Supplementary Information for:

Foxa1 and Foxa2 maintain the metabolic and secretory features of mature β-cell

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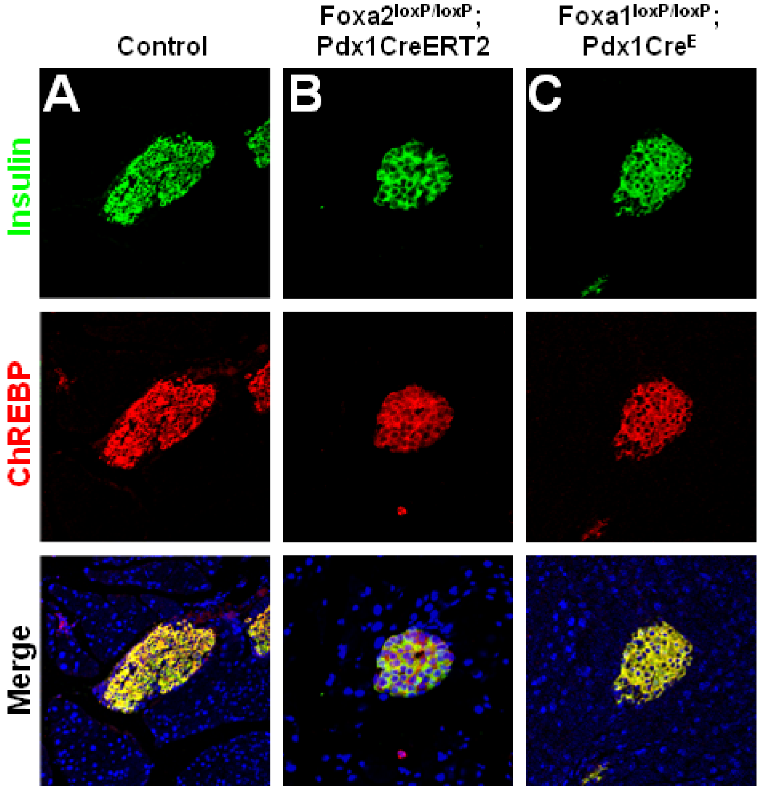
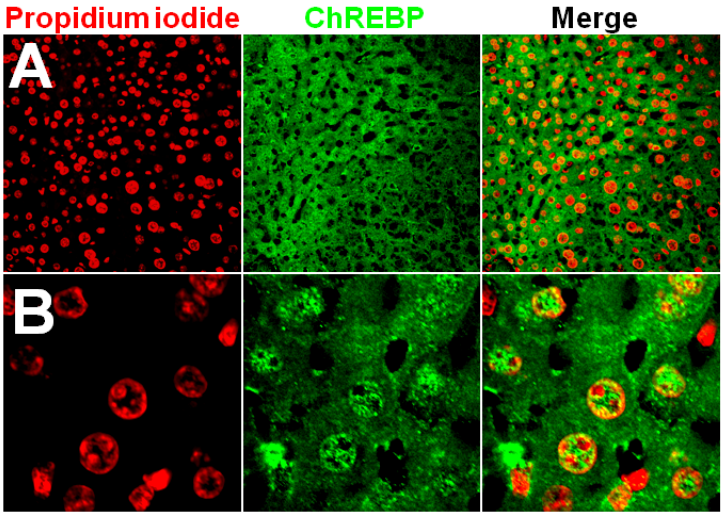
Supplementary Figure 1. Normal ChREBP expression level is maintained in *Foxa1*-deficient and *Foxa2*-deficient mouse islets.

(A-C) Control, *Foxa1*$^{loxP/loxP}$*;Pdx1Cre* and *Foxa2*$^{loxP/loxP}$*;Pdx1CreERT2* mouse pancreas were stained for ChREBP (red) and Insulin (green). Nuclei were counterstained by DAPI in blue.



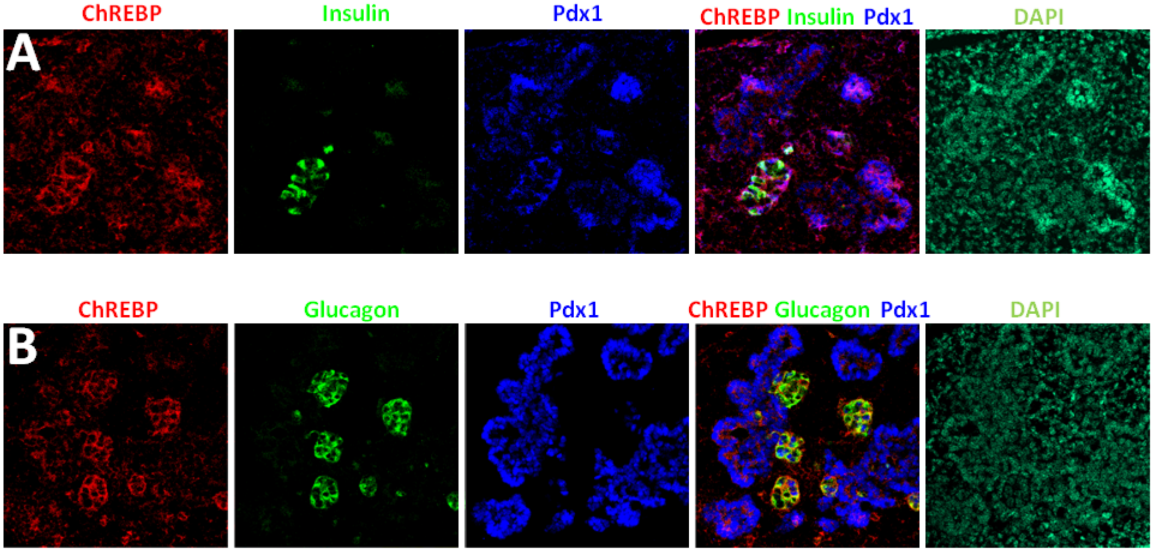
Supplementary Figure 2. Cytoplasmic ChREBP staining is found in wild type liver cells.

(A-B) Wild type liver sections were stained for ChREBP (green) and propidium iodide (red).



Supplementary Figure 3. ChREBP expression becomes enriched in differentiated endocrine cells.

(A-B) ChREBP (red) was co-stained with Pdx1 (blue), and Insulin (green in A) or Glucagon (green in B) in E12.5 pancreas.



Supplementary Table 1. Microarray data sets joined from previous *Foxa2*$^{loxP/loxP}$*;Pdx1CreERT2* study (Experiment #349) and current *Foxa1*$^{loxP/loxP}$*;Foxa2*$^{loxP/loxP}$*;Pdx1CreERT2* experiment (#536). Fold changes are highlighted in yellow and green for compound mutant islet and for *Foxa2*-deficient islet, respectively.

GeneName	ProbeName	TranscriptID	Description	536_FC	536_FDR	536_Pvalue	536_Ranking	536_Call	349_FC	349_FDR	349_Pvalue	349_Ranking
				FOXA1 and FOXA2					FOXA2 only			
Penk1	A_51_P102987	NM_001002927	preproenkephalin 1	19.424	0	0.01967	138	M	A_51_P102	33.49	0.23748	5453
Afm	A_52_P425734	NM_145146	afamin	8.049	0.55	0.03041	183	P	1.042	30.75	0.56071	9114
Lmo1	A_52_P331762	NM_057173	LIM domain only 1	7.869	0	0.00773	29	P	-1.121	3.01	0.0383	1457
Svil	A_51_P344301	AK021019	supervillin	6.789	0	0.01239	40	P	-1.029	45.68	0.49548	8515
6330403K07Rik	A_51_P417251	NM_134022	RIKEN cDNA 6330403K07 gene	6.714	4.65	0.11802	906	P	2.008	0	0.00841	310
Enpp3	A_51_P332917	BC005527	ectonucleotide pyrophosphatase/phosph	5.379	3.78	0.0868	613	P	-1.042	44.4	0.49497	8513
Sgk2	A_51_P384230	NM_013731	serum/glucocorticoid regulated kinase 2	4.757	0	0.01385	59	P	1.147	3.46	0.02439	1005
Dapp1	A_52_P422172	NM_011932	dual adaptor for phosphotyrosine and 3-p	4.647	0	0.0212	131	P	1.056	28.13	0.48193	8334
Sez6	A_52_P871	AK032277	seizure related gene 6	3.801		0.2249	1455	A	-1.007	49.48	0.89082	11974
Sparcl1	A_52_P64356	NM_010097	SPARC-like 1 (mast9, hevin)	3.776	7.45	0.1716	1340	M	2.856	0	0.00627	156
Nqo1	A_51_P424338	NM_008706	NAD(P)H dehydrogenase, quinone 1	3.716	1.85	0.06906	431	M	1.183	3.01	0.0227	963
Cpa4	A_52_P158376	NM_027926	carboxypeptidase A4	3.559	6.91	0.13833	1094	P	1.166	3.46	0.02307	974
3110001A13Rik	A_51_P521084	NM_025626	RIKEN cDNA 3110001A13 gene	3.443	13.61	0.26351	3046	P	1.559	0	0.00584	42
D1Ertd471e	A_51_P452533	BC035277	DNA segment, Chr 1, ERATO Doi 471, expr	3.396	6.57	0.13087	1030	P	1.577	0	0.00584	7
Sox6	A_52_P475356	NM_011445	SRY-box containing gene 6	3.248	6.57	0.12793	1001	P	1.046	25.31	0.32591	6626
Mmd	A_51_P298991	AK036131	predicted gene, OTTMUSG00000001284	3.225	1.29	0.03457	207	P	1.31	1.17	0.01435	603
Kntc1	A_51_P408071	NM_001042421	kinetochore associated 1	3.209	7.45	0.15022	1246	P	1.12	8.32	0.09755	3048
Epb4.1l4a	A_51_P513898	NM_013512	erythrocyte protein band 4.1-like 4a	3.146	6.57	0.1228	945	P	1.043	28.13	0.41666	7703
9030425E11Rik	A_51_P206144	NM_133733	RIKEN cDNA 9030425E11 gene	3.09	6.91	0.1396	1117	P	1.025	40.63	0.80501	11220
Vldlr	A_51_P500044	AK036010	very low density lipoprotein receptor	3.05	0	0.01529	70	P	1.138	9.71	0.19896	4881
Asb3	A_52_P649786	AK038897	ankyrin repeat and SOCS box-containing p	3.039	28.61	0.41654	6932	P	-1.003	49.48	0.98574	12935
Slc39a8	A_52_P485939	NM_026228	solute carrier family 39 (metal ion transpo	3.032	5.15	0.10304	782	P	2.181	0.35	0.04166	1576
Pard6g	A_51_P425657	NM_053117	par-6 partitioning defective 6 homolog ga	3.018	0.55	0.02209	133	P	1.012	42.43	0.88003	11858
Igsf4a	A_52_P116204	NM_001025600	cell adhesion molecule 1	2.994	2.87	0.06417	391	P	1.66	0	0.00584	22
Oat	A_51_P141535	NM_016978	ornithine aminotransferase	2.939	2.4	0.06148	366	P	-1.142	2.53	0.03076	1215
Nnat	A_52_P484956	NM_010923	neuronatin	2.918	5.86	0.10991	844	P	-1.061	36.07	0.26774	5910
1190002N15Rik	A_52_P394291	NM_001033145	RIKEN cDNA 1190002N15 gene	2.896	0	0.01766	110	P	1.444	0.24	0.00584	32
Capn6	A_52_P474089	NM_007603	calpain 6	2.883	4.11	0.0868	615	P	1.1	9.71	0.10367	3181
Fdps	A_52_P593965	AK077979	farnesyl diphosphate synthetase	2.858	10.33	0.19826	1929	P	-1.03	45.68	0.50559	8642
Moxd1	A_51_P493987	NM_021509	monooxygenase, DBH-like 1	2.753	1.85	0.05412	321	P	1.063	25.31	0.42886	7813
Col6a3	A_52_P479262	XM_897036	procollagen, type VI, alpha 3	2.7	10.33	0.1849	1700	P	1.119	13.58	0.26039	5822
Gast	A_52_P236233	NM_010257	gastrin	2.689	4.65	0.0868	614	P	1.112	8.32	0.07325	2483
Zfp185	A_52_P384264	NM_009549	zinc finger protein 185	2.607	1.85	0.04796	287	P	1.11	9.71	0.1388	3815
Slc38a5	A_51_P400269	NM_172479	solute carrier family 38, member 5	2.572	3.78	0.07004	458	P	1.386	1.58	0.03268	1286
Dlk1	A_51_P135618	L12721	delta-like 1 homolog (Drosophila)	2.554	12.21	0.23102	2399	P	-1.155	2.04	0.03017	1204
Dach2	A_51_P126167	NM_033605	dachshund 2 (Drosophila)	2.515	0.77	0.02553	151	P	2.145	0	0.00584	16
Mrc1	A_51_P439248	NM_008625	mannose receptor, C type 1	2.471	1.29	0.03399	202	P	1.083	11.33	0.12478	3596
Chgb	A_52_P652560	AK044172	chromogranin B	2.388	3.78	0.06683	421	P	2.603	0	0.00367	1
Adamts2	A_51_P164817	AK029026	a disintegrin-like and metallopeptidase (re	2.377	10.84	0.19103	1820	P	-1.003	49.48	0.96986	12743
Degs1	A_51_P498890	NM_007853	degenerative spermatocyte homolog 1 (D	2.366	1.29	0.06234	364	M	1.264	3.01	0.04735	1771
Pax1	A_51_P145322	NM_008780	paired box gene 1	2.359		0.33699	2645	A	1.019	40.63	0.74976	10785
Fbp1	A_51_P474701	NM_019395	fructose bisphosphatase 1	2.354	3.82	0.06906	446	P	-1.27	0.66	0.0146	619
Dcamkl1	A_52_P563818	NM_019978	doublecortin-like kinase 1	2.338	8.15	0.15615	1298	P	-1.005	49.48	0.91531	12221
Fbln1	A_51_P154417	NM_010180	fibulin 1	2.338	25.79	0.3647	5490	P	1	49.48	0.99613	13025
Pdgfra	A_51_P345649	NM_011058	platelet derived growth factor receptor, a	2.334	16.01	0.24565	2724	P	1.019	40.63	0.76472	10891
Ttyh1	A_51_P428384	NM_021324	tweety homolog 1 (Drosophila)	2.33	0.77	0.02663	158	P	1.093	19.02	0.3867	7357
Dhh	A_52_P232637	NM_007857	desert hedgehog	2.322	6.91	0.12332	960	P	1.009	42.43	0.83579	11495
Scd2	A_51_P129464	NM_009128	stearoyl-Coenzyme A desaturase 2	2.319	3.78	0.09507	648	M	1.462	1.32	0.03814	1444
Asb4	A_52_P594756	NM_023048	ankyrin repeat and SOCS box-containing p	2.304	8.15	0.14404	1182	P	1.17	5.75	0.09575	3009
Cdh11	A_52_P437795	NM_009866	cadherin 11	2.299	13.61	0.24363	2650	P	-1.019	49.39	0.73433	10621
Sdc2	A_51_P157255	NM_008304	syndecan 2	2.299	1.85	0.0442	266	P	1.223	11.33	0.37912	7270

Asph	A_52_P625171	NM_133723	aspartate-beta-hydroxylase	2.298	9.39	0.16264	1390	P	1.186	3.46	0.03137	1238
Dpt	A_51_P116651	NM_019759	dermatopontin	2.28	10.33	0.17663	1590	P	1.272	5.75	0.15965	4213
Rasgrp1	A_52_P487303	NM_011246	RAS guanyl releasing protein 1	2.278	28.61	0.37646	5792	P	1.758	0	0.00584	10
E030049G20Rik	A_51_P379478	NM_172484	RIKEN cDNA E030049G20 gene	2.256	18.5	0.27048	3159	P	1.078	16.2	0.26671	5896
Dpep1	A_51_P227345	NM_007876	dipeptidase 1 (renal)	2.244	12.21	0.22227	2237	P	-1.055	43.15	0.50642	8649
Col1a1	A_52_P525107	NM_007742	procollagen, type I, alpha 1	2.24	25.79	0.34902	5082	P	1.09	13.58	0.164	4282
Dlgh1	A_52_P499541	XM_924111	discs, large homolog 1 (Drosophila)	2.231	1.58	0.041	250	P	1.061	19.02	0.25085	5658
Snca	A_51_P509643	NM_001042451	synuclein, alpha	2.228	23.47	0.32119	4400	P	1.015	42.43	0.92817	12373
Flrt3	A_52_P476935	NM_178382	fibronectin leucine rich transmembrane p	2.209	28.61	0.3844	6017	P	1	42.43	0.99989	10872
Rerg	A_51_P305508	NM_181988	RAS-like, estrogen-regulated, growth-inhi	2.207	18.5	0.2729	3261	P	1.108	19.02	0.45812	8078
Camta1	A_52_P617512	XM_355539	calmodulin binding transcription activato	2.201	7.45	0.12319	954	P	1.066	16.2	0.20664	5002
2810055G20Rik	A_52_P502332	AK033222	RIKEN cDNA 2810055G20 gene	2.199	5.86	0.09225	682	P	-1.153	3.01	0.03997	1526
Rasl11b	A_51_P293938	NM_026878	RAS-like, family 11, member B	2.193	9.39	0.15198	1257	P	-1.006	49.48	0.9162	12230
Fzd7	A_52_P552665	NM_008057	frizzled homolog 7 (Drosophila)	2.184	1.21	0.02965	179	P	1.401	1.62	0.04505	1675
Angptl6	A_52_P319199	NM_145154	angiopoietin-like 6	2.154	4.11	0.07147	474	P	-1.073	30.75	0.23652	5443
Gfra3	A_51_P520426	NM_010280	glial cell line derived neurotrophic factor	2.141	8.15	0.1373	1085	P	-1.165	1.62	0.02979	1187
Aldob	A_51_P337269	NM_144903	aldolase 2, B isoform	2.127	49.93	0.59973	13428	P	1.058	19.02	0.23823	5461
Ppp2r2b	A_51_P220278	NM_028392	protein phosphatase 2 (formerly 2A), regu	2.12	1.85	0.04543	273	P	1.033	30.75	0.49807	8560
Mmp7	A_51_P426096	NM_010810	matrix metallopeptidase 7	2.103	69.29	0.83609	19007	M	-1.035	45.05	0.50522	8629
Clybl	A_52_P88818	NM_029556	citrate lyase beta like	2.096	1.29	0.03523	219	P	1.083	16.2	0.21313	5086
Odz4	A_52_P144368	AK147579	odd Oz/ten-m homolog 4 (Drosophila)	2.093	3.78	0.06649	413	P	1.073	13.58	0.1702	4387
Cacna1g	A_51_P466910	NM_009783	calcium channel, voltage-dependent, T ty	2.09	20.94	0.28406	3514	P	1.189	3.01	0.02193	928
H6pd	A_52_P83549	NM_173371	hexose-6-phosphate dehydrogenase (gluc	2.086	12.21	0.2021	1971	P	-1.027	47.43	0.62692	9690
Postn	A_51_P489192	NM_015784	periostin, osteoblast specific factor	2.086	18.5	0.2659	3079	P	-1.099	16.2	0.14477	3940
Comt	A_51_P129895	NM_007744	catechol-O-methyltransferase	2.082	4.11	0.07471	517	P	1.053	30.75	0.59745	9428
Olfm1	A_51_P137236	NM_019498	olfactomedin 1	2.078	20.94	0.30385	3964	P	1.202	3.46	0.03912	1480
2310028N02Rik	A_51_P251552	NM_025864	RIKEN cDNA 2310028N02 gene	2.066	1.85	0.09095	601	M	-1.117	11.33	0.14431	3928
Aldh1l2	A_52_P498193	NM_153543	aldehyde dehydrogenase 1 family, memb	2.064	1.58	0.04513	269	P	1.061	25.31	0.41732	7712
Auts2	A_51_P398191	AK147478	autism susceptibility candidate 2	2.062	9.39	0.15792	1320	P	1.147	16.2	0.4504	7997
Gap43	A_51_P290065	NM_008083	growth associated protein 43	2.062	23.47	0.32211	4423	P	1.896	0.24	0.01703	737
Rcor2	A_51_P306689	NM_054048	REST corepressor 2	2.056	4.11	0.07465	502	P	1.075	16.2	0.23701	5448
Mpp6	A_51_P265327	NM_019939	membrane protein, palmitoylated 6 (MAG	2.046	1.29	0.03882	237	P	-1.122	9.71	0.10651	3213
Uchl1	A_52_P24308	NM_011670	ubiquitin carboxy-terminal hydrolase L1	2.029	35.45	0.45533	8063	P	1.04	36.07	0.7143	10440
Gnas	A_51_P326769	AK047990	GNAS (guanine nucleotide binding protei	2.028	31.88	0.41042	6749	P	1.184	8.32	0.18428	4644
Dars	A_52_P596635	AK077820	aspartyl-tRNA synthetase	2.023	28.61	0.38302	5996	P	1.12	11.33	0.178	4536
Prodh2	A_51_P457446	NM_019546	proline dehydrogenase (oxidase) 2	2.017	10.84	0.1849	1708	P	1.102	9.71	0.08423	2755
Enpp2	A_51_P401974	NM_015744	ectonucleotide pyrophosphatase/phosph	2.005	5.86	0.13644	981	M	-1.105	6.98	0.06646	2330
Sim1	A_51_P239994	NM_011376	single-minded homolog 1 (Drosophila)	1.994	16.01	0.24235	2582	P	1.061	16.2	0.1817	4608
Fkbp1a	A_52_P416810	AK085599	FK506 binding protein 1a	1.992	10.84	0.1769	1603	P	-1.075	33.49	0.31065	6459
Crim1	A_52_P46447	AK053197	cysteine rich transmembrane BMP regula	1.979	12.21	0.19826	1928	P	1.145	13.58	0.36528	7103
Pitrm1	A_51_P474960	NM_145131	pitrilysin metallepetidase 1	1.972	1.21	0.03678	230	P	1.153	4.63	0.03971	1519
Rps6ka5	A_51_P255945	NM_153587	ribosomal protein S6 kinase, polypeptide	1.971	6.91	0.10809	824	P	1.313	1.17	0.01251	504
Lpl	A_51_P259296	NM_008509	lipoprotein lipase	1.97	1.85	0.09561	651	M	1.295	2.53	0.04414	1651
Lmo3	A_51_P118188	NM_207222	LIM domain only 3	1.965	20.94	0.28781	3571	P	1.082	11.33	0.10441	3195
Acpp	A_52_P119060	NM_207668	acid phosphatase, prostate	1.964	53.87	0.62723	12682	M	-1.012	49.48	0.85722	11650
Tubb6	A_51_P421140	NM_026473	tubulin, beta 6	1.958	20.94	0.28377	3507	P	-1.086	33.49	0.38457	7333
2210408F21Rik	A_52_P307142	XM_895387	RIKEN cDNA 2210408F21 gene	1.956	6.57	0.09988	751	P	1.358	0.92	0.01251	523
Pfkp	A_52_P572045	NM_019703	phosphofructokinase, platelet	1.945	1.29	0.0419	255	P	1.015	42.43	0.85145	11603
Tle4	A_51_P346543	NM_011600	transducin-like enhancer of split 4, homol	1.943	4.65	0.1373	1011	M	1.44	0.24	0.00637	172
Gyk	A_52_P120066	NM_212444	glycerol kinase	1.94	23.47	0.30455	4015	P	1.008	42.43	0.86714	11733
Flna	A_52_P582722	XM_920628	filamin, alpha	1.937		0.40486	4448	A	1.045	28.13	0.48793	8422
Aak1	A_51_P284686	NM_001040106	AP2 associated kinase 1	1.931	6.91	0.1085	833	P	1.239	2.04	0.01927	810
Tbc1d1	A_51_P293516	NM_019636	TBC1 domain family, member 1	1.928	1.29	0.04173	252	P	1.369	0.66	0.00977	361

E2f1	A_52_P587611	NM_007891	E2F transcription factor 1	1.926	16.01	0.23499	2442	P	1.112	6.98	0.05792	2083
2010004A03Rik	A_51_P268234	NM_029646	RIKEN cDNA 2010004A03 gene	1.921	20.94	0.27386	3292	P	-1.191	1.32	0.02595	1073
Hmox1	A_51_P263965	NM_010442	heme oxygenase (decycling) 1	1.92	16.01	0.23607	2464	P	1.093	19.02	0.41142	7618
Cbfb	A_52_P586157	NM_022309	core binding factor beta	1.915	10.33	0.16388	1415	P	1.097	13.58	0.23277	5394
Trib3	A_51_P331570	NM_175093	tribbles homolog 3 (Drosophila)	1.912	20.94	0.26884	3131	P	1.11	8.32	0.07692	2572
Gpd1	A_52_P16419	NM_010271	glycerol-3-phosphate dehydrogenase 1 (s	1.911	10.33	0.15824	1330	P	1	49.48	0.99923	13048
Dcn	A_51_P334104	NM_007833	decorin	1.909	18.5	0.25347	2858	P	1.04	30.75	0.51989	8753
Ptger4	A_52_P223473	AK051137	prostaglandin E receptor 4 (subtype EP4)	1.909		0.43053	4076	A	-1.019	49.48	0.904	12131
1500032D16Rik	A_52_P170054	NM_030087	RIKEN cDNA 1500032D16 gene	1.908	2.87	0.10961	776	M	1.166	6.98	0.11145	3310
Scp2	A_52_P1084657	AK087232		1.906		0.26762	2101	A	1.106	19.02	0.43821	7904
Cryz	A_51_P435198	NM_009968	crystallin, zeta	1.9	5.86	0.09133	652	P	1.28	1.62	0.02145	902
Epha7	A_52_P306236	AK033903	Eph receptor A7	1.898	10.33	0.16749	1461	P	1.065	25.31	0.47406	8234
Phyhipl	A_52_P661327	NM_178621	phytanoyl-CoA hydroxylase interacting pr	1.895	6.91	0.10304	793	P	1.011	42.43	0.82193	11378
Ssbp2	A_52_P522977	NM_024272	single-stranded DNA binding protein 2	1.882	2.87	0.06278	384	P	-1.055	42.43	0.40226	7538
Gdnf	A_51_P147777	NM_010275	glial cell line derived neurotrophic factor	1.881		0.43918	4220	A	1.031	33.49	0.57453	9223
Rps6ka6	A_52_P507665	NM_025949	ribosomal protein S6 kinase polypeptide	1.881	4.65	0.08003	558	P	-1.051	45.05	0.64944	9878
Fgd2	A_52_P260994	NM_013710	FYVE, RhoGEF and PH domain containing	1.876	1.85	0.05518	341	P	1.076	16.2	0.2431	5545
Acad9	A_52_P73208	AK049931	acyl-Coenzyme A dehydrogenase family, r	1.871	6.91	0.10722	819	P	-1.171	2.53	0.04872	1817
3321401G04Rik	A_52_P250578	AK132148	RIKEN cDNA 3321401G04 gene	1.867	2.87	0.06484	401	P	1.003	42.43	0.95758	12640
Ogfrl1	A_52_P175342	XM_129809	opioid growth factor receptor-like 1	1.86	5.86	0.0915	662	P	-1.089	22.1	0.18583	4664
Galnt10	A_52_P1028560	AK082774	UDP-N-acetyl-alpha-D-galactosamine:poly	1.856	49.93	0.37281	4067	M	-1.154	1.62	0.02757	1117
Lamp2	A_52_P636724	AK078193	lysosomal-associated membrane protein	1.851	16.01	0.23388	2421	P	1.165	3.01	0.01933	814
Adamts5	A_52_P70231	AK046558	a disintegrin-like and metallopeptidase (r	1.846	8.15	0.13482	1066	M	1.001	42.43	0.99046	12989
Tnfrsf10b	A_52_P10134	NM_020275	tumor necrosis factor receptor superfami	1.843	38.68	0.39052	5372	M	-1.1	11.33	0.10311	3174
Hebp1	A_51_P376347	NM_013546	heme binding protein 1	1.839	23.47	0.29034	3624	P	1.083	16.2	0.22626	5289
Esr1	A_51_P474658	NM_007956	estrogen receptor 1 (alpha)	1.838	10.84	0.25357	2029	M	1.019	38.4	0.70466	10356
Sox5	A_51_P500318	NM_011444	SRY-box containing gene 5	1.838		0.45319	4451	A	1.007	42.43	0.94576	12548
Rab3il1	A_51_P451759	BC020147	RAB3A interacting protein (rabin3)-like 1	1.837	7.45	0.11112	853	P	1.19	2.53	0.01648	706
D230012E17Rik	A_52_P222981	AK033485	RIKEN cDNA D230012E17 gene	1.836	10.33	0.16042	1344	P	-1.123	13.58	0.16913	4371
Col3a1	A_51_P515605	NM_009930	procollagen, type III, alpha 1	1.835	13.61	0.21221	2092	P	1.244	2.53	0.03416	1314
Ing4	A_52_P647226	AK046126	inhibitor of growth family, member 4	1.832	20.94	0.27429	3294	P	1.041	28.13	0.42552	7784
Dach1	A_51_P356552	NM_007826	dachshund 1 (Drosophila)	1.83	10.33	0.16264	1387	P	-1.094	9.71	0.08302	2729
Col5a2	A_51_P247883	NM_007737	procollagen, type V, alpha 2	1.826	5.15	0.08421	588	P	1.013	42.43	0.77383	10951
Adarb1	A_52_P665604	AK006823	adenosine deaminase, RNA-specific, B1	1.824	10.33	0.16528	1433	P	1.379	0.92	0.0146	624
Cox7a2l	A_51_P434803	NM_009187	cytochrome c oxidase subunit VIIa polype	1.824	4.65	0.14112	1051	M	1.267	4.63	0.12227	3548
Umod	A_52_P312806	NM_009470	uromodulin	1.823		0.49177	6338	A	1.114	13.58	0.25649	5752
Dner	A_52_P671132	NM_152915	delta/notch-like EGF-related receptor	1.818	7.45	0.17491	1379	M	-1.043	40.63	0.31571	6533
Tmed6	A_51_P258176	NM_025458	transmembrane emp24 protein transport	1.816	25.79	0.33558	4788	P	1.213	3.01	0.03779	1435
Fn3k	A_51_P398525	NM_022014	fructosamine 3 kinase	1.813	12.21	0.19392	1862	P	-1.077	30.75	0.29147	6222
Itgav	A_52_P30341	AK052514	integrin alpha V	1.813	18.5	0.24373	2654	P	1.245	2.53	0.03311	1292
Gdf10	A_51_P185247	NM_145741	growth differentiation factor 10	1.812	9.39	0.1498	1242	P	1.149	9.71	0.17322	4429
Nefl	A_51_P339934	NM_010910	neurofilament, light polypeptide	1.805	10.84	0.16749	1460	P	1.058	22.1	0.29656	6288
Gucy1a3	A_52_P452540	NM_021896	guanylate cyclase 1, soluble, alpha 3	1.803	12.21	0.19726	1896	P	1.185	5.75	0.10129	3133
Zfp207	A_52_P381341	AK164121	zinc finger protein 207	1.803	13.61	0.19756	1908	P	-1.062	44.4	0.67365	10084
Gpr146	A_51_P316379	NM_030258	G protein-coupled receptor 146	1.8	9.39	0.14282	1165	P	1.025	36.07	0.63764	9785
Slc34a1	A_51_P498442	NM_011392	solute carrier family 34 (sodium phosphat	1.799	10.84	0.15198	1225	M	-1.073	19.02	0.12581	3624
AW146020	A_52_P27849	AK077263	expressed sequence AW146020	1.793		0.44411	5256	A	-1.024	47.43	0.61706	9602
Spred1	A_51_P422996	NM_033524	sprouty protein with EVH-1 domain 1, rel	1.79		0.4699	4757	A	1.106	16.2	0.31099	6468
Cldn2	A_52_P251450	NM_016675	claudin 2	1.788	72.2	0.82667	25816	P	-1.15	2.04	0.03054	1210
Evc	A_52_P476431	NM_021292	Ellis van Creveld gene homolog (human)	1.788	6.57	0.09968	749	P	1.087	13.58	0.15653	4156
App	A_51_P318104	M18373	amyloid beta (A4) precursor protein	1.784	12.21	0.1859	1728	P	1.453	0.24	0.0063	169
Dpp4	A_51_P467110	NM_010074	dipeptidylpeptidase 4	1.784	9.39	0.19756	1657	M	1.122	11.33	0.22271	5250
Fxr1h	A_52_P166681	AK020641	fragile X mental retardation gene 1, autos	1.783	8.15	0.12849	1010	P	1.006	42.43	0.93342	12416

Idi1	A_52_P441634	NM_177960	isopentenyl-diphosphate delta isomerase	1.779	13.61	0.2021	1970	P	-1.109	43.15	0.68243	10161
Sema3b	A_52_P426698	NM_001042779	sema domain, immunoglobulin domain (I	1.775	35.45	0.43315	7453	P	-1.091	22.1	0.18898	4707
Insig1	A_52_P393392	NM_153526	insulin induced gene 1	1.774	10.84	0.17552	1580	P	-1.213	22.1	0.43222	7860
Slc5a1	A_52_P669128	NM_019810	solute carrier family 5 (sodium/glucose c	1.773	35.45	0.43567	7513	P	1.505	0.56	0.01695	733
Gdf3	A_51_P217039	NM_008108	growth differentiation factor 3	1.764	25.79	0.24145	2479	P	-1.019	49.47	0.74363	10738
Tnc	A_51_P291438	NM_011607	tenascin C	1.763	12.21	0.1849	1698	P	-1.08	16.2	0.11626	3403
Mrpl1	A_52_P86073	NM_001039084	mitochondrial ribosomal protein L1	1.76	9.39	0.14222	1157	P	1.101	13.58	0.25329	5700
Ccrn4l	A_51_P189777	NM_009834	CCR4 carbon catabolite repression 4-like (	1.759	6.91	0.16264	1271	M	-1.188	1.62	0.03962	1508
Cd81	A_51_P223443	NM_133655	CD 81 antigen	1.758	35.45	0.43065	6112	M	1.155	6.98	0.09505	2998
Il16	A_52_P558502	AK038014	interleukin 16	1.758	6.91	0.10221	765	P	1.081	11.33	0.10136	3134
2700092H06Rik	A_51_P110220	AK083290	RIKEN cDNA 2700092H06 gene	1.755	25.79	0.31761	4312	P	1.061	22.1	0.37012	7165
Ppp1r1a	A_51_P293538	NM_021391	protein phosphatase 1, regulatory (inhibit	1.755	6.57	0.16264	1237	M	1.214	2.04	0.0156	665
Fmod	A_51_P207622	NM_021355	fibromodulin	1.754	20.94	0.27669	3358	P	1.051	25.31	0.43286	7870
Aldh1a1	A_51_P334942	NM_013467	aldehyde dehydrogenase family 1, subfam	1.753	28.61	0.33757	4859	P	1.156	9.71	0.20244	4937
Cav1	A_52_P306845	NM_007616	caveolin, caveolae protein 1	1.752	8.15	0.13299	1054	P	-1.087	42.43	0.60076	9459
Clcn3	A_52_P462049	AK036501	chloride channel 3	1.751	18.5	0.25084	2796	P	1.212	1.62	0.01278	542
Mrpl50	A_52_P432780	NM_178603	mitochondrial ribosomal protein L50	1.751	20.94	0.25347	2863	P	1.131	9.71	0.15934	4203
Spp1	A_51_P358765	NM_009263	secreted phosphoprotein 1	1.751	53.87	0.59378	13158	P	2.227	0.24	0.01278	544
Nfia	A_52_P231217	AK050320	nuclear factor I/A	1.749	23.47	0.2848	3522	P	1.073	25.31	0.49031	8434
Eif2c1	A_52_P313035	NM_153403	eukaryotic translation initiation factor 2C,	1.747	38.68	0.29829	3091	M	1.131	6.98	0.05903	2107
Phka2	A_51_P368950	AK018208	phosphorylase kinase alpha 2	1.747	20.94	0.26649	3092	P	-1.326	0.51	0.01177	472
Commd1	A_51_P218205	NM_144514	COMM domain containing 1	1.744	10.33	0.16264	1392	P	1.048	25.31	0.3411	6779
4932408B21Rik	A_52_P512137	NM_172535	IQ motif and ubiquitin domain containing	1.742		0.37646	4808	A	-1.094	40.63	0.58625	9308
Tbl1xr1	A_51_P292057	NM_030732	transducin (beta)-like 1X-linked receptor	1.74	10.33	0.16091	1359	P	1.467	0.24	0.00591	106
Dapk1	A_52_P445346	AK009701	death associated protein kinase 1	1.737	45.92	0.53335	10824	P	1.067	19.02	0.30947	6430
Hlx1	A_51_P179701	NM_008250	H2.0-like homeo box 1 (Drosophila)	1.736	28.61	0.354	5219	P	-1.208	1.58	0.03605	1400
Itm2a	A_51_P516870	NM_008409	integral membrane protein 2A	1.736	45.92	0.51314	10068	P	1.119	8.32	0.09118	2927
Fzd6	A_52_P217710	NM_008056	frizzled homolog 6 (Drosophila)	1.735	9.39	0.14282	1164	P	1.153	3.82	0.03466	1327
C330050A14Rik	A_52_P89002	AK084600	RIKEN cDNA C330050A14 gene	1.732		0.47441	5941	A	1.035	30.75	0.44272	7941
Il17rc	A_52_P48976	AK033890	interleukin 17 receptor C	1.731	49.93	0.37939	5438	M	-1.108	13.58	0.13456	3756
Ptprz1	A_51_P206405	XM_888896	protein tyrosine phosphatase, receptor ty	1.728	10.33	0.15741	1312	P	1.197	5.75	0.12523	3606
Trim24	A_52_P148571	AK084870	tripartite motif protein 24	1.728		0.49127	5156	A	1.071	19.02	0.25196	5682
Lrp1	A_52_P202045	AK078273	low density lipoprotein receptor-related p	1.727	9.39	0.1441	1186	P	-1.01	49.48	0.90658	12159
Prrx1	A_51_P209778	NM_001025570	paired related homeobox 1	1.723	8.15	0.13061	1028	P	-1.303	0.51	0.00697	215
Plec1	A_52_P1100772	AK089422	plectin 1	1.72	6.91	0.208	1770	M	-1.146	6.98	0.1174	3428
Scml2	A_52_P134598	NM_133194	sex comb on midleg-like 2 (Drosophila)	1.72	9.39	0.1416	1144	P	-1.01	49.48	0.83907	11523
Sema5b	A_52_P385824	BC052397	sema domain, seven thrombospondin rep	1.719	35.45	0.30252	3377	M	1.025	38.4	0.72778	10549
Mapk6	A_51_P193925	AK011505	mitogen-activated protein kinase 6	1.717	28.61	0.34663	5037	P	1.137	6.98	0.06941	2384
Paqr9	A_52_P450934	NM_198414	progestin and adipoQ receptor family me	1.717	10.33	0.16221	1365	P	1.097	11.33	0.12271	3556
Ppargc1a	A_52_P5945	AK032149	peroxisome proliferative activated recept	1.716	13.61	0.19726	1897	P	1.098	9.71	0.07774	2588
Vapb	A_51_P323443	NM_019806	vesicle-associated membrane protein, ass	1.716	6.57	0.09691	723	P	1.502	0	0.00584	19
4930519N13Rik	A_52_P402663	AK019685	RIKEN cDNA 4930519N13 gene	1.715	7.45	0.12136	932	P	1.084	22.1	0.45861	8088
Csf1	A_51_P195506	NM_007778	colony stimulating factor 1 (macrophage)	1.707	18.5	0.22995	2350	P	-1.051	38.4	0.294	6270
Cd68	A_51_P120470	NM_009853	CD68 antigen	1.705	12.21	0.19042	1810	P	1.059	19.02	0.24617	5592
Pcna	A_51_P396351	NM_011045	proliferating cell nuclear antigen	1.705	25.79	0.30418	3999	P	-1.123	19.02	0.26039	5824
Hsd3b1	A_51_P421418	NM_008293	hydroxy-delta-5-steroid dehydrogenase, 3	1.698	3.78	0.07471	514	M	1.023	36.07	0.63317	9747
Mtx2	A_52_P101260	NM_016804	metaxin 2	1.695	18.5	0.24333	2614	P	-1.04	44.4	0.49494	8509
Ccr2	A_52_P580853	AK162705		1.693	35.45	0.42959	7331	P	1.081	19.02	0.34895	6859
Rab5b	A_52_P407022	NM_177411	RAB5B, member RAS oncogene family	1.689	38.68	0.4443	7782	P	1.168	5.75	0.06523	2296
Ttc15	A_51_P299655	AK086217	tetratricopeptide repeat domain 15	1.689		0.50395	5466	A	-1.059	30.75	0.19623	4840
5330426P16Rik	A_51_P507234	XM_992800	RIKEN cDNA 5330426P16 gene	1.686	45.92	0.51378	10082	P	-1.081	16.2	0.11108	3300
Tcte1	A_51_P488103	NM_013688	t-complex-associated testis expressed 1	1.686	23.47	0.28827	3583	P	-1.162	1.62	0.02808	1139
Apoe	A_51_P171999	NM_009696	apolipoprotein E	1.685	23.47	0.32361	3702	M	1.058	22.1	0.31769	6555

Cfh	A_52_P309381	NM_009888	complement component factor h	1.681	28.61	0.3524	5174	P	1.015	42.43	0.85819	11664
Diap2	A_52_P843369	AK040942	diaphanous homolog 2 (Drosophila)	1.679		0.32647	3696	A	1.042	25.31	0.34094	6778
Rnf19	A_51_P277444	NM_013923	ring finger protein (C3HC4 type) 19	1.676	7.45	0.12178	939	P	1.329	2.04	0.0494	1826
Sncaip	A_52_P59264	NM_026408	synuclein, alpha interacting protein (synp	1.676	3.82	0.07997	542	P	1.058	19.02	0.22415	5269
Slit2	A_51_P496569	NM_178804	slit homolog 2 (Drosophila)	1.675	35.45	0.39534	6398	P	1.109	8.32	0.08418	2752
Pik4cb	A_51_P202320	NM_175356	phosphatidylinositol 4-kinase, catalytic, b	1.674	10.33	0.15619	1300	P	1.15	4.63	0.03695	1407
Pggt1b	A_52_P607331	AK087098	protein geranylgeranyltransferase type I,	1.673	18.5	0.23874	2526	P	-1.216	0.92	0.01509	644
Mif	A_52_P321733	NM_010798	macrophage migration inhibitory factor	1.671	6.91	0.10911	836	P	1.064	19.02	0.24091	5513
Rarres2	A_52_P466147	NM_027852	retinoic acid receptor responder (tazarote	1.67	7.45	0.11684	895	P	1.115	16.2	0.41974	7725
H19	A_51_P142196	AK145379	H19 fetal liver mRNA	1.666	72.2	0.76076	15746	M	1.131	13.58	0.34968	6868
Lox	A_51_P300493	NM_010728	lysyl oxidase	1.666	45.92	0.51894	10314	P	1.005	42.43	0.94157	12497
Exosc9	A_52_P295955	AK083794	exosome component 9	1.665	31.88	0.29606	2607	M	-1.057	42.43	0.41601	7697
Tgfbi	A_51_P212754	NM_009369	transforming growth factor, beta induced	1.665	18.5	0.24049	2555	P	1.044	30.75	0.52699	8815
Fmo2	A_52_P1138659	AK009224	flavin containing monooxygenase 2	1.662	6.91	0.1102	846	P	1.006	42.43	0.96884	12734
Atp2a2	A_52_P1156808	AK080543	ATPase, Ca++ transporting, cardiac muscle	1.66	18.5	0.23595	2460	P	1.037	28.13	0.36824	7137
Snx6	A_52_P85875	NM_026998	sorting nexin 6	1.66	18.5	0.23742	2481	P	1.312	3.46	0.08784	2835
Ifih1	A_51_P387810	NM_027835	interferon induced with helicase C domai	1.659	7.45	0.11273	869	P	1.236	2.04	0.02177	914
Col14a1	A_51_P326529	NM_181277	procollagen, type XIV, alpha 1	1.655	57.76	0.64378	15885	P	1.44	1.62	0.04508	1504
Pls3	A_51_P271614	NM_145629	plastin 3 (T-isoform)	1.655	5.86	0.17353	1360	M	1.199	5.75	0.09289	2962
Ctsf	A_52_P660945	NM_019861	cathepsin F	1.653	3.78	0.08018	562	P	-1.087	28.13	0.25085	5656
Serping1	A_51_P376238	NM_009776	serine (or cysteine) peptidase inhibitor, cl	1.652	10.84	0.16991	1478	P	1.117	5.75	0.04379	1637
AI427515	A_51_P425167	NM_173016	expressed sequence AI427515	1.647	16.01	0.20511	2011	P	1.211	3.46	0.04159	1573
Pou6f2	A_51_P148684	NM_175006	POU domain, class 6, transcription factor	1.647	18.5	0.22708	2314	P	1.094	11.33	0.11939	3487
B930037P14Rik	A_52_P150654	AK037118	RIKEN cDNA B930037P14 gene	1.645	45.92	0.5101	9937	P	-1.005	49.48	0.9709	12751
2410025L10Rik	A_51_P363525	NM_028596	RIKEN cDNA 2410025L10 gene	1.644	20.94	0.261	3004	P	-1.278	0.51	0.0093	337
Gdf8	A_51_P384901	NM_010834	growth differentiation factor 8	1.644	10.33	0.15198	1261	M	1.02	38.4	0.6913	10247
Mest	A_51_P124535	NM_008590	mesoderm specific transcript	1.644	42.28	0.49127	9267	P	1.253	1.62	0.01485	636
Rad18	A_51_P480855	NM_021385	RAD18 homolog (S. cerevisiae)	1.638	9.39	0.1416	1146	P	-1.02	49	0.7132	10431
Arsb	A_52_P105801	AK140163	arylsulfatase B	1.636	28.61	0.32734	4568	P	-1.053	40.63	0.35632	6971
Tmeff2	A_52_P229052	NM_019790	transmembrane protein with EGF-like and	1.633	23.47	0.27143	3200	P	1.017	40.63	0.79691	11152
Pacsin3	A_51_P223084	AK014830	protein kinase C and casein kinase substra	1.631	49.93	0.42383	6894	P	-1.085	19.02	0.13742	3796
Slc27a2	A_52_P154971	NM_011978	solute carrier family 27 (fatty acid transpo	1.631	49.93	0.54443	11172	P	1.135	13.58	0.33314	6716
Copz1	A_52_P779205	AK028719		1.629	28.61	0.33839	4896	P	1.12	9.71	0.1319	3708
Mdh1	A_52_P470451	AK077724	malate dehydrogenase 1, NAD (soluble)	1.627	38.68	0.44142	7697	M	1.22	4.63	0.09033	2903
Gdf9	A_51_P220806	NM_008110	growth differentiation factor 9	1.626	61.79	0.56738	10516	P	-1.033	45.05	0.49414	8491
Rhebl1	A_52_P354123	NM_026967	Ras homolog enriched in brain like 1	1.625	20.94	0.26618	3085	P	1.17	3.82	0.03962	1510
Cntfr	A_51_P184184	NM_016673	ciliary neurotrophic factor receptor	1.624	35.45	0.41615	6929	P	1.136	8.32	0.09066	2909
Kctd12	A_51_P371912	NM_177715	potassium channel tetramerisation doma	1.624	8.15	0.1295	1021	P	1.224	3.46	0.04398	1646
Ndufb8	A_52_P252539	AK028070	NADH dehydrogenase (ubiquinone) 1 bet	1.623	16.01	0.2189	2182	P	1.138	8.32	0.09282	2959
Olfml3	A_51_P191782	NM_133859	olfactomedin-like 3	1.622	53.87	0.61137	14013	P	1.089	9.71	0.09157	2930
Ifitm1	A_52_P541802	NM_026820	interferon induced transmembrane prote	1.619	25.79	0.29875	3819	P	-1.018	49.48	0.79542	11140
D5Ertd579e	A_52_P203773	AK083736	DNA segment, Chr 5, ERATO Doi 579, expr	1.618	10.84	0.1716	1514	P	1.393	0.75	0.01251	511
Calca	A_51_P290826	NM_007587	calcitonin/calcitonin-related polypeptide,	1.615	13.61	0.19135	1827	P	-1.069	33.49	0.28906	6201
Snrpb2	A_52_P638637	NM_021335	U2 small nuclear ribonucleoprotein B	1.614	12.21	0.20335	1934	P	1.358	1.17	0.01781	756
Fzd9	A_51_P511015	AK021164	frizzled homolog 9 (Drosophila)	1.612	31.88	0.35343	5198	P	1.085	11.33	0.10217	3158
Sms	A_52_P545192	AK049780	spermine synthase	1.606	35.45	0.35679	4591	P	1.028	33.49	0.50203	8602
9030409G11Rik	A_52_P590339	BC022941	RIKEN cDNA 9030409G11 gene	1.605	49.93	0.42023	6526	M	-1.008	49.48	0.95294	12603
Hdhd3	A_51_P465582	NM_024257	haloacid dehalogenase-like hydrolase dor	1.605	13.61	0.19756	1905	P	-1.045	43.15	0.42028	7733
Niban	A_51_P467798	NM_022018	niban protein	1.603	35.45	0.39458	6336	P	-1.087	19.02	0.15385	4112
5730508B09Rik	A_52_P23308	NM_027482	RIKEN cDNA 5730508B09 gene	1.599	23.47	0.28891	3604	P	-1.001	49.48	0.9828	12885
6330569M22Rik	A_52_P400234	AK035833	RIKEN cDNA 6330569M22 gene	1.597	84.56	0.67613	12159	M	1.037	30.75	0.55846	9087
Fst	A_51_P381821	NM_008046	follistatin	1.597	31.88	0.29265	3544	M	1.037	28.13	0.39291	7434
Fuca1	A_51_P108757	NM_024243	fucosidase, alpha-L- 1, tissue	1.594	8.15	0.13196	1043	P	-1.221	1.1	0.01949	823

