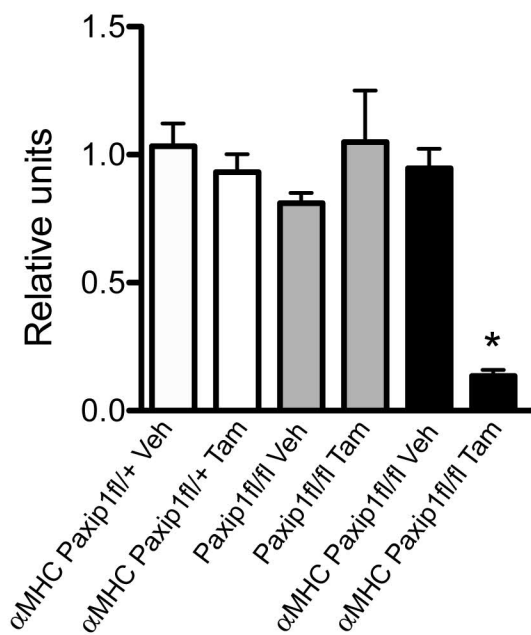


Supplemental figure 1. Genetic and tamoxifen controls. Kcnip2 gene expression by qPCR was measured in *Paxip1^{fl/+}* and *Paxip1^{fl/fl}* mice with and without the aMHC^{MCM} transgene and with and without tamoxifen. Mice were injected with tamoxifen or vehicle at 8 weeks of age. Four weeks later ventricular tissue was harvested and qPCR was run for Kcnip2 gene expression (n=2-3/group). *p<0.05 vs. all other groups. Data are means±SD.

Supplemental figure 2. H3K4me3 marks at the 5' regulatory region of the

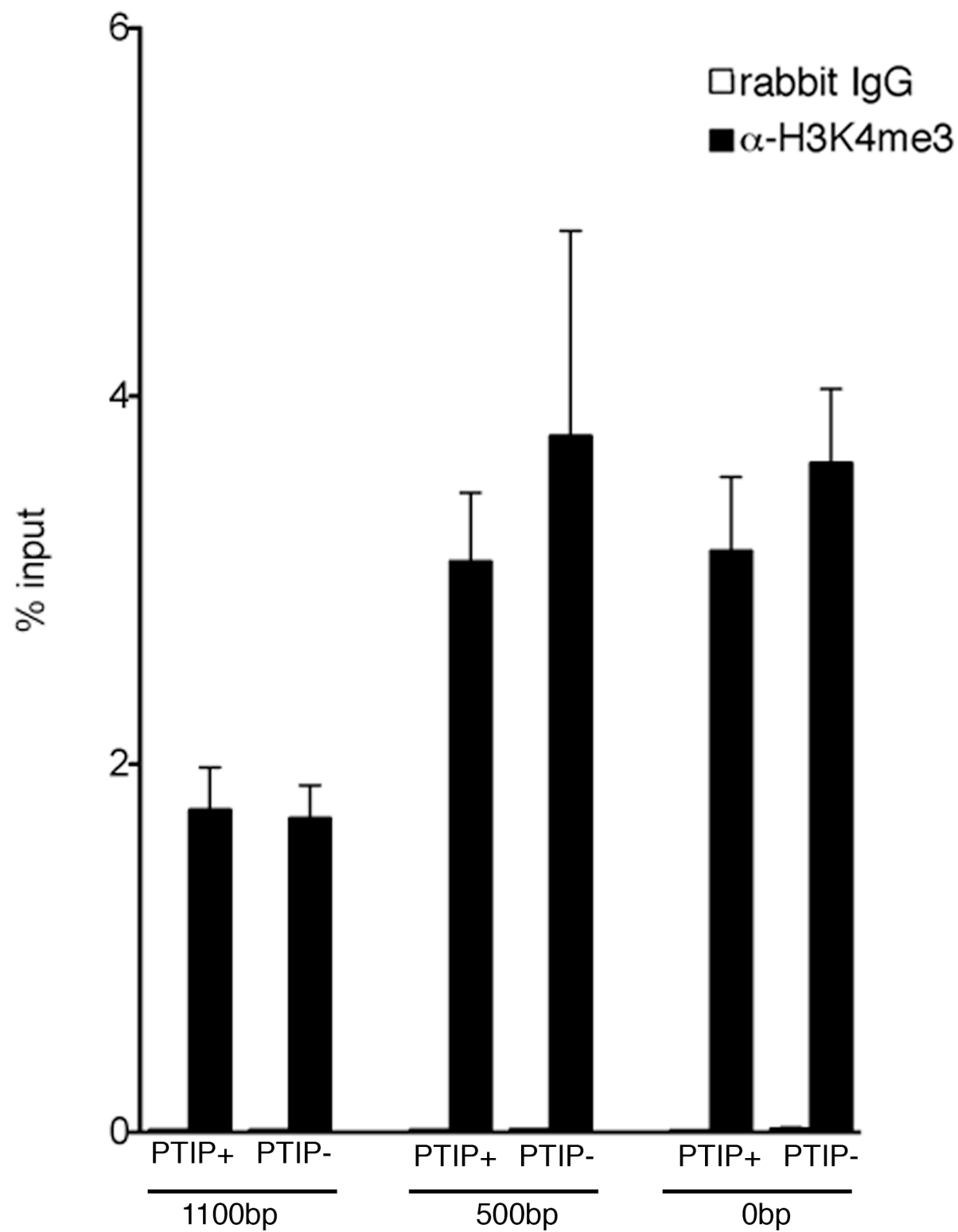
***Nppb* gene.** ChIP was performed to study H3K4me3 enrichment at the *Nppb* 5' regulatory region. **A.** A schematic of the *Nppb* transcript is shown. Boxes are exons and lines connecting boxes are introns. Filled or darkened boxes are coding sequence, whereas empty, unfilled boxes are UTR (untranslated region). Primers were designed that amplify DNA at 1100bp (Primer 1), 500bp (Primer 2), and 0bp (Primer 3) relative to the first recognized ATG site (arrow tip). **B.** IP was performed with 20ug of chromatin using 2ug of anti-rabbit IgG (□) and 2ug of anti-H3K4me3 antibody (Abcam 8580) (■) in PTIP+(n=4) and PTIP- (n=4) mice. Enrichment for H3K4me3 marks are shown at primer set 1 (left), primer set 2 (middle) and primer set 3 (right). Data are represented as % input and bars show means $\pm$ SD.



A



B



Supplemental table 1. Summary of array analysis for PTIP- and *ptip*^{fl/fl} mice.

