subunit 8	8.11 ± 0.07	8.3 ± 0.01	8.29 ± 0.05	8.15 ± 0.06	0.77485	0.66175	0.00968
TC0500000305.mm.1	Emilin1	elastin microfibril interfacer 1	7.6 ± 0.08	7.82 ± 0.03	7.89 ± 0.08	7.63 ± 0.04	0.39322	0.76721	0.00268
TC1200001109.mm.1	Eml1	echinoderm microtubule associated protein like 1	8.75 ± 0.09	8.82 ± 0.03	8.9 ± 0.07	8.59 ± 0.06	0.76799	0.20128	0.00894
TC0700000290.mm.1	Eml2	echinoderm microtubule associated protein like 2	7.53 ± 0.03	7.62 ± 0.03	7.67 ± 0.05	7.57 ± 0.01	0.10354	0.79314	0.00644
TC0600001606.mm.1	Emp1	epithelial membrane protein 1	9.66 ± 0.07	9.51 ± 0.06	9.66 ± 0.07	9.31 ± 0.09	0.22809	0.0043	0.14589
TC1600001191.mm.1	Emp2	epithelial membrane protein 2	10.18 ± 0.1	10.29 ± 0.05	10.47 ± 0.07	10.13 ± 0.06	0.26053	0.26373	0.00837
TC1700001034.mm.1	Emr1	EGF-like module containing, mucin-like, hormone receptor-lik	7.65 ± 0.06	7.3 ± 0.1	7.6 ± 0.05	7.13 ± 0.12	0.26453	0.00049	0.46209
TC0900001768.mm.1	Endod1	endonuclease domain containing 1	8.22 ± 0.08	8.45 ± 0.01	8.39 ± 0.05	8.2 ± 0.04	0.61401	0.58415	0.0018
TC1500002155.mm.1	Endou	endonuclease, polyU-specific	5.08 ± 0.04	5.48 ± 0.1	5.19 ± 0.08	5.47 ± 0.08	0.5962	0.00055	0.49214
TC1100002004.mm.1	Endov	endonuclease V	6.58 ± 0.03	6.74 ± 0.02	6.72 ± 0.02	6.71 ± 0.03	0.03956	0.01239	0.00441
TC0300002926.mm.1	Enpep	glutamyl aminopeptidase	8.01 ± 0.05	7.94 ± 0.07	8.18 ± 0.06	7.84 ± 0.1	0.78884	0.00758	0.12414
TC0200005462.mm.1	Entpd2	ectonucleoside triphosphate diphosphohydrolase 2	8.51 ± 0.05	8.34 ± 0.03	8.68 ± 0.05	8.31 ± 0.06	0.08714	0.00011	0.01934
TC0900001561.mm.1	Eomes	eomesodermin homolog (Xenopus laevis)	4.61 ± 0.03	4.79 ± 0.06	4.72 ± 0	4.78 ± 0.04	0.21811	0.00827	0.18402
TC0600002169.mm.1	Epha1	Eph receptor A1	5.74 ± 0.03	5.92 ± 0.02	5.94 ± 0.02	5.87 ± 0.05	0.07153	0.14585	0.0028
TC1400002266.mm.1	Ephx2	epoxide hydrolase 2, cytoplasmic	9.43 ± 0.2	9.12 ± 0.25	8.7 ± 0.27	9.87 ± 0.1	0.74071	0.13357	0.00232
TC0100001787.mm.1	Eprs	glutamyl-prolyl-tRNA synthetase	9.07 ± 0.02	8.88 ± 0.03	8.85 ± 0.04	8.74 ± 0.08	0.00242	0.00863	0.38767
TC0400001164.mm.1	Eps15	epidermal growth factor receptor pathway substrate 15	8.6 ± 0.04	8.41 ± 0.05	8.57 ± 0.04	8.33 ± 0.11	0.53102	0.00793	0.64806
TC0600003342.mm.1	Eps8	epidermal growth factor receptor pathway substrate 8	7.4 ± 0.05	7.14 ± 0.04	7.24 ± 0.03	7.1 ± 0.04	0.06954	0.00107	0.35827
TC0700000300.mm.1	Ercc2	excision repair cross-complementing rodent repair deficiency,	7.14 ± 0.01	7.17 ± 0	7.21 ± 0.02	7.18 ± 0.01	0.00631	0.86129	0.01899
TC1900001346.mm.1	Ermp1	endoplasmic reticulum metallopeptidase 1	8.89 ± 0.08	8.68 ± 0.08	8.92 ± 0.05	8.67 ± 0.08	0.81639	0.00369	0.82415
TC0500002272.mm.1	Evc	Ellis van Creveld gene syndrome	7.4 ± 0.07	7.55 ± 0.03	7.71 ± 0.08	7.45 ± 0.04	0.0734	0.47387	0.00381

Supplemental Table I

Annotations			Summary Statistics				2 way ANOVA p-values		
Probe Set ID	Symbol	Description	XY sh	XY Or	XX sh	XX Or	XY vs XX	Sh vs Or	Intrxn
TC0500000423.mm.1	Evc2	Ellis van Creveld syndrome 2	7.34 ± 0.06	7.53 ± 0.02	7.55 ± 0.05	7.45 ± 0	0.11973	0.23905	0.00386
TC1100003326.mm.1	Evi2b	ecotropic viral integration site 2b	6.16 ± 0.07	5.92 ± 0.09	6.15 ± 0.05	5.88 ± 0.13	0.76362	0.00912	0.91493
TC1200001236.mm.1	Exoc3l4	exocyst complex component 3-like 4	5.84 ± 0.02	5.98 ± 0.01	6.05 ± 0.05	6.04 ± 0.06	0.00354	0.10555	0.05064
TC1300001814.mm.1	F13a1	coagulation factor XIII, A1 subunit	9.13 ± 0.1	8.56 ± 0.04	9 ± 0.07	8.46 ± 0.03	0.28602	7.2E-06	0.85233
TC1300002462.mm.1	F2r	coagulation factor II (thrombin) receptor	8.9 ± 0.07	8.94 ± 0.06	9.08 ± 0.09	8.62 ± 0.12	0.57547	0.03819	0.00753
TC0300001639.mm.1	Fabp4	fatty acid binding protein 4, adipocyte	11.92 ± 0.12	11.63 ± 0.15	11.41 ± 0.2	11.96 ± 0.02	0.32838	0.58602	0.00458
TC1000000508.mm.1	Fabp7	fatty acid binding protein 7, brain	7.95 ± 0.69	6.62 ± 0.48	5.88 ± 0.46	8.09 ± 0.33	0.71676	0.33806	0.00873
TC0700003657.mm.1	Fah	fumarylacetoacetate hydrolase	8 ± 0.13	7.71 ± 0.13	7.53 ± 0.11	7.89 ± 0.03	0.12871	0.91316	0.00616
TC1400001439.mm.1	Fam107a	family with sequence similarity 107, member A	7.63 ± 0.2	7.08 ± 0.08	6.96 ± 0.04	6.64 ± 0.04	0.00362	0.01914	0.82703
TC1100001459.mm.1	Fam117a	family with sequence similarity 117, member A	6.5 ± 0.03	6.65 ± 0.02	6.56 ± 0.01	6.71 ± 0.06	0.20076	0.00201	0.74025
TC1300001947.mm.1	Fam120a	family with sequence similarity 120, member A	9.72 ± 0.03	9.63 ± 0.02	9.68 ± 0.02	9.59 ± 0.03	0.15756	0.00493	0.77326
TC0600002381.mm.1	Fam13a	family with sequence similarity 13, member A	8.12 ± 0.2	7.77 ± 0.16	7.02 ± 0.21	7.99 ± 0.1	0.0228	0.13741	0.00216
TC0700001015.mm.1	Fam169b	family with sequence similarity 169, member B	4.44 ± 0.03	4.7 ± 0.05	4.6 ± 0.03	4.66 ± 0.04	0.15961	0.00132	0.02525
TC1700001673.mm.1	Fam173a	family with sequence similarity 173, member A	6.87 ± 0.04	6.86 ± 0.03	6.83 ± 0.04	7.03 ± 0.01	0.17339	0.03625	0.00347
TC0900001633.mm.1	Fam198a	family with sequence similarity 198, member A	6.46 ± 0.06	6.71 ± 0.03	6.71 ± 0.06	6.56 ± 0.08	0.36966	0.38916	0.00397
TC1100003993.mm.1	Fam20a	family with sequence similarity 20, member A	6.43 ± 0.05	6.4 ± 0.03	6.65 ± 0.08	6.23 ± 0.07	0.70072	0.00246	0.00547
TC1100002945.mm.1	Fam211a	family with sequence similarity 211, member A	7.24 ± 0.06	7.46 ± 0.04	7.39 ± 0.05	7.31 ± 0.02	0.69036	0.09032	0.00466
TC0500003208.mm.1	Fam216a	family with sequence similarity 216, member A	7.09 ± 0.01	7.05 ± 0.02	7.09 ± 0.02	7 ± 0.03	0.2899	0.00447	0.19775
TC1300000395.mm.1	Fam50b	family with sequence similarity 50, member B	4.63 ± 0.03	4.92 ± 0.08	4.65 ± 0.02	4.71 ± 0.05	0.05097	0.00519	0.05013
TC0200005496.mm.1	Fam78a	family with sequence similarity 78, member A	5.65 ± 0.02	5.88 ± 0.02	5.75 ± 0.03	5.91 ± 0.1	0.24903	0.00213	0.55773
TC1200001446.mm.1	Fam84a	family with sequence similarity 84, member A	6.38 ± 0.12	6.8 ± 0.09	6.7 ± 0.03	6.31 ± 0.1	0.33663	0.92124	0.00112
TC1400001315.mm.1	Farp1	FERM, RhoGEF (Arhgef) and pleckstrin domain protein 1 (ch	7.8 ± 0.02	7.62 ± 0.03	7.79 ± 0.01	7.74 ± 0.06	0.13233	0.00618	0.12108
TC1200002242.mm.1	Fbln5	fibulin 5	10.78 ± 0.11	11.05 ± 0.05	11.04 ± 0.07	10.68 ± 0.12	0.73083	0.8628	0.00366
TC0200001939.mm.1	Fbln7	fibulin 7	8.41 ± 0.11	8.74 ± 0.03	8.92 ± 0.11	8.54 ± 0.1	0.13224	0.79992	0.00248
TC0200004525.mm.1	Fbn1	fibrillin 1	9.78 ± 0.09	9.54 ± 0.05	9.78 ± 0.09	9.11 ± 0.05	0.01522	4.6E-05	0.00906
TC1300000688.mm.1	Fbxl21	F-box and leucine-rich repeat protein 21	4.51 ± 0.02	4.55 ± 0.02	4.67 ± 0.05	4.6 ± 0.03	0.00564	0.79796	0.08056
TC1500001285.mm.1	Fbxl7	F-box and leucine-rich repeat protein 7	6.3 ± 0.05	6.5 ± 0.05	6.43 ± 0.01	6.35 ± 0.03	0.90876	0.19663	0.00617
TC0400002570.mm.1	Fbxo10	F-box protein 10	6.96 ± 0.04	7.03 ± 0.02	7.05 ± 0.03	6.96 ± 0.03	0.41206	0.94335	0.00567
TC0500001302.mm.1	Fbxo21	F-box protein 21	8.6 ± 0.07	8.41 ± 0.08	8.32 ± 0.07	8.57 ± 0.03	0.23726	0.89033	0.00314
TC1000001686.mm.1	Fbxo5	F-box protein 5	5.89 ± 0.02	6.02 ± 0.03	5.92 ± 0.05	5.99 ± 0.03	0.82968	0.00614	0.26394
TC0500003136.mm.1	Fbxw8	F-box and WD-40 domain protein 8	8.25 ± 0.01	8.2 ± 0.01	8.23 ± 0.02	8.16 ± 0.02	0.04869	0.00079	0.58588
TC0100003533.mm.1	Fcer1g	Fc receptor, IgE, high affinity I, gamma polypeptide	7.7 ± 0.06	7.55 ± 0.07	7.71 ± 0.06	7.39 ± 0.08	0.32395	0.00515	0.18284

Supplemental Table I

Annotations			Summary Statistics				2 way ANOVA p-values		
Probe Set ID	Symbol	Description	XY sh	XY Or	XX sh	XX Or	XY vs XX	Sh vs Or	Intrxn
TC0300002506.mm.1	Fcgr1	Fc receptor, IgG, high affinity I	6.41 ± 0.09	6.02 ± 0.05	6.1 ± 0.03	6 ± 0.06	0.05125	0.00532	0.08926
TC0100003522.mm.1	Fcgr2b	Fc receptor, IgG, low affinity IIb	7.29 ± 0.07	6.84 ± 0.13	6.93 ± 0.04	6.67 ± 0.04	0.00792	0.00092	0.41773
TC0100003524.mm.1	Fcgr3	Fc receptor, IgG, low affinity III	7.93 ± 0.04	7.6 ± 0.07	7.57 ± 0.03	7.37 ± 0.05	7.7E-05	0.00023	0.37386
TC0800002441.mm.1	Fcho1	FCH domain only 1	6.01 ± 0.05	6.12 ± 0.02	6.02 ± 0.04	6.23 ± 0.06	0.24808	0.00541	0.3599
TC0200003165.mm.1	Fcna	ficolin A	7.33 ± 0.03	6.99 ± 0.06	7.19 ± 0.05	7.04 ± 0.09	0.58926	0.00153	0.15453
TC0300002284.mm.1	Fcrls	Fc receptor-like S, scavenger receptor	7.47 ± 0.08	7.31 ± 0.05	7.66 ± 0.05	7.18 ± 0.12	0.60347	0.00205	0.05801
TC0100002593.mm.1	Fev	FEV (ETS oncogene family)	6.16 ± 0.04	6.34 ± 0.02	6.31 ± 0.05	6.44 ± 0.07	0.02248	0.00916	0.63402
TC1900000545.mm.1	Ffar4	free fatty acid receptor 4	7.25 ± 0.2	7.57 ± 0.2	6.84 ± 0.2	8.14 ± 0.26	0.94653	0.00583	0.01837
TC0X00001508.mm.1	Fgd1	FYVE, RhoGEF and PH domain containing 1	6.69 ± 0.07	6.83 ± 0.02	6.93 ± 0.03	6.74 ± 0.05	0.18212	0.68142	0.00533
TC1100003064.mm.1	Fgf11	fibroblast growth factor 11	7.43 ± 0.06	7.55 ± 0.03	7.77 ± 0.06	7.55 ± 0.03	0.00823	0.27126	0.01081
TC0X00002292.mm.1	Fgf13	fibroblast growth factor 13	5.96 ± 0.04	6.11 ± 0.02	6.19 ± 0.04	6.07 ± 0	0.0058	0.45742	0.00052
TC0X00001062.mm.1	Fgf16	fibroblast growth factor 16	5.48 ± 0.04	5.73 ± 0.03	5.73 ± 0.04	5.82 ± 0.09	0.00657	0.00899	0.16932
TC1400000829.mm.1	Fgf9	fibroblast growth factor 9	5.75 ± 0.02	5.84 ± 0.02	5.77 ± 0.02	5.91 ± 0.05	0.16644	0.0024	0.32044
TC0100002261.mm.1	Fhl2	four and a half LIM domains 2	7.1 ± 0.06	7.11 ± 0.02	7.25 ± 0.06	7.01 ± 0.04	0.32345	0.08928	0.00816
TC0400002315.mm.1	Fhl5	four and a half LIM domains 5	7.9 ± 0.14	7.35 ± 0.09	7.93 ± 0.1	7.09 ± 0.23	0.568	0.00075	0.27507
TC0X00001667.mm.1	Figf	c-fos induced growth factor	8.87 ± 0.08	8.82 ± 0.02	9.15 ± 0.12	8.55 ± 0.15	0.8779	0.008	0.01328
TC0200003643.mm.1	Fign	fidgetin	5.39 ± 0.09	4.99 ± 0.07	5.26 ± 0.04	5.09 ± 0.08	0.89338	0.00396	0.27167
TC1500002254.mm.1	Fignl2	fidgetin-like 2	5.89 ± 0.08	6.06 ± 0.06	6.27 ± 0.06	6.21 ± 0.09	0.00979	0.76732	0.33609
TC0200005091.mm.1	Fitm2	fat storage-inducing transmembrane protein 2	8.27 ± 0.14	7.96 ± 0.14	7.69 ± 0.17	8.18 ± 0.05	0.09899	0.79812	0.00475
TC0200002263.mm.1	Fkbp1a	FK506 binding protein 1a	9.18 ± 0.03	9.09 ± 0.02	9.13 ± 0.02	9.02 ± 0.03	0.08472	0.00679	0.62834
TC1900001026.mm.1	Fkbp2	FK506 binding protein 2	10.14 ± 0.05	10.1 ± 0.03	10.28 ± 0.03	10.22 ± 0.05	0.00655	0.26323	0.83997
TC1200000951.mm.1	Flrt2	fibronectin leucine rich transmembrane protein 2	7.72 ± 0.1	7.42 ± 0.07	7.68 ± 0.11	7.21 ± 0.08	0.32959	0.0027	0.21637
TC0500003629.mm.1	Flt1	FMS-like tyrosine kinase 1	8.19 ± 0.08	7.99 ± 0.1	7.88 ± 0.09	8.15 ± 0.03	0.19777	0.99126	0.00523
TC1700001605.mm.1	Flywch2	FLYWCH family member 2	5.55 ± 0.04	5.68 ± 0.01	5.65 ± 0.02	5.79 ± 0.07	0.02942	0.00656	0.9702
TC0100003401.mm.1	Fmo1	flavin containing monooxygenase 1	9.89 ± 0.09	9.49 ± 0.05	9.96 ± 0.07	9.56 ± 0.08	0.5579	0.0001	0.7697
TC0100003406.mm.1	Fmo3	flavin containing monooxygenase 3	8.75 ± 0.4	7.96 ± 0.12	7.95 ± 0.16	6.79 ± 0.11	0.00645	0.00698	0.27694
TC0500002183.mm.1	Fndc4	fibronectin type III domain containing 4	6.82 ± 0.04	6.87 ± 0.02	6.93 ± 0.02	6.78 ± 0.03	0.34885	0.26068	0.00133
TC0400001514.mm.1	Fndc5	fibronectin type III domain containing 5	6.4 ± 0.07	6.58 ± 0.03	6.42 ± 0.05	6.66 ± 0.08	0.45496	0.00568	0.62967
TC0700003845.mm.1	Folr2	folate receptor 2 (fetal)	9.16 ± 0.05	8.61 ± 0.11	9.21 ± 0.09	8.64 ± 0.08	0.59861	1.3E-05	0.8605
TC1300001115.mm.1	Foxd1	forkhead box D1	6.21 ± 0.04	6.32 ± 0.05	6.47 ± 0.09	6.44 ± 0.02	0.00544	0.39343	0.22012
TC0600001393.mm.1	Foxj2	forkhead box J2	8.26 ± 0.08	8.32 ± 0.06	8.55 ± 0.07	8.21 ± 0.06	0.20519	0.06822	0.00854
TC0900001242.mm.1	Foxl2	forkhead box L2	5.74 ± 0.06	6.04 ± 0.09	6 ± 0.05	6.09 ± 0.06	0.03234	0.00889	0.10881

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Annotations			Summary Statistics				2 way ANOVA p-values		
Probe Set ID	Symbol	Description	XY sh	XY Or	XX sh	XX Or	XY vs XX	Sh vs Or	Intrxn
TC0300000376.mm.1	Foxo1	forkhead box O1	8.5 ± 0.05	8.61 ± 0.05	8.58 ± 0.03	8.4 ± 0.06	0.1701	0.47963	0.00898
TC0200004919.mm.1	Foxs1	forkhead box S1	6.91 ± 0.12	6.81 ± 0.05	7.62 ± 0.11	6.7 ± 0.06	0.00871	0.00013	0.00094
TC0600002802.mm.1	Frmd4b	FERM domain containing 4B	7.27 ± 0.07	7.05 ± 0	7 ± 0.02	6.98 ± 0.04	0.0072	0.04425	0.12602
TC1200000596.mm.1	Frmd6	FERM domain containing 6	8.45 ± 0.04	8.42 ± 0.07	8.65 ± 0.07	8.24 ± 0.09	0.8106	0.00667	0.00928
TC0300001198.mm.1	Frrs1	ferric-chelate reductase 1	7.07 ± 0.04	6.87 ± 0.05	6.99 ± 0.03	6.85 ± 0.03	0.37385	0.00112	0.651
TC1600000536.mm.1	Fstl1	follistatin-like 1	10.91 ± 0.12	11.01 ± 0.04	11.05 ± 0.07	10.64 ± 0.08	0.38171	0.20293	0.00833
TC0300001528.mm.1	Fubp1	far upstream element (FUSE) binding protein 1	7.3 ± 0.04	7.16 ± 0.05	7.06 ± 0.03	7.06 ± 0.08	0.00631	0.18357	0.20074
TC0400001668.mm.1	Fuca1	fucosidase, alpha-L- 1, tissue	9.35 ± 0.02	9.26 ± 0.02	9.44 ± 0.04	9.32 ± 0.03	0.02838	0.00247	0.54556
TC1100001694.mm.1	Fzd2	frizzled homolog 2 (Drosophila)	8.68 ± 0.07	8.97 ± 0.07	9.03 ± 0.06	8.91 ± 0.05	0.03125	0.16796	0.00663
TC0100002470.mm.1	Fzd5	frizzled homolog 5 (Drosophila)	7.62 ± 0.04	7.81 ± 0.07	7.96 ± 0.07	7.68 ± 0.03	0.04206	0.48878	0.00044
TC1800000060.mm.1	Fzd8	frizzled homolog 8 (Drosophila)	7.26 ± 0.07	7.45 ± 0.08	7.84 ± 0.13	7.16 ± 0.17	0.23433	0.05117	0.00222
TC0700001345.mm.1	Gab2	growth factor receptor bound protein 2-associated protein 2	8.89 ± 0.07	8.78 ± 0.02	9.05 ± 0.09	8.62 ± 0.13	0.9258	0.00911	0.0598
TC0100000948.mm.1	Gal3st2	galactose-3-O-sulfotransferase 2	4.79 ± 0.05	4.97 ± 0.04	4.89 ± 0.08	5.04 ± 0.01	0.09697	0.00503	0.68238
TC0500000229.mm.1	Galnt11	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylga	7.44 ± 0.04	7.43 ± 0.03	7.33 ± 0.03	7.16 ± 0.09	0.00483	0.15213	0.09831
TC1200000740.mm.1	Galnt16	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylga	8.46 ± 0.12	8.78 ± 0.05	8.62 ± 0.11	8.42 ± 0.05	0.4958	0.36029	0.0082
TC0800002256.mm.1	Galnt7	UDP-N-acetyl-alpha-D-galactosamine: polypeptide N-acetylga	6.18 ± 0.04	6.12 ± 0.02	6.06 ± 0.02	6.03 ± 0.04	0.00833	0.26973	0.92573
TC0600000661.mm.1	Gars	glycyl-tRNA synthetase	9.16 ± 0.1	8.92 ± 0.09	8.86 ± 0.07	9.09 ± 0.05	0.2496	0.67325	0.00789
TC1100000859.mm.1	Gas7	growth arrest specific 7	7.5 ± 0.07	7.21 ± 0.05	7.41 ± 0.04	7.25 ± 0.06	0.95686	0.0076	0.57007
TC1800000091.mm.1	Gata6	GATA binding protein 6	9.36 ± 0.13	9.63 ± 0.06	9.81 ± 0.06	9.41 ± 0.13	0.22002	0.6245	0.00533
TC0200004511.mm.1	Gatm	glycine amidinotransferase (L-arginine:glycine amidinotransfe	7.65 ± 0.31	6.76 ± 0.14	6.6 ± 0.15	7.39 ± 0.2	0.54905	0.94559	0.00497
TC0300000750.mm.1	Gba	glucosidase, beta, acid	8.29 ± 0.05	8.03 ± 0.02	8.14 ± 0.04	7.92 ± 0.09	0.05905	0.0011	0.992
TC1500000663.mm.1	Gcat	glycine C-acetyltransferase (2-amino-3-ketobutyrate-coenzym	6.14 ± 0.02	6.27 ± 0	6.29 ± 0.01	6.31 ± 0.03	0.00161	0.01133	0.08886
TC1900001253.mm.1	Gda	guanine deaminase	7.78 ± 0.09	7.13 ± 0.12	7.34 ± 0.05	6.97 ± 0.08	0.01002	0.00016	0.24457
TC0300000994.mm.1	Gdap2	ganglioside-induced differentiation-associated-protein 2	7.99 ± 0.04	7.88 ± 0.03	7.82 ± 0.04	7.66 ± 0.09	0.00348	0.03132	0.52549
TC0700001385.mm.1	Gdpd5	glycerophosphodiester phosphodiesterase domain containing	6.8 ± 0.03	6.82 ± 0.02	6.9 ± 0.02	6.86 ± 0.01	0.00557	0.73374	0.14896
TC0400000092.mm.1	Gem	GTP binding protein (gene overexpressed in skeletal muscle)	7.51 ± 0.16	7.91 ± 0.06	8 ± 0.12	7.53 ± 0.08	0.70712	0.68695	0.0042
TC0X00001679.mm.1	Gemin8	gem (nuclear organelle) associated protein 8	4.46 ± 0	4.51 ± 0.03	4.48 ± 0.01	4.43 ± 0.02	0.09709	0.94254	0.0039
TC1100000526.mm.1	Gfpt2	glutamine fructose-6-phosphate transaminase 2	8.74 ± 0.17	8.12 ± 0.08	8.64 ± 0.09	8.03 ± 0.11	0.66366	0.00071	0.80432
TC1400002756.mm.1	Ggact	gamma-glutamylamine cyclotransferase	7.67 ± 0.01	7.54 ± 0.03	7.69 ± 0.01	7.54 ± 0.07	0.7675	0.00237	0.87823
TC1500001136.mm.1	Ghr	growth hormone receptor	8.24 ± 0.07	7.84 ± 0.08	7.95 ± 0.07	7.91 ± 0.06	0.09254	0.0054	0.01459
TC0500001625.mm.1	Gigyf1	GRB10 interacting GYF protein 1	7.55 ± 0.02	7.69 ± 0.01	7.68 ± 0.02	7.68 ± 0.02	0.00558	0.00326	0.00349
TC0600003501.mm.1	Gimap5	GTPase, IMAP family member 5	5.33 ± 0.03	5.5 ± 0.02	5.46 ± 0.02	5.43 ± 0	0.53665	0.0138	0.00099

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Annotations			Summary Statistics				2 way ANOVA p-values		
Probe Set ID	Symbol	Description	XY sh	XY Or	XX sh	XX Or	XY vs XX	Sh vs Or	Intrxn
TC0100000971.mm.1	Gin1	gypsy retrotransposon integrase 1	5.06 ± 0.07	4.93 ± 0.04	5.12 ± 0.07	4.92 ± 0.05	0.92805	0.00824	0.87955
TC0800000930.mm.1	Gipc1	GIPC PDZ domain containing family, member 1	8.1 ± 0.03	8.13 ± 0.02	8.21 ± 0.04	8.2 ± 0.03	0.00652	0.51088	0.42016
TC0900001939.mm.1	Glb1l2	galactosidase, beta 1-like 2	7.03 ± 0.07	6.62 ± 0.07	6.76 ± 0.05	6.67 ± 0.11	0.13296	0.00569	0.05512
TC0200000517.mm.1	Gle1	GLE1 RNA export mediator (yeast)	7.16 ± 0.03	7.25 ± 0.01	7.22 ± 0.02	7.16 ± 0.02	0.71255	0.45816	0.00564
TC1000003113.mm.1	Gli1	GLI-Kruppel family member GLI1	6.64 ± 0.03	6.66 ± 0.02	6.76 ± 0.04	6.71 ± 0.03	0.00479	0.74184	0.1592
TC1300000105.mm.1	Gli3	GLI-Kruppel family member GLI3	6.49 ± 0.05	6.53 ± 0.03	6.67 ± 0.04	6.45 ± 0.04	0.18454	0.06381	0.00482
TC0400000458.mm.1	Glipr2	GLI pathogenesis-related 2	7.79 ± 0.02	7.71 ± 0.04	7.86 ± 0.04	7.64 ± 0.04	0.87156	0.00207	0.04729
TC0500002927.mm.1	Glmn	glomulin, FKBP associated protein	5.61 ± 0.02	5.47 ± 0.06	5.6 ± 0.03	5.5 ± 0.04	0.65516	0.00997	0.71184
TC0800000798.mm.1	Glt25d1	glycosyltransferase 25 domain containing 1	8.2 ± 0.07	8.32 ± 0.04	8.27 ± 0.04	8.09 ± 0.04	0.21082	0.85154	0.00824
TC0700002415.mm.1	Gltscr2	glioma tumor suppressor candidate region gene 2	8.25 ± 0.03	8.42 ± 0.03	8.46 ± 0.03	8.44 ± 0.05	0.00642	0.04312	0.01446
TC0100001387.mm.1	Glul	glutamate-ammonia ligase (glutamine synthetase)	10.82 ± 0.1	10.49 ± 0.1	10.28 ± 0.11	10.67 ± 0.09	0.0586	0.98596	0.00169
TC1600001151.mm.1	Glyr1	glyoxylate reductase 1 homolog (Arabidopsis)	8.78 ± 0.01	8.76 ± 0.06	8.64 ± 0.01	8.68 ± 0.03	0.00713	0.73071	0.36318
TC0400000384.mm.1	Gm7819	SubName: Full=4933409K07Rik protein;	7.64 ± 0.11	7.4 ± 0.07	7.54 ± 0.08	7.22 ± 0.1	0.13324	0.00882	0.72978
TC0500001995.mm.1	Gnai1	guanine nucleotide binding protein (G protein), alpha inhibitin	9.76 ± 0.05	9.61 ± 0.04	9.56 ± 0.03	9.37 ± 0.11	0.00694	0.0297	0.70687
TC1800000694.mm.1	Gnal	guanine nucleotide binding protein, alpha stimulating, olfactor	6.02 ± 0.32	5.15 ± 0.09	4.98 ± 0.06	5.6 ± 0.14	0.30688	0.78347	0.0065
TC0200002700.mm.1	Gnas	GNAS (guanine nucleotide binding protein, alpha stimulating)	7.45 ± 0.07	7.37 ± 0.02	7.29 ± 0.04	7.53 ± 0.03	0.6845	0.17079	0.00289
TC0500003737.mm.1	Gnb2	guanine nucleotide binding protein (G protein), beta 2	7.89 ± 0.04	7.92 ± 0.02	7.99 ± 0.01	8.03 ± 0.03	0.00446	0.2576	0.7761
TC0400004179.mm.1	Gng10	guanine nucleotide binding protein (G protein), gamma 10	8.01 ± 0.03	8.16 ± 0.03	8.11 ± 0.02	8.07 ± 0.03	0.59338	0.04124	0.00282
TC1000002520.mm.1	Gng7	guanine nucleotide binding protein (G protein), gamma 7	5.97 ± 0.03	6.06 ± 0.01	6.07 ± 0.01	6.08 ± 0.03	0.00954	0.02123	0.0508
TC0700000241.mm.1	Gng8	guanine nucleotide binding protein (G protein), gamma 8	5.9 ± 0.05	6.21 ± 0.05	6.2 ± 0.05	6.15 ± 0.04	0.03029	0.01629	0.0027
TC1400001665.mm.1	Gnl3	guanine nucleotide binding protein-like 3 (nucleolar)	7.39 ± 0.05	7.4 ± 0.04	7.3 ± 0.01	7.23 ± 0.04	0.00783	0.52557	0.24796
TC1300002119.mm.1	Golm1	golgi membrane protein 1	7.47 ± 0.06	7.26 ± 0.04	7.35 ± 0.02	7.21 ± 0.06	0.22362	0.00838	0.7436
TC1900001691.mm.1	Gpam	glycerol-3-phosphate acyltransferase, mitochondrial	8.86 ± 0.2	8.48 ± 0.23	8.05 ± 0.23	9.11 ± 0.17	0.43727	0.25418	0.00227
TC1200000848.mm.1	Gpatch2l	G patch domain containing 2 like	7.08 ± 0.03	7.16 ± 0.01	7.2 ± 0.04	7.02 ± 0.05	0.98264	0.23362	0.0021
TC0X00002211.mm.1	Gpc3	glypican 3	9.53 ± 0.09	9.74 ± 0.02	9.44 ± 0.04	9.71 ± 0.12	0.6454	0.00449	0.99749
TC1400001253.mm.1	Gpc6	glypican 6	9.26 ± 0.11	9.53 ± 0.03	9.45 ± 0.07	9.15 ± 0.07	0.35249	0.95418	0.00311
TC0800000348.mm.1	Gpr124	G protein-coupled receptor 124	7.87 ± 0.05	7.92 ± 0	8.12 ± 0.08	7.87 ± 0.06	0.05247	0.15723	0.00886
TC1200002440.mm.1	Gpr132	G protein-coupled receptor 132	5.09 ± 0.07	5.4 ± 0.05	5.24 ± 0.05	5.31 ± 0.04	0.88531	0.00855	0.09377
TC0500001501.mm.1	Gpr133	G protein-coupled receptor 133	8.93 ± 0.14	8.16 ± 0.05	8.67 ± 0.09	7.96 ± 0.07	0.10072	1.5E-05	0.889
TC0300002050.mm.1	Gpr171	G protein-coupled receptor 171	5.11 ± 0.02	5.44 ± 0.05	5.27 ± 0.08	5.41 ± 0.09	0.38668	0.00256	0.21238
TC1400002744.mm.1	Gpr18	G protein-coupled receptor 18	5 ± 0.04	5.54 ± 0.06	5.32 ± 0.15	5.46 ± 0.11	0.23746	0.00305	0.0498
TC0X00000169.mm.1	Gpr34	G protein-coupled receptor 34	4.86 ± 0.05	4.58 ± 0.07	5.1 ± 0.12	4.65 ± 0.13	0.12299	0.00195	0.3606

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Probe Set ID	Symbol	Description	XY sh	XY Or	XX sh	XX Or	XY vs XX	Sh vs Or	Intrxn
TC0X00000653.mm.1	Gpr50	G-protein-coupled receptor 50	4.29 ± 0.02	4.41 ± 0.03	4.33 ± 0.02	4.43 ± 0.06	0.46436	0.00784	0.88527
TC0800001126.mm.1	Gpr56	G protein-coupled receptor 56	8.45 ± 0.13	8.11 ± 0.06	8.02 ± 0.06	8.3 ± 0.03	0.29999	0.92391	0.00774
TC0X00001633.mm.1	Gpr64	G protein-coupled receptor 64	5.41 ± 0.08	4.85 ± 0.04	5.35 ± 0.09	5.01 ± 0.07	0.38193	8.1E-05	0.24273
TC0200000445.mm.1	Gpsm1	G-protein signalling modulator 1 (AGS3-like, C. elegans)	6.67 ± 0.02	6.82 ± 0.01	6.81 ± 0.02	6.82 ± 0.04	0.01732	0.00999	0.02199
TC0800000991.mm.1	Gpt2	glutamic pyruvate transaminase (alanine aminotransferase) 2	7.64 ± 0.15	7.1 ± 0.09	7.05 ± 0.06	7.23 ± 0.05	0.06318	0.14908	0.00668
TC1100000638.mm.1	Gpx3	glutathione peroxidase 3	10.32 ± 0.13	9.34 ± 0.15	9.82 ± 0.13	9.72 ± 0.06	0.67879	0.00085	0.00385
TC0700002792.mm.1	Gramd1a	GRAM domain containing 1A	7.68 ± 0.01	7.66 ± 0.01	7.59 ± 0.02	7.68 ± 0.02	0.03913	0.03068	0.00285
TC1500000700.mm.1	Grap2	GRB2-related adaptor protein 2	5.73 ± 0.05	6.13 ± 0.04	5.8 ± 0.07	6.08 ± 0.08	0.89787	0.00014	0.5098
TC1500000580.mm.1	Grina	glutamate receptor, ionotropic, N-methyl D-aspartate-associa	9.37 ± 0.18	8.87 ± 0.12	8.8 ± 0.12	9.36 ± 0.04	0.73929	0.9088	0.0014
TC1900000866.mm.1	Grk5	G protein-coupled receptor kinase 5	8.98 ± 0.11	8.86 ± 0.08	9.16 ± 0.02	8.7 ± 0.09	0.91014	0.00492	0.07767
TC0500001944.mm.1	Grm3	glutamate receptor, metabotropic 3	5.53 ± 0.16	5.88 ± 0.07	6.2 ± 0.1	5.79 ± 0.1	0.02247	0.94504	0.00557
TC1100001688.mm.1	Grn	granulin	9.01 ± 0.03	8.93 ± 0.02	8.97 ± 0.04	8.83 ± 0.03	0.09889	0.00783	0.26387
TC1100003156.mm.1	Gsg2	germ cell-specific gene 2	4.41 ± 0.06	4.75 ± 0.09	4.51 ± 0.05	4.43 ± 0.06	0.10535	0.06989	0.00783
TC0200000636.mm.1	Gsn	gelsolin	12.12 ± 0.04	11.86 ± 0.02	12.11 ± 0.03	11.79 ± 0.1	0.62616	0.0002	0.47156
TC0100000135.mm.1	Gsta3	glutathione S-transferase, alpha 3	6.02 ± 0.2	5.41 ± 0.15	6.06 ± 0.1	5.52 ± 0.07	0.83047	0.00131	0.63088
TC0300002728.mm.1	Gstm4	glutathione S-transferase, mu 4	7.81 ± 0.05	7.88 ± 0.05	8.04 ± 0.01	7.99 ± 0.02	0.00286	0.66064	0.39457
TC1000002383.mm.1	Gstt1	glutathione S-transferase, theta 1	7.92 ± 0.07	8.17 ± 0.02	8.37 ± 0.09	8.13 ± 0.08	0.01183	0.95843	0.00392
TC1000002385.mm.1	Gstt2	glutathione S-transferase, theta 2	6.27 ± 0.06	6.31 ± 0.04	6.13 ± 0.05	6.44 ± 0.06	0.91152	0.00656	0.03279
TC1000003226.mm.1	Gstt3	glutathione S-transferase, theta 3	6.4 ± 0.06	6.53 ± 0.01	6.62 ± 0.05	6.46 ± 0.05	0.09084	0.99412	0.00698
TC0500001798.mm.1	Gtf3a	general transcription factor III A	8.02 ± 0.03	8.13 ± 0.03	8.2 ± 0.04	8.08 ± 0.02	0.07721	0.65259	0.0047
TC0300002220.mm.1	Gucy1a3	guanylate cyclase 1, soluble, alpha 3	9.43 ± 0.06	9.38 ± 0.04	9.74 ± 0.07	9.26 ± 0.1	0.10544	0.00435	0.00373
TC0X00002556.mm.1	Gyk	glycerol kinase	8.19 ± 0.21	7.94 ± 0.22	7.51 ± 0.14	8.5 ± 0.19	0.45402	0.17988	0.00326
TC1700000743.mm.1	H2-M10.5	histocompatibility 2, M region locus 10.5	4.33 ± 0.05	4.53 ± 0.04	4.3 ± 0.04	4.5 ± 0.06	0.41445	0.00258	0.83137
TC1700002071.mm.1	H2-M2	histocompatibility 2, M region locus 2	4.8 ± 0.02	5.16 ± 0.08	4.83 ± 0.05	4.99 ± 0.04	0.20168	0.00026	0.06841
TC1700000614.mm.1	H2-Oa	histocompatibility 2, O region alpha locus	4.89 ± 0.1	5.43 ± 0.05	5.27 ± 0.11	5.51 ± 0.1	0.0707	0.00335	0.2782
TC1500000402.mm.1	Has2as	HAS2 antisense RNA (non-protein coding)	5.06 ± 0.03	4.9 ± 0.04	5.09 ± 0.05	4.87 ± 0.07	0.86277	0.00212	0.47403
TC0800002421.mm.1	Haus8	4HAUS augmin-like complex, subunit 8	7.17 ± 0.1	7.29 ± 0.04	7.05 ± 0.04	6.9 ± 0.02	0.00671	0.79743	0.03564
TC1700000315.mm.1	Hcfc1r1	host cell factor C1 regulator 1 (XPO1-dependent)	7.59 ± 0.03	7.68 ± 0.03	7.78 ± 0.03	7.63 ± 0.05	0.13233	0.29256	0.00809
TC0700002758.mm.1	Hcst	hematopoietic cell signal transducer	5.74 ± 0.04	5.96 ± 0.04	5.85 ± 0.06	6.03 ± 0.09	0.13951	0.00463	0.69294
TC0100002833.mm.1	Hdlbp	high density lipoprotein (HDL) binding protein	10.52 ± 0.04	10.32 ± 0.01	10.27 ± 0.02	10.14 ± 0.06	0.00016	0.00207	0.5785
TC1600000475.mm.1	Heg1	HEG homolog 1 (zebrafish)	10.21 ± 0.1	10.04 ± 0.05	10.24 ± 0.03	9.84 ± 0.04	0.40559	0.00267	0.06574
TC0X00000919.mm.1	Heph	hephaestin	6.32 ± 0.1	5.99 ± 0.05	6.07 ± 0.01	5.9 ± 0.14	0.05344	0.00929	0.28995