Pik3c2a	A_52_P563489	AK013614	phosphatidylinositol 3-kinase, C2 domain	1.594	49.93	0.57624	10823	M	1.144	5.75	0.06194	2190
Mcm6	A_51_P360492	NM_008567	minichromosome maintenance deficient	1.593	25.79	0.29815	3769	P	1.082	11.33	0.13256	3720
Sh3gl2	A_52_P196161	NM_019535	SH3-domain GRB2-like 2	1.593	16.01	0.20466	1997	P	1.268	1.17	0.01002	378
Chn2	A_52_P302587	NM_023543	chimerin (chimaerin) 2	1.592	23.47	0.26547	3073	P	1.001	42.43	0.98495	12929
Tbc1d14	A_51_P486449	NM_133910	TBC1 domain family, member 14	1.592	13.61	0.19341	1860	P	-1.122	9.71	0.11815	3441
Enpp5	A_51_P362104	NM_032003	ectonucleotide pyrophosphatase/phosph	1.59	4.65	0.09678	717	P	1.024	38.4	0.73571	10641
Garnl3	A_52_P537376	AK084611	GTPase activating RANGAP domain-like 3	1.586	25.79	0.29937	3834	P	-1.113	6.98	0.06449	2267
Pygb	A_51_P485810	NM_153781	brain glycogen phosphorylase	1.583	10.33	0.15198	1256	P	1.149	4.63	0.03732	1421
T	A_51_P285725	NM_009309	brachyury	1.583		0.68467	7984	A	1.04	28.13	0.37192	7192
Agpat3	A_51_P425490	NM_053014	1-acylglycerol-3-phosphate O-acyltransfe	1.582	12.21	0.182	1648	P	-1.194	1.1	0.01648	705
Sat1	A_52_P640282	NM_009121	spermidine/spermine N1-acetyl transfera	1.582	31.88	0.37646	5801	P	1.254	2.04	0.02049	882
Echdc2	A_51_P477414	NM_026728	enoyl Coenzyme A hydratase domain con	1.581	31.88	0.34986	5118	P	-1.252	0.51	0.00932	339
Nfat5	A_52_P177904	AK045123	nuclear factor of activated T-cells 5	1.579	8.15	0.13808	1092	P	1.025	38.4	0.7417	10701
Col1a2	A_51_P182303	NM_007743	procollagen, type I, alpha 2	1.577	18.5	0.2353	2445	P	-1.042	42.43	0.32562	6621
C1qb	A_51_P351860	NM_009777	complement component 1, q subcompon	1.573	7.45	0.12174	936	P	1.01	42.43	0.92251	12290
Nin	A_52_P597696	NM_008697	ninein	1.573	12.21	0.1859	1730	P	-1.051	36.07	0.246	5585
Pkm2	A_51_P428913	D38379	pyruvate kinase, muscle	1.573	7.45	0.14655	1150	P	1.087	19.02	0.34172	6792
Col6a2	A_51_P279639	NM_146007	procollagen, type VI, alpha 2	1.572	20.94	0.24748	2743	P	1.13	8.32	0.10096	3124
Ngfrap1	A_51_P408155	NM_009750	nerve growth factor receptor (TNFRSF16)	1.572	13.61	0.26436	2592	M	-1.036	46.3	0.63446	9759
Sfrp1	A_51_P352296	NM_013834	secreted frizzled-related sequence protei	1.572	28.61	0.3145	4244	P	1.051	30.75	0.66916	10041
Zdhhc21	A_52_P168505	NM_026647	zinc finger, DHHC domain containing 21	1.572	45.92	0.52052	10368	P	1.043	25.31	0.31686	6549
Cd63	A_51_P511810	NM_001042580	Cd63 antigen	1.57	18.5	0.29726	3149	M	1.348	3.01	0.07851	2615
Map3k7ip2	A_52_P242400	AK086230	mitogen-activated protein kinase kinase	1.569		0.30777	3356	A	1.311	5.75	0.21473	5111
Papss2	A_51_P258551	AK029185	3'-phosphoadenosine 5'-phosphosulfate	1.569	42.28	0.45401	8029	P	1.644	0.24	0.01058	405
Plat	A_51_P301566	NM_008872	plasminogen activator, tissue	1.568	28.61	0.32076	4385	P	1.108	11.33	0.20807	5024
Aars	A_52_P567035	AK087291	alanyl-tRNA synthetase	1.567	42.28	0.30716	3916	P	1.005	42.43	0.94037	12482
Fibp	A_51_P518246	NM_021438	fibroblast growth factor (acidic) intracellu	1.567	23.47	0.26693	3099	P	1.072	16.2	0.22129	5225
Hmgcs1	A_52_P119039	AK078743	3-hydroxy-3-methylglutaryl-Coenzyme A	1.567	53.87	0.57766	12378	P	-1.217	25.31	0.47848	8290
Tcf4	A_52_P521101	NM_013685	transcription factor 4	1.566	20.94	0.24021	2541	P	1.037	28.13	0.38403	7330
Rab27a	A_52_P426740	NM_023635	RAB27A, member RAS oncogene family	1.564	83.36	0.7703	19968	P	1.125	9.71	0.12083	3506
Tiparp	A_51_P514961	NM_178892	TCDD-inducible poly(ADP-ribose) polyme	1.564	57.76	0.64769	15996	P	1.324	3.46	0.11108	3297
B230120H23Rik	A_52_P522379	NM_178084	RIKEN cDNA B230120H23 gene	1.56	9.39	0.14314	1168	P	-1.142	6.98	0.11996	3493
Gas5	A_51_P366867	X59728	growth arrest specific 5	1.559	25.79	0.36307	4582	M	1.132	6.98	0.06629	2327
Id4	A_52_P449871	NM_031166	inhibitor of DNA binding 4	1.558	25.79	0.30153	3900	P	1.031	42.43	0.88809	11941
4930506M07Rik	A_51_P200561	NM_175172	RIKEN cDNA 4930506M07 gene	1.556	6.91	0.21349	1850	M	1.147	8.32	0.14431	3926
Bloc1s1	A_52_P546540	NM_015740	biogenesis of lysosome-related organelle	1.556	10.84	0.17066	1498	P	1.098	11.33	0.12406	3580
Rad50	A_52_P101496	BC002033	RAD50 homolog (S. cerevisiae)	1.556		0.57183	6803	A	1.112	8.32	0.06339	2245
3110049J23Rik	A_52_P241619	NM_026085	RIKEN cDNA 3110049J23 gene	1.554	20.94	0.24642	2736	P	-1.019	49.48	0.78435	11047
Ddit3	A_52_P533146	NM_007837	DNA-damage inducible transcript 3	1.554	57.76	0.61689	14219	P	-1.042	43.75	0.41589	7693
Mpp7	A_52_P57889	AK141108	membrane protein, palmitoylated 7 (MA	1.554	16.01	0.20919	2057	P	-1.16	3.01	0.04505	1680
Six1	A_52_P586679	NM_009189	sine oculis-related homeobox 1 homolog	1.552		0.32985	4483	A	1.058	19.02	0.21643	5135
Pclo	A_52_P141641	AB083477	piccolo (presynaptic cytomatrix protein)	1.551	28.61	0.32081	4391	P	1.209	5.75	0.1388	3816
Aaas	A_52_P242199	AK051635	achalasia, adrenocortical insufficiency, ala	1.548	49.93	0.51754	9832	M	1.055	22.1	0.34062	6775
Pik3c3	A_52_P287683	NM_181414	phosphoinositide-3-kinase, class 3	1.547	13.61	0.19693	1893	P	1.037	36.07	0.75681	10836
Fgf14	A_52_P1011	NM_010201	fibroblast growth factor 14	1.546	20.94	0.259	2980	P	1.243	3.82	0.08197	2703
Zfhx1b	A_52_P596008	NM_015753	zinc finger E-box binding homeobox 2	1.546	31.88	0.35438	5230	P	1.013	40.63	0.75469	10822
Nrk	A_51_P461005	NM_013724	Nik related kinase	1.545	61.79	0.21493	1849	M	1.067	22.1	0.40439	7561
Zfp644	A_51_P118822	AK044814	zinc finger protein 644	1.542	57.76	0.429	6757	M	1.127	5.75	0.0408	1552
Vav3	A_52_P613596	NM_020505	vav 3 oncogene	1.54	18.5	0.22777	2317	P	1.127	6.98	0.05934	2130
Atf5	A_51_P269216	NM_030693	activating transcription factor 5	1.539	23.47	0.33423	3957	M	-1.046	43.75	0.4904	8440
Prps2	A_52_P32864	NM_026662	phosphoribosyl pyrophosphate synthetas	1.539	13.61	0.19014	1809	P	-1.083	33.49	0.35146	6895
D12Ertd551e	A_52_P683432	ENSMUST00000070837	DNA segment, Chr 12, ERATO Doi 551, ex	1.538	10.84	0.1716	1524	P	1.144	4.63	0.03391	1312
Nrip1	A_52_P413584	AK078829	nuclear receptor interacting protein 1	1.538	4.65	0.10711	817	P	1.466	0.24	0.00957	345

Ly86	A_51_P465350	NM_010745	lymphocyte antigen 86	1.537	45.92	0.49841	9567	P	1.039	30.75	0.54878	9010
Gng3	A_51_P391291	NM_010316	guanine nucleotide binding protein (G prc	1.535	61.79	0.68148	17501	P	-1.138	11.33	0.17475	4467
Sema3a	A_52_P679511	AK053115	sema domain, immunoglobulin domain (I	1.534	38.68	0.37749	4190	M	1.166	11.33	0.33055	6676
Gcg	A_51_P406253	NM_008100	glucagon	1.533	75.14	0.82865	19307	M	1.541	0.24	0.00627	155
Tuba1	A_51_P169745	NM_011653	tubulin, alpha 1A	1.533	10.33	0.22589	2074	M	-1.035	47.92	0.75525	10826
Slc4a3	A_51_P321743	AK161240	solute carrier family 4 (anion exchanger),	1.532	53.87	0.59813	13364	P	1.075	13.58	0.14616	3964
Eprs	A_52_P653684	NM_029735	glutamyl-prolyl-tRNA synthetase	1.529	28.61	0.31409	4226	P	1.181	3.46	0.02801	1129
Rab12	A_51_P296027	NM_024448	RAB12, member RAS oncogene family	1.529	10.33	0.15403	1288	P	1.355	0.24	0.00584	67
Arhgap24	A_51_P199725	NM_146161	Rho GTPase activating protein 24	1.528	10.33	0.15273	1277	P	1.024	36.07	0.61123	9540
Fntb	A_52_P235241	NM_145927	farnesyltransferase, CAAX box, beta	1.528	8.15	0.14112	1130	P	-1.027	46.3	0.53618	8904
Stmn2	A_51_P164998	NM_025285	stathmin-like 2	1.527	61.79	0.69977	18368	P	-1.117	5.75	0.06262	2217
Centg2	A_52_P947926	AK083235	centaurin, gamma 2	1.526	16.01	0.21119	2082	P	1.229	3.01	0.03511	1347
C530008M17Rik	A_51_P395206	AK016430	RIKEN cDNA C530008M17 gene	1.524	45.92	0.33775	4008	M	1.03	36.07	0.72121	10505
Mare	A_51_P169783	AK086378	alpha globin regulatory element containir	1.524	25.79	0.29726	3750	P	-1.119	6.98	0.06612	2324
Pcolce	A_51_P371942	NM_008788	procollagen C-endopeptidase enhancer p	1.523	23.47	0.259	2971	P	-1.22	1.1	0.01985	847
Col5a1	A_51_P414637	NM_015734	procollagen, type V, alpha 1	1.522	31.88	0.37281	5685	P	1.03	36.07	0.71352	10434
Mdk	A_51_P225665	NM_010784	midkine	1.521	10.33	0.15704	1311	P	-1.137	3.82	0.05135	1885
1810008A18Rik	A_52_P665335	NM_133998	RIKEN cDNA 1810008A18 gene	1.52	25.79	0.2912	3646	P	1.017	40.63	0.80618	11237
Sh3bgrl3	A_51_P344752	NM_080559	SH3 domain binding glutamic acid-rich pr	1.52	31.88	0.37123	5646	P	1.053	30.75	0.63197	9737
Maf	A_51_P379230	NM_001025577	avian musculoaponeurotic fibrosarcoma (	1.519	23.47	0.261	3003	P	1.1	9.71	0.08254	2713
Nsmaf	A_52_P674053	NM_010945	neutral sphingomyelinase (N-SMase) activ	1.518	28.61	0.31382	4222	P	1.113	6.98	0.05411	1979
Titf1	A_52_P216427	NM_009385	thyroid transcription factor 1	1.517		0.50704	7230	A	1.06	22.1	0.29086	6216
Wtap	A_52_P425790	NM_175394	Wilms' tumour 1-associating protein	1.517	12.21	0.1859	1731	P	1.228	5.75	0.13742	3798
Tro	A_52_P72831	NM_019548	trophinin	1.515	49.93	0.5494	11400	P	-1.105	25.31	0.31283	6489
Arhgap6	A_52_P561746	NM_009707	Rho GTPase activating protein 6	1.514	12.21	0.26436	2593	M	1.146	4.63	0.03906	1473
Rasl12	A_51_P105927	NM_001033158	RAS-like, family 12	1.513	38.68	0.42411	7170	P	1.12	8.32	0.08432	2758
Mpp1	A_51_P124568	NM_008621	membrane protein, palmitoylated	1.512	7.45	0.13275	1052	P	1.167	8.32	0.14368	3918
Col8a1	A_52_P282058	NM_007739	procollagen, type VIII, alpha 1	1.511	65.79	0.70237	18525	P	1.022	36.07	0.58835	9323
Elp4	A_52_P297050	NM_023876	elongation protein 4 homolog (S. cerevisia	1.511	6.91	0.12934	1019	P	-1.156	5.75	0.1064	3211
Pja1	A_52_P141123	NM_008853	praja1, RING-H2 motif containing	1.511	20.94	0.23863	2520	P	-1.3	1.18	0.04706	1759
Rcn1	A_51_P305437	NM_009037	reticulocalbin 1	1.509	10.84	0.26363	2581	M	1.208	3.82	0.05367	1970
Zfhx4	A_52_P81413	AK084213	zinc finger homeodomain 4	1.508	42.28	0.52829	9337	M	1.064	16.2	0.20719	5010
Ass1	A_51_P338713	M31690	argininosuccinate synthetase 1	1.507	49.93	0.52487	10532	P	1.041	25.31	0.35256	6910
Ptprd	A_52_P605266	NM_011211	protein tyrosine phosphatase, receptor ty	1.507	18.5	0.22992	2346	P	1.077	16.2	0.22995	5348
Rbpms	A_51_P350332	NM_019733	RNA binding protein gene with multiple s	1.507	10.33	0.16239	1374	P	1.167	3.82	0.03602	1395
Commd9	A_51_P232705	NM_029635	COMM domain containing 9	1.506	10.33	0.16388	1417	P	-1.117	8.32	0.08895	2869
Epm2aip1	A_52_P37522	NM_175266	EPM2A (laforin) interacting protein 1	1.506	49.93	0.5505	11449	P	-1.097	38.4	0.50432	8623
Serpine2	A_51_P268094	NM_009255	serine (or cysteine) peptidase inhibitor, cl	1.505	20.94	0.24811	2756	P	-1.04	45.05	0.55068	9035
Aldoa	A_51_P216905	NM_007438	aldolase 1, A isoform	1.504	35.45	0.4384	6278	M	-1.174	3.01	0.05733	2071
Grb10	A_52_P115787	NM_010345	growth factor receptor bound protein 10	1.504	28.61	0.37925	4916	M	1.373	0.24	0.00591	111
Cdkal1	A_52_P335259	NM_144536	CDK5 regulatory subunit associated prote	1.503	20.94	0.32751	3789	M	-1.014	49.48	0.75336	10810
Fgfr2	A_51_P432403	NM_010207	fibroblast growth factor receptor 2	1.503		0.53362	7347	A	1.091	13.58	0.22894	5343
Pacsin1	A_52_P531693	NM_178365	protein kinase C and casein kinase substra	1.502	28.61	0.32361	4460	P	1.028	33.49	0.53923	8934
0610038F07Rik	A_52_P209973	AK083578	RIKEN cDNA 0610038F07 gene	1.501	45.92	0.49696	9514	P	-1.001	49.48	0.97829	12826
BC023829	A_52_P1128182	ENSMUST00000101506	cDNA sequence BC023829	1.501	12.21	0.1825	1673	P	1.145	5.75	0.05496	2006
C1r	A_51_P384318	NM_023143	complement component 1, r subcompone	1.501	35.45	0.37646	5780	P	1.048	28.13	0.47441	8258
Ttyh3	A_52_P196105	NM_175274	tweety homolog 3 (Drosophila)	1.5	25.79	0.28103	3462	P	1.204	3.01	0.03267	1283
Tpk1	A_52_P156540	NM_013861	thiamine pyrophosphokinase	1.499	25.79	0.29955	3852	P	-1.102	11.33	0.11028	3278
Zfp503	A_51_P126626	NM_145459	zinc finger protein 503	1.497	12.21	0.17622	1585	P	1.141	8.32	0.11384	3358
Fgd4	A_52_P164236	AK042588	FYVE, RhoGEF and PH domain containing	1.496	6.91	0.13335	1059	P	-1.024	49.22	0.77661	10965
Prnp	A_51_P483280	NM_011170	prion protein	1.495	7.45	0.15519	1266	P	1.11	9.71	0.11364	3347
Ptn	A_52_P10793	NM_008973	pleiotrophin	1.495	10.33	0.1626	1378	P	1.568	1.32	0.05346	1968
Them2	A_51_P502422	NM_025790	thioesterase superfamily member 2	1.495	20.94	0.24343	2637	P	-1.035	44.4	0.43631	7898

Gabrb3	A_52_P532006	NM_008071	gamma-aminobutyric acid (GABA-A) recep	1.494	25.79	0.29853	3795	P	-1.082	38.4	0.47423	8243
Sox17	A_52_P365096	NM_011441	SRY-box containing gene 17	1.493		0.80833	20030	A	1.08	11.33	0.11944	3488
Rpl21	A_52_P653937	NM_019647	ribosomal protein L21	1.492	13.61	0.19861	1938	P	-1.12	13.58	0.17138	4402
Mbp	A_51_P349205	NM_010777	myelin basic protein	1.491	25.79	0.2984	3790	P	1.28	3.46	0.07211	2440
Adamts6	A_52_P604149	AK030315	a disintegrin-like and metallopeptidase (r	1.49	31.88	0.34137	4951	P	-1.212	0.66	0.01059	409
Lrp4	A_52_P635078	NM_172668	low density lipoprotein receptor-related p	1.49	57.76	0.61855	14338	P	1.019	40.63	0.77306	10944
Pcsk1n	A_52_P459657	AK076137	proprotein convertase subtilisin/kexin typ	1.49	42.28	0.45116	7948	P	1.072	13.58	0.13909	3831
Shprh	A_52_P209748	AK037266	SNF2 histone linker PHD RING helicase	1.49	20.94	0.24333	2622	P	1.003	42.43	0.97949	12837
6530401C20Rik	A_51_P114634	NM_173405	RIKEN cDNA 6530401C20 gene	1.489	25.79	0.30153	3904	P	-1.276	0.56	0.01398	586
Gmfb	A_52_P492176	NM_022023	glia maturation factor, beta	1.489	38.68	0.41502	6898	P	-1.393	0.51	0.01802	768
Mtap2	A_52_P1068259	AK048375	microtubule-associated protein 2	1.489	49.93	0.55565	11604	P	1.15	6.98	0.09767	3056
Tm6sf1	A_52_P237948	NM_145375	transmembrane 6 superfamily member 1	1.489	12.21	0.1821	1653	P	1.035	30.75	0.46036	8102
Glp1r	A_51_P275077	NM_021332	glucagon-like peptide 1 receptor	1.488	20.94	0.25155	2818	P	1.061	19.02	0.23172	5377
Sdccag1	A_52_P561170	AK041450	serologically defined colon cancer antigen	1.488	20.94	0.2826	2984	M	1.068	19.02	0.33564	6741
2310022K01Rik	A_51_P124008	AK009476	RIKEN cDNA 2310022K01 gene	1.487	31.88	0.34672	5046	P	1.197	5.75	0.11298	3338
Myt1l	A_52_P639028	AK049967	myelin transcription factor 1-like	1.487	25.79	0.28089	3460	P	1.008	42.43	0.90281	12121
Ctss	A_51_P423981	NM_021281	cathepsin S	1.486	25.79	0.29875	3816	P	1.051	33.49	0.68926	10234
Colec12	A_52_P527625	NM_130449	collectin sub-family member 12	1.485	28.61	0.3245	4493	P	1.359	1.32	0.02536	1045
Fem1a	A_52_P225592	AK005979	feminization 1 homolog a (C. elegans)	1.485	25.79	0.24428	2575	M	-1.042	42.43	0.34537	6825
Serpinc1	A_52_P409746	NM_080844	serine (or cysteine) peptidase inhibitor, cl	1.483	31.88	0.36607	5517	P	1.012	42.43	0.83453	11489
Eln	A_52_P609972	NM_007925	elastin	1.482	28.61	0.32851	4628	P	1.035	42.43	0.89691	12028
Spats2	A_52_P231453	NM_139140	spermatogenesis associated, serine-rich 2	1.482	8.15	0.15116	1253	P	1.03	36.07	0.62314	9651
Gdf15	A_52_P532982	NM_011819	growth differentiation factor 15	1.481	12.21	0.18106	1637	P	-1.009	49.48	0.84369	11550
Opa1	A_52_P153645	AK053861	optic atrophy 1 homolog (human)	1.481	12.21	0.2794	2927	M	1.122	5.75	0.04735	1774
Ngfr	A_52_P236448	NM_033217	nerve growth factor receptor (TNFR super	1.478	65.79	0.70132	18447	P	1.263	6.98	0.20651	4995
Mnt	A_52_P477431	NM_010813	max binding protein	1.477	28.61	0.32851	4626	P	1.037	30.75	0.52956	8828
Clec14a	A_52_P566665	NM_025809	C-type lectin domain family 14, member a	1.476	35.45	0.37674	5810	P	-1.01	49.48	0.8227	11390
Exosc8	A_51_P500806	AK047257	exosome component 8	1.476		0.61745	7865	A	-1.093	16.2	0.12533	3610
Pmp22	A_51_P258529	NM_008885	peripheral myelin protein	1.476	20.94	0.24458	2689	P	1.081	25.31	0.53909	8932
Hsd3b7	A_51_P435911	NM_133943	hydroxy-delta-5-steroid dehydrogenase, 3	1.474	16.01	0.208	2035	P	1.213	3.82	0.07272	2463
Snap91	A_51_P311199	NM_013669	synaptosomal-associated protein 91	1.471	31.88	0.3333	4753	P	-1.061	38.4	0.35146	6896
Abcc9	A_51_P328850	NM_021041	ATP-binding cassette, sub-family C (CFTR/	1.469	38.68	0.42256	7127	P	1.076	22.1	0.41314	7656
Bambi	A_51_P248819	NM_026505	BMP and activin membrane-bound inhibi	1.469	18.5	0.23102	2395	P	1.025	36.07	0.59225	9356
Gpx3	A_51_P292008	NM_008161	glutathione peroxidase 3	1.469	31.88	0.41931	5804	M	1.516	0.24	0.00897	325
Zwint	A_51_P163378	ENSMUST00000020081	ZW10 interactor	1.469	13.61	0.2912	3063	M	1.225	4.63	0.08702	2820
Rtn3	A_52_P218009	AK053372	reticulon 3	1.468	10.33	0.16317	1403	P	1.187	3.01	0.0225	960
Ttc21b	A_51_P221176	AK010712	tetratricopeptide repeat domain 21B	1.468		0.30248	3213	A	1.06	19.02	0.25294	5695
Creb3l4	A_51_P497882	NM_030080	cAMP responsive element binding protein	1.466	61.79	0.6784	17373	P	1.079	16.2	0.24977	5636
Apoa2	A_51_P128973	NM_013474	apolipoprotein A-II	1.465	53.87	0.59193	13030	P	-1.053	38.4	0.27714	6056
Cda	A_52_P469502	NM_028176	cytidine deaminase	1.465	45.92	0.49339	9374	P	-1.042	40.63	0.32279	6593
D630045J12Rik	A_51_P363214	XM_974678	RIKEN cDNA D630045J12 gene	1.465	10.33	0.17066	1502	P	1.075	16.2	0.21909	5192
Rab22a	A_51_P369106	NM_024436	RAB22A, member RAS oncogene family	1.464	28.61	0.31761	4310	P	-1.063	33.49	0.26039	5817
Scly	A_51_P133369	NM_016717	selenocysteine lyase	1.464	38.68	0.40754	6658	P	1.218	5.75	0.11617	3400
2410016F19Rik	A_52_P627793	NM_026113	RIKEN cDNA 2410016F19 gene	1.462	28.61	0.32561	4518	P	-1.128	3.82	0.04333	1624
4921533L14Rik	A_51_P402480	AK173166	RIKEN cDNA 4921533L14 gene	1.462	25.79	0.28682	3540	P	1.054	30.75	0.66173	9986
Atp5f1	A_52_P631514	AK081249	ATP synthase, H+ transporting, mitochond	1.462	45.92	0.48921	9214	P	1.015	42.43	0.80391	11208
Brp44l	A_52_P595687	NM_018819	brain protein 44-like	1.462	10.33	0.1677	1466	P	1.096	11.33	0.11452	3375
Myo1d	A_52_P211737	NM_177390	myosin ID	1.462	53.87	0.59251	13045	P	-1.184	1.18	0.02085	890
Txnl4b	A_51_P286327	NM_175646	thioredoxin-like 4B	1.461	9.39	0.16251	1376	P	1.035	30.75	0.43834	7905
0610037D15Rik	A_51_P321405	NM_026714	RIKEN cDNA 0610037D15 gene	1.46	35.45	0.37183	5657	P	-1.079	33.49	0.37093	7183
Aco1	A_52_P299115	NM_007386	aconitase 1	1.46	20.94	0.24913	2775	P	1.117	8.32	0.07158	2426
Egfr	A_52_P5855	AK049452	epidermal growth factor receptor	1.46	10.33	0.26547	2639	M	1.105	9.71	0.0911	2924
Sst	A_51_P262489	NM_009215	somatostatin	1.459	65.79	0.74533	15928	M	1.109	16.2	0.35439	6946

Wdr33	A_52_P438682	BC064745	WD repeat domain 33	1.459	20.94	0.23776	2494	P	-1.053	42.43	0.43315	7877
5730601F06Rik	A_52_P722599	XM_977869	RIKEN cDNA 5730601F06 gene	1.458	31.88	0.3531	5186	P	-1.064	40.63	0.41314	7657
Arhgef18	A_51_P400490	AK041423	rho/rac guanine nucleotide exchange fact	1.458		0.75317	9315	A	1.158	5.75	0.07263	2456
Foxp4	A_52_P307628	NM_028767	forkhead box P4	1.458	38.68	0.42594	7236	P	-1.057	36.07	0.28628	6179
Slc37a4	A_51_P385598	NM_008063	solute carrier family 37 (glucose-6-phosp	1.458	10.84	0.17808	1610	P	1.118	9.71	0.1095	3252
AW549877	A_52_P102413	NM_145930	expressed sequence AW549877	1.457	20.94	0.24026	2548	P	1.261	3.82	0.0814	2688
Enah	A_52_P282000	AK020248	enabled homolog (Drosophila)	1.457	35.45	0.37686	5816	P	1.229	3.82	0.06513	2286
Pgm5	A_51_P451052	NM_175013	phosphoglucomutase 5	1.457	61.79	0.66276	16699	P	1.025	33.49	0.55128	9047
Il1b	A_51_P212782	NM_008361	interleukin 1 beta	1.456	35.45	0.36307	5464	P	1.29	5.75	0.17839	4546
Ociad2	A_51_P338886	NM_026950	OCIA domain containing 2	1.456	18.5	0.23063	2367	P	1.108	8.32	0.07192	2432
Psd	A_51_P251205	NM_028627	pleckstrin and Sec7 domain containing	1.456	45.92	0.51629	8276	M	-1.386	0.51	0.00584	28
9430079B08Rik	A_52_P625975	AK035049	RIKEN cDNA 9430079B08 gene	1.455	10.84	0.18127	1643	P	1.009	42.43	0.90103	12105
Fzd1	A_52_P597634	NM_021457	frizzled homolog 1 (Drosophila)	1.455	16.01	0.21494	2120	P	1.071	16.2	0.20515	4975
Uhmk1	A_52_P614133	AK028977	U2AF homology motif (UHM) kinase 1	1.455	28.61	0.32081	4390	P	1.011	42.43	0.83151	11476
Dpysl5	A_51_P130719	NM_023047	dihydropyrimidinase-like 5	1.452	42.28	0.46928	8160	M	1.016	42.43	0.83907	11518
0610016J10Rik	A_52_P94347	AK033228	mediator of cell motility 1	1.451	53.87	0.43241	7147	M	1.105	8.32	0.06523	2297
Fstl1	A_51_P215106	NM_008047	follistatin-like 1	1.451	28.61	0.30934	4147	P	1.008	42.43	0.86776	11740
Kcnn2	A_51_P309854	NM_080465	potassium intermediate/small conductan	1.451	23.47	0.26004	2997	P	1.095	22.1	0.52549	8803
Hint3	A_51_P290819	NM_025798	histidine triad nucleotide binding protein	1.449	13.61	0.19306	1852	P	-1.007	49.48	0.89284	11989
Rtn4	A_52_P379337	NM_194054	reticulon 4	1.449	20.94	0.24841	2764	P	1.241	2.53	0.03311	1294
BC019943	A_51_P300960	NM_144927	cDNA sequence BC019943	1.448	16.01	0.20511	2013	P	1.037	30.75	0.51414	8715
Hoxb2	A_51_P257789	AK036636	homeo box B2	1.448	35.45	0.38302	5994	P	1.045	25.31	0.30884	6426
Pask	A_51_P223709	NM_080850	PAS domain containing serine/threonine	1.448	23.47	0.27116	3173	P	-1.024	48.39	0.704	10347
Ndufb4	A_51_P434269	NM_026610	NADH dehydrogenase (ubiquinone) 1 bet	1.447	31.88	0.33757	4282	M	1.036	30.75	0.53168	8855
Tbpl1	A_51_P387690	AK028621	TATA box binding protein-like 1	1.446	45.92	0.49546	9452	P	1.182	4.63	0.06742	2348
Prim2	A_52_P1115939	AK047274		1.444		0.57069	9393	A	1.007	42.43	0.94617	12554
Rabgap1l	A_52_P506529	NM_001038621	RAB GTPase activating protein 1-like	1.442	23.47	0.27514	3314	P	1.05	22.1	0.26529	5877
Golph3	A_52_P244162	BC031445	golgi phosphoprotein 3	1.441	35.45	0.36552	5509	P	1	49.48	0.99571	13015
Il12b	A_51_P385812	NM_008352	interleukin 12b	1.441	49.93	0.52633	9250	M	-1.183	2.04	0.03933	1492
E2f3	A_52_P583458	BC059262	E2F transcription factor 3	1.44	25.79	0.28104	3466	P	-1.106	4.63	0.05224	1930
Gpld1	A_51_P402583	NM_008156	glycosylphosphatidylinositol specific phos	1.44	18.5	0.22953	2330	P	1.062	25.31	0.48291	8359
Prkcn	A_52_P94495	AK050059	protein kinase C, nu	1.439		0.31447	3475	A	1.065	19.02	0.23133	5368
Mrpl15	A_52_P190506	AK017820		1.438	49.93	0.51432	10098	P	1.115	9.71	0.13892	3818
Cacna1h	A_52_P588378	AB041801	calcium channel, voltage-dependent, T ty	1.436	53.87	0.45481	5871	M	-1.076	25.31	0.16629	4319
Tyrobp	A_51_P261517	NM_011662	TYRO protein tyrosine kinase binding prot	1.435	38.68	0.42094	7072	P	-1.196	1.62	0.04061	1545
Islr	A_51_P140742	NM_012043	immunoglobulin superfamily containing	1.434	31.88	0.34722	5054	P	1.116	8.32	0.09218	2947
Sema6d	A_51_P415755	AK052232	sema domain, transmembrane domain (T	1.434	38.68	0.41089	6769	P	1.142	5.75	0.06227	2202
Rhot1	A_52_P655239	AK043323	ras homolog gene family, member T1	1.433	18.5	0.2301	2360	P	1.104	8.32	0.07994	2652
Sepw1	A_51_P474078	NM_009156	selenoprotein W, muscle 1	1.433	28.61	0.39052	5124	M	-1.003	49.48	0.9608	12670
Zfp521	A_51_P214985	NM_145492	zinc finger protein 521	1.433	49.93	0.51764	10227	P	-1.002	49.48	0.97673	12812
Impa1	A_52_P13537	NM_018864	inositol (myo)-1(or 4)-monophosphatase	1.431	16.01	0.30923	3447	M	1.182	6.98	0.14231	3890
Mmp2	A_52_P341736	NM_008610	matrix metallopeptidase 2	1.431	35.45	0.37331	5699	P	1.003	42.43	0.96168	12680
Nqo2	A_52_P35581	ENSMUST00000058978	NAD(P)H dehydrogenase, quinone 2	1.431	28.61	0.31826	4335	P	-1.179	3.82	0.10297	3171
Pdlim2	A_51_P472726	NM_145978	PDZ and LIM domain 2	1.431	35.45	0.37952	5902	P	1.06	19.02	0.23219	5382
Gbf1	A_52_P421716	AK041959	golgi-specific brefeldin A-resistance facto	1.43	49.93	0.46206	7961	P	1.025	36.07	0.59692	9415
Slc30a9	A_52_P134914	AK033990	solute carrier family 30 (zinc transporter),	1.43	8.15	0.16423	1419	P	1.001	42.43	0.98357	12901
Rasd2	A_51_P394631	XM_204287	RASD family, member 2	1.429	38.68	0.4265	7251	P	-1.003	49.48	0.94118	12493
Esd	A_52_P611000	NM_016903	esterase D/formylglutathione hydrolase	1.427	45.92	0.48893	9202	P	1.019	40.63	0.76694	10915
0610007N19Rik	A_52_P670812	AK002304	RIKEN cDNA 0610007N19 gene	1.426	31.88	0.33423	4763	P	-1.021	48.7	0.67865	10127
Il10rb	A_51_P344507	AK018347	interleukin 10 receptor, beta	1.426		0.61003	9300	A	1.062	25.31	0.46693	8177
Nrxn3	A_52_P39644	NM_172544	neurexin III	1.426	25.79	0.27555	3202	M	1.123	13.58	0.2935	6264
Acaa2	A_51_P125260	NM_177470	acetyl-Coenzyme A acyltransferase 2 (mit	1.425	45.92	0.48984	9237	P	-1.199	0.75	0.01251	509
Hsbp1	A_52_P544555	NM_024219	heat shock factor binding protein 1	1.425	38.68	0.41119	6796	P	1.162	3.82	0.03605	1399

Lama2	A_52_P652859	NM_008481	laminin, alpha 2	1.424	49.93	0.50268	9753	P	1.124	8.32	0.08715	2823
Prkar2b	A_51_P221062	NM_011158	protein kinase, cAMP dependent regulato	1.422	20.94	0.28561	3414	P	1.388	0.24	0.00623	130
Rab6	A_51_P209873	NM_024287	RAB6, member RAS oncogene family	1.422	23.47	0.27264	3235	P	1.44	0.24	0.00638	176
Sdpr	A_51_P277336	NM_138741	serum deprivation response	1.421	28.61	0.31826	4342	P	-1.029	46.85	0.62301	9645
2410022L05Rik	A_51_P357422	NM_025556	RIKEN cDNA 2410022L05 gene	1.42	10.84	0.1859	1722	P	1.062	33.49	0.73801	10663
Ctgf	A_51_P157042	NM_010217	connective tissue growth factor	1.42	35.45	0.4813	8240	P	-1.027	48.39	0.74343	10735
Perp	A_51_P317941	NM_022032	PERP, TP53 apoptosis effector	1.42	45.92	0.49127	9268	P	1.05	25.31	0.39393	7450
5730437N04Rik	A_51_P411389	NM_027457	RIKEN cDNA 5730437N04 gene	1.419	38.68	0.42074	7054	P	-1.022	47.92	0.62058	9629
Adrb3	A_51_P179442	AF193027	adrenergic receptor, beta 3	1.419		0.35185	4802	A	1.095	9.71	0.08605	2792
Eif4ebp1	A_51_P330428	NM_007918	eukaryotic translation initiation factor 4E	1.419	23.47	0.26479	3065	P	1.037	28.13	0.41015	7611
Fdxr	A_51_P461578	NM_007997	ferredoxin reductase	1.419	35.45	0.38472	6025	P	-1.166	1.18	0.01679	724
Dsp	A_51_P101460	AK077574	desmoplakin	1.418	23.47	0.26547	3071	P	1.548	0.3	0.01444	610
Rph3a	A_52_P211949	NM_011286	rabphilin 3A	1.418	16.01	0.4374	5467	M	-1.111	9.71	0.08874	2861
2410129H14Rik	A_52_P644972	NM_175245	RIKEN cDNA 2410129H14 gene	1.417	57.76	0.59334	13079	P	1.196	3.82	0.06038	2159
Gtf2h2	A_52_P291509	BC016231	general transcription factor II H, polypept	1.417	20.94	0.24498	2707	P	1.01	42.43	0.82879	11443
2610528K11Rik	A_51_P364391	NM_175184	RIKEN cDNA 2610528K11 gene	1.416	28.61	0.31768	4320	P	1.023	38.4	0.64811	9866
8430419K02Rik	A_51_P212012	BC050140	RIKEN cDNA 8430419K02 gene	1.416		0.31599	3937	A	-1.173	1.58	0.02536	1052
Cbx5	A_52_P544760	NM_007626	chromobox homolog 5 (Drosophila HP1a)	1.416	31.88	0.33775	4885	P	1.16	8.32	0.15188	4062
Dock8	A_51_P331886	AK038316	dedicator of cytokinesis 8	1.416	25.79	0.26547	2987	M	-1.003	49.48	0.9532	12607
Rpl22	A_52_P391718	NM_009079	ribosomal protein L22	1.416	13.61	0.20532	2017	P	1.152	11.33	0.30021	6320
Usp11	A_51_P315673	NM_145628	ubiquitin specific peptidase 11	1.416	16.01	0.21984	2201	P	1.303	1.62	0.02494	1033
Crsp6	A_51_P429951	NM_144933	cofactor required for Sp1 transcriptional a	1.415	23.47	0.29034	3094	M	-1.056	42.43	0.43364	7884
Mpv17l	A_51_P352738	NM_033564	Mpv17 transgene, kidney disease mutant	1.415	28.61	0.31256	4208	P	-1.05	40.63	0.34362	6803
Fbn1	A_51_P467224	NM_007993	fibrillin 1	1.414	49.93	0.5298	10741	P	1.055	25.31	0.4147	7673
Mcm4	A_52_P231545	AK083618	minichromosome maintenance deficient	1.414		0.50108	6572	A	1.024	36.07	0.64644	9859
Apoc3	A_52_P574306	NM_023114	apolipoprotein C-III	1.412	61.79	0.64601	15933	P	1.181	3.82	0.04159	1572
Cox6c	A_51_P343323	NM_053071	cytochrome c oxidase, subunit VIc	1.412	12.21	0.19102	1819	P	1.02	38.4	0.68432	10185
Foxn2	A_52_P431139	NM_180974	forkhead box N2	1.412		0.49749	6489	A	1.144	5.75	0.05529	2014
Pigk	A_51_P197175	NM_178016	phosphatidylinositol glycan anchor biosyr	1.412	49.93	0.49841	9594	P	1.01	42.43	0.90099	12101
Slc39a10	A_51_P223498	NM_172653	solute carrier family 39 (zinc transporter),	1.412	12.21	0.19672	1887	P	-1.071	42.43	0.51228	8696
Xrcc2	A_52_P510694	AK085093	X-ray repair complementing defective rep	1.412		0.78047	9884	A	-2.015	0	0.00584	68
Utrn	A_52_P504624	AK020881	utrophin	1.411		0.6625	8968	A	1.08	19.02	0.40651	7583
1300018I05Rik	A_51_P223177	NM_028791	RIKEN cDNA 1300018I05 gene	1.409	35.45	0.37783	5874	P	-1.028	47.43	0.65627	9940
Acly	A_51_P261718	NM_134037	ATP citrate lyase	1.408	10.84	0.2154	2071	P	1.562	0.24	0.01141	443
Mmd2	A_51_P257885	NM_175217	monocyte to macrophage differentiation-	1.408	31.88	0.32851	4603	P	1.015	42.43	0.77883	10973
Myl7	A_51_P246345	NM_022879	myosin, light polypeptide 7, regulatory	1.408	49.93	0.53335	10825	P	1.063	13.58	0.16598	4314
Atcay	A_51_P209697	NM_178662	ataxia, cerebellar, Cayman type homolog	1.407	42.28	0.44606	7835	P	1.074	19.02	0.30864	6424
B430316J06Rik	A_52_P1027808	AK046698	RIKEN cDNA B430316J06 gene	1.407	28.61	0.30999	4160	P	-1.057	45.05	0.68459	10188
Lmna	A_52_P137765	NM_019390	lamin A	1.407	69.29	0.76648	22003	P	1.157	8.32	0.1238	3576
Npm1	A_51_P467410	NM_008722	nucleophosmin 1	1.407	23.47	0.35984	4520	M	1.155	9.71	0.17956	4567
Serpinb12	A_51_P518909	NM_027971	serine (or cysteine) peptidase inhibitor, cl	1.407		0.54386	7563	A	-1.256	0.51	0.00809	306
Thbs2	A_51_P461877	NM_011581	thrombospondin 2	1.407		0.6654	9036	A	-1.163	1.32	0.02087	893
Fads1	A_51_P358112	NM_146094	fatty acid desaturase 1	1.406	31.88	0.33299	4738	P	-1.009	49.48	0.88372	11903
Tekt2	A_51_P109933	NM_011902	tektin 2	1.405	84.52	0.52245	9133	P	1.019	40.63	0.71928	10485
0610010O12Rik	A_52_P227937	BC028765	RIKEN cDNA 0610010O12 gene	1.404	31.88	0.33231	4706	P	1.207	3.82	0.05681	2053
Cetn3	A_51_P229105	NM_007684	centrin 3	1.403	42.28	0.45789	8133	P	-1.12	6.98	0.07614	2558
E030003F13Rik	A_52_P113672	BB529627	RIKEN cDNA E030003F13 gene	1.403	38.68	0.39107	6202	P	1.113	9.71	0.10424	3190
Snx5	A_51_P134844	NM_024225	sorting nexin 5	1.403	23.47	0.27361	3281	P	1.166	3.82	0.03166	1245
3222402P14Rik	A_51_P270960	BC031532	RIKEN cDNA 3222402P14 gene	1.402	25.79	0.28718	3556	P	1.403	0.24	0.00731	247
Gnptg	A_51_P491017	AK078230	N-acetylglucosamine-1-phosphotransfera	1.402	25.79	0.29583	3713	P	1.078	13.58	0.15508	4134
Ndrg2	A_51_P176352	NM_013864	N-myc downstream regulated gene 2	1.402	57.76	0.61456	14141	P	1.081	11.33	0.12856	3667
Plcb1	A_52_P18262	BC058710	phospholipase C, beta 1	1.402	25.79	0.27669	3346	P	1.245	1.17	0.00965	349
Plscr4	A_52_P671794	NM_178711	phospholipid scramblase 4	1.402	45.92	0.4813	8980	P	-1.118	11.33	0.1445	3932

Phgdh	A_51_P408729	NM_016966	3-phosphoglycerate dehydrogenase	1.401	13.61	0.20804	2039	P	-1.018	49.48	0.78083	10999
1110031B06Rik	A_52_P231079	NM_144521	RIKEN cDNA 1110031B06 gene	1.4	25.79	0.29119	3644	P	1.034	30.75	0.44499	7960
Baz2a	A_52_P191135	AK035400	bromodomain adjacent to zinc finger dom	1.4	28.61	0.32122	4409	P	1.084	25.31	0.5677	9183
Cyp3a11	A_51_P355301	NM_007818	cytochrome P450, family 3, subfamily a, p	1.4	75.14	0.84186	27211	P	1.022	38.4	0.73869	10673
Rtn1	A_52_P424959	NM_153457	reticulon 1	1.4	53.87	0.57306	12138	P	1.073	19.02	0.35084	6885
Hoxb9	A_52_P973575	NM_008270	homeo box B9	1.399	28.61	0.29875	3808	P	1.017	42.43	0.85845	11667
Unc5c	A_52_P380301	NM_009472	unc-5 homolog C (C. elegans)	1.399	35.45	0.37449	5726	P	1.193	4.63	0.06275	2223
Hebp2	A_51_P159612	NM_019487	heme binding protein 2	1.398	61.79	0.65765	16468	P	-1.031	49.22	0.8213	11375
Myh10	A_52_P680681	NM_175260	myosin, heavy polypeptide 10, non-muscl	1.398	28.61	0.32311	4442	P	1.681	0	0.00584	9
Fbxo21	A_52_P184145	NM_145564	F-box protein 21	1.396	23.47	0.27194	3212	P	-1.276	0.51	0.01023	385
Rhob	A_52_P89567	NM_007483	ras homolog gene family, member B	1.396	31.88	0.34185	4961	P	1.14	11.33	0.29228	6240
2900011O08Rik	A_51_P264656	NM_144518	RIKEN cDNA 2900011O08 gene	1.395	75.14	0.81009	24700	P	1.041	28.13	0.42548	7783
Ifit3	A_52_P663686	AK077243	similar to interferon-induced protein with	1.395	53.87	0.58129	12619	P	1.008	42.43	0.88348	11898
Tbxas1	A_51_P448664	NM_011539	thromboxane A synthase 1, platelet	1.395	23.47	0.26814	3119	P	1.01	42.43	0.81997	11358
A630018P17Rik	A_51_P162564	NM_001007577	RIKEN cDNA A630018P17 gene	1.394	53.87	0.55785	11672	P	1.099	16.2	0.31551	6531
Col6a1	A_51_P474496	NM_009933	procollagen, type VI, alpha 1	1.394	35.45	0.35722	5320	P	1.006	42.43	0.89053	11967
Edn3	A_52_P20753	NM_007903	endothelin 3	1.394	49.93	0.51279	10050	P	1.048	30.75	0.59423	9379
Pdk4	A_51_P350453	NM_013743	pyruvate dehydrogenase kinase, isoenzyn	1.394	53.87	0.60815	10948	M	-1.091	25.31	0.24747	5609
Rab3b	A_52_P339959	NM_023537	RAB3B, member RAS oncogene family	1.394	53.87	0.54536	11214	P	1.135	8.32	0.09166	2935
Cnot4	A_52_P795551	AK079480		1.393		0.59916	9020	A	-1.069	25.31	0.16463	4289
Park7	A_51_P229852	NM_020569	Parkinson disease (autosomal recessive, e	1.393	12.21	0.27794	2994	M	-1.011	49.48	0.87471	11811
Ppara	A_51_P348334	NM_011144	peroxisome proliferator activated recepto	1.393		0.61088	9333	A	-1.027	45.68	0.52732	8817
Pcsk1	A_52_P164524	NM_013628	proprotein convertase subtilisin/kexin typ	1.392	10.33	0.19103	1822	P	1.103	11.33	0.1615	4245
Psmc2	A_51_P108701	NM_011188	proteasome (prosome, macropain) 26S su	1.392	23.47	0.26119	3011	P	1.166	3.82	0.03916	1486
Rprm	A_52_P627967	NM_023396	reprimo, TP53 dependent G2 arrest medi	1.392	35.45	0.37154	5654	P	-1.162	1.58	0.02249	950
Aldh7a1	A_51_P470414	NM_138600	aldehyde dehydrogenase family 7, memb	1.391	38.68	0.40754	6657	P	-1.193	1.58	0.02906	1171
Pabpc1	A_52_P204023	AK005009	poly A binding protein, cytoplasmic 1	1.391	28.61	0.31692	4290	P	1.074	19.02	0.34767	6845
2610030H06Rik	A_52_P224373	BC028317	RIKEN cDNA 2610030H06 gene	1.39	20.94	0.25357	2880	P	-1.019	49.22	0.71961	10495
Mrpl49	A_52_P485433	NM_026246	mitochondrial ribosomal protein L49	1.39	28.61	0.30876	4126	P	-1.01	49.48	0.81205	11297
Neo1	A_52_P269003	NM_008684	neogenin	1.39	12.21	0.20104	1960	P	1.242	1.62	0.01565	668
Il6	A_51_P217218	NM_031168	interleukin 6	1.389	72.2	0.80326	24270	P	1.142	19.02	0.53987	8942
Rps28	A_51_P335671	CA467389	ribosomal protein S28	1.389	18.5	0.33753	4051	M	-1.036	45.05	0.53126	8846
Ctsl	A_51_P253547	NM_009984	cathepsin L	1.388	31.88	0.34941	5107	P	1.111	9.71	0.11009	3270
5730420B22Rik	A_51_P411264	NM_172597	RIKEN cDNA 5730420B22 gene	1.387	20.94	0.25495	2916	P	1	42.43	0.99997	13054
Ndufa4	A_52_P552832	NM_010886	NADH dehydrogenase (ubiquinone) 1 alpl	1.387	38.68	0.41052	6758	P	1.213	3.46	0.04581	1715
Pbx3	A_52_P406028	AK086310	pre B-cell leukemia transcription factor 3	1.387		0.51629	6912	A	1.117	6.98	0.05908	2108
Pdcd6ip	A_52_P188975	NM_011052	programmed cell death 6 interacting prot	1.387	16.01	0.22227	2239	P	1.232	2.04	0.01985	846
Foxa3	A_52_P64707	NM_008260	forkhead box A3	1.386	31.88	0.3356	4790	P	1.097	11.33	0.11899	3467
Gli3	A_51_P171288	AK048009	GLI-Kruppel family member GLI3	1.386	53.87	0.56612	11900	P	1.105	8.32	0.07279	2474
Rapgef1	A_52_P203322	NM_001039087	Rap guanine nucleotide exchange factor (	1.386	65.79	0.49339	7788	M	1.087	9.71	0.09238	2954
Sema5a	A_52_P409076	NM_009154	sema domain, seven thrombospondin rep	1.386	38.68	0.39931	6501	P	-1.073	40.63	0.45787	8076
Kdelc2	A_51_P501656	NM_212445	KDEL (Lys-Asp-Glu-Leu) containing 2	1.385	18.5	0.23742	2489	P	1.208	5.75	0.10699	3218
Tuba6	A_52_P503809	NM_009448	tubulin, alpha 1B	1.385	25.79	0.29757	3757	P	1.053	28.13	0.51724	8734
Hip1r	A_51_P440460	NM_145070	huntingtin interacting protein 1 related	1.384	12.21	0.20607	2022	P	1.023	36.07	0.61616	9592
Tcp1	A_52_P4271	AK150666	t-complex protein 1	1.384	18.5	0.23595	2458	P	1.08	13.58	0.173	4425
1100001I22Rik	A_51_P243288	NM_001005859	ribosomal protein L34	1.383	31.88	0.41848	5769	M	-1.005	49.48	0.93057	12393
Ccni	A_52_P663349	AK047232	cyclin I	1.383	79.26	0.37387	4749	M	1.152	5.75	0.07233	2448
Fzd4	A_51_P361220	NM_008055	frizzled homolog 4 (Drosophila)	1.383	53.87	0.55884	11698	P	-1.015	49.48	0.90792	12178
Wasl	A_52_P96782	NM_028459	Wiskott-Aldrich syndrome-like (human)	1.383	61.79	0.66117	16608	P	1.271	3.01	0.06348	2247
3526401B18Rik	A_52_P1042732	AK014386	RIKEN cDNA 3526401B18 gene	1.382	65.79	0.68923	17883	P	-1.017	49.39	0.71279	10424
Dhrs4	A_51_P352381	NM_030686	dehydrogenase/reductase (SDR family) m	1.382	42.28	0.44544	7802	P	1.064	25.31	0.49613	8530
Gnai3	A_51_P237695	NM_010306	guanine nucleotide binding protein, alpha	1.382	23.47	0.29265	3548	P	1.227	3.01	0.04231	1592
Vps35	A_52_P235108	NM_022997	vacuolar protein sorting 35	1.382	38.68	0.39016	6179	P	1.053	30.75	0.6778	10118