Probe	Symbol	Description	GenBank	Gene	UniGene	t-statistic	p-value	Fold Change	PTIP-			<i>ptip</i> ^{fl/fl}		
									PTIP- 1	PTIP- 2	PTIP- 3	<i>ptip</i> ^{fl/fl} 1	<i>ptip</i> ^{fl/fl} 2	<i>ptip</i> ^{fl/fl} 3
1429651_at	Phacr3	phosphatase and actin regulator 3	AV339670	74189	Mm.44413	23.12	0	2.35	7.69169	7.82264	7.75237	5.08698	5.38266	5.46967
1455346_at	Masp1	mannan-binding lectin serine peptidase 1	BB477214	17174	Mm.1213	-18.51	0.001	-1.96	4.3479	4.56572	4.62619	6.55265	6.38162	6.58597
1436619_at	D630045 M09Rik	RIKEN cDNA D630045M09 gene	BG069496	432777	Mm.415319	-17.68	0.001	-2.59	5.95005	5.62521	5.4017	7.75811	8.15761	8.18183
1428986_at	Slc17a7	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 7	BQ175176	72961	Mm.255631	17.39	0.001	2.02	9.06188	9.07116	9.03699	6.81795	6.81324	7.14716
1435720_at	Kcnd3	potassium voltage-gated channel, Shal-related family, member 3	AW045978	56543	Mm.44530	-16.1	0.001	-1.46	8.82501	8.68044	8.83306	10.2057	10.1794	10.2967
1420672_at	Kcne1	potassium voltage-gated channel, Isk-related subfamily, member 1	NM_008424	16509	Mm.299425	-16.03	0.001	-2.63	5.43217	5.82208	6.118	8.64985	8.38703	8.63153
1435057_x_at	Polr1e	polymerase (RNA) I polypeptide E	BE334128	64424	Mm.282932	-15.45	0.001	-1.51	8.34708	8.18126	8.11468	9.72298	9.56392	9.72123
1425400_a_at	Cited4	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 4	BC025116	56222	Mm.272646	-15.1	0.001	-1.6	4.49762	4.25057	4.27751	5.61626	5.87184	5.9606
1430036_at	2310015B20Rik	RIKEN cDNA 2310015B20 gene	AK009351	69563	Mm.64672	-14.44	0.001	-1.77	6.55607	6.90888	6.48966	8.48392	8.28579	8.37901
1421558_at	Y2	brachyury 2	NM_013682	21331	Mm.311080	13.99	0.001	1.42	7.83301	7.5159	7.52648	6.22552	6.20142	6.12755
1448889_at	Slc38a4	solute carrier family 38, member 4	NM_027052	69354	Mm.250980	-13.88	0.001	-1.92	4.95127	5.2739	5.24048	7.5548	7.25981	6.99238
1423303_at	Paxip1	PAX interacting (with transcription-activation domain) protein 1	AW742928	55982	Mm.277190	-13.46	0.001	-2	6.33997	5.89849	5.89837	7.80427	7.71455	8.09921
1452779_at	3110006E14Rik	RIKEN cDNA 3110006E14 gene	AK014009	76980	Mm.23960	13.16	0.001	1.24	8.92022	8.96642	8.89991	7.94916	7.67525	7.63299
1438778_at			BB083574		Mm.9213	13.14	0.001	1.4	5.43284	5.17822	5.10224	3.5716	3.76809	3.80412
1421244_at	Esr1	estrogen receptor 1 (alpha)	NM_007956	13982	Mm.463262	12.96	0.001	6.87	12.5404	12.5697	12.5857	8.49182	5.9978	5.14499
1428613_at	LdhD	lactate dehydrogenase D	AW105779	52815	Mm.271578	12.95	0.001	1.6	9.6937	9.21251	9.35229	7.85312	7.61011	7.836
1460433_at	Entpd6	ectonucleoside triphosphate diphosphohydrolase 6	BM204496	12497	Mm.275524	-12.78	0.001	-1.11	8.46534	8.40712	8.37026	9.53746	9.41101	9.53278
1425774_at	1500001A10Rik	RIKEN cDNA 1500001A10 gene	BC024130	68955	Mm.146779	12.69	0.001	1.65	7.7872	8.03624	8.26113	6.274	6.59291	6.4702
1419695_at	St8sia1	ST8 alpha-N-acetyl-neuraminidase alpha-2,8-sialyltransferase 1	NM_011374	20449	Mm.260838	12.63	0.001	2.06	5.25133	5.45376	5.32398	3.83089	3.52527	3.09067
1428111_at	Slc38a4	solute carrier family 38, member 4	AK003626	69354	Mm.250980	-12.59	0.001	-1.35	6.94868	7.20346	7.0775	8.65851	8.54562	8.35179
1441962_at	Alox5	arachidonate 5-lipoxygenase	BB079625	11689	Mm.41072	-12.35	0.001	-2	6.02122	5.56021	6.15497	7.92494	7.80743	8.08726
1426915_at	Dapk1	death associated protein kinase 1	BC021490	69635	Mm.24103	-12.34	0.001	-1.17	8.70309	8.52367	8.58088	9.91836	9.64219	9.78476
1421035_a_at	Magi3	membrane associated guanylate kinase, WW and PDZ domain containing 3	BB329638	99470	Mm.264849	-12.3	0.001	-1.21	7.74765	7.44755	7.47886	8.74395	8.65544	8.75395
1421117_at	Dst	dystonin	NM_010081	13518	Mm.336625	12.15	0.001	1.12	5.16008	5.34924	5.14675	4.16153	4.09197	4.04647
1457038_at	Frem2	Fras1 related extracellular matrix protein 2	BM201912	242022	Mm.38378	-12.1	0.001	-1.74	5.5653	5.92128	5.41118	7.60097	7.22208	7.27782
1434052_at	Al593442	expressed sequence Al593442	AV327193	330941	Mm.335160	-12.08	0.001	-3.1	3.79753	4.83371	4.11216	6.38758	7.50249	7.3991
1450101_a_at	Magi3	membrane associated guanylate kinase, WW and PDZ domain containing 3	BB329638	99470	Mm.264849	-11.92	0.001	-1.1	7.56222	7.51179	7.54271	8.45826	8.55405	8.69811
1418028_at	Dct	dopachrome tautomerase	NM_010024	13190	Mm.19987	11.6	0.001	1.34	6.30862	6.57735	6.55704	5.3879	4.97764	5.23113
1451550_at	Ephb3	Eph receptor B3	BC014822	13845	Mm.6972	-11.46	0.001	-1.06	4.9698	5.0343	4.82655	6.00834	5.94188	5.95879
1423302_a_at	Paxip1	PAX interacting (with transcription-activation domain) protein 1	AW742928	55982	Mm.277190	-11.42	0.001	-1.58	6.10087	5.46361	5.78404	7.50027	7.20134	7.38048
1449198_a_at	St3gal5	ST3 beta-galactosidase alpha-2,3-sialyltransferase 5	BB829192	20454	Mm.38248	-11.38	0.001	-1.01	9.08113	9.31248	9.17239	10.2083	10.2261	10.1869
1449619_s_at	Arhgap9	Rho GTPase activating protein 9	AU043488	216445	Mm.227198	-11.36	0.001	-1.15	7.43823	7.47596	7.25125	8.58801	8.38563	8.50804
1433691_at	Ppp1r3c	protein phosphatase 1, regulatory (inhibitor) subunit 3C	BQ176864	53412	Mm.24724	-11.35	0.001	-1.04	9.6534	9.55681	9.64696	10.8306	10.5618	10.6822
1432698_at	2900024I21Rik	RIKEN cDNA 2900024I21 gene	AK013589	72845		11.34	0.001	1.43	6.6964	6.76971	6.83067	5.83882	5.17088	5.36778
1454943_a_at	Paxip1	PAX interacting (with transcription-activation domain) protein 1	BM935413	55982	Mm.277190	-11.27	0.002	-1.58	6.12401	5.97949	5.92012	7.76918	7.21075	7.65512
1444026_at	Al593442	expressed sequence Al593442	BF658761	330941	Mm.335160	-11.23	0.002	-3.15	4.71052	4.6269	5.17234	6.86126	8.51976	8.15012
1436231_at	2900052N01Rik	RIKEN cDNA 2900052N01 gene	AU067665	73040	Mm.265384	11.06	0.002	3.77	7.72091	8.72478	8.20126	4.5112	3.57565	4.84144
1458773_at	B4galt1	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 1	BG072304	14595	Mm.15622	-11.04	0.002	-1.38	3.91394	3.74151	3.46296	4.84588	5.04617	4.97673
1417151_a_at	Nlr2	neurotensin receptor 2	NM_008747	18217	Mm.281715	-10.96	0.002	-1.92	6.70109	5.89325	6.10363	7.77969	7.90292	8.18733
1442554_s_at	Kalrn	kalirin, RhoGEF kinase	BG066934	545156	Mm.450612	-10.86	0.002	-1.14	3.82821	3.63251	3.86257	4.86101	5.09811	4.89592

1457495_at	2900052N01Rik	RIKEN cDNA 2900052N01 gene	BB426699	73040	Mm.265384	10.83	0.002	3.07	5.36907	6.99322	6.15993	3.47113	2.9394	3.18528
1428484_at	Osbpl3	oxysterol binding protein-like 3	AK004768	71720	Mm.44153 Mm.392849	-10.82	0.002	-1.16	8.81245	8.85703	8.63243	9.78499	9.73697	9.93878
1419058_at	Polr1e	polymerase (RNA) I polypeptide E	NM_022811	64424	Mm.282932	-10.77	0.002	-2.29	7.54129	6.74687	7.10583	8.5942	9.66656	9.39751
1454608_x_at	Ttr	transthyretin	BG141874	22139	Mm.2108	10.55	0.002	1.97	6.71847	6.97259	7.41508	4.74849	5.20188	5.32021
1459626_at			AW108268			10.55	0.002	1.89	7.12494	7.74056	7.3478	5.88298	5.7871	5.33194
1445226_at	BC023969	cDNA sequence BC023969	BI664409	407828	Mm.442125	10.47	0.002	1.76	4.04322	4.48972	4.60726	3.0559	2.95883	2.57262
1429593_at	Slc38a2	solute carrier family 38, member 2	BB030482	67760	Mm.46754	-10.45	0.002	-1.3	7.80101	7.46992	7.42753	8.72853	8.61036	8.89311
1429169_at	Rbm3	RNA binding motif protein 3	AK011224	19652	Mm.128512 Mm.360569	-10.45	0.002	-1.01	4.61708	4.91496	4.85734	5.85514	5.89609	5.80907
1421387_at	Kremen1	knirle containing transmembrane protein 1	NM_032396	84035	Mm.209989	10.42	0.002	1.09	5.88393	5.83557	5.92696	5.17886	4.74437	4.77223
1431043_at	Kbtbd5	kelch repeat and BTB (POZ) domain containing 5	W78395	72330	Mm.45734	10.41	0.002	1.34	9.88543	9.35759	9.664	8.13874	8.44699	8.24773
1456918_at	Raph1	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1	BB667412	77300	Mm.440325	-10.39	0.002	-1.21	7.21241	7.10695	7.28106	8.08962	8.34364	8.54491
1455400_at	Ddah1	dimethylarginine dimethylaminohydrolase 1	BB770857	69219	Mm.234247	-10.24	0.002	-1.83	6.30721	6.61243	6.13553	8.58059	8.34008	7.92993
1419606_a_at	Tnnt1	troponin T1, skeletal, slow	NM_011618	21955	Mm.358643	-10.06	0.002	-1.06	9.34371	9.09774	9.27392	10.2269	10.1524	10.3764
1430068_at	C030011L09Rik	RIKEN cDNA C030011L09 gene	BB356045	77316	Mm.126426	-9.89	0.002	-1.31	3.77868	4.0416	3.80283	5.67275	5.03178	5.14219
1419358_at	Sorcs2	sorcin-related VPS10 domain containing receptor 2	NM_030889	81840	Mm.34113	-9.85	0.002	-1.42	7.6728	7.69733	7.47785	9.09729	8.64321	9.10759
1452203_at	Obfc2a	oligonucleotide/oligosaccharide-binding fold containing 2A	AV313559	109019	Mm.196290	-9.76	0.002	-1.13	8.51767	9.03749	8.81918	9.9944	9.97525	9.92592
1436275_at	Kcnip2	Kv channel-interacting protein 2	AW490636	80906	Mm.213204	-9.73	0.002	-1.33	10.9818	10.3799	10.4965	11.6542	11.8354	11.9317
1445764_at			BB515119			-9.88	0.002	-2.45	5.94785	7.01713	5.94709	8.39995	8.49864	8.72791
1424123_at	Flvcr2	feline leukemia virus subgroup C cellular receptor family, member 2	BC011209	217721	Mm.301076	-9.65	0.002	-1.47	5.53919	6.34375	6.03531	7.57662	7.42965	7.50815
1425870_a_at	Kcnip2	Kv channel-interacting protein 2	AF439339	80906	Mm.213204	-9.64	0.002	-1.66	6.31966	6.42155	6.45914	7.35037	8.40602	8.0652
1450659_at	Rgs7	regulator of G protein signaling 7	NM_011880	24012	Mm.7956	-9.55	0.002	-1.24	4.81224	4.59032	5.03069	6.28391	6.21549	6.07831
1451922_at	Lman1l	lectin, mannose-binding 1 like	BC020188	235416	Mm.295630	9.45	0.003	1.66	4.84358	5.27693	5.46656	3.3124	3.9626	3.59184
1428614_at	Ldhf	lactate dehydrogenase D	AW105779	52815	Mm.27589 Mm.271578	9.45	0.003	1.57	10.5894	10.5727	10.448	9.02814	8.48871	9.10364
1416588_at	Ptprn	protein tyrosine phosphatase, receptor type, N	NM_008985	19275	Mm.2902	9.41	0.003	1.26	8.73806	8.57322	8.84524	7.62935	7.76414	7.37744
1419625_at	Hspa1l	heat shock protein 1-like	NM_013558	15482	Mm.14287 Mm.471680	9.41	0.003	1.64	8.15118	8.03967	8.29256	6.9191	6.93362	6.3565
1451806_at	Fbnp1	formin binding protein 1	BC003867	14269	Mm.440993	9.37	0.003	1.19	6.2368	6.28477	6.04233	5.38524	4.95648	4.85566
1432556_a_at	3100002J23Rik	RIKEN cDNA 3100002J23 gene	AK013920	75429	Mm.296819	9.34	0.003	2.22	5.41363	4.78783	5.80018	3.6758	3.21092	3.26483
1438602_s_at	Masp1	mannan-binding lectin serine peptidase 1	BB732340	17174	Mm.1213	-9.26	0.003	-1.13	3.96632	3.75325	3.94322	4.89698	4.80899	5.15239
1454995_at	Ddah1	dimethylarginine dimethylaminohydrolase 1	AW556888	69219	Mm.234247	-9.25	0.003	-1.73	6.6114	6.00564	6.55027	8.21457	8.52895	8.01014
1456813_at			AI854058			9.24	0.003	1.08	9.51512	9.81648	9.66399	8.73268	8.37175	8.66349
1445673_at	2900052N01Rik	RIKEN cDNA 2900052N01 gene	BE955394	73040	Mm.265384	9.2	0.003	2.97	5.53265	7.3117	6.52058	3.2802	3.21942	3.76455
1436013_at	Gsg1l	GSG1-like	AI852434	269994	Mm.39599	-9.01	0.003	-1.07	5.9543	5.89047	6.0811	6.86711	6.9062	7.19712
1428891_at	9130213B05Rik	RIKEN cDNA 9130213B05 gene	AK008716	231440	Mm.5002	-8.91	0.003	-1.1	10.3682	10.5069	10.315	11.9392	11.4564	11.3899
1446331_at	Ptgr	prostaglandin F receptor	AV244075	19220	Mm.331442 Mm.460678	-8.88	0.003	-1.24	4.08403	3.49643	3.72313	4.77189	4.8175	5.06543
1429299_at	Ddah1	dimethylarginine dimethylaminohydrolase 1	BE283964	69219	Mm.234247	-8.83	0.003	-1.62	4.52784	4.64344	4.14957	5.90946	6.30991	5.7871
1426806_at	Obfc2a	oligonucleotide/oligosaccharide-binding fold containing 2A	AV313559	109019	Mm.196290	-8.8	0.003	-1.18	6.71765	7.31512	7.01554	8.20396	8.37507	8.15255
1428960_at	4933434I06Rik	RIKEN cDNA 4933434I06 gene	AK017056	71233	Mm.27658	8.69	0.003	2.29	7.65772	8.37744	8.72671	6.24893	6.64294	5.98229
1442721_at			AW489203			8.67	0.003	1.31	5.07181	4.4507	4.74982	3.78473	3.54661	3.31975
1436097_x_at	Arhgap9	Rho GTPase activating protein 9	BB327418	216445	Mm.227198	-8.64	0.003	-1.08	6.97773	7.24464	6.81885	8.22984	8.01978	7.99233
1423084_at	B3gal2	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 2	BB223909	26878	Mm.285580 Mm.461846	-8.64	0.003	-1.68	2.49252	2.62825	2.03395	4.54576	3.94195	3.81431
1424940_s_at	BC022687	cDNA sequence BC022687	BC022687	217887	Mm.186678	8.61	0.003	1.14	6.57056	6.80875	6.58737	5.49721	5.2055	5.61665
1450028_a_at	Lanc2	Lanc2 (bacterial lipoteichoic synthetase component C)-like 2	NM_133737	71835	Mm.274904	8.58	0.003	1.5	8.82492	9.57843	9.00998	8.04339	7.52659	7.57405