Supplemental Table I

Annotations			Summary Statistics				2 way ANOVA p-values		
Probe Set ID	Symbol	Description	XY sh	XY Or	XX sh	XX Or	XY vs XX	Sh vs Or	Intrxn
TC0700000936.mm.1	Herc2	hect (homologous to the E6-AP (UBE3A) carboxyl terminus) c	8.23 ± 0.05	8.06 ± 0.04	7.98 ± 0.03	7.93 ± 0.07	0.0043	0.09323	0.37121
TC0800001106.mm.1	Herpud1	homocysteine-inducible, endoplasmic reticulum stress-inducil	9.25 ± 0.04	9.49 ± 0.05	8.9 ± 0.01	9.29 ± 0.04	9.9E-06	1.5E-06	0.11213
TC1100002060.mm.1	Hexdc	hexosaminidase (glycosyl hydrolase family 20, catalytic doma	6.1 ± 0.02	6.19 ± 0	6.15 ± 0.02	6.15 ± 0	0.53126	0.00787	0.00617
TC0300001616.mm.1	Hey1	hairy/enhancer-of-split related with YRPW motif 1	7.19 ± 0.11	7.24 ± 0.04	7.07 ± 0.05	7.47 ± 0.07	0.35445	0.00918	0.10712
TC0100003827.mm.1	Hhat	hedgehog acyltransferase	5.53 ± 0.04	5.59 ± 0.02	5.68 ± 0.03	5.55 ± 0.01	0.12576	0.22904	0.00794
TC0600002109.mm.1	Hipk2	homeodomain interacting protein kinase 2	9.19 ± 0.15	8.94 ± 0.12	8.93 ± 0.12	9.31 ± 0.04	0.91416	0.96656	0.00725
TC1300000255.mm.1	Hist1h2bc	histone cluster 1, H2bc	9.57 ± 0.05	9.35 ± 0.03	9.5 ± 0.06	9.32 ± 0.09	0.27054	0.00278	0.55
TC0300000930.mm.1	Hist2h2be	histone cluster 2, H2be	7.27 ± 0.07	7.19 ± 0.09	7.46 ± 0.06	6.97 ± 0.14	0.75426	0.00513	0.06556
TC1100000712.mm.1	Hist3h2ba	histone cluster 3, H2ba	6.43 ± 0.04	6.51 ± 0.02	6.36 ± 0.04	6.64 ± 0.07	0.41604	0.00099	0.04319
TC1100003529.mm.1	Hlf	hepatic leukemia factor	6.76 ± 0.08	7.32 ± 0.13	6.39 ± 0.03	7.27 ± 0.08	0.02993	1.9E-06	0.08631
TC1300001353.mm.1	Hmgcs1	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1	9.93 ± 0.24	9.42 ± 0.21	9.28 ± 0.15	9.98 ± 0.08	0.5828	0.86276	0.00434
TC1600002139.mm.1	Hmgn1	high mobility group nucleosomal binding domain 1	7.4 ± 0.05	7.57 ± 0.03	7.53 ± 0.02	7.49 ± 0	0.34176	0.07126	0.00524
TC0800000843.mm.1	Hmgxb4	HMG box domain containing 4	6.66 ± 0.04	6.76 ± 0.01	6.85 ± 0.04	6.68 ± 0.05	0.20681	0.42746	0.00515
TC1000000836.mm.1	Hmha1	histocompatibility (minor) HA-1	6.76 ± 0.03	6.95 ± 0.02	6.85 ± 0.04	6.97 ± 0.08	0.22766	0.00487	0.53887
TC0800000742.mm.1	Homer3	homer homolog 3 (Drosophila)	6.92 ± 0.02	7.03 ± 0.02	7.07 ± 0.02	7.03 ± 0.02	0.0063	0.1489	0.00773
TC1400002069.mm.1	Homez	homeodomain leucine zipper-encoding gene	5.44 ± 0.02	5.39 ± 0.01	5.46 ± 0.03	5.34 ± 0.03	0.45488	0.00355	0.0974
TC0600002284.mm.1	Hoxa10	homeobox A10	6.6 ± 0.03	6.6 ± 0.03	6.96 ± 0.11	6.54 ± 0.05	0.02364	0.00419	0.00407
TC0600002285.mm.1	Hoxa11	homeobox A11	5.12 ± 0.04	5.13 ± 0.04	5.49 ± 0.07	5.13 ± 0.06	0.00604	0.00485	0.00471
TC1100001492.mm.1	Hoxb9	homeobox B9	6.59 ± 0.02	6.76 ± 0.03	6.68 ± 0.01	6.67 ± 0.02	0.79486	0.0014	0.00086
TC0800002905.mm.1	Hp	haptoglobin	9.91 ± 0.08	8.62 ± 0.28	8.98 ± 0.23	9.08 ± 0.18	0.20454	0.00736	0.00249
TC0400001720.mm.1	Hp1bp3	heterochromatin protein 1, binding protein 3	8.68 ± 0.04	8.76 ± 0.03	8.76 ± 0.03	8.34 ± 0.13	0.02779	0.02588	0.00198
TC0600002404.mm.1	Hpgds	hematopoietic prostaglandin D synthase	6.31 ± 0.08	6.05 ± 0.07	6.45 ± 0.09	6.07 ± 0.1	0.33237	0.0042	0.45767
TC1900001532.mm.1	Hpse2	heparanase 2	6.57 ± 0.13	5.91 ± 0.06	6.5 ± 0.14	5.78 ± 0.13	0.56957	0.00011	0.66018
TC0100003836.mm.1	Hsd11b1	hydroxysteroid 11-beta dehydrogenase 1	6.43 ± 0.06	6.28 ± 0.06	6.59 ± 0.05	6.15 ± 0.04	0.98973	0.00011	0.04794
TC0700004630.mm.1	Hsd3b7	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid d	7.26 ± 0.06	7.08 ± 0.06	7.1 ± 0.05	7.18 ± 0.03	0.30213	0.15134	0.00959
TC1100001346.mm.1	Hsf5	heat shock transcription factor family member 5	4.2 ± 0.02	4.41 ± 0.06	4.32 ± 0.04	4.41 ± 0.05	0.27149	0.00772	0.22556
TC1700002151.mm.1	Hsp90ab1	heat shock protein 90 alpha (cytosolic), class B member 1	12.22 ± 0.09	12.07 ± 0.05	11.94 ± 0.03	11.88 ± 0.03	0.00481	0.23447	0.8008
TC1000002627.mm.1	Hsp90b1	heat shock protein 90, beta (Grp94), member 1	11.21 ± 0.1	10.94 ± 0.04	11.05 ± 0.06	10.72 ± 0.05	0.04075	0.00238	0.33409
TC1200000679.mm.1	Hspa2	heat shock protein 2	5.93 ± 0.05	6.25 ± 0.08	6.07 ± 0.06	5.97 ± 0.01	0.23737	0.08316	0.00279
TC1100002725.mm.1	Hspa4	heat shock protein 4	9.97 ± 0.04	9.9 ± 0.04	9.83 ± 0.02	9.75 ± 0.05	0.00376	0.08714	0.70093
TC0500001590.mm.1	Hspb1	heat shock protein 1	9.62 ± 0.15	9.57 ± 0.18	9.34 ± 0.08	8.79 ± 0.08	0.00472	0.10829	0.03995
TC0900002751.mm.1	Htr1b	5-hydroxytryptamine (serotonin) receptor 1B	8.17 ± 0.21	8.4 ± 0.11	8.52 ± 0.14	7.7 ± 0.17	0.42158	0.14396	0.00574

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TC0900002245.mm.1	Htr3a	5-hydroxytryptamine (serotonin) receptor 3A	8.41 ± 0.78	7.18 ± 0.47	5.69 ± 0.27	8.62 ± 0.34	0.40427	0.09413	0.00446
TC1900001435.mm.1	Htr7	5-hydroxytryptamine (serotonin) receptor 7	4.55 ± 0.03	4.72 ± 0.04	4.57 ± 0.03	4.71 ± 0.06	0.99349	0.00267	0.80409
TC0700001913.mm.1	Htra1	HtrA serine peptidase 1	9.36 ± 0.1	9.62 ± 0.04	9.51 ± 0.06	9.23 ± 0.06	0.1849	0.96466	0.00239
TC0500002252.mm.1	Htra3	HtrA serine peptidase 3	9.11 ± 0.07	8.97 ± 0.04	9.13 ± 0.02	8.84 ± 0.1	0.42673	0.00565	0.25116
TC0800001902.mm.1	Htra4	HtrA serine peptidase 4	8.32 ± 0.24	7.53 ± 0.09	8.15 ± 0.15	7.54 ± 0.17	0.97091	0.00541	0.9898
TC0500001382.mm.1	Hvcn1	hydrogen voltage-gated channel 1	5.84 ± 0.07	6.23 ± 0.07	6.17 ± 0.09	6.3 ± 0.08	0.04265	0.00869	0.21998
TC0400001305.mm.1	Hyi	hydroxypyruvate isomerase homolog (E. coli)	7.59 ± 0.04	7.74 ± 0.01	7.77 ± 0.03	7.81 ± 0.06	0.00449	0.02253	0.13755
TC1300000572.mm.1	Iars	isoleucine-tRNA synthetase	8.61 ± 0.05	8.45 ± 0.02	8.35 ± 0.01	8.26 ± 0.08	0.00094	0.04119	0.52291
TC0500001023.mm.1	Ibsp	integrin binding sialoprotein	4.09 ± 0.05	4 ± 0.05	4.46 ± 0.13	4.06 ± 0.03	0.01519	0.00503	0.0581
TC0200002298.mm.1	Id1	inhibitor of DNA binding 1	8.56 ± 0.04	8.78 ± 0.11	8.23 ± 0.08	8.56 ± 0.04	0.00109	0.00175	0.38643
TC1900001454.mm.1	Ide	insulin degrading enzyme	9.6 ± 0.14	9.57 ± 0.07	9.23 ± 0.1	9.29 ± 0.05	0.00242	0.63429	0.30486
TC1700000703.mm.1	Ier3	immediate early response 3	6.99 ± 0.04	7.28 ± 0.06	6.77 ± 0.04	7.24 ± 0.08	0.05045	1.7E-05	0.14396
TC0100003599.mm.1	Ifi202b	interferon activated gene 202B	5.48 ± 0.11	4.74 ± 0.09	4.86 ± 0.06	4.59 ± 0.05	0.0019	0.00015	0.04898
TC0100003888.mm.1	Ifi204	interferon activated gene 204	8.35 ± 0.17	7.57 ± 0.13	7.69 ± 0.07	7.48 ± 0.11	0.03185	0.0058	0.10334
TC1200002269.mm.1	Ifi27l2a	interferon, alpha-inducible protein 27 like 2A	9.7 ± 0.15	8.59 ± 0.2	9.06 ± 0.12	8.9 ± 0.13	0.24725	0.00093	0.00735
TC0600003422.mm.1	Ifltd1	intermediate filament tail domain containing 1	5.42 ± 0.06	5.65 ± 0.04	5.86 ± 0.09	5.56 ± 0.08	0.02143	0.6507	0.00191
TC1200001663.mm.1	Ifrd1	interferon-related developmental regulator 1	7.52 ± 0.07	7.53 ± 0.07	7.34 ± 0.04	7.15 ± 0.07	0.0007	0.15281	0.1576
TC0900001377.mm.1	Ifrd2	interferon-related developmental regulator 2	8.11 ± 0.04	8.27 ± 0.02	7.96 ± 0.01	8.21 ± 0.04	0.00481	5.3E-05	0.118
TC0600001288.mm.1	Ift122	intraflagellar transport 122	6.57 ± 0.01	6.56 ± 0	6.59 ± 0.02	6.51 ± 0.02	0.60655	0.00484	0.01568
TC1500001826.mm.1	Ift27	intraflagellar transport 27	7.17 ± 0.04	7.25 ± 0.03	7.34 ± 0.06	7.2 ± 0.01	0.11789	0.54779	0.0099
TC1200000846.mm.1	Ift43	intraflagellar transport 43 homolog (Chlamydomonas)	8.29 ± 0.13	8.44 ± 0.04	8.58 ± 0.07	8.01 ± 0.16	0.59151	0.10017	0.00592
TC0900000829.mm.1	Igdcc4	immunoglobulin superfamily, DCC subclass, member 4	6.18 ± 0.03	6.36 ± 0.04	6.31 ± 0.02	6.37 ± 0.04	0.0601	0.00569	0.15576
TC1000001066.mm.1	Igf1	insulin-like growth factor 1	7.42 ± 0.09	7.09 ± 0.04	7.17 ± 0.06	6.82 ± 0.15	0.02967	0.00575	0.73027
TC1700000355.mm.1	Igfals	insulin-like growth factor binding protein, acid labile subunit	5.21 ± 0.09	4.96 ± 0.13	4.65 ± 0.14	5.18 ± 0.05	0.12197	0.23218	0.00278
TC1100002195.mm.1	Igfbp3	insulin-like growth factor binding protein 3	7.23 ± 0.21	7.4 ± 0.14	6.6 ± 0.15	7.47 ± 0.15	0.13325	0.0098	0.06263
TC1500001089.mm.1	Igfbp6	insulin-like growth factor binding protein 6	9.01 ± 0.11	8.47 ± 0.08	8.96 ± 0.07	8.58 ± 0.04	0.366	0.0003	0.70688
TC0400002587.mm.1	Igfbpl1	insulin-like growth factor binding protein-like 1	5.61 ± 0.03	5.79 ± 0.03	5.68 ± 0.05	5.85 ± 0.11	0.24484	0.00884	0.88024
TC1200002537.mm.1	Igha	Igha immunoglobulin heavy constant alpha	5.67 ± 0.09	6.04 ± 0.1	6.12 ± 0.1	6.65 ± 0.19	0.00162	0.00477	0.38945
TC1200002540.mm.1	Ighg1	immunoglobulin heavy constant gamma 1 (G1m marker)	4.16 ± 0.04	4.51 ± 0.06	4.3 ± 0.07	4.54 ± 0.09	0.36415	0.00104	0.64732
TC1200002539.mm.1	Ighg2b	immunoglobulin heavy constant gamma 2B	5.24 ± 0.06	5.55 ± 0.15	5.73 ± 0.23	6.52 ± 0.4	0.00797	0.03529	0.30992
TC1200002541.mm.1	Ighg3	Ighg3 Immunoglobulin heavy constant gamma 3	4.85 ± 0.04	4.96 ± 0.01	4.97 ± 0.03	5.21 ± 0.08	0.00169	0.00251	0.12938
TC1200002613.mm.1	Ighv1-20	immunoglobulin heavy variable V1-20	3.85 ± 0.04	3.9 ± 0.08	3.95 ± 0.21	4.74 ± 0.2	0.00775	0.0147	0.01963

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TC1200002617.mm.1	Ighv1-26	immunoglobulin heavy variable 1-26	4.15 ± 0.11	4.49 ± 0.16	4.7 ± 0.21	5.26 ± 0.24	0.00382	0.03461	0.45951
TC1200002593.mm.1	Ighv13-2	Ighv13-2 immunoglobulin heavy variable 13-2	4.9 ± 0.11	5.05 ± 0.1	4.76 ± 0.13	5.43 ± 0.06	0.43026	0.00396	0.01775
TC1200002620.mm.1	Ighv1-34	immunoglobulin heavy variable 1-34	5.47 ± 0.11	5.83 ± 0.23	5.76 ± 0.24	6.67 ± 0.2	0.01945	0.00918	0.12032
TC1200002655.mm.1	Ighv1-75	immunoglobulin heavy variable 1-75	4.71 ± 0.15	4.99 ± 0.14	4.95 ± 0.12	5.74 ± 0.2	0.01114	0.00687	0.07647
TC1200002664.mm.1	Ighv1-85	immunoglobulin heavy variable 1-85	4.66 ± 0.12	4.85 ± 0.14	4.77 ± 0.17	5.71 ± 0.18	0.01295	0.00483	0.01348
TC1200002554.mm.1	Ighv5-2	immunoglobulin heavy variable 5-2	3.8 ± 0.11	4.22 ± 0.05	4.08 ± 0.06	4.13 ± 0.05	0.20962	0.00957	0.03172
TC1200002558.mm.1	Ighv5-6	immunoglobulin heavy variable 5-6	4.43 ± 0.08	4.98 ± 0.2	4.6 ± 0.21	4.98 ± 0.1	0.49628	0.00781	0.51024
TC1200002583.mm.1	Ighv9-1	immunoglobulin heavy variable 9-1	5.11 ± 0.08	5.55 ± 0.18	5.35 ± 0.1	5.84 ± 0.17	0.07082	0.00463	0.80813
TC0600000811.mm.1	Igkj3	immunoglobulin kappa joining 3	5.2 ± 0.1	5.81 ± 0.11	5.53 ± 0.1	5.79 ± 0.19	0.32333	0.00793	0.27478
TC0600003517.mm.1	Igkv1-110	immunoglobulin kappa variable 1-110	6.42 ± 0.1	8.04 ± 0.42	7.25 ± 0.25	7.97 ± 0.25	0.18694	0.00074	0.1168
TC0600003513.mm.1	Igkv1-122	immunoglobulin kappa chain variable 1-122	6.3 ± 0.1	7.54 ± 0.35	6.87 ± 0.18	7.62 ± 0.14	0.13264	0.0003	0.24686
TC0600003507.mm.1	Igkv1-132	immunoglobulin kappa variable 1-132	4.2 ± 0.1	4.7 ± 0.05	4.69 ± 0.12	4.89 ± 0.12	0.00682	0.00538	0.20605
TC0600003506.mm.1	Igkv1-133	immunoglobulin kappa variable 1-133	4.65 ± 0.14	5.17 ± 0.04	5 ± 0.25	5.73 ± 0.19	0.02734	0.00419	0.45202
TC0600002445.mm.1	Igkv12-38	immunoglobulin kappa chain variable 12-38	4.49 ± 0.03	4.73 ± 0.1	4.53 ± 0.02	4.76 ± 0.07	0.58984	0.0025	0.99968
TC0600003596.mm.1	Igkv6-14	immunoglobulin kappa variable 6-14	4.95 ± 0.12	5.2 ± 0.03	5.22 ± 0.04	5.61 ± 0.14	0.00607	0.01022	0.41044
TC0600003595.mm.1	Igkv6-15	immunoglobulin kappa variable 6-15	4.42 ± 0.17	4.71 ± 0.12	5.26 ± 0.38	6.19 ± 0.38	0.00143	0.06031	0.21897
TC0600002448.mm.1	Igkv8-34	Igkv8-34 immunoglobulin kappa variable 8-34	6.07 ± 0.02	6.23 ± 0.05	6.08 ± 0.05	6.22 ± 0.05	0.96779	0.00433	0.69275
TC0100002597.mm.1	Ihh	Indian hedgehog	5.78 ± 0.09	6.01 ± 0.07	5.83 ± 0.07	6.04 ± 0.08	0.33932	0.0063	0.53411
TC1100003680.mm.1	Ikzf3	IKAROS family zinc finger 3	5.07 ± 0.07	5.57 ± 0.06	5.37 ± 0.08	5.69 ± 0.14	0.07861	0.00122	0.50612
TC0400000381.mm.1	Il11ra1	interleukin 11 receptor, alpha chain 1	7.55 ± 0.07	7.77 ± 0.02	7.77 ± 0.06	7.62 ± 0.02	0.36714	0.37191	0.00249
TC0200000222.mm.1	Il15ra	interleukin 15 receptor, alpha chain	6.66 ± 0.07	6.6 ± 0.07	6.41 ± 0.05	6.72 ± 0.08	0.18016	0.21624	0.00914
TC0100000295.mm.1	Il1r1	interleukin 1 receptor, type I	8.77 ± 0.12	8.74 ± 0.08	9.01 ± 0.08	8.37 ± 0.12	0.57524	0.00709	0.01213
TC0100000297.mm.1	Il1rl2	interleukin 1 receptor-like 2	6.15 ± 0.06	5.62 ± 0.05	5.95 ± 0.06	5.55 ± 0.11	0.12992	4.1E-05	0.54051
TC0700001794.mm.1	Il21r	interleukin 21 receptor	5.42 ± 0.02	5.63 ± 0.02	5.46 ± 0.06	5.7 ± 0.09	0.31696	0.00112	0.7531
TC0700004287.mm.1	Il27	interleukin 27	5.38 ± 0.03	5.6 ± 0.04	5.49 ± 0.04	5.64 ± 0.09	0.30034	0.00979	0.70619
TC0800002565.mm.1	Il27ra	interleukin 27 receptor, alpha	6.47 ± 0.03	6.68 ± 0.05	6.55 ± 0.02	6.58 ± 0.03	0.64737	0.00655	0.04302
TC1300002679.mm.1	Il31ra	interleukin 31 receptor A	5.79 ± 0.1	5.55 ± 0.04	5.54 ± 0	5.31 ± 0.01	0.00532	0.00613	0.77742
TC0300002357.mm.1	Il6ra	interleukin 6 receptor, alpha	7.69 ± 0.08	7.38 ± 0.04	7.51 ± 0.01	7.31 ± 0.02	0.05377	0.0006	0.50287
TC1500001197.mm.1	Il7r	interleukin 7 receptor	5.44 ± 0.11	5.73 ± 0.1	5.32 ± 0.04	5.29 ± 0.06	0.00744	0.16244	0.09161
TC0100001533.mm.1	Ildr2	immunoglobulin-like domain containing receptor 2	7 ± 0.06	6.8 ± 0.03	7.17 ± 0.12	6.74 ± 0.05	0.30899	0.00118	0.08248
TC0800000091.mm.1	Ing1	inhibitor of growth family, member 1	7.49 ± 0.04	7.64 ± 0.02	7.56 ± 0.01	7.55 ± 0.01	0.88618	0.0217	0.00791
TC1300000113.mm.1	Inhba	inhibin beta-A	7.44 ± 0.1	7.64 ± 0.03	7.84 ± 0.08	7.37 ± 0.11	0.43335	0.16968	0.00153

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TC0100002945.mm.1	Inhbb	inhibin beta-B	6.61 ± 0.07	6.83 ± 0.09	6.98 ± 0.03	6.98 ± 0.07	0.00302	0.20395	0.18459
TC0600002326.mm.1	Inmt	indolethylamine N-methyltransferase	9.11 ± 0.11	8.6 ± 0.15	8.99 ± 0.07	8.6 ± 0.07	0.70328	0.00155	0.7016
TC0400001425.mm.1	Inpp5b	inositol polyphosphate-5-phosphatase B	7.16 ± 0.03	7.1 ± 0.05	7.24 ± 0.04	7 ± 0.03	0.86863	0.00328	0.03654
TC0800001608.mm.1	Insr	insulin receptor	8.33 ± 0.07	8.31 ± 0.03	8.07 ± 0.07	8.14 ± 0.03	0.00206	0.71526	0.4111
TC1400002863.mm.1	Ipo4	importin 4	7.76 ± 0.02	7.68 ± 0	7.66 ± 0.01	7.61 ± 0.03	0.00107	0.00677	0.80639
TC0700001620.mm.1	Ipo7	importin 7	8.84 ± 0.05	8.84 ± 0.05	8.69 ± 0.03	8.61 ± 0.07	0.00295	0.46566	0.44558
TC1300002463.mm.1	Iqgap2	IQ motif containing GTPase activating protein 2	7.67 ± 0.2	6.81 ± 0.1	7 ± 0.06	6.76 ± 0.08	0.04989	0.0035	0.09265
TC0X00001538.mm.1	Iqsec2	IQ motif and Sec7 domain 2	7.54 ± 0.03	7.61 ± 0	7.68 ± 0.02	7.63 ± 0.02	0.00524	0.93454	0.03242
TC0800003193.mm.1	Irf2bp2	interferon regulatory factor 2 binding protein 2	8.92 ± 0.09	9.1 ± 0.05	9.09 ± 0.02	8.85 ± 0.08	0.66971	0.75807	0.00943
TC1200002110.mm.1	Irf2bpl	interferon regulatory factor 2 binding protein-like	8.18 ± 0.07	8.24 ± 0.04	8.45 ± 0.05	8.11 ± 0.1	0.27493	0.07683	0.0085
TC0300000709.mm.1	Isg20l2	interferon stimulated exonuclease gene 20-like 2	6.88 ± 0.04	6.79 ± 0.06	6.89 ± 0.07	6.51 ± 0.11	0.09243	0.00685	0.05676
TC0200002089.mm.1	Ism1	isthmin 1 homolog (zebrafish)	7.21 ± 0.07	6.83 ± 0.04	7.17 ± 0.07	6.64 ± 0.06	0.07215	4.5E-06	0.22481
TC1800000590.mm.1	Isoc1	isochorismatase domain containing 1	8.72 ± 0.21	8.27 ± 0.12	8.27 ± 0.12	8.67 ± 0.06	0.72166	0.73626	0.00963
TC0800000756.mm.1	Isyna1	myo-inositol 1-phosphate synthase A1	7.86 ± 0.07	7.93 ± 0.03	8.06 ± 0.05	7.82 ± 0.04	0.27535	0.14908	0.00667
TC0900000791.mm.1	Itga11	integrin alpha 11	6.76 ± 0.04	6.83 ± 0.02	6.97 ± 0.02	6.76 ± 0.05	0.07177	0.07194	0.00233
TC0900001563.mm.1	Itga9	integrin alpha 9	10.25 ± 0.18	10.49 ± 0.06	10.51 ± 0.09	10.02 ± 0.07	0.52612	0.40401	0.0073
TC0700001875.mm.1	Itgam	integrin alpha M	7.21 ± 0.06	6.89 ± 0.12	7.05 ± 0.05	6.63 ± 0.06	0.02384	0.00042	0.40414
TC1100001730.mm.1	Itgb3	integrin beta 3	8.83 ± 0.19	8.97 ± 0.03	9.3 ± 0.13	8.46 ± 0.18	0.98555	0.05559	0.00653
TC1600000480.mm.1	Itgb5	integrin beta 5	10.6 ± 0.13	10.83 ± 0.05	10.9 ± 0.07	10.54 ± 0.08	0.78043	0.67458	0.00563
TC0200002945.mm.1	Itih2	inter-alpha trypsin inhibitor, heavy chain 2	7.92 ± 0.16	8.48 ± 0.06	8.26 ± 0.08	8.13 ± 0.06	0.93169	0.06695	0.00758
TC1100002602.mm.1	Itk	IL2 inducible T cell kinase	4.89 ± 0.04	5.48 ± 0.15	4.88 ± 0.07	5.21 ± 0.12	0.15463	0.00066	0.25816
TSUnmapped000000	Itlnb	intelectin b	4.58 ± 0.03	4.77 ± 0.07	4.75 ± 0.02	4.9 ± 0.08	0.01321	0.00653	0.62673
TC0100001707.mm.1	Itpkb	inositol 1,4,5-trisphosphate 3-kinase B	8.58 ± 0.05	8.71 ± 0.03	8.63 ± 0.02	8.79 ± 0.02	0.13769	0.00182	0.54338
TC0600002296.mm.1	Jazf1	JAZF zinc finger 1	6.87 ± 0.04	7.02 ± 0.05	7.02 ± 0.07	6.87 ± 0.05	0.92574	0.85221	0.00827
TC0400003079.mm.1	Jun	Jun oncogene	8.79 ± 0.07	9.1 ± 0.11	9.44 ± 0.13	9.08 ± 0.09	0.01495	0.5743	0.00983
TC0800000760.mm.1	Jund	Jun proto-oncogene related gene d	9.14 ± 0.06	9.36 ± 0.04	9.42 ± 0.05	9.22 ± 0.07	0.26397	0.91039	0.00368
TC0600003295.mm.1	Kap	kidney androgen regulated protein	7.98 ± 1.12	3.58 ± 0.06	4.07 ± 0.27	3.54 ± 0.07	0.014	0.00364	0.01567
TC0900000025.mm.1	Kbtbd3	kelch repeat and BTB (POZ) domain containing 3	5.74 ± 0.04	5.8 ± 0.02	5.84 ± 0.04	5.65 ± 0.03	0.80648	0.16577	0.00154
TC0600003163.mm.1	Kcna1	potassium voltage-gated channel, shaker-related subfamily, r	8.25 ± 0.3	7.33 ± 0.26	7.01 ± 0.17	7.95 ± 0.27	0.44866	0.69816	0.00844
TC0600003164.mm.1	Kcna6	potassium voltage-gated channel, shaker-related, subfamily,	6.05 ± 0.2	5.51 ± 0.07	5.27 ± 0.12	5.89 ± 0.09	0.33054	0.53599	0.0029
TC0700000843.mm.1	Kcna7	potassium voltage-gated channel, shaker-related subfamily, r	5.18 ± 0.02	5.37 ± 0.07	5.17 ± 0.05	5.36 ± 0.07	0.78108	0.00371	0.92609
TC0200004556.mm.1	Kcnip3	Kv channel interacting protein 3, calsenilin	7.12 ± 0.06	7.08 ± 0.05	7.41 ± 0.06	7.21 ± 0.03	0.00099	0.06652	0.11873

Supplemental Table I

Annotations			Summary Statistics				2 way ANOVA p-values		
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TC0100001611.mm.1	Kcnj10	potassium inwardly-rectifying channel, subfamily J, member 1	5.69 ± 0.24	5.1 ± 0.13	4.99 ± 0.04	5.59 ± 0.1	0.72154	0.76301	0.00489
TC1700002699.mm.1	Kcnk12	potassium channel, subfamily K, member 12	3.93 ± 0.07	4.18 ± 0.03	4.01 ± 0.04	4.27 ± 0.13	0.24863	0.00457	0.91402
TC1200001416.mm.1	Kcns3	potassium voltage-gated channel, delayed-rectifier, subfamily	6.03 ± 0.03	6.24 ± 0.09	5.94 ± 0.05	6.21 ± 0.03	0.22226	0.00063	0.55823
TC0500003060.mm.1	Kctd10	potassium channel tetramerisation domain containing 10	8.65 ± 0.12	8.79 ± 0.04	8.92 ± 0.08	8.56 ± 0.09	0.63191	0.36666	0.00912
TC0800002821.mm.1	Kctd19	potassium channel tetramerisation domain containing 19	4.86 ± 0.02	5 ± 0.01	4.95 ± 0.02	5.06 ± 0.08	0.10608	0.00934	0.85319
TC0900000639.mm.1	Kdelc2	KDEL (Lys-Asp-Glu-Leu) containing 2	8.26 ± 0.1	8.38 ± 0.05	8.45 ± 0.07	8.05 ± 0.1	0.59195	0.18911	0.00673
TC0X00001541.mm.1	Kdm5c	lysine (K)-specific demethylase 5C	7.84 ± 0.03	7.82 ± 0.02	8.22 ± 0.02	8.17 ± 0.05	1.9E-07	0.22306	0.85326
TC0Y00000005.mm.1	Kdm5d	lysine (K)-specific demethylase 5D	5.96 ± 0.05	5.77 ± 0.05	4.13 ± 0.04	4.08 ± 0.08	1.5E-13	0.05549	0.25922
TC0X00000190.mm.1	Kdm6a	lysine (K)-specific demethylase 6A	7.36 ± 0.08	7.41 ± 0.06	8.01 ± 0.05	7.83 ± 0.12	1.8E-05	0.49639	0.1434
TC0700001791.mm.1	Kdm8	lysine (K)-specific demethylase 8	6.01 ± 0.04	6.17 ± 0.02	6.27 ± 0.06	6.13 ± 0.03	0.03606	0.95457	0.00411
TC0400004035.mm.1	Kif1b	kinesin family member 1B	9.34 ± 0.19	8.9 ± 0.09	8.72 ± 0.09	9.2 ± 0.07	0.25931	0.8697	0.00376
TC1500002071.mm.1	Kif21a	kinesin family member 21A	7.76 ± 0.6	6.55 ± 0.24	5.97 ± 0.2	7.53 ± 0.23	0.44107	0.53269	0.00691
TC0700003406.mm.1	Klf13	Kruppel-like factor 13	7.88 ± 0.07	7.97 ± 0.06	7.77 ± 0.04	7.66 ± 0.08	0.00805	0.93046	0.1218
TC0600001074.mm.1	Klf15	Kruppel-like factor 15	7.82 ± 0.02	7.95 ± 0.03	7.78 ± 0.04	7.93 ± 0.06	0.63337	0.00255	0.86815
TC1900000373.mm.1	Klf9	Kruppel-like factor 9	10.79 ± 0.16	10.72 ± 0.07	10.31 ± 0.03	10.36 ± 0.06	0.00403	0.71576	0.90673
TC1500000873.mm.1	Klhdc7b	kelch domain containing 7B	4.44 ± 0.05	4.67 ± 0.06	4.53 ± 0.06	4.66 ± 0.07	0.36566	0.00601	0.30358
TC0X00001955.mm.1	Klhl13	kelch-like 13	6.76 ± 0.04	6.72 ± 0.05	6.94 ± 0.04	6.54 ± 0.11	0.89494	0.00591	0.01266
TC0800002314.mm.1	Klhl2	kelch-like 2, Mayven	7.28 ± 0.08	6.76 ± 0.12	6.81 ± 0.02	6.69 ± 0.06	0.00299	0.00097	0.02115
TC0700001098.mm.1	Klhl25	kelch-like 25	6.85 ± 0.02	6.95 ± 0.02	7.05 ± 0.03	6.96 ± 0.03	0.00139	0.85437	0.00402
TC0100000894.mm.1	Klhl30	kelch-like 30	6.15 ± 0.14	6.39 ± 0.02	6.61 ± 0.05	6.25 ± 0.04	0.12989	0.44129	0.00781
TC0800001429.mm.1	Klhl36	kelch-like 36	6.58 ± 0.05	6.67 ± 0.03	6.84 ± 0.04	6.73 ± 0.06	0.00573	0.7731	0.07226
TC0700000773.mm.1	Klk10	kallikrein related-peptidase 10	7.87 ± 0.23	7.35 ± 0.12	7.72 ± 0.05	7.11 ± 0.1	0.41906	0.00659	0.49824
TC0700000771.mm.1	Klk12	kallikrein related-peptidase 12	5.54 ± 0.02	5.72 ± 0.06	5.66 ± 0.02	5.78 ± 0.07	0.07473	0.00821	0.5122
TC1600000501.mm.1	Kpna1	karyopherin (importin) alpha 1	7.53 ± 0.04	7.47 ± 0.08	7.35 ± 0.03	7.3 ± 0.08	0.00927	0.27014	0.86279
TC1700002723.mm.1	Kpna2	karyopherin (importin) alpha 2	7.34 ± 0.06	7.28 ± 0.05	6.81 ± 0.07	7.01 ± 0.04	8.9E-06	0.20219	0.0398
TC1100002131.mm.1	Kremen1	kringle containing transmembrane protein 1	7.14 ± 0.04	7.16 ± 0.03	7.39 ± 0.06	7.17 ± 0.02	0.00692	0.02373	0.01195
TC1500001084.mm.1	Krt18	keratin 18	6.12 ± 0.06	6.53 ± 0.13	6.24 ± 0.06	6.35 ± 0.04	0.90702	0.00339	0.04443
TC1500002278.mm.1	Krt4	keratin 4	4.4 ± 0.03	4.57 ± 0.03	4.5 ± 0.04	4.55 ± 0.04	0.19717	0.00673	0.05828
TC1500002273.mm.1	Krt73	keratin 73	4.93 ± 0.03	5.14 ± 0.03	5.13 ± 0.06	5.05 ± 0.05	0.20014	0.17335	0.00565
TC1500002261.mm.1	Krt84	keratin 84	4.72 ± 0.04	4.96 ± 0.05	4.82 ± 0.05	4.98 ± 0.1	0.40714	0.00882	0.61477
TC1000001919.mm.1	Lama2	laminin, alpha 2	8.59 ± 0.1	8.24 ± 0.02	8.35 ± 0.11	8.06 ± 0.11	0.07474	0.00873	0.98911
TC1800000103.mm.1	Lama3	laminin, alpha 3	5.89 ± 0.03	6.03 ± 0.04	6.04 ± 0.03	5.96 ± 0.04	0.24071	0.36788	0.00664