Asgr2	A_51_P484842	NM_007493	asialoglycoprotein receptor 2	1.381	45.92	0.45371	6681	M	-1.112	5.75	0.0596	2137
Hdc	A_51_P254656	NM_008230	histidine decarboxylase	1.381	53.87	0.57311	12147	P	1.006	42.43	0.94631	10814
Map3k5	A_52_P656714	NM_008580	mitogen activated protein kinase kinase k	1.381	35.45	0.35734	5347	P	1.153	9.71	0.2268	5310
Ahnak	A_51_P365344	NM_009643	AHNAK nucleoprotein (desmoyokin)	1.38	31.88	0.33154	4700	P	1.017	40.63	0.7248	10521
C330018D20Rik	A_52_P241725	AK021208	RIKEN cDNA C330018D20 gene	1.38	31.88	0.32995	4667	P	1.133	5.75	0.04464	1663
Xab1	A_51_P234462	NM_133756	XPA binding protein 1	1.379	28.61	0.32293	4437	P	-1.073	22.1	0.14398	3921
Acp1	A_52_P432037	NM_021330	acid phosphatase 1, soluble	1.378	42.28	0.42411	7181	P	1.077	16.2	0.19813	4869
Sgce	A_52_P27864	NM_011360	sarcoglycan, epsilon	1.378	38.68	0.40981	6728	P	1.117	9.71	0.15392	4113
1700020C11Rik	A_51_P175699	NM_026443	RIKEN cDNA 1700020C11 gene	1.377	20.94	0.25808	2965	P	1.016	40.63	0.78944	11083
Bcar1	A_51_P375227	NM_009954	breast cancer anti-estrogen resistance 1	1.377	25.79	0.28009	3422	P	1.05	22.1	0.29717	6294
Itpr1	A_51_P269663	NM_010585	inositol 1,4,5-triphosphate receptor 1	1.377	31.88	0.42422	5966	M	1.086	13.58	0.17186	4405
Apbb1	A_51_P344249	NM_009685	amyloid beta (A4) precursor protein-bindi	1.376	16.01	0.22462	2262	P	1.086	11.33	0.11364	3349
Bbx	A_51_P388691	NM_027444	bobby sox homolog (Drosophila)	1.376	31.88	0.33274	4733	P	1.048	33.49	0.71415	10438
Mapk8	A_51_P357182	NM_016700	mitogen activated protein kinase 8	1.376	53.87	0.57786	12410	P	1.018	40.63	0.81493	11325
Rab6b	A_51_P276418	NM_173781	RAB6B, member RAS oncogene family	1.376	12.21	0.20804	2036	P	-1.018	49.39	0.72185	10509
Slc26a3	A_52_P31381	NM_021353	solute carrier family 26, member 3	1.376	77.44	0.83547	22938	M	1.032	30.75	0.45693	8069
Zswim6	A_52_P663005	AK037945	zinc finger, SWIM domain containing 6	1.376	28.61	0.3128	4209	P	-1.039	43.75	0.39542	7466
2610301B20Rik	A_51_P425768	NM_026005	RIKEN cDNA 2610301B20 gene	1.373	10.84	0.2048	2000	P	1.013	42.43	0.78065	10991
Adamts1	A_52_P213932	NM_009621	a disintegrin-like and metallopeptidase (re	1.373	57.76	0.61718	14261	P	1.151	16.2	0.47883	8297
Fbxl17	A_52_P268279	XM_925135	F-box and leucine-rich repeat protein 17	1.373	20.94	0.35717	4441	M	1.048	28.13	0.41344	7661
Mmp16	A_51_P195775	NM_019724	matrix metallopeptidase 16	1.373	20.94	0.24428	2660	P	1.057	19.02	0.24312	5551
Rnaset2	A_51_P310100	AK029149	ribonuclease T2B	1.373	31.88	0.34829	5065	P	1.053	25.31	0.43136	7846
Hdgfrp3	A_52_P545066	NM_013886	hepatoma-derived growth factor, related	1.372	25.79	0.29672	3743	P	-1.011	49.48	0.82262	11383
Lgmn	A_51_P110576	NM_011175	legumain	1.372	12.21	0.21423	2108	P	1.303	2.53	0.04603	1729
Cyp4v3	A_52_P302345	NM_133969	cytochrome P450, family 4, subfamily v, p	1.371	20.94	0.25385	2895	P	1.364	1.17	0.02177	919
Ing3	A_52_P154880	NM_023626	inhibitor of growth family, member 3	1.371	31.88	0.33676	4826	P	1.113	9.71	0.1255	3615
Bphl	A_51_P283876	NM_026512	biphenyl hydrolase-like (serine hydrolase,	1.37	18.5	0.3228	3902	M	1.26	1.17	0.00965	350
Mast1	A_51_P196113	NM_019945	microtubule associated serine/threonine	1.37	61.79	0.63452	15441	P	1.093	13.58	0.17698	4516
Ndn	A_52_P451644	NM_010882	necdin	1.37	49.93	0.51541	10132	P	1.218	2.53	0.02825	1144
Pfkfb1	A_51_P359586	NM_008824	6-phosphofructo-2-kinase/fructose-2,6-bi	1.37	25.79	0.28357	3499	P	1.07	16.2	0.16689	4327
Pign	A_51_P221274	NM_013784	phosphatidylinositol glycan anchor biosyr	1.37	53.87	0.53563	10907	P	1.1	11.33	0.16485	4293
Stard4	A_52_P384574	NM_133774	StAR-related lipid transfer (START) domai	1.369	20.94	0.259	2972	P	1.121	11.33	0.1985	4873
Plek	A_51_P238357	NM_019549	pleckstrin	1.368	53.87	0.55993	11751	P	1.228	3.82	0.0814	2689
Rars	A_52_P288614	NM_025936	arginyl-tRNA synthetase	1.368	61.79	0.67716	17337	P	-1.075	28.13	0.2124	5083
Asxl1	A_52_P549405	NM_001039939	additional sex combs like 1 (Drosophila)	1.367	45.92	0.46785	8466	P	1.065	19.02	0.26891	5932
Mtch1	A_52_P126162	NM_019880	mitochondrial carrier homolog 1 (C. elega	1.367	57.76	0.62843	11534	M	1.02	38.4	0.68632	10208
Obfc1	A_52_P340692	NM_175360	oligonucleotide/oligosaccharide-binding f	1.367	31.88	0.3333	4747	P	1.097	9.71	0.10041	3112
Slc11a1	A_51_P186476	NM_013612	solute carrier family 11 (proton-coupled d	1.367	42.28	0.44218	7717	P	1.058	22.1	0.30041	6324
D13Wsu177e	A_51_P474158	NM_178605	DNA segment, Chr 13, Wayne State Unive	1.366	23.47	0.27555	3330	P	1.028	36.07	0.67849	10125
Nol4	A_52_P167317	NM_199024	nucleolar protein 4	1.366	20.94	0.2527	2846	P	1.311	1.17	0.01278	541
Rorc	A_51_P282930	NM_011281	RAR-related orphan receptor gamma	1.365	45.92	0.46179	8265	P	1.118	19.02	0.47441	8251
Bmpr2	A_51_P492648	AK140220	bone morphogenic protein receptor, type	1.364	31.88	0.32642	4551	P	1.077	19.02	0.32816	6651
Chrdl1	A_52_P674808	ENSMUST00000074660	chordin-like 1	1.364	75.14	0.83638	26840	P	1.015	42.43	0.83421	11487
Flrt2	A_52_P615362	BC067058	fibronectin leucine rich transmembrane p	1.364	69.29	0.73504	20451	P	1.087	16.2	0.23558	5425
Nelf	A_51_P169886	NM_001039386	nasal embryonic LHRH factor	1.364	20.94	0.24522	2712	P	1.096	9.71	0.2511	5229
Pdgfd	A_52_P636948	AK141551	platelet-derived growth factor, D polypep	1.364	53.87	0.57305	12136	P	1.043	28.13	0.39069	7402
Rassf6	A_51_P491916	NM_028478	Ras association (RalGDS/AF-6) domain far	1.364	53.87	0.53484	10885	P	1.135	3.82	0.03143	1239
2610024B07Rik	A_51_P473633	AK035191	RIKEN cDNA 2610024B07 gene	1.363	49.93	0.50253	9747	P	1.214	3.46	0.04227	1590
Usp18	A_51_P164219	NM_011909	ubiquitin specific peptidase 18	1.363	31.88	0.34447	4989	P	1.22	5.75	0.11669	3414
Mll3	A_52_P448569	XM_001002522	myeloid/lymphoid or mixed-lineage leuke	1.361	31.88	0.34663	5040	P	1.048	25.31	0.33009	6663
Ppp1r7	A_52_P630502	NM_023200	protein phosphatase 1, regulatory (inhibi	1.361	35.45	0.35168	5158	P	1.087	11.33	0.12962	3681
Rbm28	A_51_P437787	NM_026650	RNA binding motif protein 28	1.361	28.61	0.32302	4439	P	-1.139	4.63	0.06215	2197
Cspg2	A_52_P251703	D28599	versican	1.36	53.87	0.54946	11423	P	-1.031	47.43	0.69606	10284

Narg1	A_52_P191341	AK078042	NMDA receptor-regulated gene 1	1.36	38.68	0.40388	6578	P	1.02	38.4	0.66474	10002
Trim37	A_52_P252127	NM_197987	tripartite motif protein 37	1.36	20.94	0.25244	2833	P	1.067	16.2	0.16269	4268
Apex1	A_51_P473576	NM_009687	apurinic/apyrimidinic endonuclease 1	1.359	18.5	0.24033	2550	P	-1.143	1.62	0.02547	1057
Mlf1	A_51_P205106	NM_010801	myeloid leukemia factor 1	1.359	53.87	0.55338	11542	P	-1.016	49.47	0.72103	10503
Ttc7b	A_51_P136699	XM_127105	tetratricopeptide repeat domain 7B	1.359	31.88	0.3472	5053	P	1.197	3.46	0.04397	1645
Arhgef17	A_52_P119301	XM_133692	Rho guanine nucleotide exchange factor (	1.358	31.88	0.33775	4882	P	1.052	22.1	0.31555	6532
Jak1	A_52_P106463	NM_146145	Janus kinase 1	1.358	38.68	0.39052	6184	P	1.259	2.53	0.04276	1605
Slc1a2	A_51_P477875	NM_011393	solute carrier family 1 (glial high affinity g	1.358	72.2	0.80189	24158	P	1.141	6.98	0.07515	2539
Upf3a	A_52_P263386	AK033239	UPF3 regulator of nonsense transcripts ho	1.358	61.79	0.51785	9845	M	-1.017	49.48	0.73985	10684
Ap1g1	A_51_P197965	AK037086	adaptor protein complex AP-1, gamma 1 s	1.357	49.93	0.4763	8472	M	1.153	5.75	0.06361	2249
2610020C11Rik	A_52_P211037	NM_028130	RIKEN cDNA 2610020C11 gene	1.356	25.79	0.28744	3562	P	-1.29	0.51	0.00627	165
Msh2	A_52_P159095	AK051960	mutS homolog 2 (E. coli)	1.356	61.79	0.58783	12305	M	1.033	36.07	0.65314	9900
Creb3	A_52_P231714	NM_013497	cAMP responsive element binding protein	1.354	53.87	0.52805	10662	P	1.036	30.75	0.43307	7871
Gas1	A_51_P157083	NM_008086	growth arrest specific 1	1.354	23.47	0.27137	3192	P	1.027	33.49	0.551	9040
Mas1	A_51_P152623	NM_008552	MAS1 oncogene	1.354	72.2	0.73506	19219	P	-1.037	46.3	0.63048	9723
Sc4mol	A_51_P209372	NM_025436	sterol-C4-methyl oxidase-like	1.354	18.5	0.27911	3139	P	-1.07	47.43	0.82428	11404
BC053994	A_52_P556390	BC096528	RIKEN cDNA A230067G21 gene	1.353	42.28	0.38549	5824	M	-1.282	0.51	0.00901	327
Gabarapl1	A_52_P633410	NM_020590	gamma-aminobutyric acid (GABA(A)) rece	1.353	28.61	0.41521	5707	M	1.205	2.53	0.01962	836
Lpp	A_52_P260856	AK050035	LIM domain containing preferred transloc	1.352	18.5	0.24348	2643	P	1.254	2.53	0.03097	1221
Ppp3ca	A_52_P513099	AK036998		1.352	38.68	0.39414	6277	P	1.277	1.17	0.01132	440
Spag9	A_51_P312896	AK030165	sperm associated antigen 9	1.352	49.93	0.49059	9248	P	1.519	0.3	0.01279	555
Vim	A_52_P287532	AK033175	vimentin	1.352		0.33488	4411	A	-1.246	3.46	0.14558	3955
1110033M05Rik	A_52_P185797	AK037713	RIKEN cDNA 1110033M05 gene	1.351	65.79	0.69235	18047	P	1.071	16.2	0.21191	5072
Ccng1	A_52_P612803	NM_009831	cyclin G1	1.351	25.79	0.40383	5446	M	1.096	9.71	0.10799	3233
Gfm2	A_52_P378937	AK052633	G elongation factor, mitochondrial 2	1.351	28.61	0.30828	4120	P	-1.092	28.13	0.31512	6527
Hbb-b1	A_52_P213909	NM_008220	hemoglobin, beta adult major chain	1.351	65.79	0.68445	17635	P	1.123	25.31	0.6291	9707
Phf20l1	A_52_P286605	BC052212	PHD finger protein 20-like 1	1.351	10.84	0.21677	2165	P	1.081	13.58	0.13407	3745
Slc1a4	A_52_P273098	NM_018861	solute carrier family 1 (glutamate/neutral	1.351	31.88	0.34409	4982	P	1.136	11.33	0.21612	5131
Trpm4	A_52_P303100	NM_175130	transient receptor potential cation chann	1.351	25.79	0.28362	3504	P	-1.008	49.48	0.87183	11780
1700093K21Rik	A_51_P326555	AK007052	RIKEN cDNA 1700093K21 gene	1.35	49.93	0.43418	7195	M	1.006	42.43	0.91054	12195
Igf2bp1	A_52_P620742	AK085396	insulin-like growth factor 2 mRNA binding	1.35		0.66845	9743	A	-1.303	0.75	0.02905	1170
Blvra	A_51_P363103	NM_026678	biliverdin reductase A	1.349	28.61	0.31744	4303	P	-1.033	46.85	0.64576	9855
Ubl3	A_52_P487246	NM_011908	ubiquitin-like 3	1.349	18.5	0.32165	3882	M	1.227	1.58	0.01141	448
Nsg1	A_51_P358755	NM_010942	neuron specific gene family member 1	1.348	35.45	0.37282	5689	P	-1.095	28.13	0.2983	6300
Cask	A_51_P167232	NM_009806	calcium/calmodulin-dependent serine pro	1.347	35.45	0.35125	5149	P	-1.006	49.48	0.91966	12271
D730040F13Rik	A_51_P455429	NM_175518	RIKEN cDNA D730040F13 gene	1.347		0.63941	10080	A	1.11	9.71	0.08996	2896
Mrps27	A_52_P615312	NM_173757	mitochondrial ribosomal protein S27	1.347	20.94	0.26372	3056	P	-1.047	42.43	0.36542	7105
Reg3g	A_51_P354126	NM_011260	regenerating islet-derived 3 gamma	1.346	77.44	0.84731	27579	P	-1.031	45.68	0.50535	8635
Fbxw8	A_52_P216539	NM_172721	F-box and WD-40 domain protein 8	1.345	31.88	0.34602	5031	P	1.067	16.2	0.2074	5014
LOC380687	A_52_P479958	NM_001001978	predicted gene, EG622339	1.345	12.21	0.2268	2310	P	1.035	36.07	0.74374	10741
Mre11a	A_51_P446678	NM_018736	meiotic recombination 11 homolog A (S. c	1.344	53.87	0.56738	11958	P	-1.028	47.43	0.64455	9838
9630050M13Rik	A_51_P231587	XM_194000	RIKEN cDNA 9630050M13 gene	1.343	28.61	0.30828	4119	P	1.279	1.32	0.01469	627
Creb5	A_52_P137529	AK051306	cAMP responsive element binding protein	1.343	79.26	0.84604	19615	M	-1.02	47.92	0.63506	9762
Dab2	A_51_P157994	NM_001037905	disabled homolog 2 (Drosophila)	1.343	25.79	0.28122	3471	P	-1.064	38.4	0.38356	7321
Npepl1	A_52_P435670	NM_213733	aminopeptidase-like 1	1.343	23.47	0.27555	3328	P	-1.001	49.48	0.98171	12872
Pank1	A_51_P123320	AK019493	pantothenate kinase 1	1.343	45.92	0.38011	5460	M	1.107	8.32	0.05927	2123
Supt3h	A_51_P510663	NM_178652	suppressor of Ty 3 homolog (S. cerevisiae	1.343	31.88	0.32642	4543	P	-1.183	3.46	0.07728	2584
Pam	A_52_P494289	AK053025	peptidylglycine alpha-amidating monooxy	1.342	53.87	0.54946	11420	P	1.101	9.71	0.08013	2659
Tuba4	A_52_P676271	NM_009447	tubulin, alpha 4A	1.342	42.28	0.41613	6923	P	1.146	6.98	0.09998	3104
Igf1	A_52_P306327	AK050118	insulin-like growth factor 1	1.341	72.2	0.77139	22285	M	1.138	8.32	0.13213	3714
Numbl	A_51_P158355	U96441	numb-like	1.341	31.88	0.3333	4748	P	1.07	19.02	0.25674	5761
Trim35	A_52_P383913	AK020775	tripartite motif-containing 35	1.341	35.45	0.35412	5222	P	1.078	13.58	0.15587	4148
C030010B13Rik	A_51_P482279	AK030794		1.34	61.79	0.64119	15739	P	-1.105	13.58	0.14548	3952

Gstt1	A_51_P179664	NM_008185	glutathione S-transferase, theta 1	1.34	35.45	0.37749	5869	P	-1.115	19.02	0.23951	5476
Sh3d19	A_52_P273169	XM_994427	SH3 domain protein D19	1.34	18.5	0.25063	2792	P	1.084	11.33	0.11933	3474
A430106J12Rik	A_52_P578876	AK051140	RIKEN cDNA A430106J12 gene	1.338	65.79	0.67635	17324	P	1.097	13.58	0.1973	4858
Egfl7	A_52_P15122	NM_178444	EGF-like domain 7	1.338	38.68	0.38297	5975	P	-1.081	22.1	0.1523	4072
Ensa	A_52_P222021	NM_019561	endosulfine alpha	1.338	42.28	0.44291	7748	P	1.166	3.82	0.03267	1284
Msra	A_51_P299243	NM_026322	methionine sulfoxide reductase A	1.338	42.28	0.43444	7484	P	1.123	11.33	0.26073	5829
Tgfb1i1	A_51_P366344	NM_009365	transforming growth factor beta 1 induce	1.338	25.79	0.29949	3842	P	1.009	42.43	0.88455	11922
Rdh13	A_52_P269334	AK089458	retinol dehydrogenase 13 (all-trans and 9	1.337	42.28	0.42844	7306	P	-1.041	45.05	0.60121	9463
Smarca2	A_52_P388829	NM_011416	SWI/SNF related, matrix associated, actin	1.337	49.93	0.51595	10164	P	1.109	9.71	0.11933	3476
Uchl3	A_52_P537050	NM_016723	ubiquitin carboxyl-terminal esterase L3 (u	1.337	42.28	0.4222	7114	P	-1.157	2.04	0.03443	1323
Ccr1	A_52_P616356	NM_009912	chemokine (C-C motif) receptor 1	1.336		0.72464	10525	A	-1.289	0.51	0.0067	209
Ndufa7	A_52_P347591	NM_023202	NADH dehydrogenase (ubiquinone) 1 alp	1.336	28.61	0.41554	5714	M	1.038	33.49	0.61383	9565
Adamts20	A_52_P242480	AK090358	a disintegrin-like and metallopeptidase (r	1.335	75.14	0.82805	25893	P	-1.05	40.63	0.34054	6774
Cdc25b	A_51_P474431	NM_023117	cell division cycle 25 homolog B (S. pomb	1.335	38.68	0.40075	6530	P	-1.067	36.07	0.3246	6613
Tle6	A_52_P368591	NM_053254	transducin-like enhancer of split 6, homol	1.335	57.76	0.60024	13445	P	1.028	33.49	0.55885	9095
Uba52	A_52_P475889	NM_019883	ubiquitin A-52 residue ribosomal protein	1.335	38.68	0.35096	4775	P	1.042	30.75	0.50539	8639
Cpeb1	A_52_P462296	NM_007755	cytoplasmic polyadenylation element bin	1.334	18.5	0.37908	4914	M	1.204	8.32	0.20058	4912
Slc4a1	A_51_P196972	NM_011403	solute carrier family 4 (anion exchanger),	1.334	42.28	0.44218	7719	P	-1.181	1.58	0.02885	1161
Lztfl1	A_52_P215597	NM_033322	leucine zipper transcription factor-like 1	1.333	31.88	0.33008	4675	P	-1.048	43.15	0.44979	7991
Mab21l2	A_51_P327206	NM_011839	mab-21-like 2 (C. elegans)	1.333	25.79	0.28279	3375	P	1.047	30.75	0.5337	8875
Thoc1	A_52_P243025	NM_153552	THO complex 1	1.333	53.87	0.55923	11710	P	1.11	13.58	0.27226	5987
2700049A03Rik	A_51_P196226	BC043104	RIKEN cDNA 2700049A03 gene	1.332	20.94	0.25894	2968	P	1.052	22.1	0.32409	6601
9130404D08Rik	A_52_P38456	AK081612	RIKEN cDNA 9130404D08 gene	1.332	61.79	0.50238	8070	M	1.103	9.71	0.11501	3378
Tardbp	A_52_P299292	NM_001008546	TAR DNA binding protein	1.332	25.79	0.28781	3576	P	1.107	11.33	0.18638	4677
Aebp1	A_51_P336770	NM_009636	AE binding protein 1	1.331	49.93	0.51764	10241	P	-1.073	28.13	0.1894	4712
Ccnc	A_52_P456674	NM_016746	cyclin C	1.331	38.68	0.38285	5973	P	-1.041	44.4	0.53045	8836
Ireb2	A_52_P680908	NM_022655	iron responsive element binding protein	1.331	49.93	0.49949	9639	P	-1.003	49.48	0.96931	12739
Pcmt1	A_51_P225853	NM_008786	protein-L-isoaspartate (D-aspartate) O-m	1.331	28.61	0.30389	3980	P	1.097	13.58	0.19009	4720
Serpinf2	A_51_P174176	NM_008878	serine (or cysteine) peptidase inhibitor, cl	1.331	69.29	0.63638	14442	M	1.084	13.58	0.14276	3901
Sh3bgrl	A_52_P426513	NM_019989	SH3-binding domain glutamic acid-rich pr	1.331	25.79	0.41455	5691	M	1.11	11.33	0.15029	4041
Ubl5	A_52_P188134	NM_025401	ubiquitin-like 5	1.331	53.87	0.52245	10430	P	-1.095	16.2	0.12613	3633
Spna1	A_51_P501069	NM_011465	spectrin alpha 1	1.33		0.82935	11001	A	-1.035	45.68	0.54537	8987
Thbs1	A_52_P337086	NM_011580	thrombospondin 1	1.33	57.76	0.59941	13419	P	-1.02	49.48	0.82791	11439
AV249152	A_51_P235853	NM_145425	expressed sequence AV249152	1.329	53.87	0.54741	11307	P	1.049	25.31	0.317	6551
BC003965	A_51_P357838	XM_128528	cDNA sequence BC003965	1.329	49.93	0.49694	9505	P	1.048	30.75	0.55707	9080
Gnai2	A_51_P432484	NM_008138	guanine nucleotide binding protein, alph	1.329	25.79	0.29965	3854	P	1.073	13.58	0.16225	4262
9630020C08Rik	A_52_P623511	AK080592	neuron navigator 3	1.328	72.2	0.78154	22833	P	1.019	38.4	0.67768	10116
Cpa3	A_51_P214127	NM_007753	carboxypeptidase A3, mast cell	1.327		0.60428	9158	A	-1.061	33.49	0.2463	5594
Pycr1	A_51_P503896	ENSMUST00000026133	pyrroline-5-carboxylate reductase 1	1.327	23.47	0.28012	3427	P	-1.127	5.75	0.07515	2538
Cry1	A_51_P302204	NM_007771	cryptochrome 1 (photolyase-like)	1.326	12.21	0.24026	2549	P	1.079	22.1	0.44389	7954
Eps15	A_52_P360595	BC048783	epidermal growth factor receptor pathwa	1.326	28.61	0.30439	4009	P	1.202	5.75	0.12486	3600
Exo1	A_51_P239984	NM_012012	exonuclease 1	1.326	57.76	0.51941	9451	M	-1.045	40.63	0.31472	6520
Ghitm	A_52_P246749	NM_078478	growth hormone inducible transmembra	1.326	25.79	0.41752	5749	M	1.206	4.63	0.08867	2858
Hdgf	A_52_P339791	NM_008231	hepatoma-derived growth factor	1.326	35.45	0.35793	5373	P	1.172	5.75	0.08145	2693
Cdkn1a	A_51_P363947	NM_007669	cyclin-dependent kinase inhibitor 1A (P21	1.325	53.87	0.5437	11150	P	1.291	3.01	0.06486	2279
Usp15	A_52_P124812	AK122301	ubiquitin specific peptidase 15	1.325	31.88	0.34305	4977	P	1.04	28.13	0.39135	7413
Chm	A_52_P236373	NM_018818	choroidermia	1.324	25.79	0.29265	3547	M	1.069	22.1	0.43143	7851
Dusp9	A_52_P648601	NM_029352	dual specificity phosphatase 9	1.324	65.79	0.53635	9058	M	1.099	9.71	0.08313	2730
Rab11fip5	A_52_P529360	NM_001003955	RAB11 family interacting protein 5 (class I	1.324	53.87	0.55674	11643	P	-1.028	47.43	0.67517	10100
Rassf2	A_51_P355802	NM_175445	Ras association (RalGDS/AF-6) domain fa	1.324		0.73574	10804	A	1.014	42.43	0.86564	11726
Klf4	A_51_P213544	NM_010637	Kruppel-like factor 4 (gut)	1.323	65.79	0.72438	15130	M	1.042	28.13	0.46213	8128
Npc2	A_51_P347961	NM_023409	Niemann Pick type C2	1.323	45.92	0.47077	8572	P	1.001	42.43	0.99758	13034
Ralgds	A_51_P509518	NM_009058	ral guanine nucleotide dissociation stimul	1.323	57.76	0.58585	12819	P	-1.022	49.47	0.78401	11043

Rnaseh2a	A_51_P424128	ENSMUST00000065049	ribonuclease H2, large subunit	1.323	28.61	0.32456	4498	P	-1.008	49.48	0.87157	11776
Rragd	A_52_P490032	NM_027491	Ras-related GTP binding D	1.323	42.28	0.41313	6856	P	1.075	16.2	0.18947	4714
4933439F18Rik	A_51_P511745	NM_025757	RIKEN cDNA 4933439F18 gene	1.322	35.45	0.35929	5386	P	1.018	40.63	0.80166	11195
Atox1	A_51_P346153	NM_009720	ATX1 (antioxidant protein 1) homolog 1 (y	1.322	38.68	0.40199	6549	P	1.07	19.02	0.32686	6638
Bspry	A_51_P421559	NM_138653	B-box and SPRY domain containing	1.322	42.28	0.41069	6762	P	1.061	19.02	0.28685	6184
Hc	A_51_P155323	NM_010406	hemolytic complement	1.322	45.92	0.47609	8839	P	-1.067	38.4	0.38568	7344
Lhx1	A_51_P452119	NM_008498	LIM homeobox protein 1	1.322	38.68	0.40939	6712	P	1.065	19.02	0.28883	6199
Phb	A_51_P165934	NM_008831	prohibitin	1.322	31.88	0.3333	4754	P	1.051	22.1	0.27579	6037
Smurf1	A_51_P181227	NM_001038627	SMAD specific E3 ubiquitin protein ligase	1.322	53.87	0.52271	10440	P	-1.039	44.4	0.49496	8510
Tmem38b	A_51_P181865	NM_028053	transmembrane protein 38B	1.321	42.28	0.4272	7278	P	-1.133	4.63	0.05657	2045
Derl2	A_52_P84275	NM_033562	Der1-like domain family, member 2	1.32	25.79	0.41761	5752	M	1.097	16.2	0.30529	6386
Tom1l2	A_51_P202162	NM_001039093	target of myb1-like 2 (chicken)	1.32	61.79	0.62089	13684	M	1.109	9.71	0.11024	3273
Wnt6	A_51_P482571	M89800	wingless-related MMTV integration site 6	1.32	38.68	0.39458	6349	P	-1.118	16.2	0.18985	4719
Epb4.1l1	A_52_P270490	NM_001003815	erythrocyte protein band 4.1-like 1	1.319	35.45	0.36697	5541	P	1.105	8.32	0.06237	2205
Gnb1	A_52_P304858	NM_008142	guanine nucleotide binding protein, beta	1.319	38.68	0.47485	7212	M	1.056	16.2	0.1986	4878
Mesdc2	A_52_P574974	NM_023403	mesoderm development candiate 2	1.319	61.79	0.65843	16505	P	1	42.43	0.99732	13032
Sdcbp	A_51_P249494	NM_016807	syndecan binding protein	1.319	38.68	0.48742	7507	M	1.325	3.46	0.11387	3364
Acsl1	A_52_P597618	NM_007981	acyl-CoA synthetase long-chain family me	1.318	12.21	0.24458	2702	P	1.015	42.43	0.81045	11284
Cad	A_52_P16102	NM_023525	carbamoyl-phosphate synthetase 2, aspai	1.318	53.87	0.53335	10835	P	-1.075	28.13	0.19855	4877
Mgst1	A_52_P549827	NM_019946	microsomal glutathione S-transferase 1	1.318	79.26	0.88759	30115	P	1.05	28.13	0.4417	7933
Stag1	A_52_P673971	NM_009282	stromal antigen 1	1.318	53.87	0.52633	10573	P	1.059	22.1	0.32601	6629
Chfr	A_52_P327971	NM_172717	checkpoint with forkhead and ring finger	1.317	61.79	0.65288	16242	P	1.015	42.43	0.84226	11537
H3f3b	A_52_P217875	NM_008211	H3 histone, family 3B	1.317	35.45	0.36757	5574	P	1.067	28.13	0.59219	9353
Ldb2	A_51_P388517	NM_001077398	LIM domain binding 2	1.317	61.79	0.62328	14604	P	-1.024	49.48	0.82099	11369
Zfp609	A_52_P455352	NM_172536	zinc finger protein 609	1.317	53.87	0.50395	9427	M	1.004	42.43	0.93833	12464
Centd2	A_51_P437247	NM_001040111	centaurin, delta 2	1.316	35.45	0.36115	5425	P	-1.003	49.48	0.94576	12549
Kcnj8	A_51_P312795	NM_008428	potassium inwardly-rectifying channel, su	1.316	69.29	0.71645	19310	P	1.022	38.4	0.63996	9811
Ndufab1	A_51_P208801	NM_028177	NADH dehydrogenase (ubiquinone) 1, alp	1.316	53.87	0.55244	11506	P	1.157	4.63	0.04865	1812
Nr4a1	A_51_P239654	NM_010444	nuclear receptor subfamily 4, group A, me	1.316	84.52	0.81285	23502	P	1.229	8.32	0.21716	5156
Sod1	A_51_P367381	NM_011434	superoxide dismutase 1, soluble	1.316	57.76	0.63575	11759	M	1.108	16.2	0.31601	6534
BC004004	A_52_P448466	NM_030561	cDNA sequence BC004004	1.315	42.28	0.43451	7488	P	-1.15	9.71	0.18379	4636
Tceb2	A_52_P1182012	NM_026305	transcription elongation factor B (SIII), po	1.315	38.68	0.40143	6538	P	-1.002	49.48	0.98019	12848
Tgfb2	A_51_P317640	NM_009367	transforming growth factor, beta 2	1.315	38.68	0.39453	6328	P	1.079	13.58	0.18656	4679
2210010L05Rik	A_52_P388163	NM_178081	RIKEN cDNA 2210010L05 gene	1.314	42.28	0.41119	6792	P	1.245	2.53	0.03528	1360
5730596K20Rik	A_52_P594927	NM_146091	RIKEN cDNA 5730596K20 gene	1.314	38.68	0.39765	6454	P	1.053	30.75	0.5743	9222
Gpr4	A_51_P295806	NM_175668	G protein-coupled receptor 4	1.314	79.26	0.80717	23116	P	1.035	30.75	0.4643	8154
Fkbp10	A_51_P216965	NM_010221	FK506 binding protein 10	1.313	35.45	0.36627	5524	P	1.009	42.43	0.84595	11573
Mocs3	A_51_P146813	XM_130596	molybdenum cofactor synthesis 3	1.313	13.61	0.25143	2812	P	1.036	30.75	0.47083	8208
Ogt	A_52_P658241	BC037194	O-linked N-acetylglucosamine (GlcNAc) tr	1.313	25.79	0.30634	4060	P	-1.083	19.02	0.12967	3684
Rab8b	A_51_P366836	NM_173413	RAB8B, member RAS oncogene family	1.313	57.76	0.60906	13891	P	1.018	40.63	0.78383	11040
Timm9	A_51_P421804	NM_013896	translocase of inner mitochondrial memb	1.313	38.68	0.39447	6308	P	1.022	40.63	0.77399	10953
Bhlhb9	A_51_P323081	NM_198161	basic helix-loop-helix domain containing,	1.312	25.79	0.30389	3979	P	1.035	28.13	0.40686	7587
Ndufa3	A_52_P69702	NM_025348	NADH dehydrogenase (ubiquinone) 1 alpl	1.312	31.88	0.34902	5090	P	-1.049	42.43	0.35417	6940
Rpl5	A_51_P183732	NM_016980	ribosomal protein L5	1.312	53.87	0.5953	10577	M	1.176	2.53	0.01861	789
Timm10	A_51_P348624	NM_013899	translocase of inner mitochondrial memb	1.312	38.68	0.39458	6348	P	1.103	13.58	0.2134	5090
Usp19	A_51_P136845	NM_027804	ubiquitin specific peptidase 19	1.312	35.45	0.37749	5867	P	-1.228	0.75	0.01384	583
Rpl30	A_51_P268914	NM_009083	ribosomal protein L30	1.311	31.88	0.44734	6517	M	-1.043	46.3	0.71375	10436
Ubap1	A_51_P480062	NM_023305	ubiquitin-associated protein 1	1.311	35.45	0.35535	5251	P	-1.021	48.7	0.70508	10361
Wsb1	A_51_P271370	NM_001042565	WD repeat and SOCS box-containing 1	1.311	57.76	0.57363	12182	P	-1.031	46.85	0.6291	9705
Ylpm1	A_52_P615158	AK054220	YLP motif containing 1	1.311	35.45	0.35717	5310	P	1.205	3.82	0.06577	2308
Aven	A_52_P547730	AK034962	apoptosis, caspase activation inhibitor	1.31	61.79	0.65776	16485	P	-1.039	43.75	0.40349	7548
Btf3	A_51_P482600	AK006780	basic transcription factor 3	1.31	57.76	0.59336	13102	P	1.169	8.32	0.15095	4053
Clock	A_52_P334677	NM_007715	circadian locomoter output cycles kaput	1.31	31.88	0.34833	5070	P	1.084	22.1	0.42915	7819

Hccs	A_52_P241797	AK028608	holocytochrome c synthetase	1.31	42.28	0.43862	7593	P	1.04	28.13	0.41573	7687
Tead1	A_51_P422603	NM_009346	TEA domain family member 1	1.31	61.79	0.6422	15810	P	1.125	6.98	0.05044	1864
Vamp2	A_52_P240905	NM_009497	vesicle-associated membrane protein 2	1.31	42.28	0.43701	7541	P	1.05	25.31	0.41711	7709
Cdc42se2	A_51_P340013	NM_178626	CDC42 small effector 2	1.309	35.45	0.3596	5392	P	1.092	8.32	0.07384	2504
Lgi4	A_51_P217386	NM_144556	leucine-rich repeat LGI family, member 4	1.309	53.87	0.53335	10844	P	-1.067	28.13	0.19116	4751
Magi1	A_52_P44205	NM_001029850	membrane associated guanylate kinase,	1.309	65.79	0.70123	18444	P	-1.017	49.48	0.7401	10687
Ndrg3	A_51_P346722	NM_013865	N-myc downstream regulated gene 3	1.309	12.21	0.2527	2835	P	1.175	3.82	0.04595	1723
Prep	A_52_P90124	NM_011156	prolyl endopeptidase	1.309	42.28	0.42082	7061	P	1.108	6.98	0.05211	1916
Setbp1	A_52_P230167	NM_053099	SET binding protein 1	1.309	53.87	0.519	10315	P	1.056	19.02	0.24053	5499
Coro2b	A_52_P538995	NM_175484	coronin, actin binding protein, 2B	1.308	53.87	0.54744	11315	P	-1.069	36.07	0.36669	7122
Crem	A_52_P460957	NM_013498	cAMP responsive element modulator	1.308	72.2	0.77774	22634	P	1.379	2.53	0.08551	2786
Efnb2	A_51_P380970	NM_010111	ephrin B2	1.308	57.76	0.59361	13130	P	1.037	30.75	0.46191	8122
Fn1	A_51_P100856	NM_010233	fibronectin 1	1.308		0.47461	6857	A	-1.066	36.07	0.35082	6881
Ablim1	A_52_P489778	AK154082	actin-binding LIM protein 1	1.307	49.93	0.49841	9588	P	1.141	6.98	0.09557	3008
Atp5g2	A_52_P287002	NM_026468	ATP synthase, H+ transporting, mitochon	1.307	20.94	0.41119	5610	M	-1.042	44.4	0.51164	8684
Cmya5	A_51_P493016	AJ511265	cardiomyopathy associated 5	1.307	45.92	0.39529	6139	M	-1.022	49	0.72705	10534
Nfe2l1	A_51_P491720	NM_008686	nuclear factor, erythroid derived 2,-like 1	1.307	42.28	0.50441	8003	M	1.259	1.62	0.01586	685
Uaca	A_51_P437336	NM_028283	uveal autoantigen with coiled-coil domai	1.307	49.93	0.49105	9257	P	-1.087	13.58	0.10452	3197
Ntf3	A_52_P525161	NM_008742	neurotrophin 3	1.306	57.76	0.5707	12084	P	1.121	11.33	0.23872	5465
Tgfbr1	A_52_P4538	NM_009370	transforming growth factor, beta receptor	1.306	31.88	0.41653	6102	M	1.09	13.58	0.15679	4163
1110029E03Rik	A_51_P385010	NM_172866	RIKEN cDNA 1110029E03 gene	1.305	42.28	0.37527	5527	M	1.031	33.49	0.52116	8761
Blvrb	A_51_P460844	NM_144923	biliverdin reductase B (flavin reductase (	1.305	42.28	0.43796	7562	P	-1.016	49.48	0.7657	10899
Hdac11	A_51_P213334	NM_144919	histone deacetylase 11	1.304	31.88	0.33133	4692	P	-1.002	49.48	0.96667	12718
Map2k6	A_52_P395242	AK086722	mitogen activated protein kinase kinase 6	1.304	53.87	0.43943	7333	P	1.115	16.2	0.35815	6987
Ywhaz	A_52_P644465	AK050511	tyrosine 3-monooxygenase/tryptophan 5	1.304	45.92	0.47135	8619	P	1.222	3.82	0.06486	2275
Zyx	A_51_P473252	NM_011777	zyxin	1.304	53.87	0.52866	10698	P	-1.074	28.13	0.19142	4757
Atp1b3	A_52_P572950	NM_007502	ATPase, Na+/K+ transporting, beta 3 poly	1.303	18.5	0.2678	3110	P	1.115	11.33	0.2196	5201
Fhl5	A_51_P465843	NM_021318	four and a half LIM domains 5	1.303		0.75532	11336	A	1.101	9.71	0.09454	2991
Rpl17	A_52_P123268	NM_001002239	ribosomal protein L17	1.303	42.28	0.50298	7967	M	1.14	9.71	0.17836	4545
2610024E20Rik	A_52_P666824	NM_146084	RIKEN cDNA 2610024E20 gene	1.302	38.68	0.39279	6239	P	1.173	3.82	0.04505	1671
Epha3	A_52_P276955	NM_010140	Eph receptor A3	1.302	42.28	0.40939	6709	P	1.094	13.58	0.21503	5123
Ftl1	A_52_P501733	NM_010240	ferritin light chain 1	1.302	49.93	0.56327	9556	M	-1.18	1.62	0.03516	1353
Slc11a2	A_51_P388737	NM_008732	solute carrier family 11 (proton-coupled	1.302	42.28	0.42597	7239	P	1.061	19.02	0.22274	5252
Apln	A_51_P209327	NM_013912	apelin	1.301	57.76	0.58584	12817	P	1.002	42.43	0.98171	12869
St8sia4	A_51_P236267	NM_009183	ST8 alpha-N-acetyl-neuraminide alpha-2,	1.301	65.79	0.66333	16722	P	1.032	33.49	0.60143	9465
Vps29	A_52_P456071	NM_019780	vacuolar protein sorting 29 (S. pombe)	1.301	49.93	0.49715	9518	P	-1.062	42.43	0.49735	8552
2610036L11Rik	A_52_P609024	AK141272	RIKEN cDNA 2610036L11 gene	1.3	23.47	0.29354	3686	P	1.127	6.98	0.05375	1972
2810410C14Rik	A_52_P18775	NM_175471	RIKEN cDNA 2810410C14 gene	1.3	38.68	0.38487	6039	P	-1.243	0.56	0.01004	379
Calm2	A_52_P402305	NM_007589	calmodulin 2	1.3	38.68	0.50041	7874	M	1.284	3.01	0.07093	2415
Huwe1	A_52_P617552	AK031374	HECT, UBA and WWE domain containing	1.3	35.45	0.36107	5419	P	1.1	9.71	0.1166	3412
Dcxr	A_52_P98100	AK161732	dicarbonyl L-xylulose reductase	1.299	45.92	0.423	6228	M	-1.005	49.48	0.92231	12285
Gli2	A_52_P357829	XM_136212	GLI-Kruppel family member GLI2	1.299		0.49841	7470	A	-1.06	38.4	0.32562	6620
Mgat1	A_52_P90337	NM_010794	mannoside acetylglucosaminyltransferase	1.299	61.79	0.636	15532	M	1.086	28.13	0.65026	9885
Rab36	A_52_P247057	NM_029781	RAB36, member RAS oncogene family	1.299	57.76	0.59721	12719	P	1.03	33.49	0.5498	9018
Rps19	A_52_P129131	AK031403	ribosomal protein S19	1.299		0.8462	11439	A	-1.014	49.48	0.83739	11509
Slit3	A_51_P301809	NM_011412	slit homolog 3 (Drosophila)	1.299	65.79	0.66121	16623	P	1.008	42.43	0.91405	12210
1700020O03Rik	A_52_P303595	NM_027405	RIKEN cDNA 1700020O03 gene	1.298	25.79	0.29894	3827	P	-1.065	40.63	0.41683	7705
2310021P13Rik	A_51_P402805	AK029263	RIKEN cDNA 2310021P13 gene	1.298	49.93	0.5101	9945	P	-1.003	49.48	0.93769	12455
Ankrd24	A_52_P351758	AK019475	ankyrin repeat domain 24	1.298	53.87	0.52694	10604	P	1.106	11.33	0.14642	3972
Elf4	A_51_P448856	NM_019680	E74-like factor 4 (ets domain transcriptio	1.298	38.68	0.39458	6339	M	1.137	5.75	0.04155	1571
Jagn1	A_51_P150608	NM_026365	jagunal homolog 1 (Drosophila)	1.298	23.47	0.29098	3637	P	1.119	8.32	0.10123	3130
Pex13	A_52_P322555	NM_023651	peroxisomal biogenesis factor 13	1.298	42.28	0.43073	7385	P	-1.024	48.39	0.66718	10022
Rnf24	A_51_P339356	NM_178607	ring finger protein 24	1.298	53.87	0.40489	6387	P	1.097	11.33	0.1233	3567

Rpl27a	A_51_P132459	NM_011975	ribosomal protein L27a	1.298	45.92	0.45858	8159	P	1.074	19.02	0.29008	6211
Wdr55	A_51_P381743	NM_026464	WD repeat domain 55	1.298	23.47	0.2894	3612	P	-1.227	0.75	0.03963	1337
Anxa5	A_51_P426754	NM_009673	annexin A5	1.297	35.45	0.44185	7413	P	1.404	0.75	0.01469	628
Arid5b	A_52_P660812	BC082312		1.297	38.68	0.39458	6347	P	1.01	42.43	0.8769	11826
C1galt1c1	A_52_P382376	AK161729	C1GALT1-specific chaperone 1	1.297	65.79	0.5115	9167	M	1.016	42.43	0.8965	12026
Plod2	A_51_P396570	NM_011961	procollagen lysine, 2-oxoglutarate 5-dioxy	1.296	35.45	0.37747	5844	P	1.112	9.71	0.12728	3650
2610036D13Rik	A_52_P24382	NM_029282	RIKEN cDNA 2610036D13 gene	1.295	28.61	0.32338	4456	P	1.092	8.32	0.07325	2482
4930534B04Rik	A_51_P355258	NM_181815	RIKEN cDNA 4930534B04 gene	1.295	61.79	0.61819	14299	P	1.032	30.75	0.47083	8211
Atpif1	A_52_P276412	AK011886	ATPase inhibitory factor 1	1.295	53.87	0.52599	10558	P	1.007	42.43	0.90099	12096
Oxct1	A_52_P430058	NM_024188	3-oxoacid CoA transferase 1	1.295	45.92	0.44572	7816	P	1.108	9.71	0.12199	3545
Ppt2	A_52_P238816	NM_019441	palmitoyl-protein thioesterase 2	1.295	35.45	0.3596	5391	P	1.112	8.32	0.07152	2423
Tarsl1	A_52_P392591	NM_027931	threonyl-tRNA synthetase 2, mitochondri	1.295	53.87	0.53797	10974	P	1.017	40.63	0.73205	10592
Api5	A_52_P644903	AK078801	apoptosis inhibitor 5	1.294	65.79	0.69097	17960	P	1.139	6.98	0.09226	2951
Ctsd	A_51_P384629	NM_009983	cathepsin D	1.294	45.92	0.4705	7861	P	-1.071	33.49	0.26935	5946
Adora1	A_52_P172272	NM_001008533	adenosine A1 receptor	1.293	45.92	0.45812	8142	P	-1.349	0.51	0.00584	54
BC005537	A_52_P561394	AK051292	cDNA sequence BC005537	1.293	45.92	0.45467	8040	P	1.215	3.01	0.02835	1152
Blm	A_51_P314418	NM_007550	Bloom syndrome homolog (human)	1.293	53.87	0.51911	10317	P	1.006	42.43	0.91088	12197
Cxcl2	A_51_P217463	NM_009140	chemokine (C-X-C motif) ligand 2	1.293	81.02	0.89894	30907	P	-1.087	36.07	0.42186	7747
Gabarap	A_51_P295312	NM_019749	gamma-aminobutyric acid receptor assoc	1.293	45.92	0.53391	8816	M	1.117	11.33	0.21111	5056
Pknox1	A_52_P431894	NM_016670	Pbx/knotted 1 homeobox	1.293	31.88	0.34379	4980	P	-1.01	49.48	0.91764	12244
Vat1	A_52_P79639	NM_012037	vesicle amine transport protein 1 homolo	1.293	49.93	0.48536	9083	P	1.113	9.71	0.11104	3295
8030451K01Rik	A_52_P320202	AK220477	RIKEN cDNA 8030451K01 gene	1.292	38.68	0.39534	6399	P	-1.027	46.85	0.59776	9432
Mrg1	A_52_P277641	NM_010825	myeloid ecotropic viral integration site-re	1.292	20.94	0.29057	3635	P	1.622	0.24	0.00661	193
Nr2f1	A_52_P275700	NM_010151	nuclear receptor subfamily 2, group F, me	1.292	57.76	0.55863	11684	P	1.125	8.32	0.1018	3140
Prkra	A_51_P345836	NM_011871	protein kinase, interferon inducible doubl	1.292	18.5	0.27843	3403	P	-1.129	6.98	0.08461	2778
Anxa1	A_51_P283590	NM_010730	annexin A1	1.291	79.26	0.89437	30616	P	1.006	42.43	0.9352	12435
Ccbl2	A_51_P392577	NM_173763	cysteine conjugate-beta lyase 2	1.291	77.44	0.83703	26876	P	1.053	25.31	0.45011	7993
D1Ertd161e	A_52_P110646	NM_026187	DNA segment, Chr 1, ERATO Doi 161, expr	1.291	42.28	0.41016	6741	P	1.104	8.32	0.06487	2280
Pafah1b2	A_51_P461844	NM_008775	platelet-activating factor acetylhydrolase,	1.291	53.87	0.53699	10940	P	1.127	9.71	0.12852	3664
D3Ertd300e	A_51_P362771	NM_019995	DNA segment, Chr 3, ERATO Doi 300, expr	1.29	53.87	0.51659	10200	P	-1.045	40.63	0.31099	6471
E130308A19Rik	A_51_P109541	NM_001015681	RIKEN cDNA E130308A19 gene	1.29	25.79	0.30372	3951	P	1.084	13.58	0.20476	4961
Idh3g	A_51_P136729	NM_008323	isocitrate dehydrogenase 3 (NAD+), gamn	1.29	38.68	0.49177	7610	M	-1.022	48.39	0.66366	9994
Jam2	A_52_P374846	NM_023844	junction adhesion molecule 2	1.29	49.93	0.48372	9034	P	-1.013	49.48	0.83992	11528
Prdx6	A_52_P388359	NM_007453	peroxiredoxin 6	1.29	49.93	0.49961	9245	P	1.021	38.4	0.70707	10384
Sgpp1	A_52_P42221	NM_030750	sphingosine-1-phosphate phosphatase 1	1.29	23.47	0.29875	3801	P	1.207	5.75	0.11855	3450
Smarca1	A_51_P461404	NM_053123	SWI/SNF related, matrix associated, actin	1.29	53.87	0.52791	10655	P	1.206	3.46	0.04256	1601
Synj2	A_52_P188172	NM_011523	synaptojanin 2	1.29	20.94	0.28615	3534	P	1.012	42.43	0.88003	11859
Bmf	A_52_P78830	NM_138313	Bcl2 modifying factor	1.289		0.76761	11654	A	1.091	13.58	0.16853	4360
Evi2b	A_52_P508999	NM_146023	ecotropic viral integration site 2b	1.289		0.69651	11694	A	-1.002	49.48	0.97107	12755
2010315L10Rik	A_52_P181235	NM_025917	RIKEN cDNA 2010315L10 gene	1.288	53.87	0.55338	11543	P	1.048	33.49	0.66531	10004
Celsr1	A_51_P440743	NM_009886	cadherin EGF LAG seven-pass G-type rece	1.288	72.2	0.75317	21297	P	-1.061	36.07	0.29307	6257
Cycs	A_51_P261671	NM_007808	cytochrome c, somatic	1.288	45.92	0.44972	7905	P	1.075	19.02	0.28401	6138
Rwdd2	A_52_P554436	NM_027100	RWD domain containing 2	1.288	45.92	0.45944	8193	P	-1.011	49.48	0.81977	11354
C920006C10Rik	A_52_P298593	AK052176	RIKEN cDNA C920006C10 gene	1.287	49.93	0.47485	8790	P	1.087	11.33	0.13454	3753
Golt1b	A_52_P37665	NM_025872	golgi transport 1 homolog B (S. cerevisiae	1.287	42.28	0.43224	7407	P	1.022	42.43	0.85845	11668
Ptpn21	A_52_P329825	NM_011877	protein tyrosine phosphatase, non-recept	1.287	23.47	0.29829	3784	P	1.167	3.82	0.03362	1307
Ttc3	A_51_P137947	NM_009441	tetratricopeptide repeat domain 3	1.287	38.68	0.39694	6172	P	1.067	25.31	0.45153	8006
5330401P04Rik	A_52_P51854	NM_172654	RIKEN cDNA 5330401P04 gene	1.286	57.76	0.57565	12295	P	-1.055	38.4	0.2923	6242
Arhgap12	A_51_P214837	NM_001039692	Rho GTPase activating protein 12	1.286	49.93	0.49273	9359	P	1.127	6.98	0.06279	2227
B930042K01Rik	A_52_P113345	AK040303	RIKEN cDNA B930042K01 gene	1.286	77.44	0.8594	28196	P	-1.013	49.48	0.77614	10960
Bub3	A_52_P110040	NM_009774	budding uninhibited by benzimidazoles 3	1.286	20.94	0.28891	3606	P	1.013	42.43	0.79824	11165
Cobl	A_52_P451485	NM_172496	cordon-bleu	1.286	49.93	0.4977	9544	P	1.01	42.43	0.80954	11274
Ctsb	A_51_P465148	NM_007798	cathepsin B	1.286	53.87	0.60426	10833	M	1.143	5.75	0.05931	2128