1458455_at	Abra	actin-binding Rho activating protein	BB296103	223513	Mm.148913	8.58	0.003	1.48	10.0412	10.1312	9.79685	8.83596	8.72725	8.2344
1429704_at	Lrp2bp	Lrp2 binding protein	AK007202	67620	Mm.383914	8.56	0.003	1.2	4.04526	3.63673	3.92981	2.89433	2.90848	2.54672
1449462_at	3110049J23Rik	RIKEN cDNA 3110049J23 gene	NM_026085	67307	Mm.368563	8.55	0.003	1.18	7.70909	8.26602	7.95353	6.9322	6.98407	6.70886
1438613_at	Kcna4	potassium voltage-gated channel, shaker-related subfamily, member 4	BB131475	16492	Mm.142718	-8.54	0.003	-1.07	6.57107	6.81629	6.5392	8.0492	7.76601	7.58237
1438261_at	Cited4	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 4	AW702005	56222	Mm.272646	-8.49	0.003	-1.49	4.59595	4.31454	4.51852	5.1345	6.1321	6.03703
1420991_at	Ankrd1	ankyrin repeat domain 1 (cardiac muscle)	AK009959	107765	Mm.10279	-8.49	0.003	-1.75	10.1477	10.4896	9.85573	11.276	12.1592	11.7254
1434363_x_at	Paxip1	PAX interacting (with transcription-activation domain) protein 1	BM935413	55982	Mm.277190	-8.44	0.004	-1.13	6.52612	6.50334	6.47388	7.14748	7.45689	7.7557
1423026_at	Rad51c	Rad51 homolog c (S. cerevisiae)	NM_053269	114714	Mm.37376	8.27	0.004	1.04	5.12187	5.07405	5.08402	4.57813	4.07461	3.94845
1445263_at			BF148780			8.23	0.004	1.71	5.45225	4.76753	5.37826	4.09956	3.19392	3.60844
1426036_a_at	Pde1c	phosphodiesterase 1C	L76944	18575	Mm.5145	8.22	0.004	1.18	8.36331	8.94826	8.83347	7.2919	7.7556	7.59307
1436309_at	Neto2	neuropilin (NRP) and tolloid (TLL)-like 2	BB125651	74513	Mm.471668	-8.18	0.004	-1.09	3.16091	2.69238	2.81094	4.27621	3.76507	3.94111
1432913_at	Lrrc52	leucine rich repeat containing 52	AK015134	240899	Mm.159799	8.09	0.004	1.85	6.25775	6.56446	5.7754	4.37953	3.79406	4.32175
1458115_at	4930512H18Rik	RIKEN cDNA 4930512H18 gene	BB472574	75111	Mm.440931	8.06	0.004	1.81	5.69015	6.03247	6.02074	5.30618	4.0403	4.03695
1451410_a_at	Crip3	cysteine-rich protein 3	AF367970	114570	Mm.25158	8.05	0.004	1.69	7.25779	7.41912	8.07626	6.1608	6.28646	6.01225
1444386_at	Pde1c	phosphodiesterase 1C	BB388392	18575	Mm.5145	8.02	0.004	1.36	4.88966	5.66334	5.13374	3.86487	3.64809	3.94427
1424885_at	Klhc8a	kelch domain containing 8A	BC011135	213417	Mm.39723	-7.99	0.004	-1.25	7.75421	7.48986	8.06458	9.08923	8.98077	9.21007
1437644_at	B3gal12	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 2	BB083643	26878	Mm.461846	-7.97	0.004	-1.22	3.14052	3.51937	3.75036	4.88946	4.99434	4.7307
1433556_at	Cen1a1	centaurin, alpha 1	AV264037	231821	Mm.297819	7.97	0.004	1.15	6.29533	6.6758	6.27985	5.53614	5.38596	5.09889
1436251_at	Pde1c	phosphodiesterase 1C	BB131735	18575	Mm.5145	7.91	0.004	1.39	7.26259	7.91526	7.45764	6.59331	5.86215	6.18457
1447480_at	Fgf14	fibroblast growth factor 14	BB801162	14169	Mm.439768	-7.84	0.004	-1.31	4.55109	3.84118	4.123	5.11462	5.24538	5.57453
1442586_at	Socs2	suppressor of cytokine signaling 2	BB456057	216233	Mm.440128	-7.81	0.004	-1.35	7.00015	6.42425	6.42792	7.25348	7.9288	7.93818
1455913_x_at	Ttr	transthyretin	AV152953	22139	Mm.2108	7.76	0.005	1.55	5.33266	5.00675	5.70613	3.48595	3.79028	4.07838
1429130_at	Tlc25	tetratricopeptide repeat domain 25	AK016657	74407	Mm.31590	7.75	0.005	1.02	4.69828	5.07728	4.95609	3.91017	4.18475	3.81431
1457899_at	Kalrn	kalirin, RhoGEF kinase	BG066934	545156	Mm.450612	-7.74	0.005	-1.01	4.66124	4.28126	4.15808	5.25706	5.14348	5.3341
1435928_at	6430548M08Rik	RIKEN cDNA 6430548M08 gene	AV271124	234797	Mm.101958	7.73	0.005	1.03	6.03848	5.94467	6.21493	5.46571	5.24248	4.98179
1452480_at	4930529M08Rik	RIKEN cDNA 4930529M08 gene	BC024760	78774	Mm.451992	7.7	0.005	1.28	4.15258	4.59259	4.72807	3.87889	3.189	3.29151
1415885_at	Chgb	chromogranin B	NM_007694	12653	Mm.255241	7.7	0.005	1.46	5.5567	6.23361	6.10406	5.21664	4.31337	4.60242
1442804_at	Fgr	Gardner-Rasheed feline sarcoma viral (Fgr) oncogene homolog	BB165085	14191	Mm.271665	7.7	0.005	1.67	3.63251	4.11306	4.45137	3.19884	2.70893	2.41486
1417346_at	Pycard	PYD and CARD domain containing ribonuclease, RNase A family, 10 (non-active)	BG084230	66824	Mm.24163	-7.69	0.005	-1.38	8.26906	7.82049	7.85766	8.57776	9.55706	9.29551
1453215_at	Rnase10		AK015573	75019	Mm.318775	7.66	0.005	1.62	5.01872	5.43042	4.73063	2.65193	3.21318	3.461
1425213_at	6430514L14Rik	RIKEN cDNA 6430514L14 gene	BC025646	76886	Mm.44355	7.65	0.005	1.1	7.96425	8.02384	8.24133	6.93984	7.36623	6.92423
1458913_at	4831440E17Rik	RIKEN cDNA 4831440E17 gene	AV245490	320965	Mm.468586	-7.65	0.005	-1.1	3.33924	3.09371	3.06214	3.65964	4.12608	4.33578
1442064_at	AW556556	expressed sequence AW556556	AI452057	106817	Mm.440584	-7.63	0.005	-1.29	5.44179	5.02848	4.99773	5.66024	6.46931	6.42749
1422997_s_at	Aco12	acyl-CoA thioesterase 2	NM_134188	171210	Mm.371675	-7.57	0.005	-1.57	5.96314	6.38032	6.84855	7.83285	8.36489	8.13786
1421441_at	Angpt1	angiotensinogen 1	NM_009640	11600	Mm.309336	-7.54	0.005	-1.37	6.07438	6.14002	5.8494	7.07025	7.77986	7.15946
1457110_at	Pank1	pantothenate kinase 1	BB440150	75735	Mm.24742	7.53	0.005	1.25	8.03122	8.29141	7.70619	6.33076	6.51597	6.73542
1448562_at	Upp1	uridine phosphorylase 1	NM_009477	22271	Mm.4610	-7.48	0.005	-1.17	6.01799	5.93909	6.2999	7.05891	7.66085	7.25292
1439821_at	Lrp2bp	Lrp2 binding protein	BB075157	67620	Mm.383914	7.48	0.005	1.61	8.27317	7.99164	7.93539	7.24271	5.93399	6.45236
1428216_s_at	Tomm7	translocase of outer mitochondrial membrane 7 homolog (yeast)	BB609428	66169	Mm.291868	7.39	0.005	1.18	5.55142	5.48553	5.61768	3.65026	4.35445	4.52885
1449065_at	Aco11	acyl-CoA thioesterase 1	NM_012006	26897	Mm.1978	-7.34	0.005	-2.02	5.34219	5.1387	6.20632	7.51787	8.07203	7.79648
1442988_at	A630001O12Rik	RIKEN cDNA A630001O12 gene	BB667542	414091	Mm.240068	7.31	0.005	1.12	5.92735	5.69338	5.98129	4.64261	4.45415	4.95057
1420342_at	Gdap10	ganglioside-induced differentiation-associated-protein 10	NM_010268	14546	Mm.440246	-7.3	0.005	-1.71	5.95916	5.7164	5.68144	6.43896	7.17628	7.71084
1446736_at	Tbl1x	transducin (beta)-like 1 X-linked	BM198618	21372	Mm.258476	-7.27	0.005	-1.03	5.84192	6.08664	6.29427	6.83663	7.10708	7.30394
1429870_at	Tnik	TRAF2 and NCK interacting kinase	BB021125	665113	Mm.126193	-7.25	0.005	-1.43	5.64889	4.8724	5.50765	6.43652	6.6074	6.97108
1455973_at	OTTMUSG00000005148	predicted gene, OTTMUSG00000005148	BB738659	626870	Mm.369429	7.25	0.005	1.57	4.98202	6.0037	5.15048	3.85752	3.58561	3.79915
1460509_at	B3gal11	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 1	AK018190	26877	Mm.226435 Mm.393260 Mm.468937	-7.25	0.005	-1.1	3.64958	4.40099	4.09605	4.99125	5.31689	5.16676
1427340_at	Rgs6	regulator of G-protein signaling 6	BB274058	50779	Mm.153013	-7.22	0.005	-1.36	4.11932	4.38524	3.89419	6.13114	5.4624	5.2615