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Annotations			Summary Statistics				2 way ANOVA p-values		
Probe Set ID	Symbol	Description	XY sh	XY Or	XX sh	XX Or	XY vs XX	Sh vs Or	Intrxn
TC1200000263.mm.1	Lamb1	laminin B1	8.12 ± 0.13	7.75 ± 0.1	7.52 ± 0.13	7.9 ± 0.03	0.06221	0.99381	0.0051
TC0100003273.mm.1	Lamc1	laminin, gamma 1	9.94 ± 0.05	9.72 ± 0.02	9.71 ± 0.04	9.45 ± 0.05	9.2E-05	0.00017	0.41181
TC0200000559.mm.1	Lamc3	laminin gamma 3	7.5 ± 0.08	7.6 ± 0.03	7.84 ± 0.1	7.52 ± 0.03	0.07783	0.10709	0.00823
TC0800000123.mm.1	Lamp1	lysosomal-associated membrane protein 1	11.42 ± 0.01	11.34 ± 0.02	11.47 ± 0.03	11.32 ± 0.03	0.65344	0.0005	0.19311
TC0X00000108.mm.1	Lancl3	LanC lantibiotic synthetase component C-like 3 (bacterial)	8.24 ± 0.09	8.36 ± 0.07	8.58 ± 0.12	7.96 ± 0.17	0.8961	0.0765	0.00549
TC0800002471.mm.1	Large	like-glycosyltransferase	9.44 ± 0.15	9.16 ± 0.08	9.33 ± 0.06	8.82 ± 0.08	0.11958	0.00659	0.15594
TC0700004273.mm.1	Lat	linker for activation of T cells	5.81 ± 0.02	6.25 ± 0.09	5.88 ± 0.06	6.28 ± 0.15	0.5711	0.00033	0.80851
TC1700001147.mm.1	Lbh	limb-bud and heart	9.58 ± 0.07	9.76 ± 0.07	9.89 ± 0.08	9.64 ± 0.07	0.1733	0.75079	0.00806
TC0200002426.mm.1	Lbp	lipopolysaccharide binding protein	9.87 ± 0.12	8.99 ± 0.09	9.77 ± 0.04	8.93 ± 0.15	0.65143	4.4E-06	0.9333
TC0900002766.mm.1	Lca5	Leber congenital amaurosis 5 (human)	5.84 ± 0.05	5.92 ± 0.04	5.95 ± 0.03	5.78 ± 0.04	0.91946	0.43674	0.00672
TC0300002410.mm.1	Lce1j	late cornified envelope 1J	4.45 ± 0.03	4.57 ± 0.05	4.5 ± 0.03	4.66 ± 0.07	0.13726	0.00957	0.73714
TC0400003602.mm.1	Lck	lymphocyte protein tyrosine kinase	5.28 ± 0.04	5.72 ± 0.12	5.4 ± 0.06	5.73 ± 0.14	0.58896	0.00157	0.71768
TC1800000714.mm.1	Ldlrad4	low density lipoprotein receptor class A domain containing 4	9.01 ± 0.13	9.37 ± 0.04	9.36 ± 0.09	9.02 ± 0.09	0.98596	0.91981	0.00378
TC0300001330.mm.1	Lef1	lymphoid enhancer binding factor 1	4.95 ± 0.04	5.39 ± 0.11	4.91 ± 0.09	5.29 ± 0.14	0.43386	0.00106	0.78202
TC0900001016.mm.1	Leo1	Leo1, Paf1/RNA polymerase II complex component, homolog	7.31 ± 0.09	7.21 ± 0.11	7.84 ± 0.02	7.2 ± 0.07	0.01993	0.00026	0.01579
TC0600003122.mm.1	Leprel2	leprecan-like 2	8.18 ± 0.09	8.37 ± 0.06	8.36 ± 0.06	8.15 ± 0.03	0.9708	0.87809	0.00688
TC1900001051.mm.1	Lgals12	lectin, galactose binding, soluble 12	10 ± 0.14	9.46 ± 0.2	9.31 ± 0.27	9.81 ± 0.03	0.24168	0.70543	0.00664
TC1100002314.mm.1	Lgalsl	lectin, galactoside binding-like	9.38 ± 0.08	9.47 ± 0.04	9.6 ± 0.07	9.23 ± 0.05	0.93308	0.07905	0.00343
TC0500002411.mm.1	Lgi2	leucine-rich repeat LGI family, member 2	8.43 ± 0.11	7.92 ± 0.05	8.2 ± 0.08	7.64 ± 0.17	0.07756	0.00069	0.61788
TC0200001627.mm.1	Lgr4	leucine-rich repeat-containing G protein-coupled receptor 4	7.57 ± 0.05	7.42 ± 0.02	7.28 ± 0.04	7.28 ± 0.1	0.00528	0.36879	0.33841
TC1000003214.mm.1	Lilrb4	leukocyte immunoglobulin-like receptor, subfamily B, member	7.26 ± 0.17	7 ± 0.21	6.77 ± 0.18	6.36 ± 0.11	0.00515	0.06195	0.74344
TC1100003914.mm.1	Limd2	LIM domain containing 2	7.2 ± 0.03	7.43 ± 0.04	7.33 ± 0.03	7.47 ± 0.05	0.07651	0.0006	0.36462
TC0100001712.mm.1	Lin9	lin-9 homolog (C. elegans)	5.34 ± 0.01	5.43 ± 0.02	5.25 ± 0.04	5.38 ± 0.05	0.05193	0.00633	0.5468
TC0700002632.mm.1	Lipe	lipase, hormone sensitive	9.31 ± 0.15	9.05 ± 0.19	8.84 ± 0.21	9.53 ± 0.08	0.71686	0.38423	0.00597
TC1800001478.mm.1	Lman1	lectin, mannose-binding, 1	8.23 ± 0.04	8.11 ± 0.04	8.11 ± 0.02	7.96 ± 0.06	0.00692	0.00649	0.86253
TC0500003619.mm.1	Lnx2	ligand of numb-protein X 2	8.21 ± 0.06	8.25 ± 0.02	8.52 ± 0.05	8.18 ± 0.05	0.0642	0.00403	0.00367
TC0800002060.mm.1	Lonrf1	LON peptidase N-terminal domain and ring finger 1	6.81 ± 0.07	7.11 ± 0.08	6.37 ± 0.1	6.85 ± 0.06	0.00131	0.00012	0.44383
TC0X00000319.mm.1	Lonrf3	LON peptidase N-terminal domain and ring finger 3	5.14 ± 0.03	5.28 ± 0.02	5.52 ± 0.08	5.16 ± 0.05	0.01836	0.03945	0.0002
TC1800001334.mm.1	Lox	lysyl oxidase	9.89 ± 0.14	9.79 ± 0.07	10.11 ± 0.08	9.23 ± 0.14	0.18428	0.00109	0.00507
TC0800000707.mm.1	Lpl	lipoprotein lipase	10.97 ± 0.15	10.41 ± 0.23	10.09 ± 0.19	10.83 ± 0.04	0.12941	0.77281	0.00109
TC1700002315.mm.1	Lrg1	leucine-rich alpha-2-glycoprotein 1	7.08 ± 0.05	6.47 ± 0.09	6.71 ± 0.07	6.66 ± 0.08	0.1923	0.00063	0.00179
TC1900000882.mm.1	Lrp5	low density lipoprotein receptor-related protein 5	8.77 ± 0.07	8.78 ± 0.02	9.02 ± 0.04	8.65 ± 0.04	0.30431	0.00393	0.00386

Supplemental Table I

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TC1000000566.mm.1	Lrrc20	leucine rich repeat containing 20	7.06 ± 0.06	7.04 ± 0.03	7.22 ± 0.03	7.34 ± 0.08	0.00216	0.6258	0.11564
TC0700003434.mm.1	Lrrk1	leucine-rich repeat kinase 1	7.32 ± 0.05	7.44 ± 0.04	7.47 ± 0.05	7.35 ± 0.02	0.39952	0.87213	0.00972
TC0600001189.mm.1	Lrrn1	leucine rich repeat protein 1, neuronal	6.59 ± 0.05	6.37 ± 0.06	6.77 ± 0.03	6.41 ± 0.04	0.02445	3.6E-05	0.10229
TC1700000673.mm.1	Ltb	lymphotoxin B	6.01 ± 0.05	6.4 ± 0.06	6.24 ± 0.09	6.49 ± 0.11	0.08402	0.00193	0.54763
TC1900000082.mm.1	Ltbp3	latent transforming growth factor beta binding protein 3	9.03 ± 0.08	9.28 ± 0.05	9.23 ± 0.05	9.06 ± 0.05	0.68859	0.6964	0.00874
TC1700000410.mm.1	Luc7l	Luc7 homolog (S. cerevisiae)-like	6.48 ± 0.02	6.48 ± 0.04	6.38 ± 0.02	6.39 ± 0.03	0.00639	0.91091	0.80574
TC0400000811.mm.1	Lurap1l	leucine rich adaptor protein 1-like	6.13 ± 0.07	5.82 ± 0.03	5.99 ± 0.05	5.66 ± 0.07	0.02765	9.4E-05	0.87431
TC1500001728.mm.1	Ly6a	lymphocyte antigen 6 complex, locus A	11.12 ± 0.04	10.61 ± 0.06	10.95 ± 0.07	10.6 ± 0.08	0.21806	1.1E-05	0.32276
TC1500001729.mm.1	Ly6c1	lymphocyte antigen 6 complex, locus C1	9.23 ± 0.03	8.75 ± 0.07	8.99 ± 0.06	8.81 ± 0.02	0.0976	1.4E-05	0.01178
TC1500001730.mm.1	Ly6c2	lymphocyte antigen 6 complex, locus C2	10.65 ± 0.02	10.09 ± 0.09	10.4 ± 0.05	10.15 ± 0.04	0.13145	5.1E-06	0.01823
TC1500001718.mm.1	Ly6d	lymphocyte antigen 6 complex, locus D	5.82 ± 0.12	6.34 ± 0.09	6.2 ± 0.11	6.4 ± 0.11	0.08808	0.0081	0.21206
TC1500001727.mm.1	Ly6i	lymphocyte antigen 6 complex, locus I	6.19 ± 0.07	5.93 ± 0.06	6.08 ± 0.02	5.9 ± 0.05	0.33251	0.0029	0.59372
TC0100000103.mm.1	Ly96	lymphocyte antigen 96	9.18 ± 0.08	8.9 ± 0.04	9.29 ± 0.1	9.03 ± 0.08	0.10994	0.00765	0.9507
TC1200002166.mm.1	Lysmd1	LysM, putative peptidoglycan-binding, domain containing 1	7.14 ± 0.02	7.05 ± 0.01	6.99 ± 0.05	6.93 ± 0.07	0.00817	0.15158	0.80427
TC0700004104.mm.1	Lyve1	lymphatic vessel endothelial hyaluronan receptor 1	9.44 ± 0.12	8.85 ± 0.1	9.05 ± 0.09	8.68 ± 0.11	0.04932	0.00146	0.53167
TC1000002930.mm.1	Lyz1	lysozyme 1	9.36 ± 0.04	9.12 ± 0.07	9.26 ± 0.09	8.75 ± 0.12	0.02063	0.00071	0.08057
TC1000002929.mm.1	Lyz2	lysozyme 2	11.2 ± 0.06	10.99 ± 0.09	11.12 ± 0.08	10.59 ± 0.12	0.02634	0.00143	0.07479
TC0800002359.mm.1	Lzts1	leucine zipper, putative tumor suppressor 1	4.94 ± 0.02	4.98 ± 0.01	4.97 ± 0	5.02 ± 0.03	0.0275	0.00881	0.9825
TC0200005052.mm.1	Mafb	v-maf musculoaponeurotic fibrosarcoma oncogene family, pr	7.6 ± 0.05	7.34 ± 0.05	7.41 ± 0.02	7.3 ± 0.06	0.07591	0.0044	0.29865
TC0200004501.mm.1	Mageb3	melanoma antigen, family B, 3	4.59 ± 0.04	4.71 ± 0.02	4.78 ± 0.04	4.65 ± 0.05	0.13668	0.83221	0.00887
TC0600002763.mm.1	Magi1	membrane associated guanylate kinase, WW and PDZ doma	7.39 ± 0.03	7.37 ± 0.02	7.56 ± 0.05	7.28 ± 0.04	0.22125	0.00237	0.00312
TC0600003266.mm.1	Magohb	mago-nashi homolog B (Drosophila)	5.15 ± 0.04	5.08 ± 0.06	5.24 ± 0.03	4.96 ± 0.07	0.76566	0.00616	0.07703
TC0200004563.mm.1	Mal	myelin and lymphocyte protein, T cell differentiation protein	7.89 ± 0.29	7.14 ± 0.15	6.95 ± 0.15	7.73 ± 0.19	0.72864	0.6227	0.00886
TC1900000984.mm.1	Malat1	metastasis associated lung adenocarcinoma transcript 1 (nor	11.72 ± 0.1	11.53 ± 0.08	11.3 ± 0.05	11.4 ± 0.04	0.00432	0.64324	0.0908
TC0200004564.mm.1	Mall	mal, T cell differentiation protein-like	8.31 ± 0.13	7.93 ± 0.04	7.96 ± 0.04	7.67 ± 0.08	0.00887	0.00513	0.95349
TC0300001960.mm.1	Maml3	mastermind like 3 (Drosophila)	6.28 ± 0.05	6.4 ± 0.01	6.4 ± 0.02	6.49 ± 0.04	0.01076	0.00837	0.68264
TC1000002175.mm.1	Man1a	mannosidase 1, alpha	8.89 ± 0.05	8.5 ± 0.07	8.74 ± 0.03	8.53 ± 0.08	0.54517	0.00049	0.27389
TC0400003742.mm.1	Man1c1	mannosidase, alpha, class 1C, member 1	8.74 ± 0.09	8.46 ± 0.02	8.67 ± 0.06	8.39 ± 0.07	0.73643	0.005	0.56334
TC1700001062.mm.1	Man2a1	mannosidase 2, alpha 1	9.6 ± 0.08	9.17 ± 0.11	9.37 ± 0.05	8.95 ± 0.11	0.04592	0.00062	0.69217
TC0800000983.mm.1	Man2b1	mannosidase 2, alpha B1	8.52 ± 0.04	8.4 ± 0.02	8.5 ± 0.03	8.19 ± 0.07	0.034	0.00042	0.03264
TC0300001373.mm.1	Manba	mannosidase, beta A, lysosomal	6.81 ± 0.04	6.84 ± 0.02	6.89 ± 0.05	6.67 ± 0.04	0.32005	0.02663	0.00673
TC0600003305.mm.1	Mansc1	MANSC domain containing 1	6.79 ± 0.03	6.8 ± 0.08	7.01 ± 0.05	6.9 ± 0.03	0.00774	0.43909	0.20647

Supplemental Table I

Annotations			Summary Statistics				2 way ANOVA p-values		
Probe Set ID	Symbol	Description	XY sh	XY Or	XX sh	XX Or	XY vs XX	Sh vs Or	Intrxn
TC0X00001892.mm.1	Maob	monoamine oxidase B	9.23 ± 0.16	8.75 ± 0.08	8.86 ± 0.04	9.08 ± 0.07	0.80875	0.2442	0.0066
TC0200001809.mm.1	Map1a	microtubule-associated protein 1 A	7.47 ± 0.08	7.32 ± 0.02	7.57 ± 0.06	7.19 ± 0.08	0.80477	0.00675	0.04917
TC1100000771.mm.1	Map2k3	mitogen-activated protein kinase kinase 3	8.23 ± 0.05	8.3 ± 0.02	8.15 ± 0.04	8.11 ± 0.06	0.00862	0.77482	0.277
TC0400001607.mm.1	Map3k6	mitogen-activated protein kinase kinase kinase 6	7.67 ± 0.15	7.44 ± 0.07	7.19 ± 0.02	7.05 ± 0.05	0.00154	0.17898	0.94339
TC0700000519.mm.1	Map4k1	mitogen-activated protein kinase kinase kinase kinase 1	5.97 ± 0.04	6.2 ± 0.03	6.1 ± 0.06	6.24 ± 0.07	0.11616	0.00277	0.46467
TC0100000289.mm.1	Map4k4	mitogen-activated protein kinase kinase kinase kinase 4	8.84 ± 0.04	8.68 ± 0.08	8.88 ± 0.02	8.64 ± 0.07	0.86755	0.00286	0.57534
TC1500002038.mm.1	Mapk12	mitogen-activated protein kinase 12	6.87 ± 0.02	6.95 ± 0.03	6.83 ± 0.03	6.94 ± 0.04	0.57811	0.00723	0.74413
TC0900002676.mm.1	Mapk6	mitogen-activated protein kinase 6	8.02 ± 0.06	7.73 ± 0.05	7.79 ± 0.05	7.63 ± 0.02	0.00487	0.00052	0.20031
TC1000003095.mm.1	Mar9	membrane-associated ring finger (C3HC4) 9	5.68 ± 0.04	5.85 ± 0.04	5.84 ± 0.03	5.93 ± 0.04	0.0079	0.00362	0.26206
TC0600002491.mm.1	Mat2a	methionine adenosyltransferase II, alpha	10.1 ± 0.03	10.09 ± 0.07	9.87 ± 0.06	9.95 ± 0.04	0.00184	0.52032	0.35324
TC1100002548.mm.1	Mat2b	methionine adenosyltransferase II, beta	7.26 ± 0.03	7.34 ± 0.03	7.2 ± 0.02	7.29 ± 0.02	0.0592	0.00948	0.85972
TC1600001439.mm.1	Mb21d2	Mab-21 domain containing 2	7.13 ± 0.03	7.15 ± 0.08	7.31 ± 0.03	7.05 ± 0.06	0.35086	0.04439	0.00711
TC1800000788.mm.1	Mbd1	methyl-CpG binding domain protein 1	7.92 ± 0.1	8.18 ± 0.13	7.6 ± 0.04	7.69 ± 0.07	0.00195	0.03326	0.20011
TC1400001303.mm.1	Mbnl2	muscleblind-like 2	8.93 ± 0.04	8.88 ± 0.02	8.79 ± 0.02	8.8 ± 0.05	0.00906	0.55952	0.47371
TC1800000869.mm.1	Mbp	myelin basic protein	7.36 ± 0.12	7.1 ± 0.08	6.98 ± 0.11	7.55 ± 0.13	0.53459	0.13103	0.00513
TC1700002686.mm.1	Mcfd2	multiple coagulation factor deficiency 2	7.94 ± 0.02	7.92 ± 0.01	7.9 ± 0.01	7.89 ± 0.01	0.00518	0.19404	0.41956
TC0300001488.mm.1	Mcoln3	mucolipin 3	4.25 ± 0.03	4.48 ± 0.07	4.35 ± 0.02	4.4 ± 0.03	0.95425	0.00513	0.05959
TC1500002206.mm.1	Mcrs1	microspherule protein 1	7.27 ± 0.02	7.3 ± 0	7.35 ± 0.02	7.3 ± 0.01	0.00318	0.44875	0.00223
TC0200004129.mm.1	Mdk	midkine	6.49 ± 0.04	6.83 ± 0.05	6.73 ± 0.05	6.8 ± 0.08	0.07092	0.00216	0.02837
TC1700000900.mm.1	Mea1	male enhanced antigen 1	7.43 ± 0.02	7.44 ± 0.04	7.51 ± 0.01	7.57 ± 0.04	0.00536	0.40085	0.32292
TC1000002484.mm.1	Med16	mediator complex subunit 16	7.9 ± 0.04	7.99 ± 0.03	8.11 ± 0.04	8.08 ± 0.02	0.00188	0.62135	0.16615
TC0200003203.mm.1	Med22	mediator complex subunit 22	7.19 ± 0.01	7.26 ± 0.03	7.26 ± 0.02	7.19 ± 0.01	0.92156	0.69557	0.0014
TC1100003687.mm.1	Med24	mediator complex subunit 24	7.33 ± 0.01	7.28 ± 0.03	7.47 ± 0.03	7.32 ± 0.02	0.00211	0.00046	0.05405
TC0500000489.mm.1	Med28	mediator of RNA polymerase II transcription, subunit 28 homo	7.19 ± 0.02	7.12 ± 0.04	7.23 ± 0.02	7.06 ± 0.04	0.79725	0.00069	0.09551
TC0500003722.mm.1	Medag	mesenteric estrogen dependent adipogenesis	8.48 ± 0.07	8.26 ± 0.03	8.63 ± 0.07	8.05 ± 0.19	0.95988	0.00256	0.07072
TC1200000331.mm.1	Meox2	mesenchyme homeobox 2	7.09 ± 0.1	6.83 ± 0.04	7.24 ± 0.06	6.89 ± 0.11	0.34792	0.00249	0.80225
TC0500003462.mm.1	Mepce	methylphosphate capping enzyme	7.46 ± 0.03	7.56 ± 0.01	7.49 ± 0.03	7.54 ± 0.01	0.63792	0.00336	0.22003
TC1000001544.mm.1	Mettl1	methyltransferase like 1	6.87 ± 0.02	6.81 ± 0.01	6.76 ± 0.03	6.76 ± 0.02	0.0074	0.34078	0.49148
TC1200001868.mm.1	Mettl21d	methyltransferase like 21D	5.6 ± 0.04	5.72 ± 0.03	5.77 ± 0.04	5.6 ± 0.03	0.61631	0.31866	0.00173
TC1000000356.mm.1	Mettl24	methyltransferase like 24	6.82 ± 0.08	7.18 ± 0.04	7.15 ± 0.02	6.99 ± 0.04	0.29442	0.1071	0.00057
TC1500001040.mm.1	Mettl7a1	methyltransferase like 7A1	9.35 ± 0.06	9.1 ± 0.06	9.08 ± 0.03	9.28 ± 0.06	0.42692	0.76796	0.00128
TC1100000780.mm.1	Mfap4	microfibrillar-associated protein 4	9.85 ± 0.16	10.24 ± 0.1	10.03 ± 0.1	9.69 ± 0.11	0.21708	0.70195	0.00844

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Annotations			Summary Statistics				2 way ANOVA p-values		
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TC0700003552.mm.1	Mfge8	milk fat globule-EGF factor 8 protein	10.32 ± 0.12	10.43 ± 0.05	10.58 ± 0.08	10.2 ± 0.05	0.68782	0.21537	0.0088
TC1600000421.mm.1	Mfi2	antigen p97 (melanoma associated) identified by monoclonal	5.64 ± 0.02	5.76 ± 0.01	5.76 ± 0.04	5.94 ± 0.09	0.00717	0.00879	0.65658
TC1500001093.mm.1	Mfsd5	major facilitator superfamily domain containing 5	7.87 ± 0.03	7.85 ± 0.02	7.74 ± 0.02	7.78 ± 0.03	0.00324	0.64389	0.26207
TC1100000874.mm.1	Mfsd6l	major facilitator superfamily domain containing 6-like	5.08 ± 0.05	5.52 ± 0.11	5.31 ± 0.04	5.31 ± 0.07	0.89717	0.00864	0.00824
TC1200000563.mm.1	Mgat2	mannoside acetylglucosaminyltransferase 2	8.59 ± 0.06	8.49 ± 0.05	8.47 ± 0.03	8.25 ± 0.04	0.00655	0.01732	0.19907
TC1100000941.mm.1	Mgl2	macrophage galactose N-acetyl-galactosamine specific lectin	7.8 ± 0.05	7.47 ± 0.09	7.55 ± 0.03	7.34 ± 0.04	0.00618	0.00038	0.42842
TC0600001639.mm.1	Mgst1	microsomal glutathione S-transferase 1	8.16 ± 0.1	7.69 ± 0.16	7.59 ± 0.15	8.04 ± 0.05	0.27793	0.79379	0.00144
TC0100003725.mm.1	Mia3	melanoma inhibitory activity 3	8.28 ± 0.04	8.09 ± 0.04	8.11 ± 0.01	7.95 ± 0.09	0.01773	0.00901	0.97202
TC1900000465.mm.1	Minpp1	multiple inositol polyphosphate histidine phosphatase 1	8.05 ± 0.02	7.99 ± 0.02	7.93 ± 0	7.87 ± 0.07	0.00994	0.18429	0.73787
TC1900001429.mm.1	Mir107	microRNA 107	4.24 ± 0.09	4.79 ± 0.14	4.36 ± 0.09	4.72 ± 0.06	0.8801	0.0012	0.58109
TC1200002238.mm.1	Mir1190	microRNA 1190	6.72 ± 0.03	6.84 ± 0.03	6.7 ± 0.06	6.93 ± 0.08	0.57239	0.00842	0.29473
TC0300002985.mm.1	Mir1895	microRNA 1895	4.75 ± 0.03	4.87 ± 0.02	4.78 ± 0.05	4.93 ± 0.07	0.22236	0.00852	0.86644
TC0600003113.mm.1	Mir200c	microRNA 200c	3.99 ± 0.07	4.35 ± 0.06	4.09 ± 0.05	4.38 ± 0.14	0.64091	0.0047	0.90838
TC0800002576.mm.1	Mir3074-2	microRNA 3074-2	5.76 ± 0.03	5.79 ± 0.02	5.73 ± 0.01	5.91 ± 0.02	0.05494	0.00039	0.0151
TC0500000388.mm.1	Mir3097	microRNA 3097	7.32 ± 0.05	7.46 ± 0.08	7.29 ± 0.04	7.49 ± 0.05	0.90146	0.00623	0.79623
TC0400003027.mm.1	Mir31	microRNA 31	4.5 ± 0.02	4.47 ± 0.06	4.64 ± 0.08	4.72 ± 0.07	0.00674	0.74397	0.25533
TC0800002936.mm.1	Mir3473d	microRNA 3473d	5.7 ± 0.05	5.82 ± 0.04	5.6 ± 0.05	5.81 ± 0.05	0.20233	0.00512	0.31008
TC0100002595.mm.1	Mir375	microRNA 375	6.09 ± 0.07	6.68 ± 0.11	6.35 ± 0.12	6.61 ± 0.19	0.64602	0.00799	0.31676
TC0X00002311.mm.1	Mir505	microRNA 505	4.75 ± 0.03	4.86 ± 0.08	4.6 ± 0.09	4.84 ± 0.02	0.24826	0.00968	0.37075
TC1200001876.mm.1	Mir681	microRNA 681	6.29 ± 0.08	6.62 ± 0.03	6.43 ± 0.06	6.65 ± 0.11	0.57603	0.00874	0.8149
TC1700001393.mm.1	Mir692-1	microRNA 692-1	9.59 ± 0.05	9.25 ± 0.08	9.54 ± 0.11	9.41 ± 0.07	0.47589	0.00976	0.20743
TC1200001172.mm.1	Mir758	microRNA 758	5.54 ± 0.03	5.79 ± 0.07	5.62 ± 0.07	6 ± 0.17	0.16967	0.00603	0.43429
TC1300001941.mm.1	Mirlet7d	microRNA let7d	6.13 ± 0.07	6.08 ± 0.03	5.97 ± 0.1	5.71 ± 0.12	0.00953	0.10048	0.24962
TC1800000953.mm.1	Mkx	mohawk homeobox	5.07 ± 0.06	5.18 ± 0.01	5.48 ± 0.11	5.17 ± 0.02	0.00619	0.15215	0.0039
TC1900000444.mm.1	Mlana	melan-A	4.68 ± 0.04	5.05 ± 0.05	4.91 ± 0.05	5.01 ± 0.02	0.05724	0.00012	0.00878
TC1100001543.mm.1	Mllt6	myeloid/lymphoid or mixed-lineage leukemia (trithorax homol	8.19 ± 0.03	8.31 ± 0.01	8.42 ± 0.04	8.34 ± 0.02	0.00059	0.44549	0.00506
TC1400000745.mm.1	Mmp14	matrix metallopeptidase 14 (membrane-inserted)	8.99 ± 0.07	8.95 ± 0.09	9.25 ± 0.06	8.67 ± 0.16	0.88727	0.00778	0.01799
TC0200002542.mm.1	Mmp9	matrix metallopeptidase 9	7.3 ± 0.06	7.06 ± 0.07	7.47 ± 0.03	7.16 ± 0.07	0.04815	0.00045	0.61666
TC0X00001932.mm.1	mmu-mir-5617	mmu-mir-5617	6.93 ± 0.03	7.19 ± 0.02	7.06 ± 0.06	7.26 ± 0.11	0.18951	0.00514	0.87671
TC0500000874.mm.1	mmu-mir-6415	mmu-mir-6415	5.58 ± 0.06	5.86 ± 0.03	5.7 ± 0.05	5.65 ± 0.05	0.40418	0.02972	0.00447
TC1000002452.mm.1	mmu-mir-6907	mmu-mir-6907	6.15 ± 0.02	6.38 ± 0.06	6.09 ± 0.06	6.39 ± 0.06	0.4941	0.00015	0.3882
TC1900000115.mm.1	mmu-mir-6989	mmu-mir-6989	8.8 ± 0.06	9.2 ± 0.03	8.92 ± 0.07	9.08 ± 0.16	0.95941	0.00781	0.20812

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Annotations			Summary Statistics				2 way ANOVA p-values		
Probe Set ID	Symbol	Description	XY sh	XY Or	XX sh	XX Or	XY vs XX	Sh vs Or	Intrxn
TC0900001443.mm.1	mmu-mir-7089	mmu-mir-7089	6.7 ± 0.06	6.92 ± 0.06	6.79 ± 0.03	6.97 ± 0.1	0.27997	0.00847	0.65272
TC1000002711.mm.1	mmu-mir-7211	mmu-mir-7211	6.97 ± 0.05	7.27 ± 0.03	7.17 ± 0.04	7.28 ± 0.08	0.08907	0.00239	0.12866
TC0200001439.mm.1	mmu-mir-7221	mmu-mir-7221	5.47 ± 0.06	5.74 ± 0.05	5.5 ± 0.07	5.8 ± 0.11	0.35339	0.00104	0.90686
TC0100003889.mm.1	Mnda	myeloid cell nuclear differentiation antigen	7.46 ± 0.17	6.72 ± 0.12	6.86 ± 0.06	6.57 ± 0.13	0.02932	0.00364	0.19305
TC1100001050.mm.1	Mnt	max binding protein	7.6 ± 0.04	7.7 ± 0.02	7.62 ± 0.02	7.73 ± 0.02	0.18337	0.00071	0.80078
TC0700004550.mm.1	Mob2	MOB kinase activator 2	8.39 ± 0.14	8.36 ± 0.05	8.74 ± 0.09	8.09 ± 0.1	0.51841	0.01077	0.0068
TC0X00003038.mm.1	Morf4l2	mortality factor 4 like 2	8.27 ± 0.06	8.17 ± 0.05	8.05 ± 0.03	7.87 ± 0.09	0.00335	0.11227	0.31342
TC0X00002470.mm.1	Mpp1	membrane protein, palmitoylated	7.93 ± 0.05	7.61 ± 0.06	7.66 ± 0.04	7.55 ± 0.1	0.03147	0.00638	0.1496
TC0600000591.mm.1	Mpp6	membrane protein, palmitoylated 6 (MAGUK p55 subfamily m	8.28 ± 0.12	7.89 ± 0.08	8.23 ± 0.03	7.73 ± 0.08	0.46741	0.00065	0.3166
TC0100001578.mm.1	Mpz	myelin protein zero	7.94 ± 0.29	7.08 ± 0.21	6.84 ± 0.27	8.09 ± 0.26	0.82096	0.27897	0.00371
TC0200000245.mm.1	Mrc1	mannose receptor, C type 1	9.49 ± 0.06	8.93 ± 0.1	9.39 ± 0.08	8.9 ± 0.13	0.58119	0.00011	0.86326
TC0700002080.mm.1	Mrpl23	mitochondrial ribosomal protein L23	7.33 ± 0.03	7.47 ± 0.02	7.49 ± 0.01	7.51 ± 0.03	0.00731	0.03978	0.14248
TC1400000744.mm.1	Mrpl52	mitochondrial ribosomal protein L52	7.45 ± 0.04	7.51 ± 0.03	7.61 ± 0.03	7.64 ± 0.06	0.00612	0.40686	0.85056
TC1900000216.mm.1	Ms4a4a	membrane-spanning 4-domains, subfamily A, member 4A	7.36 ± 0.29	6.38 ± 0.11	6.25 ± 0.08	6 ± 0.05	0.00548	0.01962	0.20444
TC1900000226.mm.1	Ms4a4d	membrane-spanning 4-domains, subfamily A, member 4D	7.87 ± 0.09	7.71 ± 0.05	7.85 ± 0.09	7.31 ± 0.18	0.10557	0.00866	0.07713
TC1900000225.mm.1	Ms4a6b	membrane-spanning 4-domains, subfamily A, member 6B	5.68 ± 0.09	5.35 ± 0.04	5.28 ± 0.1	5.12 ± 0.08	0.004	0.01742	0.45682
TC1900000221.mm.1	Ms4a6c	membrane-spanning 4-domains, subfamily A, member 6C	7.52 ± 0.13	6.93 ± 0.09	6.94 ± 0.07	6.5 ± 0.14	0.00174	0.00143	0.78008
TC1900001137.mm.1	Ms4a6d	membrane-spanning 4-domains, subfamily A, member 6D	7.51 ± 0.15	6.93 ± 0.07	6.99 ± 0.07	6.59 ± 0.04	0.00342	0.00121	0.79426
TC1900001131.mm.1	Ms4a7	membrane-spanning 4-domains, subfamily A, member 7	5.25 ± 0.08	5 ± 0.07	5.06 ± 0.06	4.82 ± 0.06	0.02077	0.00464	0.93778
TC0800002102.mm.1	Msr1	macrophage scavenger receptor 1	6.15 ± 0.11	5.72 ± 0.07	5.85 ± 0.07	5.58 ± 0.07	0.0614	0.00315	0.67744
TC0500002275.mm.1	Msx1	homeobox, msh-like 1	5.68 ± 0.01	5.79 ± 0.03	5.88 ± 0.03	5.95 ± 0.11	0.00725	0.12391	0.73849
TC0800001095.mm.1	Mt1	metallothionein 1	11.02 ± 0.09	10.69 ± 0.07	10.64 ± 0.03	10.47 ± 0.04	0.00078	0.00276	0.31021
TC0800001094.mm.1	Mt2	metallothionein 2	10.38 ± 0.18	9.51 ± 0.1	9.52 ± 0.04	9 ± 0.14	0.00054	0.0005	0.41966
TC0X00002267.mm.1	Mtap7d3	MAP7 domain containing 3	5.96 ± 0.07	5.72 ± 0.1	6.23 ± 0.12	5.71 ± 0.14	0.21186	0.004	0.19035
TC1000000015.mm.1	Mthfd1l	methylenetetrahydrofolate dehydrogenase (NADP+ depender	6.19 ± 0.1	6.29 ± 0.05	5.8 ± 0.03	6.23 ± 0.04	0.01974	0.00066	0.09013
TC0600002565.mm.1	Mthfd2	methylenetetrahydrofolate dehydrogenase (NAD+ dependent	6.94 ± 0.14	6.43 ± 0.1	6.79 ± 0.08	6.28 ± 0.05	0.3201	0.00065	0.73416
TC0400001924.mm.1	Mthfr	5,10-methylenetetrahydrofolate reductase	6.89 ± 0.05	7.03 ± 0.01	7.14 ± 0.04	7 ± 0.02	0.00742	0.77105	0.00163
TC0700004547.mm.1	Muc6	mucin 6, gastric	4.86 ± 0.02	5 ± 0.03	4.92 ± 0.02	5.04 ± 0.08	0.29583	0.00992	0.81454
TC0X00001367.mm.1	Mum1l1	melanoma associated antigen (mutated) 1-like 1	6.17 ± 0.08	6.18 ± 0.05	6.23 ± 0.06	5.8 ± 0.1	0.07715	0.02822	0.00878
TC1400000316.mm.1	Mustn1	musculoskeletal, embryonic nuclear protein 1	9.57 ± 0.12	9.68 ± 0.04	9.93 ± 0.07	9.32 ± 0.17	0.89619	0.06036	0.00567
TC0700004660.mm.1	Mvp	major vault protein	8.01 ± 0.02	8.04 ± 0.02	8.11 ± 0.02	8.03 ± 0.01	0.03924	0.12812	0.00616
TC0400002095.mm.1	Mxra8	matrix-remodelling associated 8	8.6 ± 0.1	8.82 ± 0.04	8.88 ± 0.07	8.6 ± 0.05	0.58057	0.8133	0.00525