Dbp	A_51_P180492	NM_016974	D site albumin promoter binding protein	1.286	77.44	0.83451	26581	P	-1.067	33.49	0.27701	6053
Mthfs	A_51_P338197	AK081946	5, 10-methenyltetrahydrofolate synthetas	1.286	57.76	0.58539	12791	P	-1.197	1.18	0.01749	747
Rpl7	A_51_P496480	NM_011291	ribosomal protein L7	1.286	42.28	0.42074	7050	P	1.084	16.2	0.26507	5873
Ncor1	A_51_P457744	AK038502	nuclear receptor co-repressor 1	1.285	23.47	0.29819	3775	P	-1.2	1.18	0.01947	822
Rpl10	A_51_P495895	NM_052835	ribosomal protein 10	1.285	23.47	0.43969	6314	M	1.081	19.02	0.31065	6457
BC054438	A_51_P397446	AK038244	cDNA sequence BC054438	1.284	42.28	0.42805	7294	P	1.081	25.31	0.52202	8770
Commd8	A_52_P112721	NM_178599	COMM domain containing 8	1.284	53.87	0.54468	11188	P	-1.149	4.63	0.07628	2562
Ppp1r9a	A_52_P159490	NM_181595	protein phosphatase 1, regulatory (inhibit	1.284	42.28	0.42199	7103	P	1.07	16.2	0.23272	5390
Cugbp2	A_51_P182471	NM_010160	CUG triplet repeat, RNA binding protein 2	1.283	42.28	0.52633	8578	M	1.042	28.13	0.45234	8021
Tnfrsf1a	A_52_P192426	NM_011609	tumor necrosis factor receptor superfami	1.283	61.79	0.62451	14675	P	1.133	8.32	0.08819	2850
Pde1a	A_51_P327016	NM_016744	phosphodiesterase 1A, calmodulin-depen	1.282	42.28	0.41931	7003	P	1.023	38.4	0.69683	10290
Pemt	A_51_P193093	NM_008819	phosphatidylethanolamine N-methyltrans	1.281	45.92	0.4714	8628	P	-1.022	49.22	0.75804	10853
Spin	A_51_P195135	NM_011462	spindlin 1	1.281	31.88	0.47364	7156	M	1.11	9.71	0.11077	3284
Lmo2	A_51_P223686	NM_008505	LIM domain only 2	1.28	57.76	0.5773	12372	P	1.067	16.2	0.16315	4274
Mthfd2	A_52_P184149	NM_008638	methylenetetrahydrofolate dehydrogenas	1.28	53.87	0.51595	10165	P	-1.073	28.13	0.21652	5144
Sumo1	A_52_P236354	AK020140		1.28		0.76231	17567	A	1.084	28.13	0.66863	10031
Hrsp12	A_52_P59681	NM_008287	heat-responsive protein 12	1.279	53.87	0.51764	10231	P	1.102	11.33	0.16591	4308
Mdm4	A_52_P174937	NM_008575	transformed mouse 3T3 cell double minu	1.279	57.76	0.59334	13093	P	1.097	19.02	0.39909	7506
Ncald	A_52_P673722	NM_134094	neurocalcin delta	1.279	49.93	0.48167	9000	P	1.193	6.98	0.13679	3785
Nrp1	A_52_P174942	AK040447	neuropilin 1	1.279	77.44	0.63941	13656	M	1.178	5.75	0.10129	3132
Sema4a	A_51_P195066	NM_013658	sema domain, immunoglobulin domain (I	1.279	25.79	0.31599	4269	P	1.091	11.33	0.13908	3828
Ubl4	A_52_P637730	NM_145405	ubiquitin-like 4	1.279	45.92	0.47123	8611	P	-1.082	19.02	0.12604	3630
Wif1	A_51_P484526	NM_011915	Wnt inhibitory factor 1	1.279	72.2	0.58616	12228	M	1.045	25.31	0.36472	7087
Hook1	A_52_P13897	NM_030014	hook homolog 1 (Drosophila)	1.278	49.93	0.4726	8673	P	1.111	8.32	0.08211	2708
Psat1	A_51_P317427	NM_177420	phosphoserine aminotransferase 1	1.278	75.14	0.79387	23755	P	1.193	8.32	0.22782	5330
Syn1	A_51_P420684	NM_013680	synapsin I	1.278	57.76	0.59334	13096	P	-1.337	0.51	0.00731	251
Gns	A_52_P408476	NM_029364	glucosamine (N-acetyl)-6-sulfatase	1.277	42.28	0.41841	6979	P	1.141	8.32	0.12865	3673
Tex10	A_52_P221696	AK132870	testis expressed gene 10	1.277	45.92	0.4705	8552	P	-1.083	19.02	0.12552	3619
Tor3a	A_52_P52357	BC052851	torsin family 3, member A	1.276	38.68	0.38867	6151	P	-1.001	49.48	0.97856	12829
2900064A13Rik	A_51_P204286	AK033552	RIKEN cDNA 2900064A13 gene	1.275	35.45	0.37114	5644	P	1.032	36.07	0.70826	10391
Entpd6	A_51_P379399	NM_172117	ectonucleoside triphosphate diphosphohy	1.275	42.28	0.42411	7186	P	1.124	11.33	0.19966	4897
Gls	A_51_P488024	AK031899	glutaminase	1.275	28.61	0.33299	4741	P	1.215	3.82	0.07233	2449
Pogk	A_52_P476690	NM_175170	pogo transposable element with KRAB do	1.275	31.88	0.34854	5075	P	-1.038	44.4	0.47798	8286
Zfp566	A_51_P437478	NM_152814	zinc finger protein 566	1.275	38.68	0.38958	6169	P	-1.057	38.4	0.32773	6646
BC026657	A_51_P304002	AK020491	enhancer trap locus 4	1.274	61.79	0.65199	16172	P	1.042	28.13	0.37996	7279
Crp	A_51_P105554	NM_007768	C-reactive protein, pentraxin-related	1.274	57.76	0.49334	9005	P	1.147	8.32	0.15301	4088
Hcn3	A_52_P655508	ENSMUST00000029686	hyperpolarization-activated, cyclic nucleo	1.274	45.92	0.45434	8031	P	-1.081	25.31	0.20732	5011
Rps15a	A_52_P577019	NM_170669	ribosomal protein S15a	1.274	45.92	0.55478	9363	M	-1.022	49.48	0.82999	11450
Tfpi	A_51_P383210	AF016313	tissue factor pathway inhibitor	1.274		0.67422	12680	A	1.109	13.58	0.25347	5708
Araf	A_52_P673489	AK133797	v-raf murine sarcoma 3611 viral oncogene	1.273	49.93	0.47299	8711	P	1.218	2.53	0.02327	979
Cln8	A_52_P541134	NM_012000	ceroid-lipofuscinosis, neuronal 8	1.273	38.68	0.39526	6375	P	1.11	9.71	0.09869	3079
Dhcr24	A_51_P482711	NM_053272	24-dehydrocholesterol reductase	1.273	72.2	0.76477	21899	P	-1.12	8.32	0.08456	2776
Prdm5	A_51_P347448	NM_027547	PR domain containing 5	1.273	57.76	0.58248	12646	P	-1.003	49.48	0.94037	12481
Ptpn11	A_52_P641185	NM_011202	protein tyrosine phosphatase, non-recept	1.273	28.61	0.32974	4664	P	1.035	30.75	0.50929	8668
Camk2d	A_52_P428745	NM_001025439	calcium/calmodulin-dependent protein ki	1.272	31.88	0.34833	5071	P	-1.006	49.48	0.90494	12144
Wdr1	A_51_P184773	NM_011715	WD repeat domain 1	1.272	77.44	0.8411	20133	M	1.262	1.58	0.01485	637
Mpp2	A_51_P462978	NM_016695	membrane protein, palmitoylated 2 (MAC	1.271	61.79	0.60765	13810	P	-1.002	49.48	0.97747	12816
Adamts18	A_52_P488683	AK035797	a disintegrin-like and metallopeptidase (r	1.27	38.68	0.3999	6514	P	1.008	42.43	0.92002	12274
Ak1	A_51_P452876	NM_021515	adenylate kinase 1	1.27	38.68	0.39483	6369	P	1.149	9.71	0.17362	4438
AW124694	A_51_P319551	AK149180	kinesin family member 3A	1.27	38.68	0.38777	6118	P	1.245	4.63	0.12625	3640
Crsp3	A_52_P596054	AK028545	cofactor required for Sp1 transcriptional a	1.27	31.88	0.34944	5109	P	1.013	42.43	0.7994	11173
Grik1	A_51_P282609	NM_146072	glutamate receptor, ionotropic, kainate 1	1.27		0.64363	10236	A	1.039	25.31	0.35632	6968
Stxbp5	A_52_P234695	XM_896388	syntaxin binding protein 5 (tomosyn)	1.27	20.94	0.30377	3962	P	1.001	42.43	0.97941	12834

Tal1	A_51_P255853	NM_011527	T-cell acute lymphocytic leukemia 1	1.27	57.76	0.58746	12888	P	1	49.48	0.99892	13057
Zfp423	A_51_P328439	NM_033327	zinc finger protein 423	1.27	57.76	0.60731	13060	P	-1.048	42.43	0.36458	7082
Acy1	A_51_P166288	NM_025371	aminoacylase 1	1.269	49.93	0.49512	9443	P	1.001	42.43	0.9932	13004
Eya4	A_52_P295933	AK045060	eyes absent 4 homolog (Drosophila)	1.269	69.29	0.62328	13778	P	1.095	9.71	0.08213	2709
Fbxo25	A_51_P324551	NM_025785	F-box protein 25	1.269	45.92	0.45291	8000	P	1.091	11.33	0.12116	3513
Itm2b	A_52_P99411	NM_008410	integral membrane protein 2B	1.269	31.88	0.48647	7479	M	1.152	5.75	0.05211	1917
Khdrbs2	A_51_P223724	NM_133235	KH domain containing, RNA binding, signa	1.269	65.79	0.6915	18009	P	-1.309	0.92	0.03814	1443
Mthfd1	A_52_P282279	NM_138745	methylenetetrahydrofolate dehydrogenas	1.269	35.45	0.37749	5865	P	1.2	4.63	0.08606	2795
Prnpip1	A_52_P616591	NM_080469	prion protein interacting protein 1	1.269	38.68	0.38483	6031	P	-1.006	49.48	0.96755	12724
Tomm70a	A_51_P520660	NM_138599	translocase of outer mitochondrial memb	1.269	31.88	0.35734	5345	P	1.042	25.31	0.3307	6682
Ero1l	A_51_P481693	NM_015774	ERO1-like (S. cerevisiae)	1.268	49.93	0.50238	9727	P	1.198	3.82	0.05148	1894
Hoxa2	A_51_P501803	NM_010451	homeo box A2	1.268	75.14	0.81907	25366	P	1.106	9.71	0.11412	3369
Adra2c	A_52_P428345	NM_007418	adrenergic receptor, alpha 2c	1.267	79.26	0.81115	23421	M	1.101	6.98	0.05742	2077
As3mt	A_51_P282227	NM_020577	arsenic (+3 oxidation state) methyltransfe	1.267	42.28	0.42204	7105	P	-1.001	49.48	0.98123	12857
Jmjd1a	A_52_P133965	NM_001038695	jumonji domain containing 1A	1.267	31.88	0.35723	5334	P	1.076	25.31	0.498	8557
B230112C05Rik	A_52_P488623	XM_619141	RIKEN cDNA B230112C05 gene	1.266	35.45	0.36532	5503	P	1.09	11.33	0.11329	3343
Pfdn5	A_52_P208604	NM_027044	prefoldin 5	1.266	49.93	0.51637	8858	M	-1.055	44.4	0.62786	9701
AW060207	A_51_P378558	NM_144911	expressed sequence AW060207	1.265	35.45	0.37749	5850	P	-1.113	8.32	0.07782	2596
Cops2	A_52_P259087	NM_009939	COP9 (constitutive photomorphogenic) ho	1.265	45.92	0.45956	8203	P	1.04	30.75	0.54902	9012
Eif3s5	A_51_P516452	NM_025344	eukaryotic translation initiation factor 3, s	1.265	42.28	0.41219	6827	P	-1.067	36.07	0.33104	6686
Fyn	A_51_P177667	NM_008054	Fyn proto-oncogene	1.265	49.93	0.48078	8967	P	1.001	42.43	0.98392	12908
Rps3	A_51_P318642	NM_012052	ribosomal protein S3	1.265	38.68	0.5132	8201	M	1.149	11.33	0.2964	6286
Eif4b	A_52_P390114	NM_145625	eukaryotic translation initiation factor 4B	1.264	53.87	0.54252	11093	P	1.149	8.32	0.11515	3384
Mast2	A_52_P261151	AK086418	microtubule associated serine/threonine	1.264	69.29	0.73001	17395	M	-1.036	45.68	0.59197	9352
Mphosph10	A_52_P463578	NM_026483	M-phase phosphoprotein 10 (U3 small nu	1.264	23.47	0.31651	4279	P	-1.002	49.48	0.9753	12790
Prdx5	A_51_P174591	NM_012021	peroxiredoxin 5	1.264	45.92	0.43972	7635	P	-1.227	1.1	0.01999	851
Zfp91	A_52_P301243	AK040976	zinc finger protein 91	1.264	28.61	0.33591	4805	P	1.003	42.43	0.96856	12729
0610037L13Rik	A_52_P613953	NM_028754	RIKEN cDNA 0610037L13 gene	1.263	49.93	0.47157	8633	P	1.09	13.58	0.16182	4257
2310061C15Rik	A_51_P140368	NM_026844	RIKEN cDNA 2310061C15 gene	1.263	61.79	0.61828	14311	P	-1.025	47.43	0.62359	9653
Anapc1	A_52_P384594	AK090134	anaphase promoting complex subunit 1	1.263	53.87	0.53827	11000	P	1.124	6.98	0.05733	2072
Arl6ip1	A_51_P301964	NM_019419	ADP-ribosylation factor-like 6 interacting p	1.263	45.92	0.45812	8141	P	1.073	16.2	0.23272	5393
Bckdha	A_51_P466148	NM_007533	branched chain ketoacid dehydrogenase E	1.263	23.47	0.31825	4330	P	-1.219	0.66	0.01045	399
Cited2	A_51_P478548	U86445	Cbp/p300-interacting transactivator, with	1.263	69.29	0.73204	20348	P	-1.042	43.75	0.42795	7800
Map1lc3b	A_51_P126177	NM_026160	microtubule-associated protein 1 light cha	1.263	28.61	0.4082	6177	P	1.054	28.13	0.51175	8685
Mt1	A_52_P423810	AK154954	metallothionein 1	1.263	49.93	0.48724	9166	P	-1.081	19.02	0.1217	3540
Cd2bp2	A_52_P530958	NM_027353	CD2 antigen (cytoplasmic tail) binding pro	1.262	28.61	0.3362	4817	P	1.07	22.1	0.36826	7140
Hist1h2be	A_51_P235426	NM_178194	histone cluster 1, H2be	1.262	49.93	0.49127	9276	P	1.267	9.71	0.36478	7091
Mgea5	A_52_P504786	NM_023799	meningioma expressed antigen 5 (hyaluro	1.262	42.28	0.43312	7445	P	-1.016	49.48	0.72735	10541
Pcca	A_51_P484254	NM_144844	propionyl-Coenzyme A carboxylase, alpha	1.262	49.93	0.49929	9636	P	1.011	42.43	0.84609	11575
4930413O22Rik	A_51_P428595	AK032310	centrosome and spindle pole associated p	1.261	65.79	0.66674	16888	P	1.228	5.75	0.14879	4023
Irx3	A_51_P518757	NM_008393	Iroquois related homeobox 3 (Drosophila	1.261	61.79	0.61855	14364	P	1.025	33.49	0.55676	9079
Itpr2	A_51_P468269	AB012393	inositol 1,4,5-triphosphate receptor 2	1.261		0.65565	10566	A	-1.045	43.75	0.4574	8072
Vrk1	A_52_P555672	NM_001029844	vaccinia related kinase 1	1.261	69.29	0.7015	18467	P	-1.134	4.63	0.05574	2023
Nfic	A_52_P551496	NM_026756	nuclear factor I/C	1.26	57.76	0.56391	11840	P	1.053	22.1	0.28082	6099
Rnf20	A_52_P411401	AK087860	ring finger protein 20	1.26	49.93	0.47299	8712	M	1.061	19.02	0.2404	5495
Rps7	A_51_P127545	NM_011300	ribosomal protein S7	1.26	45.92	0.54774	9162	M	1.04	30.75	0.53978	8939
Brms1l	A_52_P377703	NM_001037756	breast cancer metastasis-suppressor 1-lik	1.259	38.68	0.40405	6595	P	1.051	22.1	0.26315	5856
Akt1	A_51_P237553	NM_009652	thymoma viral proto-oncogene 1	1.258	65.79	0.68448	17640	P	1.093	11.33	0.14718	3985
Akt3	A_52_P130835	NM_011785	thymoma viral proto-oncogene 3	1.258	35.45	0.37749	5863	P	1.18	8.32	0.20543	4979
Bgn	A_52_P162486	NM_007542	biglycan	1.258	57.76	0.57961	12473	P	-1.05	38.4	0.27939	6085
Eif3s8	A_52_P455089	XM_993422	eukaryotic translation initiation factor 3, s	1.258	45.92	0.43868	7597	P	-1.122	9.71	0.12611	3631
Lad1	A_51_P116932	NM_133664	ladinin	1.258	75.14	0.80746	24552	P	-1.038	45.05	0.5031	8610
Nrxn1	A_52_P362651	AK037724	neurexin I	1.258	61.79	0.60279	13572	P	-1.117	8.32	0.07903	2631

Rtn4rl1	A_52_P94401	NM_177708	reticulon 4 receptor-like 1	1.258	31.88	0.35661	5270	P	-1.015	49.48	0.74228	10704
Trub2	A_52_P427064	NM_145520	TruB pseudouridine (psi) synthase homol	1.258	53.87	0.51076	9980	P	-1.003	49.48	0.94253	12505
Cct4	A_52_P236176	AK011873	chaperonin subunit 4 (delta)	1.257	53.87	0.5359	10912	P	1.496	0.24	0.00584	80
Fbxw2	A_52_P643001	BC003834	F-box and WD-40 domain protein 2	1.257	35.45	0.36771	5582	P	1.046	25.31	0.3774	7246
Fgfr1op2	A_52_P493620	NM_026218	FGFR1 oncogene partner 2	1.257	31.88	0.3584	5383	P	1.176	3.82	0.04112	1558
Gcap14	A_52_P102798	NM_027045	granule cell antiserum positive 14	1.257	45.92	0.44218	7711	P	1.052	30.75	0.6066	9499
Gpx4	A_51_P462448	NM_001037741	glutathione peroxidase 4	1.257	42.28	0.43626	7519	P	1.037	28.13	0.37227	7200
Ipo11	A_52_P499934	NM_029665	importin 11	1.257	25.79	0.33064	4680	P	1.063	22.1	0.36031	7026
Nfe2l2	A_52_P523835	AK029360	nuclear factor, erythroid derived 2, like 2	1.257	38.68	0.39447	6311	P	-1.022	49.39	0.78625	11057
Plscr2	A_51_P251022	NM_008880	phospholipid scramblase 2	1.257	61.79	0.60024	13457	P	1.108	13.58	0.30536	6387
9130213B05Rik	A_51_P114577	AK161172	RIKEN cDNA 9130213B05 gene	1.256	61.79	0.6071	13765	P	1.032	40.63	0.84317	11545
Adrbk1	A_51_P460302	NM_130863	adrenergic receptor kinase, beta 1	1.256	57.76	0.54927	11393	P	-1.05	40.63	0.35281	6920
D19Bwg1357e	A_52_P276343	NM_177474	DNA segment, Chr 19, Brigham & Womer	1.256	42.28	0.42411	7178	P	1.03	33.49	0.50427	8622
Gna13	A_52_P185343	AK011851	guanine nucleotide binding protein, alpha	1.256	53.87	0.5298	10740	P	1.114	11.33	0.2123	5080
Klhl5	A_51_P395405	BC057606	kelch-like 5 (Drosophila)	1.256	69.29	0.71151	19044	P	1.035	30.75	0.50013	8580
Nab1	A_52_P318438	NM_008667	Ngfi-A binding protein 1	1.256	38.68	0.38848	6148	P	1.044	30.75	0.60513	9493
Sema3e	A_51_P483438	NM_011348	sema domain, immunoglobulin domain (I	1.256	38.68	0.40631	6642	P	1.094	11.33	0.12232	3549
Snx27	A_52_P19329	AK147452	sorting nexin family member 27	1.255	57.76	0.6422	12482	M	-1.201	0.75	0.01251	528
Tcf21	A_51_P459944	NM_011545	transcription factor 21	1.255	53.87	0.53279	10818	P	1.056	22.1	0.29288	6250
5330417C22Rik	A_51_P182131	NM_001033304	RIKEN cDNA 5330417C22 gene	1.254	45.92	0.46836	8478	P	1.366	1.1	0.01492	641
Kctd5	A_52_P61758	NM_027008	potassium channel tetramerisation doma	1.254	72.2	0.74464	20827	P	1.014	42.43	0.85811	11655
Pygl	A_51_P452779	NM_133198	liver glycogen phosphorylase	1.254	57.76	0.5773	12373	P	-1.116	22.1	0.2892	6202
Rabggtb	A_51_P314763	NM_011231	RAB geranylgeranyl transferase, b subunit	1.254	69.29	0.70847	18863	P	1.143	6.98	0.08963	2885
Serpinb6a	A_51_P191375	NM_009254	serine (or cysteine) peptidase inhibitor, cl	1.254	65.79	0.66394	16790	P	1.187	6.98	0.15575	4144
Sugt1	A_52_P414718	NM_026474	SGT1, suppressor of G2 allele of SKP1 (S.	1.254	42.28	0.43495	7505	P	1.071	25.31	0.48497	8383
Txnl5	A_51_P349878	NM_026559	thioredoxin-like 5	1.254	31.88	0.35713	5293	P	-1.008	49.48	0.94283	12507
Xpo1	A_52_P89259	AK052007	exportin 1, CRM1 homolog (yeast)	1.254	61.79	0.64671	15952	P	1.067	16.2	0.1791	4555
2010208K18Rik	A_51_P329879	NM_028095	RIKEN cDNA 2010208K18 gene	1.253	61.79	0.63638	15547	P	1.193	3.82	0.04407	1648
Ednrb	A_51_P262964	NM_007904	endothelin receptor type B	1.253	31.88	0.36016	5401	P	1.047	33.49	0.67916	10134
Lrrc3b	A_51_P362089	NM_146052	leucine rich repeat containing 3B	1.253	69.29	0.71091	19013	P	1.04	28.13	0.4147	7675
Rpl35a	A_51_P509107	NM_021338	ribosomal protein L35a	1.253	57.76	0.6422	11971	M	-1.016	49.48	0.89507	12010
Tpcn1	A_52_P476560	NM_145853	two pore channel 1	1.253	65.79	0.68819	17844	P	-1.115	8.32	0.08418	2753
Uxs1	A_51_P501550	NM_026430	UDP-glucuronate decarboxylase 1	1.253	45.92	0.44523	7797	P	-1.067	40.63	0.44094	7929
Atrx	A_51_P413366	NM_009530	alpha thalassemia/mental retardation syr	1.252	57.76	0.56738	11947	P	1.196	3.82	0.06328	2240
Dll1	A_51_P306017	NM_007865	delta-like 1 (Drosophila)	1.252	53.87	0.52764	10626	P	1.082	11.33	0.11376	3356
Eif4e3	A_52_P287338	NM_025829	eukaryotic translation initiation factor 4E	1.252	65.79	0.64966	16079	P	1.122	5.75	0.04556	1709
F2rl2	A_51_P261164	NM_010170	coagulation factor II (thrombin) receptor-	1.252		0.59676	12708	A	-1.013	49.48	0.86853	11748
Hgfac	A_51_P101545	NM_019447	hepatocyte growth factor activator	1.252	49.93	0.49841	9595	P	1.023	38.4	0.74033	10690
Mrpl13	A_51_P428715	NM_026759	mitochondrial ribosomal protein L13	1.252	35.45	0.38302	5989	P	1.04	33.49	0.59745	9427
Spg21	A_52_P219966	NM_138584	spastic paraplegia 21 homolog (human)	1.252	35.45	0.38011	5928	P	1.208	3.01	0.03553	1376
Tnfrsf12a	A_51_P131408	NM_013749	tumor necrosis factor receptor superfami	1.252	69.29	0.70335	18585	P	-1.234	1.1	0.02229	941
AA536717	A_52_P242445	NM_001024512	expressed sequence AA536717	1.251	42.28	0.41801	6963	P	1.1	16.2	0.30973	6440
Akr1b3	A_52_P346706	NM_009658	aldo-keto reductase family 1, member B3	1.251	61.79	0.62845	14928	P	1.046	25.31	0.32695	6640
Eef1g	A_51_P401471	AK011951	eukaryotic translation elongation factor 1	1.251	65.79	0.67257	17199	P	-1.013	49.48	0.79325	11123
Hspa12b	A_51_P130332	NM_028306	heat shock protein 12B	1.251	53.87	0.52683	10590	P	-1.023	48.39	0.6878	10217
Psmc6	A_51_P509941	BC043044	proteasome (prosome, macropain) 26S su	1.251	31.88	0.3571	5289	P	1.077	16.2	0.26904	5935
Rasgrp3	A_52_P198435	NM_207246	RAS, guanyl releasing protein 3	1.251	53.87	0.54024	11038	P	1.118	6.98	0.05634	2038
Ube2l6	A_52_P214740	NM_019949	ubiquitin-conjugating enzyme E2L 6	1.251	45.92	0.466	8413	P	1.002	42.43	0.97353	12771
3300001M20Rik	A_52_P525837	NM_175113	RIKEN cDNA 3300001M20 gene	1.25	31.88	0.36381	5473	P	-1.008	49.48	0.85207	11615
Cd2ap	A_51_P229076	NM_009847	CD2-associated protein	1.25	53.87	0.50783	9898	P	1.129	13.58	0.28196	6116
Dap	A_52_P576442	NM_146057	death-associated protein	1.25	49.93	0.57665	9920	M	1.197	6.98	0.14384	3919
Ndufs6	A_52_P685828	NM_010888	NADH dehydrogenase (ubiquinone) Fe-S	1.25	42.28	0.4196	7013	P	-1.063	33.49	0.24609	5590
Nos3	A_51_P139651	NM_008713	nitric oxide synthase 3, endothelial cell	1.25	53.87	0.51279	10058	P	1.073	30.75	0.67432	10090

Pet112l	A_51_P397375	NM_144896	PET112-like (yeast)	1.25	57.76	0.57961	12458	P	-1.148	5.75	0.10386	3185
Smpd1	A_51_P429209	NM_011421	sphingomyelin phosphodiesterase 1, acid	1.25	61.79	0.64119	15736	P	-1.016	49.48	0.83037	11457
Abca5	A_51_P284646	NM_147219	ATP-binding cassette, sub-family A (ABC1)	1.249	53.87	0.5295	10718	P	1.1	9.71	0.1171	3421
Bre	A_51_P197365	NM_181279	brain and reproductive organ-expressed p	1.249	23.47	0.33533	4782	P	-1.141	8.32	0.12284	3559
Efemp2	A_51_P160544	NM_021474	epidermal growth factor-containing fibuli	1.249	45.92	0.46442	8365	P	1.006	42.43	0.90449	12141
Garnl1	A_52_P39372	BC010340	GTPase activating RANGAP domain-like 1	1.249	72.2	0.74659	20913	P	1.031	33.49	0.55467	9058
Gcat	A_51_P159402	NM_013847	glycine C-acetyltransferase (2-amino-3-ke	1.249	57.76	0.57174	12109	P	-1.036	46.3	0.60908	9514
Rab20	A_51_P417854	NM_011227	RAB20, member RAS oncogene family	1.249	61.79	0.63533	15490	P	1.027	33.49	0.56634	9174
Skp1a	A_52_P10458	NM_011543	S-phase kinase-associated protein 1A	1.249	45.92	0.45115	7945	P	1.168	3.01	0.01925	805
2310008H04Rik	A_51_P428226	NM_146068	RIKEN cDNA 2310008H04 gene	1.248	35.45	0.39187	6214	P	1.157	6.98	0.12116	3524
2810423E13Rik	A_52_P623352	AK084485	major facilitator superfamily domain cont	1.248	31.88	0.37009	5623	P	-1.01	49.48	0.88251	11886
Pax7	A_51_P295131	NM_011039	paired box gene 7	1.248	69.29	0.64119	14711	M	1.029	33.49	0.50787	8659
Hba-a1	A_52_P208681	M10466	hemoglobin alpha, adult chain 2	1.247	75.14	0.82282	25603	P	1.235	8.32	0.25768	5776
Plrg1	A_51_P436796	NM_016784	pleiotropic regulator 1, PRL1 homolog (Ar	1.247	53.87	0.50433	9847	P	-1.223	0.75	0.01384	584
Rpl4	A_52_P376829	NM_024212	ribosomal protein L4	1.247	57.76	0.6416	11936	M	1.061	19.02	0.2199	5205
Wwp2	A_51_P386358	NM_025830	WW domain containing E3 ubiquitin prote	1.247	49.93	0.47485	8793	P	1.098	9.71	0.10429	3191
Herc3	A_51_P249313	NM_028705	hect domain and RLD 3	1.246	35.45	0.43852	7316	P	1.178	6.98	0.11364	3348
Lmo6	A_52_P1048	AK079845	LIM domain only 6	1.246	82.34	0.82596	22309	M	-1.286	0.56	0.01529	651
Timp1	A_51_P512384	NM_001044384	tissue inhibitor of metalloproteinase 1	1.246	53.87	0.5101	9943	P	-1.056	33.49	0.21868	5183
Unc5a	A_52_P541095	NM_153131	unc-5 homolog A (C. elegans)	1.246	72.2	0.76922	22164	P	-1.035	44.4	0.46108	8119
2410012H22Rik	A_51_P236829	ENSMUST00000072916	RIKEN cDNA 2410012H22 gene	1.245	53.87	0.5306	10758	P	1.132	5.75	0.04205	1584
Akt2	A_51_P408044	NM_007434	thymoma viral proto-oncogene 2	1.245	57.76	0.56738	11957	P	1.066	19.02	0.28968	6206
D330001F17Rik	A_51_P249385	AK090131	RIKEN cDNA D330001F17 gene	1.245	61.79	0.62723	14803	P	1.059	19.02	0.26009	5809
D5Ertd593e	A_52_P645855	NM_175096	DNA segment, Chr 5, ERATO Doi 593, expr	1.245	69.29	0.70545	18694	P	1.061	19.02	0.2226	5249
Ybx2	A_51_P455488	NM_016875	Y box protein 2	1.245	61.79	0.60052	13481	P	-1.123	19.02	0.24053	5498
Zdhhc17	A_51_P348672	NM_172554	zinc finger, DHHC domain containing 17	1.245	57.76	0.55103	11469	P	1.094	13.58	0.18728	4687
Zfp291	A_51_P393161	AK173175	zinc finger protein 291	1.245	45.92	0.46016	8219	P	1.078	19.02	0.29192	6230
Cutl1	A_52_P442676	NM_198602	cut-like 1 (Drosophila)	1.244	69.29	0.71449	19198	P	1.103	11.33	0.19192	4764
Igbp1	A_51_P222092	NM_008784	immunoglobulin (CD79A) binding protein	1.244	69.29	0.72827	20129	P	1.137	9.71	0.18147	4600
Raf1	A_52_P412600	NM_029780	v-raf-leukemia viral oncogene 1	1.244	49.93	0.48895	9204	P	1.149	4.63	0.0421	1588
AA986860	A_51_P340829	NM_177604	expressed sequence AA986860	1.243	75.14	0.80691	24510	P	-1.146	2.53	0.03502	1343
AU040320	A_51_P351351	AK053479	expressed sequence AU040320	1.243	38.68	0.4	6522	P	-1.067	28.13	0.18589	4666
Fasn	A_51_P321126	NM_007988	fatty acid synthase	1.243	69.29	0.70381	18608	P	-1.031	46.3	0.59891	9440
Galnt11	A_52_P129706	AK079811	UDP-N-acetyl-alpha-D-galactosamine:poly	1.243	69.29	0.72951	20197	P	1.02	38.4	0.72016	10498
Trap1	A_51_P402435	NM_026508	TNF receptor-associated protein 1	1.243	57.76	0.58539	12799	P	1	49.48	0.99613	13017
Centd3	A_52_P195018	NM_139206	centaurin, delta 3	1.242	49.93	0.49059	9244	P	-1.041	43.75	0.42186	7748
Gsk3b	A_52_P641629	NM_019827	glycogen synthase kinase 3 beta	1.242	45.92	0.44589	7828	P	1.148	5.75	0.06335	2242
Hmgb3	A_51_P138548	NM_008253	high mobility group box 3	1.242	49.93	0.47599	8826	P	1.421	0.24	0.00584	63
Kif2a	A_52_P150327	NM_008442	kinesin family member 2A	1.242	38.68	0.39615	6407	M	-1.024	47.43	0.61032	9530
Plekha1	A_52_P215469	NM_133942	pleckstrin homology domain containing, f	1.242	38.68	0.40388	6581	P	1.215	2.53	0.02518	1037
Rnf4	A_52_P349540	AK037465	ring finger protein 4	1.242	53.87	0.51294	10063	P	1.198	5.75	0.12614	3635
1300018J18Rik	A_51_P340947	NM_027905	RIKEN cDNA 1300018J18 gene	1.241	69.29	0.73204	20349	P	1.091	9.71	0.09879	3084
Brd8	A_52_P676492	NM_030147	bromodomain containing 8	1.241	75.14	0.79356	23718	P	1.056	28.13	0.54935	9016
Chchd5	A_52_P324694	NM_025395	coiled-coil-helix-coiled-coil-helix domain c	1.241	25.79	0.35096	5133	P	-1.016	49.48	0.79225	11118
Fasl	A_52_P77106	NM_010177	Fas ligand (TNF superfamily, member 6)	1.241		0.58218	9801	A	-1.13	4.63	0.05863	2095
Mrpl47	A_52_P595537	BC029173	mitochondrial ribosomal protein L47	1.241	65.79	0.68647	17762	P	1.008	42.43	0.88251	11890
Nipbl	A_51_P299681	AK016861	Nipped-B homolog (Drosophila)	1.241	69.29	0.69938	18348	P	1.149	9.71	0.22821	5333
Snap23	A_52_P155778	NM_009222	synaptosomal-associated protein 23	1.241	38.68	0.40316	6566	P	1.17	8.32	0.14813	4010
Ttc8	A_51_P507899	NM_029553	tetratricopeptide repeat domain 8	1.241	35.45	0.39278	6237	P	1.282	1.58	0.01786	763
Vps41	A_51_P412338	NM_172120	vacuolar protein sorting 41 (yeast)	1.241	38.68	0.41235	6835	P	1.05	22.1	0.27425	6018
2410016O06Rik	A_51_P350395	AK078791	RIKEN cDNA 2410016O06 gene	1.24	69.29	0.71259	15658	M	1.085	13.58	0.16984	4380
Cdc40	A_52_P657240	AK004569	cell division cycle 40 homolog (yeast)	1.24	45.92	0.4683	8474	P	1.042	33.49	0.70554	10366
D5Wsu178e	A_52_P630563	NM_027652	DNA segment, Chr 5, Wayne State Univer	1.24	61.79	0.60754	13791	P	-1.069	25.31	0.15676	4161

Elac2	A_52_P649236	BC023134	elaC homolog 2 (E. coli)	1.24	49.93	0.49861	9623	P	1.038	30.75	0.53147	8854
Fkbp7	A_51_P415607	NM_010222	FK506 binding protein 7	1.24	45.92	0.44386	7770	P	-1.042	46.85	0.71595	10450
Kng1	A_52_P151983	NM_023125	kininogen 1	1.24		0.7596	11964	A	1.094	19.02	0.46769	8185
Myo1b	A_52_P355934	NM_010863	myosin IB	1.24	42.28	0.43241	7432	P	1.177	4.63	0.053	1953
Pard3	A_52_P633612	NM_001013580	par-3 (partitioning defective 3) homolog (	1.24	65.79	0.665	16811	P	1.029	36.07	0.61452	9569
Pipox	A_51_P337195	NM_008952	pipecolic acid oxidase	1.24	75.14	0.81625	25168	P	1.04	28.13	0.42866	7811
Plg	A_52_P662013	NM_008877	plasminogen	1.24		0.66137	13199	A	1.132	5.75	0.04735	1769
Tcf1	A_51_P302626	NM_009327	transcription factor 1	1.24	65.79	0.66929	16995	P	1.005	42.43	0.94108	12489
Tsn	A_52_P415351	NM_011650	translin	1.24	28.61	0.35837	5380	P	1.193	3.82	0.04712	1764
5730403B10Rik	A_52_P683178	NM_025670	RIKEN cDNA 5730403B10 gene	1.239	53.87	0.52412	10484	P	1.06	22.1	0.36525	7097
3110001D03Rik	A_51_P212183	NM_025849	RIKEN cDNA 3110001D03 gene	1.238	28.61	0.36593	5515	P	-1.012	49.48	0.86373	11716
Cyfip1	A_51_P403005	NM_011370	cytoplasmic FMR1 interacting protein 1	1.238	31.88	0.3765	5802	P	1.118	9.71	0.15833	4190
Nlgn1	A_52_P497105	AK083116	neuroligin 1	1.238	69.29	0.60907	13178	M	1.1	9.71	0.10562	3205
Rab13	A_51_P387473	NM_026677	RAB13, member RAS oncogene family	1.238	61.79	0.59364	13136	P	1.067	19.02	0.29693	6290
Trp53inp1	A_52_P503387	NM_021897	transformation related protein 53 inducib	1.238	57.76	0.57665	12331	P	-1.146	5.75	0.08637	2812
2010003O02Rik	A_51_P119588	AK008077	RIKEN cDNA 2010003O02 gene	1.237	35.45	0.44053	7048	P	-1.023	47.43	0.60143	9466
Dusp3	A_51_P461748	NM_028207	dual specificity phosphatase 3 (vaccinia vi	1.237	65.79	0.68577	17717	P	-1.112	8.32	0.07865	2617
Lxn	A_51_P487813	NM_016753	latexin	1.237	65.79	0.6531	16265	P	1.102	9.71	0.08446	2766
Tbca	A_51_P489966	NM_009321	tubulin cofactor a	1.237	38.68	0.54007	8947	M	1.076	25.31	0.54469	8981
Usp33	A_52_P234004	AK047530	ubiquitin specific peptidase 33	1.237	61.79	0.61718	14263	P	-1.035	43.75	0.4127	7650
Hsd17b7	A_52_P566605	NM_010476	hydroxysteroid (17-beta) dehydrogenase	1.236	35.45	0.38285	5971	P	-1.105	13.58	0.14548	3954
Rpl37	A_52_P150675	NM_026069	ribosomal protein L37	1.236	42.28	0.54946	9217	M	1.054	30.75	0.59387	9374
Arhgap5	A_52_P617762	AK039081	Rho GTPase activating protein 5	1.235	53.87	0.53228	10795	P	1.049	33.49	0.70373	10346
Gtpbp1	A_51_P256510	NM_013818	GTP binding protein 1	1.235	49.93	0.47599	8458	M	-1.013	49.48	0.85811	11661
Pdcd5	A_51_P178435	NM_019746	programmed cell death 5	1.235	53.87	0.53849	11010	P	-1.039	45.68	0.62761	9693
Smoc1	A_51_P443403	NM_022316	SPARC related modular calcium binding 1	1.235	38.68	0.39887	6483	P	-1.062	28.13	0.17475	4469
Usp30	A_51_P161413	AK162153	ubiquitin specific peptidase 30	1.235	72.2	0.74324	20749	P	1.091	9.71	0.09238	2953
Vdac3	A_51_P137971	NM_011696	voltage-dependent anion channel 3	1.235	49.93	0.49955	9642	P	1.043	30.75	0.59497	9392
Axl	A_52_P311787	NM_009465	AXL receptor tyrosine kinase	1.234	57.76	0.54815	11346	P	1.04	33.49	0.64644	9856
Maoa	A_51_P125355	NM_173740	monoamine oxidase A	1.234	61.79	0.60476	13672	P	-1.022	49	0.73205	10590
Ndufa9	A_51_P280492	NM_025358	NADH dehydrogenase (ubiquinone) 1 alp	1.234	65.79	0.69989	13937	M	1.17	8.32	0.20155	4930
Pfn2	A_52_P359061	NM_019410	profilin 2	1.234	42.28	0.42844	7305	P	1.126	11.33	0.24091	5505
Rpl7a	A_52_P548790	NM_013721	ribosomal protein L7a	1.234	35.45	0.53469	8835	M	1.152	8.32	0.1687	4363
Atp6v1h	A_52_P112888	NM_133826	ATPase, H+ transporting, lysosomal V1 su	1.233	57.76	0.55296	11532	P	1.087	16.2	0.28533	6149
Lactb2	A_51_P379373	NM_145381	lactamase, beta 2	1.233	61.79	0.61718	14255	P	-1.139	4.63	0.07277	2468
Sec61b	A_52_P93886	NM_024171	Sec61 beta subunit	1.233	53.87	0.61824	11220	M	1.057	28.13	0.54173	8960
Zbed3	A_52_P27371	AK138671		1.233	82.34	0.87103	27353	M	-1.159	1.62	0.02609	1077
AI314180	A_52_P652459	AK038775	expressed sequence AI314180	1.232	45.92	0.45706	8106	P	-1.089	19.02	0.1534	4100
Ctsh	A_52_P51078	NM_007801	cathepsin H	1.232	57.76	0.58439	12741	P	1.012	42.43	0.80555	11225
Gja7	A_52_P285041	NM_008122	gap junction membrane channel protein a	1.232	61.79	0.60436	13650	P	-1.005	49.48	0.95439	12621
Gnb4	A_52_P640474	NM_013531	guanine nucleotide binding protein, beta	1.232	57.76	0.56738	11950	P	1.197	5.75	0.11684	3416
Gpr124	A_51_P282523	NM_054044	G protein-coupled receptor 124	1.232	38.68	0.42003	7021	P	1.19	3.82	0.05071	1874
Paics	A_52_P449768	NM_025939	phosphoribosylaminoimidazole carboxyla	1.232	57.76	0.57969	12479	P	1.053	22.1	0.3306	6679
Phf8	A_51_P117369	NM_177201	PHD finger protein 8	1.232		0.72548	12598	A	1.09	9.71	0.09269	2957
Wdfy3	A_52_P409778	NM_172882	WD repeat and FYVE domain containing 3	1.232	65.79	0.6531	16262	M	1.064	22.1	0.35695	6979
Zdhhc6	A_51_P416439	NM_001033573	zinc finger, DHHC domain containing 6	1.232	57.76	0.5748	12232	P	1.049	19.02	0.25261	5689
Plcd1	A_51_P239766	NM_019676	phospholipase C, delta 1	1.231	57.76	0.58305	12699	P	1.142	3.82	0.03066	1212
Dctn2	A_51_P435333	NM_027151	dynactin 2	1.23	35.45	0.39347	6263	P	-1.108	9.71	0.09181	2940
Gck	A_51_P106294	NM_010292	glucokinase	1.23	53.87	0.52912	10702	P	1.069	13.58	0.1475	3992
Got1	A_51_P370700	NM_010324	glutamate oxaloacetate transaminase 1, s	1.23	49.93	0.49479	9420	P	1.106	13.58	0.21473	5109
Smarce1	A_52_P37517	AK017922	SWI/SNF related, matrix associated, actin	1.23	72.2	0.7617	21721	P	1.137	5.75	0.05066	1871
2410003P15Rik	A_52_P660765	AK028574	RIKEN cDNA 2410003P15 gene	1.229	69.29	0.68819	16989	M	1.086	13.58	0.14842	4019
5730472N09Rik	A_51_P146432	NM_175392	RIKEN cDNA 5730472N09 gene	1.229	38.68	0.41157	6814	P	-1.241	0.75	0.0148	632

Map2k7	A_52_P70381	AK028772	mitogen activated protein kinase kinase 7	1.229	77.44	0.83461	26641	P	1.117	11.33	0.17748	4521
Rfxdc1	A_51_P151848	NM_177306	regulatory factor X domain containing 1	1.229	49.93	0.48647	9128	P	1.101	16.2	0.33619	6744
Adpgk	A_51_P266143	NM_028121	ADP-dependent glucokinase	1.228	45.92	0.45073	7926	P	1.262	2.04	0.02475	1025
E030018N11Rik	A_52_P110541	NM_001033380	RIKEN cDNA E030018N11 gene	1.228	42.28	0.42396	7161	P	-1.079	22.1	0.15941	4207
Rnf12	A_52_P104761	NM_011276	ring finger protein 12	1.228	57.76	0.54327	11122	P	1.047	25.31	0.36912	7154
Rpl23a	A_51_P127516	NM_207523	ribosomal protein L23a	1.228	38.68	0.5481	9168	M	1.031	33.49	0.55635	9077
Tbx3	A_52_P183368	NM_011535	T-box 3	1.228	69.29	0.69847	18302	P	-1.069	30.75	0.22666	5302
Ube2n	A_52_P387803	NM_080560	ubiquitin-conjugating enzyme E2N	1.228	49.93	0.4726	8693	P	1.197	2.53	0.02191	926
Zfp143	A_52_P496173	NM_009281	zinc finger protein 143	1.228	72.2	0.7414	20666	P	1.042	28.13	0.41816	7716
D230040A04Rik	A_52_P545914	AK039302	RIKEN cDNA D230040A04 gene	1.227	53.87	0.51941	10322	P	1.061	25.31	0.47083	8206
Dym	A_52_P896	AK080149	dymeclin	1.227		0.894	12459	A	1.019	38.4	0.71017	10401
Lgals1	A_51_P465281	NM_008495	lectin, galactose binding, soluble 1	1.227	69.29	0.73013	20278	P	1.025	36.07	0.6241	9658
4631424J17Rik	A_52_P1124217	AV338080		1.226	61.79	0.59903	13387	P	1.187	5.75	0.09023	2900
Btg2	A_52_P35217	NM_007570	B-cell translocation gene 2, anti-proliferat	1.226	72.2	0.7477	20968	P	-1.065	36.07	0.3392	6767
Epb4.1l2	A_52_P335201	NM_013511	erythrocyte protein band 4.1-like 2	1.226	49.93	0.47364	8748	P	1.123	11.33	0.22103	5219
Rpl13	A_52_P668076	NM_016738	ribosomal protein L13	1.226	69.29	0.75846	16404	M	-1.072	33.49	0.32064	6573
Rps16	A_51_P416995	NM_013647	ribosomal protein S16	1.226	45.92	0.58248	10138	M	1.046	25.31	0.3853	7342
Ube2v2	A_52_P118390	NM_023585	ubiquitin-conjugating enzyme E2 variant	1.226	35.45	0.39529	6383	P	1.013	42.43	0.80001	11176
2610029G23Rik	A_52_P272936	NM_026312	RIKEN cDNA 2610029G23 gene	1.225	72.2	0.76648	22009	P	1.017	42.43	0.82868	11441
Chchd7	A_52_P788229	AK145105	coiled-coil-helix-coiled-coil-helix domain	1.225	35.45	0.40584	6631	P	-1.05	42.43	0.37996	7275
Csad	A_51_P268529	ENSMUST00000023805	cysteine sulfinic acid decarboxylase	1.225	53.87	0.50712	9889	P	-1.003	49.48	0.95533	12625
Dscr1	A_52_P617327	NM_019466	Down syndrome critical region homolog 1	1.225	61.79	0.59581	13278	P	1.001	42.43	0.98495	12932
Myst2	A_51_P202699	AK078483	MYST histone acetyltransferase 2	1.225	83.36	0.90191	29187	M	-1.104	11.33	0.10402	3186
Plekhb2	A_51_P356705	NM_145516	pleckstrin homology domain containing, f	1.225	49.93	0.47555	8811	P	-1.086	25.31	0.24091	5504
Rb1cc1	A_51_P332100	NM_009826	RB1-inducible coiled-coil 1	1.225	57.76	0.568	11982	P	1.001	42.43	0.97618	12808
Rpl10a	A_52_P407086	NM_011287	ribosomal protein L10A	1.225	49.93	0.59565	10587	M	1.15	9.71	0.21179	5068
Trrap	A_52_P304469	AK147241	transformation/transcription domain-ass	1.225	49.93	0.47627	8842	P	-1.344	0.51	0.00627	158
1810035L17Rik	A_51_P367040	NM_026958	RIKEN cDNA 1810035L17 gene	1.224	31.88	0.3921	6222	P	1.046	30.75	0.61752	9607
9130227C08Rik	A_52_P124320	AK122247	RIKEN cDNA 9130227C08Rik gene	1.224	49.93	0.49899	9626	P	-1.082	22.1	0.17785	4531
C530043G21Rik	A_52_P388001	AK034081	RIKEN cDNA C530043G21 gene	1.224	69.29	0.72253	19816	P	1.085	13.58	0.15824	4185
Capzb	A_52_P428784	AK007209	capping protein (actin filament) muscle Z-	1.224		0.70802	15859	A	-1.1	11.33	0.08963	2884
Serpina11	A_52_P423296	NM_199314	serine (or cysteine) peptidase inhibitor, cl	1.224		0.47476	8037	A	1.028	33.49	0.54705	8997
Sestd1	A_52_P408237	AK044401	SEC14 and spectrin domains 1	1.224	31.88	0.3921	6220	P	1.167	6.98	0.12962	3682
Smo	A_51_P258766	NM_176996	smoothened homolog (Drosophila)	1.224	28.61	0.37646	5796	P	1.131	5.75	0.05026	1859
Stard3nl	A_51_P172688	NM_024270	STARD3 N-terminal like	1.224	45.92	0.47093	8599	P	-1.16	1.62	0.02735	1111
Vcl	A_52_P190973	NM_009502	vinculin	1.224	42.28	0.42411	7182	P	1.185	3.82	0.05166	1900
Vti1b	A_51_P438692	NM_016800	vesicle transport through interaction with	1.224	31.88	0.46319	7659	P	1.042	30.75	0.51573	8725
Arhgef2	A_51_P502701	NM_008487	rho/rac guanine nucleotide exchange fact	1.223	53.87	0.52419	10500	P	1.151	6.98	0.10199	3155
Nap1l1	A_51_P506787	NM_015781	nucleosome assembly protein 1-like 1	1.223	45.92	0.58125	10096	M	1.295	3.01	0.07233	2447
Rps27a	A_51_P128945	NM_001033865	ribosomal protein S27a	1.223	72.2	0.76568	16687	M	-1.052	38.4	0.27522	6029
Serpinb9b	A_51_P406780	NM_011452	serine (or cysteine) peptidase inhibitor, cl	1.223	75.14	0.80444	24393	M	-1.096	16.2	0.13742	3795
Sgk	A_51_P118237	NM_011361	serum/glucocorticoid regulated kinase	1.223	38.68	0.55089	9253	M	1.03	38.4	0.80093	11187
Smarcad1	A_52_P45551	NM_007958	SWI/SNF-related, matrix-associated actin-	1.223	53.87	0.53807	10993	P	1.132	9.71	0.14826	4011
1700081L11Rik	A_51_P281164	XM_001000446	RIKEN cDNA 1700081L11 gene	1.222		0.89757	12559	A	-1.084	19.02	0.12598	3627
1810020G14Rik	A_52_P70027	BC100533	RIKEN cDNA 1810020G14 gene	1.222	53.87	0.51548	10145	P	-1.087	38.4	0.50017	8581
Frg1	A_51_P267544	NM_013522	FSHD region gene 1	1.222	38.68	0.42405	7167	P	1.046	30.75	0.54284	8968
Nhp2l1	A_52_P2081	U95114	NHP2 non-histone chromosome protein 2	1.222	42.28	0.43972	7630	P	1.075	25.31	0.49069	8447
Zfp608	A_52_P598224	NM_175751	zinc finger protein 608	1.222	61.79	0.62968	15043	P	1.165	11.33	0.34462	6818
Mtf2	A_51_P264995	S78454	metal response element binding transcrip	1.221	49.93	0.5012	9685	P	1.07	16.2	0.17078	4396
Nufip1	A_52_P643784	NM_013745	nuclear fragile X mental retardation prote	1.221	57.76	0.54188	11082	P	1.011	42.43	0.91857	12252
8430427H17Rik	A_51_P475853	AK029844	RIKEN cDNA 8430427H17 gene	1.22		0.89849	12590	A	-1.146	2.53	0.03104	1228
Armc6	A_52_P287328	NM_133972	armadillo repeat containing 6	1.22	38.68	0.58532	10588	M	1.106	8.32	0.05919	2117
Bapx1	A_52_P90603	U87957	bagpipe homeobox gene 1 homolog (Dros	1.22		0.78351	12635	A	-1.082	19.02	0.14341	3911