1422092_at	Pfkfb2	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 2	BC018418	18640	Mm.249861	7.15	0.006	1.03	4.98452	4.64562	5.00738	4.31454	4.01157	3.76728
1437866_at	Dusp18	dual specificity phosphatase 18	AV276425	75219	Mm.32588	7.07	0.006	1.06	9.53116	9.8355	9.7158	9.22157	8.78149	8.50745
1439066_at	Angpt1	angiotensinogen 1	BB453314	11600	Mm.309336	-7.06	0.006	-1.07	8.90805	8.8871	8.92943	10.2056	10.3286	9.79747
1458701_at	Prei4	preimplantation protein 4	BB550273	74182	Mm.211211 Mm.448334	-7.05	0.006	-1.72	4.8698	4.84497	4.45518	5.14242	6.4927	6.44105
1438596_at	Hectd2	HECT domain containing 2	AW114007	226098	Mm.61107	7.02	0.006	1.5	5.49153	6.07679	6.16674	4.95485	4.90665	4.31991
1450557_at	Scn4a	sodium channel, voltage-gated, type IV, alpha	NM_133199	110880	Mm.432528	-6.98	0.006	-1.33	3.92552	4.02421	3.60111	4.28421	5.26948	5.11748
1434553_at	Tmem56	transmembrane protein 56	BB667728	99887	Mm.26088	6.97	0.006	1.84	6.60725	6.67696	7.5407	5.93736	5.13294	5.3526
1425631_at	Ppp1r3c	protein phosphatase 1, regulatory (inhibitor) subunit 3C	U89924	53412	Mm.24724	-6.97	0.006	-1.29	5.09707	5.42359	5.35621	5.94161	7.01368	6.55743
1429271_at	9130011E15Rik	RIKEN cDNA 9130011E15 gene	AK018607	71617	Mm.210949	6.93	0.006	1.25	9.78199	9.48728	9.03839	8.08665	7.8227	8.07217
AFFX-	Ttrc	transferrin receptor	AFFX-	22042	Mm.28683	-6.93	0.006	-1.24	5.88954	6.78312	6.54602	7.81297	7.5268	7.80236
1423410_at	Meig1	meiosis expressed gene 1	BF021951	104362	Mm.2688	-6.87	0.006	-1.31	4.14465	4.79202	3.98781	5.29171	5.57997	5.50662
1444159_at	Pip4k2a	phosphatidylinositol-5-phosphate 4-kinase, type II, alpha	BM243903	18718	Mm.313977	-6.85	0.006	-1.03	5.13854	4.99846	4.84174	5.7756	5.64403	6.12003
1455679_at	Obfc2a	oligonucleotide/oligosaccharide-binding fold containing 2A	BE457727	109019	Mm.196290	-6.84	0.006	-1.24	7.36627	8.17458	7.88768	9.50148	9.28954	8.9701
1441497_at	AA388235	expressed sequence AA388235	AV364133	433100	Mm.380381	6.77	0.007	1.3	4.87637	5.57146	5.46597	4.68053	4.25929	3.92664
1418835_at	Phl1a1	pleckstrin homology-like domain, family	NM_009344	21664	Mm.31117	-6.76	0.007	-1.09	8.7343	8.64344	8.82624	10.2994	10.1552	9.66817
1425985_s_a	Masp1	mannan-binding lectin serine peptidase 1	AB049755	17174	Mm.1213	-6.7	0.007	-1.39	3.29917	4.24336	3.74084	4.5713	5.08179	5.3007
1417812_a_a	Lamb3	laminin, beta 3	NM_008484	16780	Mm.435441	6.68	0.007	1.25	9.61308	9.72053	10.2002	8.59839	9.07332	8.62528
1420735_at	Gabbr2	gamma-aminobutyric acid (GABA-C) receptor, subunit rho 2	AF024621	14409	Mm.6227	-6.66	0.007	-1.07	4.28136	4.50133	4.42421	5.03277	5.20669	5.68399
1427602_at	Dep1	diabetic embryopathy 1	BB626684	170624	Mm.406761 Mm.441701	-6.63	0.007	-1.13	3.13442	2.94638	3.07052	3.34456	4.32235	4.24925
1454392_at	9230112J17Rik	RIKEN cDNA 9230112J17 gene	BB174628	77749	Mm.410770	-6.62	0.007	-1.06	6.49002	7.10005	7.19856	8.24319	7.99023	8.15677
1429298_at	Ddah1	dimethylarginine dimethylaminohydrolase 1	BE283964	69219	Mm.234247	-6.58	0.007	-1.44	6.26777	6.42438	6.23941	8.53445	8.06008	7.44837
1455234_at	B3galt1	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 1	BB795733	26877	Mm.226435 Mm.393260 Mm.468937 Mm.406761 Mm.441701	-6.54	0.007	-1.01	4.68589	4.86651	4.32265	5.80687	5.49595	5.47061
1438892_at	Dep1	diabetic embryopathy 1	BB088198	170624	Mm.441701	-6.49	0.007	-1.15	4.40854	4.12716	4.15799	4.62639	5.16962	5.53561
1424249_a_a	Arhgap9	Rho GTPase activating protein 9	BC024535	216445	Mm.227198	-6.49	0.007	-1.12	7.41216	7.80888	7.24775	9.07681	8.43544	8.46694
1458167_at	4833412E19Rik	RIKEN cDNA 4833412E19 gene	AA409371	73905	Mm.101958	-6.48	0.007	-1.2	3.49617	3.63251	3.68395	4.33405	4.4769	5.07534
1430109_at	6430548M08Rik	RIKEN cDNA 6430548M08 gene	BF465109	234797	Mm.101958	6.42	0.008	1.02	7.6827	8.05275	7.72975	7.14042	7.03118	6.60071
1446894_at	Arnt2	aryl hydrocarbon receptor nuclear translocator 2	BB117494	11864	Mm.38594	6.35	0.008	1.45	6.0124	6.28437	6.06822	5.12782	5.18905	4.35378
1459741_x_a	Ucp2	uncoupling protein 2 (mitochondrial, proton carrier)	AW108044	22228	Mm.171378	6.35	0.008	1.59	10.8528	10.5634	11.4627	9.69899	9.93923	9.39693
1430623_s_a	Obfc2a	oligonucleotide/oligosaccharide-binding fold containing 2A	AV263881	109019	Mm.196290	-6.33	0.008	-1.29	7.54114	8.55926	8.05283	8.976	9.60532	9.33402
1430886_at	1700112E06Rik	RIKEN cDNA 1700112E06 gene	BB246912	76633	Mm.361010	6.33	0.008	1.25	7.07516	6.50595	6.73858	5.47347	5.97357	5.29434
1448566_at	Slc40a1	solute carrier family 40 (iron-regulated transporter), member 1	AF226613	53945	Mm.28756	-6.31	0.008	-1.19	5.36129	5.30692	5.51461	6.08639	7.10689	6.52162
1439112_at	2810442I21Rik	RIKEN cDNA 2810442I21 gene	BE456545	72735	Mm.268598	6.31	0.008	1.33	5.62603	5.63692	5.53442	4.70771	3.65188	4.42063
1449545_at	Fgf18	fibroblast growth factor 18	NM_008005	14172	Mm.339812	6.28	0.008	1.08	7.58911	8.10124	8.17067	6.73813	7.30874	6.88532
1445534_at	Flnb	filamin, beta	BM206272	286940	Mm.28095	-6.27	0.008	-1.01	4.2729	4.19571	3.80719	5.0413	4.69828	5.09601
1460521_a_a	Obfc2a	oligonucleotide/oligosaccharide-binding fold containing 2A	AK015312	109019	Mm.196290	-6.26	0.008	-1.57	5.59926	6.449	6.00916	6.5451	7.90604	7.65171
1444315_at	D630024D03Rik	RIKEN cDNA D630024D03 gene	BB499985	414116	Mm.150222	6.25	0.008	1.91	6.96196	6.97023	7.5597	5.08585	4.69828	5.78057
1433944_at	LOC668215	hypothetical LOC668215	AV256030	668215	Mm.394223	6.19	0.008	1.08	7.72847	8.28115	8.12384	7.12779	7.38582	6.8395
1423141_at	Lipa	lysosomal acid lipase A	AI596237	16889	Mm.157545	6.19	0.008	1.07	7.44579	8.12544	7.82827	7.37405	6.76747	6.67098