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TC1000001840.mm.1	Myb	myeloblastosis oncogene	4.34 ± 0.04	5 ± 0.25	4.47 ± 0.01	5.17 ± 0.3	0.45723	0.00295	0.86369
TC0700002966.mm.1	Mybpc2	myosin binding protein C, fast-type	5.48 ± 0.02	5.72 ± 0.02	5.62 ± 0.01	5.64 ± 0.09	0.47185	0.00743	0.02102
TC1100000880.mm.1	Myh10	myosin, heavy polypeptide 10, non-muscle	9.9 ± 0.16	10.32 ± 0.07	10.3 ± 0.08	9.98 ± 0.12	0.76694	0.64463	0.00809
TC1000003145.mm.1	Myl6	myosin, light polypeptide 6, alkali, smooth muscle and non-m	11.58 ± 0.06	11.77 ± 0.05	11.79 ± 0.04	11.58 ± 0.06	0.58487	0.9023	0.00204
TC0200002303.mm.1	Mylk2	myosin, light polypeptide kinase 2, skeletal muscle	6.66 ± 0.12	7.07 ± 0.07	6.98 ± 0.05	6.73 ± 0.06	0.78739	0.43136	0.00329
TC0100002308.mm.1	Myo1b	myosin IB	6.95 ± 0.16	6.36 ± 0.09	6.34 ± 0.08	6.56 ± 0.03	0.10649	0.13608	0.00335
TC0900001009.mm.1	Myo5a	myosin VA	8.15 ± 0.18	7.63 ± 0.09	7.65 ± 0.11	8.01 ± 0.07	0.59984	0.47364	0.00392
TC0100001481.mm.1	Myoc	myocilin	5.96 ± 0.14	6.32 ± 0.13	6.51 ± 0.09	6.59 ± 0.07	0.00603	0.13481	0.38586
TC0500003685.mm.1	N4bp2l1	NEDD4 binding protein 2-like 1	5.83 ± 0.06	5.73 ± 0.07	5.61 ± 0.05	5.88 ± 0.03	0.40992	0.22501	0.00343
TC1100001638.mm.1	Naglu	alpha-N-acetylglucosaminidase (Sanfilippo disease IIIB)	7.4 ± 0.05	7.55 ± 0.03	7.56 ± 0.04	7.43 ± 0.01	0.45966	0.61872	0.00105
TC1600001155.mm.1	Nagpa	N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucos	7.45 ± 0.04	7.54 ± 0.02	7.6 ± 0.03	7.49 ± 0.03	0.10225	0.75153	0.00593
TC1300002530.mm.1	Naip2	NLR family, apoptosis inhibitory protein 2	6.01 ± 0.02	5.9 ± 0.05	6.02 ± 0.02	5.87 ± 0.04	0.69301	0.00214	0.66281
TC0700000219.mm.1	Napa	N-ethylmaleimide sensitive fusion protein attachment protein	8.14 ± 0.05	8.04 ± 0.03	8.03 ± 0.04	8.15 ± 0.02	0.68696	0.95107	0.00931
TC0200004813.mm.1	Napb	N-ethylmaleimide sensitive fusion protein attachment protein	8.4 ± 0.76	6.89 ± 0.33	6.05 ± 0.15	8 ± 0.32	0.38205	0.48424	0.0089
TC1100002062.mm.1	Narf	nuclear prelamin A recognition factor	7.43 ± 0.07	7.51 ± 0.04	7.24 ± 0.05	7.29 ± 0.03	0.00277	0.22238	0.68258
TC0700000049.mm.1	Nat14	N-acetyltransferase 14	6.67 ± 0.08	6.8 ± 0.03	6.87 ± 0.01	6.67 ± 0.06	0.29986	0.88357	0.00523
TC1200000110.mm.1	Nbas	neuroblastoma amplified sequence	7.58 ± 0.04	7.44 ± 0.01	7.4 ± 0.04	7.21 ± 0.09	0.00251	0.01091	0.5358
TC1500000871.mm.1	Ncaph2	non-SMC condensin II complex, subunit H2	7.71 ± 0.01	7.75 ± 0.01	7.74 ± 0.01	7.71 ± 0.01	0.99107	0.48539	0.00302
TC0200000549.mm.1	Ncs1	neuronal calcium sensor 1	7.7 ± 0.09	7.51 ± 0.02	7.7 ± 0.08	7.37 ± 0.07	0.71105	0.00915	0.16762
TC0X00001893.mm.1	Ndp	Norrie disease (pseudoglioma) (human)	5.35 ± 0.06	5.61 ± 0.11	5.96 ± 0.08	5.6 ± 0.12	0.0095	0.41203	0.00755
TC0200005006.mm.1	Ndrg3	N-myc downstream regulated gene 3	8.58 ± 0.1	8.44 ± 0.06	8.44 ± 0.07	8.72 ± 0.06	0.71885	0.69133	0.00643
TC0300002879.mm.1	Ndst3	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 3	4.71 ± 0.02	4.88 ± 0.05	4.62 ± 0.02	4.77 ± 0.04	0.02074	0.00028	0.6207
TC1900000986.mm.1	Neat1	nuclear paraspeckle assembly transcript 1 (non-protein codin	8.25 ± 0.12	8.07 ± 0.05	7.85 ± 0.02	8.1 ± 0.04	0.0172	0.9242	0.0084
TC0400002238.mm.1	Necab1	N-terminal EF-hand calcium binding protein 1	6.88 ± 0.77	5.38 ± 0.23	4.78 ± 0.23	6.68 ± 0.32	0.62973	0.50723	0.00929
TC1400000965.mm.1	Nefl	neurofilament, light polypeptide	7.89 ± 0.83	6.14 ± 0.56	5.21 ± 0.18	7.66 ± 0.31	0.47916	0.4087	0.00568
TC1400002297.mm.1	Nefm	neurofilament, medium polypeptide	5.93 ± 0.24	5.6 ± 0.12	5.2 ± 0.07	6.03 ± 0.12	0.52602	0.10759	0.00787
TC0200000702.mm.1	Nek6	NIMA (never in mitosis gene a)-related expressed kinase 6	7.47 ± 0.06	7.35 ± 0.03	7.5 ± 0.02	7.34 ± 0.06	0.88295	0.008	0.90375
TC0200002705.mm.1	Nelfcd	negative elongation factor complex member C/D, Th1l	7.02 ± 0.02	6.95 ± 0.03	6.92 ± 0.02	7.02 ± 0.02	0.51656	0.74218	0.00263
TC0100003805.mm.1	Nenf	neuron derived neurotrophic factor	8.45 ± 0.05	8.63 ± 0.03	8.66 ± 0.03	8.55 ± 0	0.05006	0.17441	0.00036
TC0100000817.mm.1	Neu2	neuraminidase 2	5.07 ± 0.03	5.24 ± 0.05	5.31 ± 0.02	5.27 ± 0.03	0.00415	0.13016	0.02308
TC0700003806.mm.1	Neu3	neuraminidase 3	6.75 ± 0.06	7.01 ± 0.04	6.92 ± 0.03	6.9 ± 0.02	0.339	0.00797	0.0028
TC1300002013.mm.1	Nfil3	nuclear factor, interleukin 3, regulated	6.41 ± 0.1	6.69 ± 0.02	7.08 ± 0.04	6.64 ± 0.11	0.00643	0.16682	0.00182

Supplemental Table I

Annotations			Summary Statistics				2 way ANOVA p-values		
Probe Set ID	Symbol	Description	XY sh	XY Or	XX sh	XX Or	XY vs XX	Sh vs Or	Intrxn
TC1900000689.mm.1	Nfkb2	nuclear factor of kappa light polypeptide gene enhancer in B	7.19 ± 0.03	7.27 ± 0.01	7.31 ± 0.01	7.2 ± 0.04	0.53624	0.34018	0.00553
TC1200001768.mm.1	Nfkbia	nuclear factor of kappa light polypeptide gene enhancer in B	8.87 ± 0.06	9 ± 0.08	8.64 ± 0.06	8.71 ± 0.05	0.00262	0.06876	0.40644
TC1600001742.mm.1	Nfkbiz	nuclear factor of kappa light polypeptide gene enhancer in B	6.33 ± 0.05	6.49 ± 0.05	6.45 ± 0.04	6.28 ± 0.04	0.25874	0.74862	0.00544
TC1300000087.mm.1	Nid1	nidogen 1	10.18 ± 0.06	9.67 ± 0.06	9.98 ± 0.04	9.57 ± 0.09	0.05638	1.2E-05	0.53045
TC1300002747.mm.1	Nim1	serine/threonine-protein kinase NIM1	5.49 ± 0.02	5.56 ± 0.01	5.48 ± 0.02	5.54 ± 0.01	0.3376	0.00326	0.84034
TC1100000053.mm.1	Nipsnap1	4-nitrophenylphosphatase domain and non-neuronal SNAP25	6.99 ± 0.09	6.88 ± 0.03	6.88 ± 0.05	7.17 ± 0.02	0.17857	0.2091	0.00389
TC0200005426.mm.1	Nkain4	Na+/K+ transporting ATPase interacting 4	6.77 ± 0.03	6.75 ± 0.01	6.95 ± 0.03	6.83 ± 0.02	6.2E-05	0.01136	0.0287
TC1300002304.mm.1	Nkd2	naked cuticle 2 homolog (Drosophila)	6.23 ± 0.03	6.25 ± 0.02	6.4 ± 0.05	6.26 ± 0.01	0.00876	0.10368	0.01208
TC1400000972.mm.1	Nkx3-1	NK-3 transcription factor, locus 1 (Drosophila)	7.82 ± 0.11	7.51 ± 0.07	7.96 ± 0.08	7.41 ± 0.18	0.55703	0.00616	0.18441
TC0700004481.mm.1	Nkx6-2	NK6 homeobox 2	6.4 ± 0.06	6.65 ± 0.05	6.51 ± 0.05	6.7 ± 0.09	0.21019	0.0043	0.62523
TC0700000351.mm.1	Nlrp5	NLR family, pyrin domain containing 5	4.97 ± 0.03	4.89 ± 0.03	5.09 ± 0.06	4.98 ± 0.01	0.00534	0.04588	0.4307
TC0900002239.mm.1	Nnmt	nicotinamide N-methyltransferase	6.59 ± 0.04	6.29 ± 0.07	6.34 ± 0.02	6.13 ± 0.1	0.00591	0.00172	0.51897
TC0800002878.mm.1	Nob1	NIN1/RPN12 binding protein 1 homolog (S. cerevisiae)	7.01 ± 0.02	7.14 ± 0.02	7.1 ± 0.01	7.07 ± 0.01	0.68004	0.02157	0.00198
TC0600002323.mm.1	Nod1	nucleotide-binding oligomerization domain containing 1	7.72 ± 0.04	7.56 ± 0.03	7.66 ± 0.01	7.58 ± 0.04	0.44307	0.00196	0.21114
TC0600001448.mm.1	Nop2	NOP2 nucleolar protein	7.75 ± 0.03	7.72 ± 0	7.67 ± 0.01	7.7 ± 0.01	0.00793	0.42448	0.06595
TC0200001972.mm.1	Nop56	NOP56 ribonucleoprotein	6.83 ± 0.02	6.83 ± 0.02	6.74 ± 0.02	6.71 ± 0.05	0.00392	0.73173	0.43004
TC1700000348.mm.1	Noxo1	NADPH oxidase organizer 1	5.34 ± 0.03	5.57 ± 0.04	5.54 ± 0.03	5.6 ± 0.04	0.01159	0.00268	0.04889
TC0100000282.mm.1	Npas2	neuronal PAS domain protein 2	6.98 ± 0.29	7.07 ± 0.13	9.14 ± 0.11	7.07 ± 0.08	0.00024	8.5E-05	0.00023
TC1800000994.mm.1	Npc1	Niemann Pick type C1	7.91 ± 0.02	7.87 ± 0.02	7.78 ± 0.05	7.82 ± 0.02	0.00895	0.92599	0.12739
TC0100003280.mm.1	Npl	N-acetylneuraminate pyruvate lyase	6.24 ± 0.04	6.09 ± 0.07	6.13 ± 0.03	5.96 ± 0.06	0.04512	0.00962	0.90146
TC1100004204.mm.1	Nploc4	nuclear protein localization 4 homolog (S. cerevisiae)	9.38 ± 0.04	9.24 ± 0.05	9.18 ± 0.04	9.29 ± 0.03	0.04341	0.56159	0.00494
TC1900001587.mm.1	Npm3	nucleoplasmin 3	7.93 ± 0.07	8.1 ± 0.04	8.01 ± 0.02	7.86 ± 0.02	0.09886	0.99472	0.00694
TC0500001756.mm.1	Nptx2	neuronal pentraxin 2	6.51 ± 0.07	6.72 ± 0.05	6.54 ± 0.07	6.73 ± 0.05	0.66393	0.0074	0.78523
TC1700001635.mm.1	Npw	neuropeptide W	6.48 ± 0.02	6.73 ± 0.07	6.51 ± 0.06	6.73 ± 0.12	0.86263	0.00644	0.86794
TC0600000588.mm.1	Npy	neuropeptide Y	9.91 ± 0.71	8.11 ± 0.62	6.53 ± 0.47	9.86 ± 0.26	0.28618	0.1306	0.00118
TC1100003688.mm.1	Nr1d1	nuclear receptor subfamily 1, group D, member 1	10.12 ± 0.12	10.03 ± 0.07	8.71 ± 0.26	10.06 ± 0.1	0.00112	0.00081	0.00073
TC1400001499.mm.1	Nr1d2	nuclear receptor subfamily 1, group D, member 2	9.86 ± 0.13	10.03 ± 0.03	8.31 ± 0.19	9.82 ± 0.02	1.2E-05	4.4E-06	0.0002
TC0700002970.mm.1	Nr1h2	nuclear receptor subfamily 1, group H, member 2	7.8 ± 0.03	7.85 ± 0.03	7.97 ± 0.02	7.91 ± 0.02	0.00061	0.89516	0.03751
TC0800000854.mm.1	Nr3c2	nuclear receptor subfamily 3, group C, member 2	7.05 ± 0.08	7.35 ± 0.06	7.51 ± 0.06	7.42 ± 0.05	0.00289	0.22671	0.0208
TC0400000529.mm.1	Nr4a3	nuclear receptor subfamily 4, group A, member 3	7.15 ± 0.18	7.04 ± 0.1	6.57 ± 0.14	6.48 ± 0.18	0.00631	0.76239	0.77171
TC0X00001532.mm.1	n-R5s14	nuclear encoded rRNA 5S 14	4.43 ± 0.04	4.75 ± 0.05	4.51 ± 0.03	4.76 ± 0.06	0.32211	3.5E-05	0.41713
TC0700003632.mm.1	n-R5s154	nuclear encoded rRNA 5S 154	4.11 ± 0.01	4.31 ± 0.09	4.03 ± 0.05	4.32 ± 0.09	0.5261	0.00197	0.47731

Supplemental Table I

Annotations			Summary Statistics				2 way ANOVA p-values		
Probe Set ID	Symbol	Description	XY sh	XY Or	XX sh	XX Or	XY vs XX	Sh vs Or	Intrxn
TC0500001554.mm.1	n-R5s178	nuclear encoded rRNA 5S 178	5.18 ± 0.03	5.3 ± 0.03	5.24 ± 0.05	5.52 ± 0.05	0.00371	0.0003	0.07566
TC1500000680.mm.1	n-R5s40	nuclear encoded rRNA 5S 40	4.05 ± 0.05	4.14 ± 0.08	3.8 ± 0.09	3.91 ± 0.06	0.00671	0.12397	0.89941
TC1200001736.mm.1	n-R5s58	nuclear encoded rRNA 5S 58	4.46 ± 0.04	4.58 ± 0.05	4.67 ± 0.03	4.64 ± 0.04	0.00543	0.29925	0.08397
TC0900000789.mm.1	n-R5s84	nuclear encoded rRNA 5S 84	4.1 ± 0.07	4.2 ± 0.06	4.03 ± 0.06	4.36 ± 0.09	0.28026	0.00365	0.24322
TC0900000852.mm.1	n-R5s85	nuclear encoded rRNA 5S 85	4.47 ± 0.08	4.95 ± 0.02	4.64 ± 0.05	4.53 ± 0.15	0.12317	0.08677	0.00886
TC0900003133.mm.1	n-R5s90	nuclear encoded rRNA 5S 90	6.21 ± 0.03	6.15 ± 0.01	6.18 ± 0.03	6.35 ± 0.03	0.0113	0.07669	0.00077
TC0900002332.mm.1	Nrg4	neuregulin 4	7.48 ± 0.17	7.2 ± 0.2	6.81 ± 0.21	7.49 ± 0.11	0.15981	0.5057	0.00866
TC1700002336.mm.1	Nrtn	neurturin	7.11 ± 0.04	7.33 ± 0.05	7.36 ± 0.04	7.41 ± 0.08	0.00535	0.01627	0.09297
TC0900001128.mm.1	Nt5e	5 nucleotidase, ecto	7.01 ± 0.09	6.74 ± 0.1	7.01 ± 0.09	6.65 ± 0.08	0.88372	0.00802	0.43213
TC0600003155.mm.1	Ntf3	neurotrophin 3	6.85 ± 0.15	7.33 ± 0.05	7.42 ± 0.07	6.91 ± 0.1	0.60543	0.77995	0.00065
TC1100003013.mm.1	Ntn1	netrin 1	9.56 ± 0.12	9.8 ± 0.04	9.9 ± 0.08	9.56 ± 0.07	0.4945	0.69704	0.00487
TC0700001684.mm.1	Nucb2	nucleobindin 2	8.87 ± 0.09	8.73 ± 0.02	8.93 ± 0.06	8.5 ± 0.12	0.54239	0.00902	0.04589
TC1200002445.mm.1	Nudt14	nudix (nucleoside diphosphate linked moiety X)-type motif 14	5.74 ± 0.03	5.75 ± 0.04	5.84 ± 0.02	5.94 ± 0.07	0.00657	0.29191	0.20322
TC0900002988.mm.1	Nudt16	nudix (nucleoside diphosphate linked moiety X)-type motif 16	6.93 ± 0.03	7.04 ± 0.04	7.09 ± 0.02	7.02 ± 0.02	0.0268	0.38124	0.00652
TC0600002722.mm.1	Nup210	nucleoporin 210	5.57 ± 0.06	5.81 ± 0.02	5.69 ± 0.06	5.84 ± 0.06	0.30249	0.00708	0.54832
TC0700004152.mm.1	Nup35	nucleoporin 35	6.78 ± 0.02	6.58 ± 0.03	6.8 ± 0.09	6.72 ± 0.03	0.13686	0.00794	0.17504
TC1500000797.mm.1	Nup50	nucleoporin 50	8.67 ± 0.02	8.62 ± 0.04	8.4 ± 0.03	8.5 ± 0.06	0.00031	0.5259	0.1046
TC1100003117.mm.1	Nup88	nucleoporin 88	6.16 ± 0.02	6.19 ± 0.04	6.09 ± 0.02	6.07 ± 0.04	0.00749	0.86698	0.44511
TC0800001097.mm.1	Nup93	nucleoporin 93	6.74 ± 0.03	6.7 ± 0.02	6.69 ± 0.01	6.6 ± 0.02	0.00961	0.03103	0.17765
TC1000000469.mm.1	Nus1	nuclear undecaprenyl pyrophosphate synthase 1 homolog (S	9.1 ± 0.04	9.05 ± 0.06	8.92 ± 0.02	8.89 ± 0.06	0.00329	0.36899	0.8073
TC0800000831.mm.1	Nwd1	NACHT and WD repeat domain containing 1	5.58 ± 0.03	5.7 ± 0.02	5.65 ± 0.02	5.79 ± 0.06	0.07032	0.00419	0.8717
TC0600000067.mm.1	Nxph1	neurexophilin 1	5.64 ± 0.03	5.86 ± 0.08	5.87 ± 0.03	5.74 ± 0.06	0.30983	0.39765	0.00602
TC0X00001402.mm.1	Nxt2	nuclear transport factor 2-like export factor 2	7.1 ± 0.05	7.17 ± 0.01	7.3 ± 0.04	7.13 ± 0.04	0.057	0.27912	0.00642
TC0700004409.mm.1	Oat	ornithine aminotransferase	10.02 ± 0.09	10.27 ± 0.04	10.15 ± 0.06	9.86 ± 0.12	0.18255	0.91776	0.00543
TC1200000142.mm.1	Odc1	ornithine decarboxylase, structural 1	9.07 ± 0.07	8.93 ± 0.04	8.82 ± 0.03	8.65 ± 0.07	0.00076	0.03188	0.58968
TC1500000288.mm.1	Odf1	outer dense fiber of sperm tails 1	4.48 ± 0.06	4.75 ± 0.04	4.6 ± 0.02	4.55 ± 0.03	0.27077	0.02639	0.00412
TC0300002629.mm.1	Olfml3	olfactomedin-like 3	6.39 ± 0.04	6.29 ± 0.04	6.46 ± 0.03	6.31 ± 0.02	0.11173	0.00721	0.27656
TC1100000517.mm.1	Olfr1381	olfactory receptor 1381	5.54 ± 0.02	5.82 ± 0.05	5.74 ± 0.02	5.67 ± 0.1	0.57334	0.07267	0.00488
TC1900001145.mm.1	Olfr1417	olfactory receptor 1417	4.82 ± 0.02	5.11 ± 0.15	4.75 ± 0.04	5 ± 0.09	0.3289	0.00614	0.73848
TC0800000811.mm.1	Olfr373	olfactory receptor 373	4.6 ± 0.06	4.95 ± 0.09	4.67 ± 0.1	4.93 ± 0.09	0.99197	0.00611	0.83733
TC0100001636.mm.1	Olfr433	olfactory receptor 433	4.11 ± 0.06	4.33 ± 0.06	4.16 ± 0.04	4.39 ± 0.07	0.50014	0.00304	0.83735
TC0700002005.mm.1	Olfr523	olfactory receptor 523	5.37 ± 0.04	5.47 ± 0.05	5.6 ± 0.06	5.64 ± 0.08	0.00533	0.32053	0.69971

Supplemental Table I

Annotations			Summary Statistics				2 way ANOVA p-values		
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TC0700001510.mm.1	Olfr632	olfactory receptor 632	5.14 ± 0.06	5.55 ± 0.06	5.36 ± 0.03	5.24 ± 0.14	0.64765	0.09664	0.0059
TC0700001532.mm.1	Olfr661	olfactory receptor 661	4.1 ± 0.02	4.22 ± 0.06	4.14 ± 0.01	4.22 ± 0.02	0.42388	0.00974	0.51581
TC0700003957.mm.1	Olfr666	olfactory receptor 666	4.16 ± 0.07	4.4 ± 0.1	4.12 ± 0.01	4.39 ± 0.09	0.57322	0.00681	0.71676
TC0700003972.mm.1	Olfr686	olfactory receptor 686	5.17 ± 0.05	5.12 ± 0.05	5.24 ± 0.03	5.29 ± 0.04	0.00851	0.69952	0.44129
TC0X00002689.mm.1	Ophn1	oligophrenin 1	6.73 ± 0.03	6.49 ± 0.07	6.61 ± 0.03	6.56 ± 0.05	0.40399	0.00372	0.0337
TC0100003098.mm.1	Optc	opticin	6.18 ± 0.08	6.4 ± 0.05	6.37 ± 0.09	6.16 ± 0.05	0.90244	0.73686	0.00794
TC1000003097.mm.1	Os9	amplified in osteosarcoma	9.04 ± 0.03	8.93 ± 0.02	8.97 ± 0.02	8.89 ± 0.03	0.1702	0.00816	0.87725
TC1900000237.mm.1	Osbp	oxysterol binding protein	9.1 ± 0.03	9.17 ± 0.02	9.05 ± 0.04	8.97 ± 0.06	0.00731	0.88237	0.06112
TC1600000464.mm.1	Osbpl11	oxysterol binding protein-like 11	8.33 ± 0.03	8.22 ± 0.1	7.99 ± 0.09	8.19 ± 0.01	0.00917	0.61458	0.02495
TC0600002250.mm.1	Osbpl3	oxysterol binding protein-like 3	7.58 ± 0.1	7.76 ± 0.05	7.74 ± 0.08	7.39 ± 0.09	0.33073	0.47228	0.0045
TC1500001167.mm.1	Osmr	oncostatin M receptor	8.69 ± 0.13	8.39 ± 0.06	8.5 ± 0.04	8.11 ± 0.1	0.05151	0.00562	0.4835
TC0300002944.mm.1	Ostc	oligosaccharyltransferase complex subunit	8.88 ± 0.06	8.79 ± 0.05	8.81 ± 0.05	8.36 ± 0.14	0.01539	0.00936	0.02476
TC0200000316.mm.1	Otud1	OTU domain containing 1	7.84 ± 0.04	8.11 ± 0.08	8.2 ± 0.08	8 ± 0.05	0.06305	0.56899	0.0028
TC0300000491.mm.1	P2ry1	purinergic receptor P2Y, G-protein coupled 1	6.38 ± 0.09	6.06 ± 0.1	6.38 ± 0.08	6.1 ± 0.05	0.88922	0.00125	0.52699
TC0300002054.mm.1	P2ry12	purinergic receptor P2Y, G-protein coupled 12	5.93 ± 0.09	5.59 ± 0.05	6.04 ± 0.17	5.65 ± 0.1	0.43569	0.00464	0.7983
TC0700003829.mm.1	P2ry6	pyrimidinergic receptor P2Y, G-protein coupled, 6	7.93 ± 0.07	7.75 ± 0.04	7.95 ± 0.1	7.55 ± 0.08	0.37097	0.00319	0.09967
TC1000000531.mm.1	P4ha1	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-	9.32 ± 0.22	9.02 ± 0.13	8.82 ± 0.07	8.51 ± 0.02	0.00968	0.12942	0.67289
TC0700004225.mm.1	Palb2	partner and localizer of BRCA2	4.57 ± 0.03	4.64 ± 0	4.65 ± 0	4.71 ± 0.03	0.00817	0.01541	0.82791
TC0800002300.mm.1	Palld	palladin, cytoskeletal associated protein	6.99 ± 0.06	6.97 ± 0.01	7.31 ± 0.08	6.79 ± 0.06	0.19474	0.00061	0.00061
TC0300002815.mm.1	Palmd	palmdelphin	8.25 ± 0.16	7.79 ± 0.1	7.69 ± 0.17	8.18 ± 0.04	0.41491	0.89052	0.00267
TC0200001523.mm.1	Pamr1	peptidase domain containing associated with muscle regener	7.31 ± 0.09	7.65 ± 0.05	7.47 ± 0.05	7.37 ± 0.05	0.65702	0.04993	0.00325
TC1100000383.mm.1	Pank3	pantothenate kinase 3	10.09 ± 0.15	9.63 ± 0.16	9.35 ± 0.13	9.83 ± 0.1	0.05648	0.95231	0.00348
TC1900000467.mm.1	Papss2	3-phosphoadenosine 5-phosphosulfate synthase 2	9.16 ± 0.09	8.87 ± 0.04	9.1 ± 0.06	8.77 ± 0.11	0.54784	0.00515	0.57667
TC0900000750.mm.1	Parp6	poly (ADP-ribose) polymerase family, member 6	7.44 ± 0.11	7.21 ± 0.07	7.07 ± 0.09	7.41 ± 0.04	0.1857	0.75803	0.00304
TC1500000787.mm.1	Parvg	parvin, gamma	5.74 ± 0.05	6 ± 0.01	5.83 ± 0.03	6.05 ± 0.07	0.2226	0.00027	0.84405
TC1100000007.mm.1	Patz1	POZ (BTB) and AT hook containing zinc finger 1	5.89 ± 0.03	6 ± 0.02	5.93 ± 0.02	5.94 ± 0.01	0.83938	0.00977	0.01923
TC1000001270.mm.1	Pawr	PRKC, apoptosis, WT1, regulator	8.6 ± 0.18	8.95 ± 0.06	9.1 ± 0.09	8.65 ± 0.07	0.39068	0.7408	0.00532
TC0200002184.mm.1	Pax1	paired box gene 1	6.52 ± 0.06	6.7 ± 0.02	6.82 ± 0.05	6.62 ± 0.05	0.03021	0.96329	0.00133
TC0400002562.mm.1	Pax5	paired box gene 5	5.56 ± 0.06	5.93 ± 0.06	5.81 ± 0.1	6 ± 0.07	0.08295	0.00438	0.39252
TC0X00001054.mm.1	Pbdc1	polysaccharide biosynthesis domain containing 1	5.54 ± 0.04	5.58 ± 0.07	5.88 ± 0.04	5.6 ± 0.03	0.00198	0.01317	0.00625
TC1000000596.mm.1	Pbld1	phenazine biosynthesis-like protein domain containing 1	5.16 ± 0.03	5.24 ± 0.01	5.15 ± 0.05	5.33 ± 0.05	0.37668	0.00954	0.21597
TC0300000765.mm.1	Pbxip1	pre B cell leukemia transcription factor interacting protein 1	9.36 ± 0.16	9.71 ± 0.08	9.72 ± 0.11	9.33 ± 0.09	0.91628	1	0.00655

Supplemental Table I

Annotations			Summary Statistics				2 way ANOVA p-values		
Probe Set ID	Symbol	Description	XY sh	XY Or	XX sh	XX Or	XY vs XX	Sh vs Or	Intrxn
TC0X00001178.mm.1	Pcdh11x	protocadherin 11 X-linked	5.16 ± 0.02	5.11 ± 0.03	5.28 ± 0.06	5.05 ± 0.05	0.46108	0.00797	0.03764
TC1800000374.mm.1	Pcdhb17	protocadherin beta 17	6.41 ± 0.08	6.64 ± 0.05	6.74 ± 0.06	6.4 ± 0.12	0.55381	0.50882	0.00302
TC1800000378.mm.1	Pcdhb21	protocadherin beta 21	5.22 ± 0.06	5.24 ± 0.03	5.28 ± 0.04	4.96 ± 0.04	0.02625	0.00513	0.00555
TC0200002538.mm.1	Pcif1	PDX1 C-terminal inhibiting factor 1	7.58 ± 0.03	7.68 ± 0.02	7.79 ± 0.04	7.66 ± 0.01	0.00759	0.64572	0.00182
TC0200002683.mm.1	Pck1	phosphoenolpyruvate carboxykinase 1, cytosolic	10.86 ± 0.13	10.6 ± 0.2	9.86 ± 0.33	10.95 ± 0.05	0.08485	0.08466	0.0032
TC1000002400.mm.1	Pcnt	pericentrin (kendrin)	7.36 ± 0.05	7.48 ± 0.02	7.48 ± 0.03	7.38 ± 0.03	0.57741	0.586	0.00558
TC0500003738.mm.1	Pcolce	procollagen C-endopeptidase enhancer protein	8.29 ± 0.07	8.07 ± 0.04	8.24 ± 0.05	7.96 ± 0.03	0.37645	0.00116	0.24041
TC1600002175.mm.1	Pcp4	Purkinje cell protein 4	6.68 ± 0.09	6.72 ± 0.08	7.36 ± 0.16	6.76 ± 0.09	0.00574	0.01376	0.0129
TC1900001219.mm.1	Pcsk5	proprotein convertase subtilisin/kexin type 5	7.1 ± 0.07	7.31 ± 0.04	7.28 ± 0.03	7.06 ± 0.03	0.55417	0.91313	0.00097
TC0900000839.mm.1	Pdcd7	programmed cell death 7	6.48 ± 0.04	6.6 ± 0.02	6.7 ± 0.05	6.55 ± 0.03	0.04585	0.61686	0.00339
TC0700004536.mm.1	Pddc1	Parkinson disease 7 domain containing 1	6.84 ± 0.02	6.82 ± 0.03	6.96 ± 0.02	6.88 ± 0.01	0.00149	0.02498	0.30345
TC0700001669.mm.1	Pde3b	phosphodiesterase 3B, cGMP-inhibited	9.52 ± 0.13	9.09 ± 0.19	8.78 ± 0.19	9.36 ± 0.05	0.0824	0.82562	0.00288
TC0500003482.mm.1	Pdgfa	platelet derived growth factor, alpha	8.13 ± 0.07	8.25 ± 0.04	8.24 ± 0.04	8.09 ± 0.03	0.99889	0.88148	0.00862
TC0900000035.mm.1	Pdgfd	platelet-derived growth factor, D polypeptide	9.65 ± 0.18	10.06 ± 0.08	10.08 ± 0.07	9.62 ± 0.14	0.99456	0.86929	0.0067
TC0500000709.mm.1	Pdgfra	platelet derived growth factor receptor, alpha polypeptide	9.36 ± 0.07	9.21 ± 0.06	9.76 ± 0.08	9.09 ± 0.17	0.21264	0.0015	0.0279
TC0200001812.mm.1	Pdia3	protein disulfide isomerase associated 3	10.99 ± 0.08	10.79 ± 0.04	10.87 ± 0.05	10.56 ± 0.09	0.05453	0.00599	0.21291
TC0600002212.mm.1	Pdia4	protein disulfide isomerase associated 4	10.08 ± 0.11	9.76 ± 0.05	9.84 ± 0.07	9.37 ± 0.09	0.00773	0.00145	0.23192
TC1600001548.mm.1	Pdia5	protein disulfide isomerase associated 5	7.75 ± 0.07	7.86 ± 0.05	7.9 ± 0.04	7.62 ± 0.06	0.5274	0.2414	0.00632
TC1200000139.mm.1	Pdia6	protein disulfide isomerase associated 6	10.26 ± 0.08	9.99 ± 0.04	10.03 ± 0.06	9.69 ± 0.04	0.00158	0.00057	0.33204
TC1900001484.mm.1	Pdlim1	PDZ and LIM domain 1 (elfin)	8.71 ± 0.16	8.94 ± 0.07	8.99 ± 0.08	8.53 ± 0.11	0.69679	0.41878	0.00918
TC1400002333.mm.1	Pdlim2	PDZ and LIM domain 2	7.01 ± 0.05	7.08 ± 0.01	7.23 ± 0.03	7.1 ± 0.01	0.00162	0.67046	0.00489
TC1100002755.mm.1	Pdlim4	PDZ and LIM domain 4	7.36 ± 0.04	7.48 ± 0.04	7.58 ± 0.04	7.45 ± 0.05	0.03468	0.9164	0.00941
TC1000002453.mm.1	Pdxk	pyridoxal (pyridoxine, vitamin B6) kinase	7.88 ± 0.05	8.05 ± 0.05	7.87 ± 0.05	8.08 ± 0.05	0.86228	0.00664	0.40631
TC0X00002435.mm.1	Pdzd4	PDZ domain containing 4	6.18 ± 0.03	6.28 ± 0.03	6.27 ± 0.03	6.21 ± 0.01	0.50107	0.29984	0.00314
TC1500000907.mm.1	Pdzrn4	PDZ domain containing RING finger 4	5.43 ± 0.05	5.66 ± 0.03	5.76 ± 0.04	5.7 ± 0.07	0.00351	0.14865	0.01269
TC0400002139.mm.1	Penk	preproenkephalin	8.24 ± 0.11	7.39 ± 0.08	7.85 ± 0.03	7.48 ± 0.11	0.16689	2.2E-05	0.02878
TC0700000647.mm.1	Pepd	peptidase D	7.44 ± 0.05	7.26 ± 0.07	7.22 ± 0.04	7.34 ± 0.02	0.10541	0.34533	0.00529
TC1100000900.mm.1	Per1	period circadian clock 1	7.94 ± 0.12	8.38 ± 0.11	7.33 ± 0.09	8.14 ± 0.14	0.00603	6.5E-05	0.23696
TC0100002801.mm.1	Per2	period circadian clock 2	7.81 ± 0.13	8.39 ± 0.15	6.96 ± 0.06	7.92 ± 0.07	0.00017	6.8E-06	0.25702
TC0400004074.mm.1	Per3	period circadian clock 3	6.71 ± 0.09	6.95 ± 0.09	5.84 ± 0.05	6.86 ± 0.02	2.7E-05	6.8E-07	0.00022
TC0500000843.mm.1	Pf4	platelet factor 4	7.78 ± 0.04	7.47 ± 0.06	7.99 ± 0.1	7.6 ± 0.1	0.04862	0.0005	0.64598
TC0X00001502.mm.1	Pfkfb1	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 1	6.3 ± 0.1	5.92 ± 0.12	5.82 ± 0.12	6.24 ± 0.03	0.29051	0.91558	0.001