Dhrs1	A_51_P293901	NM_026819	dehydrogenase/reductase (SDR family) m	1.22	57.76	0.56182	11792	P	1.004	42.43	0.93901	12469
Nrf1	A_52_P376269	NM_010938	nuclear respiratory factor 1	1.22	61.79	0.60503	13687	P	1.015	40.63	0.76406	10886
Pdk1	A_52_P277654	AK165090	pyruvate dehydrogenase kinase, isoenzyn	1.22	38.68	0.41119	6787	P	1.107	13.58	0.30561	6388
Psmb5	A_51_P269728	NM_011186	proteasome (prosome, macropain) subun	1.22	61.79	0.62738	14826	P	-1.072	33.49	0.27258	5991
Top1	A_52_P218132	AK083930	topoisomerase (DNA) I	1.22	61.79	0.58491	12771	P	1.169	4.63	0.0481	1799
Bhlhb3	A_51_P451176	NM_024469	basic helix-loop-helix domain containing,	1.219	57.76	0.55993	11750	P	-1.017	49.48	0.82519	11418
Hoxa4	A_52_P443588	NM_008265	homeo box A4	1.219	61.79	0.63332	15382	P	1.005	42.43	0.93769	12451
Htatip2	A_51_P228883	NM_016865	HIV-1 tat interactive protein 2, homolog (	1.219	75.14	0.80564	24451	P	-1.149	3.01	0.03953	1503
Mmp11	A_51_P293087	NM_008606	matrix metallopeptidase 11	1.219	61.79	0.59991	13433	P	1.034	30.75	0.43044	7830
Mrrf	A_52_P169295	NM_026422	mitochondrial ribosome recycling factor	1.219	57.76	0.57439	12212	P	-1.026	48.39	0.73259	10607
Wee1	A_52_P160078	NM_009516	wee 1 homolog (S. pombe)	1.219	57.76	0.57861	12422	P	-1.043	43.75	0.46898	8192
Atp6v1e1	A_52_P303388	NM_007510	VATPase, H+ transporting, lysosomal V1 s	1.218	61.79	0.62828	14903	P	-1.006	49.48	0.96587	12710
Limk2	A_52_P393755	NM_010718	LIM motif-containing protein kinase 2	1.218	61.79	0.62092	14508	P	-1.04	45.05	0.53169	8861
Pkd2l2	A_52_P210909	NM_016927	polycystic kidney disease 2-like 2	1.218	65.79	0.65262	16233	P	1.113	6.98	0.05512	2013
Rps3a	A_51_P292357	NM_016959	ribosomal protein S3a	1.218	45.92	0.58491	10235	M	-1.295	0.51	0.0122	490
Asna1	A_51_P469531	NM_019652	arsA (bacterial) arsenite transporter, ATP-	1.217	75.14	0.79241	23626	P	-1.041	43.15	0.36929	7158
Cct2	A_52_P369232	NM_007636	chaperonin subunit 2 (beta)	1.217	65.79	0.67305	17219	P	1.16	3.82	0.03601	1391
Mrps5	A_52_P333241	AK047438	mitochondrial ribosomal protein S5	1.217	49.93	0.48762	9172	P	-1.071	22.1	0.14194	3887
Stx8	A_51_P356308	NM_018768	syntaxin 8	1.217	38.68	0.42029	7028	P	1.096	13.58	0.1811	4595
Ubr1	A_52_P636629	AK037771	ubiquitin protein ligase E3 component n-r	1.217	61.79	0.59447	13220	P	1.205	2.04	0.01427	600
Cwf19l1	A_51_P212679	XM_901651	CWF19-like 1, cell cycle control (S. pombe	1.216	65.79	0.64906	16057	P	1.022	38.4	0.71364	10435
Ddx1	A_52_P424563	NM_134040	DEAD (Asp-Glu-Ala-Asp) box polypeptide	1.216	45.92	0.45467	8048	P	1.161	9.71	0.24061	5500
Entpd5	A_51_P480046	NM_001026214	ectonucleoside triphosphate diphosphoh	1.216	75.14	0.79529	23840	P	1.128	8.32	0.09648	3025
Gpd2	A_52_P373938	AK079336	glycerol phosphate dehydrogenase 2, mit	1.216	57.76	0.55666	11636	P	-1.089	13.58	0.10916	3245
Mrps22	A_51_P362903	NM_025485	mitochondrial ribosomal protein S22	1.216	45.92	0.45072	7924	P	-1.045	44.4	0.55068	9034
Pcnx	A_52_P102223	NM_018814	pecanex homolog (Drosophila)	1.216	53.87	0.52825	10667	P	1.149	3.82	0.03137	1236
Rab1	A_52_P631081	NM_008996	RAB1, member RAS oncogene family	1.216	53.87	0.71858	16221	M	1.238	3.82	0.07219	2443
Slc25a4	A_51_P108334	NM_007450	solute carrier family 25 (mitochondrial ca	1.216	45.92	0.51785	8908	M	-1.034	46.85	0.6775	10111
5730427N09Rik	A_51_P284166	NM_021552	RIKEN cDNA 5730427N09 gene	1.215	31.88	0.39458	6352	P	1.017	40.63	0.71611	10459
Alb1	A_51_P160713	NM_009654	albumin 1	1.215	65.79	0.65402	16307	P	-1.303	0.51	0.00645	179
Cnot6l	A_52_P436464	NM_144910	CCR4-NOT transcription complex, subunit	1.215	57.76	0.58305	12689	P	1.046	30.75	0.59474	9385
Fuca2	A_52_P441949	NM_025799	fucosidase, alpha-L- 2, plasma	1.215	75.14	0.78251	22904	P	-1.474	0	0.00584	18
Gpc6	A_52_P224829	NM_001079844	glypican 6	1.215	28.61	0.52719	9280	M	1.075	13.58	0.14533	3949
Laptm4b	A_52_P470316	NM_033521	lysosomal-associated protein transmemb	1.215	42.28	0.43663	7535	P	-1.045	44.4	0.55907	9099
2400001E08Rik	A_51_P338674	NM_025605	RIKEN cDNA 2400001E08 gene	1.214	45.92	0.46206	8286	P	1.084	11.33	0.12278	3558
Anapc5	A_52_P143847	NM_021505	anaphase-promoting complex subunit 5	1.214	53.87	0.55251	10523	P	1.012	42.43	0.9012	12106
Rpl19	A_51_P415162	NM_009078	ribosomal protein L19	1.214	57.76	0.6354	11743	M	1.03	30.75	0.482	8338
Rps25	A_51_P274768	NM_024266	ribosomal protein S25	1.214	77.44	0.84202	20184	M	1.035	38.4	0.76979	10929
Sdha	A_51_P410823	NM_023281	succinate dehydrogenase complex, subun	1.214	31.88	0.39711	6439	P	1.119	8.32	0.0996	3097
Ubc	A_52_P238556	NM_019639	ubiquitin C	1.214	57.76	0.64373	12022	M	1.089	11.33	0.14341	3910
Cfl2	A_51_P302149	NM_007688	cofilin 2, muscle	1.213	45.92	0.45858	8165	P	1.443	2.04	0.07534	2541
Erbb2ip	A_51_P148512	AK079640	Erbb2 interacting protein	1.213	69.29	0.70795	18825	P	1.028	33.49	0.56587	9169
Erp29	A_51_P133670	NM_026129	endoplasmic reticulum protein 29	1.213	57.76	0.57363	12168	P	1.073	16.2	0.20543	4980
Psenen	A_51_P374268	NM_025498	presenilin enhancer 2 homolog (C. elegan	1.213	38.68	0.56935	9721	M	-1.021	49.22	0.75078	10795
Senp2	A_52_P101972	AK009212	SUMO/sentrin specific peptidase 2	1.213	57.76	0.54987	11431	P	-1.233	0.75	0.0148	633
Wwp1	A_52_P165455	NM_177327	WW domain containing E3 ubiquitin prot	1.213	65.79	0.64012	15679	P	-1.079	33.49	0.36413	7074
2010305A19Rik	A_52_P504342	NM_027250	RIKEN cDNA 2010305A19 gene	1.212	57.76	0.55882	11691	P	1.064	19.02	0.24091	5510
E430025E21Rik	A_52_P685310	NM_153548	RIKEN cDNA E430025E21 gene	1.212	53.87	0.53141	10781	P	1.012	42.43	0.86005	11681
Flt1	A_52_P650151	AK084177	FMS-like tyrosine kinase 1	1.212	45.92	0.46016	8221	P	-1.005	49.48	0.92932	12381
Pop5	A_51_P490198	NM_026398	processing of precursor 5, ribonuclease P/	1.212	49.93	0.48917	9208	P	-1.153	3.01	0.04588	1721
Qk	A_51_P434670	NM_021881	quaking	1.212	61.79	0.60765	13814	P	1.1	9.71	0.08012	2657
Rap1a	A_51_P228632	NM_145541	RAS-related protein-1a	1.212	57.76	0.56213	11797	P	1.103	9.71	0.11206	3317
Rps11	A_52_P169005	AK002987	ribosomal protein S11	1.212	38.68	0.56811	9689	M	1.037	33.49	0.59766	9429

St6gal2	A_52_P519924	AK129462	beta galactoside alpha 2,6 sialyltransferas	1.212	65.79	0.59503	11974	M	-1.223	0.51	0.00921	332
Dnajc8	A_51_P264478	NM_172400	DnaJ (Hsp40) homolog, subfamily C, mem	1.211	38.68	0.42094	7087	P	1.063	19.02	0.28592	6166
Fbxo7	A_51_P188135	NM_153195	F-box protein 7	1.211	53.87	0.51255	10037	P	1.088	11.33	0.11754	3429
Hnrpul1	A_52_P243307	NM_144922	heterogeneous nuclear ribonucleoprotei	1.211	72.2	0.77314	22407	P	1.17	2.53	0.01663	714
Mbd1	A_52_P131423	AK007371	methyl-CpG binding domain protein 1	1.211	65.79	0.67305	17224	M	1.07	19.02	0.24589	5582
Snn	A_52_P295067	NM_009223	stannin	1.211	61.79	0.6189	14396	P	1.022	36.07	0.59423	9380
Adra1a	A_52_P424778	NM_013461	adrenergic receptor, alpha 1a	1.21	65.79	0.67859	17385	P	-1.077	25.31	0.16736	4335
Rps24	A_52_P100002	AK135247	ribosomal protein S24	1.21	65.79	0.65952	16563	P	1.001	42.43	0.98055	12850
Rps9	A_51_P436928	NM_029767	ribosomal protein S9	1.21	53.87	0.62794	11517	M	1.091	16.2	0.28604	6171
1700080G18Rik	A_51_P154840	XM_001000195	RIKEN cDNA 1700080G18 gene	1.209	75.14	0.7912	23541	P	1.017	40.63	0.70826	10393
Aatf	A_52_P37658	NM_019816	apoptosis antagonizing transcription fact	1.209	57.76	0.56706	11932	P	1.077	13.58	0.134	3742
Chchd3	A_52_P598478	AK145337	coiled-coil-helix-coiled-coil-helix domain	1.209	75.14	0.77768	22630	P	-1.072	22.1	0.14735	3988
Gtpbp4	A_52_P670725	NM_027000	GTP binding protein 4	1.209	61.79	0.62329	14605	P	1.127	16.2	0.40049	7522
Idh1	A_51_P132978	NM_010497	isocitrate dehydrogenase 1 (NADP+), solu	1.209	75.14	0.78974	23414	P	1.149	11.33	0.27354	6005
Snx15	A_52_P462106	AK165527		1.209	61.79	0.59402	13174	P	1.095	19.02	0.37526	7224
Xpo6	A_52_P1091624	AK088433	exportin 6	1.209		0.71703	14218	A	1.131	8.32	0.12354	3569
Adipor2	A_51_P257151	AK046591	adiponectin receptor 2	1.208	61.79	0.61882	14386	P	1.093	13.58	0.1687	4364
Arl6	A_51_P146576	NM_019665	ADP-ribosylation factor-like 6	1.208	61.79	0.59116	13016	P	1.028	40.63	0.87198	11785
Arsa	A_51_P310649	NM_009713	arylsulfatase A	1.208	72.2	0.76216	21756	P	1.074	19.02	0.27823	6066
Cbx3	A_52_P397231	AK017958	chromobox homolog 3 (Drosophila HP1 g	1.208	83.95	0.78136	20060	M	1.081	19.02	0.34462	6817
Cox7a2	A_52_P37894	NM_009945	cytochrome c oxidase, subunit VIIa 2	1.208	75.14	0.80515	18219	M	1.075	22.1	0.39637	7485
Dgcr6	A_51_P118712	NM_010047	DiGeorge syndrome critical region gene 6	1.208	53.87	0.52791	10654	P	1.116	9.71	0.10184	3145
Efhd2	A_52_P429308	NM_025994	EF hand domain containing 2	1.208	61.79	0.60643	13749	P	-1.04	43.75	0.40275	7546
Exosc2	A_51_P195023	NM_144886	exosome component 2	1.208	53.87	0.5181	10271	P	-1.247	0.51	0.00731	248
Igf2bp3	A_51_P302336	NM_023670	insulin-like growth factor 2 mRNA binding	1.208	69.29	0.6901	17928	P	1.329	0.24	0.00584	102
Pcsk5	A_52_P544043	BC013068	proprotein convertase subtilisin/kexin typ	1.208	65.79	0.63638	15558	P	-1.327	0.51	0.00654	192
Ppargc1b	A_51_P294891	NM_133249	peroxisome proliferative activated recept	1.208	53.87	0.50704	9888	P	1.037	28.13	0.40407	7559
Rps20	A_52_P5210	NM_026147	ribosomal protein S20	1.208	57.76	0.64276	11989	M	1.006	42.43	0.96431	12698
Atp6v1b2	A_51_P190845	NM_007509	ATPase, H+ transporting, lysosomal V1 su	1.207	49.93	0.49788	9551	P	1.201	2.04	0.01651	708
Dnaja1	A_51_P303346	NM_008298	DnaJ (Hsp40) homolog, subfamily A, mem	1.207	65.79	0.65972	16576	P	-1.302	0.66	0.02044	879
Fgfr3	A_51_P322906	NM_008010	fibroblast growth factor receptor 3	1.207	49.93	0.50315	9805	P	1.1	19.02	0.45346	8032
Lims2	A_51_P151862	NM_144862	LIM and senescent cell antigen like domai	1.207	61.79	0.61973	14440	P	-1.01	49.48	0.83625	11498
Myct1	A_52_P13389	NM_026793	myc target 1	1.207	35.45	0.41496	6893	P	-1.037	46.3	0.63636	9775
Txndc9	A_52_P345777	NM_172054	thioredoxin domain containing 9	1.207	53.87	0.52825	10671	P	-1.106	19.02	0.22137	5228
Bap1	A_52_P680311	NM_027088	Brca1 associated protein 1	1.206	81.02	0.89165	28451	M	1.131	6.98	0.05481	1999
Lepr	A_52_P247900	U42467	leptin receptor	1.206	53.87	0.53797	10985	P	-1.172	3.01	0.05718	2067
Ptgs1	A_51_P279100	NM_008969	prostaglandin-endoperoxide synthase 1	1.206	69.29	0.69665	18223	P	1.01	42.43	0.89809	12043
Rdh14	A_52_P169198	AK014097	retinol dehydrogenase 14 (all-trans and 9	1.206	45.92	0.4726	8685	P	1.183	3.46	0.03605	1398
Rit1	A_52_P515370	AK168254	Ras-like without CAAX 1	1.206	45.92	0.4726	8671	P	1.134	5.75	0.05188	1907
Sfxn5	A_51_P234864	NM_178639	sideroflexin 5	1.206	61.79	0.63034	15141	P	-1.045	42.43	0.33697	6750
Ucp2	A_52_P499675	NM_011671	uncoupling protein 2 (mitochondrial, prot	1.206		0.81904	13829	A	1.174	4.63	0.06242	2208
Cdc2l5	A_52_P585621	AK173265	cell division cycle 2-like 5 (cholinesterase-	1.205	69.29	0.71151	19046	P	1.029	33.49	0.53852	8922
Es1	A_52_P342860	NM_007954	esterase 1	1.205	83.36	0.92749	31144	M	1.133	6.98	0.05661	2046
Isl2	A_51_P334335	NM_027397	insulin related protein 2 (islet 2)	1.205	82.34	0.92253	33235	M	-1.077	22.1	0.13908	3829
Mrps14	A_51_P293612	NM_025474	mitochondrial ribosomal protein S14	1.205	53.87	0.5233	10462	P	1.045	33.49	0.64368	9823
Phip	A_51_P375431	XM_358384	pleckstrin homology domain interacting p	1.205	65.79	0.65572	16363	P	1.037	33.49	0.66052	9978
Scpep1	A_51_P118417	NM_029023	serine carboxypeptidase 1	1.205	72.2	0.77015	22198	P	-1.1	13.58	0.12083	3505
Ypel5	A_51_P311694	NM_027166	yippee-like 5 (Drosophila)	1.205	49.93	0.48921	9212	P	1.127	8.32	0.11241	3321
2900010J23Rik	A_51_P444401	AK039840	RIKEN cDNA 2900010J23 gene	1.204	72.2	0.72951	20196	P	1.204	3.01	0.02825	1148
Adcy7	A_51_P441622	NM_007406	adenylate cyclase 7	1.204	69.29	0.71674	19330	P	-1.033	45.68	0.53576	8893
Cdk5rap3	A_52_P151949	NM_030248	CDK5 regulatory subunit associated prote	1.204	65.79	0.65596	16389	P	1.056	25.31	0.47406	8236
Echdc3	A_51_P475378	NM_024208	enoyl Coenzyme A hydratase domain con	1.204	69.29	0.696	18182	P	1.035	30.75	0.42883	7812
Eng	A_51_P268563	NM_007932	endoglin	1.204	65.79	0.6375	15595	P	1.085	11.33	0.13126	3692

Hibch	A_51_P178735	NM_146108	3-hydroxyisobutyryl-Coenzyme A hydrola	1.204	35.45	0.41934	7007	P	1.023	38.4	0.71821	10472
Rragc	A_52_P202725	NM_017475	Ras-related GTP binding C	1.204	49.93	0.49841	9605	P	1.186	2.53	0.01896	798
Wnt8a	A_51_P240811	NM_009290	wingless-related MMTV integration site 8	1.204		0.90781	12842	A	1.068	13.58	0.14235	3892
Atp6v1f	A_51_P310539	NM_025381	ATPase, H+ transporting, lysosomal V1 su	1.203	65.79	0.56811	10967	P	-1.091	30.75	0.33009	6662
Pafah1b1	A_52_P181038	AK147309	platelet-activating factor acetylhydrolase,	1.203	57.76	0.56736	11943	P	1.027	38.4	0.72735	10542
Rpl24	A_52_P405893	NM_024218	ribosomal protein L24	1.203	65.79	0.71034	14380	M	-1.193	3.01	0.06822	2369
Col15a1	A_51_P159792	NM_009928	procollagen, type XV	1.202	72.2	0.72815	20127	P	1.035	30.75	0.49613	8527
Cops5	A_52_P240090	AK133073	COP9 (constitutive photomorphogenic) h	1.202	65.79	0.65861	16527	P	1.008	42.43	0.88007	11861
Mvp	A_52_P46085	NM_080638	major vault protein	1.202	61.79	0.61067	13985	P	1.257	2.04	0.02358	988
Ndrg1	A_51_P405606	NM_010884	N-myc downstream regulated gene 1	1.202	61.79	0.60523	13699	P	1.202	2.04	0.01366	576
Ndufb2	A_51_P361184	NM_026612	NADH dehydrogenase (ubiquinone) 1 bet	1.202	49.93	0.61474	11108	M	-1.078	22.1	0.15998	4215
Prrg2	A_52_P329917	NM_022999	proline-rich Gla (G-carboxyglutamic acid)	1.202	65.79	0.63405	15406	P	-1.035	45.05	0.50219	8604
Rora	A_52_P652950	AK087905	RAR-related orphan receptor alpha	1.202	65.79	0.65148	16134	P	-1.046	43.15	0.38617	7349
Snx2	A_51_P347177	NM_026386	sorting nexin 2	1.202	61.79	0.60922	13903	P	-1.029	46.85	0.58692	9313
Ttc1	A_52_P451041	NM_133795	tetratricopeptide repeat domain 1	1.202	72.2	0.75517	21408	P	1.101	9.71	0.08544	2781
1600012F09Rik	A_51_P309618	NM_025904	RIKEN cDNA 1600012F09 gene	1.201	53.87	0.5246	10524	P	-1.099	11.33	0.09869	3077
Cast	A_52_P638903	AK037098	calpastatin	1.201	45.92	0.46466	8373	P	1.056	28.13	0.52089	8760
Fmo1	A_52_P408245	AK034946	flavin containing monooxygenase 1	1.201	61.79	0.60052	13475	P	1.1	9.71	0.08551	2785
Gata6	A_52_P176245	NM_010258	GATA binding protein 6	1.201	75.14	0.78158	22839	P	-1.166	1.62	0.0271	1102
Gdf6	A_52_P28960	NM_013526	growth differentiation factor 6	1.201		0.64627	11736	A	1.128	11.33	0.21849	5175
Mga	A_52_P474871	NM_013720	MAX gene associated	1.201	61.79	0.58294	12665	P	1.13	6.98	0.0795	2647
Ncam1	A_52_P684037	NM_010875	neural cell adhesion molecule 1	1.201	49.93	0.49385	9400	P	1.058	22.1	0.31071	6461
Prdx3	A_51_P100828	NM_007452	peroxiredoxin 3	1.201	57.76	0.57322	12150	P	1.037	30.75	0.46758	8183
Abcd4	A_51_P138760	NM_008992	ATP-binding cassette, sub-family D (ALD),	1.2	69.29	0.6835	17573	P	1.017	38.4	0.68976	10238
Ap2b1	A_51_P213641	NM_001035854	adaptor-related protein complex 2, beta 1	1.2	65.79	0.65228	16194	P	1.099	8.32	0.07034	2406
Atp6v1g1	A_51_P140171	NM_024173	ATPase, H+ transporting, lysosomal V1 su	1.2	75.14	0.81786	18815	M	1.069	28.13	0.55992	9109
Atrnl1	A_52_P584293	NM_181415	attractin like 1	1.2	69.29	0.68802	17825	P	1.149	3.46	0.0243	1003
D130062J10Rik	A_52_P723436	AK051660	RIKEN cDNA D130062J10 gene	1.2	65.79	0.65687	16422	M	1	42.43	0.99655	13021
H2afz	A_52_P468268	NM_016750	H2A histone family, member Z	1.2	61.79	0.60369	13614	P	1.075	28.13	0.63491	9761
Hmgcs2	A_51_P116039	NM_008256	3-hydroxy-3-methylglutaryl-Coenzyme A s	1.2		0.773	16670	A	-1.196	5.75	0.1534	4099
Hoxa1	A_51_P351975	NM_010449	homeo box A1	1.2	81.02	0.83461	24849	M	1.065	22.1	0.31613	6541
Neu1	A_52_P58524	NM_010893	neuraminidase 1	1.2	53.87	0.52764	10622	P	1.099	22.1	0.49376	8483
Ppp1r16b	A_52_P449974	NM_153089	protein phosphatase 1, regulatory (inhibit	1.2	49.93	0.53102	9849	M	1.051	25.31	0.40049	7521
Rpl35	A_51_P132715	NM_025592	ribosomal protein L35	1.2	49.93	0.61247	11068	M	-1.064	43.75	0.59225	9357
Zfp341	A_51_P330701	NM_199304	zinc finger protein 341	1.2	61.79	0.60765	13809	P	-1.006	49.48	0.9357	12444
5830417I10Rik	A_52_P443443	AY040842	RIKEN cDNA 5830417I10 gene	1.199	65.79	0.65195	16167	P	1.078	11.33	0.12116	3522
6530403A03Rik	A_52_P169028	NM_026382	RIKEN cDNA 6530403A03 gene	1.199	72.2	0.74552	20871	P	1.127	19.02	0.47613	8273
Kctd2	A_51_P272448	NM_183285	potassium channel tetramerisation doma	1.199	45.92	0.46682	8434	P	1.161	3.82	0.03558	1381
Psmd10	A_51_P225123	NM_016883	proteosome (prosome, macropain) 26S su	1.199	72.2	0.76438	21886	P	-1.022	48.7	0.72187	10510
Syne1	A_51_P305777	NM_153399	synaptic nuclear envelope 1	1.199	65.79	0.6532	16281	P	-1.077	25.31	0.16343	4276
Atp5o	A_51_P365521	NM_138597	ATP synthase, H+ transporting, mitochon	1.198	49.93	0.62794	11511	M	1.09	11.33	0.11006	3268
Prelp	A_52_P486260	NM_054077	proline arginine-rich end leucine-rich rep	1.198	72.2	0.76368	21867	P	1.038	28.13	0.39045	7397
Zfp180	A_52_P224818	NM_001045486	zinc finger protein 180	1.198		0.91029	12919	A	1.042	30.75	0.47882	8296
Dot1l	A_52_P207728	NM_199322	DOT1-like, histone H3 methyltransferase (	1.197	69.29	0.68762	17805	P	-1.133	4.63	0.05927	2125
E230022H04Rik	A_51_P168172	AK030009	AMME chromosomal region gene 1-like	1.197	82.34	0.84679	25695	P	1.197	4.63	0.08375	2748
Eef1a1	A_51_P118765	NM_010106	eukaryotic translation elongation factor 1	1.197	75.14	0.82024	18929	M	1.166	4.63	0.0453	1700
Efha1	A_51_P441782	NM_028643	EF hand domain family A1	1.197	45.92	0.4726	8689	P	1.253	3.01	0.04276	1609
Ilk	A_51_P138651	NM_010562	integrin linked kinase	1.197	53.87	0.51739	10210	P	1.092	11.33	0.12271	3555
Nme3	A_51_P395111	NM_019730	expressed in non-metastatic cells 3	1.197	45.92	0.47599	8821	P	1.059	19.02	0.21716	5155
Rab32	A_51_P293688	NM_026405	RAB32, member RAS oncogene family	1.197	77.44	0.83348	26369	P	1.092	19.02	0.40749	7591
Tbx19	A_52_P95930	NM_032005	T-box 19	1.197	45.92	0.48392	9049	M	1.048	28.13	0.51414	8714
Adamts10	A_52_P671784	NM_172619	a disintegrin-like and metallopeptidase (r	1.196	57.76	0.57504	11740	M	1.092	9.71	0.08026	2667
Lbp	A_51_P454008	NM_008489	lipopolysaccharide binding protein	1.196	65.79	0.65853	16521	P	1.047	25.31	0.38785	7372

Mki67ip	A_51_P250647	NM_026472	Mki67 (FHA domain) interacting nucleola	1.196	57.76	0.54744	11319	P	1.061	28.13	0.55557	9072
Psmc4	A_52_P10254	NM_011874	proteasome (prosome, macropain) 26S su	1.196	42.28	0.45748	8122	P	-1.113	19.02	0.21374	5093
Rab11fip4	A_52_P40832	AK147344	RAB11 family interacting protein 4 (class I	1.196	61.79	0.60906	13897	P	1.227	3.46	0.05543	2017
Rps15	A_51_P195997	NM_009091	ribosomal protein S15	1.196	53.87	0.63042	11603	M	1.033	38.4	0.79018	11094
Ahr	A_51_P449133	NM_013464	aryl-hydrocarbon receptor	1.195	57.76	0.54463	11184	P	-1.068	28.13	0.19731	4860
Commd10	A_51_P362209	NM_178377	COMM domain containing 10	1.195	57.76	0.55303	11535	P	-1.035	46.3	0.6291	9704
Lrpap1	A_52_P583973	NM_013587	low density lipoprotein receptor-related p	1.195	61.79	0.59402	13172	P	1.079	19.02	0.3314	6693
Osbpl2	A_51_P173212	NM_144500	oxysterol binding protein-like 2	1.195	53.87	0.52692	10602	P	1.154	5.75	0.05734	2073
Padi2	A_51_P280117	NM_008812	peptidyl arginine deiminase, type II	1.195	81.02	0.88793	30136	P	1.172	9.71	0.27088	5968
Pcdh18	A_52_P555789	NM_130448	protocadherin 18	1.195	65.79	0.74437	16833	M	-1.016	49.48	0.7315	10587
1810047C23Rik	A_52_P282302	AK046862	RIKEN cDNA 1810047C23 gene	1.194	61.79	0.62217	14543	P	1.02	38.4	0.70719	10385
Arhgap10	A_52_P51564	NM_030113	Rho GTPase activating protein 10	1.194	81.02	0.70294	13063	M	-1.117	25.31	0.35264	6911
Chrac1	A_52_P106537	NM_053068	chromatin accessibility complex 1	1.194	57.76	0.58129	12613	P	-1.006	49.48	0.89318	11994
Edem1	A_52_P86417	NM_138677	ER degradation enhancer, mannosidase a	1.194	61.79	0.59596	13290	P	1.022	36.07	0.60895	9513
Mfsd1	A_51_P500550	NM_025813	major facilitator superfamily domain cont	1.194	49.93	0.51039	9952	P	-1.112	8.32	0.08606	2797
Nme1	A_51_P253904	NM_008704	expressed in non-metastatic cells 1, prote	1.194	61.79	0.6022	13541	P	-1.028	46.85	0.62229	9638
Otub1	A_51_P443393	NM_134150	OTU domain, ubiquitin aldehyde binding	1.194	69.29	0.75317	16210	M	-1.019	49.22	0.73074	10578
Rpl6	A_52_P23041	NM_011290	ribosomal protein L6	1.194	49.93	0.62014	11311	M	-1.105	28.13	0.34767	6846
Rps29	A_52_P158090	NM_009093	ribosomal protein S29	1.194	42.28	0.60024	10726	M	1.01	42.43	0.87739	11835
Chrnb1	A_51_P475342	NM_009601	cholinergic receptor, nicotinic, beta polyp	1.193	69.29	0.68505	17668	P	1.097	16.2	0.2807	6098
Cpeb4	A_52_P595824	NM_026252	cytoplasmic polyadenylation element bin	1.193	75.14	0.80281	24238	P	1.144	8.32	0.13823	3805
Flywch1	A_51_P373589	AK034869	FLYWCH-type zinc finger 1	1.193	61.79	0.58305	12697	P	1.063	19.02	0.2573	5768
Gosr2	A_51_P270939	NM_019650	golgi SNAP receptor complex member 2	1.193	72.2	0.7421	20700	P	1.121	8.32	0.08867	2859
Psmd14	A_52_P652212	NM_021526	proteasome (prosome, macropain) 26S su	1.193	61.79	0.61213	14078	P	-1.097	13.58	0.11815	3440
Sfrs14	A_51_P147714	NM_172755	splicing factor, arginine/serine-rich 14	1.193	53.87	0.52284	10444	P	-1.067	36.07	0.35214	6907
Slc31a1	A_52_P563655	NM_175090	solute carrier family 31, member 1	1.193	49.93	0.6061	12350	P	1.102	16.2	0.35396	6936
Zfp236	A_51_P417321	AK156842	zinc finger protein 236	1.193	69.29	0.72057	19572	P	1.216	6.98	0.1683	4349
2610301G19Rik	A_52_P288495	BC021475	RIKEN cDNA 2610301G19 gene	1.192	69.29	0.6888	17020	M	-1.096	8.32	0.06763	2355
Gdf2	A_51_P245156	NM_019506	growth differentiation factor 2	1.192		0.75984	13751	A	1.056	19.02	0.24886	5629
Metap2	A_51_P345046	NM_019648	methionine aminopeptidase 2	1.192	57.76	0.57399	12192	P	1.109	11.33	0.1894	4713
Pnpo	A_51_P246754	NM_134021	pyridoxine 5'-phosphate oxidase	1.192	75.14	0.78656	23167	P	1.429	0.24	0.00637	173
Gclm	A_51_P320089	NM_008129	glutamate-cysteine ligase , modifier subu	1.191	61.79	0.62297	14582	P	1.205	2.53	0.01889	793
Gnl3	A_51_P377376	NM_178846	guanine nucleotide binding protein-like 3	1.191	65.79	0.63497	15476	P	1.134	11.33	0.21645	5142
Hspe1	A_51_P436368	NM_008303	heat shock protein 1 (chaperonin 10)	1.191	65.79	0.66118	16619	P	1.23	3.01	0.0353	1365
Macf1	A_51_P115315	AK089453	microtubule-actin crosslinking factor 1	1.191	53.87	0.52753	10619	P	1.058	25.31	0.47428	8244
Nol8	A_52_P442722	BC058699	nucleolar protein 8	1.191	75.14	0.77139	22328	P	-1.017	49.48	0.9007	12086
Pthr1	A_51_P327874	NM_011199	parathyroid hormone receptor 1	1.191	77.44	0.8447	27369	P	1.096	9.71	0.09438	2985
Rian	A_52_P102630	AB063319	RNA imprinted and accumulated in nucle	1.191	69.29	0.6965	18198	P	1.731	0	0.00584	5
Rkhd2	A_52_P264161	NM_001039214	ring finger and KH domain containing 2	1.191	75.14	0.65853	13078	M	1.077	22.1	0.41301	7654
Smarcd1	A_51_P101765	NM_031842	SWI/SNF related, matrix associated, actin	1.191	61.79	0.59446	13216	P	1.183	9.71	0.27536	6030
Tgfb3	A_51_P124748	NM_009368	transforming growth factor, beta 3	1.191	72.2	0.72387	19966	P	1.047	25.31	0.36346	7068
2310008H09Rik	A_51_P301207	NM_023197	RIKEN cDNA 2310008H09 gene	1.19	61.79	0.62272	14565	P	-1.18	1.18	0.01696	734
Ces6	A_51_P443339	NM_133960	carboxylesterase 6	1.19	69.29	0.71858	19431	P	1.064	19.02	0.24023	5489
Id2	A_52_P240542	NM_010496	inhibitor of DNA binding 2	1.19	69.29	0.7075	18803	P	1.394	2.53	0.07422	2510
Nola1	A_51_P274992	NM_026578	nucleolar protein family A, member 1 (H/	1.19	42.28	0.46509	8389	P	-1.058	40.63	0.41248	7639
Sra1	A_51_P226053	NM_025291	steroid receptor RNA activator 1	1.19	53.87	0.5136	10079	P	1.04	30.75	0.53785	8918
Stk39	A_51_P183940	NM_016866	serine/threonine kinase 39, STE20/SPS1 h	1.19	57.76	0.55186	11490	P	-1.134	4.63	0.0621	2196
Tac2	A_51_P415087	NM_009312	tachykinin 2	1.19	75.14	0.78992	23430	P	-1.344	0.51	0.00623	135
Wac	A_52_P1084604	AK079535	WW domain containing adaptor with coil	1.19	61.79	0.61645	14204	P	-1.018	49.48	0.83907	11517
0610007C21Rik	A_51_P256759	NM_027855	RIKEN cDNA 0610007C21 gene	1.189	57.76	0.67069	12906	M	1.095	13.58	0.25195	5678
AF397014	A_51_P397200	NM_138654	RIKEN cDNA 5033411D12 gene	1.189	72.2	0.74163	20679	P	-1.033	45.68	0.57761	9244
Bnc1	A_52_P676819	NM_007562	basonuclin 1	1.189		0.91525	13040	A	-1.051	38.4	0.27767	6060
Commd2	A_51_P237775	NM_175095	COMM domain containing 2	1.189	77.44	0.82727	25859	P	-1.301	0.51	0.00627	162

Pik3r2	A_51_P417725	NM_008841	phosphatidylinositol 3-kinase, regulatory	1.189	42.28	0.46559	8396	P	1.12	5.75	0.04385	1638
Prkrir	A_52_P405193	NM_028410	protein-kinase, interferon-inducible doub	1.189	61.79	0.60436	13651	P	1.078	13.58	0.16594	4310
Sfrs12	A_52_P569594	AK081447	splicing factor, arginine/serine-rich 12	1.189	57.76	0.55993	11752	P	1.106	22.1	0.57318	9212
Zfp367	A_51_P431996	NM_175494	zinc finger protein 367	1.189	61.79	0.58531	12779	P	-1.08	22.1	0.14714	3983
2610101N10Rik	A_52_P294174	NM_026476	RIKEN cDNA 2610101N10 gene	1.188	53.87	0.52245	10431	P	1.097	11.33	0.14488	3946
5830415L20Rik	A_51_P438028	AK020011	RIKEN cDNA 5830415L20 gene	1.188	69.29	0.69841	18292	P	1.03	33.49	0.51573	8730
Cd14	A_51_P172853	NM_009841	CD14 antigen	1.188	65.79	0.67032	17064	P	-1.43	0.51	0.01278	549
Foxo3a	A_52_P373852	AK079567	forkhead box O3a	1.188	69.29	0.68995	17077	P	1.023	36.07	0.62628	9682
Rpe	A_52_P867286	AK039429		1.188	75.14	0.7874	23216	P	1.116	11.33	0.22391	5267
Vcam1	A_51_P210956	NM_011693	vascular cell adhesion molecule 1	1.188	77.44	0.8344	26481	P	1.042	38.4	0.81731	11341
2010007H12Rik	A_51_P103865	NM_027242	RIKEN cDNA 2010007H12 gene	1.187	69.29	0.7094	18908	P	-1.389	0.51	0.00584	39
Acbd3	A_52_P58006	NM_133225	acyl-Coenzyme A binding domain contain	1.187	65.79	0.6562	16398	P	1.168	2.53	0.01782	762
Derl1	A_51_P217236	NM_024207	Der1-like domain family, member 1	1.187	57.76	0.54934	11398	P	1.173	3.82	0.04247	1597
Dpysl2	A_51_P468899	NM_009955	dihydropyrimidinase-like 2	1.187	72.2	0.73083	20313	P	1.022	42.43	0.86753	11734
Gabra1	A_52_P377537	NM_010250	gamma-aminobutyric acid (GABA-A) rece	1.187	61.79	0.61522	14171	P	-1.111	5.75	0.05502	2010
Pdk3	A_52_P99622	NM_145630	pyruvate dehydrogenase kinase, isoenzy	1.187	42.28	0.46785	8468	P	1.017	38.4	0.69374	10271
Tnfrsf1b	A_52_P228621	NM_011610	tumor necrosis factor receptor superfami	1.187		0.73182	19076	A	1.058	22.1	0.3489	6857
Btd	A_51_P196158	NM_025295	biotinidase	1.186	65.79	0.65158	16140	P	1.022	38.4	0.71097	10410
Cdkn2c	A_51_P513720	U19596	cyclin-dependent kinase inhibitor 2C (p18	1.186	61.79	0.6062	13737	P	-1.146	5.75	0.08819	2849
Plce1	A_52_P415335	AK122521	phospholipase C, epsilon 1	1.186	75.14	0.79472	23806	P	1.14	8.32	0.12601	3628
Prkag2	A_51_P460869	NM_145401	protein kinase, AMP-activated, gamma 2	1.186	61.79	0.67999	13200	M	1.3	2.04	0.04067	1546
Txndc11	A_52_P150988	NM_029582	thioredoxin domain containing 11	1.186	49.93	0.49923	9635	P	-1.226	0.75	0.01444	611
Zfpm2	A_52_P255261	AK033131	zinc finger protein, multitype 2	1.186	65.79	0.67018	17046	P	1.067	19.02	0.25689	5764
Acaca	A_51_P439426	NM_133360	acetyl-Coenzyme A carboxylase alpha	1.185	38.68	0.59971	11709	M	-1.383	0.51	0.00584	83
Apex2	A_52_P417148	NM_029943	apurinic/apyrimidinic endonuclease 2	1.185	57.76	0.55389	11559	P	1.022	40.63	0.79669	11147
D12Ertd553e	A_51_P253883	NM_029758	DNA segment, Chr 12, ERATO Doi 553, ex	1.185	81.02	0.91066	32004	P	1.11	9.71	0.1238	3575
Ercc5	A_51_P368332	NM_011729	excision repair cross-complementing rode	1.185	61.79	0.60523	13701	P	1.006	42.43	0.9227	12301
Pcbp4	A_51_P194377	NM_021567	poly(rC) binding protein 4	1.185	49.93	0.49756	9535	P	1.057	25.31	0.3976	7496
2210015D19Rik	A_52_P588917	XM_900750	RIKEN cDNA 2210015D19 gene	1.184	77.44	0.82154	25478	P	1.037	28.13	0.41607	7699
Arhgef7	A_52_P26357	AK129064	Rho guanine nucleotide exchange factor (	1.184	79.26	0.86001	28227	P	-1.006	49.48	0.93351	12418
Bxdc1	A_51_P375187	NM_001042556	brix domain containing 1	1.184	61.79	0.60436	13655	P	-1.05	42.43	0.36039	7027
Hat1	A_51_P369636	NM_026115	histone aminotransferase 1	1.184	77.44	0.81539	25119	P	1.015	42.43	0.78145	11005
Hck	A_51_P499918	NM_010407	hemopoietic cell kinase	1.184	81.02	0.89437	30615	P	1.004	42.43	0.93817	12463
Rufy1	A_51_P163694	NM_172557	RUN and FYVE domain containing 1	1.184	61.79	0.58783	12900	P	1.059	25.31	0.47848	8289
Cdkn1c	A_51_P339540	NM_009876	cyclin-dependent kinase inhibitor 1C (P57	1.183	72.2	0.76244	21779	P	-1.14	3.01	0.03602	1394
Etv3	A_51_P148227	NM_012051	ets variant gene 3	1.183	57.76	0.79935	17270	M	1.162	5.75	0.0807	2674
Farslb	A_51_P353360	NM_011811	phenylalanyl-tRNA synthetase, beta subu	1.183	72.2	0.75861	21540	P	1.056	22.1	0.31305	6494
Hoxc5	A_52_P283656	NM_175730	homeo box C5	1.183		0.91818	13156	A	-1.068	36.07	0.3533	6928
Mrpl46	A_51_P335916	NM_023331	mitochondrial ribosomal protein L46	1.183	72.2	0.7513	21143	P	-1.016	49.48	0.735	10627
Ndufb9	A_51_P177552	NM_023172	NADH dehydrogenase (ubiquinone) 1 bet	1.183	49.93	0.49576	9470	P	1.073	13.58	0.14909	4031
Psmd4	A_52_P12869	AB029144	proteasome (prosome, macropain) 26S su	1.183	77.44	0.81287	24894	P	1.073	13.58	0.15931	4200
Umps	A_52_P197627	NM_009471	uridine monophosphate synthetase	1.183	49.93	0.51432	10100	P	1.015	42.43	0.84094	11532
2810028N01Rik	A_52_P29646	NM_028315	DIS3 mitotic control homolog (S. cerevisia	1.182	72.2	0.72231	19782	P	-1.146	6.98	0.10954	3253
Abcb7	A_52_P360650	XM_907304	ATP-binding cassette, sub-family B (MDR/	1.182	53.87	0.542	11083	P	1.107	13.58	0.285	6146
Dctn4	A_52_P201627	NM_026302	dynactin 4	1.182	65.79	0.72346	15070	M	-1.153	3.01	0.04002	1530
Fbxl19	A_52_P364386	NM_172748	F-box and leucine-rich repeat protein 19	1.182	69.29	0.69049	17937	P	-1.079	28.13	0.23887	5469
Golph3l	A_52_P820985	NM_146133	golgi phosphoprotein 3-like	1.182	61.79	0.60765	13799	P	1.094	22.1	0.52431	8791
Ier2	A_51_P481325	NM_010499	immediate early response 2	1.182	77.44	0.81447	25021	P	1.196	13.58	0.39897	7502
Rpl18a	A_51_P446229	NM_029751	Ribosomal protein L18A	1.182	49.93	0.6417	11938	M	1.031	38.4	0.75153	10801
St13	A_52_P484550	NM_133726	suppression of tumorigenicity 13	1.182	69.29	0.69575	18174	P	1.075	25.31	0.56462	9158
Uros	A_51_P257832	NM_009479	uroporphyrinogen III synthase	1.182	75.14	0.80419	24363	P	1.064	22.1	0.38628	7352
Atp6v0b	A_51_P404236	NM_033617	ATPase, H+ transporting, lysosomal V0 su	1.181	75.14	0.79846	24011	P	-1.075	38.4	0.40976	7607
D7Ertd715e	A_52_P145433	AK035508	DNA segment, Chr 7, ERATO Doi 715, exp	1.181	65.79	0.64978	16090	P	1.023	36.07	0.63129	9728

Mlh1	A_51_P180724	NM_026810	mutL homolog 1 (E. coli)	1.181	45.92	0.49273	9356	P	-1.236	0.66	0.01141	450
Pdhx	A_51_P149946	NM_175094	pyruvate dehydrogenase complex, compo	1.181	75.14	0.80313	24263	P	-1.097	6.98	0.06513	2285
Peo1	A_51_P261585	NM_153796	progressive external ophthalmoplegia 1 (I	1.181	42.28	0.50829	9516	M	-1.194	1.62	0.03969	1518
Pgea1	A_51_P470311	NM_028634	PKD2 interactor, golgi and endoplasmic re	1.181	53.87	0.53797	10982	P	-1.051	36.07	0.26039	5823
Ppil2	A_51_P473456	NM_144954	peptidylprolyl isomerase (cyclophilin)-like	1.181	45.92	0.49214	9340	P	1.005	42.43	0.938	12461
Tgfbr3	A_51_P255899	NM_011578	transforming growth factor, beta receptor	1.181	65.79	0.64679	15956	P	1.063	25.31	0.4864	8400
Tmem45a	A_51_P288876	NM_019631	transmembrane protein 45a	1.181	83.36	0.9524	35756	P	1.112	13.58	0.3004	6323
1500035H01Rik	A_52_P217796	NM_023831	RIKEN cDNA 1500035H01 gene	1.18	61.79	0.59937	13415	P	-1.019	49	0.69325	10270
Cited4	A_52_P426768	NM_019563	Cbp/p300-interacting transactivator, with	1.18	77.44	0.84631	27507	P	1.022	36.07	0.615	9576
D10Jhu81e	A_51_P118320	NM_138601	DNA segment, Chr 10, Johns Hopkins Univ	1.18	65.79	0.6703	17061	P	-1.14	5.75	0.09076	2910
Fkbp5	A_52_P481493	NM_010220	FK506 binding protein 5	1.18	65.79	0.62794	14870	P	1.045	30.75	0.54978	9017
Rnf34	A_51_P509211	NM_030564	ring finger protein 34	1.18	53.87	0.5229	10453	P	1.056	28.13	0.52201	8768
Sfxn1	A_51_P431576	AK044490	sideroflexin 1	1.18	65.79	0.64492	15908	P	-1.015	49.48	0.81975	11353
Txn2	A_51_P207310	U85089	thioredoxin 2	1.18	57.76	0.62558	12262	M	-1.084	43.75	0.16545	3948
Ugdh	A_51_P137953	NM_009466	UDP-glucose dehydrogenase	1.18	57.76	0.57477	12231	P	1.064	19.02	0.26315	5853
Wdr31	A_51_P432724	NM_023597	WD repeat domain 31	1.18	65.79	0.65776	16481	P	-1.03	46.85	0.64368	9825
1500011J06Rik	A_51_P327418	NM_025438	arginine/serine-rich coiled-coil 2	1.179	65.79	0.65715	16452	P	1.048	25.31	0.33208	6703
Ddx46	A_52_P106739	NM_145975	DEAD (Asp-Glu-Ala-Asp) box polypeptide	1.179	53.87	0.52487	10530	P	1.071	13.58	0.15736	4171
Gli1	A_51_P518548	NM_010296	GLI-Kruppel family member GLI1	1.179	83.95	0.75902	18691	M	1.061	22.1	0.29244	6244
Pou2f1	A_51_P361492	NM_198934	POU domain, class 2, transcription factor	1.179	53.87	0.53631	10920	P	1.091	11.33	0.109	3242
Rpl29	A_52_P217069	NM_009082	ribosomal protein L29	1.179	49.93	0.5664	10893	P	1.009	42.43	0.86044	11684
Usp3	A_51_P330630	NM_144937	ubiquitin specific peptidase 3	1.179	65.79	0.62794	14857	P	1.048	28.13	0.46898	8195
1110038D17Rik	A_52_P225822	AK036914	RIKEN cDNA 1110038D17 gene	1.178	65.79	0.63237	15350	P	1.081	11.33	0.12036	3502
Asah1	A_51_P509098	NM_019734	N-acylsphingosine amidohydrolase 1	1.178	45.92	0.49852	9610	P	1.021	40.63	0.74287	10716
Cds2	A_52_P253915	NM_138651	CDP-diacylglycerol synthase (phosphatida	1.178	65.79	0.65256	16211	P	1.013	42.43	0.91558	12222
Galnt1	A_51_P209518	NM_013814	UDP-N-acetyl-alpha-D-galactosamine:poly	1.178	69.29	0.68577	17724	P	-1.001	49.48	0.99567	13016
Ldhd	A_52_P161454	NM_027570	lactate dehydrogenase D	1.178	65.79	0.65625	16399	P	-1.01	49.48	0.86781	11741
Med6	A_51_P332359	NM_027213	mediator of RNA polymerase II transcripti	1.178	65.79	0.66359	16750	P	1.078	16.2	0.25121	5665
Mnab	A_52_P274486	AK051094	ring finger and CCCH-type zinc finger dom	1.178	72.2	0.7366	20502	P	1.064	25.31	0.45651	8062
Rpl38	A_51_P227332	NM_001048057	ribosomal protein L38	1.178	77.44	0.84547	20324	M	1.055	30.75	0.63014	9717
Rps10	A_51_P169156	NM_025963	ribosomal protein S10	1.178	61.79	0.70241	14066	M	1.097	16.2	0.31883	6562
Slc30a1	A_51_P300572	NM_009579	solute carrier family 30 (zinc transporter),	1.178	49.93	0.5101	9933	P	1.241	2.53	0.03473	1330
Slc3a2	A_51_P472901	NM_008577	solute carrier family 3 (activators of dibas	1.178	72.2	0.78777	17467	M	1.166	6.98	0.11019	3271
Vkorc1	A_51_P395555	NM_178600	vitamin K epoxide reductase complex, sub	1.178	65.79	0.78425	20538	P	1.148	4.63	0.04586	1718
Ccnl1	A_51_P351481	NM_019937	cyclin L1	1.177	75.14	0.7761	22533	P	1.015	42.43	0.79037	11095
Cdc2l1	A_52_P365803	BC052920	cell division cycle 2-like 1	1.177	72.2	0.7437	20759	P	-1.019	49.39	0.73014	10574
E2f6	A_52_P349216	AK035116	E2F transcription factor 6	1.177	72.2	0.72005	19538	P	1.166	6.98	0.10973	3261
Gc	A_51_P349961	NM_008096	group specific component	1.177	77.44	0.84032	27116	P	-1.216	1.18	0.0297	1184
Glo1	A_51_P480982	NM_025374	glyoxalase 1	1.177	53.87	0.65848	12480	M	1.046	30.75	0.51573	8726
Hprt1	A_51_P239673	NM_013556	hypoxanthine guanine phosphoribosyl tra	1.177	69.29	0.74664	15964	M	1.275	3.46	0.08194	2701
Mrpl23	A_51_P193130	NM_011288	mitochondrial ribosomal protein L23	1.177	49.93	0.51764	10237	P	-1.052	40.63	0.31681	6546
Rpl26	A_51_P363515	NM_009080	ribosomal protein L26	1.177	57.76	0.67557	13046	M	-1.015	49.48	0.78383	11041
Slc27a3	A_51_P133252	NM_011988	solute carrier family 27 (fatty acid transpo	1.177	61.79	0.58459	12747	P	1.033	30.75	0.47591	8269
Srpx2	A_51_P425047	NM_026838	sushi-repeat-containing protein, X-linked	1.177	61.79	0.62327	14600	P	-1.093	11.33	0.09324	2968
Stx12	A_51_P252363	NM_133887	syntaxin 12	1.177	53.87	0.54443	11177	P	-1.058	38.4	0.32115	6576
Stx4a	A_51_P495492	NM_009294	syntaxin 4A (placental)	1.177	57.76	0.57043	12069	P	1.003	42.43	0.96107	12676
Zfr	A_52_P213318	NM_011767	zinc finger RNA binding protein	1.177	61.79	0.62384	14630	P	1.114	8.32	0.06417	2259
Cdc25c	A_51_P279575	NM_009860	cell division cycle 25 homolog C (S. pomb	1.176	79.26	0.87403	29184	P	1.055	22.1	0.27929	6082
Hace1	A_51_P512947	NM_172473	HECT domain and ankyrin repeat containi	1.176	57.76	0.56085	11772	P	-1.259	0.51	0.00977	355
Rab25	A_52_P149577	NM_016899	RAB25, member RAS oncogene family	1.176	65.79	0.6531	16267	P	-1.085	28.13	0.26317	5858
Rai14	A_52_P385229	NM_030690	retinoic acid induced 14	1.176	69.29	0.68708	17781	P	1.077	19.02	0.36136	7032
Sc5d	A_52_P67637	AK080673	sterol-C5-desaturase (fungal ERG3, delta-	1.176	57.76	0.58264	12659	P	1.032	33.49	0.59555	9405
Timm50	A_52_P682990	NM_025616	translocase of inner mitochondrial memb	1.176	65.79	0.65378	16299	P	1.12	8.32	0.08461	2777