1440330_at	Hist1h1e	histone cluster 1, H1e	BB490701	50709	Mm.170587	6.15	0.009	1.52	6.16565	6.96773	6.63732	5.39008	5.66717	4.83454
1419619_at	Krt80	keratin 80	NM_028770	74127	Mm.440055	6.13	0.009	1.38	5.39919	5.98659	6.47252	5.00618	4.72036	4.81602
1443503_at	Ihpk3	inositol hexaphosphate kinase 3	BB515192	271424	Mm.209679	-6.13	0.009	-1.4	5.52489	5.41784	4.69973	6.14322	6.17181	6.53054
1427358_at	Dapk1	death associated protein kinase 1	BC026671	69635	Mm.24103	-6.13	0.009	-1.3	4.68281	4.07325	4.69828	5.07646	6.08532	5.87865
1416889_at	Tnni2	troponin I, skeletal, fast 2	NM_009405	21953	Mm.39469	-6.12	0.009	-1.06	6.44071	6.41397	6.20042	7.78778	6.93136	7.46416
1448188_at	Ucp2	uncoupling protein 2 (mitochondrial, proton carrier)	BC012697	22228	Mm.171378	6.11	0.009	1.57	11.5009	11.124	12.0558	9.99176	10.6072	10.0289
1431372_at	SrpK2	serine/arginine-rich protein specific kinase 2	AK014004	20817	Mm.288728	-6.11	0.009	-1.29	5.00457	4.73006	5.13926	5.66808	5.97168	6.55723
1441608_at	Cacna2d1	calcium channel, voltage-dependent, alpha2/delta subunit 1	BB559910	12293	Mm.159842	-6.08	0.009	-1.22	4.64786	4.29347	4.07252	4.59284	5.46494	5.54784
1441236_at	Slc9a3	solute carrier family 9 (sodium/hydrogen exchanger), member 3	AV373598	105243	Mm.261564	-6.08	0.009	-1.24	3.32931	4.23089	3.40058	5.04327	4.75975	4.79936
1444148_at	LOC497253	hypothetical LOC497253	AI552426	497253		-6.08	0.009	-1.13	5.42205	5.19381	4.66916	6.10075	5.878	6.10672
1459740_s_at	Ucp2	uncoupling protein 2 (mitochondrial, proton carrier)	AW108044	22228	Mm.171378	6.07	0.009	1.7	10.8514	10.6089	11.5503	9.62991	10.0036	9.30238
1445565_at	Hist1h1e	histone cluster 1, H1e	BE688907	50709	Mm.170587	6.03	0.009	1.3	8.85703	8.59598	8.66427	7.49231	7.96469	7.11776
1445498_at	Ryr2	ryanodine receptor 2, cardiac	AW552101	20191	Mm.239871	-6	0.009	-1.42	8.08117	7.14	7.75927	8.82938	8.66915	9.32317
1434862_at	Fut2	fucosyltransferase 2	AV371838	14344	Mm.290046	-5.98	0.009	-1.37	3.91424	3.99713	3.76785	4.02642	5.26217	5.37911
1441597_at	Ankhd1	ankyrin repeat and KH domain containing 1	BB084168	108857	Mm.24790	-5.97	0.009	-1.09	4.10063	4.45192	4.26892	4.79534	5.07803	5.58872
1442732_at	Hadhb	hydroxyacyl-Coenzyme A dehydrogenase/3-ketoacyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), beta subunit	BB181461	231086	Mm.291463	-5.96	0.009	-1.15	7.29571	6.87877	6.63959	7.58517	7.66295	8.13479
1421584_at	Opm4	opsin 4 (melanopsin)	NM_013887	30044	Mm.272060	-5.95	0.009	-1.04	5.40604	4.81949	5.50358	6.10765	6.29951	6.44108
1440678_at	Ltbp1	latent transforming growth factor beta	BM119516	268977	Mm.269747	-5.92	0.01	-1.01	4.63974	4.36621	4.58958	5.18008	5.21337	5.76133
1436731_at	Zfp385b	zinc finger protein 385B	BB333374	241494	Mm.126649	-5.89	0.01	-1.21	6.78714	6.99806	6.24002	7.47779	7.95415	7.64666
1432280_at	2310007L24Rik	RIKEN cDNA 2310007L24 gene	AK009213	75573	Mm.159539	-5.89	0.01	-1.3	4.42224	3.91708	3.77285	4.88911	4.76294	5.44763
1422966_a_a	Tfrc	transferrin receptor	BB810450	22042	Mm.28683	-5.89	0.01	-1.33	5.03241	6.23703	5.89059	7.27506	6.90671	7.24526
1459745_at	Ubap2	ubiquitin-associated protein 2	AI506718	68926	Mm.41864	-5.89	0.01	-1.07	5.14787	5.89639	5.21612	6.19743	6.30057	6.51357
1446812_at	LOC100040515	hypothetical protein LOC100040515	BB667300	100040515	Mm.229304	-5.88	0.01	-1.03	6.79944	6.7758	7.04863	7.60787	8.39475	7.8482
1443455_at	Cuedc1	CUE domain containing 1	AV375943	103841	Mm.374846	-5.87	0.01	-1.16	5.17595	5.04277	5.28895	5.53736	6.18627	6.59208
1446045_at	AU024581	expressed sequence AU024581	BG069074	102243	Mm.442359	-5.85	0.01	-1.05	3.34319	2.99909	3.13442	3.32818	4.21994	4.30172
1444663_at	Vezf1	vascular endothelial zinc finger 1	BB546415	22344	Mm.46628	-5.82	0.01	-1.04	4.76889	4.41625	4.3931	4.86989	5.28562	5.68945
1453745_at	2700038G22Rik	RIKEN cDNA 2700038G22 gene	AK012332	67194	Mm.426395	5.78	0.01	1.1	6.78504	7.17958	6.45257	5.89415	5.69645	5.46221
1425164_a_a	Phkg1	phosphorylase kinase gamma 1	J03293	18682	Mm.3159	5.77	0.01	1.19	9.1277	9.78113	9.57252	9.26244	8.21244	8.27326
1445032_at	Dapk1	death associated protein kinase 1	AW491158	69635	Mm.24103	-5.76	0.01	-1.46	3.96706	3.3515	4.19406	4.86961	5.08993	5.66767
1433667_at	Lgi3	leucine-rich repeat LGI family, member 3	BB187947	213469	Mm.41708	-5.75	0.011	-1.05	4.70186	4.83223	4.39074	5.19914	5.29478	5.78638
1451270_at	Dusp18	dual specificity phosphatase 18	BC020036	75219	Mm.32588	5.72	0.011	1.05	8.99818	9.74246	9.58321	8.66197	8.77051	8.30904
1449969_at	Tmod4	tropomodulin 4	NM_016712	50874	Mm.71935	-5.71	0.011	-1.43	8.8644	8.51387	7.84555	9.13687	9.85844	9.54896
1434449_at	Aqp4	aquaporin 4	BB193413	11829	Mm.250786	5.7	0.011	1.05	8.9018	9.3153	9.30216	8.361	8.61016	7.98044
1446464_at	Psmc4	proteasome (prosome, macropain)	BB384493	103554	Mm.240066	-5.68	0.011	-1.33	4.1913	3.73277	4.25471	4.41531	5.4003	5.64989
1422315_x_a	Phkg1	phosphorylase kinase gamma 1	NM_011079	18682	Mm.3159	5.67	0.011	1.2	9.4816	10.0893	9.84085	9.61289	8.58394	8.50447
1432787_at	6720420G18Rik	RIKEN cDNA 6720420G18 gene	AK020112	77072	Mm.446079	-5.66	0.011	-1.6	4.13072	3.60322	3.53358	4.00986	5.01159	5.54124
1429594_at	Slc38a2	solute carrier family 38, member 2	BB030482	67760	Mm.46754	-5.62	0.011	-1.03	6.34948	7.07919	6.56156	8.11095	7.85748	7.53137
1453646_at	3110005L21Rik	RIKEN cDNA 3110005L21 gene	BM219138	73104		-5.6	0.012	-1.21	6.27013	5.88992	5.55427	6.23394	6.81286	7.1314
1459256_at	Nrp2	neuropilin 2	BB328920	18187	Mm.266341	-5.58	0.012	-1.01	5.82189	5.15291	5.41951	5.77423	6.37438	6.55924
1443551_at	Atp2a2	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	BB216071	11938	Mm.227583	-5.56	0.012	-1.2	5.8109	5.49303	5.53239	5.73565	6.6788	6.97504
1460294_at	Atp8a2	ATPase, aminophospholipid transporter-like, class I, type 8A, member 2	NM_015803	50769	Mm.319599	5.51	0.012	1.03	7.63231	8.44656	8.26671	7.42295	6.8732	7.26838
1458830_at	Fgfl4	fibroblast growth factor 14	BB023508	14169	Mm.439768	-5.5	0.012	-1.41	5.26801	4.42907	4.44731	5.6831	5.47363	6.24856
1451537_at	Chil3l1	chitinase 3-like 1	BC005611	12654	Mm.38274	5.5	0.012	1.28	6.21781	5.19628	6.1061	4.28987	4.84908	4.60742
1423406_at	Sv2a	synaptic vesicle glycoprotein 2 a	BC026494	64051	Mm.200365	-5.48	0.012	-1.09	4.97218	5.51785	5.2181	6.22578	5.86505	6.55787
1446324_at	Cacna2d1	calcium channel, voltage-dependent, alpha2/delta subunit 1	BB451211	12293	Mm.159842	-5.41	0.013	-2.35	4.6945	3.54368	4.31025	5.24224	5.7733	7.09683
1426007_a_a	Ubx3	UBX domain containing 3	BC027099	212190	Mm.292226	5.4	0.013	1.08	8.88536	9.06086	9.64003	8.67024	8.40093	8.20541