Supplemental Table I

Annotations			Summary Statistics				2 way ANOVA p-values		
Probe Set ID	Symbol	Description	XY sh	XY Or	XX sh	XX Or	XY vs XX	Sh vs Or	Intrxn
TC0200002961.mm.1	Pfkfb3	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3	8.26 ± 0.15	8.26 ± 0.08	7.71 ± 0.14	8.42 ± 0.09	0.06034	0.04134	0.00544
TC1300001395.mm.1	Pfkp	phosphofructokinase, platelet	7.89 ± 0.07	7.65 ± 0.05	7.63 ± 0.04	7.72 ± 0.05	0.0888	0.1403	0.00738
TC1200000032.mm.1	Pfn4	profilin family, member 4	4.32 ± 0.03	4.34 ± 0.06	4.52 ± 0.04	4.5 ± 0.05	0.00143	0.98717	0.70652
TC1700001846.mm.1	Pglyrp2	peptidoglycan recognition protein 2	4.56 ± 0.04	4.76 ± 0.06	4.68 ± 0.02	4.86 ± 0.06	0.05791	0.00249	0.89251
TC0900002779.mm.1	Pgm3	phosphoglucomutase 3	6.75 ± 0.08	6.52 ± 0.09	6.75 ± 0.05	6.36 ± 0.08	0.45813	0.00238	0.24223
TC1900001286.mm.1	Pgm5	phosphoglucomutase 5	10.24 ± 0.16	10.52 ± 0.07	10.67 ± 0.11	10.15 ± 0.1	0.72981	0.41285	0.00564
TC1700000426.mm.1	Phf1	PHD finger protein 1	7.93 ± 0.02	8.03 ± 0.02	8.11 ± 0.02	8.13 ± 0.03	4.1E-05	0.02076	0.12694
TC0200003354.mm.1	Phf19	PHD finger protein 19	5.81 ± 0.03	5.99 ± 0.04	5.86 ± 0.01	5.87 ± 0.04	0.41193	0.00712	0.01188
TC1100000935.mm.1	Phf23	PHD finger protein 23	7.36 ± 0.01	7.48 ± 0.03	7.41 ± 0.03	7.45 ± 0.04	0.74338	0.00901	0.11283
TC1000001301.mm.1	Phlda1	pleckstrin homology-like domain, family A, member 1	7.37 ± 0.07	7.04 ± 0.09	7.47 ± 0.11	6.99 ± 0.08	0.65605	0.0005	0.32879
TC0100000112.mm.1	Pi15	peptidase inhibitor 15	10.13 ± 0.13	10.38 ± 0.05	10.48 ± 0.12	9.73 ± 0.2	0.32345	0.10298	0.00246
TC1700000502.mm.1	Pi16	peptidase inhibitor 16	8.35 ± 0.09	8.25 ± 0.06	8.61 ± 0.07	8.19 ± 0.04	0.15648	0.00359	0.03699
TC0300000956.mm.1	Pias3	protein inhibitor of activated STAT 3	7.15 ± 0.03	7.22 ± 0.02	7.26 ± 0.02	7.19 ± 0.01	0.08516	0.85793	0.00695
TC0100002690.mm.1	Pid1	phosphotyrosine interaction domain containing 1	6.41 ± 0.02	6.34 ± 0.02	6.49 ± 0.02	6.28 ± 0.04	0.653	0.00011	0.02515
TC1600002118.mm.1	Pigp	phosphatidylinositol glycan anchor biosynthesis, class P	7.15 ± 0.01	7.25 ± 0.01	7.24 ± 0.01	7.26 ± 0.02	0.00339	0.00159	0.01379
TC0400003711.mm.1	Pigv	phosphatidylinositol glycan anchor biosynthesis, class V	6.72 ± 0.02	6.88 ± 0.03	6.89 ± 0.04	6.8 ± 0.01	0.17328	0.45156	0.00064
TC1300002553.mm.1	Pik3r1	phosphatidylinositol 3-kinase, regulatory subunit, polypeptide	10.06 ± 0.05	9.81 ± 0.09	10.15 ± 0.06	9.66 ± 0.15	0.90452	0.00194	0.16602
TC0400001250.mm.1	Pik3r3	phosphatidylinositol 3 kinase, regulatory subunit, polypeptide	6.98 ± 0.04	6.81 ± 0.07	6.94 ± 0.08	6.6 ± 0.14	0.14666	0.00981	0.31662
TC0700004634.mm.1	Pira2	paired-Ig-like receptor A2	6.35 ± 0.05	6.23 ± 0.08	6.26 ± 0.03	6.03 ± 0.05	0.01516	0.00447	0.39421
TC0700000030.mm.1	Pira6	paired-Ig-like receptor A6	6.56 ± 0.03	6.39 ± 0.1	6.47 ± 0.04	6.24 ± 0.06	0.08071	0.00642	0.53527
TC1100000845.mm.1	Pirt	phosphoinositide-interacting regulator of transient receptor pc	7.16 ± 0.77	5.77 ± 0.44	4.87 ± 0.09	7.15 ± 0.31	0.55963	0.29026	0.00664
TC1100003948.mm.1	Pitpnc1	phosphatidylinositol transfer protein, cytoplasmic 1	6.83 ± 0.11	6.55 ± 0.05	6.43 ± 0.11	6.71 ± 0.03	0.14889	0.90019	0.00552
TC1100003137.mm.1	Pitpnm3	PITPNM family member 3	6.57 ± 0.03	6.74 ± 0.03	6.79 ± 0.05	6.69 ± 0.01	0.02705	0.32435	0.00144
TC1400002337.mm.1	Piwil2	piwi-like RNA-mediated gene silencing 2	5.07 ± 0.02	5.21 ± 0.04	5.13 ± 0.02	5.19 ± 0.04	0.37909	0.00314	0.11393
TC1700001236.mm.1	Pkdcc	protein kinase domain containing, cytoplasmic	8.37 ± 0.11	8.53 ± 0.04	8.95 ± 0.11	8.31 ± 0.08	0.06495	0.02613	0.00069
TC1600001604.mm.1	Pla1a	phospholipase A1 member A	6.5 ± 0.07	6.24 ± 0.05	6.41 ± 0.07	6.27 ± 0.08	0.5331	0.00703	0.27008
TC0400001733.mm.1	Pla2g2d	phospholipase A2, group IID	6.9 ± 0.09	6.95 ± 0.05	7.29 ± 0.06	7.31 ± 0.11	0.00105	0.84769	0.9119
TC1700000835.mm.1	Pla2g7	phospholipase A2, group VII (platelet-activating factor acetylh	7.82 ± 0.13	7.54 ± 0.16	7.4 ± 0.15	7.94 ± 0.13	0.60095	0.65282	0.00537
TC1400001604.mm.1	Plac9a	placenta specific 9a	9.74 ± 0.07	9.75 ± 0.04	9.98 ± 0.06	9.66 ± 0.06	0.11121	0.05442	0.00668
TC1400001612.mm.1	Plac9b	placenta specific 9b	9.24 ± 0.08	9.22 ± 0.04	9.49 ± 0.05	9.11 ± 0.08	0.1422	0.02273	0.00818
TC1400000176.mm.1	Plau	plasminogen activator, urokinase	7.23 ± 0.08	6.81 ± 0.1	7.04 ± 0.05	6.69 ± 0.06	0.07178	0.00023	0.66668
TC0200004418.mm.1	Plcb2	phospholipase C, beta 2	5.39 ± 0.05	5.57 ± 0.02	5.48 ± 0.03	5.59 ± 0.05	0.25321	0.00483	0.51237

Supplemental Table I

Annotations			Summary Statistics				2 way ANOVA p-values		
Probe Set ID	Symbol	Description	XY sh	XY Or	XX sh	XX Or	XY vs XX	Sh vs Or	Intrxn
TC0800001903.mm.1	Plekha2	pleckstrin homology domain-containing, family A (phosphoinc	7.77 ± 0.05	7.85 ± 0.02	8.02 ± 0.05	7.71 ± 0.1	0.30262	0.12848	0.00554
TC0700003823.mm.1	Plekhb1	pleckstrin homology domain containing, family B (evectins) m	8.19 ± 0.19	7.73 ± 0.11	7.77 ± 0.07	8.37 ± 0.15	0.30401	0.42348	0.00731
TC1200000682.mm.1	Plekhg3	pleckstrin homology domain containing, family G (with RhoGe	8.22 ± 0.16	8.5 ± 0.08	8.66 ± 0.09	8.14 ± 0.09	0.68858	0.35163	0.00473
TC0400003888.mm.1	Plekhm2	pleckstrin homology domain containing, family M (with RUN d	7.71 ± 0.05	7.76 ± 0	7.87 ± 0.03	7.66 ± 0.05	0.44002	0.10493	0.0053
TC0400004173.mm.1	Plekhn1	pleckstrin homology domain containing, family N member 1	5.26 ± 0.04	5.5 ± 0.03	5.37 ± 0.03	5.41 ± 0.05	0.72527	0.00314	0.01915
TC0400004004.mm.1	Plod1	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 1	8.56 ± 0.05	8.35 ± 0.05	8.34 ± 0.02	8.21 ± 0.04	0.00244	0.00555	0.63825
TC0X00001338.mm.1	Plp1	proteolipid protein (myelin) 1	8.51 ± 0.37	7.52 ± 0.15	7.37 ± 0.11	8.21 ± 0.19	0.65334	0.90188	0.008
TC1500001934.mm.1	Pmm1	phosphomannomutase 1	7.48 ± 0.09	7.44 ± 0.06	7.3 ± 0.05	7.64 ± 0.05	0.87065	0.09835	0.00729
TC0X00002431.mm.1	Pnck	pregnancy upregulated non-ubiquitously expressed CaM kina	7.57 ± 0.06	7.81 ± 0.05	7.84 ± 0.05	7.7 ± 0.02	0.07922	0.22648	0.00122
TC1400000574.mm.1	Pnp	purine-nucleoside phosphorylase	8.23 ± 0.06	7.98 ± 0.07	7.81 ± 0.03	8.03 ± 0.03	0.00267	0.64974	0.00037
TC1400000575.mm.1	Pnp2	purine-nucleoside phosphorylase 2	8.49 ± 0.05	8.28 ± 0.06	8.1 ± 0.06	8.32 ± 0.03	0.00483	0.99929	0.00117
TC0700002053.mm.1	Pnpla2	patatin-like phospholipase domain containing 2	10.96 ± 0.14	10.59 ± 0.17	10.28 ± 0.24	11.07 ± 0.06	0.35087	0.38702	0.00205
TC0800000011.mm.1	Pnpla6	patatin-like phospholipase domain containing 6	7.14 ± 0.05	6.98 ± 0.02	6.95 ± 0.04	7.07 ± 0.02	0.26183	0.61356	0.00382
TC0400002373.mm.1	Pnrc1	proline-rich nuclear receptor coactivator 1	8.17 ± 0.05	8.38 ± 0.05	8.49 ± 0.03	8.34 ± 0.02	0.00347	0.41314	0.00039
TC1000001203.mm.1	Poc1b	POC1 centriolar protein homolog B (Chlamydomonas)	7.29 ± 0.04	7.38 ± 0.01	7.52 ± 0.04	7.3 ± 0.07	0.10703	0.15262	0.00439
TC0400004216.mm.1	Podn	podocan	9.2 ± 0.06	8.95 ± 0.07	9.33 ± 0.06	8.82 ± 0.1	0.85862	0.00032	0.06152
TC1100002155.mm.1	Pold2	polymerase (DNA directed), delta 2, regulatory subunit	7.49 ± 0.02	7.61 ± 0.01	7.68 ± 0.03	7.66 ± 0.03	0.00069	0.11333	0.0399
TC1900000036.mm.1	Pold4	polymerase (DNA-directed), delta 4	7.73 ± 0.05	7.91 ± 0.03	8.15 ± 0.07	7.97 ± 0.02	0.0003	0.78661	0.0033
TC0600000839.mm.1	Polr1a	polymerase (RNA) I polypeptide A	7.02 ± 0.03	6.9 ± 0.04	7.01 ± 0.03	6.84 ± 0.05	0.25843	0.00192	0.66242
TC1000002488.mm.1	Polr2e	polymerase (RNA) II (DNA directed) polypeptide E	7.41 ± 0.03	7.42 ± 0.02	7.49 ± 0.03	7.58 ± 0.03	0.00328	0.20315	0.11538
TC1500000667.mm.1	Polr2f	polymerase (RNA) II (DNA directed) polypeptide F	8.98 ± 0.03	9.02 ± 0.01	9.15 ± 0.06	9.09 ± 0.03	0.00547	0.71198	0.22767
TC0700004542.mm.1	Polr2l	polymerase (RNA) II (DNA directed) polypeptide L	6.8 ± 0.03	6.8 ± 0.05	6.62 ± 0.05	6.75 ± 0.03	0.00784	0.18358	0.07336
TC0600001805.mm.1	Pon1	paraoxonase 1	8.69 ± 0.16	7.16 ± 0.23	7.85 ± 0.16	7.41 ± 0.1	0.08124	4.8E-05	0.00498
TC0700002880.mm.1	Pop4	processing of precursor 4, ribonuclease P/MRP family, (S. ce	8.18 ± 0.06	8.02 ± 0.04	7.94 ± 0.04	7.86 ± 0.1	0.00591	0.05664	0.48991
TC0500001584.mm.1	Por	P450 (cytochrome) oxidoreductase	9.09 ± 0.04	8.94 ± 0.09	8.48 ± 0.07	8.94 ± 0.03	0.00022	0.02647	0.00021
TC0900000615.mm.1	Pou2af1	POU domain, class 2, associating factor 1	5.62 ± 0.05	5.97 ± 0.1	5.89 ± 0.1	6.19 ± 0.1	0.01728	0.00279	0.87828
TC1000000571.mm.1	Ppa1	pyrophosphatase (inorganic) 1	9.05 ± 0.19	8.36 ± 0.16	8.16 ± 0.13	8.6 ± 0.05	0.04446	0.37371	0.00229
TC1300001270.mm.1	Ppap2a	phosphatidic acid phosphatase type 2A	9.71 ± 0.1	9.48 ± 0.09	9.64 ± 0.06	9.13 ± 0.14	0.09858	0.0048	0.1116
TC0400001091.mm.1	Ppap2b	phosphatidic acid phosphatase type 2B	10.51 ± 0.07	10.14 ± 0.05	10.56 ± 0.05	9.98 ± 0.14	0.57717	8.1E-05	0.15833
TC1800001338.mm.1	Ppic	peptidylprolyl isomerase C	9.29 ± 0.09	9.21 ± 0.08	9.04 ± 0.04	8.74 ± 0.12	0.0023	0.07059	0.18438
TC1700001781.mm.1	Ppil1	peptidylprolyl isomerase (cyclophilin)-like 1	7.09 ± 0.03	7.21 ± 0.01	7.2 ± 0.01	7.17 ± 0.01	0.24179	0.10196	0.00562
TC1600001154.mm.1	Ppl	periplakin	7.71 ± 0.05	7.58 ± 0.03	7.53 ± 0.06	7.39 ± 0.05	0.00822	0.04757	0.57435

Supplemental Table I

Annotations			Summary Statistics				2 way ANOVA p-values		
Probe Set ID	Symbol	Description	XY sh	XY Or	XX sh	XX Or	XY vs XX	Sh vs Or	Intrxn
TC0900003003.mm.1	Ppm1m	protein phosphatase 1M	8.33 ± 0.07	8.21 ± 0.06	8.22 ± 0.04	8.39 ± 0.02	0.94093	0.84459	0.00813
TC0700003818.mm.1	Ppme1	protein phosphatase methylesterase 1	8.65 ± 0.08	8.53 ± 0.05	8.3 ± 0.04	8.22 ± 0.09	0.00084	0.30422	0.86568
TC1700001075.mm.1	Ppp4r1	protein phosphatase 4, regulatory subunit 1	7.96 ± 0.05	7.97 ± 0.03	7.9 ± 0.02	7.83 ± 0.03	0.00874	0.25808	0.48212
TC0X00003239.mm.1	Prdx4	peroxiredoxin 4	8.33 ± 0.07	8.5 ± 0.05	8.49 ± 0.05	8.24 ± 0.1	0.6167	0.76626	0.00835
TC0100000055.mm.1	Prex2	phosphatidylinositol-3,4,5-trisphosphate-dependent Rac exch	8.39 ± 0.08	8.28 ± 0.08	8.09 ± 0.1	8.42 ± 0.06	0.22304	0.32476	0.0093
TC1200001602.mm.1	Prkar2b	protein kinase, cAMP dependent regulatory, type II beta	10.45 ± 0.18	10.17 ± 0.26	9.54 ± 0.36	10.76 ± 0.1	0.33548	0.12489	0.00446
TC1400001659.mm.1	Prkcd	protein kinase C, delta	8.01 ± 0.09	7.98 ± 0.03	8.26 ± 0.08	7.73 ± 0.1	0.93854	0.00532	0.00732
TC0700003978.mm.1	Prkcdbp	protein kinase C, delta binding protein	9.33 ± 0.11	9.38 ± 0.01	9.53 ± 0.06	9.03 ± 0.06	0.53149	0.02275	0.0019
TC0200000211.mm.1	Prkcq	protein kinase C, theta	5.84 ± 0.06	5.98 ± 0.05	5.74 ± 0.05	5.97 ± 0.08	0.39103	0.00971	0.43274
TC0900000210.mm.1	Prkcsh	protein kinase C substrate 80K-H	8.38 ± 0.03	8.32 ± 0.03	8.28 ± 0.02	8.19 ± 0.01	0.00036	0.01827	0.44656
TC0500002814.mm.1	Prkg2	protein kinase, cGMP-dependent, type II	5.91 ± 0.07	5.59 ± 0.05	6.17 ± 0.1	5.61 ± 0.08	0.04809	6.1E-05	0.07538
TC0100000883.mm.1	Prlh	prolactin releasing hormone	7.16 ± 0.03	7.56 ± 0.08	7.3 ± 0.11	7.52 ± 0.18	0.56513	0.00861	0.36021
TC1600001201.mm.1	Prm2	protamine 2	6.11 ± 0.03	6.37 ± 0.06	6.15 ± 0.03	6.28 ± 0.11	0.73756	0.0074	0.27867
TC0700002980.mm.1	Prmt1	protein arginine N-methyltransferase 1	8.19 ± 0.02	8.25 ± 0.01	8.26 ± 0.02	8.18 ± 0.03	0.84614	0.90418	0.00674
TC0200002026.mm.1	Prnp	prion protein	6.78 ± 0.05	6.72 ± 0.03	6.58 ± 0.02	6.66 ± 0.04	0.00273	0.86302	0.04261
TC1800001177.mm.1	Prob1	proline rich basic protein 1	5.63 ± 0.04	5.82 ± 0.07	5.9 ± 0.03	5.73 ± 0.04	0.06624	0.81979	0.00133
TC0X00001382.mm.1	Prps1	phosphoribosyl pyrophosphate synthetase 1	9.08 ± 0.09	8.57 ± 0.08	8.51 ± 0.02	8.5 ± 0.1	0.00226	0.0089	0.01183
TC1500001101.mm.1	Prr13	proline rich 13	6.8 ± 0.07	6.43 ± 0.07	6.71 ± 0.04	6.49 ± 0.04	0.9968	0.00066	0.37822
TC1700000090.mm.1	Prr18	proline rich region 18	5.21 ± 0.03	5.42 ± 0.02	5.36 ± 0.05	5.48 ± 0.07	0.04238	0.00366	0.46149
TC0200004204.mm.1	Prr5l	proline rich 5 like	6.14 ± 0.02	6.21 ± 0	6.3 ± 0.02	6.21 ± 0.02	0.00085	0.47861	0.00094
TC1300001573.mm.1	Prss16	protease, serine, 16 (thymus)	4.61 ± 0.03	4.8 ± 0.02	4.69 ± 0.03	4.86 ± 0.07	0.1633	0.00141	0.93039
TC0900000980.mm.1	Prtg	protogenin homolog (Gallus gallus)	4.72 ± 0.01	4.78 ± 0	4.78 ± 0	4.83 ± 0.03	0.00582	0.00513	0.75532
TC0700000461.mm.1	Prx	periaxin	6.57 ± 0.02	6.69 ± 0.04	6.64 ± 0.02	6.76 ± 0.06	0.07051	0.0036	0.81812
TC0200000383.mm.1	Psd4	pleckstrin and Sec7 domain containing 4	5.57 ± 0.04	5.75 ± 0.02	5.65 ± 0.05	5.75 ± 0.04	0.49257	0.00465	0.38975
TC1100001777.mm.1	Psmc5	protease (prosome, macropain) 26S subunit, ATPase 5	8.41 ± 0.04	8.34 ± 0.07	8.2 ± 0.03	8.22 ± 0.04	0.00397	0.58086	0.36379
TC1600000286.mm.1	Psmd2	proteasome (prosome, macropain) 26S subunit, non-ATPase	9.41 ± 0.03	9.27 ± 0.06	9.21 ± 0.03	9.22 ± 0.03	0.00567	0.10982	0.06193
TC0400001593.mm.1	Ptafr	platelet-activating factor receptor	7.35 ± 0.11	7.08 ± 0.04	7.35 ± 0.03	6.99 ± 0.07	0.71742	0.00168	0.46908
TC1700002190.mm.1	Ptcra	pre T cell antigen receptor alpha	6.09 ± 0.02	6.28 ± 0.04	6.18 ± 0.04	6.23 ± 0.05	0.71468	0.00835	0.12512
TC1900000471.mm.1	Pten	phosphatase and tensin homolog	9.92 ± 0.04	9.75 ± 0.02	9.69 ± 0.02	9.64 ± 0.06	0.00188	0.02583	0.21579
TC0200000228.mm.1	Pter	phosphotriesterase related	7.01 ± 0.02	6.92 ± 0.04	7.09 ± 0.04	6.94 ± 0.03	0.20484	0.00127	0.48427
TC1400000477.mm.1	Ptger2	prostaglandin E receptor 2 (subtype EP2)	4.08 ± 0.04	4.24 ± 0.04	4.13 ± 0	4.08 ± 0.04	0.21707	0.08213	0.00394
TC0300002595.mm.1	Ptgfrn	prostaglandin F2 receptor negative regulator	8.83 ± 0.06	8.79 ± 0.02	8.96 ± 0.08	8.54 ± 0.08	0.45755	0.00503	0.00602

Supplemental Table I

Annotations			Summary Statistics				2 way ANOVA p-values		
Probe Set ID	Symbol	Description	XY sh	XY Or	XX sh	XX Or	XY vs XX	Sh vs Or	Intrxn
TC0400002744.mm.1	Ptgr1	prostaglandin reductase 1	6.53 ± 0.03	6.45 ± 0.03	6.48 ± 0.03	6.3 ± 0.05	0.01685	0.00245	0.0731
TC0900003116.mm.1	Pth1r	parathyroid hormone 1 receptor	7.28 ± 0.04	7.28 ± 0.04	7.45 ± 0.02	7.39 ± 0.06	0.00913	0.45759	0.56782
TC0200002990.mm.1	Ptpla	protein tyrosine phosphatase-like (proline instead of catalytic	8.02 ± 0.07	8.19 ± 0.04	8.04 ± 0.01	7.88 ± 0.06	0.02733	0.8983	0.00839
TC1600000489.mm.1	Ptplb	protein tyrosine phosphatase-like (proline instead of catalytic	9.8 ± 0.15	9.31 ± 0.17	9.34 ± 0.17	9.86 ± 0.09	0.9446	0.77427	0.0029
TC0300001064.mm.1	Ptpn22	protein tyrosine phosphatase, non-receptor type 22 (lymphoic	4.88 ± 0.03	5 ± 0.02	4.79 ± 0.04	4.74 ± 0.12	0.00844	0.67344	0.28253
TC0100001244.mm.1	Ptpn7	protein tyrosine phosphatase, non-receptor type 7	5.87 ± 0.05	6.1 ± 0.05	5.98 ± 0.03	6.13 ± 0.07	0.19114	0.00252	0.4313
TC0600000193.mm.1	Ptprz1	protein tyrosine phosphatase, receptor type Z, polypeptide 1	8.94 ± 0.2	9.39 ± 0.08	9.32 ± 0.08	8.86 ± 0.16	0.74513	0.88293	0.00813
TC1300001789.mm.1	Pxdc1	PX domain containing 1	7.86 ± 0.11	8.19 ± 0.05	8.15 ± 0.08	7.87 ± 0.09	0.92988	0.7667	0.00483
TC1200000253.mm.1	Pxdn	peroxidasin homolog (Drosophila)	8.59 ± 0.03	8.27 ± 0.05	8.29 ± 0.04	8.2 ± 0.04	0.0002	7.3E-05	0.00439
TC1900000117.mm.1	Pygm	muscle glycogen phosphorylase	8.64 ± 0.14	8.95 ± 0.05	9.12 ± 0.11	8.67 ± 0.12	0.38485	0.53915	0.00538
TC1400002325.mm.1	R3hcc1	R3H domain and coiled-coil containing 1	6.98 ± 0.02	7.04 ± 0.01	7.14 ± 0.05	7.08 ± 0.03	0.00235	0.8835	0.05406
TC0100001129.mm.1	R3hdm1	R3H domain containing 1	8.17 ± 0.03	8.01 ± 0.01	8.01 ± 0.03	7.98 ± 0.04	0.00477	0.00661	0.04472
TC1700001686.mm.1	Rab11fip3	RAB11 family interacting protein 3 (class II)	7.72 ± 0.04	7.82 ± 0.03	7.82 ± 0.04	7.67 ± 0.04	0.84016	0.67574	0.00267
TC0600002610.mm.1	Rab11fip5	RAB11 family interacting protein 5 (class I)	7.85 ± 0.03	7.76 ± 0.03	7.92 ± 0.02	7.81 ± 0.01	0.00914	0.0014	0.41953
TC0300000360.mm.1	Rab33b	RAB33B, member of RAS oncogene family	7.85 ± 0.05	7.94 ± 0.06	7.95 ± 0.04	7.73 ± 0.04	0.26921	0.21573	0.00745
TC0100001779.mm.1	Rab3gap2	RAB3 GTPase activating protein subunit 2	8.23 ± 0.05	8.05 ± 0.03	7.86 ± 0.05	7.87 ± 0.08	0.00049	0.25428	0.17052
TC1900000184.mm.1	Rab3il1	RAB3A interacting protein (rabin3)-like 1	6.76 ± 0.01	6.77 ± 0.01	6.86 ± 0.02	6.77 ± 0.02	0.00776	0.06428	0.00471
TC1500002059.mm.1	Rabl2	RAB, member of RAS oncogene family-like 2	6.66 ± 0.03	6.57 ± 0.01	6.59 ± 0.03	6.49 ± 0.02	0.02798	0.00854	0.4537
TC0100000886.mm.1	Ramp1	receptor (calcitonin) activity modifying protein 1	6.86 ± 0.11	7.03 ± 0.07	7.11 ± 0.08	6.72 ± 0.12	0.86246	0.36822	0.00947
TC1500002289.mm.1	Rarg	retinoic acid receptor, gamma	7.4 ± 0.03	7.49 ± 0.02	7.52 ± 0.02	7.45 ± 0	0.06801	0.41885	0.00433
TC1700001844.mm.1	Rasal3	RAS protein activator like 3	5.46 ± 0.04	5.72 ± 0.04	5.55 ± 0.06	5.75 ± 0.07	0.38596	0.00062	0.69137
TC0800000847.mm.1	Rasd2	RASD family, member 2	5.52 ± 0.03	5.75 ± 0.03	5.51 ± 0.06	5.81 ± 0.05	0.38315	2.9E-05	0.63594
TC0200004396.mm.1	Rasgrp1	RAS guanyl releasing protein 1	5.65 ± 0.06	6.06 ± 0.11	5.76 ± 0.11	6.06 ± 0.16	0.6724	0.00747	0.70176
TC0500001796.mm.1	Rasl11a	RAS-like, family 11, member A	6.79 ± 0.06	6.96 ± 0.02	7.38 ± 0.05	6.8 ± 0.05	0.00177	0.00151	1E-05
TC0500000699.mm.1	Rasl11b	RAS-like, family 11, member B	7.52 ± 0.12	7.79 ± 0.07	8.15 ± 0.13	7.38 ± 0.09	0.38767	0.02854	0.00044
TC1000003047.mm.1	Rassf3	Ras association (RalGDS/AF-6) domain family member 3	9.5 ± 0.12	9.67 ± 0.07	9.98 ± 0.09	9.47 ± 0.09	0.17307	0.11577	0.00373
TC0600002978.mm.1	Rassf4	Ras association (RalGDS/AF-6) domain family member 4	7.36 ± 0.04	7.17 ± 0.07	7.09 ± 0.05	6.98 ± 0.07	0.00279	0.036	0.67484
TC0600001722.mm.1	Rassf8	Ras association (RalGDS/AF-6) domain family (N-terminal) m	7.97 ± 0.07	8.13 ± 0.05	8.13 ± 0.04	7.91 ± 0.06	0.70906	0.77975	0.00367
TC0400001024.mm.1	Raver2	ribonucleoprotein, PTB-binding 2	6.22 ± 0.03	6.12 ± 0.03	6.43 ± 0.11	6.11 ± 0.03	0.10795	0.00301	0.06795
TC0200004894.mm.1	Rbck1	RanBP-type and C3HC4-type zinc finger containing 1	7.23 ± 0.02	7.29 ± 0	7.34 ± 0.02	7.31 ± 0.02	0.0068	0.55972	0.02974
TSUnmapped000000	Rbm14-rbm4	Rbm14-Rbm4 readthrough (Rbm14-rbm4), transcript variant	7.43 ± 0.02	7.55 ± 0.04	7.31 ± 0.04	7.3 ± 0.06	0.00039	0.21866	0.13599
TC0300000953.mm.1	Rbm8a	RNA binding motif protein 8a	8.77 ± 0.04	8.94 ± 0.06	8.8 ± 0.04	8.71 ± 0.05	0.10057	0.31391	0.00955

Supplemental Table I

Annotations			Summary Statistics				2 way ANOVA p-values		
Probe Set ID	Symbol	Description	XY sh	XY Or	XX sh	XX Or	XY vs XX	Sh vs Or	Intrxn
TC0200003607.mm.1	Rbms1	RNA binding motif, single stranded interacting protein 1	7.85 ± 0.01	7.75 ± 0.04	7.87 ± 0.02	7.76 ± 0.05	0.68454	0.00627	0.9609
TC0900001232.mm.1	Rbp1	retinol binding protein 1, cellular	11.04 ± 0.12	11.33 ± 0.05	11.39 ± 0.08	11.06 ± 0.08	0.44827	0.92097	0.00271
TC1700000839.mm.1	Rcan2	regulator of calcineurin 2	8.95 ± 0.16	9.22 ± 0.07	9.32 ± 0.08	8.93 ± 0.08	0.59677	0.73166	0.00799
TC0900000678.mm.1	Rcn2	reticulocalbin 2	7.77 ± 0.07	7.94 ± 0.03	7.97 ± 0.05	7.63 ± 0.1	0.61905	0.43062	0.00211
TC1100001664.mm.1	Rdm1	RAD52 motif 1	6.94 ± 0.04	7.11 ± 0.03	7.27 ± 0.02	7.19 ± 0.02	1.5E-05	0.20837	0.00155
TC0700002491.mm.1	Relb	avian reticuloendotheliosis viral (v-rel) oncogene related B	6.8 ± 0.03	6.89 ± 0.01	6.97 ± 0.03	6.91 ± 0.03	0.00525	0.70424	0.0252
TC0X00003301.mm.1	Reps2	RALBP1 associated Eps domain containing protein 2	7.34 ± 0.15	6.68 ± 0.06	7.17 ± 0.03	6.94 ± 0.08	0.4415	0.00165	0.10242
TC0600000854.mm.1	Retsat	retinol saturase (all trans retinol 13,14 reductase)	7.94 ± 0.21	7.77 ± 0.17	7.58 ± 0.2	8.36 ± 0.09	0.95254	0.27405	0.00743
TC0200003206.mm.1	Rexo4	REX4, RNA exonuclease 4 homolog (S. cerevisiae)	6.87 ± 0.02	6.99 ± 0.03	6.91 ± 0.02	6.87 ± 0.02	0.15876	0.06665	0.00316
TC0100002356.mm.1	Rftn2	raftlin family member 2	7.7 ± 0.14	7.86 ± 0.04	8.28 ± 0.08	7.76 ± 0.09	0.03987	0.10758	0.00628
TC0100003264.mm.1	Rgl1	ral guanine nucleotide dissociation stimulator,-like 1	8.05 ± 0.04	7.89 ± 0.04	8 ± 0.04	7.92 ± 0.05	0.72029	0.00847	0.3262
TC0100003604.mm.1	Rgs7	regulator of G protein signaling 7	7.77 ± 0.13	7.65 ± 0.05	7.26 ± 0.12	7.8 ± 0.08	0.07964	0.09917	0.00569
TC1100002471.mm.1	Rhbdf1	rhomboid family 1 (Drosophila)	7.48 ± 0.03	7.59 ± 0.02	7.56 ± 0.02	7.5 ± 0.02	0.8722	0.20095	0.00181
TC1100004122.mm.1	Rhbdf2	rhomboid 5 homolog 2 (Drosophila)	6.95 ± 0.03	7.08 ± 0.01	7.03 ± 0	7.01 ± 0.02	0.9362	0.05636	0.00704
TC1000000656.mm.1	Rhobtb1	Rho-related BTB domain containing 1	7.59 ± 0.12	8.17 ± 0.11	7.67 ± 0.05	7.77 ± 0.04	0.19228	0.00218	0.0185
TC0500003225.mm.1	Rhof	ras homolog gene family, member f	5.41 ± 0.05	5.54 ± 0.04	5.44 ± 0.04	5.57 ± 0.05	0.42817	0.00586	0.85019
TC0500000627.mm.1	Rhoh	ras homolog gene family, member H	4.8 ± 0.02	5.04 ± 0.07	4.81 ± 0.04	5.05 ± 0.06	0.86074	0.00045	0.9238
TC0X00003424.mm.1	Rhox3h	reproductive homeobox 3H	4.49 ± 0.03	4.67 ± 0.03	4.64 ± 0.03	4.58 ± 0.03	0.29658	0.03715	0.00067
TC1200001142.mm.1	Rian	RNA imprinted and accumulated in nucleus	5.78 ± 0.1	5.39 ± 0.01	5.32 ± 0.06	5.32 ± 0.04	0.00662	0.05148	0.04373
TC0200002166.mm.1	Rin2	Ras and Rab interactor 2	7.46 ± 0.1	7.54 ± 0.04	7.88 ± 0.05	7.42 ± 0.09	0.08676	0.04147	0.00567
TC0800001226.mm.1	Rltpr	RGD motif, leucine rich repeats, tropomodulin domain and pr	5.84 ± 0.04	5.96 ± 0.04	5.87 ± 0.05	6.09 ± 0.08	0.14907	0.0053	0.33072
TC1100002695.mm.1	Rmnd5b	required for meiotic nuclear division 5 homolog B (S. cerevisi	7.15 ± 0.02	7.21 ± 0	7.26 ± 0.02	7.2 ± 0.02	0.03966	0.66448	0.0097
TC0200003512.mm.1	Rnd3	Rho family GTPase 3	9.56 ± 0.12	9.61 ± 0.11	10.27 ± 0.16	9.44 ± 0.16	0.0816	0.01072	0.00757
TC1700001639.mm.1	Rnf151	ring finger protein 151	4.27 ± 0.03	4.51 ± 0.02	4.46 ± 0.07	4.58 ± 0.09	0.04423	0.00953	0.37057
TC0100002887.mm.1	Rnf152	ring finger protein 152	6.43 ± 0.13	6.41 ± 0.08	6.27 ± 0.09	6.78 ± 0.07	0.58209	0.07604	0.00982
TC0400002788.mm.1	Rnf183	ring finger protein 183	5.26 ± 0.03	5.41 ± 0.03	5.32 ± 0.01	5.39 ± 0.04	0.5	0.0025	0.1553
TC1100001315.mm.1	Rnft1	ring finger protein, transmembrane 1	8.45 ± 0.11	8.35 ± 0.07	8.74 ± 0.04	8.24 ± 0.13	0.38985	0.00676	0.0574
TC0700004522.mm.1	Rnh1	ribonuclease/angiogenin inhibitor 1	8.38 ± 0.01	8.35 ± 0.02	8.48 ± 0.03	8.31 ± 0.03	0.17041	0.00305	0.00992
TC0100003124.mm.1	Rnpep	arginyl aminopeptidase (aminopeptidase B)	7.63 ± 0.04	7.48 ± 0.03	7.63 ± 0.02	7.53 ± 0.04	0.79866	0.00194	0.33256
TSUnmapped000000	Rora	RAR-related orphan receptor alpha (Rora), transcript variant	8.54 ± 0.09	8.74 ± 0.03	8.68 ± 0.1	8.28 ± 0.11	0.10842	0.3338	0.00372
TC0800003058.mm.1	RP24-286J21.5	novel transcript	4.71 ± 0.05	5.02 ± 0.05	4.86 ± 0.08	4.93 ± 0.05	0.52838	0.00449	0.04326
TC0400003779.mm.1	Rpl11	ribosomal protein L11	6.67 ± 0.01	6.73 ± 0.01	6.72 ± 0.01	6.78 ± 0.03	0.02174	0.00461	0.95367