Vps28	A_52_P143121	NM_025842	vacuolar protein sorting 28 (yeast)	1.176	57.76	0.54911	11390	P	1.05	25.31	0.32279	6594
Aga	A_51_P119544	NM_001005847	aspartylglucosaminidase	1.175	69.29	0.70517	18681	P	1.125	6.98	0.06256	2211
Akap13	A_52_P414750	XM_133543	A kinase (PRKA) anchor protein 13	1.175	61.79	0.70266	15125	M	1.008	42.43	0.90206	12110
Dusp16	A_51_P242634	AF345951	dual specificity phosphatase 16	1.175	61.79	0.59355	13116	P	-1.01	49.48	0.82285	11392
Eif5b	A_51_P479659	NM_198303	eukaryotic translation initiation factor 5B	1.175	75.14	0.807	24523	P	-1.063	33.49	0.2718	5978
Ets1	A_52_P258291	NM_011808	E26 avian leukemia oncogene 1, 5' domai	1.175	81.02	0.91011	31953	P	-1.013	49.48	0.7827	11017
Pdk2	A_51_P426276	NM_133667	pyruvate dehydrogenase kinase, isoenzyn	1.175	65.79	0.66265	16694	P	-1.275	0.51	0.00756	282
Rps8	A_52_P284672	NM_009098	ribosomal protein S8	1.175	69.29	0.70849	18864	P	-1.142	8.32	0.12664	3643
Tagln2	A_52_P35240	NM_178598	transgelin 2	1.175	53.87	0.54602	11248	P	-1.002	49.48	0.97376	12775
B4galt1	A_51_P155257	NM_022305	UDP-Gal:betaGlcNAc beta 1,4- galactosylt	1.174	61.79	0.60459	13665	P	1.112	11.33	0.19654	4846
D1Bwg1363e	A_51_P153904	NM_001001566	DNA segment, Chr 1, Brigham & Women's	1.174	75.14	0.77263	22378	P	1.034	33.49	0.61332	9554
Ddx41	A_51_P345927	NM_134059	DEAD (Asp-Glu-Ala-Asp) box polypeptide	1.174	57.76	0.57942	12445	P	-1.292	0.51	0.00623	133
Lrp2	A_51_P322000	XM_130308	low density lipoprotein receptor-related p	1.174		0.81096	18175	A	1.066	13.58	0.1549	4126
Meox2	A_51_P383001	NM_008584	mesenchyme homeobox 2	1.174	75.14	0.80251	24193	P	1.044	36.07	0.74695	10765
Ncbp2	A_52_P83321	NM_026554	nuclear cap binding protein subunit 2	1.174	69.29	0.70898	18893	P	-1.049	40.63	0.31325	6495
Nfatc3	A_52_P333419	NM_010901	nuclear factor of activated T-cells, cytopla	1.174	57.76	0.5801	12504	P	1.105	9.71	0.09218	2948
Rbms3	A_51_P497451	NM_178660	RNA binding motif, single stranded intera	1.174	75.14	0.79372	23737	P	1.218	2.04	0.01643	700
4930402H24Rik	A_51_P293575	AK089462	RIKEN cDNA 4930402H24 gene	1.173	57.76	0.57556	12272	P	1.061	19.02	0.27129	5974
Adm	A_51_P265571	NM_009627	adrenomedullin	1.173	69.29	0.69373	18102	P	1.103	16.2	0.3233	6596
Atp5j	A_51_P100866	NM_016755	ATP synthase, H+ transporting, mitochon	1.173	57.76	0.57971	12484	P	1.031	33.49	0.53586	8898
C3	A_52_P133594	NM_009778	complement component 3	1.173	77.44	0.66333	14868	M	-1.118	8.32	0.0808	2679
F8	A_51_P289239	NM_007977	coagulation factor VIII	1.173	69.29	0.7097	18928	P	-1.346	0.51	0.00627	147
Hdhd2	A_52_P450675	NM_001039201	haloacid dehalogenase-like hydrolase dor	1.173	69.29	0.67216	17158	P	-1.025	48.39	0.69861	10304
Hp1bp3	A_52_P224778	NM_010470	heterochromatin protein 1, binding prote	1.173	75.14	0.77732	22591	P	1.197	4.63	0.07882	2624
Igsf3	A_51_P231482	AK019524	immunoglobulin superfamily, member 3	1.173	77.44	0.82443	25674	P	1.003	42.43	0.93754	12447
Msr1	A_52_P127130	NM_031195	macrophage scavenger receptor 1	1.173	42.28	0.63286	12907	M	1.005	42.43	0.91107	12200
Ppih	A_51_P300759	NM_028677	peptidyl prolyl isomerase H	1.173	61.79	0.61855	14347	P	1.131	8.32	0.12167	3535
Psmc5	A_52_P657435	NM_008950	protease (prosome, macropain) 26S subu	1.173	53.87	0.5295	10714	P	-1.025	47.43	0.61206	9546
Rpl36a	A_52_P197926	NM_019865	ribosomal protein L36a	1.173	65.79	0.71944	14765	M	1.022	40.63	0.84549	11567
Sqstm1	A_51_P119077	NM_011018	sequestosome 1	1.173	49.93	0.65368	12324	M	1.174	3.46	0.03174	1247
Zfp289	A_52_P466993	NM_023854	zinc finger protein 289	1.173	49.93	0.51792	10262	P	-1.179	1.18	0.01962	833
1700021K19Rik	A_52_P263490	NM_172615	RIKEN cDNA 1700021K19 gene	1.172		0.73378	15121	A	-1.252	0.51	0.00744	268
E330036I19Rik	A_51_P122582	NM_144915	diacylglycerol lipase, beta	1.172	77.44	0.82952	26013	P	-1.035	45.68	0.54088	8952
Ephb4	A_52_P542612	NM_010144	Eph receptor B4	1.172	75.14	0.78047	22798	P	1.045	33.49	0.66858	10030
Mpp5	A_52_P402881	BC075698	membrane protein, palmitoylated 5 (MAG	1.172	61.79	0.61973	14433	P	-1.008	49.48	0.90099	12098
Pax4	A_51_P514224	NM_011038	paired box gene 4	1.172	65.79	0.58969	11766	M	-1.237	1.32	0.04507	1693
Prdm2	A_51_P176998	XM_898822	PR domain containing 2, with ZNF domair	1.172	72.2	0.58725	12279	M	-1.191	2.04	0.04712	1763
Prkag1	A_52_P273546	NM_016781	protein kinase, AMP-activated, gamma 1	1.172	53.87	0.53038	10752	P	1.006	42.43	0.93923	12473
Rpl13a	A_51_P235311	NM_009438	ribosomal protein L13a	1.172	69.29	0.76604	16705	M	1.016	42.43	0.89628	12016
Shoc2	A_51_P185941	NM_019658	soc-2 (suppressor of clear) homolog (C. el	1.172	61.79	0.60322	13600	P	-1.021	49.47	0.77211	10943
Ube2m	A_52_P665386	NM_145578	ubiquitin-conjugating enzyme E2M (UBC1	1.172	42.28	0.49188	9318	P	1.091	11.33	0.1534	4096
Wasf1	A_51_P322801	NM_031877	WASP family 1	1.172	72.2	0.75318	21301	P	-1.113	6.98	0.06647	2333
2010012C16Rik	A_51_P187018	NM_025564	RIKEN cDNA 2010012C16 gene	1.171	61.79	0.62672	14774	P	1.006	42.43	0.92381	12332
5230400G24Rik	A_51_P287931	NM_029409	RIKEN cDNA 5230400G24 gene	1.171	57.76	0.68445	13350	M	-1.049	44.4	0.59881	9436
Abi3	A_51_P185906	NM_025659	ABI gene family, member 3	1.171	81.02	0.8844	29956	P	1.056	22.1	0.31065	6456
Cdadc1	A_52_P327791	AK032600	cytidine and dCMP deaminase domain co	1.171	69.29	0.68154	17503	P	1.007	42.43	0.89442	12005
Mef2a	A_52_P290579	NM_001033713	myocyte enhancer factor 2A	1.171	53.87	0.5467	11290	P	1.011	42.43	0.81576	11333
Mib1	A_52_P437884	BC083072	mindbomb homolog 1 (Drosophila)	1.171	42.28	0.56539	10868	P	1.203	3.46	0.03904	1469
Mtrr	A_52_P58318	NM_172480	5-methyltetrahydrofolate-homocysteine r	1.171	61.79	0.61962	14425	P	-1.039	43.75	0.40359	7553
Mylip	A_52_P248343	NM_153789	myosin regulatory light chain interacting p	1.171	75.14	0.64538	13978	M	-1.008	49.48	0.89551	12014
Nid2	A_51_P315666	NM_008695	nidogen 2	1.171	72.2	0.73378	20408	P	1.127	6.98	0.0659	2316
Ptges2	A_51_P349008	NM_133783	prostaglandin E synthase 2	1.171	65.79	0.63447	15433	P	-1.044	38.4	0.29799	6299
Rbpsuh	A_52_P100028	NM_009035	recombination signal binding protein for i	1.171	53.87	0.53797	10978	P	1.125	8.32	0.11024	3272

Rps6	A_51_P344734	NM_009096	ribosomal protein S6	1.171	61.79	0.70381	14131	M	1.165	9.71	0.2199	5206
Rps6kb2	A_52_P277335	AK090093	ribosomal protein S6 kinase, polypeptide	1.171	72.2	0.71858	19436	P	1.091	9.71	0.08296	2727
Sidt2	A_51_P269303	AK081177	SID1 transmembrane family, member 2	1.171	72.2	0.72946	20191	P	1.018	38.4	0.67517	10097
Wbp5	A_51_P139848	NM_011712	WW domain binding protein 5	1.171	65.79	0.71641	14646	M	1.124	16.2	0.45518	8050
Zfp395	A_52_P654080	NM_199029	zinc finger protein 395	1.171	83.95	0.70327	16258	M	1.037	33.49	0.66434	9999
1600020E01Rik	A_52_P617171	BC029726	RIKEN cDNA 1600020E01 gene	1.17	75.14	0.77853	22679	P	-1.129	3.01	0.03532	1369
Ercc4	A_51_P210082	NM_015769	excision repair cross-complementing rode	1.17	75.14	0.77895	22702	P	-1.009	49.48	0.87155	11772
Fubp1	A_52_P438578	NM_057172	far upstream element (FUSE) binding prot	1.17	65.79	0.65578	16381	P	1.184	4.63	0.05995	2153
Lin7c	A_52_P124279	NM_011699	lin-7 homolog C (C. elegans)	1.17	53.87	0.54626	11262	P	1	49.48	0.99863	13044
Lsm1	A_51_P206655	NM_026032	LSM1 homolog, U6 small nuclear RNA ass	1.17	65.79	0.62845	14925	P	1.103	11.33	0.16599	4317
Orc4l	A_52_P376535	NM_011958	origin recognition complex, subunit 4-like	1.17	75.14	0.7931	23694	P	-1.174	2.04	0.04067	1550
Pdgfb	A_51_P175262	NM_011057	platelet derived growth factor, B polypept	1.17	49.93	0.51164	9998	P	-1.038	45.68	0.59635	9411
Pfkfb3	A_52_P362917	NM_133232	6-phosphofructo-2-kinase/fructose-2,6-b	1.17		0.79485	15507	A	1.037	33.49	0.59709	9417
Pklr	A_51_P176042	NM_013631	pyruvate kinase liver and red blood cell	1.17	65.79	0.62738	14822	P	1.077	16.2	0.22252	5246
Rpl37a	A_51_P441263	NM_009084	ribosomal protein L37a	1.17	65.79	0.73334	15608	M	-1.113	19.02	0.22274	5254
Eef2	A_52_P605455	NM_007907	eukaryotic translation elongation factor 2	1.169	61.79	0.59916	13397	P	1.305	2.53	0.05139	1887
Glipr1	A_51_P371051	NM_028608	GLI pathogenesis-related 1 (glioma)	1.169	65.79	0.65034	16106	P	1.057	25.31	0.37242	7202
Nfrkb	A_52_P43456	AK036381	nuclear factor related to kappa B binding	1.169	75.14	0.79255	23645	P	1.012	42.43	0.93323	12411
Sertad2	A_52_P238242	NM_021372	SERTA domain containing 2	1.169	57.76	0.55923	11721	P	1.08	16.2	0.21788	5167
Tmem4	A_51_P342082	NM_019953	transmembrane protein 4	1.169	65.79	0.66359	16755	P	1.013	42.43	0.85958	11675
0610007P06Rik	A_51_P251717	NM_026304	lethal, Chr 7, Rinchik 6	1.168	72.2	0.7163	19297	P	1.194	4.63	0.08013	2661
Cdk5	A_51_P157895	NM_007668	cyclin-dependent kinase 5	1.168	61.79	0.60024	13452	P	-1.143	2.04	0.02732	1108
Creb1	A_52_P517730	NM_009952	cAMP responsive element binding protei	1.168	61.79	0.61645	14206	P	1.057	16.2	0.20101	4916
Dad1	A_51_P189905	ENSMUST00000022781	defender against cell death 1	1.168	61.79	0.70918	14321	M	1.068	30.75	0.73134	10582
Dnm2	A_52_P271614	NM_001039520	dynamin 2	1.168	57.76	0.57556	12277	P	1.142	9.71	0.16704	4330
Extl3	A_51_P208321	NM_018788	exostoses (multiple)-like 3	1.168	61.79	0.60906	13889	P	-1.039	44.4	0.47929	8304
Gata2	A_51_P516625	NM_008090	GATA binding protein 2	1.168	57.76	0.57768	12392	P	1.01	42.43	0.88912	11953
Il28ra	A_52_P621588	NM_174851	interleukin 28 receptor alpha	1.168	61.79	0.61195	14065	P	-1.01	49.48	0.93769	12453
Pld2	A_51_P357759	NM_008876	phospholipase D2	1.168	69.29	0.68129	17484	P	-1.102	16.2	0.14805	4004
Txnl2	A_51_P157634	NM_023140	thioredoxin-like 2	1.168	65.79	0.63846	15634	P	1.003	42.43	0.93762	12449
Blzf1	A_51_P378009	NM_025505	basic leucine zipper nuclear factor 1	1.167	49.93	0.51629	10175	P	-1.061	36.07	0.28666	6182
Hbld2	A_52_P167189	NM_026921	iron-sulfur cluster assembly 1 homolog (S	1.167	61.79	0.70887	14300	M	1.127	5.75	0.03933	1493
Htatsf1	A_51_P347452	NM_028242	HIV TAT specific factor 1	1.167	72.2	0.7334	20404	P	-1.012	49.48	0.78435	11046
Il1a	A_52_P100926	NM_010554	interleukin 1 alpha	1.167	79.26	0.85577	28024	P	1.17	3.01	0.02042	874
Rorb	A_52_P74320	NM_001043354	RAR-related orphan receptor beta	1.167		0.82089	16423	A	-1.051	38.4	0.29296	6254
Stxbp2	A_51_P134070	NM_011503	syntaxin binding protein 2	1.167	69.29	0.69282	18060	P	-1.103	19.02	0.21142	5060
Zfp85-rs1	A_52_P560116	U29505	zinc finger protein 85, related sequence 1	1.167	57.76	0.58473	12755	P	1.049	28.13	0.42002	7730
Agl	A_51_P334444	XM_131166	amylo-1,6-glucosidase, 4-alpha-glucanotr	1.166	61.79	0.60024	13444	P	1.1	16.2	0.38104	7284
Arvcf	A_51_P164539	NM_033474	armadillo repeat gene deleted in velo-car	1.166	69.29	0.70795	18823	P	1.065	19.02	0.22046	5216
Cml1	A_51_P235604	NM_023160	camello-like 1	1.166	65.79	0.64133	15758	P	-1.045	44.4	0.52699	8816
Gpc3	A_52_P23225	NM_016697	glypican 3	1.166	77.44	0.83252	26289	P	1.113	19.02	0.48617	8395
Il2	A_51_P114222	NM_008366	interleukin 2	1.166		0.84744	15083	A	1.125	9.71	0.16458	4288
Nhlrc2	A_52_P571661	NM_025811	NHL repeat containing 2	1.166	57.76	0.58125	12581	P	1.093	13.58	0.22108	5220
Ppm1f	A_51_P224564	NM_176833	protein phosphatase 1F (PP2C domain co	1.166	57.76	0.58125	12592	P	1.05	28.13	0.46306	8140
Sec23ip	A_51_P283639	NM_001029982	Sec23 interacting protein	1.166	75.14	0.77781	22654	P	1.017	42.43	0.83579	11494
Spcs1	A_51_P149775	NM_026911	signal peptidase complex subunit 1 homo	1.166	72.2	0.78224	17282	M	1.321	1.32	0.01781	761
Zbtb20	A_52_P657844	AK038731	zinc finger and BTB domain containing 20	1.166	65.79	0.62876	14956	P	1.045	25.31	0.34641	6831
Cetn2	A_52_P482825	NM_019405	centrin 2	1.165	65.79	0.63509	15483	P	1.073	25.31	0.51391	8709
H2-Ke6	A_51_P344407	NM_013543	H2-K region expressed gene 6	1.165	69.29	0.68295	17539	P	1.144	8.32	0.11205	3316
Idh3a	A_51_P268559	NM_029573	isocitrate dehydrogenase 3 (NAD+) alpha	1.165	61.79	0.61831	14313	P	1.131	5.75	0.04349	1632
Irak1	A_51_P106743	NM_008363	interleukin-1 receptor-associated kinase 1	1.165	61.79	0.60384	13626	P	1.313	3.46	0.09408	2982
Mef2c	A_51_P135802	NM_025282	myocyte enhancer factor 2C	1.165	57.76	0.56348	11822	P	1.075	13.58	0.16853	4361
Mtif2	A_52_P201446	NM_133767	mitochondrial translational initiation fact	1.165	65.79	0.65628	16406	P	1.061	22.1	0.37996	7276

Osgep	A_51_P310548	NM_133676	O-sialoglycoprotein endopeptidase	1.165	65.79	0.66508	16826	P	1.073	16.2	0.24091	5503
Pgrmc1	A_51_P144581	NM_016783	progesterone receptor membrane compo	1.165	42.28	0.50277	9774	P	1.171	5.75	0.07811	2609
Rps27	A_51_P511199	NM_027015	ribosomal protein S27	1.165	45.92	0.66359	12671	M	1.109	8.32	0.06516	2293
Sybl1	A_51_P364421	NM_011515	synaptobrevin like 1	1.165	53.87	0.67248	12979	M	-1.045	46.3	0.70466	10352
Taf5	A_51_P263220	NM_177342	TAF5 RNA polymerase II, TATA box binding	1.165	61.79	0.60354	13605	P	1.094	9.71	0.0963	3022
Ube2b	A_52_P564625	AK161008	ubiquitin-conjugating enzyme E2B, RAD6	1.165	57.76	0.58074	12523	P	1.087	19.02	0.36302	7060
Ubxd1	A_51_P391926	NM_024432	UBX domain containing 1	1.165	53.87	0.54927	11392	P	-1.275	0.51	0.00804	298
1110059E24Rik	A_51_P490348	NM_025423	RIKEN cDNA 1110059E24 gene	1.164	49.93	0.5246	10526	P	-1.089	16.2	0.1189	3462
Cyc1	A_51_P295610	NM_025567	cytochrome c-1	1.164	61.79	0.59361	13126	P	-1.167	1.32	0.02003	855
E130112L23Rik	A_51_P435731	NM_198249	RIKEN cDNA E130112L23 gene	1.164	38.68	0.66508	13361	M	-1.309	0.51	0.00619	129
Fbxl3	A_52_P451600	NM_015822	F-box and leucine-rich repeat protein 3	1.164	53.87	0.5494	11401	P	1.126	8.32	0.08375	2744
Lctl	A_51_P336070	NM_145835	lactase-like	1.164	69.29	0.84589	21813	M	1.215	1.62	0.01291	559
Myl9	A_51_P308298	BC055439	myosin, light polypeptide 9, regulatory	1.164	77.44	0.80638	24472	P	-1.039	45.68	0.60313	9472
Ncl	A_52_P429650	NM_010880	nucleolin	1.164	57.76	0.57081	12087	P	1.075	19.02	0.36008	7019
Papss1	A_51_P196127	NM_011863	3'-phosphoadenosine 5'-phosphosulfate s	1.164	57.76	0.58125	12572	P	1.173	2.53	0.0173	742
Pon2	A_51_P280928	NM_183308	paraoxonase 2	1.164	57.76	0.5808	12540	P	-1.18	4.63	0.12227	3547
Ppp1r10	A_52_P258507	AK004266	protein phosphatase 1, regulatory subuni	1.164	57.76	0.56283	11810	P	1.03	33.49	0.58612	9305
Ptbp1	A_52_P234619	NM_001077363	polypyrimidine tract binding protein 1	1.164	65.79	0.66333	16713	P	1.138	6.98	0.06611	2323
Rps5	A_51_P174335	NM_009095	ribosomal protein S5	1.164	72.2	0.79305	17721	M	1.18	8.32	0.19298	4794
Strbp	A_52_P121525	NM_009261	spermatid perinuclear RNA binding prote	1.164	72.2	0.75437	21366	P	-1.025	47.92	0.67257	10076
Txndc10	A_51_P507324	NM_198295	thioredoxin domain containing 10	1.164	61.79	0.62401	14654	P	1.001	42.43	0.99	12986
2810430M08Rik	A_51_P186053	NM_026041	ribosomal RNA processing 15 homolog (S	1.163	61.79	0.60961	13921	P	1.097	13.58	0.25033	5648
Acad8	A_51_P244052	NM_025862	acyl-Coenzyme A dehydrogenase family, r	1.163	65.79	0.65713	16448	P	1.02	38.4	0.67006	10044
BC002199	A_51_P318497	NM_145964	cDNA sequence BC002199	1.163	53.87	0.54821	11347	P	1.194	3.01	0.02469	1020
Bclaf1	A_52_P18897	NM_001025393	BCL2-associated transcription factor 1	1.163	72.2	0.71212	19070	P	1.048	30.75	0.59726	9420
D030022P06Rik	A_52_P419632	AK154145	RIKEN cDNA D030022P06 gene	1.163	75.14	0.77107	22256	P	-1.032	46.85	0.67797	10122
H13	A_52_P341161	BC056977	histocompatibility 13	1.163	69.29	0.69849	18304	P	1.071	16.2	0.22666	5303
Mphosph6	A_51_P453010	NM_026758	M phase phosphoprotein 6	1.163	72.2	0.75269	21250	P	1.184	3.82	0.04181	1578
Pcaf	A_52_P87955	NM_020005	p300/CBP-associated factor	1.163	61.79	0.59402	13168	P	1.013	42.43	0.7827	11019
Ubap2	A_51_P286411	NM_026872	ubiquitin-associated protein 2	1.163	69.29	0.7004	18396	P	1.066	19.02	0.31065	6455
Cox6a1	A_51_P311540	NM_007748	cytochrome c oxidase, subunit VI a, polyp	1.162	53.87	0.68383	13327	M	-1.068	40.63	0.47325	8230
Racgap1	A_51_P243750	NM_012025	Rac GTPase-activating protein 1	1.162	61.79	0.61013	13950	P	1.072	22.1	0.37093	7182
Usp34	A_52_P172453	AK033182	ubiquitin specific peptidase 34	1.162	57.76	0.57165	12103	P	-1.025	48.7	0.71908	10475
Wdr18	A_51_P317115	NM_175450	WD repeat domain 18	1.162	61.79	0.59305	13061	P	-1.087	22.1	0.19196	4771
Acyp1	A_51_P145735	NM_025421	acylphosphatase 1, erythrocyte (common	1.161	75.14	0.78002	22744	P	1.078	16.2	0.26935	5945
Dnajc14	A_52_P95921	NM_028873	DnaJ (Hsp40) homolog, subfamily C, mem	1.161	69.29	0.71034	18966	P	1.099	11.33	0.15644	4153
Gmps	A_52_P489531	AK136966	guanine monphosphate synthetase	1.161	65.79	0.63638	15544	P	1.089	9.71	0.09771	3060
Jarid1a	A_51_P249689	AK043170	jumonji, AT rich interactive domain 1A (Rb	1.161	72.2	0.73001	20238	M	-1.099	28.13	0.29943	6306
Limk1	A_51_P484030	NM_010717	LIM-domain containing, protein kinase	1.161	65.79	0.62914	15000	P	1.044	30.75	0.52026	8758
Nr2f2	A_52_P155713	AK012573	nuclear receptor subfamily 2, group F, me	1.161	77.44	0.8198	25402	P	1.133	13.58	0.30779	6414
Psmd13	A_52_P50512	NM_011875	proteasome (prosome, macropain) 26S su	1.161	72.2	0.7491	21035	P	-1.159	11.33	0.22287	5256
Stard3	A_51_P154973	NM_021547	START domain containing 3	1.161	72.2	0.74715	20943	P	-1.254	0.56	0.01077	417
Top2b	A_52_P183062	AK052306	topoisomerase (DNA) II beta	1.161		0.88993	16111	A	1.106	9.71	0.09505	2999
Zfp26	A_52_P566487	XM_977451	zinc finger protein 26	1.161	45.92	0.58909	11746	P	-1.013	49.48	0.86948	11756
4632413K17Rik	A_51_P382331	AK014574	amplified in osteosarcoma	1.16		0.65262	14290	A	1.098	9.71	0.11145	3308
4930482L21Rik	A_52_P617272	AK015611	RIKEN cDNA 4930482L21 gene	1.16	65.79	0.65572	16364	P	1.074	13.58	0.16092	4229
9130221D24Rik	A_52_P146403	NM_029953	RIKEN cDNA 9130221D24 gene	1.16	77.44	0.83662	26863	M	-1.105	9.71	0.09132	2929
Acvr1b	A_51_P402391	NM_007395	activin A receptor, type 1B	1.16		0.7174	14233	A	1.14	11.33	0.28147	6106
Alg2	A_51_P123060	NM_019998	asparagine-linked glycosylation 2 homolo	1.16	69.29	0.7652	16676	M	1.401	1.17	0.01933	813
Atbf1	A_52_P574618	NM_007496	AT motif binding factor 1	1.16	69.29	0.67252	17197	P	1.058	19.02	0.25284	5693
Gpi1	A_51_P426886	NM_008155	glucose phosphate isomerase 1	1.16	61.79	0.7073	14238	M	1.172	2.53	0.01625	696
Jtb	A_52_P603976	NM_206924	jumping translocation breakpoint	1.16	65.79	0.73827	15727	M	-1.055	44.4	0.62307	9648
Mafg	A_52_P240754	NM_010756	v-maf musculoaponeurotic fibrosarcoma	1.16	72.2	0.74163	20675	P	1.135	11.33	0.24553	5575

P4ha1	A_51_P458067	NM_011030	procollagen-proline, 2-oxoglutarate 4-diox	1.16	72.2	0.72493	20010	P	1.002	42.43	0.97517	12787
Zfp9	A_52_P315910	AB010325	zinc finger protein 9	1.16	61.79	0.59548	13262	P	1.001	42.43	0.9814	12860
2410004L22Rik	A_51_P249544	NM_029621	RIKEN cDNA 2410004L22 gene	1.159	75.14	0.79711	23933	P	1.061	19.02	0.2754	6031
Adcy4	A_51_P229911	NM_080435	adenylate cyclase 4	1.159	77.44	0.82276	25590	P	-1.015	49.48	0.8006	11179
D5Ertd135e	A_51_P231364	AK088165	DNA segment, Chr 5, ERATO Doi 135, expr	1.159	42.28	0.51932	10319	P	-1.078	25.31	0.1683	4356
Gpiap1	A_52_P127459	AK133891	cell cycle associated protein 1	1.159	65.79	0.64935	16074	P	1.044	28.13	0.44677	7978
Mrpl52	A_52_P315111	NM_026851	mitochondrial ribosomal protein L52	1.159	61.79	0.6241	14660	P	-1.065	25.31	0.15736	4170
Pxn	A_52_P317416	AK084243	paxillin	1.159		0.93084	13513	A	-1.035	45.05	0.52813	8821
Senp7	A_52_P88722	NM_025483	SUMO1/sentrin specific peptidase 7	1.159	65.79	0.65802	16497	P	1.058	19.02	0.25617	5746
Spata5	A_51_P192429	NM_021343	spermatogenesis associated 5	1.159	49.93	0.54172	11067	P	1.038	28.13	0.37715	7243
Spon1	A_51_P151902	NM_145584	spondin 1, (f-spondin) extracellular matrix	1.159	75.14	0.7629	21810	P	1.038	28.13	0.39055	7401
2610204L23Rik	A_52_P214416	AK162160	RIKEN cDNA 2610204L23 gene	1.158	65.79	0.65776	16486	P	1.123	13.58	0.34767	6844
Apcs	A_51_P354165	NM_011318	serum amyloid P-component	1.158	61.79	0.61855	14355	P	-1.028	47.92	0.70508	10363
Atp6v0e	A_51_P336874	NM_025272	ATPase, H+ transporting, lysosomal V0 su	1.158	72.2	0.77427	17010	M	1.042	36.07	0.74823	10775
AU040829	A_51_P254019	AK053220	expressed sequence AU040829	1.158		0.81213	16064	A	1.125	5.75	0.04689	1746
Cse1l	A_52_P470518	NM_023565	chromosome segregation 1-like (S. cerevis	1.158	77.44	0.82564	25727	P	-1.106	13.58	0.1217	3538
Plekhj1	A_51_P196509	NM_023900	pleckstrin homology domain containing, f	1.158	57.76	0.57363	12179	P	1.054	25.31	0.43881	7912
Rpl11	A_51_P394524	NM_025919	ribosomal protein L11	1.158	69.29	0.77288	16962	M	1.204	2.53	0.02026	866
Seh1l	A_52_P352967	BC027244	SEH1-like (S. cerevisiae	1.158	77.44	0.83513	26707	P	1.104	13.58	0.24813	5619
Slc25a25	A_51_P193176	NM_146118	solute carrier family 25 (mitochondrial ca	1.158	77.44	0.83461	26667	P	1.001	42.43	0.98717	12950
Slc6a9	A_51_P351872	NM_008135	solute carrier family 6 (neurotransmitter t	1.158	75.14	0.76651	22013	P	-1.037	48.7	0.80857	11273
Snrpd2	A_51_P475279	NM_026943	small nuclear ribonucleoprotein D2	1.158	75.14	0.76918	22161	P	1.067	19.02	0.27879	6072
1110059P08Rik	A_52_P73374	AK085518	Vps20-associated 1 homolog (S. cerevisiae	1.157	61.79	0.60208	13529	P	1.078	16.2	0.24886	5630
Adprh	A_52_P289022	AF244347	ADP-ribosylarginine hydrolase	1.157	75.14	0.79472	23801	P	1.076	19.02	0.27646	6050
AI314976	A_52_P505584	NM_207219	expressed sequence AI314976	1.157	72.2	0.74637	20902	P	1.128	6.98	0.0689	2374
Arl1	A_51_P195393	NM_025859	ADP-ribosylation factor-like 1	1.157	57.76	0.64752	13050	M	1.075	22.1	0.44278	7944
C330007P06Rik	A_52_P137086	AK021190	RIKEN cDNA C330007P06 gene	1.157	72.2	0.74317	20728	P	-1.038	45.05	0.53126	8844
D12Ertd647e	A_52_P86693	NM_026790	DNA segment, Chr 12, ERATO Doi 647, exp	1.157	69.29	0.67764	17358	P	1.026	40.63	0.85305	11618
Lilrb4	A_51_P241457	NM_013532	leukocyte immunoglobulin-like receptor, s	1.157	65.79	0.65991	16585	P	1.011	42.43	0.82428	11402
Lztr1	A_52_P75985	NM_025808	leucine-zipper-like transcriptional regulato	1.157	53.87	0.56567	11890	P	1.177	3.46	0.02595	1075
Prkce	A_51_P352782	AK017901	protein kinase C, epsilon	1.157	72.2	0.79485	17808	M	1.067	13.58	0.1484	4018
Pscd4	A_51_P231398	NM_028195	pleckstrin homology, Sec7 and coiled/coil	1.157	77.44	0.83461	26630	P	-1.032	45.05	0.47319	8228
Tmepai	A_51_P449777	NM_022995	transmembrane, prostate androgen induc	1.157	77.44	0.81643	25177	M	1.23	6.98	0.18739	4690
Tusc2	A_52_P123354	NM_019742	tumor suppressor candidate 2	1.157	65.79	0.65628	16403	P	-1.051	42.43	0.36472	7088
Capza2	A_51_P496845	NM_007604	capping protein (actin filament) muscle Z-	1.156	72.2	0.73001	20250	P	1.111	11.33	0.19502	4815
Mfn2	A_51_P266774	NM_133201	mitofusin 2	1.156	75.14	0.79372	23735	P	1.099	16.2	0.38172	7303
Mrpl36	A_51_P450123	NM_053163	mitochondrial ribosomal protein L36	1.156	61.79	0.61717	14244	P	-1.218	0.75	0.012	484
Msl31	A_51_P332481	NM_010832	male-specific lethal-3 homolog 1 (Drosop	1.156	61.79	0.59629	13312	P	1.075	19.02	0.32475	6616
Rin3	A_51_P111562	NM_177620	Ras and Rab interactor 3	1.156	53.87	0.5658	11892	P	-1.162	1.58	0.02361	991
Rnf149	A_52_P128283	NM_001033135	ring finger protein 149	1.156	57.76	0.58539	12804	P	1.162	3.46	0.02469	1019
Rpl9	A_51_P301734	NM_011292	ribosomal protein L9	1.156	53.87	0.69103	13601	M	1.048	30.75	0.57494	9227
Slc20a1	A_51_P408631	NM_015747	solute carrier family 20, member 1	1.156	77.44	0.82861	25929	P	1.04	30.75	0.49834	8566
1700034H14Rik	A_51_P395842	NM_025969	RIKEN cDNA 1700034H14 gene	1.155	77.44	0.81371	24956	P	1.046	28.13	0.4813	8322
Fancl	A_51_P127934	NM_025923	Fanconi anemia, complementation group	1.155	65.79	0.66519	16836	P	1.059	22.1	0.31065	6458
Mkrn1	A_52_P642207	NM_018810	makorin, ring finger protein, 1	1.155	49.93	0.54443	11173	P	-1.017	49.48	0.74205	10702
1300017J02Rik	A_51_P249274	NM_027918	RIKEN cDNA 1300017J02 gene	1.154	57.76	0.57971	12496	P	-1.11	9.71	0.10282	3167
Amotl1	A_51_P210708	XM_976419	angiomotin-like 1	1.154	75.14	0.79115	23514	P	-1.004	49.48	0.95631	12632
Ccs	A_51_P193536	NM_016892	copper chaperone for superoxide dismuta	1.154	69.29	0.69665	18208	P	-1.012	49.48	0.79418	11129
Eef1a2	A_51_P485862	NM_007906	eukaryotic translation elongation factor 1	1.154	75.14	0.67482	16457	M	1.068	16.2	0.17956	4566
Mapk8ip3	A_51_P264388	NM_013931	mitogen-activated protein kinase 8 intera	1.154	69.29	0.70795	18839	P	1.056	22.1	0.31851	6560
Mbtd1	A_51_P360963	NM_134012	mbt domain containing 1	1.154	57.76	0.57961	12470	P	1.053	25.31	0.35881	6992
Rac3	A_51_P455946	NM_133223	RAS-related C3 botulinum substrate 3	1.154	61.79	0.60024	13456	P	1.073	13.58	0.16545	4303
Trpc2	A_52_P34381	NM_011644	transient receptor potential cation chann	1.154	69.29	0.70666	17794	P	1.135	5.75	0.05313	1961

Abhd10	A_52_P259530	NM_172511	abhydrolase domain containing 10	1.153	69.29	0.68339	17571	P	1.127	9.71	0.17517	4483
Hpca	A_52_P287246	NM_010471	hippocalcin	1.153		0.81874	16353	A	1.031	33.49	0.51445	8716
Mrps15	A_51_P333099	NM_025544	mitochondrial ribosomal protein S15	1.153	69.29	0.69529	18162	P	1.009	42.43	0.88436	11910
Slc29a1	A_51_P289836	NM_022880	solute carrier family 29 (nucleoside transp	1.153	65.79	0.63878	15649	P	1.065	16.2	0.18159	4606
St3gal2	A_52_P408530	NM_178048	ST3 beta-galactoside alpha-2,3-sialyltrans	1.153	69.29	0.67154	17114	P	-1.12	4.63	0.05188	1905
2310047H23Rik	A_52_P465964	AK046071	RIKEN cDNA 2310047H23 gene	1.152		0.82089	16425	A	-1.094	36.07	0.44517	7963
3110003A17Rik	A_51_P214679	BC098509	RIKEN cDNA 3110003A17 gene	1.152	49.93	0.54934	11395	P	1.12	11.33	0.23607	5435
Ctps	A_51_P251357	NM_016748	cytidine 5'-triphosphate synthase	1.152	65.79	0.74041	15787	M	1.02	38.4	0.6554	9922
E130103I17Rik	A_52_P674196	NM_181316	Bardet-Biedl syndrome 9	1.152	72.2	0.71027	18958	P	1.079	11.33	0.12478	3597
Ganab	A_52_P594215	NM_008060	alpha glucosidase 2 alpha neutral subunit	1.152	65.79	0.65943	16557	P	1.149	4.63	0.03814	1442
Gnl3l	A_52_P101416	NM_198110	guanine nucleotide binding protein-like 3	1.152	57.76	0.64388	14935	P	-1.044	43.75	0.48306	8362
Mitf	A_52_P100140	NM_008601	microphthalmia-associated transcription	1.152	77.44	0.80242	24170	M	-1.274	2.04	0.09627	3020
Tyms	A_52_P292651	NM_021288	thymidylate synthase	1.152	69.29	0.70619	18716	P	-1.068	25.31	0.15043	4043
2410003K15Rik	A_52_P343853	AK031878	RIKEN cDNA 2410003K15 gene	1.151	77.44	0.72064	18446	P	1.047	30.75	0.60313	9475
6230416J20Rik	A_51_P288026	NM_173400	RIKEN cDNA 6230416J20 gene	1.151	65.79	0.65402	16313	P	-1.111	9.71	0.0911	2923
Gcsh	A_52_P390625	NM_026572	glycine cleavage system protein H (amino	1.151	72.2	0.74353	20757	P	1.179	3.46	0.02935	1178
Mbd2	A_51_P256337	AF072244	methyl-CpG binding domain protein 2	1.151	65.79	0.64638	15940	P	1.141	5.75	0.05867	2097
Mcm10	A_51_P212682	NM_027290	minichromosome maintenance deficient	1.151	65.79	0.69547	17297	M	-1.086	28.13	0.27701	6055
Tbc1d15	A_52_P120904	NM_025706	TBC1 domain family, member 15	1.151	65.79	0.63827	15632	P	1.064	22.1	0.37451	7217
Tfb2m	A_52_P69325	NM_008249	transcription factor B2, mitochondrial	1.151	69.29	0.69465	18145	P	1.082	13.58	0.16225	4261
Yme1l1	A_52_P575874	AK163649	YME1-like 1 (S. cerevisiae)	1.151	69.29	0.70134	18456	P	1.091	16.2	0.31396	6512
4932416N17Rik	A_52_P558609	NM_177562	RIKEN cDNA 4932416N17 gene	1.15	75.14	0.77632	22546	P	-1.241	0.66	0.01176	471
Acadm	A_51_P319879	NM_007382	acyl-Coenzyme A dehydrogenase, mediu	1.15	61.79	0.61519	14168	P	1.201	11.33	0.37093	7184
Dck	A_52_P602719	NM_007832	deoxycytidine kinase	1.15	79.26	0.86863	28804	P	1.801	0	0.00584	8
Efna5	A_51_P218009	NM_010109	ephrin A5	1.15	75.14	0.81815	23883	M	1.081	13.58	0.1951	4819
Fau	A_51_P178761	NM_007990	Finkel-Biskis-Reilly murine sarcoma virus (	1.15	61.79	0.73575	15664	M	1.03	36.07	0.65794	9954
Rbms1	A_52_P189038	AK161102	RNA binding motif, single stranded intera	1.15	69.29	0.68448	17649	P	1.006	42.43	0.94037	12483
Spock2	A_52_P221756	NM_052994	sparc/osteonectin, cwcv and kazal-like do	1.15	77.44	0.80292	24246	P	-1.01	49.48	0.93149	12401
Stam	A_51_P242663	NM_011484	signal transducing adaptor molecule (SH3	1.15	65.79	0.66728	16911	P	1.235	2.53	0.03237	1268
Tmem33	A_51_P400527	NM_028975	transmembrane protein 33	1.15	65.79	0.65628	16402	P	1.038	33.49	0.5827	9285
Trim27	A_52_P601446	AK049314	tripartite motif protein 27	1.15	79.26	0.86518	27008	M	1.044	28.13	0.4855	8390
Uqcr	A_51_P300143	NM_025650	ubiquinol-cytochrome c reductase (6.4kD	1.15	65.79	0.63553	15505	P	1.033	33.49	0.53762	8916
9430040K09Rik	A_52_P86165	AK020461	RIKEN cDNA 9430040K09 gene	1.149	65.79	0.64292	15848	P	-1.287	0.51	0.00619	122
Cd28	A_52_P162967	NM_007642	CD28 antigen	1.149		0.82443	16564	A	-1.147	16.2	0.28314	6120
Cdc91l1	A_52_P222709	NM_001004721	CDC91 cell division cycle 91-like 1 (S. cere	1.149	69.29	0.66861	16974	P	1.048	30.75	0.58282	9290
Crispld1	A_51_P249749	NM_031402	cysteine-rich secretory protein LCCL doma	1.149	81.02	0.9061	31516	P	1.019	38.4	0.70459	10351
Dhfr	A_51_P461444	L26316	dihydrofolate reductase	1.149	69.29	0.67216	17156	P	1.048	22.1	0.26972	5949
Fkbp4	A_51_P185175	NM_010219	FK506 binding protein 4	1.149	65.79	0.63295	15373	P	1.287	6.98	0.22527	5276
Kifap3	A_52_P363301	NM_010629	kinesin-associated protein 3	1.149	75.14	0.77995	22735	P	-1.057	40.63	0.36238	7053
Nipa2	A_51_P197354	NM_023647	non imprinted in Prader-Willi/Angelman s	1.149	69.29	0.6857	17691	P	-1.181	1.18	0.02042	876
Pea15	A_51_P411253	NM_011063	phosphoprotein enriched in astrocytes 15	1.149	75.14	0.7554	21430	P	1.056	28.13	0.49697	8541
Peg10	A_52_P377723	NM_001040611	paternally expressed 10	1.149	81.02	0.8984	30853	P	1.203	2.53	0.01679	725
St3gal3	A_52_P155692	NM_009176	ST3 beta-galactoside alpha-2,3-sialyltrans	1.149	65.79	0.64844	16032	P	-1.011	49.48	0.92414	12335
Aldh2	A_52_P13109	AK163452	aldehyde dehydrogenase 2, mitochondria	1.148	75.14	0.77957	22724	P	1.046	25.31	0.3105	6452
Gfra1	A_52_P311022	NM_010279	glial cell line derived neurotrophic factor	1.148	81.02	0.89461	30633	P	1.053	22.1	0.31972	6565
Grcc10	A_51_P320114	NM_013535	gene rich cluster, C10 gene	1.148	61.79	0.72733	15356	M	-1.093	16.2	0.13414	3751
Mrps26	A_52_P542958	NM_207207	mitochondrial ribosomal protein S26	1.148	77.44	0.83423	26448	P	-1.196	0.75	0.01294	563
Slc41a1	A_51_P393726	NM_173865	solute carrier family 41, member 1	1.148	72.2	0.74379	20761	P	1.037	30.75	0.52265	8776
Ank1	A_51_P269375	NM_031158	ankyrin 1, erythroid	1.147	83.36	0.90814	29696	M	-1.469	0.51	0.00584	51
Arl3	A_51_P107265	NM_019718	ADP-ribosylation factor-like 3	1.147	61.79	0.62413	14662	P	-1.056	36.07	0.2801	6095
Cct3	A_52_P685666	NM_009836	chaperonin subunit 3 (gamma)	1.147	79.26	0.84866	27658	P	-1.02	49.48	0.78083	11001
Cdgap	A_52_P400999	NM_020260	Cdc42 GTPase-activating protein	1.147	72.2	0.7216	19724	P	1.057	22.1	0.29373	6266
Cul2	A_52_P483544	NM_029402	cullin 2	1.147	61.79	0.61522	14174	P	1.004	42.43	0.94174	12498

D19Ertd386e	A_52_P486482	NM_177464	DNA segment, Chr 19, ERATO Doi 386, ex	1.147	61.79	0.62449	14672	P	1.077	16.2	0.25423	5727
Ehd2	A_52_P340595	NM_153068	EH-domain containing 2	1.147	49.93	0.80622	17525	M	1.054	28.13	0.53051	8837
Imp4	A_51_P322465	NM_178601	IMP4, U3 small nucleolar ribonucleoprote	1.147	57.76	0.58727	12882	P	1.022	38.4	0.68236	10156
Sypl	A_51_P129299	NM_013635	synaptophysin-like protein	1.147	69.29	0.66951	17002	P	1.174	6.98	0.1097	3258
Zkscan1	A_52_P322364	NM_133906	zinc finger with KRAB and SCAN domains	1.147	65.79	0.72069	18454	P	-1.067	25.31	0.16548	4305
2610005L07Rik	A_52_P7105	NM_001033456	RIKEN cDNA 6820431F20 gene	1.146	49.93	0.56391	11837	P	1.093	13.58	0.19606	4838
2700085E05Rik	A_51_P154196	NM_026029	glyoxalase domain containing 4	1.146	75.14	0.77055	22221	P	-1.052	40.63	0.36387	7070
Adcy2	A_51_P337523	NM_153534	adenylate cyclase 2	1.146	82.34	0.90089	29085	M	1.081	11.33	0.12364	3570
Anp32b	A_51_P388432	NM_130889	acidic nuclear phosphoprotein 32 family,	1.146	65.79	0.64388	15893	P	1.09	22.1	0.49451	8496
Ap3b2	A_51_P486681	NM_021492	adaptor-related protein complex 3, beta	1.146	75.14	0.76834	22137	P	1.148	9.71	0.21777	5166
Bcl7c	A_52_P368262	AK038789	B-cell CLL/lymphoma 7C	1.146	75.14	0.76552	21942	P	1	42.43	0.99729	13033
Lrrn3	A_52_P146719	NM_010733	leucine rich repeat protein 3, neuronal	1.146	77.44	0.82767	25869	P	1.079	11.33	0.11878	3458
Pld3	A_52_P614336	NM_011116	phospholipase D family, member 3	1.146	65.79	0.66067	16594	P	1.001	42.43	0.98171	12864
Ppia	A_52_P265542	NM_008907	peptidylprolyl isomerase A	1.146	72.2	0.79875	17951	M	1.059	28.13	0.52026	8755
Rps13	A_51_P327469	NM_026533	ribosomal protein S13	1.146	53.87	0.71537	14599	M	1.123	9.71	0.13386	3738
6230427J02Rik	A_51_P248857	NM_026597	RIKEN cDNA 6230427J02 gene	1.145	75.14	0.71948	17344	M	1.005	42.43	0.94592	12551
Anks1	A_51_P141932	NM_181413	ankyrin repeat and SAM domain containi	1.145	77.44	0.82821	25900	P	-1.231	0.75	0.01444	608
Eif4a1	A_51_P113527	NM_144958	eukaryotic translation initiation factor 4A	1.145	77.44	0.83401	19634	M	1.022	40.63	0.82285	11394
Epor	A_51_P435339	NM_010149	erythropoietin receptor	1.145	75.14	0.68383	16789	M	1.143	5.75	0.05435	1985
Fkbp3	A_52_P531175	NM_013902	FK506 binding protein 3	1.145	61.79	0.62794	14847	P	-1.125	5.75	0.0694	2383
Gpr135	A_52_P275678	NM_181752	G protein-coupled receptor 135	1.145	72.2	0.75046	21097	P	1.072	16.2	0.19727	4855
Hoxb1	A_51_P485014	NM_008266	homeo box B1	1.145		0.93951	13728	A	1.056	19.02	0.24127	5517
Hspb7	A_51_P346445	NM_013868	heat shock protein family, member 7 (car	1.145	49.93	0.58738	12289	M	1.148	5.75	0.07034	2404
Irf6	A_52_P47598	AK087631	interferon regulatory factor 6	1.145	72.2	0.72951	20208	M	1.067	13.58	0.16181	4250
Mtch2	A_51_P135394	NM_019758	mitochondrial carrier homolog 2 (C. elega	1.145	75.14	0.77781	22647	P	1.127	9.71	0.13456	3754
Nedd1	A_51_P315634	NM_008682	neural precursor cell expressed, develop	1.145	72.2	0.74301	20717	P	-1.052	43.75	0.51006	8674
Phr1	A_51_P498670	AK079289	pam, highwire, rpm 1	1.145	65.79	0.65228	16181	P	1.054	28.13	0.4907	8449
Recc1	A_51_P406638	NM_011258	replication factor C (activator 1) 1	1.145	57.76	0.59026	12971	P	-1.046	40.63	0.31668	6545
Sdf4	A_51_P213706	NM_011341	stromal cell derived factor 4	1.145	75.14	0.79	23458	P	-1.009	49.48	0.9157	12223
Trim2	A_51_P196596	NM_030706	tripartite motif protein 2	1.145	49.93	0.56391	11835	P	1.124	6.98	0.05052	1867
Ywhab	A_52_P112958	NM_018753	tyrosine 3-monooxygenase/tryptophan 5	1.145	57.76	0.59453	13223	P	1.237	1.32	0.00985	369
0910001L09Rik	A_52_P316405	ENSMUST00000062067	RIKEN cDNA 0910001L09 gene	1.144	72.2	0.72707	20057	P	1.058	19.02	0.24401	5565
2010107E04Rik	A_51_P128287	NM_027360	RIKEN cDNA 2010107E04 gene	1.144	61.79	0.73835	15735	M	1.12	13.58	0.33379	6724
Bcs1l	A_52_P104782	NM_025784	BCS1-like (yeast)	1.144	69.29	0.70386	18624	P	1.065	16.2	0.18469	4648
Cul5	A_52_P268378	NM_027807	cullin 5	1.144	65.79	0.66247	16688	P	-1.065	40.63	0.43397	7888
F8a	A_51_P459679	NM_007978	factor 8-associated gene A	1.144	72.2	0.73591	20487	P	1.064	16.2	0.20602	4985
Fen1	A_52_P502684	NM_007999	flap structure specific endonuclease 1	1.144	72.2	0.72464	19984	P	-1.15	4.63	0.07528	2540
Fmo5	A_52_P1147453	AK137645	flavin containing monooxygenase 5	1.144		0.88794	16392	A	1.106	13.58	0.21864	5181
Git2	A_52_P467588	NM_019834	G protein-coupled receptor kinase-intera	1.144	77.44	0.81227	24835	P	-1.07	40.63	0.44425	7957
Hbb-y	A_51_P350058	NM_008221	hemoglobin Y, beta-like embryonic chain	1.144	82.34	0.85442	26217	M	1.053	19.02	0.24252	5533
Kpna2	A_51_P474643	NM_010655	karyopherin (importin) alpha 2	1.144	72.2	0.73067	20300	P	-1.084	25.31	0.18959	4715
Napg	A_51_P170008	NM_028017	N-ethylmaleimide sensitive fusion protei	1.144	53.87	0.57953	12451	P	1.132	8.32	0.08963	2882
Pbef1	A_51_P387235	NM_021524	pre-B-cell colony-enhancing factor 1	1.144	75.14	0.78665	23176	P	-1.017	49.48	0.92783	12370
Psmb1	A_51_P367162	NM_011185	proteasome (prosome, macropain) subun	1.144	72.2	0.73717	20528	P	1.022	38.4	0.7132	10430
Rpa2	A_51_P234308	NM_011284	replication protein A2	1.144	69.29	0.69975	18367	P	1.12	8.32	0.07728	2582
Rps12	A_51_P349435	NM_011295	ribosomal protein S12	1.144	82.34	0.92744	23954	M	1.03	40.63	0.82212	11381
Tcf12	A_52_P20048	M97635	transcription factor 12	1.144	61.79	0.62638	14747	P	-1.134	3.01	0.03757	1432
Tpi1	A_51_P433824	NM_009415	triosephosphate isomerase 1	1.144	69.29	0.67248	17182	P	1.027	36.07	0.67763	10113
Trappc2	A_51_P102631	NM_025432	trafficking protein particle complex 2	1.144	72.2	0.71976	19499	P	1.03	38.4	0.75753	10847
Fbxl5	A_52_P39533	NM_178729	F-box and leucine-rich repeat protein 5	1.143	79.26	0.8375	26894	P	1.027	38.4	0.77854	10972
Matr3	A_51_P156348	NM_010771	matrin 3	1.143	69.29	0.70255	18543	P	1.12	13.58	0.31369	6502
Mthfr	A_52_P413947	NM_010840	5,10-methylenetetrahydrofolate reductas	1.143	65.79	0.64819	16014	P	1.056	22.1	0.29093	6218
Pigx	A_51_P399217	NM_024464	phosphatidylinositol glycan anchor biosy	1.143	75.14	0.77512	22508	P	-1.126	5.75	0.07277	2470