1437355_at	Zoche5	zinc finger, CCHC domain containing 5	BQ126004	213436	Mm.85581	5.4	0.013	1.41	5.25353	5.19917	6.08325	5.00283	4.13734	4.3173
1422967_a_a	Trfc	transferrin receptor	BB810450	22042	Mm.28683	-5.35	0.013	-1.89	3.73504	4.59118	5.16704	6.66683	6.05281	6.97597
1446673_at	D330013E07Rik	RIKEN cDNA D330013E07 gene	BB475442	319525	Mm.447615	-5.34	0.014	-1.12	5.3814	5.10355	5.18905	5.93187	5.82687	6.59828
1447510_at	C530014P21Rik	RIKEN cDNA C530014P21 gene	AI467086	399604	Mm.449558	-5.33	0.014	-1.24	5.58886	5.15567	5.01269	5.61886	6.04317	6.6398
1458505_at	LOC552901	hypothetical LOC552901	AW546414	552901	Mm.443869	-5.33	0.014	-1.03	6.207	5.80704	5.61603	6.26112	6.53128	6.98097
1429639_at	Prei4	preimplantation protein 4	AK009137	74182	Mm.211211	-5.3	0.014	-1.5	8.60223	7.74325	7.72804	8.19942	9.30429	9.58246
1428987_at	Dynlrb2	dynein light chain roadblock-type 2	AK005789	75465	Mm.23114	5.27	0.014	1.1	3.18258	4.11051	3.29877	2.59488	2.49549	2.26222
1429032_at	Micalc1	MICAL C-terminal like	AK014911	70877	Mm.291129	-5.26	0.014	-1.07	5.90882	5.2206	6.02641	6.44791	6.92647	6.95284
1423619_at	Rasd1	RAS, dexamethasone-induced 1	BB217136	19416	Mm.3903	5.23	0.015	1.09	6.41522	7.07327	7.20139	5.93585	6.3412	5.78835
1457535_at	4932438A13Rik	RIKEN cDNA 4932438A13 gene	BB465997	229227	Mm.207907	-5.21	0.015	-1.36	5.20243	4.48379	4.47323	4.7949	5.95984	6.13785
1429732_at	Ppp1r1c	protein phosphatase 1, regulatory (inhibitor) subunit 1C	AK016334	75276	Mm.257373	5.2	0.015	1.38	5.72396	5.55821	4.71219	3.87194	3.37127	3.7928
1454833_at	Rpl35	ribosomal protein L35	AI467654	66489	Mm.345333	-5.18	0.015	-1.11	6.5186	5.90902	5.62508	6.71339	6.66232	7.09982
1434442_at	Stbd1	starch binding domain 1	BB667844	52331	Mm.21965	-5.15	0.015	-1.44	5.71498	6.53898	5.59327	8.26795	7.24608	7.11301
1441992_at	Rab14	RAB14, member RAS oncogene family	BM217857	68365	Mm.198264	-5.14	0.015	-1.05	5.99559	5.48663	5.38842	5.7239	6.53177	6.70498
1455650_at			AA016705			-5.13	0.015	-1.48	4.0212	2.72617	3.16409	4.02176	4.31847	4.9409
1452257_at	Bdh1	3-hydroxybutyrate dehydrogenase, type 1	BF322712	71911	Mm.293470	5.09	0.016	1.14	11.2673	10.6474	10.7803	8.84001	9.45686	9.92059
1458022_at	D830039M14Rik	RIKEN cDNA D830039M14 gene	BB185401	320949	Mm.347744	5.05	0.016	1.09	7.76034	8.11278	8.08863	7.9431	7.08018	6.7413
1440093_at	Ednra	endothelin receptor type A	BB238381	13617	Mm.283168	-5.05	0.016	-1.06	4.3461	4.23642	4.3461	4.31529	5.34397	5.56299
1432059_x_a_t	5031425E22Rik	RIKEN cDNA 5031425E22 gene	AK017143	75977	Mm.425231	5.02	0.016	1.09	4.42422	5.34479	5.45022	3.8669	4.1157	4.24781
1446154_at			BB131186		Mm.463293	5.01	0.016	2.17	8.70237	8.60502	8.4762	6.04224	5.13267	6.96015
1439554_at	Scmh1	sex comb on midleg homolog 1	AV323498	29871	Mm.427014	-4.98	0.017	-1.02	4.86946	4.3577	4.51494	4.61636	5.5285	5.71975
1443799_at			AV348753		Mm.447554	-4.94	0.017	-1.98	6.19084	4.85934	5.10528	7.46201	6.20341	7.59576
1452661_at	Trfc	transferrin receptor	AK011596	22042	Mm.28683	-4.92	0.017	-1.01	10.5378	10.8453	11.1743	12.0847	11.5674	12.185
1450791_at	Nppb	natriuretic peptide precursor type B	NM_008726	18158	Mm.2740	-4.92	0.017	-1.12	9.90456	10.6403	10.9155	11.7141	12.1188	11.6868
1441494_at	Rb1	retinoblastoma 1	BB160773	19645	Mm.273862	-4.88	0.018	-1.15	3.13442	3.32992	2.77035	3.85255	3.58711	4.36544
1457455_at	Suhw4	suppressor of hairy wing homolog 4 (Drosophila)	BB430212	235469	Mm.392319	-4.88	0.018	-1.12	6.72689	6.14562	6.06158	6.5208	7.05907	7.54314
1457824_at	LOC331000	similar to putative scramblase	AI504076	331000	Mm.464262	-4.86	0.018	-1.07	4.47359	4.85002	4.8612	5.13588	5.50947	6.13685
1432788_at	6720420G18Rik	RIKEN cDNA 6720420G18 gene	AK020112	77072	Mm.446079	-4.84	0.018	-1.46	2.60952	2.74192	2.83645	2.93129	3.84962	4.61583
1444281_at	Camk2d	calcium/calmodulin-dependent protein kinase II, delta	BB519823	108058	Mm.255822	-4.83	0.018	-1.05	5.75899	5.77662	5.5822	6.31284	6.18348	6.98997
1456623_at	tpm1	tropomyosin 1, alpha	BM232388	22003	Mm.121878	-4.8	0.019	-1.08	7.55362	8.07141	7.10947	8.20619	8.43905	8.54231
1459737_s_a_t	Ttr	transthyretin	AA408768	22139	Mm.2108	4.77	0.019	1.31	6.0842	6.28968	6.64346	4.06843	4.86795	5.46552
1438327_at	Zfp385b	zinc finger protein 385B	BE981788	241494	Mm.126649	-4.72	0.02	-1.43	5.85097	6.046	4.84754	6.37508	6.89281	6.68567
1457198_at	Nrp1	neuropilin 1	AV291009	18186	Mm.271745	-4.71	0.02	-1.16	6.77141	6.3821	6.52046	7.18369	7.11524	8.01691
1460241_a_a_t	St3gal5	ST3 beta-galactoside alpha-2,3-sialyltransferase 5	BB829192	20454	Mm.38248	-4.67	0.02	-1	5.73439	5.91286	6.1339	5.99085	7.24028	7.09395
1432840_at	E130116L18Rik	RIKEN cDNA E130116L18 gene	AK021392	77870	Mm.246718	-4.67	0.02	-1.17	5.25216	4.08505	4.67586	5.51912	5.41662	6.02473
AFFX-	Trfc	transferrin receptor	AFFX-	22042	Mm.28683	-4.65	0.02	-1.18	2.93352	3.57331	3.55328	4.36124	4.04659	4.93904
1449133_at	Spr1a	small proline-rich protein 1A	NM_009264	20753	Mm.331191	4.63	0.021	1.27	5.19759	5.19759	5.95638	4.64261	3.83197	4.59565
1455695_at	St8sia1	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 1	BI736113	20449	Mm.260838	4.6	0.021	1	5.84546	5.58429	5.59507	5.72482	4.65607	4.44565
1434943_at	BC023055A730020	cDNA sequence BC023055	BF464669	226123	Mm.259441	4.58	0.021	1.31	7.88922	7.57416	8.09444	7.21392	7.27214	6.26275
1442396_at	M07Rik	RIKEN cDNA A730020M07 gene	BB503768	319738	Mm.65320	-4.58	0.021	-1.03	4.12362	4.39592	5.03901	5.85794	5.53381	5.8652
1439290_at	Fxr1	fragile X mental retardation gene 1, autosomal homolog	BM213145	14359	Mm.259021	-4.56	0.022	-1.04	5.17886	5.66705	5.21209	5.2657	6.4927	6.46331
1460431_at	Gcnt1	glucosaminyl (N-acetyl) transferase 1, core 2	AK017462	14537	Mm.244825	-4.56	0.022	-2.08	6.82426	6.93519	7.67821	10.2176	8.20947	9.87175
1429743_at	6720468P15Rik	RIKEN cDNA 6720468P15 gene	BG068031	78073	Mm.12411	4.56	0.022	1.03	4.40808	4.14964	5.05441	3.45732	3.81527	3.71898
1421040_a_a_t	Gsta2	glutathione S-transferase, alpha 2 (Yc2)	NM_008182	14858	Mm.422778	4.56	0.022	1.16	6.02678	5.41237	4.92645	3.71945	4.40394	3.96108
1426959_at	Bdh1	3-hydroxybutyrate dehydrogenase, type 1	BF322712	71911	Mm.293470	4.55	0.022	1.47	10.0172	10.0938	10.2476	8.21859	7.84307	9.1467
1460511_at	Pkp2	plakophilin 2	AK004731	67451	Mm.2252	-4.54	0.022	-1.14	8.01338	7.30601	7.80165	8.13107	8.45926	9.14709
1422155_at	Hist2h3c2	histone cluster 2, H3c2	BC015270	97114	Mm.358797	4.54	0.022	1.08	7.19797	5.89364	6.23967	5.26301	5.44907	5.14039
1422679_s_a_t	Ctr9	Ctr9, Pat1/RNA polymerase II complex	BB459423	22083	Mm.255858	4.54	0.022	1.58	9.75183	9.57421	9.57956	9.90004	8.07523	7.71146