Supplemental Table I

Annotations			Summary Statistics				2 way ANOVA p-values		
Probe Set ID	Symbol	Description	XY sh	XY Or	XX sh	XX Or	XY vs XX	Sh vs Or	Intrxn
TC0800001508.mm.1	Rpl13	ribosomal protein L13	8.05 ± 0.04	8.18 ± 0.01	8.23 ± 0.02	8.15 ± 0.04	0.02467	0.39474	0.00451
TC0800002412.mm.1	Rpl18a	ribosomal protein L18A	11.08 ± 0.02	11.22 ± 0.03	11.27 ± 0.03	11.25 ± 0.04	0.00313	0.0544	0.01541
TC1600000460.mm.1	Rpl35a	ribosomal protein L35A	6.41 ± 0.02	6.48 ± 0.02	6.53 ± 0.02	6.45 ± 0.04	0.07029	0.95736	0.00875
TC1700001012.mm.1	Rpl36	ribosomal protein L36	9.21 ± 0.03	9.29 ± 0.04	9.42 ± 0.05	9.44 ± 0.06	0.00163	0.39302	0.52474
TC0100000609.mm.1	Rpl37a	ribosomal protein L37a	8.52 ± 0.03	8.69 ± 0.06	8.74 ± 0.03	8.62 ± 0.06	0.0837	0.58488	0.00486
TC1100001874.mm.1	Rpl38	ribosomal protein L38	9.78 ± 0.02	9.92 ± 0.02	9.92 ± 0.03	9.99 ± 0.03	0.00134	0.0015	0.13947
TC0900002450.mm.1	Rplp1	ribosomal protein, large, P1	11.21 ± 0.03	11.27 ± 0.04	11.43 ± 0.06	11.35 ± 0.06	0.00464	0.9317	0.1369
TC0700002052.mm.1	Rplp2	ribosomal protein, large P2	7.05 ± 0.04	7.16 ± 0.02	7.19 ± 0.01	7.27 ± 0.05	0.00559	0.03792	0.88943
TC0600001027.mm.1	Rpn1	ribophorin I	10.2 ± 0.07	10.04 ± 0.03	10.07 ± 0.04	9.78 ± 0.07	0.01088	0.00371	0.16098
TC0200002844.mm.1	Rpp38	ribonuclease P/MRP 38 subunit	8.57 ± 0.02	8.71 ± 0.02	8.61 ± 0.03	8.7 ± 0.06	0.55251	0.00497	0.45769
TC1700001742.mm.1	Rps10	ribosomal protein S10	7.41 ± 0.02	7.48 ± 0.04	7.54 ± 0.02	7.53 ± 0.02	0.00394	0.16176	0.11332
TC0800000440.mm.1	Rps12l2	ribosomal protein S12-like 2	10.83 ± 0.04	10.91 ± 0.04	10.93 ± 0.01	10.78 ± 0.06	0.87989	0.51471	0.00958
TC1800000616.mm.1	Rps14	ribosomal protein S14	6.14 ± 0.02	6.28 ± 0.04	6.38 ± 0.02	6.32 ± 0.04	0.00012	0.13024	0.00219
TC0700000495.mm.1	Rps16	ribosomal protein S16	8.33 ± 0.04	8.46 ± 0.03	8.5 ± 0.01	8.4 ± 0.05	0.09083	0.56326	0.00692
TC0700000401.mm.1	Rps19	ribosomal protein S19	6.99 ± 0.03	7.07 ± 0.01	7.08 ± 0.01	7.14 ± 0.03	0.00428	0.00946	0.55785
TC1700000349.mm.1	Rps2	ribosomal protein S2	6.96 ± 0.02	7.04 ± 0.01	7.05 ± 0.01	7.07 ± 0.02	0.00073	0.00859	0.06896
TC0200002785.mm.1	Rps21	ribosomal protein S21	8.15 ± 0.03	8.31 ± 0.04	8.31 ± 0.01	8.23 ± 0.04	0.18304	0.23415	0.00203
TC0700003798.mm.1	Rps3	ribosomal protein S3	7.19 ± 0.03	7.32 ± 0.02	7.36 ± 0.01	7.28 ± 0.04	0.02009	0.33567	0.00104
TC0700000151.mm.1	Rps5	ribosomal protein S5	8.38 ± 0.03	8.53 ± 0.04	8.61 ± 0.01	8.58 ± 0.01	7.8E-05	0.02708	0.003
TC0400003362.mm.1	Rps8	ribosomal protein S8	7.67 ± 0.03	7.77 ± 0.02	7.76 ± 0.02	7.65 ± 0.06	0.71505	0.98256	0.00746
TC0800002807.mm.1	Rrad	Ras-related associated with diabetes	8.4 ± 0.27	9.06 ± 0.21	9.31 ± 0.14	8.59 ± 0.04	0.40207	0.71347	0.00669
TC0700004132.mm.1	Rras2	related RAS viral (r-ras) oncogene homolog 2	7.79 ± 0.04	7.9 ± 0.06	7.76 ± 0.03	7.71 ± 0.03	0.00942	0.65281	0.07457
TC1700000550.mm.1	Rrp1b	ribosomal RNA processing 1 homolog B (S. cerevisiae)	6.04 ± 0.03	6.17 ± 0.03	6.12 ± 0.02	6.03 ± 0.03	0.24079	0.44725	0.00208
TC1100003566.mm.1	Rsad1	radical S-adenosyl methionine domain containing 1	6.83 ± 0.01	6.94 ± 0.03	6.67 ± 0.04	6.94 ± 0.08	0.11939	0.00108	0.12048
TC0400001433.mm.1	Rspo1	R-spondin homolog (Xenopus laevis)	7.5 ± 0.03	7.44 ± 0.07	7.75 ± 0.06	7.56 ± 0.07	0.00441	0.05049	0.21089
TC1500001457.mm.1	Rspo2	R-spondin 2 homolog (Xenopus laevis)	4.84 ± 0.02	4.76 ± 0.04	5.1 ± 0.04	4.81 ± 0.05	0.00119	0.00015	0.01746
TC1200001902.mm.1	Rtn1	reticulon 1	7.41 ± 0.27	7.02 ± 0.2	6.66 ± 0.06	7.58 ± 0.09	0.81423	0.12646	0.00786
TC1100001063.mm.1	Rtn4rl1	reticulon 4 receptor-like 1	6.97 ± 0.04	6.83 ± 0.05	7.36 ± 0.09	7.02 ± 0.02	0.00018	0.00089	0.10005
TC0400000435.mm.1	Rusc2	RUN and SH3 domain containing 2	7.4 ± 0.06	7.61 ± 0.05	7.52 ± 0.05	7.42 ± 0.03	0.79209	0.2083	0.00568
TC0100001554.mm.1	Rxrg	retinoid X receptor gamma	6.63 ± 0.1	6.6 ± 0.06	6.44 ± 0.11	6.88 ± 0.05	0.94265	0.08153	0.00802
TC0300000853.mm.1	S100a10	S100 calcium binding protein A10 (calpactin)	6.81 ± 0.06	6.47 ± 0.07	6.5 ± 0.03	6.42 ± 0.04	0.00618	0.00219	0.03871
TC0300000806.mm.1	S100a3	S100 calcium binding protein A3	4.92 ± 0.04	5.2 ± 0.07	5.11 ± 0.04	5.23 ± 0.09	0.06844	0.00394	0.16397

Supplemental Table I

Annotations			Summary Statistics				2 way ANOVA p-values		
Probe Set ID	Symbol	Description	XY sh	XY Or	XX sh	XX Or	XY vs XX	Sh vs Or	Intrxn
TC0300000807.mm.1	S100a4	S100 calcium binding protein A4	6.55 ± 0.1	6.88 ± 0.1	6.74 ± 0.06	6.47 ± 0.05	0.26961	0.64777	0.00323
TC0300000810.mm.1	S100a7a	S100 calcium binding protein A7A	5.51 ± 0.08	5.85 ± 0.05	5.78 ± 0.08	5.54 ± 0.11	0.83673	0.49781	0.00289
TC0900001864.mm.1	S1pr5	sphingosine-1-phosphate receptor 5	5.43 ± 0.03	5.65 ± 0.07	5.7 ± 0.08	5.78 ± 0.07	0.00605	0.02457	0.24392
TC1400000507.mm.1	Samd4	sterile alpha motif domain containing 4	8.76 ± 0.13	9.03 ± 0.06	9.06 ± 0.07	8.64 ± 0.1	0.81241	0.61147	0.00278
TC1000000572.mm.1	Sar1a	SAR1 gene homolog A (S. cerevisiae)	10.75 ± 0.04	10.7 ± 0.06	10.61 ± 0.02	10.49 ± 0.06	0.00579	0.14872	0.3741
TC0200003214.mm.1	Sardh	sarcosine dehydrogenase	7.13 ± 0.02	7.21 ± 0.01	7.17 ± 0.01	7.15 ± 0.01	0.63855	0.01801	0.00173
TC1900000961.mm.1	Sart1	squamous cell carcinoma antigen recognized by T cells 1	7.32 ± 0.02	7.36 ± 0.01	7.36 ± 0.01	7.32 ± 0.01	0.8221	0.52812	0.00303
TC1000001716.mm.1	Sash1	SAM and SH3 domain containing 1	8.75 ± 0.04	8.73 ± 0.07	9.03 ± 0.05	8.6 ± 0.1	0.33915	0.00588	0.01087
TC0X00000427.mm.1	Sash3	SAM and SH3 domain containing 3	6.22 ± 0.01	6.43 ± 0.04	6.33 ± 0.06	6.47 ± 0.06	0.09715	0.00126	0.38303
TC1400000938.mm.1	Scara5	scavenger receptor class A, member 5 (putative)	8.61 ± 0.08	8.31 ± 0.01	8.69 ± 0.05	8.19 ± 0.08	0.99175	4.3E-05	0.07725
TC0500003271.mm.1	Scarb1	scavenger receptor class B, member 1	7.88 ± 0.13	7.56 ± 0.09	7.54 ± 0.09	7.84 ± 0.03	0.71455	0.90091	0.0071
TC1600000225.mm.1	Scarf2	scavenger receptor class F, member 2	7.78 ± 0.09	8.02 ± 0.06	8.11 ± 0.05	7.91 ± 0.03	0.0872	0.68069	0.00358
TC1000000388.mm.1	Scml4	sex comb on midleg-like 4 (Drosophila)	5.38 ± 0.02	5.45 ± 0.02	5.39 ± 0.03	5.46 ± 0.02	0.62629	0.00593	0.98358
TC0400003234.mm.1	Scp2	sterol carrier protein 2, liver	8.97 ± 0.12	8.67 ± 0.15	8.52 ± 0.14	9.01 ± 0.04	0.41052	0.66359	0.00288
TC1700000471.mm.1	Scube3	signal peptide, CUB domain, EGF-like 3	9.28 ± 0.22	9.79 ± 0.09	9.69 ± 0.1	9.25 ± 0.1	0.76246	0.74192	0.0079
TC1200000069.mm.1	Sdc1	syndecan 1	7.3 ± 0.02	7.35 ± 0.02	7.53 ± 0.06	7.33 ± 0.04	0.01144	0.04348	0.00474
TC0500001337.mm.1	Sds	serine dehydratase	5.17 ± 0.04	5.44 ± 0.02	5.33 ± 0.01	5.41 ± 0.08	0.321	0.00388	0.09549
TC0700003016.mm.1	Sec1	secretory blood group 1	5.57 ± 0.03	5.69 ± 0.04	5.75 ± 0.03	5.79 ± 0.08	0.00564	0.04899	0.29143
TC1800000682.mm.1	Sec11c	SEC11 homolog C (S. cerevisiae)	6.9 ± 0.02	6.84 ± 0.04	6.95 ± 0.02	6.86 ± 0.03	0.48518	0.00954	0.76184
TC1100000033.mm.1	Sec14l3	SEC14-like 3 (S. cerevisiae)	4.65 ± 0.02	4.72 ± 0.01	4.69 ± 0.01	4.83 ± 0.07	0.04916	0.00894	0.39667
TC0200002150.mm.1	Sec23b	SEC23B (S. cerevisiae)	8 ± 0.05	7.84 ± 0.05	7.78 ± 0.04	7.7 ± 0.06	0.00798	0.06745	0.6183
TC0100001495.mm.1	Sele	selectin, endothelial cell	4.52 ± 0.02	4.72 ± 0.07	4.36 ± 0.06	4.41 ± 0.05	0.00053	0.03149	0.15039
TC1100000015.mm.1	Selm	selenoprotein M	8.03 ± 0.06	8.05 ± 0.04	8.23 ± 0.05	8.11 ± 0.02	0.00509	0.63576	0.0669
TC0500000131.mm.1	Sema3c	sema domain, immunoglobulin domain (Ig), short basic doma	9.5 ± 0.14	9.76 ± 0.06	9.79 ± 0.09	9.4 ± 0.11	0.97167	0.74682	0.00833
TC1400000325.mm.1	Sema3g	sema domain, immunoglobulin domain (Ig), short basic doma	6.93 ± 0.05	6.79 ± 0.02	6.75 ± 0.06	6.88 ± 0.04	0.21299	0.65248	0.00516
TC1500000002.mm.1	Sepp1	selenoprotein P, plasma, 1	7.65 ± 0.04	7.47 ± 0.02	7.7 ± 0.03	7.51 ± 0.09	0.31092	0.00354	0.87578
TC0700004318.mm.1	Sept1	septin 1	5.83 ± 0.05	6.17 ± 0.02	5.97 ± 0.05	6.17 ± 0.07	0.28312	0.00029	0.33887
TC0400003629.mm.1	Serinc2	serine incorporator 2	6.65 ± 0.04	6.79 ± 0.03	6.92 ± 0.04	6.93 ± 0.12	0.0068	0.2761	0.3259
TC1200002288.mm.1	Serpina12	serine (or cysteine) peptidase inhibitor, clade A (alpha-1 antip	4.51 ± 0.02	4.7 ± 0.06	4.52 ± 0.03	4.72 ± 0.1	0.93176	0.00521	0.88654
TC1200002289.mm.1	Serpina3c	serine (or cysteine) peptidase inhibitor, clade A, member 3C	7.81 ± 0.21	6.69 ± 0.14	6.92 ± 0.09	6.61 ± 0.29	0.03586	0.00394	0.07828
TC1200001044.mm.1	Serpina3k	serine (or cysteine) peptidase inhibitor, clade A, member 3K	6.19 ± 0.26	5.24 ± 0.22	5.4 ± 0.01	5.02 ± 0.13	0.04488	0.0097	0.29062
TC1200001047.mm.1	Serpina3n	serine (or cysteine) peptidase inhibitor, clade A, member 3N	9.52 ± 0.18	8.29 ± 0.23	8.96 ± 0.09	7.7 ± 0.19	0.01186	1.8E-05	0.73697

Supplemental Table I

Annotations			Summary Statistics				2 way ANOVA p-values		
Probe Set ID	Symbol	Description	XY sh	XY Or	XX sh	XX Or	XY vs XX	Sh vs Or	Intrxn
TC0100001031.mm.1	Serpinb8	serine (or cysteine) peptidase inhibitor, clade B, member 8	6.47 ± 0.07	6.3 ± 0.06	6.24 ± 0.06	6.06 ± 0.07	0.00566	0.03064	0.72383
TC1300000364.mm.1	Serpinb9	serine (or cysteine) peptidase inhibitor, clade B, member 9	7.98 ± 0.07	8.11 ± 0.04	8.33 ± 0.09	7.92 ± 0.12	0.28998	0.16656	0.00507
TC1300000365.mm.1	Serpinb9b	serine (or cysteine) peptidase inhibitor, clade B, member 9b	4.52 ± 0.04	4.65 ± 0.04	4.68 ± 0.03	4.56 ± 0.03	0.3068	0.81264	0.00347
TC0100002645.mm.1	Serpine2	serine (or cysteine) peptidase inhibitor, clade E, member 2	11.05 ± 0.16	11.37 ± 0.07	11.34 ± 0.08	10.98 ± 0.1	0.74655	0.99362	0.00884
TC0200003880.mm.1	Serping1	serine (or cysteine) peptidase inhibitor, clade G, member 1	11.63 ± 0.06	11.49 ± 0.02	11.72 ± 0.05	11.38 ± 0.1	0.8424	0.00546	0.07693
TC0700003797.mm.1	Serpinh1	serine (or cysteine) peptidase inhibitor, clade H, member 1	8.55 ± 0.09	8.47 ± 0.05	8.54 ± 0.07	8.11 ± 0.05	0.03006	0.00512	0.01516
TC0700000460.mm.1	Sertad1	SERTA domain containing 1	6.93 ± 0.02	7.18 ± 0.03	7.1 ± 0.03	7.14 ± 0.08	0.18248	0.00531	0.03052
TC0100003830.mm.1	Sertad4	SERTA domain containing 4	6.36 ± 0.04	6.44 ± 0.01	6.61 ± 0.07	6.42 ± 0.02	0.00731	0.40252	0.00316
TC1800001640.mm.1	Setbp1	SET binding protein 1	8.54 ± 0.14	8.87 ± 0.07	8.85 ± 0.08	8.57 ± 0.08	0.87307	0.72238	0.00965
TC0800002927.mm.1	Sf3b3	splicing factor 3b, subunit 3	8.34 ± 0.05	8.32 ± 0.03	8.24 ± 0.02	8.07 ± 0.09	0.00946	0.11435	0.16125
TC0400001477.mm.1	Sfpq	splicing factor proline/glutamine rich (polypyrimidine tract binc	7.05 ± 0.05	7.04 ± 0.07	6.81 ± 0.04	6.88 ± 0.09	0.00661	0.68554	0.56358
TC1300000623.mm.1	Sfxn1	sideroflexin 1	9.12 ± 0.09	8.78 ± 0.12	8.85 ± 0.1	9.07 ± 0.02	0.7708	0.34064	0.00456
TC1000000171.mm.1	Sgk1	serum/glucocorticoid regulated kinase 1	6.99 ± 0.09	7.11 ± 0.06	6.76 ± 0.02	6.83 ± 0.06	0.00295	0.13687	0.62751
TC0300002959.mm.1	Sgms2	sphingomyelin synthase 2	8.42 ± 0.13	8.35 ± 0.04	8.2 ± 0.06	7.89 ± 0.07	0.00639	0.14516	0.07381
TC0900001099.mm.1	Sh3bgrl2	SH3 domain binding glutamic acid-rich protein like 2	6.67 ± 0.15	6.26 ± 0.12	6.25 ± 0.12	6.63 ± 0.06	0.80443	0.84889	0.00647
TC1500002333.mm.1	Sh3bp1	SH3-domain binding protein 1	6.53 ± 0.03	6.64 ± 0.05	6.71 ± 0.04	6.61 ± 0.02	0.0421	0.70965	0.00715
TC0400003529.mm.1	Sh3d21	SH3 domain containing 21	6.51 ± 0.05	6.68 ± 0.03	6.57 ± 0.02	6.59 ± 0.04	0.97459	0.00903	0.03237
TC1100000341.mm.1	Sh3pxd2b	SH3 and PX domains 2B	7.63 ± 0.04	7.65 ± 0.02	7.77 ± 0.06	7.42 ± 0.06	0.53208	0.0083	0.0014
TC0600001821.mm.1	Shfm1	split hand/foot malformation (ectrodactyly) type 1	8.29 ± 0.03	8.32 ± 0.04	8.21 ± 0.03	8.17 ± 0.03	0.00309	0.58734	0.52189
TC1100001018.mm.1	Shpk	sedoheptulokinase	6.19 ± 0.1	5.97 ± 0.03	5.9 ± 0.07	6.19 ± 0.07	0.79192	0.53454	0.00778
TC1600001642.mm.1	Sidt1	SID1 transmembrane family, member 1	4.45 ± 0.01	4.56 ± 0.02	4.42 ± 0.05	4.56 ± 0.04	0.50692	0.00303	0.62853
TC0700004519.mm.1	Sigirr	single immunoglobulin and toll-interleukin 1 receptor (TIR) do	6.03 ± 0.02	6.15 ± 0.02	6.1 ± 0.02	6.18 ± 0.05	0.14581	0.0044	0.57772
TC0700000757.mm.1	Siglecg	sialic acid binding Ig-like lectin G	5.13 ± 0.03	5.36 ± 0.03	5.25 ± 0.03	5.42 ± 0.1	0.20713	0.00726	0.80845
TC1700001827.mm.1	Sik1	salt inducible kinase 1	7.58 ± 0.06	7.92 ± 0.02	7.49 ± 0.1	8.06 ± 0.2	0.94373	0.00152	0.25936
TC0700000511.mm.1	Sirt2	sirtuin 2 (silent mating type information regulation 2, homolog	9.41 ± 0.02	9.42 ± 0.02	9.49 ± 0.01	9.46 ± 0.02	0.00706	0.67307	0.17851
TC1200001913.mm.1	Six4	sine oculis-related homeobox 4	6.13 ± 0.05	6.28 ± 0.05	6.34 ± 0.01	6.2 ± 0.02	0.06948	0.7783	0.00175
TC0700000287.mm.1	Six5	sine oculis-related homeobox 5	7.35 ± 0.01	7.45 ± 0.04	7.51 ± 0.05	7.41 ± 0.02	0.09919	0.94844	0.0096
TC0200005003.mm.1	Sla2	Src-like-adaptor 2	5.74 ± 0.04	6.07 ± 0.05	5.83 ± 0.07	6.02 ± 0.07	0.67039	0.00051	0.25226
TC1400001189.mm.1	Slain1	SLAIN motif family, member 1	4.68 ± 0.05	4.81 ± 0.02	4.7 ± 0.05	4.83 ± 0.03	0.503	0.00532	0.7703
TC1800000583.mm.1	Slc12a2	solute carrier family 12, member 2	7.61 ± 0.11	7.21 ± 0.1	6.95 ± 0.07	7.37 ± 0.09	0.0188	0.96192	0.00094
TC1100001895.mm.1	Slc16a5	solute carrier family 16 (monocarboxylic acid transporters), m	5.06 ± 0.02	5.35 ± 0.06	5.19 ± 0.04	5.35 ± 0.08	0.25191	0.00067	0.21226
TC1000000674.mm.1	Slc16a9	solute carrier family 16 (monocarboxylic acid transporters), m	6.97 ± 0.01	6.81 ± 0.03	7.13 ± 0.04	6.74 ± 0.08	0.34036	2.5E-05	0.01423

Supplemental Table I

Annotations			Summary Statistics				2 way ANOVA p-values		
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TC1000002658.mm.1	Slc17a8	solute carrier family 17 (sodium-dependent inorganic phospha	4.84 ± 0.02	5.05 ± 0.06	4.94 ± 0.05	5.07 ± 0.09	0.26536	0.00834	0.46226
TC1900000850.mm.1	Slc18a2	solute carrier family 18 (vesicular monoamine), member 2	8.56 ± 0.83	6.92 ± 0.39	5.85 ± 0.2	8.16 ± 0.31	0.3282	0.38823	0.00652
TC0700000236.mm.1	Slc1a5	solute carrier family 1 (neutral amino acid transporter), memb	9.51 ± 0.09	9.02 ± 0.1	9.03 ± 0.07	9.19 ± 0.07	0.05501	0.04318	0.00125
TC0200001951.mm.1	Slc20a1	solute carrier family 20, member 1	6.47 ± 0.04	6.34 ± 0.02	6.27 ± 0.03	6.35 ± 0.01	0.00748	0.47111	0.00615
TC1700000124.mm.1	Slc22a2	solute carrier family 22 (organic cation transporter), member 2	6.18 ± 0.05	6 ± 0.01	5.93 ± 0.04	5.76 ± 0.1	0.00261	0.01995	0.87489
TC1300001784.mm.1	Slc22a23	solute carrier family 22, member 23	7.28 ± 0.11	7.01 ± 0.12	7.03 ± 0.14	7.4 ± 0.1	0.77473	0.95031	0.00905
TC1100002754.mm.1	Slc22a4	solute carrier family 22 (organic cation transporter), member 4	6.7 ± 0.05	6.3 ± 0.06	6.56 ± 0.02	6.37 ± 0.06	0.4187	5.1E-05	0.04522
TC1100002748.mm.1	Slc22a5	solute carrier family 22 (organic cation transporter), member 5	7.58 ± 0.07	7.41 ± 0.1	7.36 ± 0.06	7.61 ± 0.04	0.60146	0.89424	0.00529
TC0800001867.mm.1	Slc25a15	solute carrier family 25 (mitochondrial carrier ornithine transp	6.78 ± 0.05	6.61 ± 0.06	6.61 ± 0.07	6.78 ± 0.04	0.7335	0.83169	0.00472
TC0400004050.mm.1	Slc25a33	solute carrier family 25, member 33	6.38 ± 0.14	6.3 ± 0.08	5.84 ± 0.1	6.46 ± 0.11	0.10394	0.04624	0.00725
TC0800000796.mm.1	Slc27a1	solute carrier family 27 (fatty acid transporter), member 1	9.22 ± 0.14	9.03 ± 0.18	8.57 ± 0.16	9.5 ± 0.09	0.3779	0.04201	0.00127
TC0200001898.mm.1	Slc27a2	solute carrier family 27 (fatty acid transporter), member 2	7.87 ± 0.34	6.88 ± 0.19	6.08 ± 0.3	7.57 ± 0.29	0.07087	0.48984	0.0009
TC0200002549.mm.1	Slc2a10	solute carrier family 2 (facilitated glucose transporter), membe	7.54 ± 0.06	7.67 ± 0.03	7.69 ± 0.05	7.52 ± 0.02	0.65917	0.98973	0.00503
TC0100001859.mm.1	Slc30a1	solute carrier family 30 (zinc transporter), member 1	7.58 ± 0.03	7.62 ± 0.05	7.44 ± 0.03	7.51 ± 0.04	0.00548	0.08748	0.764
TC0400000698.mm.1	Slc31a1	solute carrier family 31, member 1	7.62 ± 0.35	6.86 ± 0.16	6.53 ± 0.07	7.36 ± 0.15	0.31324	0.72388	0.00806
TC1100001460.mm.1	Slc35b1	solute carrier family 35, member B1	8.36 ± 0.03	8.32 ± 0.02	8.34 ± 0.06	8.11 ± 0.06	0.01927	0.00827	0.06343
TC1100002777.mm.1	Slc36a2	solute carrier family 36 (proton/amino acid symporter), memb	8.31 ± 0.25	8.2 ± 0.2	7.69 ± 0.33	8.97 ± 0.08	0.86782	0.07373	0.0045
TC1700002811.mm.1	Slc39a7	solute carrier family 39 (zinc transporter), member 7	8.52 ± 0.03	8.44 ± 0.02	8.52 ± 0.03	8.4 ± 0.03	0.57393	0.00872	0.38947
TC1900001066.mm.1	Slc3a2	solute carrier family 3 (activators of dibasic and neutral amino	8.82 ± 0.04	8.69 ± 0.01	8.64 ± 0.02	8.75 ± 0.02	0.15667	0.81346	0.0046
TC0200001226.mm.1	Slc43a3	solute carrier family 43, member 3	10.5 ± 0.11	10.03 ± 0.05	10.38 ± 0.05	9.79 ± 0.09	0.14583	7.8E-05	0.24866
TC1500001698.mm.1	Slc45a4	solute carrier family 45, member 4	6.92 ± 0.01	6.93 ± 0.02	7.03 ± 0.01	6.93 ± 0.01	0.0035	0.00707	0.00298
TC0100000665.mm.1	Slc4a3	solute carrier family 4 (anion exchanger), member 3	7.28 ± 0.04	7.4 ± 0.03	7.47 ± 0.05	7.33 ± 0.02	0.11205	0.89319	0.00267
TC0500000819.mm.1	Slc4a4	solute carrier family 4 (anion exchanger), member 4	8.6 ± 0.2	8.27 ± 0.18	7.7 ± 0.21	8.83 ± 0.2	0.25583	0.12649	0.00179
TC0500002170.mm.1	Slc5a6	solute carrier family 5 (sodium-dependent vitamin transporter)	7.27 ± 0.13	6.92 ± 0.06	6.66 ± 0.05	6.9 ± 0.03	0.00745	0.86467	0.01098
TC0400003285.mm.1	Slc5a9	solute carrier family 5 (sodium/glucose cotransporter), membe	4.32 ± 0.01	4.46 ± 0.04	4.32 ± 0.03	4.45 ± 0.07	0.97923	0.00519	0.89744
TC0800001080.mm.1	Slc6a2	solute carrier family 6 (neurotransmitter transporter, noradren	9.34 ± 0.81	7.7 ± 0.57	6.67 ± 0.2	9.35 ± 0.32	0.54562	0.28027	0.0044
TC1800001410.mm.1	Slc6a7	solute carrier family 6 (neurotransmitter transporter, L-proline	6 ± 0.02	6.34 ± 0.03	6.11 ± 0.04	6.23 ± 0.07	0.91354	0.00011	0.02052
TC0700000655.mm.1	Slc7a10	solute carrier family 7 (cationic amino acid transporter, y+ sys	7.08 ± 0.08	7 ± 0.06	6.73 ± 0.03	7.15 ± 0.07	0.13705	0.02192	0.00196
TC0700000221.mm.1	Slc8a2	solute carrier family 8 (sodium/calcium exchanger), member 2	6.71 ± 0.11	7.04 ± 0.06	6.99 ± 0.08	6.8 ± 0.06	0.80625	0.41635	0.00957
TC1700001634.mm.1	Slc9a3r2	solute carrier family 9 (sodium/hydrogen exchanger), membe	8.66 ± 0.05	8.46 ± 0.02	8.34 ± 0.05	8.41 ± 0.01	0.00062	0.24876	0.00895
TC0700003804.mm.1	Slco2b1	solute carrier organic anion transporter family, member 2b1	8.52 ± 0.09	8.15 ± 0.05	8.43 ± 0.02	8.13 ± 0.07	0.71269	0.00068	0.99044
TC0800002518.mm.1	Smad1	SMAD family member 1	7.68 ± 0.03	7.84 ± 0.03	7.75 ± 0.02	7.73 ± 0.02	0.48998	0.01468	0.00358

Supplemental Table I

Annotations			Summary Statistics				2 way ANOVA p-values		
Probe Set ID	Symbol	Description	XY sh	XY Or	XX sh	XX Or	XY vs XX	Sh vs Or	Intrxn
TC1300001136.mm.1	Smn1	survival motor neuron 1	6.91 ± 0.02	7 ± 0.01	7.01 ± 0.02	6.97 ± 0.01	0.15022	0.40585	0.00633
TC1200000751.mm.1	Smoc1	SPARC related modular calcium binding 1	9.52 ± 0.15	9.83 ± 0.08	9.78 ± 0.08	9.32 ± 0.12	0.33273	0.57875	0.00717
TC0200002077.mm.1	Snap25	synaptosomal-associated protein 25	9.51 ± 0.87	7.84 ± 0.59	6.11 ± 0.46	9.53 ± 0.31	0.30659	0.12907	0.00283
TC0900000816.mm.1	Snapc5	small nuclear RNA activating complex, polypeptide 5	7.13 ± 0.05	7.01 ± 0.1	7.21 ± 0.05	6.92 ± 0.08	0.65463	0.00717	0.40048
TC0600000215.mm.1	Snd1	staphylococcal nuclease and tudor domain containing 1	8.41 ± 0.02	8.37 ± 0	8.37 ± 0.02	8.27 ± 0.01	0.00082	0.0015	0.0282
TC1800000310.mm.1	Snhg4	small nucleolar RNA host gene 4 (non-protein coding)	4.52 ± 0.02	4.52 ± 0.03	4.56 ± 0.01	4.6 ± 0.02	0.00866	0.29341	0.54732
TC0400002711.mm.1	SNORA43	Small nucleolar RNA SNORA43	6.69 ± 0.05	6.92 ± 0.07	6.78 ± 0.02	6.86 ± 0.02	0.95161	0.00705	0.21641
TC1100001783.mm.1	Snord104	small nucleolar RNA, C/D box 104	9.99 ± 0.05	10.23 ± 0.07	10.33 ± 0.07	10.11 ± 0.09	0.12619	0.8834	0.00543
TC0700003300.mm.1	Snord116	small nucleolar RNA, C/D box 116	8.2 ± 0.92	6.54 ± 0.46	5.73 ± 0.19	8.12 ± 0.28	0.62156	0.43793	0.00906
TC0700003329.mm.1	Snord116l2	small nucleolar RNA, C/D box 116-like 2	8.15 ± 0.92	6.41 ± 0.51	5.46 ± 0.27	8.11 ± 0.29	0.56595	0.37983	0.00606
TC0900000458.mm.1	Snord14e	small nucleolar RNA, C/D box 14E	10.29 ± 0.05	10.28 ± 0.07	10 ± 0.04	10.07 ± 0.03	0.00056	0.37371	0.61989
TC0900001635.mm.1	Snrk	SNF related kinase	8.64 ± 0.05	8.74 ± 0.09	8.39 ± 0.08	8.85 ± 0.09	0.21037	0.00421	0.01667
TC1100000333.mm.1	Snrnp25	small nuclear ribonucleoprotein 25 (U11/U12)	6.03 ± 0.03	6.1 ± 0.01	6.1 ± 0.03	6.18 ± 0.03	0.00917	0.00917	0.87729
TC1200001583.mm.1	Sntg2	syntrophin, gamma 2	6.69 ± 0.13	7.01 ± 0.04	7.1 ± 0.06	6.84 ± 0.08	0.22653	0.74723	0.00771
TC0600000609.mm.1	Snx10	sorting nexin 10	7.97 ± 0.14	7.64 ± 0.12	7.4 ± 0.18	7.98 ± 0.09	0.27595	0.59461	0.00274
TC1300002697.mm.1	Snx18	sorting nexin 18	8.69 ± 0.1	8.9 ± 0.03	9.19 ± 0.07	8.72 ± 0.11	0.10616	0.10897	0.00221
TC1000000382.mm.1	Snx3	sorting nexin 3	9.4 ± 0.02	9.35 ± 0.01	9.37 ± 0.02	9.29 ± 0.02	0.04362	0.0037	0.48953
TC0200005011.mm.1	Soga1	suppressor of glucose, autophagy associated 1	7.86 ± 0.05	7.94 ± 0.03	8 ± 0.03	7.86 ± 0.02	0.30065	0.51836	0.00601
TC1900001485.mm.1	Sorbs1	sorbin and SH3 domain containing 1	8.76 ± 0.11	8.56 ± 0.07	8.34 ± 0.11	8.74 ± 0.01	0.10385	0.51032	0.00256
TC1100003630.mm.1	Sp2	Sp2 transcription factor	7.11 ± 0.02	7.21 ± 0.02	7.21 ± 0.02	7.17 ± 0.02	0.27323	0.2108	0.00584
TC1100002783.mm.1	Sparc	secreted acidic cysteine rich glycoprotein	12.38 ± 0.05	12.23 ± 0.03	12.15 ± 0.02	11.87 ± 0.06	7E-05	0.00121	0.0704
TC1200000967.mm.1	Spata7	spermatogenesis associated 7	5.03 ± 0.02	4.95 ± 0.03	5.02 ± 0.03	4.93 ± 0.02	0.69638	0.00531	0.69638
TC0100000424.mm.1	Spats2l	spermatogenesis associated, serine-rich 2-like	7.05 ± 0.09	7.47 ± 0.06	7.26 ± 0.02	7.19 ± 0.05	0.6317	0.02674	0.00353
TC1100000789.mm.1	Specc1	sperm antigen with calponin homology and coiled-coil domair	7.12 ± 0.07	7.28 ± 0.05	7.31 ± 0.07	7.11 ± 0.02	0.59641	0.95317	0.00557
TC0300000416.mm.1	Spg20	spastic paraplegia 20, spartin (Troyer syndrome) homolog (hu	7.71 ± 0.05	7.8 ± 0.03	7.77 ± 0.03	7.63 ± 0.04	0.34727	0.84799	0.00787
TC0700002967.mm.1	Spib	Spi-B transcription factor (Spi-1/PU.1 related)	5.11 ± 0.1	5.66 ± 0.07	5.58 ± 0.1	5.74 ± 0.1	0.03005	0.00582	0.13784
TC0X00002659.mm.1	Spin4	spindlin family, member 4	6.2 ± 0.05	6.33 ± 0.08	6.27 ± 0.05	6.05 ± 0.05	0.13525	0.56418	0.00651
TC0700002720.mm.1	Spint2	serine protease inhibitor, Kunitz type 2	7.35 ± 0.11	7.7 ± 0.03	7.66 ± 0.07	7.4 ± 0.06	0.81627	0.453	0.00153
TC1800001507.mm.1	Spire1	spire homolog 1 (Drosophila)	7.81 ± 0.05	7.73 ± 0.01	7.61 ± 0.05	7.66 ± 0.05	0.00864	0.56097	0.13322
TC0700004313.mm.1	Spn	sialophorin	5.34 ± 0.03	5.57 ± 0.05	5.42 ± 0.05	5.52 ± 0.04	0.78395	0.00172	0.16438
TC0700001668.mm.1	Spon1	spondin 1, (f-spondin) extracellular matrix protein	7.47 ± 0.09	7.2 ± 0.07	7.41 ± 0.06	7.13 ± 0.06	0.64473	0.00652	0.67341
TC0600002605.mm.1	Spr	sepiapterin reductase	7.92 ± 0.02	8.02 ± 0.03	8.07 ± 0.02	8 ± 0	0.01074	0.53578	0.00325