Pkp2	A_51_P225427	NM_026163	plakophilin 2	1.143	57.76	0.60291	13584	P	-1.146	1.62	0.02493	1030
Prkar1a	A_51_P294095	NM_021880	protein kinase, cAMP dependent regulatc	1.143	77.44	0.84088	20113	M	1.546	0.24	0.01141	457
Rps23	A_51_P376165	NM_024175	ribosomal protein S23	1.143	79.26	0.8594	20786	M	1.126	9.71	0.14327	3907
4933437K13Rik	A_51_P328150	NM_028964	RIKEN cDNA 4933437K13 gene	1.142	69.29	0.70407	16747	M	1.025	33.49	0.55241	9049
6430527G18Rik	A_51_P244577	NM_145836	RIKEN cDNA 6430527G18 gene	1.142	72.2	0.74725	20952	P	1.339	1.62	0.03681	1406
6820401H01Rik	A_52_P641414	AK039998	RIKEN cDNA 6820401H01 gene	1.142	61.79	0.62003	14457	P	-1.135	8.32	0.11939	3480
Calm3	A_51_P384499	NM_007590	calmodulin 3	1.142	65.79	0.64092	15722	P	1.149	6.98	0.0993	3092
Hand2	A_51_P147850	NM_010402	heart and neural crest derivatives express	1.142	79.26	0.85062	27757	P	1.238	2.53	0.0291	1173
Kptn	A_52_P308477	NM_133727	kaptin	1.142	75.14	0.78499	23077	P	-1.022	48.39	0.6878	10219
Pex16	A_51_P395164	NM_145122	peroxisome biogenesis factor 16	1.142	75.14	0.79222	23609	P	-1.261	0.51	0.00901	329
Sulf2	A_51_P133229	NM_028072	sulfatase 2	1.142	53.87	0.57553	12268	P	1.045	25.31	0.35396	6937
Tex9	A_52_P112864	NM_009359	testis expressed gene 9	1.142	81.02	0.88598	30022	P	1.019	40.63	0.72866	10560
Tfg	A_52_P510336	AK039139	Trk-fused gene	1.142	72.2	0.79306	22265	M	1.099	9.71	0.0808	2681
Wdr45l	A_52_P680436	NM_025793	Wdr45 like	1.142	75.14	0.77322	22420	P	1.029	38.4	0.73014	10571
1110006O17Rik	A_52_P1026777	NM_001033141	RIKEN cDNA 1110006O17 gene	1.141	79.26	0.85143	27839	P	1.102	8.32	0.06486	2277
Commd4	A_51_P353592	NM_025417	COMM domain containing 4	1.141	72.2	0.71034	18972	P	-1.021	47.92	0.62272	9643
Cox5b	A_51_P141123	NM_009942	cytochrome c oxidase, subunit Vb	1.141	53.87	0.72238	14984	M	-1.113	5.75	0.05912	2113
Gng11	A_51_P136355	NM_025331	guanine nucleotide binding protein (G prc	1.141	79.26	0.87021	28907	P	1.092	25.31	0.56159	9127
Gpkow	A_51_P314584	NM_173747	G patch domain and KOW motifs	1.141	57.76	0.59813	13363	P	1.009	42.43	0.87131	11768
Rps26	A_51_P302675	NM_013765	ribosomal protein S26	1.141	72.2	0.78777	17468	M	-1.022	47.92	0.63614	9774
2700078E11Rik	A_52_P345618	NM_030197	RIKEN cDNA 2700078E11 gene	1.14	65.79	0.63878	15648	P	1.146	11.33	0.25544	5736
Apoc2	A_51_P334979	NM_009695	apolipoprotein C-II	1.14	84.22	0.96504	36991	P	-1.097	13.58	0.10716	3223
Emilin3	A_52_P45616	NM_182840	elastin microfibril interfacer 3	1.14		0.88566	16329	A	-1.202	1.1	0.01553	664
Gphn	A_52_P551594	NM_172952	gephyrin	1.14	75.14	0.75532	21421	P	-1.321	0.51	0.00584	84
Gtf2e1	A_51_P236324	NM_028812	general transcription factor II E, polypepti	1.14	69.29	0.6933	18071	P	1.09	19.02	0.35004	6875
Pspc1	A_51_P330133	NM_025682	paraspeckle protein 1	1.14	72.2	0.73378	20409	P	1.092	11.33	0.11265	3327
Tead4	A_51_P179041	D87966	TEA domain family member 4	1.14	79.26	0.83591	26816	M	1.088	11.33	0.11876	3457
Trim47	A_51_P437176	NM_172570	tripartite motif protein 47	1.14	82.34	0.9118	32141	P	1.009	42.43	0.8792	11853
Vps24	A_52_P493394	NM_025783	vacuolar protein sorting 24 (yeast)	1.14	79.26	0.83789	26946	P	-1.073	28.13	0.21645	5138
2010003J03Rik	A_51_P474688	NM_027236	RIKEN cDNA 2010003J03 gene	1.139	72.2	0.72548	20016	P	-1.006	49.48	0.92728	12368
Cic	A_52_P69351	BC035474	capicua homolog (Drosophila)	1.139	69.29	0.69991	18381	P	-1.075	30.75	0.2565	5756
Dtnbp1	A_51_P234288	AK030248		1.139		0.88336	16259	A	1.038	25.31	0.36206	7047
Ruvbl1	A_51_P465772	NM_019685	RuvB-like protein 1	1.139	65.79	0.63919	15660	P	1.001	42.43	0.99328	13007
Srpk2	A_52_P587924	NM_009274	serine/arginine-rich protein specific kinas	1.139	61.79	0.61819	14295	P	1.001	42.43	0.9918	12993
Tfdp2	A_52_P676469	NM_178667	transcription factor Dp 2	1.139	75.14	0.76244	21792	P	1.245	3.46	0.05809	2087
Txndc1	A_52_P499082	NM_028339	thioredoxin domain containing 1	1.139	77.44	0.81163	24808	P	1.138	11.33	0.30334	6358
1810029B16Rik	A_51_P306839	NM_025465	RIKEN cDNA 1810029B16 gene	1.138	81.02	0.90199	31185	P	1.025	36.07	0.63764	9786
6720458F09Rik	A_51_P325152	NM_177374	RIKEN cDNA 6720458F09 gene	1.138	77.44	0.80778	24565	P	1.001	42.43	0.98072	12852
Aplp2	A_52_P559770	NM_009691	amyloid beta (A4) precursor-like protein 2	1.138	69.29	0.67959	17429	P	1.632	3.82	0.20899	5031
BC016423	A_52_P544540	AK220437	cDNA sequence BC016423	1.138	57.76	0.60436	13646	P	-1.087	11.33	0.08637	2809
Bmp2k	A_51_P337944	NM_080708	BMP2 inducible kinase	1.138	61.79	0.61137	14014	P	1.031	30.75	0.46737	8179
Cox6b1	A_51_P448032	NM_025628	cytochrome c oxidase, subunit VIb polype	1.138	72.2	0.80216	18062	M	-1.013	49.48	0.87035	11761
Cst3	A_51_P332201	NM_009976	cystatin C	1.138	81.02	0.89905	22422	M	1.188	6.98	0.15788	4177
Npy	A_51_P454873	NM_023456	neuropeptide Y	1.138	82.34	0.93529	34208	P	-1.066	44.4	0.65421	9910
Sfrs5	A_52_P50090	NM_001079695	splicing factor, arginine/serine-rich 5 (SRp	1.138	81.02	0.894	22186	M	1.166	16.2	0.46231	8134
Slc4a4	A_51_P273800	NM_018760	solute carrier family 4 (anion exchanger),	1.138	72.2	0.73663	20506	P	1.161	9.71	0.2416	5525
2810452K22Rik	A_51_P204793	NM_026048	RIKEN cDNA 2810452K22 gene	1.137	61.79	0.61261	14101	P	1.055	22.1	0.3303	6671
Cab39l	A_52_P264905	NM_026908	calcium binding protein 39-like	1.137	61.79	0.62488	14678	P	1.193	3.01	0.02183	920
Cuedc2	A_51_P403334	NM_024192	CUE domain containing 2	1.137	75.14	0.77768	22612	P	1.118	8.32	0.08176	2697
Gtf2a1	A_52_P274315	NM_175335	general transcription factor II A, 1	1.137	77.44	0.82602	25749	P	-1.056	30.75	0.21224	5079
Hint2	A_51_P278887	NM_026871	histidine triad nucleotide binding protein	1.137	57.76	0.60961	13926	P	-1.141	6.98	0.09869	3076
Ipo7	A_52_P239403	NM_181517	importin 7	1.137	65.79	0.6419	15784	P	1.049	36.07	0.78783	11071
Itpa	A_52_P455404	NM_025922	inosine triphosphatase (nucleoside triphc	1.137	61.79	0.6297	15046	P	1.365	0.75	0.0122	491

Tkt	A_51_P394515	NM_009388	transketolase	1.137	75.14	0.79424	23766	P	1.032	30.75	0.46051	8106
Tmed7	A_51_P269997	XM_128959	transmembrane emp24 protein transport	1.137	61.79	0.63528	15489	P	1.119	8.32	0.1018	3143
Utp14a	A_52_P543040	NM_028276	UTP14, U3 small nucleolar ribonucleoprot	1.137	77.44	0.82824	25912	P	1.04	28.13	0.36826	7138
2210418O10Rik	A_52_P195535	BC048160	RIKEN cDNA 2210418O10 gene	1.136	72.2	0.71537	19243	P	1.066	16.2	0.18469	4649
3110003A22Rik	A_52_P588022	NM_026534	RIKEN cDNA 3110003A22 gene	1.136	65.79	0.64227	15818	P	-1.202	1.32	0.02967	1183
6330577E15Rik	A_51_P437188	NM_026377	RIKEN cDNA 6330577E15 gene	1.136	61.79	0.62279	14570	P	1.069	16.2	0.22657	5299
Ankrd17	A_52_P499395	AK031350	ankyrin repeat domain 17	1.136	75.14	0.7596	21605	M	1.022	38.4	0.71595	10452
C230008H04Rik	A_52_P21400	NM_176970	mitogen activated protein kinase 10	1.136	75.14	0.78804	23267	P	1.07	19.02	0.34362	6804
Chchd1	A_52_P48670	NM_025366	coiled-coil-helix-coiled-coil-helix domain	1.136	72.2	0.74403	20782	P	1.067	28.13	0.57905	9253
Eif3s6	A_52_P375037	NM_008388	eukaryotic translation initiation factor 3,	1.136	79.26	0.8473	27574	P	1.085	22.1	0.48203	8340
Fnbp1	A_52_P105840	NM_001038700	formin binding protein 1	1.136	75.14	0.77214	22353	P	1.087	13.58	0.16893	4368
Lamp1	A_51_P150648	NM_010684	lysosomal-associated membrane protein	1.136	77.44	0.85187	20572	M	1.146	5.75	0.06615	2326
Ppp1r11	A_51_P105320	NM_029632	protein phosphatase 1, regulatory (inhibit	1.136	72.2	0.73708	20523	P	1.113	16.2	0.34969	6869
Rdh10	A_52_P59318	NM_133832	retinol dehydrogenase 10 (all-trans)	1.136	65.79	0.66554	16862	P	1.153	4.63	0.03864	1461
Sfrs1	A_52_P525674	NM_173374	splicing factor, arginine/serine-rich 1 (ASF	1.136	82.34	0.91249	32265	P	1.1	13.58	0.20046	4910
Slc25a5	A_51_P475446	NM_007451	solute carrier family 25 (mitochondrial ca	1.136	77.44	0.84158	20155	M	1.134	8.32	0.1004	3107
Spbc24	A_51_P214209	NM_026282	SPC24, NDC80 kinetochore complex comp	1.136	79.26	0.84248	27240	P	1.079	16.2	0.20501	4967
Tcfl5	A_52_P299713	NM_178254	transcription factor-like 5 (basic helix-loop	1.136		0.94386	13874	A	1.027	36.07	0.60762	9505
Znrf2	A_52_P556586	NM_199143	zinc and ring finger 2	1.136	69.29	0.69144	17994	P	-1.008	49.48	0.9219	12282
Apon	A_51_P100625	NM_133996	apolipoprotein N	1.135	69.29	0.85117	23987	M	-1.015	49.48	0.73807	10665
Ches1	A_51_P172344	NM_183186	checkpoint suppressor 1	1.135	72.2	0.72464	20000	P	1.206	3.82	0.06967	2389
Cybb	A_52_P444628	NM_007807	cytochrome b-245, beta polypeptide	1.135	75.14	0.77894	22700	P	1.052	22.1	0.32686	6637
Naca	A_51_P310030	NM_013608	nascent polypeptide-associated complex	1.135	72.2	0.78992	17557	M	-1.071	40.63	0.46523	8161
Slc12a2	A_51_P275527	NM_009194	solute carrier family 12, member 2	1.135	57.76	0.60428	13640	P	1.183	3.46	0.03242	1273
4933407H18Rik	A_52_P217329	AK016722	RIKEN cDNA 4933407H18 gene	1.134	75.14	0.75532	21420	P	1.042	36.07	0.78177	11008
Akr1a4	A_51_P327295	NM_021473	aldo-keto reductase family 1, member A4	1.134	72.2	0.71367	19142	P	1.065	19.02	0.27335	6002
Fkbp14	A_52_P396239	NM_153573	FK506 binding protein 14	1.134	75.14	0.76647	22002	P	1.162	5.75	0.0781	2608
Gbas	A_51_P228276	NM_008095	glioblastoma amplified sequence	1.134	77.44	0.83448	19679	M	1.24	3.46	0.06396	2255
Rps17	A_51_P482473	NM_009092	ribosomal protein S17	1.134	72.2	0.80671	18265	M	1.033	36.07	0.74306	10727
Snrpd1	A_51_P193254	NM_009226	small nuclear ribonucleoprotein D1	1.134	75.14	0.78876	23368	P	1.035	33.49	0.61301	9549
Sox18	A_51_P472274	NM_009236	SRY-box containing gene 18	1.134	61.79	0.62081	14499	P	1.013	42.43	0.79549	11142
Tdrd3	A_52_P124440	AK078326		1.134	57.76	0.6079	13837	P	-1.18	1.32	0.02092	894
Gart	A_51_P360773	AK028982	phosphoribosylglycinamide formyltransfe	1.133		0.89165	16522	A	1.073	11.33	0.12151	3532
Gem	A_51_P318192	NM_010276	GTP binding protein (gene overexpressed	1.133	83.36	0.93874	34481	P	1.216	5.75	0.11384	3357
Rplp1	A_51_P219603	NM_018853	ribosomal protein, large, P1	1.133	65.79	0.76648	16720	M	1.011	42.43	0.92356	12330
Rps14	A_51_P361638	NM_020600	ribosomal protein S14	1.133	77.44	0.85039	20513	M	1.054	28.13	0.55846	9088
Tcea1	A_52_P493079	M18209	transcription elongation factor A (SII) 1	1.133	65.79	0.6532	16278	P	1.041	36.07	0.73795	10660
Uqcrh	A_51_P431852	NM_025641	ubiquinol-cytochrome c reductase hinge	1.133	57.76	0.74533	15930	M	1.004	42.43	0.9611	12677
Zcchc14	A_51_P496057	NM_080855	zinc finger, CCHC domain containing 14	1.133	61.79	0.63395	15394	P	-1.081	25.31	0.21716	5157
Zfyve20	A_52_P293169	AK053285	zinc finger, FYVE domain containing 20	1.133	81.02	0.88647	30053	P	1.057	22.1	0.36195	7043
1810058I24Rik	A_52_P477649	AK158055	RIKEN cDNA 1810058I24 gene	1.132	72.2	0.72438	19970	P	1.068	22.1	0.41258	7640
2810410L24Rik	A_52_P74524	NM_175239	RIKEN cDNA 2810410L24 gene	1.132	77.44	0.83277	26310	P	1.032	33.49	0.60971	9522
Fbxl14	A_52_P608542	NM_133940	F-box and leucine-rich repeat protein 14	1.132	69.29	0.69774	18262	P	1.164	3.82	0.03483	1334
Myst1	A_51_P103757	NM_026370	MYST histone acetyltransferase 1	1.132	77.44	0.8176	25256	P	-1.063	43.15	0.53576	8894
Nomo1	A_51_P105520	NM_153057	nodal modulator 1	1.132	81.02	0.80341	22872	P	-1.003	49.48	0.96863	12730
Ppef2	A_52_P413394	NM_011148	protein phosphatase, EF hand calcium-bir	1.132	82.34	0.91093	32031	P	-1.001	49.48	0.97561	12798
Ppig	A_51_P471798	AK045812	peptidyl-prolyl isomerase G (cyclophilin G	1.132	61.79	0.62385	14645	P	1.158	9.71	0.21329	5088
Taok1	A_51_P350806	BC019960	TAO kinase 1	1.132	65.79	0.66542	16857	P	1.144	3.82	0.03237	1271
Zc3hc1	A_51_P174005	NM_172735	zinc finger, C3HC type 1	1.132	72.2	0.74437	20799	P	-1.053	38.4	0.30021	6321
AI597468	A_51_P344758	ENSMUST00000075658	expressed sequence AI597468	1.131	72.2	0.74437	20790	P	1.168	5.75	0.06884	2372
Decr1	A_51_P208555	NM_026172	2,4-dienoyl CoA reductase 1, mitochondri	1.131	77.44	0.81247	24850	P	-1.02	49.39	0.73903	10682
Fech	A_51_P266763	NM_007998	ferrochelatase	1.131	69.29	0.69196	18031	P	1.131	4.63	0.0354	1372
Fignl1	A_52_P148553	NM_021891	fidgetin-like 1	1.131	79.26	0.83371	26380	P	-1.049	42.43	0.40356	7549

Map4k4	A_52_P584302	NM_008696	mitogen-activated protein kinase kinase k	1.131	75.14	0.7912	23537	P	1.013	42.43	0.7967	11148
Ndufv2	A_51_P261470	NM_028388	NADH dehydrogenase (ubiquinone) flavop	1.131	72.2	0.71369	19163	P	-1.017	49.48	0.74228	10705
Nkd2	A_51_P345549	NM_028186	naked cuticle 2 homolog (Drosophila)	1.131	69.29	0.70278	17597	M	1.042	30.75	0.48356	8367
Poldip2	A_52_P163928	NM_026389	polymerase (DNA-directed), delta interact	1.131	69.29	0.69909	18332	P	1.118	6.98	0.05486	2001
Rab11a	A_52_P444162	NM_017382	RAB11a, member RAS oncogene family	1.131	69.29	0.67859	17382	P	1.022	38.4	0.68458	10187
2310046O06Rik	A_52_P475062	BY709465	RIKEN cDNA 2310046O06 gene	1.13	75.14	0.77487	22496	P	1.086	16.2	0.2268	5308
Arpp19	A_51_P134413	NM_021548	cAMP-regulated phosphoprotein 19	1.13	72.2	0.72464	20002	P	1.075	13.58	0.15788	4178
Ddx50	A_52_P242888	BC071265	DEAD (Asp-Glu-Ala-Asp) box polypeptide	1.13	75.14	0.76328	21851	P	1.074	19.02	0.33195	6702
Dtx3	A_52_P495453	NM_030714	deltex 3 homolog (Drosophila)	1.13	79.26	0.8672	28671	P	-1.16	3.01	0.05213	1923
Eif3s12	A_51_P341025	NM_028659	eukaryotic translation initiation factor 3, s	1.13	79.26	0.84604	27488	P	-1.036	45.68	0.55036	9027
H2-Ke2	A_51_P368855	NM_010385	H2-K region expressed gene 2	1.13	75.14	0.76035	21650	P	-1.132	4.63	0.05435	1986
Rdbp	A_52_P110270	NM_001045864	RD RNA-binding protein	1.13	77.44	0.81533	25111	P	1.117	6.98	0.05285	1943
Rpl12	A_51_P356023	NM_009076	ribosomal protein L12	1.13	75.14	0.81447	18652	M	1.117	11.33	0.20651	4997
Rpl3	A_51_P519024	NM_013762	ribosomal protein L3	1.13	75.14	0.89431	24498	M	-1.095	22.1	0.1945	4809
Rps2	A_52_P277592	NM_008503	ribosomal protein S2	1.13	77.44	0.83461	19788	M	1.123	11.33	0.18052	4582
Scmh1	A_52_P499851	AK083889	sex comb on midleg homolog 1	1.13		0.87051	18341	A	1.058	25.31	0.46912	8197
Serpine1	A_52_P207173	AK040662	serine (or cysteine) peptidase inhibitor, cl	1.13	79.26	0.86697	28660	P	-1.082	22.1	0.15194	4065
Setdb1	A_52_P31717	AF546078	SET domain, bifurcated 1	1.13	49.93	0.74904	17001	M	-1.016	49.48	0.7639	10884
Trappc3	A_51_P432930	NM_013718	trafficking protein particle complex 3	1.13	77.44	0.80108	24131	P	1.054	22.1	0.2702	5961
Whrn	A_51_P303620	NM_001008791	whirlin	1.13	79.26	0.88759	28205	P	-1.012	49.48	0.85722	11649
Zfp62	A_52_P336133	ENSMUST00000061757	zinc finger protein 62	1.13	72.2	0.72092	19636	P	-1.027	46.85	0.62077	9630
Commd3	A_51_P413785	NM_147778	COMM domain containing 3	1.129	72.2	0.72376	19955	P	-1.041	45.05	0.58282	9289
Cxcl12	A_52_P685021	NM_021704	chemokine (C-X-C motif) ligand 12	1.129	65.79	0.65228	16189	P	1.162	13.58	0.39044	7396
D15Wsu75e	A_51_P187612	NM_134095	DNA segment, Chr 15, Wayne State Unive	1.129	77.44	0.81068	24742	P	1.01	42.43	0.86875	11749
Denr	A_51_P499776	NM_026603	density-regulated protein	1.129	65.79	0.65947	16560	P	1.032	33.49	0.61518	9580
Dpm1	A_51_P397834	NM_010072	dolichol-phosphate (beta-D) mannosyltra	1.129	77.44	0.82666	25793	P	1.048	25.31	0.36194	7040
Mylk	A_51_P272407	AK044527	myosin, light polypeptide kinase	1.129		0.94822	13983	A	1.006	42.43	0.96091	12673
Phgdhl1	A_51_P353856	NM_026861	phosphoglycerate dehydrogenase like 1	1.129	65.79	0.65628	16408	P	1.029	33.49	0.51338	8703
Tomm20	A_52_P310930	NM_024214	translocase of outer mitochondrial memb	1.129	69.29	0.70294	18561	P	1.132	6.98	0.0637	2250
Tsnax	A_51_P236397	NM_016909	translin-associated factor X	1.129	69.29	0.68225	17519	P	1.176	3.01	0.02356	986
Acsl5	A_52_P593037	NM_027976	acyl-CoA synthetase long-chain family me	1.128	81.02	0.8816	29745	P	-1.044	45.05	0.59219	9354
Atp5g3	A_51_P294849	NM_175015	ATP synthase, H+ transporting, mitochond	1.128	69.29	0.79214	17671	M	1.202	3.01	0.02522	1041
Bysl	A_51_P447946	NM_016859	bystin-like	1.128	72.2	0.71658	19312	P	1.14	4.63	0.04205	1587
E4f1	A_51_P463348	NM_007893	E4F transcription factor 1	1.128	81.02	0.87678	29370	P	-1.015	49.48	0.80843	11269
Fyttd1	A_52_P651078	NM_027226	forty-two-three domain containing 1	1.128	65.79	0.668	16941	P	1.115	6.98	0.05545	2020
Ostf1	A_51_P277345	NM_017375	osteoclast stimulating factor 1	1.128	72.2	0.72625	20035	P	1.182	3.01	0.0254	1054
Resp18	A_51_P178083	NM_009049	regulated endocrine-specific protein 18	1.128	77.44	0.83938	20073	M	-1.048	43.75	0.47441	8252
Rsl1d1	A_52_P362277	NM_025546	ribosomal L1 domain containing 1	1.128	79.26	0.8484	27635	P	-1.075	33.49	0.31175	6477
Ttf2	A_52_P634157	AK078759	transcription termination factor, RNA poly	1.128	82.34	0.8952	28701	M	1.005	42.43	0.93445	12426
1110003E01Rik	A_52_P451123	AK044403	RIKEN cDNA 1110003E01 gene	1.127	57.76	0.62828	14901	P	1.197	2.04	0.01285	557
2410001C21Rik	A_52_P264368	NM_025542	RIKEN cDNA 2410001C21 gene	1.127	69.29	0.68798	17816	P	1.008	42.43	0.89086	11976
Acat2	A_51_P139748	NM_009338	acetyl-Coenzyme A acetyltransferase 2	1.127	61.79	0.78559	20592	P	-1.006	49.48	0.96755	12725
Dmap1	A_52_P472120	NM_023178	DNA methyltransferase 1-associated prot	1.127	77.44	0.79725	23957	P	1.028	38.4	0.76771	10920
Hoxa13	A_52_P71789	NM_008264	homeo box A13	1.127		0.80462	17915	A	1.073	16.2	0.17373	4441
Igh-VJ558	A_51_P270661	AF029748	immunoglobulin heavy chain (J558 family	1.127	65.79	0.66804	16946	P	-1.11	11.33	0.11709	3420
Mfi2	A_51_P324351	NM_013900	antigen p97 (melanoma associated) ident	1.127	75.14	0.78723	23201	M	1.007	42.43	0.89842	12050
Rpl31	A_51_P452820	NM_053257	ribosomal protein L31	1.127	65.79	0.65748	16459	P	1.024	40.63	0.8064	11246
Rps18	A_51_P287677	NM_011296	ribosomal protein S18	1.127	75.14	0.82666	19206	M	-1.17	3.82	0.08759	2829
Sec23a	A_52_P72839	NM_009147	SEC23A (S. cerevisiae)	1.127	69.29	0.69665	18233	P	-1.039	43.75	0.65811	9208
Wdr7	A_52_P323305	AK154451	WD repeat domain 7	1.127	61.79	0.63669	15567	P	-1.106	8.32	0.07263	2457
Zadh2	A_51_P137388	NM_146090	zinc binding alcohol dehydrogenase, dom	1.127	77.44	0.80959	24676	P	-1.188	1.32	0.0235	983
Agpat1	A_51_P322612	NM_018862	1-acylglycerol-3-phosphate O-acyltransfer	1.126	81.02	0.90199	31182	P	-1.064	30.75	0.19377	4800
Clec11a	A_51_P359800	NM_009131	C-type lectin domain family 11, member a	1.126	77.44	0.81904	25363	P	-1.008	49.48	0.90281	12122

Cnot3	A_52_P487127	NM_146176	CCR4-NOT transcription complex, subunit	1.126	77.44	0.81447	25029	P	1.193	1.62	0.01227	498
Cpt1a	A_52_P219753	NM_013495	carnitine palmitoyltransferase 1a, liver	1.126	75.14	0.7874	23215	P	1.16	8.32	0.15044	4045
Cyp4a10	A_52_P6588	NM_010011	cytochrome P450, family 4, subfamily a, p	1.126	61.79	0.63542	15491	M	-1.022	48.39	0.6778	10117
Hrg	A_51_P506309	NM_053176	histidine-rich glycoprotein	1.126	61.79	0.65262	15539	M	1.077	13.58	0.12855	3666
Mtpn	A_52_P385139	NM_008098	myotrophin	1.126	69.29	0.69758	18252	P	1.23	1.32	0.00977	360
Rad51l1	A_52_P81571	NM_009014	RAD51-like 1 (S. cerevisiae)	1.126	77.44	0.81753	23839	M	-1.301	0.51	0.00627	161
Rpl23	A_52_P651894	NM_022891	ribosomal protein L23	1.126	65.79	0.77458	17022	M	1.035	36.07	0.68236	10158
Ssr1	A_52_P274028	AK078039	signal sequence receptor, alpha	1.126	72.2	0.72464	19979	P	1.146	8.32	0.15514	4138
Angptl3	A_52_P209884	AK040679	angiopoietin-like 3	1.125	69.29	0.69665	18209	P	1.003	42.43	0.96018	12659
Bat2d	A_52_P566337	AK021383	BAT2 domain containing 1	1.125	75.14	0.7818	22850	P	-1.127	13.58	0.18566	4662
Brca2	A_51_P451106	NM_009765	breast cancer 2	1.125	61.79	0.63801	15612	P	1.099	11.33	0.15194	4064
Espl1	A_52_P658437	NM_001014976	extra spindle poles-like 1 (S. cerevisiae)	1.125		0.70666	16842	A	-1.158	3.46	0.05415	1980
Fut11	A_52_P641341	NM_028428	fucosyltransferase 11	1.125	75.14	0.76244	21770	P	1.042	28.13	0.37397	7215
Gabpa	A_52_P126238	NM_008065	GA repeat binding protein, alpha	1.125	65.79	0.67268	17201	P	1.094	16.2	0.26612	5893
Garnl4	A_52_P39756	NM_001015046	GTPase activating RANGAP domain-like 4	1.125	75.14	0.78559	23100	P	1.184	5.75	0.08046	2671
Gmeb1	A_51_P520066	NM_020273	glucocorticoid modulatory element bindi	1.125	61.79	0.64034	15691	P	-1.048	44.4	0.57598	9234
Hps3	A_51_P496934	NM_080634	Hermansky-Pudlak syndrome 3 homolog (	1.125	69.29	0.70217	18513	P	1.057	28.13	0.56342	9143
Inpp5a	A_51_P364014	NM_183144	inositol polyphosphate-5-phosphatase A	1.125	69.29	0.70666	18759	P	1.184	2.53	0.01567	671
Itgam	A_52_P669155	AK170324	integrin alpha M	1.125	83.36	0.84299	25429	P	-1.061	40.63	0.42726	7790
Mgl2	A_52_P414065	NM_145137	macrophage galactose N-acetyl-galactosa	1.125	79.26	0.85249	27893	P	1.138	9.71	0.17461	4458
Mms19l	A_52_P214936	AK029840	MMS19 (MET18 S. cerevisiae)-like	1.125		0.7629	17975	A	1.03	33.49	0.5296	8829
Morf4l1	A_52_P418724	NM_001039147	mortality factor 4 like 1	1.125	77.44	0.80292	24243	P	1.167	3.01	0.02043	877
Nutf2	A_52_P668715	NM_026532	nuclear transport factor 2	1.125	75.14	0.75205	21181	P	1.119	6.98	0.06143	2179
Parn	A_52_P25567	NM_028761	poly(A)-specific ribonuclease (deadenylat	1.125	81.02	0.894	30582	P	1.077	19.02	0.30377	6362
Prkcbp1	A_51_P506015	NM_027230	protein kinase C binding protein 1	1.125	69.29	0.69196	18030	P	1.068	16.2	0.18589	4665
Rab34	A_52_P177454	AK045474	RAB34, member of RAS oncogene family	1.125	79.26	0.94373	24419	M	1.068	16.2	0.20059	4913
Tgfb1	A_51_P390715	NM_011577	transforming growth factor, beta 1	1.125	82.34	0.82288	24155	M	1.174	3.82	0.04071	1551
3632451O06Rik	A_51_P465147	NM_026142	RIKEN cDNA 3632451O06 gene	1.124	77.44	0.82885	25961	P	-1.085	28.13	0.28304	6119
Cdc26	A_52_P1180267	AK028893	cell division cycle 26	1.124		0.87686	29387	A	1.113	6.98	0.04963	1832
D6Wsu176e	A_51_P277416	NM_138587	DNA segment, Chr 6, Wayne State Univer	1.124	65.79	0.67567	17298	P	1.008	42.43	0.90263	12118
Pabpc4	A_52_P393396	NM_148917	poly A binding protein, cytoplasmic 4	1.124	79.26	0.83591	26819	P	1.055	22.1	0.28542	6156
Polr2g	A_51_P367843	NM_026329	polymerase (RNA) II (DNA directed) polyp	1.124	77.44	0.79241	23623	P	1.137	11.33	0.21655	5149
Rad23b	A_52_P600625	AK142280	RAD23b homolog (S. cerevisiae)	1.124	72.2	0.71359	19133	P	1.02	38.4	0.71128	10415
Ywhaq	A_52_P215249	AK037746	tyrosine 3-monooxygenase/tryptophan 5-	1.124	72.2	0.72137	19682	P	1.149	4.63	0.04772	1784
1500005P14Rik	A_52_P108845	XM_133283	CAP-GLY domain containing linker protein	1.123	79.26	0.85109	27803	P	1.138	4.63	0.03519	1358
Dlat	A_51_P265106	NM_145614	dihydrolipoamide S-acetyltransferase (E2	1.123	77.44	0.82962	26021	P	1.18	4.63	0.05591	2027
Hspd1	A_52_P1172972	NM_010477	heat shock protein 1 (chaperonin)	1.123	77.44	0.79266	23655	P	-1.039	43.15	0.37348	7208
Lrrc17	A_51_P301930	BC030317	leucine rich repeat containing 17	1.123	72.2	0.74784	20976	P	-1.222	0.56	0.00989	374
Mrpl30	A_51_P440904	NM_027098	mitochondrial ribosomal protein L30	1.123	79.26	0.84263	27248	P	-1.1	22.1	0.21893	5190
Ndfip1	A_51_P304879	ENSMUST00000025293	Nedd4 family interacting protein 1	1.123	72.2	0.80447	18197	M	1.202	2.53	0.02085	889
Notch1	A_51_P508510	Z11886	Notch gene homolog 1 (Drosophila)	1.123	82.34	0.84642	22135	M	1.225	4.63	0.09765	3052
Prkar2a	A_51_P217295	NM_008924	protein kinase, cAMP dependent regulat	1.123	82.34	0.80951	20062	M	1.149	5.75	0.04955	1830
Psme4	A_52_P111438	NM_134013	proteasome (prosome, macropain) activa	1.123	79.26	0.84099	27158	P	-1.116	19.02	0.234	5411
Smoc2	A_51_P213045	NM_022315	SPARC related modular calcium binding 2	1.123	69.29	0.68577	17723	P	1.119	8.32	0.07062	2413
Ube2d3	A_51_P259064	AK020443	ubiquitin-conjugating enzyme E2D 3 (UBC	1.123	57.76	0.76732	16761	M	1.191	5.75	0.08627	2806
Uqcrc2	A_51_P128648	NM_025899	ubiquinol cytochrome c reductase core pr	1.123	61.79	0.72788	17704	P	-1.084	30.75	0.31396	6509
2810030E01Rik	A_52_P455643	NM_028317	RIKEN cDNA 2810030E01 gene	1.122	81.02	0.8698	28863	P	1.035	36.07	0.69546	10282
Fusip1	A_52_P372843	AK161097	FUS interacting protein (serine-arginine ri	1.122	65.79	0.66728	16909	P	1.051	22.1	0.2897	6208
Il22ra1	A_52_P184362	NM_178257	interleukin 22 receptor, alpha 1	1.122		0.80918	18106	A	-1.267	0.51	0.0108	420
Leprotl1	A_52_P496655	NM_026609	leptin receptor overlapping transcript-like	1.122	72.2	0.7185	19418	P	1.01	42.43	0.94491	12530
Manbal	A_51_P440107	NM_026968	mannosidase, beta A, lysosomal-like	1.122	75.14	0.76313	21844	P	1.056	22.1	0.27115	5970
Mbnl3	A_52_P411264	NM_134163	muscleblind-like 3 (Drosophila)	1.122		0.95176	14090	A	1.188	4.63	0.06459	2271
Nagk	A_51_P206518	NM_019542	N-acetylglucosamine kinase	1.122	75.14	0.75744	21499	P	1.062	16.2	0.17898	4553

Prpf39	A_51_P250358	NM_177806	PRP39 pre-mRNA processing factor 39 ho	1.122	53.87	0.62876	14965	P	-1.279	0.51	0.00627	157
Rpl7l1	A_52_P343343	NM_025433	ribosomal protein L7-like 1	1.122	72.2	0.73827	20566	P	1.025	33.49	0.53859	8925
Sftpb	A_51_P269134	NM_147779	surfactant associated protein B	1.122	72.2	0.72788	17713	M	1.046	25.31	0.38299	7316
Tbcc	A_51_P388801	NM_178385	tubulin-specific chaperone c	1.122	81.02	0.8952	30662	P	1.157	3.82	0.03282	1287
Tcf2	A_51_P484311	NM_009330	transcription factor 2	1.122	61.79	0.64073	15709	P	1.179	2.53	0.01834	781
Timm17a	A_51_P167843	NM_011590	translocase of inner mitochondrial memb	1.122	61.79	0.64743	15968	P	-1.022	48.39	0.64822	9869
Zfp469	A_51_P224962	NM_178242	zinc finger protein 469	1.122	82.34	0.93084	33903	P	1.039	28.13	0.41686	7708
5730410I19Rik	A_51_P242076	NM_025666	RIKEN cDNA 5730410I19 gene	1.121	72.2	0.71763	19375	P	1.035	36.07	0.67797	10121
Taf1a	A_52_P618511	NM_021466	TATA box binding protein (Tbp)-associated	1.121	75.14	0.75006	21077	P	1.035	30.75	0.43635	7900
Tpm1	A_51_P325173	AK077713	tropomyosin 1, alpha	1.121	81.02	0.88057	29694	P	1.199	8.32	0.24471	5572
5330431N19Rik	A_51_P369294	NM_172639	RIKEN cDNA 5330431N19 gene	1.12	79.26	0.86362	28413	P	1.083	13.58	0.17007	4384
Ankib1	A_52_P155302	NM_001003909	ankyrin repeat and IBR domain containing	1.12	77.44	0.7912	23536	P	1.2	8.32	0.18704	4684
Bag1	A_51_P224505	NM_009736	Bcl2-associated athanogene 1	1.12	69.29	0.68776	17810	P	1.089	11.33	0.11932	3473
Basp1	A_52_P26794	NM_027395	brain abundant, membrane attached sign	1.12	77.44	0.80242	24178	P	1.091	25.31	0.55602	9075
Dek	A_52_P477709	NM_025900	DEK oncogene (DNA binding)	1.12	65.79	0.67211	17140	P	1.042	25.31	0.31613	6542
Eif2s3x	A_51_P256154	NM_012010	eukaryotic translation initiation factor 2, s	1.12	75.14	0.82109	18957	M	1.089	22.1	0.53135	8853
Emb	A_51_P382849	NM_010330	embigin	1.12	75.14	0.83273	19531	M	1.022	36.07	0.59408	9376
Hmgn1	A_51_P134408	AK080436	high mobility group nucleosomal binding	1.12	82.34	0.91547	32631	P	1.077	19.02	0.30574	6392
Pi4k2a	A_51_P345470	NM_145501	phosphatidylinositol 4-kinase type 2 alpha	1.12	79.26	0.83609	26824	P	1.142	6.98	0.064	2256
Rbm19	A_51_P144512	NM_028762	RNA binding motif protein 19	1.12	81.02	0.86821	28758	P	-1.276	0.51	0.00869	318
Serpina6	A_51_P133562	NM_007618	serine (or cysteine) peptidase inhibitor, cl	1.12	75.14	0.78158	22844	P	-1.043	43.75	0.42124	7741
Srpx	A_51_P316871	NM_016911	sushi-repeat-containing protein	1.12		0.78251	20471	A	1.014	42.43	0.83146	11474
Taf10	A_52_P263589	ENSMUST00000054556		1.12	77.44	0.79643	23902	P	-1.078	30.75	0.25651	5759
2610510H03Rik	A_52_P656867	NM_026620	RIKEN cDNA 2610510H03 gene	1.119	61.79	0.66133	16635	P	-1.026	46.85	0.58281	9287
3110031B13Rik	A_52_P203981	NM_026075	RIKEN cDNA 3110031B13 gene	1.119	61.79	0.64836	16023	P	1.048	30.75	0.59239	9358
A730011L01Rik	A_52_P19662	NM_177394	RIKEN cDNA A730011L01 gene	1.119	65.79	0.67248	17187	P	-1.076	40.63	0.51199	8690
Aldh16a1	A_51_P407311	NM_145954	aldehyde dehydrogenase 16 family, memb	1.119	75.14	0.75944	21592	P	-1.017	49.48	0.74857	10777
Kpnb1	A_52_P275627	NM_008379	karyopherin (importin) beta 1	1.119	69.29	0.69196	18033	P	1.176	5.75	0.09758	3051
Lsm7	A_51_P200044	NM_025349	LSM7 homolog, U6 small nuclear RNA ass	1.119	69.29	0.69975	18363	P	-1.078	22.1	0.13943	3839
M6pr	A_51_P439170	NM_010749	mannose-6-phosphate receptor, cation de	1.119	75.14	0.75932	21561	P	1.112	11.33	0.22996	5350
Me3	A_51_P396000	NM_181407	malic enzyme 3, NADP(+)-dependent, mit	1.119		0.90463	16940	A	-1.084	22.1	0.15965	4210
Punc	A_51_P436559	AK012957	putative neuronal cell adhesion molecule	1.119	81.02	0.84655	25682	M	1.062	16.2	0.19793	4866
Snx19	A_52_P337478	NM_028874	sorting nexin 19	1.119	69.29	0.70887	18877	P	1.163	3.46	0.02221	939
Atp5h	A_51_P264186	NM_027862	ATP synthase, H+ transporting, mitochond	1.118	79.26	0.87051	21233	M	-1.015	49.48	0.882	11879
Capns1	A_51_P399538	NM_009795	calpain, small subunit 1	1.118	65.79	0.68027	17450	P	1.139	6.98	0.08145	2692
Clk1	A_51_P193573	NM_001042634	CDC-like kinase 1	1.118	77.44	0.85901	20762	M	1.098	22.1	0.53498	8888
Eef1b2	A_51_P412595	NM_018796	eukaryotic translation elongation factor 1	1.118	82.34	0.91949	23587	M	1.087	19.02	0.3661	7116
Gpx1	A_52_P684378	NM_008160	glutathione peroxidase 1	1.118	72.2	0.81427	18632	M	1.22	3.01	0.03601	1392
Hs2st1	A_52_P564132	NM_011828	heparan sulfate 2-O-sulfotransferase 1	1.118	69.29	0.69709	18244	P	1.053	25.31	0.37912	7271
Irf3	A_52_P609770	AK050570	interferon regulatory factor 3	1.118	81.02	0.86758	28716	P	-1.02	48.39	0.64644	9857
Nras	A_52_P649296	NM_010937	neuroblastoma ras oncogene	1.118	77.44	0.79241	23621	P	1.087	9.71	0.09648	3026
Odz3	A_52_P206429	NM_011857	odd Oz/ten-m homolog 3 (Drosophila)	1.118	69.29	0.79372	20655	P	2.444	0	0.00584	86
Rbbp5	A_51_P516850	NM_172517	retinoblastoma binding protein 5	1.118	77.44	0.82935	25997	P	1.048	28.13	0.49593	8522
Rbm3	A_52_P262340	BC106176	RNA binding motif protein 3	1.118	82.34	0.92551	23882	M	1.056	22.1	0.27939	6089
Sfrs7	A_52_P649685	NM_146083	splicing factor, arginine/serine-rich 7	1.118	75.14	0.82885	19317	M	-1.104	42.43	0.6184	9614
Srebf2	A_52_P302001	NM_033218	sterol regulatory element binding factor 2	1.118		0.87152	18397	A	-1.056	43.75	0.53923	8933
Tceal8	A_51_P135379	NM_025703	transcription elongation factor A (SII)-like	1.118	79.26	0.84642	27530	P	1.062	25.31	0.41879	7720
1810013L24Rik	A_52_P316437	ENSMUST00000023150	RIKEN cDNA 1810013L24 gene	1.117	79.26	0.83817	26968	P	1.012	42.43	0.80555	11226
2010100O12Rik	A_51_P199148	NM_025946	RIKEN cDNA 2010100O12 gene	1.117	75.14	0.76732	22045	P	-1.058	43.15	0.51123	8680
Esrra	A_52_P198949	AK046588	estrogen related receptor, alpha	1.117	77.44	0.81287	24890	P	1.008	42.43	0.90375	12124
Gtf3c2	A_51_P354102	NM_027901	general transcription factor IIIC, polypept	1.117	72.2	0.74473	20840	P	1.149	13.58	0.37208	7197
Ppp1r12a	A_52_P437363	NM_027892	protein phosphatase 1, regulatory (inhibit	1.117	72.2	0.7198	19512	P	1.16	4.63	0.04544	1704
Qscn6l1	A_52_P138895	NM_153559	quiescin Q6-like 1	1.117	79.26	0.83883	27044	P	1.126	4.63	0.03484	1335

Rab1b	A_51_P344950	NM_029576	RAB1B, member RAS oncogene family	1.117	77.44	0.82266	25584	P	1.015	40.63	0.73517	10634
Tob1	A_51_P293339	NM_009427	transducer of ErbB-2.1	1.117	77.44	0.7912	23546	P	1.037	30.75	0.48221	8342
1200011I18Rik	A_51_P455776	NM_026177	RIKEN cDNA 1200011I18 gene	1.116	77.44	0.79306	23688	P	1.032	30.75	0.46306	8141
Coro1c	A_52_P634856	NM_011779	coronin, actin binding protein 1C	1.116	77.44	0.79365	23721	P	-1.116	16.2	0.1871	4686
Dpp3	A_52_P266435	AK039975	dipeptidylpeptidase 3	1.116	83.95	0.91932	30566	M	-1.073	25.31	0.15232	4073
Ngly1	A_51_P419111	NM_021504	N-glycanase 1	1.116	77.44	0.81753	25249	P	1.14	5.75	0.05211	1919
Rrad	A_51_P240253	NM_019662	Ras-related associated with diabetes	1.116	69.29	0.71133	19033	P	1.183	4.63	0.07192	2430
Stag2	A_51_P126540	NM_001077712	stromal antigen 2	1.116	77.44	0.81125	24796	P	1.074	13.58	0.1683	4352
Tial1	A_51_P441942	NM_009383	Tia1 cytotoxic granule-associated RNA bir	1.116	79.26	0.88103	21615	M	1.129	19.02	0.52251	8772
Uck2	A_52_P135392	BC004016	uridine-cytidine kinase 2	1.116	79.26	0.84604	27484	P	1.131	6.98	0.05741	2076
2810008M24Rik	A_51_P409761	NM_001048250	RIKEN cDNA 2810008M24 gene	1.115	77.44	0.79285	23677	P	-1.117	13.58	0.15611	4149
6720401G13Rik	A_52_P223508	AK081581	RIKEN cDNA 6720401G13 gene	1.115	82.34	0.91605	32696	P	-1.3	3.01	0.15274	4081
Ap1b1	A_51_P138348	NM_007454	adaptor protein complex AP-1, beta 1 sub	1.115	77.44	0.81591	25148	P	-1.081	19.02	0.13882	3817
C330006K01Rik	A_51_P118779	NM_172725	RIKEN cDNA C330006K01 gene	1.115	79.26	0.85807	28129	P	-1.041	44.4	0.47852	8293
Dcbld2	A_52_P56955	NM_028523	discoidin, CUB and LCCL domain containir	1.115	69.29	0.69991	18379	P	-1.022	47.43	0.60743	9504
Ddx21	A_52_P424037	NM_019553	DEAD (Asp-Glu-Ala-Asp) box polypeptide	1.115	81.02	0.90266	31221	P	-1.003	49.48	0.9761	12803
Gys1	A_52_P228932	NM_030678	glycogen synthase 1, muscle	1.115	77.44	0.76648	20890	M	1.042	28.13	0.38739	7366
Hist1h1c	A_51_P516133	NM_015786	histone cluster 1, H1c	1.115	77.44	0.84821	20429	M	1.193	13.58	0.39596	7471
Igfbp4	A_52_P257502	NM_010517	insulin-like growth factor binding protein	1.115	77.44	0.82688	25840	P	1.003	42.43	0.96945	12741
Mrps24	A_52_P507310	NM_026080	mitochondrial ribosomal protein S24	1.115	75.14	0.75595	21449	P	1.12	9.71	0.11657	3410
Rfxap	A_52_P441044	AK087489	regulatory factor X-associated protein	1.115	72.2	0.74123	20663	P	1.11	11.33	0.14894	4028
Strn	A_51_P252061	NM_011500	striatin, calmodulin binding protein	1.115	65.79	0.81287	21582	M	1.015	42.43	0.80265	11199
Aspscr1	A_51_P121652	NM_026877	alveolar soft part sarcoma chromosome r	1.114	69.29	0.70048	18405	P	1.037	30.75	0.47441	8248
Crtap	A_51_P201721	NM_019922	cartilage associated protein	1.114	75.14	0.75699	21480	P	-1.067	36.07	0.3338	6725
Efnb3	A_52_P495565	NM_007911	ephrin B3	1.114	79.26	0.83788	26928	P	-1.225	0.75	0.01279	553
Emp3	A_51_P446510	NM_010129	epithelial membrane protein 3	1.114	75.14	0.78956	23402	P	-1.081	13.58	0.09833	3072
Fbxo11	A_51_P479802	ENSMUST00000005504	F-box protein 11	1.114	77.44	0.79875	24028	P	1.192	3.82	0.04966	1839
Kctd9	A_51_P454638	NM_134073	potassium channel tetramerisation doma	1.114	69.29	0.7132	19113	P	1.127	8.32	0.08823	2854
Ptprf	A_52_P148883	NM_011213	protein tyrosine phosphatase, receptor ty	1.114	79.26	0.85117	27819	P	1.149	8.32	0.16153	4246
Pvrl2	A_51_P475858	NM_008990	poliovirus receptor-related 2	1.114	75.14	0.77047	22217	P	1.108	9.71	0.11939	3482
Slc35a5	A_52_P51198	NM_028756	solute carrier family 35, member A5	1.114	75.14	0.75588	21447	P	-1.006	49.48	0.90871	12181
Synj2bp	A_52_P662001	NM_025292	synaptojanin 2 binding protein	1.114	72.2	0.735	20445	P	1.02	38.4	0.65376	9908
Trip12	A_52_P1068111	AK041991	thyroid hormone receptor interactor 12	1.114	83.36	0.93339	34105	P	1.11	8.32	0.05981	2145
1200004M23Rik	A_51_P472659	NM_026169	RIKEN cDNA 1200004M23 gene	1.113	72.2	0.73771	20549	P	1.096	9.71	0.08544	2782
1810019J16Rik	A_51_P142258	NM_133707	RIKEN cDNA 1810019J16 gene	1.113	81.02	0.89183	30401	P	-1.103	16.2	0.15879	4193
AL033314	A_52_P467140	NM_019776	staphylococcal nuclease and tudor domai	1.113	65.79	0.68802	17829	P	1.184	6.98	0.15944	4208
Dnajc3	A_52_P329875	NM_008929	DnaJ (Hsp40) homolog, subfamily C, mem	1.113	75.14	0.77259	22374	P	-1.119	25.31	0.35602	6966
Fbxo18	A_51_P472323	NM_015792	F-box protein 18	1.113	75.14	0.77678	22563	P	1.064	19.02	0.24236	5530
Gsc	A_51_P370717	NM_010351	goosecoid	1.113		0.92907	17584	A	1.101	8.32	0.06694	2341
Klhl2	A_51_P398164	NM_178633	kelch-like 2, Mayven (Drosophila)	1.113	61.79	0.74784	18565	P	1.067	22.1	0.35017	6876
Rab18	A_52_P180210	AK034242	RAB18, member RAS oncogene family	1.113	81.02	0.8782	29492	P	1.042	30.75	0.49241	8472
Sox10	A_52_P192625	BC023356	SRY-box containing gene 10	1.113	81.02	0.83252	24669	M	1.063	19.02	0.23793	5459
Ard1	A_51_P195324	NM_019870	N-acetyltransferase ARD1 homolog (S. cer	1.112	81.02	0.87616	29341	P	1.068	16.2	0.17637	4507
BC017643	A_51_P457130	NM_144832	cDNA sequence BC017643	1.112	72.2	0.73228	20364	P	-1.185	1.58	0.02629	1082
Ciz1	A_52_P280344	NM_028412	CDKN1A interacting zinc finger protein 1	1.112	72.2	0.72221	19764	P	-1.039	45.05	0.57371	9218
Creg1	A_51_P111762	NM_011804	cellular repressor of E1A-stimulated gene	1.112	77.44	0.81378	24964	P	-1.198	2.04	0.05188	1908
Cul7	A_51_P293753	NM_025611	cullin 7	1.112	77.44	0.82149	25476	P	-1.074	30.75	0.25546	5285
Mapk1	A_51_P481788	NM_011949	mitogen activated protein kinase 1	1.112	72.2	0.73504	20450	P	1.107	9.71	0.09576	3010
Mybl2	A_51_P351144	NM_008652	myeloblastosis oncogene-like 2	1.112	72.2	0.74028	20638	P	1.091	9.71	0.0895	2879
Psma1	A_51_P469578	NM_011965	proteasome (prosome, macropain) subun	1.112	75.14	0.76881	22150	P	-1.095	13.58	0.11028	3276
Rab2b	A_51_P446132	NM_172601	RAB2B, member RAS oncogene family	1.112	77.44	0.81818	25309	P	-1.167	1.58	0.02543	1055
Senp6	A_51_P293989	NM_146003	SUMO/sentrin specific peptidase 6	1.112	77.44	0.80132	24144	P	1.057	19.02	0.25188	5677
Tarbp2	A_51_P111583	NM_009319	TAR (HIV) RNA binding protein 2	1.112	77.44	0.80216	24164	P	1.234	6.98	0.17381	4447