1445402_at	Adk	adenosine kinase	AV337434	11534	Mm.188734	-4.53	0.022	-1.09	3.43378	3.01565	3.2627	3.26834	4.07206	4.53537
1419739_at	Tpm2	tropomyosin 2, beta	AK003186	22004	Mm.646	4.52	0.022	1.39	7.77699	6.78116	7.18999	6.24022	5.02304	6.0694
1427735_at	Acta1	actin, alpha 1, skeletal muscle	M12233	11459	Mm.214950	-4.51	0.022	-1.04	10.0887	10.3085	9.44742	10.7633	11.0561	10.6679
1420349_at	Ptgfr	prostaglandin F receptor	NM_008966	19220	Mm.460678	-4.51	0.022	-1.46	5.09707	5.58385	4.26041	6.46907	5.81064	6.24778
1457894_at			BB284616			-4.5	0.022	-1.1	1.88014	2.72882	2.12547	2.41034	3.18097	3.51931
1460126_at			BG070566			-4.49	0.023	-1.11	4.35313	4.8216	4.70074	4.93355	5.37508	6.09563
1429700_at	EG668050	predicted gene, EG668050	AV000681	668050		-4.47	0.023	-1.53	5.12456	3.64957	5.11287	6.74446	6.05632	6.3544
1438493_at	01Rik	RIKEN cDNA 4933433K01 gene	AW554531	194908	Mm.344651	-4.47	0.023	-1.16	3.2549	3.50211	4.07908	3.99059	4.99921	5.12263
1424022_at	Osgin1	oxidative stress induced growth inhibitor 1	BC022135	71839	Mm.272357	4.47	0.023	1.11	7.57764	6.95455	6.38855	5.30092	5.60374	5.63886
1451580_at	Ttr	transthyretin	BC024702	22139	Mm.2108	4.46	0.023	1.19	5.48283	5.71668	6.24587	3.89888	4.56828	5.0644
1440068_at	Rfxdc2	regulatory factor X domain containing 2 homolog (human)	BB199265	319758	Mm.32081	-4.46	0.023	-2	3.28721	2.29569	2.21134	2.49248	3.97914	4.88176
1441164_at	Pip4k2b	phosphatidylinositol-5-phosphate 4-kinase, type II, beta	BG071985	108083	Mm.39700	-4.45	0.023	-1.21	7.83791	7.0747	7.73075	7.84903	8.50734	9.08539
1432746_at	21Rik	RIKEN cDNA 6030442H21 gene	AK020062	77070		-4.43	0.024	-1.14	2.50525	2.5757	2.47098	2.72766	3.17472	3.97572
1418719_at	22Rik	RIKEN cDNA 2410004L22 gene	NM_029621	76478	Mm.27355	-4.43	0.024	-1.21	6.55255	6.034	5.34274	6.36137	6.94681	6.96925
1450127_at	Gcgr	glucagon receptor	NM_008101	14527	Mm.22329	-4.43	0.024	-1.07	4.33336	3.94274	3.23721	4.50638	4.6403	4.67205
1446050_at	Magi1	membrane associated guanylate kinase, WW and PDZ domain	BG074383	14924	Mm.217216	-4.43	0.024	-1.13	4.96701	3.81872	3.83669	4.61229	5.03369	5.27456
1443797_at	Agps	alkylglycerone phosphate synthase	BB155250	228061	Mm.31227	-4.41	0.024	-1.38	2.18778	2.52071	1.95221	2.275	3.08818	3.86272
1456429_at	Malt1	mucosa associated lymphoid tissue lymphoma translocation gene 1	BB296321	240354	Mm.132613	-4.41	0.024	-1.21	7.53706	7.09438	7.22731	7.21056	8.98722	8.42627
1454551_at	02Rik	RIKEN cDNA 9530034D02 gene	AK020585	78417		-4.38	0.024	-1.07	3.10113	3.63251	2.6674	4.04772	3.69753	4.16273
1430695_at	Tlr4	toll-like receptor 4	AV230010	21898	Mm.38049	4.37	0.025	1.25	4.77374	4.83982	4.61333	2.62175	4.22957	3.22954
1443619_at	Tmem30a	transmembrane protein 30A	BB745549	69981	Mm.355034	-4.37	0.025	-1.13	7.42026	6.92868	6.90181	6.94834	7.96023	8.37308
1451811_at	Cacng6	calcium channel, voltage-dependent, gamma subunit 6	AV091458	54378	Mm.424047	-4.33	0.025	-1.2	5.45907	4.19175	5.08282	5.84204	5.75503	6.36445
1422925_at	Aco13	acyl-CoA thioesterase 3	NM_134246	171281	Mm.219001	-4.33	0.025	-1.14	2.69918	4.25255	3.6428	4.8523	4.89185	4.69828
1438878_at	16Rik	RIKEN cDNA 6430537K16 gene	AU067682	320480	Mm.440629	-4.33	0.025	-1.34	6.45756	5.23798	5.33611	6.17588	6.39613	7.12621
1433015_at	06Rik	RIKEN cDNA 6330436F06 gene	AK018204	76733		-4.32	0.026	-1.2	4.29852	3.68287	4.12558	3.97173	5.1061	5.52626
1444714_at	LOC667452	similar to Doublecortin domain containing 2B	BB529567	667452	Mm.468205	-4.32	0.026	-1.12	5.11177	4.53575	3.88154	5.13849	5.39311	5.35571
1458389_at	Klf7	Kruppel-like factor 7 (ubiquitous)	BB211886	93691	Mm.29466	-4.25	0.027	-1.05	6.00557	5.49112	6.00844	5.95281	6.70781	7.19451
1435207_at	Dixdc1	DIX domain containing 1	BB758432	330938	Mm.82598	4.24	0.027	1.43	9.24992	8.14219	7.93563	7.97089	6.822	6.55526
1435292_at	Tbc1d4	TBC1 domain family, member 4	AF023098	210789	Mm.320639	-4.22	0.027	-1.28	8.51725	7.51349	7.75424	7.7407	9.36376	9.19936
1439307_at	Cdnh2	cadherin 2	BB054169	12558	Mm.257437	-4.2	0.028	-1.37	5.74533	4.48332	4.3399	4.97884	6.19553	6.02996
1460095_at	23Rik	RIKEN cDNA 1110030E23 gene	BB347515	68681	Mm.362556	-4.17	0.028	-1.08	3.15861	2.53503	2.65917	2.54883	4.08883	3.86448
1451906_at	Ubxd3	UBX domain containing 3	BC027099	212190	Mm.292226	4.17	0.028	1.14	6.62094	7.51065	7.86649	7.01504	6.59579	6.28638
1431182_at	Hspa8	heat shock protein 8	AK004608	15481	Mm.412745	-4.16	0.029	-1.36	8.1804	7.49439	6.85391	8.93486	9.05264	8.30368
1446345_at			BB075868			-4.12	0.03	-1.03	5.62603	4.85381	4.89503	5.68781	5.52167	6.3058
1458598_at	Peg13	paternally expressed 13	BE979804	353342	Mm.440245	4.07	0.03	1.34	5.92826	6.94739	6.5486	3.97606	5.86	5.10972
1457447_at	Rb1	retinoblastoma 1	BB503322	19645	Mm.273862	-4.07	0.031	-1.05	5.74306	5.26516	5.2858	5.11274	6.4273	6.59215
1441006_at	LOC100043081	hypothetical protein LOC100043081	BB270693	100043081	Mm.458878	-4.05	0.031	-1.06	2.76048	3.17478	3.08097	3.33649	3.58939	4.45023
1439568_at	Greb1	gene regulated by estrogen in breast cancer protein	AV373997	268527		4.02	0.032	1.13	4.29028	4.30654	4.47359	4.42674	3.68188	2.91579
1429664_at	Cdk1	cyclin-dependent kinase-like 1 (CDC2-related kinase)	AI464135	71091	Mm.132325	4.02	0.032	1.08	6.58847	7.1334	7.07558	5.97911	6.64944	5.60584
1416688_at	Snap91	synaptosomal-associated protein 91	NM_013669	20616	Mm.281651	-4.02	0.032	-2.42	7.89247	7.4871	5.71242	7.2974	8.4773	9.30504
1452865_at	Lrrc27	leucine rich repeat containing 27	AK009798	76612	Mm.17757	-4	0.032	-1	8.17108	8.217	8.04398	7.76545	9.27911	9.24216
1446656_at			BB024203			-4	0.032	-1.12	5.82783	4.74415	4.47081	5.39105	5.79583	5.97912
1432867_at	17Rik	RIKEN cDNA 9230112J17 gene	BB174628	77749	Mm.410770	-4	0.032	-1.01	5.82615	7.10243	6.89888	8.17517	7.96209	7.6451
1458002_at	Mapk10	mitogen-activated protein kinase 10	BB337911	26414	Mm.472459	-3.99	0.032	-1.1	4.72625	4.64261	3.70238	4.72625	5.38674	5.15973
1446675_at	Adk	adenosine kinase	BB667305	11534	Mm.188734	-3.99	0.032	-1.05	7.29374	7.04044	6.86143	7.47945	7.41747	8.36258
1453627_at	2610020P09Rik	RIKEN cDNA 2610020P09 gene	BB153741	72153	Mm.452021	-3.99	0.033	-1.07	3.72361	4.01479	3.25117	3.47739	4.78066	4.646
1439802_at	Stk35	serine/threonine kinase 35	AV375248	67333	Mm.389329	3.87	0.036	1.51	7.17224	7.39677	7.3018	6.53487	6.80499	5.24573