Supplemental Table I

Annotations			Summary Statistics				2 way ANOVA p-values		
Probe Set ID	Symbol	Description	XY sh	XY Or	XX sh	XX Or	XY vs XX	Sh vs Or	Intrxn
TC0300000828.mm.1	Sprr2h	small proline-rich protein 2H	4.36 ± 0.03	4.45 ± 0.03	4.38 ± 0.05	4.54 ± 0.06	0.19912	0.0092	0.43302
TC0300000288.mm.1	Spry1	sprouty homolog 1 (Drosophila)	7.32 ± 0.02	7.47 ± 0.03	7.68 ± 0.03	7.45 ± 0.01	2.4E-05	0.09473	6.6E-06
TC1200001747.mm.1	Sptssa	serine palmitoyltransferase, small subunit A	8.6 ± 0.04	8.75 ± 0.08	8.78 ± 0.01	8.6 ± 0.03	0.71036	0.8352	0.00571
TC0200001859.mm.1	Sqrdl	sulfide quinone reductase-like (yeast)	7.67 ± 0.05	7.47 ± 0.05	7.6 ± 0.03	7.55 ± 0.04	0.75111	0.00596	0.06017
TC1100002664.mm.1	Sqstm1	sequestosome 1	9.14 ± 0.06	8.99 ± 0.01	8.94 ± 0.03	8.9 ± 0.05	0.00916	0.11069	0.34519
TC0100003058.mm.1	Srgap2	SLIT-ROBO Rho GTPase activating protein 2	7.49 ± 0.04	7.34 ± 0.03	7.47 ± 0.03	7.32 ± 0.07	0.81284	0.00744	0.83093
TC0400001934.mm.1	Srm	spermidine synthase	8.02 ± 0.03	7.96 ± 0.02	7.84 ± 0.05	7.84 ± 0.04	0.00202	0.6626	0.62941
TC1200000458.mm.1	Srp54a	signal recognition particle 54A	10.51 ± 0.05	10.49 ± 0.06	10.32 ± 0.06	10.21 ± 0.08	0.00361	0.38715	0.35572
TC1200000460.mm.1	Srp54b	signal recognition particle 54B	10.56 ± 0.05	10.55 ± 0.06	10.38 ± 0.06	10.29 ± 0.07	0.00326	0.47862	0.38379
TC1200000462.mm.1	Srp54c	signal recognition particle 54C	10.19 ± 0.05	10.17 ± 0.06	10.03 ± 0.07	9.9 ± 0.08	0.00545	0.31892	0.33314
TC0500000734.mm.1	Srp72	signal recognition particle 72	9.06 ± 0.03	8.92 ± 0.03	8.83 ± 0.02	8.82 ± 0.09	0.00782	0.22896	0.32766
TC0X00003417.mm.1	Srpx	sushi-repeat-containing protein	8.38 ± 0.12	7.53 ± 0.04	8.04 ± 0.09	7.27 ± 0.17	0.05537	2.1E-05	0.92198
TC0500003439.mm.1	Srrt	serrate RNA effector molecule homolog (Arabidopsis)	7.84 ± 0.02	7.82 ± 0.03	7.74 ± 0.02	7.69 ± 0.05	0.00635	0.40833	0.61416
TC0Y00000240.mm.1	Sry	sex determining region of Chr Y	7.16 ± 0.05	7.46 ± 0.05	7.87 ± 0.12	7.91 ± 0.1	1.1E-05	0.07554	0.15941
TC1900000913.mm.1	Ssh3	slingshot homolog 3 (Drosophila)	7.57 ± 0.08	7.68 ± 0.05	7.84 ± 0.05	7.61 ± 0.03	0.08591	0.47396	0.00975
TC1500001920.mm.1	St13	suppression of tumorigenicity 13	9.7 ± 0.05	9.59 ± 0.06	9.47 ± 0.05	9.48 ± 0.05	0.00637	0.38042	0.27618
TC0700004076.mm.1	St5	suppression of tumorigenicity 5	8.93 ± 0.14	9.11 ± 0.05	9.32 ± 0.08	8.77 ± 0.14	0.68608	0.17138	0.00577
TC1100004124.mm.1	St6galnac2	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-a	6.71 ± 0.01	6.58 ± 0.04	6.74 ± 0.04	6.63 ± 0.03	0.17746	0.00199	0.80278
TC1400001671.mm.1	Stab1	stabilin 1	8.01 ± 0.05	7.87 ± 0.03	7.99 ± 0.03	7.81 ± 0.04	0.51809	0.00416	0.47378
TC0X00000933.mm.1	Stard8	START domain containing 8	6.91 ± 0.01	6.82 ± 0.04	6.92 ± 0.02	6.86 ± 0.01	0.17809	0.00636	0.64503
TC1100003790.mm.1	Stat3	signal transducer and activator of transcription 3	8.73 ± 0.06	8.58 ± 0.03	8.56 ± 0.02	8.43 ± 0.01	0.00376	0.00884	0.76592
TC1100002457.mm.1	Stc2	stanniocalcin 2	5.51 ± 0.01	5.62 ± 0.04	5.52 ± 0	5.49 ± 0.02	0.02732	0.0409	0.00301
TC0500001912.mm.1	Steap2	six transmembrane epithelial antigen of prostate 2	5.76 ± 0.04	5.75 ± 0.01	5.89 ± 0.04	5.69 ± 0.05	0.18265	0.05038	0.00875
TC0500000043.mm.1	Steap4	STEAP family member 4	10.05 ± 0.06	9.43 ± 0.12	9.78 ± 0.04	9.22 ± 0.16	0.04134	7.5E-05	0.8678
TC1900001031.mm.1	Stip1	stress-induced phosphoprotein 1	9.9 ± 0.13	9.72 ± 0.13	9.5 ± 0.07	9.39 ± 0.04	0.00831	0.32526	0.96223
TC0500002274.mm.1	Stk32b	serine/threonine kinase 32B	6.39 ± 0.08	6.52 ± 0.01	6.67 ± 0.05	6.55 ± 0.02	0.00825	0.67283	0.01995
TC0300000043.mm.1	Stmn2	stathmin-like 2	10 ± 0.59	8.83 ± 0.26	8.36 ± 0.06	9.91 ± 0.21	0.68878	0.43839	0.00772
TC1100004227.mm.1	Stra13	stimulated by retinoic acid 13	8.53 ± 0.04	8.66 ± 0.03	8.74 ± 0.05	8.75 ± 0.05	0.00424	0.15143	0.31507
TSUnmapped000000	Sts	steroid sulfatase	8.09 ± 0.01	8.19 ± 0.02	8.23 ± 0.02	8.24 ± 0.05	0.00823	0.06725	0.16498
TC0900003182.mm.1	Stt3b	STT3, subunit of the oligosaccharyltransferase complex, hom	10.38 ± 0.06	10.27 ± 0.07	10.18 ± 0.02	10.11 ± 0.05	0.0046	0.09828	0.63426
TC1000001761.mm.1	Stx11	syntaxin 11	6.13 ± 0.06	6.33 ± 0.03	6.4 ± 0.04	6.27 ± 0.05	0.07098	0.64583	0.00731
TC0200005164.mm.1	Sulf2	sulfatase 2	9.91 ± 0.04	9.65 ± 0.03	9.81 ± 0.03	9.48 ± 0.07	0.02383	4.4E-05	0.28428

Supplemental Table I

Annotations			Summary Statistics				2 way ANOVA p-values		
Probe Set ID	Symbol	Description	XY sh	XY Or	XX sh	XX Or	XY vs XX	Sh vs Or	Intrxn
TC0700004291.mm.1	Sult1a1	sulfotransferase family 1A, phenol-preferring, member 1	8.86 ± 0.11	8.67 ± 0.07	8.48 ± 0.06	8.38 ± 0.13	0.00813	0.24232	0.86279
TC0500002700.mm.1	Sult1e1	sulfotransferase family 1E, member 1	5.99 ± 0.27	3.31 ± 0.06	5.6 ± 0.34	3.27 ± 0.08	0.40277	8.4E-08	0.49178
TC0800003091.mm.1	Sult5a1	sulfotransferase family 5A, member 1	6.27 ± 0.04	5.77 ± 0.06	6.51 ± 0.04	5.91 ± 0.05	0.00066	3.4E-08	0.20653
TC1000003158.mm.1	Suox	sulfite oxidase	8.12 ± 0.08	8 ± 0.07	8.02 ± 0.07	8.26 ± 0.03	0.45386	0.64783	0.00842
TC0200003205.mm.1	Surf4	surfeit gene 4	9.83 ± 0.01	9.81 ± 0.02	9.76 ± 0.02	9.7 ± 0.02	0.00084	0.07835	0.17565
TC0400002733.mm.1	Svep1	sushi, von Willebrand factor type A, EGF and pentraxin doma	8.4 ± 0.06	8.17 ± 0.04	8.27 ± 0.08	7.93 ± 0.05	0.01563	0.00056	0.26428
TC0800000968.mm.1	Syce2	synaptonemal complex central element protein 2	6.28 ± 0.03	6.38 ± 0.02	6.33 ± 0.02	6.4 ± 0.03	0.25458	0.00578	0.58096
TC1000002458.mm.1	Syde1	synapse defective 1, Rho GTPase, homolog 1 (C. elegans)	8.16 ± 0.09	8.32 ± 0.03	8.39 ± 0.03	8.18 ± 0.06	0.44086	0.76083	0.00957
TC0600001275.mm.1	Syn2	synapsin II	8.27 ± 0.55	7.3 ± 0.29	6.6 ± 0.1	8.19 ± 0.2	0.45598	0.28641	0.00763
TC1000002828.mm.1	Syt1	synaptotagmin I	8.73 ± 0.83	7.19 ± 0.56	5.75 ± 0.28	8.61 ± 0.35	0.30753	0.21432	0.00468
TC1400000372.mm.1	Syt15	synaptotagmin XV	7.67 ± 0.12	8.02 ± 0.1	8.27 ± 0.11	7.9 ± 0.06	0.03775	0.99963	0.00443
TC1800001111.mm.1	Syt4	synaptotagmin IV	8.17 ± 0.79	6.72 ± 0.51	5.6 ± 0.13	7.98 ± 0.28	0.38229	0.28029	0.00717
TC0700001280.mm.1	Sytl2	synaptotagmin-like 2	5.65 ± 0.04	5.53 ± 0.06	5.87 ± 0.06	5.54 ± 0.08	0.06073	0.00404	0.09691
TC0X00000122.mm.1	Sytl5	synaptotagmin-like 5	8.15 ± 0.22	8.04 ± 0.06	8.97 ± 0.15	7.58 ± 0.34	0.36236	0.00603	0.00895
TC1000000199.mm.1	Taar7b	trace amine-associated receptor 7B	4.36 ± 0.06	4.75 ± 0.06	4.68 ± 0.04	4.66 ± 0.04	0.14883	0.01114	0.00555
TC0200002937.mm.1	Taf3	TAF3 RNA polymerase II, TATA box binding protein (TBP)-as	6.98 ± 0.04	7.11 ± 0.02	7.12 ± 0.03	7.05 ± 0.02	0.16657	0.26862	0.00443
TC1800000124.mm.1	Taf4b	TAF4B RNA polymerase II, TATA box binding protein (TBP)-a	6.15 ± 0.02	5.94 ± 0.06	5.96 ± 0.04	6.03 ± 0.03	0.26289	0.15143	0.00455
TC0500000591.mm.1	Tbc1d1	TBC1 domain family, member 1	7.84 ± 0.08	7.95 ± 0.04	8.01 ± 0.06	7.71 ± 0.09	0.79718	0.27711	0.00964
TC1900000907.mm.1	Tbc1d10c	TBC1 domain family, member 10c	5.66 ± 0.02	5.88 ± 0.02	5.76 ± 0.03	5.96 ± 0.1	0.08207	0.00099	0.75002
TC1000002894.mm.1	Tbc1d15	TBC1 domain family, member 15	7.52 ± 0.04	7.49 ± 0.05	7.39 ± 0.02	7.36 ± 0.05	0.00906	0.66213	0.93662
TC0500001576.mm.1	Tbl2	transducin (beta)-like 2	7.7 ± 0.02	7.66 ± 0.02	7.58 ± 0.04	7.57 ± 0.05	0.00561	0.48467	0.62672
TC0300000990.mm.1	Tbx15	T-box 15	5.19 ± 0.03	5.36 ± 0.04	5.38 ± 0.04	5.3 ± 0.03	0.08204	0.22153	0.00414
TC1000000894.mm.1	Tbxa2r	thromboxane A2 receptor	6.71 ± 0.05	6.94 ± 0.05	6.97 ± 0.06	6.84 ± 0.03	0.13653	0.40866	0.00375
TC1100001566.mm.1	Tcap	titin-cap	7.68 ± 0.14	8.09 ± 0.07	7.2 ± 0.08	7.88 ± 0.09	0.01415	8E-05	0.42007
TC0X00003007.mm.1	Tceal6	transcription elongation factor A (SII)-like 6	7.86 ± 0.13	8.08 ± 0.06	8.23 ± 0.12	7.76 ± 0.14	0.68362	0.39791	0.00918
TC0X00003021.mm.1	Tceal8	transcription elongation factor A (SII)-like 8	7.66 ± 0.04	7.7 ± 0.02	7.66 ± 0.01	7.55 ± 0.03	0.07631	0.46932	0.00923
TC0400003216.mm.1	Tceanc2	transcription elongation factor A (SII) N-terminal and central d	7.02 ± 0.02	7.04 ± 0.01	7.11 ± 0.01	7.04 ± 0.01	0.00311	0.36485	0.00492
TC1700001969.mm.1	Tcf19	transcription factor 19	6.03 ± 0.05	6.14 ± 0.02	6.22 ± 0.03	6.17 ± 0.04	0.00742	0.31447	0.02635
TC1100002715.mm.1	Tcf7	transcription factor 7, T cell specific	5.69 ± 0.05	6.41 ± 0.29	5.65 ± 0.08	6.33 ± 0.26	0.69674	0.00319	0.97754
TC1800001409.mm.1	Tcof1	Treacher Collins Franceschetti syndrome 1, homolog	7.02 ± 0.03	7.12 ± 0	7.17 ± 0.02	7.14 ± 0.02	0.0024	0.12964	0.02373
TC1300001519.mm.1	Tcrg-C2	T-cell receptor gamma, constant 2	4.3 ± 0.04	4.5 ± 0.05	4.6 ± 0.06	4.58 ± 0.08	0.00773	0.18894	0.10402
TC1300000140.mm.1	Tcrg-V6	T cell receptor gamma, variable 6	4.5 ± 0.03	4.61 ± 0.04	4.83 ± 0.04	4.85 ± 0.04	7.2E-06	0.16936	0.28673

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Annotations			Summary Statistics				2 way ANOVA p-values		
Probe Set ID	Symbol	Description	XY sh	XY Or	XX sh	XX Or	XY vs XX	Sh vs Or	Intrxn
TC0900003058.mm.1	Tcta	T cell leukemia translocation altered gene	7.47 ± 0.03	7.35 ± 0.02	7.48 ± 0.03	7.38 ± 0.04	0.35825	0.00573	0.96842
TC0300002218.mm.1	Tdo2	tryptophan 2,3-dioxygenase	5.29 ± 0.27	3.91 ± 0.18	4.44 ± 0.11	3.86 ± 0.06	0.09387	0.00053	0.1472
TC0100003316.mm.1	Tdrd5	tudor domain containing 5	4.11 ± 0.03	4.25 ± 0.05	4.14 ± 0.03	4.27 ± 0.06	0.52433	0.00613	0.8388
TC0700001651.mm.1	Tead1	TEA domain family member 1	8.08 ± 0.07	7.92 ± 0.03	8.04 ± 0.07	7.76 ± 0.06	0.23678	0.00767	0.19207
TC1500000731.mm.1	Tef	thyrotroph embryonic factor	7.12 ± 0.07	7.33 ± 0.07	6.36 ± 0.05	7.23 ± 0.05	3.9E-05	8E-07	0.00048
TC1000001661.mm.1	Tespa1	thymocyte expressed, positive selection associated 1	3.97 ± 0.07	4.36 ± 0.08	4.09 ± 0.05	4.32 ± 0.13	0.83089	0.00472	0.53105
TC1100003928.mm.1	Tex2	testis expressed gene 2	8.23 ± 0.05	8.02 ± 0.04	7.99 ± 0.04	8.11 ± 0.04	0.07641	0.23951	0.00178
TC0800000126.mm.1	Tfdp1	transcription factor Dp 1	8.44 ± 0.03	8.41 ± 0.04	8.34 ± 0.01	8.3 ± 0.04	0.00492	0.28548	0.94556
TC0600001890.mm.1	Tfec	transcription factor EC	4.73 ± 0.04	4.59 ± 0.03	4.7 ± 0.05	4.43 ± 0.04	0.049	0.00028	0.10123
TC1500000488.mm.1	Tg	thyroglobulin	5.5 ± 0.04	5.62 ± 0.03	5.83 ± 0.06	5.63 ± 0.01	0.00133	0.20979	0.0016
TC1200002103.mm.1	Tgfb3	transforming growth factor, beta 3	10.22 ± 0.12	10.13 ± 0.05	10.47 ± 0.12	9.7 ± 0.14	0.63405	0.00368	0.00584
TC0700004575.mm.1	Th	tyrosine hydroxylase	9.43 ± 0.87	7.72 ± 0.5	6.5 ± 0.3	9.23 ± 0.31	0.38218	0.29112	0.00498
TC0400004083.mm.1	Thap3	THAP domain containing, apoptosis associated protein 3	6.51 ± 0.02	6.64 ± 0	6.66 ± 0.03	6.66 ± 0.04	0.00273	0.01414	0.02562
TC0200001729.mm.1	Thbs1	thrombospondin 1	9.06 ± 0.04	8.9 ± 0.14	9.06 ± 0.04	8.4 ± 0.11	0.01657	0.00042	0.01006
TC1700001484.mm.1	Thbs2	thrombospondin 2	8.11 ± 0.11	8.54 ± 0.05	8.48 ± 0.09	8.27 ± 0.09	0.52293	0.18815	0.0031
TC0300000752.mm.1	Thbs3	thrombospondin 3	7.31 ± 0.06	7.24 ± 0.02	7.31 ± 0.05	7.03 ± 0.02	0.05116	0.00257	0.02325
TC0600002460.mm.1	Thnsl2	threonine synthase-like 2 (bacterial)	6.41 ± 0.01	6.47 ± 0.03	6.52 ± 0.01	6.48 ± 0.01	0.00107	0.55106	0.00317
TC1100001580.mm.1	Thra	thyroid hormone receptor alpha	8.7 ± 0.01	8.69 ± 0.03	8.99 ± 0.05	8.74 ± 0.06	0.00055	0.00661	0.007
TC1700002595.mm.1	Thumpd2	THUMP domain containing 2	5.78 ± 0.03	5.84 ± 0.03	5.85 ± 0.01	5.7 ± 0.02	0.08803	0.04851	0.00201
TC1500000177.mm.1	Tiaf2	TGF-beta1-induced anti-apoptotic factor 2	4.31 ± 0.09	4.42 ± 0.03	4.07 ± 0.09	4.06 ± 0.08	0.00176	0.55106	0.53265
TC1600002039.mm.1	Tiam1	T cell lymphoma invasion and metastasis 1	6.58 ± 0.03	6.73 ± 0.02	6.68 ± 0	6.77 ± 0.06	0.11708	0.00986	0.55139
TC1100000484.mm.1	Timd4	T cell immunoglobulin and mucin domain containing 4	6.22 ± 0.05	5.83 ± 0.08	6.21 ± 0.07	6.01 ± 0.03	0.15885	0.00019	0.12784
TC0X00000218.mm.1	Timp1	tissue inhibitor of metalloproteinase 1	7.74 ± 0.14	7.38 ± 0.14	7.67 ± 0.08	6.87 ± 0.06	0.05175	0.00049	0.05757
TC0600002948.mm.1	Timp4	tissue inhibitor of metalloproteinase 4	8.28 ± 0.14	7.71 ± 0.09	7.94 ± 0.05	7.35 ± 0.15	0.02471	0.00072	0.6479
TC1900001273.mm.1	Tjp2	tight junction protein 2	7.71 ± 0.04	7.83 ± 0.03	7.82 ± 0.02	7.75 ± 0.01	0.49583	0.27627	0.00488
TC0X00001069.mm.1	Tlr13	toll-like receptor 13	5.09 ± 0.09	4.67 ± 0.11	4.7 ± 0.09	4.3 ± 0.04	0.00166	0.00081	0.82909
TC0100001754.mm.1	Tlr5	toll-like receptor 5	6.6 ± 0.03	6.28 ± 0.05	6.64 ± 0.05	6.37 ± 0.1	0.36927	0.0002	0.54994
TC0X00003360.mm.1	Tlr7	toll-like receptor 7	6.18 ± 0.05	5.76 ± 0.07	5.95 ± 0.06	5.66 ± 0.18	0.16154	0.00446	0.62085
TC0X00003359.mm.1	Tlr8	toll-like receptor 8	6.06 ± 0.14	5.34 ± 0.05	5.65 ± 0.09	5.14 ± 0.14	0.04776	0.00032	0.64709
TC0300002023.mm.1	Tm4sf1	transmembrane 4 superfamily member 1	10.21 ± 0.1	10.35 ± 0.08	10.66 ± 0.06	10.11 ± 0.14	0.25445	0.07861	0.00356
TC0700001178.mm.1	Tm6sf1	transmembrane 6 superfamily member 1	7.75 ± 0.04	7.74 ± 0.02	7.77 ± 0.02	7.55 ± 0.05	0.03649	0.00651	0.00764
TC0900003074.mm.1	Tma7	translational machinery associated 7 homolog (S. cerevisiae)	9.01 ± 0.04	8.83 ± 0.03	8.94 ± 0.04	8.86 ± 0.04	0.65473	0.00367	0.19457

Supplemental Table I

Annotations			Summary Statistics				2 way ANOVA p-values		
Probe Set ID	Symbol	Description	XY sh	XY Or	XX sh	XX Or	XY vs XX	Sh vs Or	Intrxn
TC1500001013.mm.1	Tmbim6	transmembrane BAX inhibitor motif containing 6	9.05 ± 0.05	8.97 ± 0.05	8.97 ± 0.04	9.1 ± 0.01	0.95268	0.97451	0.00958
TC0900001874.mm.1	Tmed1	transmembrane emp24 domain containing 1	7.25 ± 0.03	7.4 ± 0.02	7.44 ± 0.03	7.36 ± 0.02	0.03067	0.30318	0.00138
TC0500002940.mm.1	Tmed5	transmembrane emp24 protein transport domain containing 5	7.52 ± 0.12	7.37 ± 0.09	7.18 ± 0.16	7.81 ± 0.08	0.96713	0.16408	0.00271
TC1200002117.mm.1	Tmed8	transmembrane emp24 domain containing 8	7.53 ± 0.05	7.5 ± 0.03	7.37 ± 0.02	7.32 ± 0.02	0.00112	0.51075	0.38401
TC0400000535.mm.1	Tmeff1	transmembrane protein with EGF-like and two follistatin-like d	7.34 ± 0.24	6.83 ± 0.12	6.63 ± 0.12	7.19 ± 0.05	0.36694	0.78933	0.00807
TC0100000364.mm.1	Tmeff2	transmembrane protein with EGF-like and two follistatin-like d	7.22 ± 0.12	6.8 ± 0.06	7.18 ± 0.07	6.82 ± 0.11	0.75182	0.00408	0.87524
TC1100001395.mm.1	Tmem100	transmembrane protein 100	8.06 ± 0.1	7.52 ± 0.12	8.04 ± 0.16	7.42 ± 0.1	0.64081	0.0004	0.70036
TC1500000967.mm.1	Tmem106c	transmembrane protein 106C	7.63 ± 0.04	7.66 ± 0.04	7.77 ± 0.02	7.77 ± 0.03	0.00424	0.79192	0.84992
TC0500003404.mm.1	Tmem120a	transmembrane protein 120A	8.31 ± 0.1	8.09 ± 0.09	7.85 ± 0.11	8.28 ± 0.05	0.08812	0.47945	0.00161
TC0300000656.mm.1	Tmem154	transmembrane protein 154	5.92 ± 0.03	5.95 ± 0	6.04 ± 0.05	5.86 ± 0.04	0.69989	0.04972	0.00669
TC1300002506.mm.1	Tmem171	transmembrane protein 171	4.92 ± 0.05	5.19 ± 0.04	4.99 ± 0.07	5.24 ± 0.12	0.29971	0.00236	0.80062
TC0100003108.mm.1	Tmem183a	transmembrane protein 183A	8.07 ± 0.05	7.88 ± 0.04	7.73 ± 0.04	7.83 ± 0.03	0.0005	0.27738	0.0037
TC0200005516.mm.1	Tmem189	transmembrane protein 189	8.33 ± 0.05	8.21 ± 0.03	8.12 ± 0.02	8.17 ± 0.01	0.00707	0.58737	0.07916
TC1200001337.mm.1	Tmem196	transmembrane protein 196	5.05 ± 0.02	5.01 ± 0.03	5.41 ± 0.13	5.08 ± 0.04	0.00809	0.01526	0.05841
TC0200000407.mm.1	Tmem210	transmembrane protein 210	5.75 ± 0.04	6.09 ± 0.06	5.88 ± 0.09	6.14 ± 0.1	0.23523	0.0012	0.61007
TC1900001105.mm.1	Tmem216	transmembrane protein 216	5.45 ± 0.03	5.38 ± 0.02	5.42 ± 0.01	5.35 ± 0.03	0.17096	0.00801	0.95738
TC1200001974.mm.1	Tmem229b	transmembrane protein 229B	6.26 ± 0.05	6.33 ± 0.02	6.18 ± 0.03	6.13 ± 0.04	0.00564	0.42563	0.04708
TC1000000653.mm.1	Tmem26	transmembrane protein 26	5.74 ± 0.05	5.88 ± 0.01	5.93 ± 0.07	5.79 ± 0.03	0.18854	0.80041	0.00348
TC0X00003159.mm.1	Tmem29	transmembrane protein 29	4.81 ± 0.03	4.85 ± 0.02	4.98 ± 0.04	4.87 ± 0	0.00866	0.18624	0.02863
TC0300002838.mm.1	Tmem56	transmembrane protein 56	5.7 ± 0.09	5.51 ± 0.08	5.45 ± 0.07	5.76 ± 0.06	0.88741	0.57139	0.005
TC0400003747.mm.1	Tmem57	transmembrane protein 57	8.5 ± 0.02	8.59 ± 0.01	8.38 ± 0.03	8.5 ± 0.05	0.00453	0.00215	0.77583
TC1700002155.mm.1	Tmem63b	transmembrane protein 63b	7.8 ± 0.04	7.72 ± 0.02	7.69 ± 0.03	7.88 ± 0.04	0.563	0.16091	0.00096
TC0200003210.mm.1	Tmem8c	transmembrane protein 8C	4.28 ± 0.02	4.56 ± 0.04	4.45 ± 0.07	4.55 ± 0.09	0.1948	0.00582	0.15935
TC1100001209.mm.1	Tmem98	transmembrane protein 98	7.62 ± 0.12	7.83 ± 0.02	7.89 ± 0.08	7.62 ± 0.04	0.54555	0.89343	0.00842
TC1400002757.mm.1	Tmtc4	transmembrane and tetratricopeptide repeat containing 4	6.14 ± 0.02	6.22 ± 0.01	6.27 ± 0.03	6.21 ± 0	0.02252	0.85371	0.00482
TC1100001686.mm.1	Tmub2	transmembrane and ubiquitin-like domain containing 2	7 ± 0.03	6.89 ± 0.01	6.97 ± 0	7 ± 0.01	0.05634	0.11578	0.00986
TC1200001237.mm.1	Tnfaip2	tumor necrosis factor, alpha-induced protein 2	6.7 ± 0.04	6.71 ± 0.04	6.76 ± 0.02	6.48 ± 0.03	0.03784	0.00247	0.00102
TC1100000774.mm.1	Tnfrsf13b	tumor necrosis factor receptor superfamily, member 13b	5.94 ± 0.01	6.14 ± 0.03	6.05 ± 0.04	6.18 ± 0.08	0.10246	0.00263	0.39873
TC1500001939.mm.1	Tnfrsf13c	tumor necrosis factor receptor superfamily, member 13c	6.08 ± 0.08	6.61 ± 0.09	6.44 ± 0.14	6.76 ± 0.17	0.09925	0.0075	0.62755
TC0600001459.mm.1	Tnfrsf1a	tumor necrosis factor receptor superfamily, member 1a	8.63 ± 0.04	8.49 ± 0.04	8.6 ± 0.01	8.47 ± 0.03	0.40759	0.00159	0.64565
TC0400003958.mm.1	Tnfrsf8	tumor necrosis factor receptor superfamily, member 8	5.83 ± 0.02	5.97 ± 0.03	5.9 ± 0.03	6.04 ± 0.09	0.15494	0.00845	0.98819
TC1600000448.mm.1	Tnk2	tyrosine kinase, non-receptor, 2	7.9 ± 0.03	7.97 ± 0.02	8.09 ± 0.03	8.02 ± 0.01	0.00043	0.8164	0.0131

Supplemental Table I

Annotations			Summary Statistics				2 way ANOVA p-values		
Probe Set ID	Symbol	Description	XY sh	XY Or	XX sh	XX Or	XY vs XX	Sh vs Or	Intrxn
TC0100001447.mm.1	Tnr	tenascin R	7.34 ± 0.19	6.67 ± 0.07	7.82 ± 0.3	6.96 ± 0.15	0.04774	0.00301	0.49406
TC1500001931.mm.1	Tob2	transducer of ERBB2, 2	6.15 ± 0.09	6.4 ± 0.02	6.08 ± 0.05	6.39 ± 0.09	0.49957	0.00242	0.58121
TC0400002436.mm.1	Topors	topoisomerase I binding, arginine/serine-rich	7.58 ± 0.03	7.76 ± 0.05	7.67 ± 0.02	7.61 ± 0.02	0.406	0.10023	0.0023
TC0200003132.mm.1	Tor4a	torsin family 4, member A	6.18 ± 0.02	6.18 ± 0.06	6.41 ± 0.04	6.25 ± 0.02	0.00104	0.06118	0.04408
TC0800002674.mm.1	Tox3	TOX high mobility group box family member 3	5.06 ± 0.02	5.16 ± 0.03	5.05 ± 0.02	5.14 ± 0.04	0.54032	0.00893	0.88538
TC0400002529.mm.1	Tpm2	tropomyosin 2, beta	10.19 ± 0.1	10.34 ± 0.05	10.41 ± 0.07	10.1 ± 0.08	0.91536	0.45841	0.00803
TC0800000814.mm.1	Tpm4	tropomyosin 4	10.35 ± 0.06	10.25 ± 0.05	10.24 ± 0.02	10.01 ± 0.04	0.00583	0.00984	0.09358
TC1300000893.mm.1	Tppp	tubulin polymerization promoting protein	7.26 ± 0.12	6.99 ± 0.05	6.81 ± 0.12	7.3 ± 0.13	0.44816	0.41915	0.00392
TC0500001522.mm.1	Tpst1	protein-tyrosine sulfotransferase 1	7.35 ± 0.05	7.44 ± 0.02	7.48 ± 0.03	7.35 ± 0.04	0.43983	0.72916	0.00665
TC0600002240.mm.1	Tra2a	transformer 2 alpha homolog (Drosophila)	8.03 ± 0.03	8.12 ± 0.07	7.81 ± 0.1	7.9 ± 0.07	0.00846	0.17861	0.92499
TC0400001209.mm.1	Trabd2b	TraB domain containing 2B	8.19 ± 0.1	8.46 ± 0.04	8.65 ± 0.1	8.27 ± 0.14	0.23606	0.62191	0.00901
TC0200003157.mm.1	Traf2	TNF receptor-associated factor 2	7.17 ± 0.05	7.28 ± 0.01	7.4 ± 0.05	7.22 ± 0.03	0.09386	0.36484	0.00554
TC0100003835.mm.1	Traf3ip3	TRAF3 interacting protein 3	4.48 ± 0.03	4.68 ± 0.02	4.54 ± 0.04	4.65 ± 0.06	0.95666	0.00165	0.33714
TC1400000737.mm.1	Traj8	T cell receptor alpha joining 8	5.32 ± 0.12	5.81 ± 0.09	5.48 ± 0.03	5.93 ± 0.19	0.29045	0.0026	0.93267
TC1400000613.mm.1	Trav1	T cell receptor alpha variable 1	7.12 ± 0.01	7.32 ± 0.03	7.25 ± 0.03	7.42 ± 0.09	0.02589	0.00125	0.6664
TC1400000700.mm.1	Trav12-1	Trav12-1 T cell receptor alpha variable 12-1	5.21 ± 0.08	5.53 ± 0.05	5.35 ± 0.13	5.71 ± 0.11	0.16322	0.00629	0.67642
TC1400000702.mm.1	Trav12-2	T cell receptor alpha variable 12-2	4.5 ± 0.05	4.82 ± 0.07	4.55 ± 0.07	4.84 ± 0.17	0.82281	0.00912	0.94085
TC1400000646.mm.1	Trav12d-3	T cell receptor alpha variable 12D-3	4.99 ± 0.07	5.49 ± 0.06	5.06 ± 0.07	5.2 ± 0.06	0.07586	0.00087	0.03964
TC1400000677.mm.1	Trav12n-3	T cell receptor alpha variable 12N-3	4.98 ± 0.1	5.48 ± 0.06	5.03 ± 0.07	5.2 ± 0.06	0.09301	0.00231	0.12194
TC1400002817.mm.1	Trav13-3	T cell receptor alpha variable 13-3	6.4 ± 0.02	6.56 ± 0.04	6.44 ± 0.05	6.56 ± 0.05	0.46577	0.00381	0.58331
TC1400000635.mm.1	Trav13d-1	T cell receptor alpha variable 13D-1	6.46 ± 0.03	6.68 ± 0.05	6.52 ± 0.06	6.72 ± 0.08	0.38656	0.00213	0.84523
TC1400000656.mm.1	Trav13d-4	T cell receptor alpha variable 13D-4	5.54 ± 0.08	5.92 ± 0.03	5.51 ± 0.12	5.69 ± 0.07	0.06756	0.00769	0.42193
TC1400000665.mm.1	Trav13n-1	Trav13n-1 T cell receptor alpha variable 13N-1	5.99 ± 0.06	6.21 ± 0.05	5.99 ± 0.06	6.19 ± 0.09	0.83689	0.00407	0.68841
TC1400002802.mm.1	Trav14d-2	Trav14d-2 T cell receptor alpha variable 14D-2	5.04 ± 0.03	5.38 ± 0.09	5.18 ± 0.05	5.51 ± 0.14	0.12009	0.00116	0.91265
TC1400002820.mm.1	Trav14n-2	Trav14n-2 T cell receptor alpha variable 14N-2	5.04 ± 0.03	5.38 ± 0.09	5.18 ± 0.05	5.51 ± 0.14	0.12009	0.00116	0.91265
TC1400002830.mm.1	Trav15-1-dv6-1	Trav15-1-dv6-1 T cell receptor alpha variable 15-1-DV6-1	6.44 ± 0.04	6.57 ± 0.05	6.48 ± 0.04	6.64 ± 0.04	0.21111	0.00509	0.7817
TC1400000622.mm.1	Trav4d-2	T cell receptor alpha variable 4D-2	6.86 ± 0.04	7.09 ± 0.04	6.95 ± 0.06	7.09 ± 0.11	0.38554	0.00806	0.35649
TC1400000684.mm.1	Trav6n-7	T cell receptor alpha variable 6N-7	4.19 ± 0.02	4.4 ± 0.06	4.21 ± 0.05	4.42 ± 0.1	0.75974	0.00405	0.92902
TC1400000705.mm.1	Trav9-4	T cell receptor alpha variable 9-4	4.33 ± 0.05	4.71 ± 0.07	4.6 ± 0.1	4.8 ± 0.11	0.04484	0.00342	0.25547
TC0600003496.mm.1	Trbd1	T cell receptor beta, D region 1	5.27 ± 0.05	5.93 ± 0.18	5.35 ± 0.07	5.87 ± 0.21	0.92651	0.00102	0.71154
TC0600000417.mm.1	Trbv1	T cell receptor beta, variable 1	5.12 ± 0.07	5.47 ± 0.05	5.23 ± 0.09	5.43 ± 0.07	0.7253	0.00307	0.41938
TC0600000423.mm.1	Trbv12-1	T cell receptor beta, variable 12-1	4.2 ± 0.02	4.64 ± 0.1	4.24 ± 0.07	4.5 ± 0.13	0.5315	0.00119	0.31637