1448553_at	Myh7	myosin, heavy polypeptide 7, cardiac muscle, beta	NM_080728	140781	Mm.457983	3.83	0.037	1.19	10.6749	10.6409	10.6462	10.3067	10.1641	9.02263
1425471_x_at			BC003855			3.78	0.039	1.03	5.96868	4.398	5.26531	4.24503	4.31623	4.06532
1429846_at	9030411K21Rik	RIKEN cDNA 9030411K21 gene	BM250766	71557	Mm.22379	-3.76	0.04	-1.9	4.24229	3.25782	3.38191	3.22966	4.7842	5.99057
1444440_at	4121402D02Rik	RIKEN cDNA 4121402D02 gene	BB532764	74026	Mm.258352	3.71	0.041	1	4.14705	3.90377	4.47455	3.4586	3.95755	2.98053
1424612_at	Npal2	NIPA-like domain containing 2	BC016107	223473	Mm.258402	3.7	0.042	1.08	5.08581	5.01224	5.52472	5.02076	4.83098	3.88749
1440553_at	Mecr	mitochondrial trans-2-enoyl-CoA reductase	BB310008	26922	Mm.192706	-3.69	0.042	-1.52	4.74309	3.79822	3.67443	4.33062	4.60073	5.91215
1422826_at	Igfals	insulin-like growth factor binding protein, acid labile subunit	NM_008340	16005	Mm.3135	-3.64	0.044	-1.06	6.99964	5.97661	5.71369	7.73713	7.20564	6.85639
1447670_at	Psmc9	proteasome (prosome, macropain) 26S subunit, non-ATPase, 9	AV030235	67151	Mm.278997	-3.6	0.045	-1.03	4.08513	3.49715	3.02976	3.29452	4.57163	4.39709
1433579_at	Tmem30b	transmembrane protein 30B	BG068678	238257	Mm.251196	-3.56	0.047	-1.19	2.6674	2.95538	2.88309	5.10931	3.13442	4.27763
1441413_at	Cat	catalase	BM247599	12359	Mm.4215	-3.55	0.047	-1.58	5.69004	4.1617	3.87423	5.27949	5.06534	6.22333
1441181_at			BE957389			-3.51	0.048	-1.17	6.2644	5.68625	5.26518	5.96869	6.0703	7.07207
1419735_at	Csn3	casein kappa	NM_007786	12994	Mm.296303	3.5	0.049	2.6	9.66832	5.86198	8.13028	6.96956	5.8665	4.75203

Supplementary table 2. Echocardiographic data from PTIP+ and PTIP- mice at 3 months of age, 6 months of age, and 9 months of age after tamoxifen or vehicle injection.

	<u>3 months</u>				<u>6months</u>				<u>9months</u>			
Parameter	PTIP-TAM	PTIP+ TAM	PTIP-VEH	PTIP+ VEH	PTIP-TAM	PTIP+ TAM	PTIP-VEH	PTIP+ VEH	PTIP-TAM	PTIP+ TAM	PTIP-VEH	PTIP+ VEH
Age	3.38 ± 0.61	3.35 ± 0.56	3 ± 0	3 ± 0	6.15 ± 0.75	6.15 ± 0.55	5.9 ± 0	5.5 ± 0	9.19 ± 0.82	9.4 ± 0.8	9.3 ± 0	8.95 ± 0
n	12	10	6	5	12	10	6	5	12	10	6	5
Body weight (g)	25.5 ± 2.7	27.7 ± 2.8	25.7 ± 1.7	26.1 ± 1.7	28.6 ± 3.1	31.4 ± 3.0	29 ± 2	29.5 ± 2.8	30.5 ± 3.1	34.6 ± 4.3	32.6 ± 2.4	33.9 ± 3.3
Heart rate (bpm)	472 ± 40	489 ± 41	481 ± 36	491 ± 37	484 ± 35	491 ± 35	464 ± 30	488 ± 21	470 ± 40	509 ± 44	492 ± 46	507 ± 43
EF (%)	72 ± 7.5*	55 ± 9	54 ± 10	52 ± 6	72 ± 5.3*	57 ± 10	47 ± 10	54 ± 8	67 ± 5*	57 ± 11	53 ± 6	53 ± 5
FS (%)	35 ± 6.1*	24 ± 5	23 ± 6	22 ± 3.3	35 ± 4.2*	25 ± 6	19 ± 5.6	23 ± 5	31 ± 4*	25 ± 7	22 ± 3	22 ± 3
Vcf_c	2.54 ± 0.44*	1.72 ± 0.4	1.7 ± 0.4	1.6 ± 0.3	2.8 ± 0.39*	1.96 ± 0.39	1.5 ± 0.4	1.75 ± 0.3	2.5 ± 0.3*	1.89 ± 0.46	1.8 ± 0.3	1.6 ± 0.03
Ant wall diameter (mm)	0.68 ± 0.09	0.68 ± 0.08	0.66 ± 0.08	0.73 ± 0.05	0.74 ± 0.09	0.73 ± 0.11	0.67 ± 0.06	0.7 ± 0.03	0.82 ± 0.06	0.81 ± 0.11	0.78 ± 0.07	0.87 ± 0.08
LVEDD (mm)	3.83 ± 0.4	3.99 ± 0.22	3.79 ± .3	4.06 ± 0.16	3.72 ± 0.27	3.82 ± 0.35	3.59 ± 0.3	3.54 ± 0.7	4.07 ± 0.38	4.18 ± 0.44	4.02 ± 0.27	4.17 ± 0.16
E wave(mm/sec)	1129 ± 82	1074 ± 146	948 ± 105	988 ± 109	1096 ± 133	979 ± 112	826 ± 151	1063 ± 242	1061 ± 147	1031 ± 155	904 ± 125	1003 ± 123
A wave(mm/sec)	706 ± 140	669 ± 189	646 ± 101	601 ± 72	650 ± 145	597 ± 133	646 ± 64	448 ± 59	586 ± 196	670 ± 268	570 ± 126	586 ± 194
E/A ratio	1.65 ± .29	1.62 ± 0.4	1.5 ± 0.2	1.7 ± 0.3	1.75 ± 0.4	1.76 ± 0.63	1.3 ± 0.3	2.7 ± 0.3	1.93 ± 0.5	1.68 ± 0.57	1.6 ± 0.4	1.78 ± 0.56
DT (msec)	17.7 ± 4.5	11.65 ± 4.5	13.3 ± 5.7	10.8 ± 1.5	14.7 ± 7.8	11.9 ± 3.8	10.2 ± 4.6	13.1 ± .9	15.5 ± 7.0	12.4 ± 4.9	12.6 ± 1.1	9.2 ± 1.6
IVRT (msec)	17.22 ± 1.4	19.98 ± 1.93	20.3 ± 1.7	20.6 ± 4.6	15.1 ± 2.1*	20.9 ± 3.2	23.3 ± 1.6	18.9 ± 4.1	15.9 ± 1.8*	20.7 ± 2.6	20.4 ± 3.6	20.5 ± 3.8

TAM=tamoxifen, VEH= vehicle, EF= ejection fraction, FS= fractional shortening, Vcfc= velocity of circumferential fractional shortening, Ant= anterior, LVEDD= left ventricle end diastolic diameter, DT= deceleration time, IVRT= isovolumic relaxation time

*p<0.01 vs. PTIP+TAM, PTIP- VEH, PTIP- VEH

Supplemental Table 3. qPCR Primer information

KChIP2 Primers for ChIP

Location relative to first ATG	Forward	Reverse
-500	GTGAAGGGGTGAACTGGA	AGAGGTGCCTGAGAATTG
-100	GATAGGGCGCTCACACAGT	CTTCTGCTCCGCTCTCACTT
+100	GGTCTAGGGGGATGGAGTCT	AGGCCGAAAGGAGAGTTTGT

Nppb Primers for ChIP

Location relative to first ATG	Forward	Reverse
-1100	GTTTCCCTTGGGTCAGAACA	AGGACAATGACCAGGAGTGG
-500	AAGTACACGTGTGGCGATCA	TATGGCGTGACTCATGGAAA
0	CAGAGGGGTGAATTCTCAGG	CAGCTTGTGCACTGGTGTCT