Supplemental Table I

Annotations			Summary Statistics				2 way ANOVA p-values		
Probe Set ID	Symbol	Description	XY sh	XY Or	XX sh	XX Or	XY vs XX	Sh vs Or	Intrxn
TC0600003497.mm.1	Trbv12-2	T cell receptor beta, variable 12-2	5.08 ± 0.08	5.42 ± 0.07	4.93 ± 0.11	5.45 ± 0.18	0.56385	0.00238	0.40879
TC0600003493.mm.1	Trbv13-1	T cell receptor beta, variable 13-1	4.39 ± 0.11	4.84 ± 0.07	4.5 ± 0.08	4.82 ± 0.2	0.71276	0.0085	0.5598
TC0600000426.mm.1	Trbv14	T cell receptor beta, variable 14	5.36 ± 0.12	5.88 ± 0.02	5.6 ± 0.14	5.87 ± 0.1	0.44738	0.00518	0.39498
TC0600000427.mm.1	Trbv15	T cell receptor beta, variable 15	4.47 ± 0.09	4.71 ± 0.17	4.41 ± 0.06	5.01 ± 0.13	0.4039	0.00516	0.11782
TC0600000428.mm.1	Trbv16	T cell receptor beta, variable 16	4.44 ± 0.06	4.89 ± 0.09	4.65 ± 0.06	4.78 ± 0.07	0.78405	0.00251	0.0874
TC0600000419.mm.1	Trbv2	T cell receptor beta, variable 2	5.18 ± 0.04	5.67 ± 0.12	5.25 ± 0.09	5.52 ± 0.12	0.53017	0.00221	0.33911
TC0600000433.mm.1	Trbv24	Trbv24 T cell receptor beta, variable 24	4.99 ± 0.07	5.3 ± 0.05	5.16 ± 0.07	5.3 ± 0.06	0.27933	0.00577	0.2584
TC0600002157.mm.1	Trbv31	T cell receptor beta, variable 31	4.98 ± 0.07	5.43 ± 0.05	5.05 ± 0.08	5.39 ± 0.15	0.86448	0.00102	0.56734
TC1400000715.mm.1	Trdv4	T cell receptor delta variable 4	4.11 ± 0.03	4.28 ± 0.04	4.4 ± 0.06	4.24 ± 0.04	0.01965	0.85083	0.0031
TC1700000933.mm.1	Trem3	triggering receptor expressed on myeloid cells 3	4.78 ± 0.03	4.94 ± 0.02	4.81 ± 0.04	4.91 ± 0.05	0.78108	0.00379	0.56466
TC1700000935.mm.1	Treml2	triggering receptor expressed on myeloid cells-like 2	5.11 ± 0.05	5.37 ± 0.03	5.29 ± 0.05	5.44 ± 0.06	0.02907	0.001	0.33725
TC1300002762.mm.1	Trgj1	T cell receptor gamma joining 1	5.5 ± 0.08	5.71 ± 0.09	6.08 ± 0.1	6 ± 0.24	0.00773	0.64002	0.29433
TC0600002305.mm.1	Tril	TLR4 interactor with leucine-rich repeats	6.91 ± 0.13	6.45 ± 0.04	6.99 ± 0.08	6.7 ± 0.16	0.19268	0.00718	0.48947
TC0700000155.mm.1	Trim28	tripartite motif-containing 28	8.05 ± 0.04	8.15 ± 0.01	8.13 ± 0.03	8.01 ± 0.05	0.58584	0.84252	0.00754
TC0200004213.mm.1	Trim44	tripartite motif-containing 44	9.1 ± 0.02	9 ± 0.02	9.09 ± 0.01	9.03 ± 0.03	0.71829	0.00378	0.40327
TC1100004301.mm.1	Trim47	tripartite motif-containing 47	7.66 ± 0.08	7.85 ± 0.04	7.86 ± 0.03	7.76 ± 0.01	0.22577	0.2776	0.00908
TC0500003433.mm.1	Trim56	tripartite motif-containing 56	7.62 ± 0.03	7.76 ± 0.03	7.73 ± 0.02	7.63 ± 0.06	0.88182	0.56125	0.00397
TC1200001243.mm.1	Trmt61a	tRNA methyltransferase 61A	7.28 ± 0.02	7.36 ± 0.03	7.34 ± 0.02	7.27 ± 0.02	0.61729	0.80578	0.00795
TC0200001448.mm.1	Trp53i11	transformation related protein 53 inducible protein 11	8.35 ± 0.11	8.61 ± 0.05	8.82 ± 0.04	8.89 ± 0.04	0.00056	0.1052	0.41474
TC0200002574.mm.1	Trp53rk	transformation related protein 53 regulating kinase	5.72 ± 0.02	5.88 ± 0.03	5.78 ± 0.02	5.89 ± 0.08	0.36851	0.005	0.50608
TC1500001491.mm.1	Trps1	trichorhinophalangeal syndrome I (human)	6.65 ± 0.04	6.61 ± 0.02	6.7 ± 0.03	6.56 ± 0.04	0.7033	0.0091	0.28315
TC0X00003075.mm.1	Tsc22d3	TSC22 domain family, member 3	7.41 ± 0.05	7.44 ± 0.12	6.97 ± 0.04	7.23 ± 0.06	0.00101	0.03642	0.22551
TC0700000018.mm.1	Tsen34	tRNA splicing endonuclease 34 homolog (S. cerevisiae)	7.12 ± 0.02	7.18 ± 0	7.23 ± 0.02	7.22 ± 0.03	0.0038	0.23886	0.16027
TC1800001700.mm.1	Tshz1	teashirt zinc finger family member 1	8.29 ± 0.05	8.39 ± 0.04	8.47 ± 0.05	8.21 ± 0.05	0.99243	0.13651	0.00203
TC0200002632.mm.1	Tshz2	teashirt zinc finger family member 2	8.73 ± 0.05	8.43 ± 0.09	8.79 ± 0.04	8.64 ± 0.09	0.0767	0.00529	0.29843
TC0X00003398.mm.1	Tsix	X (inactive)-specific transcript, antisense	3.92 ± 0.04	4.07 ± 0.05	4.71 ± 0.05	4.76 ± 0.12	9.1E-08	0.24097	0.61976
TC0600001500.mm.1	Tspan11	tetraspanin 11	8.06 ± 0.13	7.9 ± 0.02	8.17 ± 0.07	7.74 ± 0.02	0.98641	0.00652	0.07524
TC1000003096.mm.1	Tspan31	tetraspanin 31	10.12 ± 0.04	9.99 ± 0.04	9.94 ± 0.02	9.91 ± 0.05	0.00602	0.09362	0.34247
TC0700002056.mm.1	Tspan4	tetraspanin 4	8.02 ± 0.08	8.32 ± 0.07	7.8 ± 0.01	8.21 ± 0.02	0.04631	3.3E-05	0.60286
TC1000001333.mm.1	Tspan8	tetraspanin 8	5.99 ± 0.62	4.85 ± 0.3	4.12 ± 0.03	5.9 ± 0.37	0.48717	0.36018	0.00815
TC0600003185.mm.1	Tspan9	tetraspanin 9	8.16 ± 0.1	8.04 ± 0.04	8.35 ± 0.06	7.81 ± 0.05	0.93495	0.00142	0.00924
TC1600000227.mm.1	Tssk1	testis-specific serine kinase 1	3.78 ± 0.08	4.42 ± 0.04	4.18 ± 0.17	4.35 ± 0.11	0.18534	0.00285	0.06248

Supplemental Table I

Annotations			Summary Statistics				2 way ANOVA p-values		
Probe Set ID	Symbol	Description	XY sh	XY Or	XX sh	XX Or	XY vs XX	Sh vs Or	Intrxn
TC0200000499.mm.1	Ttf1	transcription termination factor, RNA polymerase I	6.17 ± 0.02	6.23 ± 0.02	6.24 ± 0.02	6.17 ± 0.02	0.81686	0.78441	0.00423
TC0100002604.mm.1	Tuba4a	tubulin, alpha 4A	7.94 ± 0.36	7.12 ± 0.12	6.8 ± 0.11	7.67 ± 0.15	0.30149	0.81885	0.00549
TC0800001522.mm.1	Tubb3	tubulin, beta 3 class III	8.92 ± 0.68	7.69 ± 0.27	6.81 ± 0.16	8.76 ± 0.23	0.40252	0.29206	0.00627
TC1000000324.mm.1	Tube1	epsilon-tubulin 1	4.37 ± 0.03	4.57 ± 0.05	4.41 ± 0.04	4.56 ± 0.05	0.81777	0.00092	0.57254
TC0900001374.mm.1	Tusc2	tumor suppressor candidate 2	7.66 ± 0.03	7.53 ± 0.02	7.49 ± 0.06	7.7 ± 0.07	0.92442	0.44547	0.00293
TC0500002579.mm.1	Txk	TXK tyrosine kinase	4.29 ± 0.03	4.43 ± 0.02	4.3 ± 0.05	4.44 ± 0.04	0.66635	0.00212	0.82181
TC0X00003308.mm.1	Txlng	taxilin gamma	6.55 ± 0.09	6.3 ± 0.08	6.17 ± 0.1	6.39 ± 0.02	0.04865	0.61778	0.00618
TC0800001297.mm.1	Txnl4b	thioredoxin-like 4B	6.82 ± 0.08	6.67 ± 0.07	6.74 ± 0.07	6.96 ± 0.03	0.31704	0.949	0.0087
TC0100003507.mm.1	Uap1	UDP-N-acetylglucosamine pyrophosphorylase 1	8.03 ± 0.06	7.71 ± 0.07	7.66 ± 0.03	7.62 ± 0.04	0.00124	0.00711	0.02518
TC1700000531.mm.1	Ubash3a	ubiquitin associated and SH3 domain containing, A	5.28 ± 0.03	5.51 ± 0.05	5.34 ± 0.05	5.51 ± 0.07	0.57161	0.0017	0.56844
TC0500003273.mm.1	Ubc	ubiquitin C	12.9 ± 0.02	12.92 ± 0.01	12.97 ± 0.02	13 ± 0.01	0.00132	0.16003	0.59616
TC1100002706.mm.1	Ube2b	ubiquitin-conjugating enzyme E2B	7.54 ± 0.04	7.49 ± 0.03	7.35 ± 0.04	7.45 ± 0.03	0.00566	0.6387	0.0302
TC0700003365.mm.1	Ube2nl	ubiquitin-conjugating enzyme E2N-like	7.64 ± 0.03	7.57 ± 0.08	7.49 ± 0.01	7.37 ± 0.06	0.00744	0.12172	0.50136
TC0400000358.mm.1	Ube2r2	ubiquitin-conjugating enzyme E2R 2	8.76 ± 0.03	8.7 ± 0.02	8.79 ± 0.01	8.68 ± 0.03	0.90711	0.00593	0.34289
TC0900002186.mm.1	Ube4a	ubiquitination factor E4A, UFD2 homolog (S. cerevisiae)	8 ± 0.05	7.81 ± 0.03	7.76 ± 0.06	7.87 ± 0.03	0.04049	0.27555	0.00408
TC0400004039.mm.1	Ube4b	ubiquitination factor E4B, UFD2 homolog (S. cerevisiae)	8.78 ± 0.02	8.71 ± 0.01	8.68 ± 0.03	8.73 ± 0.02	0.03608	0.65774	0.00798
TC0700001749.mm.1	Ubfd1	ubiquitin family domain containing 1	7.14 ± 0.03	7.09 ± 0.02	7.03 ± 0.02	7 ± 0.04	0.00549	0.29046	0.94724
TC1700002199.mm.1	Ubr2	ubiquitin protein ligase E3 component n-recognin 2	8.55 ± 0.03	8.58 ± 0.01	8.46 ± 0.03	8.48 ± 0.04	0.00749	0.40909	0.89421
TC0500002174.mm.1	Ucn	urocortin	6.03 ± 0.02	6.35 ± 0.08	6.16 ± 0.08	6.33 ± 0.12	0.56961	0.00926	0.41032
TC1000001089.mm.1	Uhrf1bp1l	UHRF1 (ICBP90) binding protein 1-like	8.85 ± 0.08	8.68 ± 0.02	8.56 ± 0.03	8.41 ± 0.06	0.00067	0.03758	0.864
TC1100001158.mm.1	Unc119	unc-119 homolog (C. elegans)	6.95 ± 0.05	7.09 ± 0.03	7.19 ± 0.01	7.2 ± 0.05	0.0015	0.12689	0.20099
TC0500003089.mm.1	Unc119b	unc-119 homolog B (C. elegans)	7.81 ± 0.04	7.83 ± 0.02	8.06 ± 0.04	7.83 ± 0.03	0.00391	0.00454	0.00397
TC0800000132.mm.1	Upf3a	UPF3 regulator of nonsense transcripts homolog A (yeast)	7.24 ± 0.01	7.34 ± 0.02	7.34 ± 0.03	7.29 ± 0.02	0.48317	0.3637	0.00609
TC0800000783.mm.1	Use1	unconventional SNARE in the ER 1 homolog (S. cerevisiae)	7.39 ± 0.03	7.51 ± 0.01	7.54 ± 0.01	7.54 ± 0.02	0.0019	0.01974	0.02739
TC0700001492.mm.1	Usp17lc	ubiquitin specific peptidase 17-like C	4.37 ± 0.08	4.54 ± 0.06	4.45 ± 0.03	4.72 ± 0.11	0.06597	0.00652	0.75069
TC0900000497.mm.1	Usp2	ubiquitin specific peptidase 2	7.04 ± 0.04	7.16 ± 0.06	6.87 ± 0.03	7.12 ± 0.09	0.08006	0.00999	0.29627
TC0Y00000233.mm.1	Uty	ubiquitously transcribed tetratricopeptide repeat gene, Y chro	6.25 ± 0.05	6.07 ± 0.07	3.97 ± 0.01	3.92 ± 0.01	2.2E-16	0.0121	0.09928
TC0700002474.mm.1	Vasp	vasodilator-stimulated phosphoprotein	7.8 ± 0.07	7.98 ± 0.02	8 ± 0.05	7.84 ± 0	0.49724	0.85295	0.00238
TC0800001360.mm.1	Vat1l	vesicle amine transport protein 1 homolog-like (T. californica)	8.08 ± 0.63	6.66 ± 0.27	6.14 ± 0.15	7.67 ± 0.24	0.43828	0.68113	0.00717
TC0600000935.mm.1	Vax2	ventral anterior homeobox containing gene 2	6.27 ± 0.02	6.45 ± 0.05	6.35 ± 0.05	6.46 ± 0.06	0.39409	0.00912	0.5042
TC0600000933.mm.1	Vax2os1_2	Vax2os1 conserved region 2	5.66 ± 0.05	5.85 ± 0.03	5.69 ± 0.06	5.95 ± 0.11	0.31274	0.0047	0.71275
TC0300002802.mm.1	Vcam1	vascular cell adhesion molecule 1	9.11 ± 0.1	8.98 ± 0.08	8.93 ± 0.04	8.56 ± 0.08	0.00834	0.02276	0.07729

Supplemental Table I

Annotations			Summary Statistics				2 way ANOVA p-values		
Probe Set ID	Symbol	Description	XY sh	XY Or	XX sh	XX Or	XY vs XX	Sh vs Or	Intrxn
TC1300002392.mm.1	Vcan	versican	7.82 ± 0.15	7.59 ± 0.03	7.73 ± 0.12	7.23 ± 0.06	0.0956	0.00755	0.16251
TC1600000797.mm.1	Vgll3	vestigial like 3 (Drosophila)	8.59 ± 0.14	8.53 ± 0.02	9.06 ± 0.1	8.3 ± 0.12	0.19545	0.00433	0.00396
TC1700001187.mm.1	Vit	vitrin	8.03 ± 0.09	7.67 ± 0.06	8.11 ± 0.06	7.71 ± 0.1	0.31148	0.00057	0.59644
TC1700002334.mm.1	Vmac	vimentin-type intermediate filament associated coiled-coil pro	6.59 ± 0.03	6.71 ± 0.02	6.81 ± 0.04	6.78 ± 0.04	0.00059	0.19059	0.03177
TC1100003450.mm.1	Vmp1	vacuole membrane protein 1	6.95 ± 0.05	6.76 ± 0.07	6.68 ± 0.04	6.66 ± 0.03	0.00157	0.02746	0.05515
TC1000000193.mm.1	Vnn1	vanin 1	5.81 ± 0.12	5.56 ± 0.03	5.14 ± 0.03	5.54 ± 0.07	0.00184	0.19092	0.00332
TC0500001389.mm.1	Vps29	vacuolar protein sorting 29 (S. pombe)	7.04 ± 0.02	6.96 ± 0.04	6.97 ± 0.01	6.87 ± 0.03	0.00908	0.00583	0.58116
TC0500003236.mm.1	Vps33a	vacuolar protein sorting 33A (yeast)	8.33 ± 0.05	8.22 ± 0.06	8.19 ± 0.05	8.36 ± 0.04	0.85339	0.81812	0.00966
TC0800000475.mm.1	Vps37a	vacuolar protein sorting 37A (yeast)	8.37 ± 0.04	8.25 ± 0.02	8.47 ± 0.05	8.21 ± 0.11	0.70199	0.00757	0.32633
TC0500003245.mm.1	Vps37b	vacuolar protein sorting 37B (yeast)	7.38 ± 0.08	7.47 ± 0.09	7.74 ± 0.02	7.42 ± 0.01	0.03137	0.13349	0.00801
TC1700000604.mm.1	Vps52	vacuolar protein sorting 52 (yeast)	7.32 ± 0	7.31 ± 0.01	7.37 ± 0.02	7.31 ± 0.01	0.03878	0.00321	0.07561
TC0700000720.mm.1	Vstm2b	V-set and transmembrane domain containing 2B	6.84 ± 0.08	7.23 ± 0.03	7.22 ± 0.12	7.01 ± 0.03	0.37643	0.3274	0.00231
TC1200000074.mm.1	Wdr35	WD repeat domain 35	7.28 ± 0.04	7.19 ± 0.03	7.38 ± 0.07	7.05 ± 0.1	0.82609	0.00803	0.07071
TC0500001412.mm.1	Wdr66	WD repeat domain 66	5.55 ± 0.02	5.6 ± 0	5.64 ± 0.02	5.58 ± 0.02	0.04164	0.82605	0.00597
TC1900000152.mm.1	Wdr74	WD repeat domain 74	8.37 ± 0.04	8.29 ± 0.06	8.17 ± 0.02	8.1 ± 0.09	0.00347	0.1531	0.84484
TC0100000351.mm.1	Wdr75	WD repeat domain 75	7.08 ± 0.05	6.99 ± 0.03	7.07 ± 0.03	6.9 ± 0.06	0.18729	0.00688	0.57385
TC0200000392.mm.1	Wdr85	WD repeat domain 85	6.52 ± 0.05	6.6 ± 0	6.72 ± 0.04	6.56 ± 0.05	0.04325	0.57356	0.00766
TC0700001624.mm.1	Wee1	WEE 1 homolog 1 (S. pombe)	7.15 ± 0.11	7.7 ± 0.08	6.68 ± 0.03	7.21 ± 0.04	0.00011	4.4E-06	0.4443
TC0800001425.mm.1	Wfdc1	WAP four-disulfide core domain 1	9.23 ± 0.18	9.54 ± 0.08	9.5 ± 0.11	9.06 ± 0.11	0.62714	0.84086	0.00931
TC1100001264.mm.1	Wfdc17	WAP four-disulfide core domain 17	6.5 ± 0.07	6.03 ± 0.14	6.33 ± 0.16	5.83 ± 0.03	0.13722	0.00072	0.78755
TC1000001620.mm.1	Wibg	within bgcn homolog (Drosophila)	6.56 ± 0.04	6.69 ± 0.02	6.72 ± 0.03	6.75 ± 0.02	0.00281	0.01998	0.12729
TC1000001490.mm.1	Wif1	Wnt inhibitory factor 1	5.9 ± 0.07	6.35 ± 0.11	6.2 ± 0.05	6.27 ± 0.1	0.23137	0.00926	0.04716
TC0500001717.mm.1	Wipi2	WD repeat domain, phosphoinositide interacting 2	8.06 ± 0.04	7.99 ± 0.04	7.94 ± 0.03	8.1 ± 0.06	0.5885	0.59156	0.00848
TC1500000489.mm.1	Wisp1	WNT1 inducible signaling pathway protein 1	6.66 ± 0.04	6.64 ± 0.01	6.87 ± 0.09	6.54 ± 0.05	0.2099	0.01168	0.00808
TC0200002496.mm.1	Wisp2	WNT1 inducible signaling pathway protein 2	9.08 ± 0.12	9.05 ± 0.07	9.38 ± 0.17	8.6 ± 0.08	0.74849	0.00873	0.00491
TC0600003030.mm.1	Wnk1	WNK lysine deficient protein kinase 1	9.41 ± 0.03	9.29 ± 0.03	9.38 ± 0.03	9.24 ± 0.07	0.46629	0.00976	0.5779
TC0600001902.mm.1	Wnt2	wingless-related MMTV integration site 2	5.42 ± 0.02	5.5 ± 0.01	5.57 ± 0.04	5.46 ± 0.02	0.07379	0.45471	0.00316
TC1100003318.mm.1	Wsb1	WD repeat and SOCS box-containing 1	6.9 ± 0.07	6.98 ± 0.07	7.31 ± 0.12	6.76 ± 0.12	0.43187	0.02028	0.00822
TC0500001205.mm.1	Wscd2	WSC domain containing 2	6.71 ± 0.06	6.99 ± 0.05	6.89 ± 0.04	6.88 ± 0.03	0.47271	0.01251	0.00766
TC0400002271.mm.1	Wwp1	WW domain containing E3 ubiquitin protein ligase 1	9.35 ± 0.05	9.08 ± 0.06	9.31 ± 0.04	9.07 ± 0.08	0.68617	0.00066	0.90386
TC0300002025.mm.1	Wwtr1	WW domain containing transcription regulator 1	8.89 ± 0.05	8.94 ± 0.01	9.07 ± 0.06	8.83 ± 0.03	0.39802	0.04792	0.00471
TC1700002526.mm.1	Xdh	xanthine dehydrogenase	9.02 ± 0.06	8.6 ± 0.07	8.65 ± 0.03	8.58 ± 0.08	0.01101	0.00301	0.0237

Supplemental Table I

Annotations			Summary Statistics				2 way ANOVA p-values		
Probe Set ID	Symbol	Description	XY sh	XY Or	XX sh	XX Or	XY vs XX	Sh vs Or	Intrxn
TC0X00002775.mm.1	Xist	inactive X specific transcripts	4.19 ± 0.02	4.24 ± 0.04	9.88 ± 0.09	9.84 ± 0.12	1E-16	0.94263	0.53769
TC1700000882.mm.1	Xpo5	exportin 5	7.58 ± 0.02	7.53 ± 0.03	7.47 ± 0.03	7.41 ± 0.06	0.00511	0.15642	0.94547
TC1300002395.mm.1	Xrcc4	X-ray repair complementing defective repair in Chinese hams	5.43 ± 0.04	5.57 ± 0.04	5.54 ± 0.04	5.4 ± 0.06	0.50965	0.99691	0.00752
TC1600001471.mm.1	Xxylt1	xyloside xylosyltransferase 1	7.01 ± 0.02	7.17 ± 0.01	7.15 ± 0.03	7.08 ± 0.01	0.23275	0.07338	7.1E-05
TC0400001515.mm.1	Yars	tyrosyl-tRNA synthetase	6.93 ± 0.04	6.83 ± 0.03	6.74 ± 0.02	6.75 ± 0.03	0.0009	0.26219	0.14249
TC0600003268.mm.1	Ybx3	Y box protein 3	10.27 ± 0.07	10.17 ± 0.01	10.31 ± 0.01	10.13 ± 0.03	0.78823	0.0072	0.55506
TC1100003462.mm.1	Ypel2	yippee-like 2 (Drosophila)	7.98 ± 0.05	8.03 ± 0.05	8.3 ± 0.04	8.04 ± 0.03	0.00498	0.02384	0.01056
TC0200005425.mm.1	Ythdf1	YTH domain family 1	8 ± 0.01	8.05 ± 0.03	7.99 ± 0.02	7.92 ± 0.02	0.00278	0.70099	0.00946
TC0500003410.mm.1	Ywhag	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase act	7.75 ± 0.13	7.56 ± 0.09	7.36 ± 0.11	7.81 ± 0.04	0.3772	0.31563	0.00585
TC0100000255.mm.1	Zap70	zeta-chain (TCR) associated protein kinase	5.55 ± 0.03	5.79 ± 0.03	5.67 ± 0.03	5.75 ± 0.07	0.4426	0.0032	0.11281
TC0400003795.mm.1	Zbtb40	zinc finger and BTB domain containing 40	6.32 ± 0.02	6.42 ± 0.02	6.32 ± 0.02	6.34 ± 0	0.0411	0.00805	0.05777
TC0900002296.mm.1	Zc3h12c	zinc finger CCCH type containing 12C	7.19 ± 0.04	7.35 ± 0.01	7.28 ± 0.04	7.13 ± 0.06	0.18588	0.96633	0.00411
TC1000000056.mm.1	Zc3h12d	zinc finger CCCH type containing 12D	5.92 ± 0.06	6.2 ± 0.03	6.01 ± 0.1	6.21 ± 0.08	0.63484	0.00823	0.77328
TC0700000225.mm.1	Zc3h4	zinc finger CCCH-type containing 4	7.99 ± 0.02	8.04 ± 0.01	8.1 ± 0.03	7.99 ± 0.04	0.23772	0.26063	0.00887
TC1500000729.mm.1	Zc3h7b	zinc finger CCCH type containing 7B	8.35 ± 0.04	8.46 ± 0.02	8.48 ± 0.03	8.4 ± 0.03	0.33197	0.54936	0.00873
TC1300002416.mm.1	Zcchc9	zinc finger, CCHC domain containing 9	6.54 ± 0.05	6.65 ± 0.04	6.62 ± 0.03	6.44 ± 0.05	0.14538	0.34763	0.00588
TC1700000036.mm.1	Zdhhc14	zinc finger, DHHC domain containing 14	7.53 ± 0.05	7.47 ± 0.03	7.34 ± 0.02	7.34 ± 0.06	0.00718	0.84282	0.91464
TC0100000653.mm.1	Zfand2b	zinc finger, AN1 type domain 2B	6.91 ± 0.02	7 ± 0.01	7.03 ± 0.03	7.08 ± 0.04	0.00507	0.03384	0.70067
TC1000001328.mm.1	Zfc3h1	zinc finger, C3H1-type containing	7.53 ± 0.05	7.33 ± 0.04	7.53 ± 0.07	7.18 ± 0.14	0.40541	0.00497	0.35127
TC0300000017.mm.1	Zfhx4	zinc finger homeodomain 4	6.53 ± 0.03	6.28 ± 0.05	6.41 ± 0.05	6.39 ± 0.03	0.85416	0.00402	0.01207
TC0500001727.mm.1	Zfp12	zinc finger protein 12	6.69 ± 0.03	6.78 ± 0.01	6.77 ± 0.04	6.67 ± 0.02	0.80845	0.90447	0.00357
TC1700001595.mm.1	Zfp13	zinc finger protein 13	6.89 ± 0.03	6.93 ± 0.01	7.03 ± 0.04	6.89 ± 0.01	0.04164	0.14808	0.00257
TC1600000014.mm.1	Zfp174	zinc finger protein 174	5.59 ± 0.02	5.65 ± 0.02	5.66 ± 0.02	5.58 ± 0.02	0.96827	0.52079	0.00387
TC0600000542.mm.1	Zfp212	Zinc finger protein 212	7.05 ± 0.04	7.2 ± 0.02	7.19 ± 0.01	7.1 ± 0.05	0.46999	0.29144	0.00326
TC1600000009.mm.1	Zfp263	zinc finger protein 263	6.35 ± 0.03	6.45 ± 0.02	6.4 ± 0.01	6.35 ± 0.02	0.29731	0.19245	0.00647
TC0600000540.mm.1	Zfp282	zinc finger protein 282	6.51 ± 0.03	6.64 ± 0.04	6.64 ± 0.03	6.58 ± 0.03	0.17496	0.15559	0.00476
TC0700000534.mm.1	Zfp30	zinc finger protein 30	6.39 ± 0.03	6.46 ± 0.02	6.6 ± 0.03	6.41 ± 0.03	0.0222	0.02817	0.00101
TC1300001128.mm.1	Zfp366	zinc finger protein 366	7.14 ± 0.08	7.35 ± 0.06	7.06 ± 0.08	7.43 ± 0.11	0.764	0.00906	0.24893
TC1200001988.mm.1	Zfp36l1	zinc finger protein 36, C3H type-like 1	9.07 ± 0.06	9.23 ± 0.07	9.65 ± 0.07	9.15 ± 0.09	0.00682	0.01954	0.0008
TC0700000539.mm.1	Zfp383	zinc finger protein 383	6.45 ± 0.03	6.63 ± 0.03	6.51 ± 0.05	6.48 ± 0.01	0.27178	0.03226	0.00526
TC1400000935.mm.1	Zfp395	zinc finger protein 395	7.48 ± 0.03	7.55 ± 0.06	7.67 ± 0.03	7.63 ± 0.01	0.00517	0.99228	0.24636
TC1800000875.mm.1	Zfp516	zinc finger protein 516	7.13 ± 0.05	7.32 ± 0.02	7.5 ± 0.05	7.24 ± 0.04	0.01343	0.28345	0.00048

Supplemental Table I

Annotations			Summary Statistics				2 way ANOVA p-values		
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TC0400003995.mm.1	Zfp534	zinc finger protein 534	4.73 ± 0.03	4.83 ± 0.03	4.81 ± 0.03	4.68 ± 0.05	0.3638	0.8427	0.00511
TC0400003732.mm.1	Zfp593	zinc finger protein 593	5.62 ± 0.02	5.73 ± 0.01	5.77 ± 0.04	5.79 ± 0.03	0.00298	0.056	0.18073
TC1600001107.mm.1	Zfp597	zinc finger protein 597	6.17 ± 0.01	6.19 ± 0.02	6.12 ± 0.02	6.1 ± 0.03	0.00408	0.90276	0.28742
TC0700002594.mm.1	Zfp61	zinc finger protein 61	5.4 ± 0.01	5.47 ± 0.02	5.45 ± 0.02	5.43 ± 0.01	0.60272	0.11395	0.00347
TC0900001625.mm.1	Zfp651	zinc finger protein 651	8.14 ± 0.1	8.42 ± 0.01	8.44 ± 0.06	8.22 ± 0.04	0.38482	0.53725	0.00256
TC0300002460.mm.1	Zfp687	zinc finger protein 687	6.78 ± 0.01	6.83 ± 0.03	6.89 ± 0.01	6.9 ± 0.02	0.0012	0.12898	0.35787
TC0300001626.mm.1	Zfp704	zinc finger protein 704	7.94 ± 0.09	8.25 ± 0.03	8.25 ± 0.05	8.07 ± 0.04	0.27371	0.24476	0.00192
TC1300002321.mm.1	Zfp72	zinc finger protein 72	7.13 ± 0.06	7.37 ± 0.08	7.46 ± 0.09	7.08 ± 0.14	0.92465	0.40699	0.00674
TC0600002217.mm.1	Zfp746	zinc finger protein 746	7.08 ± 0.03	7.19 ± 0.02	7.21 ± 0.03	7.11 ± 0.03	0.36033	0.86646	0.00668
TC0700004324.mm.1	Zfp747	zinc finger protein 747	7.07 ± 0.05	7.19 ± 0.03	7.21 ± 0.04	7.01 ± 0.05	0.86356	0.76578	0.00192
TC0600002216.mm.1	Zfp777	zinc finger protein 777	6.94 ± 0.03	7.04 ± 0.01	7.06 ± 0.01	7.08 ± 0.03	0.0025	0.01805	0.07184
TC0700000753.mm.1	Zfp936	zinc finger protein 936	5.9 ± 0.05	6 ± 0.03	6.04 ± 0.04	5.87 ± 0.06	0.63933	0.61864	0.00828
TC1900000612.mm.1	Zfyve27	zinc finger, FYVE domain containing 27	6.83 ± 0.01	6.85 ± 0.01	6.82 ± 0.01	6.9 ± 0.03	0.28392	0.00419	0.15191
TC1400002253.mm.1	ZNRD1-AS1_2	ZNRD1 antisense RNA 1 conserved region 2	4.33 ± 0.04	4.65 ± 0.09	4.35 ± 0.1	4.63 ± 0.13	0.88367	0.00855	0.97187
TC1800001072.mm.1	Zscan30	zinc finger and SCAN domain containing 30	4.91 ± 0.04	4.96 ± 0.02	5.06 ± 0.04	4.91 ± 0.02	0.13038	0.26583	0.00848
TC0200002534.mm.1	Zswim3	zinc finger SWIM-type containing 3	6.07 ± 0.02	6 ± 0.03	6.21 ± 0.05	6.14 ± 0.03	0.00108	0.05451	0.92661
TC0900000590.mm.1	Zw10	zw10 kinetochore protein	6.68 ± 0.07	6.65 ± 0.03	6.57 ± 0.01	6.43 ± 0.07	0.00976	0.20774	0.21809
TC0600000459.mm.1	Zyx	zyxin	8.83 ± 0.13	9.09 ± 0.08	9.17 ± 0.08	8.83 ± 0.06	0.56799	0.81291	0.00753

Supplemental Table II. Primer sequences for RT-PCR.

Gene	Primer sequence
ACE	Forward: 5'-AGGTTGGGCTACTCCAGGAC-3'
	Reverse: 5'-GGTGAGTGTTGTCTGGCTTC-3'
MMP2	Forward: 5'-GGGGTCCATTTTCTTCTTCA-3'
	Reverse: 5'-CCAGCAAGTAGATGCTGCCT-3'
Collagen1	Forward: 5'-GCTCCTCTTAGGGGCCACT-3'
	Reverse: 5'-CCACGTCTCACCATTGGGG-3'
Thbs1	Forward: 5'-CAATTTTCAGGGGGGTGCTGC-3'
	Reverse: 5'-CCGTTCACCACGTTGTTGTC-3'
Xist	Purchased from QIAGEN catalog#330001 PPM68756B
Kap	Purchased from QIAGEN catalog#QT00113484
Cyp2e1	Purchased from QIAGEN catalog#QT02280278
Arntl	Purchased from QIAGEN catalog#QT00101647
Npas2	Purchased from QIAGEN catalog#QT00108647

Supplemental table III

Genes Upregulated in XY	Genes Upregulated in XX
Ddx3y	Xist
Uty	Arntl
Kdm5d	Npas2
Eif2s3y	Arhgap20
Dbp	Ighv14-1
Nr1d2	
Nr1d1	
Cyp2e1	
Cidec	
Fam13a	
Ehhadh	
Slc27a2	
Npy	
Ms4a4a	
Kap	
Dbh	
Snap25	
Pck1	
Atp1b1	
Gnal	
Syt1	
Htr3a	
Slc18a2	
Th	
Tubb3	
Tuba4a	
Ache	
Syt4	
Kcna1	
Gatm	
Ddc	
Slc31a1	
Cdh19	
Napb	
Vat1l	
Nefl	
Slc6a2	
Syn2	
Plp1	
Kif21a	
Chl1	
Pirt	
Drd2	

Cxcl13	
Tspan8	
Snord116l2	
Stmn2	
Necab1	
Mpz	
Snord116	
Fabp7	

Supplemental Table IV.

Upregulated in XY compared to XX

1. Polyamine biosynthetic process (4 genes): Amd2, Azin1, Odc1, Srm
2. Nuclear pore (6 genes): Ipo7, Kpna1, Kpna2, Nup50, Nup88, Nup93
3. Purine ribonucleotide binding (31 genes): Abcf2, Atp2b1, Baz1b, Btaf1, Cars, Cct2, Cct3, Cdk6, Ctps, Ddx21, Ddx3y, Dgkg, Eif2s3y, Eif4a1, Gnai1, Gnl3, Hsp90ab1, Hspa4, Iars, Ide, Insr, Map2k3, Map3k6, Mat2a, Psmc5, Rras2, Sar1a, Sgk1, Srp54a, Srp54b, Srp54c
4. tRNA binding (4 Genes): Cars, Mettl1, Xpo5, Yars
5. Nuclear lumen (16 genes) Ccnl2, Cfl2, Ddx21, Gnl3, Mbd1, Nop2, Nop56, Polr2l, Pop4, Psmc5, Sfpq, Srp54a, Srp54b, Srp54c, Srp72, Srrt
6. Nucleolus (8 genes): Ddx21, Gnl3, Mbd1, Nop2, Nop56, Pop4, Srp72, Wdr74
7. Transition metal ion binding (32 genes): Adamts1, Adamts9, B4galt4, B4galt5, Baz1b, Cars, Dgkg, Dnaja2, Galnt11, Galnt7, Herc2, Iars, Ide, Kdm5d, Klf13, Klf9, Luc7l, Mat2a, Mbd1, Mbnl2, Nr4a3, P4ha1, Polr2l, Prnp, Sec23b, Slc30a1, Spire1, Sqstm1, Ubr2, Uty, Zdhhc14, Zfp597
8. Protein amino acid N-linked glycosylation (3 genes): Mgat2, Prkcsh, Stt3b
9. Extracellular matrix part (7 genes): Ccdc80, Col1a1, Col1a2, Col4a1, Col5a2, Lamc1, Sparc
10. Immune response (7 genes): Ccl6, Ccl9, Cfb, Fcgr2b, Fcgr3, Il31ra, Tlr13
11. Acute inflammatory response (4 genes): Cd163, Cfb, Fcgr3, Stat3
12. Skin development (3 genes): Aars, Col1a1, Col5a2
13. Defense response (6 genes): Cd163, Cfb, Fcgr2b, Fcgr3, Stat3, Tlr13
14. Melanosome (3 genes): Pdia4, Pdia6, Snd1

Upregulated in XX compared to XY

1. Ribosome (8 genes): Mrpl23, Mrpl52, Rpl18a, Rpl36, Rplp1, Rplp2, Rps10, Ubc
2. DNA binding (20 genes): Arap1, Ddx3x, Ercc2, Foxd1, Gli1, Kcnip3, Kdm5c, Msx1, Nr1h2, Nr3c2, Pold2, Polr2e, Polr2f, Relb, Sry, Stra13, Thap3, Zfp395, Zfp593, Zfp687
3. Intracellular non-membrane-bounded organelle (18 genes): Arhgap6, Camk2n1, Cdk5rap2, Eml2, Fgd1, Grm3, Homer3, Ifltd1, Myl6, Nudt16, Pdlim2, Rpl13, Rpl35a, Rpl37a, Rps16, Sntg2, Ssh3, Ttf1
4. Positive regulation of macromolecule metabolic process (8 genes): C1qtnf2, Jun, Pawr, Pax1, Pias3, Rarg, Six4, Ttf1
5. Postsynaptic density (3 genes): Camk2n1, Grm3, Homer3
6. Structural constituent of ribosome (4 genes): Rpl13, Rpl35a, Rpl37a, Rps16
7. Death (6 genes): Dapk2, Pawr, Pdcd7, Serpinb9b, Spr, Traf2
8. Regulation of cell proliferation (6 genes): Ada, Jun, Pawr, Rarg, Six5, Wnt2

Supplemental Table V. Characteristics of XY and XX male *Ldlr*$^{-/-}$ mice infused with AngII.

	XY Sham	XY ORC	XX sham	XX ORC
Body weight (g)	28.6 ± 1	23.9 ± 0.6 **	31.3 ± 1	28.3 ± 0.8 **
Serum testosterone (ng/ml)	1.77 ± 0.85	0.07 ± 0.02 **	1.53 ± 0.64	0.14 ± 0.02 **
Plasma Renin Concentration (ng/ml)	0.37 ± 0.16	0.32 ± 0.09	0.25 ± 0.04	0.29 ± 0.05
Total serum cholesterol (mg/dl)	1617 ± 242	1450 ± 320	1797 ± 140	1670 ± 115
Systolic blood pressure (mmHg)	132 ± 3	135 ± 4	119 ± 4 *	135 ± 3 **
% Atherosclerotic lesion in aortic arch	21 ± 2	20 ± 3	19 ± 3	17 ± 2

Data are mean ± SEM from n = 9-20/group.

*, P<0.05 compared to XY within surgical treatment.

**, P<0.05 compared to sham within genotype.