6620401M08Rik	A_52_P244312	AK158571	RIKEN cDNA 6620401M08 gene	1.111	79.26	0.85452	27989	P	-1.166	13.58	0.27879	6075
Arbp	A_51_P134602	NM_007475	acidic ribosomal phosphoprotein P0	1.111	75.14	0.82983	19377	M	1.1	9.71	0.0911	2922
Cfdp1	A_51_P446978	NM_011801	craniofacial development protein 1	1.111	75.14	0.78472	23040	P	-1.014	49.48	0.79418	11130
Itch	A_52_P209852	XM_902526	itchy, E3 ubiquitin protein ligase	1.111	81.02	0.83817	25140	P	1.21	3.82	0.05472	1998
Tomm40	A_52_P495318	NM_016871	translocase of outer mitochondrial memb	1.111	75.14	0.75282	21257	P	-1.031	46.85	0.61343	9560
Trnt1	A_52_P456629	NM_027296	tRNA nucleotidyl transferase, CCA-adding	1.111	72.2	0.7491	21046	P	1.001	42.43	0.98432	12912
Vamp3	A_51_P252212	NM_009498	vesicle-associated membrane protein 3	1.111	75.14	0.75861	21538	P	1.061	25.31	0.44926	7987
Wdr34	A_51_P438461	NM_001008498	WD repeat domain 34	1.111	69.29	0.70113	18442	P	-1.04	45.68	0.64526	9848
Wdr6	A_51_P118650	NM_031392	WD repeat domain 6	1.111	81.02	0.878	29481	P	1.254	3.82	0.08255	2719
5730455P16Rik	A_51_P169564	NM_027472	RIKEN cDNA 5730455P16 gene	1.11	72.2	0.74313	20723	P	1.206	11.33	0.35276	6919
9430016H08Rik	A_51_P224468	BC071241	RIKEN cDNA 9430016H08 gene	1.11	75.14	0.7744	22477	P	1.037	30.75	0.48541	8388
Abhd6	A_52_P496497	NM_025341	abhydrolase domain containing 6	1.11	81.02	0.86821	28760	P	1.07	22.1	0.41151	7625
Atp6v0c	A_52_P601240	NM_009729	ATPase, H+ transporting, lysosomal V0 su	1.11	75.14	0.76648	22004	P	1.159	3.46	0.02567	1059
Bet1	A_51_P432449	NM_009748	blocked early in transport 1 homolog (S. c	1.11	75.14	0.78804	23266	P	-1.146	8.32	0.13222	3719
Cct5	A_51_P144783	NM_007637	chaperonin subunit 5 (epsilon)	1.11	83.95	0.85237	22451	M	1.011	42.43	0.86296	11702
D13Wsu50e	A_51_P219433	NM_138596	mediator of RNA polymerase II transcripti	1.11	77.44	0.81296	24905	P	1.006	42.43	0.971	12752
Dnpep	A_51_P128096	NM_016878	aspartyl aminopeptidase	1.11	77.44	0.81247	24844	P	-1.072	30.75	0.23	5354
Gyltl1b	A_52_P201992	AK081797	glycosyltransferase-like 1B	1.11	75.14	0.77416	22462	P	-1.177	1.32	0.02005	858
Mrps21	A_51_P509012	NM_078479	mitochondrial ribosomal protein S21	1.11	75.14	0.77599	22524	P	1.113	6.98	0.05346	1967
Nicn1	A_52_P94845	NM_025449	nicolin 1	1.11	75.14	0.78472	23048	P	1.046	30.75	0.63274	9745
Scfd1	A_52_P140299	AK049361	sec1 family domain containing 1	1.11	72.2	0.72853	20143	P	-1.078	30.75	0.25649	5753
Sdhc	A_52_P875481	AK031343		1.11	72.2	0.75092	21136	P	1.05	30.75	0.5823	9275
Tia1	A_51_P225889	NM_011585	cytotoxic granule-associated RNA binding	1.11	82.34	0.90463	31403	P	-1.069	30.75	0.22129	5224
Btbd7	A_51_P330658	AK122522	BTB (POZ) domain containing 7	1.109	82.34	0.9186	32888	P	1.084	11.33	0.09861	3074
Itk	A_52_P50623	AK037554	IL2-inducible T-cell kinase	1.109	75.14	0.77402	22457	P	-1.086	25.31	0.2332	5403
Lass4	A_51_P296528	NM_026058	longevity assurance homolog 4 (S. cerevis	1.109	77.44	0.79696	23921	P	-1.037	46.3	0.65501	9916
Sbno1	A_51_P123805	XM_355637	sno, strawberry notch homolog 1 (Drosop	1.109	72.2	0.73047	20289	P	1.113	8.32	0.06967	2388
Ttc5	A_51_P166325	BC092074	tetratricopeptide repeat domain 5	1.109	72.2	0.7471	20931	P	-1.228	0.56	0.01049	402
Tubb5	A_52_P163796	NM_011655	tubulin, beta 5	1.109	79.26	0.8299	26056	P	1.143	4.63	0.03417	1317
Cct6a	A_52_P363718	NM_009838	chaperonin subunit 6a (zeta)	1.108	81.02	0.86893	28828	P	1.13	9.71	0.16314	4273
Dlg5	A_51_P430817	AK147699	discs, large homolog 5 (Drosophila)	1.108	72.2	0.75252	21232	P	1.218	6.98	0.15718	4167
Eefsec	A_51_P340402	NM_023060	eukaryotic elongation factor, selenocystei	1.108	81.02	0.87627	29358	P	1.021	38.4	0.64449	9832
Exosc10	A_51_P391825	NM_016699	exosome component 10	1.108	77.44	0.82443	25668	P	-1.141	2.53	0.0311	1229
Gng12	A_51_P415688	NM_025278	guanine nucleotide binding protein (G pro	1.108	75.14	0.77047	22216	P	1.349	2.53	0.06194	2189
Mxd3	A_52_P190647	NM_016662	Max dimerization protein 3	1.108	61.79	0.67959	17433	P	-1.117	11.33	0.11939	3485
Nfe2l3	A_52_P423222	NM_010903	nuclear factor, erythroid derived 2, like 3	1.108	77.44	0.79709	23931	P	1.108	13.58	0.22756	5324
Nup35	A_51_P259230	NM_027091	nucleoporin 35	1.108	77.44	0.80609	24469	P	1.133	6.98	0.07614	2559
Rnf7	A_52_P43111	NM_011279	ring finger protein 7	1.108	72.2	0.74535	20863	P	1.112	9.71	0.12367	3571
Zfp655	A_52_P257665	NM_028298	zinc finger protein 655	1.108	72.2	0.72841	20140	P	-1.076	22.1	0.1549	4127
6430514L14Rik	A_51_P221510	NM_029784	RIKEN cDNA 6430514L14 gene	1.107	79.26	0.83751	26898	P	1.05	22.1	0.30281	6350
B930006L02Rik	A_52_P285674	NM_178764	RIKEN cDNA B930006L02 gene	1.107	72.2	0.72788	20100	P	1.094	16.2	0.32199	6586
Cox7b	A_51_P160664	NM_025379	cytochrome c oxidase subunit VIIb	1.107	79.26	0.88647	21849	M	1.241	4.63	0.10068	3119
D14Abb1e	A_52_P182749	XM_897688	DNA segment, Chr 14, Abbott 1 expressed	1.107	77.44	0.81746	25242	P	1.097	16.2	0.33668	6747
Foxd3	A_51_P286423	NM_010425	forkhead box D3	1.107	77.44	0.79	23455	P	1.008	42.43	0.88416	11906
Lgals8	A_51_P316981	NM_018886	lectin, galactose binding, soluble 8	1.107	77.44	0.82214	25538	P	1.03	36.07	0.67113	10061
Rap2b	A_52_P368384	NM_028712	RAP2B, member of RAS oncogene family	1.107	82.34	0.90463	31409	P	1.056	22.1	0.27384	6007
Spnb2	A_52_P492856	NM_175836	spectrin beta 2	1.107	69.29	0.71296	19100	P	1.12	13.58	0.28592	6167
Tfam	A_52_P351785	NM_009360	transcription factor A, mitochondrial	1.107	77.44	0.8176	25257	P	1.01	42.43	0.86219	11697
Zbed4	A_51_P199832	NM_181412	zinc finger, BED domain containing 4	1.107	81.02	0.90137	31065	M	1.142	6.98	0.08375	2749
6720468P15Rik	A_52_P667066	AK078497	RIKEN cDNA 6720468P15 gene	1.106	72.2	0.73001	20240	P	-1.178	1.1	0.01529	649
Clcn1	A_52_P516878	NM_013491	chloride channel 1	1.106	72.2	0.76762	19762	M	1.127	9.71	0.18151	4603
Gata4	A_51_P492355	NM_008092	GATA binding protein 4	1.106	72.2	0.75	21069	P	1.052	28.13	0.55083	9038
Gnl2	A_51_P161362	NM_145552	guanine nucleotide binding protein-like 2	1.106	79.26	0.83872	27016	P	-1.003	49.48	0.97107	12756

Mrps18b	A_52_P207964	NM_025878	mitochondrial ribosomal protein S18B	1.106	81.02	0.90183	31137	P	1.09	11.33	0.12993	3685
Mylc2b	A_52_P222888	NM_023402	myosin light chain, regulatory B	1.106	81.02	0.89568	22257	M	1.207	2.53	0.02523	1043
Rdx	A_52_P571684	NM_009041	radixin	1.106	77.44	0.80275	24220	P	1.136	9.71	0.20644	4989
Rnf11	A_51_P268117	NM_013876	ring finger protein 11	1.106	72.2	0.75205	21179	P	1.11	8.32	0.07279	2473
Tgfbr2	A_52_P3811	AK090393	transforming growth factor, beta receptor	1.106		0.9189	17454	A	-1.054	38.4	0.29214	6238
Tob2	A_52_P43100	AK013833	transducer of ERBB2, 2	1.106	77.44	0.78594	20605	M	1.05	25.31	0.3283	6653
4931406C07Rik	A_51_P445683	NM_133732	RIKEN cDNA 4931406C07 gene	1.105	77.44	0.80415	24352	P	1.097	8.32	0.07277	2465
Adh5	A_51_P404275	NM_007410	alcohol dehydrogenase 5 (class III), chi po	1.105	69.29	0.72698	20043	P	1.048	22.1	0.27	5951
Cbx1	A_51_P495012	NM_007622	chromobox homolog 1 (Drosophila HP1 b	1.105	77.44	0.79655	23908	P	1.062	19.02	0.21209	5074
Cox7c	A_52_P136153	NM_007749	cytochrome c oxidase, subunit VIIc	1.105	75.14	0.78613	23136	P	1.064	22.1	0.33368	6721
D2Wsu81e	A_51_P281663	NM_172660	DNA segment, Chr 2, Wayne State Univer	1.105	75.14	0.7888	23375	P	1.016	42.43	0.86316	11707
Dscr2	A_51_P421950	NM_019537	Down syndrome critical region homolog 2	1.105	75.14	0.76183	21742	P	1.061	25.31	0.4138	7664
Dusp1	A_51_P430900	NM_013642	dual specificity phosphatase 1	1.105	82.34	0.91591	23382	M	1.061	22.1	0.3102	6450
Isl1	A_52_P337246	NM_021459	ISL1 transcription factor, LIM/homeodom	1.105	77.44	0.86471	20972	M	1.161	4.63	0.04045	1541
Ppm1d	A_51_P131526	NM_016910	protein phosphatase 1D magnesium-depe	1.105	82.34	0.92269	33251	P	-1.013	49.48	0.77933	10983
Sap18	A_51_P386031	NM_009119	Sin3-associated polypeptide 18	1.105	77.44	0.82556	25723	P	-1.043	44.4	0.48701	8408
Sdhb	A_51_P234853	NM_023374	succinate dehydrogenase complex, subun	1.105	81.02	0.86117	28304	P	-1.262	0.56	0.01141	445
Wap	A_51_P407705	NM_011709	whey acidic protein	1.105		0.8977	19526	A	1.088	11.33	0.10965	3257
0610008C08Rik	A_51_P265685	NM_026673	RIKEN cDNA 0610008C08 gene	1.104	72.2	0.75435	21346	P	1.131	16.2	0.39175	7415
1810022K09Rik	A_52_P5394	BC045157	RIKEN cDNA 1810022K09 gene	1.104	79.26	0.87393	21352	M	1.078	16.2	0.2404	5494
Arnt2	A_52_P260696	NM_007488	aryl hydrocarbon receptor nuclear translc	1.104	82.34	0.91363	32392	P	1.057	22.1	0.29516	6275
Hdgfrp2	A_51_P400773	NM_008233	hepatoma-derived growth factor, related	1.104	79.26	0.83302	26334	P	1.049	22.1	0.28546	6157
Hrbl	A_51_P496074	NM_178162	HIV-1 Rev binding protein-like	1.104	72.2	0.73986	20615	P	-1.015	49.48	0.72759	10547
Ky	A_51_P334190	AJ293727	kyphoscoliosis peptidase	1.104	83.36	0.85918	22449	M	1.073	16.2	0.20269	4939
Psmb7	A_51_P468329	NM_011187	proteasome (prosome, macropain) subun	1.104	77.44	0.85913	20769	M	1.139	9.71	0.17942	4559
Pycrl	A_51_P482844	AK004291	pyrroline-5-carboxylate reductase-like	1.104	79.26	0.84478	27380	P	1.027	33.49	0.53861	8927
Sh3glb1	A_52_P218100	AK086477	SH3-domain GRB2-like B1 (endophilin)	1.104	81.02	0.89072	30281	P	1.129	6.98	0.07509	2536
Slc39a6	A_51_P259214	NM_139143	solute carrier family 39 (metal ion transpc	1.104	75.14	0.78103	22813	P	1.023	38.4	0.72706	10536
St6galnac4	A_52_P449104	NM_011373	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-	1.104	82.34	0.90374	31367	P	1.1	11.33	0.12491	3603
Crsp2	A_51_P281134	AB019028	cofactor required for Sp1 transcriptional a	1.103	81.02	0.87393	29170	P	-1.017	49.48	0.78354	11038
D10Ertd641e	A_52_P550684	AK037565	DNA segment, Chr 10, ERATO Doi 641, exp	1.103	79.26	0.83273	26307	P	1.025	38.4	0.7248	10520
Eif2s1	A_51_P448340	NM_026114	eukaryotic translation initiation factor 2, s	1.103	79.26	0.83342	26362	P	1.125	5.75	0.04706	1760
Fgd1	A_52_P428521	NM_008001	FYVE, RhoGEF and PH domain containing	1.103	77.44	0.81874	25341	P	-1.187	1.62	0.03502	1346
Ivns1abp	A_52_P584058	NM_001039511	influenza virus NS1A binding protein	1.103	79.26	0.83547	26792	P	1.224	2.04	0.01529	652
Pccb	A_51_P418259	NM_025835	propionyl Coenzyme A carboxylase, beta p	1.103	81.02	0.86555	28544	P	1.073	22.1	0.38497	7337
Rhoa	A_52_P110965	NM_016802	ras homolog gene family, member A	1.103	75.14	0.78996	23449	P	1.199	2.04	0.01584	682
Rpl39	A_51_P139244	NM_026055	ribosomal protein L39	1.103	81.02	0.90183	22536	M	1.056	22.1	0.34749	6842
Uhrf2	A_52_P531514	AK031036	ubiquitin-like, containing PHD and RING fi	1.103	81.02	0.8661	28570	P	1.137	8.32	0.12441	3586
Wars2	A_52_P641477	NM_027462	tryptophanyl tRNA synthetase 2 (mitocho	1.103	79.26	0.83789	26944	P	1.017	42.43	0.8974	12035
0710008K08Rik	A_51_P453167	NM_026995	RIKEN cDNA 0710008K08 gene	1.102	75.14	0.76655	22023	P	1.092	11.33	0.15103	4055
2410127E16Rik	A_52_P104581	NM_029741	RIKEN cDNA 2410127E16 gene	1.102	81.02	0.89796	30805	P	1.074	13.58	0.13256	3721
Anapc11	A_52_P238019	NM_001038230	anaphase promoting complex subunit 11	1.102	65.79	0.71449	19204	P	-1.013	49.48	0.82646	11425
Asns	A_51_P125745	NM_012055	asparagine synthetase	1.102	79.26	0.88491	21799	M	1.035	33.49	0.54989	9022
Dvl1	A_52_P234958	NM_010091	dishevelled, dsh homolog 1 (Drosophila)	1.102	82.34	0.91033	31989	P	-1.043	44.4	0.49099	8451
Ext2	A_51_P221801	NM_010163	exostoses (multiple) 2	1.102	79.26	0.83927	27060	P	1.133	5.75	0.05211	1920
Hadhb	A_51_P217990	NM_145558	hydroxyacyl-Coenzyme A dehydrogenase/	1.102	77.44	0.82494	25694	P	-1.04	45.05	0.55846	9089
Mrpl51	A_52_P24160	NM_025595	mitochondrial ribosomal protein L51	1.102	77.44	0.79823	23999	P	1.003	42.43	0.94873	12568
Nup62	A_51_P190277	NM_053074	nucleoporin 62	1.102	69.29	0.71937	19471	P	1.14	3.82	0.02789	1120
Pbxip1	A_51_P146850	NM_146131	pre-B-cell leukemia transcription factor in	1.102	81.02	0.86173	28336	P	1.075	13.58	0.15225	4068
Pcbp2	A_52_P635718	NM_011042	poly(rC) binding protein 2	1.102	75.14	0.76844	22140	P	1.149	5.75	0.05908	2110
Pelo	A_51_P175555	NM_134058	pelota homolog (Drosophila)	1.102	77.44	0.81406	24985	P	1.048	25.31	0.3303	6670
Sqle	A_51_P450487	NM_009270	squalene epoxidase	1.102	72.2	0.75215	21185	P	1.009	42.43	0.8679	11743
Tnpo3	A_52_P100042	AK045143	transportin 3	1.102	75.14	0.7763	22543	P	1.112	9.71	0.11996	3492

Ttc14	A_51_P101719	NM_025978	tetratricopeptide repeat domain 14	1.102	81.02	0.86033	28239	P	-1.032	46.3	0.62104	9633
Tusc4	A_52_P59457	NM_018879	tumor suppressor candidate 4	1.102	82.34	0.90848	31699	P	-1.182	2.04	0.04486	1668
Wwox	A_52_P406141	AK083096	WW domain-containing oxidoreductase	1.102	77.44	0.79111	23501	P	1.059	19.02	0.23591	5429
Ankrd32	A_52_P328128	AK086347	ankyrin repeat domain 32	1.101	82.34	0.909	31788	P	1.05	22.1	0.26773	5909
D19Wsu162e	A_51_P496598	NM_146099	DNA segment, Chr 19, Wayne State Unive	1.101	79.26	0.85903	28164	P	1.002	42.43	0.97003	12744
Gnb5	A_51_P185259	NM_010313	guanine nucleotide binding protein, beta	1.101	72.2	0.75724	21493	P	-1.254	0.66	0.01227	499
Hip1	A_52_P11174	AK147269	huntingtin interacting protein 1	1.101	77.44	0.7912	23540	P	-1.107	16.2	0.1601	4216
Hnrpc	A_52_P596080	AK088678	heterogeneous nuclear ribonucleoprotein	1.101	77.44	0.86773	21120	M	1.129	4.63	0.03839	1459
Ier3ip1	A_52_P445324	NM_025409	immediate early response 3 interacting pr	1.101	72.2	0.74032	20641	P	-1.001	49.48	0.99345	13008
Mastl	A_52_P996341	BC086483	microtubule associated serine/threonine	1.101	81.02	0.88507	29980	P	1.042	30.75	0.55007	9025
Mrpl38	A_52_P262997	AK013126	mitochondrial ribosomal protein L38	1.101	82.34	0.90137	31066	P	1.102	11.33	0.14582	3959
Pecam1	A_52_P349070	AK031380	platelet/endothelial cell adhesion molecu	1.101		0.89894	19611	A	-1.031	49	0.81997	11357
Psmc1	A_51_P104960	NM_008947	protease (prosome, macropain) 26S subu	1.101	77.44	0.7912	23547	P	-1.148	2.04	0.03012	1200
Snai1	A_51_P165087	NM_011427	snail homolog 1 (Drosophila)	1.101	82.34	0.90596	31512	P	-1.151	3.46	0.04748	1780
Tnf	A_51_P385099	NM_013693	tumor necrosis factor	1.101	79.26	0.82788	25879	P	1.042	28.13	0.3949	7458
Ube2e3	A_52_P174962	AK043446	ubiquitin-conjugating enzyme E2E 3, UBC	1.101	82.34	0.9153	32614	M	1.008	42.43	0.89646	12024
Vax2	A_51_P310348	NM_011912	ventral anterior homeobox containing ger	1.101		0.92079	17531	A	1.045	22.1	0.29288	6251
1700020I14Rik	A_52_P500741	AK147270	RIKEN cDNA 1700020I14 gene	1.1	82.34	0.9036	31340	P	-1.103	6.98	0.06573	2301
4930455F23Rik	A_51_P190437	NM_029115	RIKEN cDNA 4930455F23 gene	1.1	75.14	0.77139	22334	P	-1.01	49.48	0.9007	12080
6330416L07Rik	A_51_P233308	NM_176962	RIKEN cDNA 6330416L07 gene	1.1	75.14	0.76814	22112	P	-1.136	3.46	0.04529	1698
Cobll1	A_52_P631356	NM_177025	Cobl-like 1	1.1	77.44	0.82083	25437	P	-1.337	1.32	0.09017	2898
Hmgb1	A_52_P323044	NM_010439	high mobility group box 1	1.1	77.44	0.79372	23729	P	-1.033	49.22	0.83907	11522
Mafb	A_52_P495869	NM_010658	v-maf musculoaponeurotic fibrosarcoma	1.1	83.36	0.94613	24702	M	1.357	1.32	0.02177	918
Myh3	A_51_P167668	XM_354614	myosin, heavy polypeptide 3, skeletal mu	1.1		0.90299	19969	A	1.054	25.31	0.39103	7411
Notch3	A_51_P220162	NM_008716	Notch gene homolog 3 (Drosophila)	1.1	81.02	0.87476	29234	P	1.056	28.13	0.49031	8432
Smarcc1	A_51_P502184	NM_009211	SWI/SNF related, matrix associated, actin	1.1	77.44	0.80132	24146	P	-1.06	33.49	0.21827	5172
St6galnac2	A_52_P577819	AK136381	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-	1.1		0.89438	22033	A	-1.224	0.75	0.01427	598
Ccpg1	A_52_P668146	NM_028181	cell cycle progression 1	1.099	79.26	0.83233	26238	P	1.103	11.33	0.17381	4444
Crbn	A_52_P424871	NM_175357	cereblon	1.099	82.34	0.90075	31025	P	1.063	19.02	0.28832	6190
D030051N19Rik	A_51_P141180	AK083596	RIKEN cDNA D030051N19 gene	1.099	77.44	0.81316	24927	P	1.06	19.02	0.21806	5168
Mat2b	A_52_P288811	NM_134017	methionine adenosyltransferase II, beta	1.099	75.14	0.7912	23522	P	1.232	3.46	0.04965	1838
Mrpl17	A_52_P273929	NM_025301	mitochondrial ribosomal protein L17	1.099	69.29	0.73865	20578	P	-1.011	49.48	0.81635	11339
Mrps31	A_51_P319732	NM_020560	mitochondrial ribosomal protein S31	1.099	79.26	0.83788	26934	P	-1.04	43.15	0.37494	7223
Nnp1	A_51_P452352	NM_010925	ribosomal RNA processing 1 homolog (S.	1.099	69.29	0.72464	19999	P	1.103	8.32	0.0745	2519
Nup160	A_52_P157037	NM_021512	nucleoporin 160	1.099	77.44	0.90714	27382	M	-1.098	9.71	0.07782	2597
Rab2	A_52_P303928	NM_021518	RAB2, member RAS oncogene family	1.099	72.2	0.83461	19770	M	1.073	16.2	0.22576	5283
Rhoq	A_51_P338317	NM_145491	ras homolog gene family, member Q	1.099	77.44	0.80592	24465	P	1.106	9.71	0.12486	3602
Tpp2	A_52_P488720	AK040859	tripeptidyl peptidase II	1.099	81.02	0.86033	28251	P	1.108	13.58	0.25735	5770
Zfp69	A_52_P478550	NM_001005788	zinc finger protein 69	1.099	79.26	0.83448	26506	P	1.07	13.58	0.13908	3830
1700017B05Rik	A_51_P268131	AK029230	RIKEN cDNA 1700017B05 gene	1.098	83.36	0.92982	23767	M	-1.296	0.51	0.00805	300
A130038J17Rik	A_52_P225856	AK038150	RIKEN cDNA A130038J17 gene	1.098	82.34	0.91371	32411	P	1.268	1.58	0.0155	661
Crkl	A_51_P350843	NM_007764	v-crk sarcoma virus CT10 oncogene homc	1.098	77.44	0.80717	24530	P	1.052	22.1	0.25361	5711
Hmga2	A_51_P288315	NM_010441	high mobility group AT-hook 2	1.098	81.02	0.86431	28462	P	1.151	4.63	0.04375	1635
Klhl12	A_51_P311091	NM_153128	kelch-like 12 (Drosophila)	1.098	75.14	0.78992	23434	P	-1.094	16.2	0.14183	3881
Lmo7	A_52_P299446	XM_895740	LIM domain only 7	1.098	72.2	0.74032	20645	P	-1.05	40.63	0.35133	6892
Pik3r1	A_51_P511236	NM_001077495	phosphatidylinositol 3-kinase, regulatory	1.098	79.26	0.85638	28066	P	1.073	22.1	0.40819	7595
Shmt1	A_52_P673499	NM_009171	serine hydroxymethyltransferase 1 (solub	1.098		0.94205	18045	A	1.06	16.2	0.19509	4817
Tomm7	A_52_P206547	NM_025394	translocase of outer mitochondrial memb	1.098	77.44	0.81815	25307	P	-1.012	49.48	0.84183	11536
Aprt	A_52_P594768	NM_009698	adenine phosphoribosyl transferase	1.097	75.14	0.78051	22805	P	-1.193	0.75	0.01232	500
Atp5a1	A_52_P674489	NM_007505	ATP synthase, H+ transporting, mitochond	1.097	75.14	0.84953	20485	M	1.285	1.17	0.01266	534
Fyco1	A_51_P158216	NM_148925	FYVE and coiled-coil domain containing 1	1.097	77.44	0.82024	25424	P	-1.04	43.75	0.41446	7669
Insig2	A_52_P113250	NM_178082	insulin induced gene 2	1.097	81.02	0.87393	29161	P	1.18	9.71	0.22538	5278
Kars	A_51_P154222	NM_053092	lysyl-tRNA synthetase	1.097	79.26	0.83817	26958	P	1.045	25.31	0.3817	7298

Lyar	A_51_P452189	NM_025281	Ly1 antibody reactive clone	1.097	81.02	0.8925	30447	P	1.076	16.2	0.19049	4742
Maz	A_52_P673304	NM_010772	MYC-associated zinc finger protein (purin	1.097	69.29	0.72992	20224	M	-1.072	33.49	0.28324	6122
Ndufs4	A_51_P388696	NM_010887	NADH dehydrogenase (ubiquinone) Fe-S p	1.097	79.26	0.8368	26871	P	1.102	16.2	0.31073	6464
Srp14	A_51_P111544	NM_009273	signal recognition particle 14	1.097	77.44	0.85639	20703	M	1.267	1.32	0.01222	496
Sult1d1	A_51_P481721	NM_016771	sulfotransferase family 1D, member 1	1.097	82.34	0.90935	31821	P	-1.045	49.48	0.88787	11938
1810026B05Rik	A_52_P67463	AK140938	RIKEN cDNA 1810026B05 gene	1.096	79.26	0.84587	27462	P	1.081	11.33	0.13274	3726
2310076G13Rik	A_51_P429111	AK010199	RIKEN cDNA 2310076G13 gene	1.096	79.26	0.83527	26720	P	-1.123	6.98	0.07777	2595
A930008G19Rik	A_51_P374190	NM_212473	RIKEN cDNA A930008G19 gene	1.096	81.02	0.87022	28914	P	1	49.48	0.99742	13030
Apc	A_52_P675171	NM_007462	adenomatosis polyposis coli	1.096	72.2	0.75683	21475	P	1.069	22.1	0.37567	7229
Atp10a	A_51_P320022	NM_009728	ATPase, class V, type 10A	1.096	82.34	0.90362	31358	M	-1.048	42.43	0.38401	7328
Auh	A_52_P4095	AK169661	AU RNA binding protein/enoyl-coenzyme	1.096	79.26	0.85443	27969	P	1.108	6.98	0.05213	1922
AW146242	A_51_P338040	NM_146168	expressed sequence AW146242	1.096	77.44	0.80833	24608	P	1.071	16.2	0.24262	5536
Deb1	A_51_P119715	NM_026794	differentially expressed in B16F10 1	1.096	77.44	0.86843	21140	M	1.064	22.1	0.37323	7203
Ebna1bp2	A_51_P455027	NM_026932	EBNA1 binding protein 2	1.096	79.26	0.84917	27686	P	1.006	42.43	0.91764	12245
Etfa	A_51_P131084	NM_145615	electron transferring flavoprotein, alpha p	1.096	79.26	0.84642	27523	P	1.136	5.75	0.04976	1848
Fabp5	A_51_P387764	X70100	fatty acid binding protein 5, epidermal	1.096	79.26	0.83499	26697	P	-1.107	9.71	0.09513	3001
Mpst	A_51_P200529	NM_138670	mercaptopyruvate sulfurtransferase	1.096	81.02	0.89022	30259	P	1.01	42.43	0.83907	11520
Ndufa2	A_51_P384946	NM_010885	NADH dehydrogenase (ubiquinone) 1 alpl	1.096	69.29	0.83603	19908	M	-1.066	42.43	0.52537	8802
Pja2	A_52_P420712	NM_001025309	praja 2, RING-H2 motif containing	1.096	72.2	0.84158	20157	M	1.11	9.71	0.14105	3867
Plxnb2	A_52_P311068	BC031202	plexin B2	1.096	81.02	0.86064	28263	P	1.07	16.2	0.18233	4614
Psme2	A_52_P305289	NM_011190	proteasome (prosome, macropain) 28 sul	1.096	77.44	0.79266	23652	P	-1.06	42.43	0.47523	8263
Rev3l	A_51_P271665	NM_011264	REV3-like, catalytic subunit of DNA polym	1.096	81.02	0.86086	28273	P	1.029	36.07	0.68165	10150
Rpl36	A_51_P361875	NM_018730	ribosomal protein L36	1.096	69.29	0.83369	19587	M	-1.071	40.63	0.46054	8107
Srp9	A_52_P321791	AK003606	signal recognition particle 9	1.096	79.26	0.85201	27869	P	1.043	30.75	0.61461	9571
Tcf19	A_51_P505172	NM_025674	transcription factor 19	1.096	82.34	0.91999	33032	P	-1.048	43.15	0.43307	7873
1700041B20Rik	A_51_P263407	AK028913	RIKEN cDNA 1700041B20 gene	1.095	83.95	0.95478	35862	P	1.036	30.75	0.4643	8153
Acbd6	A_51_P208919	NM_028250	acyl-Coenzyme A binding domain contain	1.095	75.14	0.77768	22613	P	-1.139	4.63	0.06647	2332
B230219D22Rik	A_52_P75384	NM_181278	RIKEN cDNA B230219D22 gene	1.095	77.44	0.82254	25558	P	1.077	13.58	0.14569	3957
Bcas2	A_52_P180408	NM_026602	breast carcinoma amplified sequence 2	1.095	81.02	0.89861	22380	M	1.103	8.32	0.06445	2262
Bmpr1b	A_52_P586944	NM_007560	bone morphogenetic protein receptor, typ	1.095	83.36	0.94291	34802	P	1.001	42.43	0.97829	12824
Eral1	A_52_P464096	AK018664	Era (G-protein)-like 1 (E. coli)	1.095	77.44	0.8135	24945	P	-1.042	45.05	0.58699	9318
Gdpd5	A_51_P468464	NM_201352	glycerophosphodiester phosphodiesteras	1.095	82.34	0.91144	32102	P	-1.101	28.13	0.33845	6763
Jmjd2b	A_51_P410286	NM_172132	jumonji domain containing 2B	1.095	81.02	0.89162	30356	P	-1.079	25.31	0.16913	4375
Mcts1	A_51_P385749	NM_026902	malignant T cell amplified sequence 1	1.095	77.44	0.86047	20826	M	1.091	16.2	0.27036	5962
Psmb2	A_51_P404084	NM_011970	proteasome (prosome, macropain) subun	1.095	82.34	0.91231	32219	P	-1.147	5.75	0.10651	3212
Scamp3	A_51_P482639	NM_011886	secretory carrier membrane protein 3	1.095	79.26	0.82999	26062	P	-1.01	49.48	0.89991	12066
Snrpe	A_51_P363634	NM_009227	small nuclear ribonucleoprotein E	1.095	69.29	0.74454	20821	P	1.021	38.4	0.68383	10182
Wrn	A_52_P478236	NM_011721	Werner syndrome homolog (human)	1.095	79.26	0.8356	26808	P	1.044	25.31	0.33182	6701
Ywhae	A_52_P171715	NM_009536	tyrosine 3-monooxygenase/tryptophan 5-	1.095	81.02	0.90708	22792	M	1.222	1.58	0.01057	404
2310047O13Rik	A_51_P429472	NM_024185	RIKEN cDNA 2310047O13 gene	1.094	77.44	0.80336	24276	P	-1.124	6.98	0.08015	2664
3110050N22Rik	A_51_P266546	NM_173181	RIKEN cDNA 3110050N22 gene	1.094	75.14	0.82983	21231	M	-1.035	46.85	0.65776	9952
Aldh9a1	A_51_P106211	NM_019993	aldehyde dehydrogenase 9, subfamily A1	1.094	75.14	0.77858	22689	P	1.006	42.43	0.90768	12167
Arpc3	A_51_P129767	NM_019824	actin related protein 2/3 complex, subuni	1.094	82.34	0.89905	30925	P	1.049	19.02	0.25385	5715
Gkap1	A_51_P459320	NM_019832	G kinase anchoring protein 1	1.094	79.26	0.83233	26240	P	-1.039	43.15	0.37794	7254
Gna12	A_52_P647906	XM_986527	guanine nucleotide binding protein, alpha	1.094	81.02	0.89437	30623	P	1.071	22.1	0.38615	7348
Hmgcl	A_51_P308961	NM_008254	3-hydroxy-3-methylglutaryl-Coenzyme A l	1.094	72.2	0.76247	21803	P	1.08	19.02	0.32595	6627
Sfrs11	A_51_P149818	NM_026989	splicing factor, arginine/serine-rich 11	1.094	82.34	0.9087	31723	P	1.162	3.01	0.01963	839
Slmap	A_52_P679966	NM_032008	sarcolemma associated protein	1.094	75.14	0.78304	22941	P	1.041	30.75	0.4984	8567
Suz12	A_52_P302203	NM_199196	suppressor of zeste 12 homolog (Drosoph	1.094	77.44	0.81696	25221	P	-1.083	28.13	0.25393	5720
Ubxd2	A_52_P170610	NM_026390	UBX domain containing 2	1.094	81.02	0.86668	28630	P	1.126	5.75	0.04695	1751
Xrn2	A_52_P404403	NM_011917	5'-3' exoribonuclease 2	1.094	81.02	0.86882	28813	P	1.034	33.49	0.55297	9052
A830073O21Rik	A_51_P500726	AK080460	RIKEN cDNA A830073O21 gene	1.093	83.36	0.93538	34246	P	1.056	22.1	0.27356	6006
Crry	A_52_P295129	AK017702	complement receptor related protein	1.093	81.02	0.83461	24876	M	1.195	2.53	0.02152	905

Prkcb1	A_52_P51355	NM_008855	protein kinase C, beta 1	1.093	69.29	0.82344	22551	P	1.176	6.98	0.11081	3288
Psmb4	A_51_P155522	NM_008945	proteasome (prosome, macropain) subun	1.093	72.2	0.84642	20376	M	1.195	3.01	0.02628	1080
Rala	A_52_P672740	NM_019491	v-ral simian leukemia viral oncogene hom	1.093	72.2	0.76707	22034	P	1.115	8.32	0.08606	2796
Ube2e1	A_51_P390775	NM_009455	ubiquitin-conjugating enzyme E2E 1, UBC	1.093	72.2	0.75297	21278	P	1.113	11.33	0.15274	4084
Usp6nl	A_51_P442719	NM_181399	USP6 N-terminal like	1.093	79.26	0.82709	25853	P	-1.061	33.49	0.25261	5690
Wt1	A_52_P673458	NM_144783	Wilms tumor homolog	1.093		0.96504	14469	A	1.061	16.2	0.18027	4578
1500012F01Rik	A_52_P598309	AK005231	RIKEN cDNA 1500012F01 gene	1.092	77.44	0.92376	30876	P	-1.045	43.15	0.3932	7439
Cryzl1	A_51_P413193	NM_133679	crystallin, zeta (quinone reductase)-like 1	1.092	77.44	0.82228	25549	P	1.175	5.75	0.09306	2966
Ddx27	A_51_P138772	AK134274	DEAD (Asp-Glu-Ala-Asp) box polypeptide	1.092	77.44	0.7964	23899	P	-1.017	49.48	0.76533	10896
Dusp7	A_52_P173197	NM_153459	dual specificity phosphatase 7	1.092	77.44	0.79717	23950	P	1.146	4.63	0.04498	1670
Fth1	A_52_P49601	NM_010239	ferritin heavy chain 1	1.092	79.26	0.88417	21755	M	1.131	5.75	0.04641	1737
Lrpprc	A_52_P366116	NM_028233	leucine-rich PPR-motif containing	1.092	77.44	0.80691	24514	P	-1.12	4.63	0.05039	1863
Ndufb5	A_51_P201904	NM_025316	NADH dehydrogenase (ubiquinone) 1 bet	1.092	79.26	0.84505	27404	P	1.073	16.2	0.25309	5699
Neurog3	A_51_P175784	NM_009719	neurogenin 3	1.092	75.14	0.78014	22761	P	1.001	42.43	0.98518	12934
Psmd5	A_51_P455671	NM_080554	proteasome (prosome, macropain) 26S su	1.092	79.26	0.84365	27299	P	1.039	28.13	0.36726	7131
Sepp1	A_51_P470328	NM_001042614	selenoprotein P, plasma, 1	1.092	83.36	0.9386	24412	M	1.388	1.58	0.03553	1378
Stim2	A_51_P260008	AK142275	stromal interaction molecule 2	1.092	79.26	0.83635	26829	P	1.117	11.33	0.19986	4902
Tbrg4	A_52_P612993	AK144813	transforming growth factor beta regulate	1.092	82.34	0.92057	33085	P	-1.072	30.75	0.26157	5839
Cabin1	A_52_P93422	NM_172549	calcineurin binding protein 1	1.091	79.26	0.83077	26090	M	1.162	4.63	0.04205	1586
Csnk1g2	A_51_P297311	NM_134002	casein kinase 1, gamma 2	1.091	82.34	0.90895	31776	P	-1.045	43.15	0.4138	7667
Ecm1	A_52_P154347	NM_007899	extracellular matrix protein 1	1.091	81.02	0.88421	29925	P	1.072	13.58	0.13222	3718
F830028O17Rik	A_52_P1067	AK089821	RIKEN cDNA F830028O17 gene	1.091	81.02	0.86322	28380	P	-1.059	40.63	0.36333	7065
Glt25d1	A_52_P346581	NM_146211	glycosyltransferase 25 domain containing	1.091	79.26	0.83652	26854	P	-1.254	0.56	0.01062	412
Gtf3c4	A_52_P73214	NM_172977	general transcription factor IIIC, polypept	1.091	82.34	0.90015	31002	P	1.079	19.02	0.29943	6307
Ltbp3	A_52_P652936	NM_008520	latent transforming growth factor beta bi	1.091	77.44	0.78753	21910	M	1.083	9.71	0.09627	3019
Nol5	A_51_P496751	NM_018868	nucleolar protein 5	1.091	81.02	0.89303	30507	P	-1.101	16.2	0.16711	4333
Ran	A_52_P344910	NM_009391	RAN, member RAS oncogene family	1.091	77.44	0.8659	21012	M	1.135	8.32	0.09908	3090
Slc30a5	A_52_P65165	AK051654	solute carrier family 30 (zinc transporter),	1.091	81.02	0.8711	28980	P	1.131	8.32	0.11874	3456
1500010J02Rik	A_52_P375918	AK030876	RIKEN cDNA 1500010J02 gene	1.09		0.93315	17939	A	-1.102	19.02	0.1945	4810
4930504E06Rik	A_52_P76899	NM_133858	RIKEN cDNA 4930504E06 gene	1.09	81.02	0.87776	29463	M	-1.003	49.48	0.95081	12594
AI585793	A_52_P424197	AK033788	expressed sequence AI585793	1.09	72.2	0.76328	21852	P	1.042	30.75	0.52026	8754
Dmtf1	A_51_P405882	NM_011806	cyclin D binding myb-like transcription fac	1.09	79.26	0.83384	26393	P	-1.015	49.48	0.82721	11430
Ltbp1	A_52_P189946	NM_019919	latent transforming growth factor beta bi	1.09	79.26	0.85581	28034	P	1.024	38.4	0.76582	10901
Mrps11	A_52_P582394	NM_026498	mitochondrial ribosomal protein S11	1.09	81.02	0.88204	29793	P	-1.04	44.4	0.46054	8112
Samhd1	A_52_P136316	AK128954	SAM domain and HD domain, 1	1.09	79.26	0.86155	26833	M	1.07	16.2	0.17232	4411
2810410M20Rik	A_51_P185103	NM_024428	RIKEN cDNA 2810410M20 gene	1.089	79.26	0.83817	26998	P	1.064	16.2	0.19264	4787
C1s	A_51_P208793	NM_144938	complement component 1, s subcompon	1.089	81.02	0.89123	30306	P	-1.073	36.07	0.37192	7190
Crlz1	A_52_P429289	NM_023054	charged amino acid rich leucine zipper 1	1.089	75.14	0.78828	23301	P	1.017	40.63	0.76095	10863
Mapk7	A_51_P359017	NM_011841	mitogen activated protein kinase 7	1.089	82.34	0.91612	32703	P	-1.001	49.48	0.9828	12884
Mvd	A_51_P355943	NM_138656	mevalonate (diphospho) decarboxylase	1.089	77.44	0.82288	25614	P	1.044	25.31	0.37128	7187
Ugp2	A_52_P42242	NM_139297	UDP-glucose pyrophosphorylase 2	1.089	81.02	0.8711	28973	P	1.223	3.46	0.04586	1719
Abcb10	A_52_P571431	AK011569	ATP-binding cassette, sub-family B (MDR/	1.088	82.34	0.83938	25240	M	-1.107	19.02	0.20159	4931
Dnaja2	A_52_P510706	NM_019794	DnaJ (Hsp40) homolog, subfamily A, mem	1.088	77.44	0.80242	24179	P	1.142	8.32	0.12137	3530
Dnm1l	A_52_P66333	NM_152816	dynamin 1-like	1.088	82.34	0.91836	32868	P	-1.122	3.82	0.04696	1752
Fts	A_52_P174313	NM_010241	thymoma viral proto-oncogene 1 interact	1.088	81.02	0.8666	28621	P	1.11	8.32	0.07774	2592
Mpi1	A_51_P393897	NM_025837	mannose phosphate isomerase 1	1.088	81.02	0.87354	29142	P	1.019	38.4	0.64455	9840
Pgm2	A_51_P368074	NM_028132	phosphoglucomutase 2	1.088	75.14	0.79483	23816	P	1.062	19.02	0.25081	5655
Ptpre	A_52_P235319	NM_011212	protein tyrosine phosphatase, receptor ty	1.088	82.34	0.92533	33475	P	-1.247	0.66	0.01267	535
Qdpr	A_51_P506513	NM_024236	quinoid dihydropteridine reductase	1.088	77.44	0.80689	24504	P	1.352	9.71	0.41258	7641
Rpl8	A_51_P165046	NM_012053	ribosomal protein L8	1.088	72.2	0.85396	20637	M	1.001	42.43	0.98171	12873
Sema6c	A_51_P324251	NM_011351	sema domain, transmembrane domain (T	1.088	75.14	0.78613	23137	P	-1.151	1.32	0.02161	909
Set	A_52_P212293	AK054400	SET translocation	1.088		0.93488	17986	A	1.075	22.1	0.48529	8387
Slc23a2	A_52_P286520	NM_018824	solute carrier family 23 (nucleobase trans	1.088	75.14	0.79241	23617	P	1.205	3.01	0.03116	1232

Trim39	A_52_P601497	AK053591	tripartite motif protein 39	1.088	79.26	0.8299	26058	P	-1.235	1.18	0.02586	1064
2310016C08Rik	A_52_P321150	NM_023516	RIKEN cDNA 2310016C08 gene	1.087	82.34	0.9098	31928	P	-1.138	8.32	0.12097	3509
5430437P03Rik	A_52_P575078	NM_026636	RIKEN cDNA 5430437P03 gene	1.087	75.14	0.7912	23543	P	-1.05	40.63	0.32282	6595
BC056474	A_51_P307062	NM_001001493	cDNA sequence BC056474	1.087	75.14	0.79021	23469	P	1.065	19.02	0.26484	5872
C030011O14Rik	A_51_P339524	NM_174868	RIKEN cDNA C030011O14 gene	1.087	75.14	0.78992	23432	P	1.069	19.02	0.34167	6789
Cbx2	A_51_P300245	NM_007623	chromobox homolog 2 (Drosophila Pc cla	1.087	77.44	0.81096	23405	M	-1.313	0.51	0.01227	435
Cdk2	A_52_P651298	NM_016756	cyclin-dependent kinase 2	1.087		0.93771	18078	A	-1.196	1.18	0.02243	947
Hoxa3	A_52_P447935	NM_010452	homeo box A3	1.087	82.34	0.83334	23092	M	1.035	30.75	0.42434	7772
Myadm	A_52_P645589	AK159160	myeloid-associated differentiation marke	1.087	79.26	0.84158	27189	P	-1.218	1.1	0.01893	795
Nubp1	A_51_P123077	NM_011955	nucleotide binding protein 1	1.087	79.26	0.83461	26612	P	1.019	40.63	0.78537	11051
Pax5	A_51_P122855	NM_008782	paired box gene 5	1.087	72.2	0.82118	22411	M	-1.037	45.68	0.57127	9204
Pck2	A_52_P21659	NM_028994	phosphoenolpyruvate carboxykinase 2 (	1.087	79.26	0.83558	26804	P	1.081	13.58	0.13943	3838
Plk2	A_51_P290576	NM_152804	polo-like kinase 2 (Drosophila)	1.087	79.26	0.8447	27367	P	1.256	1.1	0.00755	275
Pmpcb	A_51_P151038	NM_028431	peptidase (mitochondrial processing) bet	1.087	81.02	0.87727	29415	P	-1.208	0.75	0.01189	473
Rnf167	A_51_P364328	AK075579	ring finger protein 167	1.087	79.26	0.83045	26078	P	1.095	9.71	0.10343	3178
Stx18	A_51_P147964	NM_026959	syntaxin 18	1.087	75.14	0.79138	23552	P	-1.125	2.53	0.03417	1315
Cyp21a1	A_52_P594116	NM_009995	cytochrome P450, family 21, subfamily a,	1.086	75.14	0.81271	21916	M	-1.033	45.05	0.49722	8547
Dhx33	A_52_P286342	NM_178367	DEAH (Asp-Glu-Ala-His) box polypeptide	1.086	81.02	0.89351	30543	P	1.131	9.71	0.19672	4848
Eif4a2	A_52_P344376	NM_013506	eukaryotic translation initiation factor 4A	1.086	82.34	0.91805	32804	P	1.025	36.07	0.59305	9366
Sod2	A_51_P172573	NM_013671	superoxide dismutase 2, mitochondrial	1.086	75.14	0.78021	22775	P	1.013	42.43	0.85137	11601
Abca3	A_51_P427317	NM_013855	ATP-binding cassette, sub-family A (ABC1)	1.085	65.79	0.80911	21745	M	1.002	42.43	0.96261	12687
Anxa6	A_51_P231979	NM_013472	annexin A6	1.085	79.26	0.85201	27863	P	1.131	5.75	0.04067	1549
Cdc42	A_52_P259214	L78075	cell division cycle 42 homolog (S. cerevisi	1.085	81.02	0.87616	29340	P	1.046	30.75	0.6266	9687
Ddx24	A_51_P277389	NM_020494	DEAD (Asp-Glu-Ala-Asp) box polypeptide	1.085	79.26	0.83883	27029	P	1.021	40.63	0.81451	11323
Fabp4	A_52_P564544	NM_024406	fatty acid binding protein 4, adipocyte	1.085	82.34	0.89818	30823	P	-1.094	40.63	0.59149	9341
Map1lc3a	A_51_P464981	NM_025735	microtubule-associated protein 1 light ch	1.085	81.02	0.89029	30261	P	1.032	33.49	0.54783	9005
Mc3r	A_51_P467278	NM_008561	melanocortin 3 receptor	1.085	77.44	0.83448	23198	M	-1.255	2.53	0.10735	3225
Psma4	A_52_P81468	NM_011966	proteasome (prosome, macropain) subun	1.085	82.34	0.90138	31083	P	1.123	8.32	0.07873	2620
Vdac2	A_51_P162253	NM_011695	voltage-dependent anion channel 2	1.085	81.02	0.89812	22352	M	1.235	1.32	0.00979	365
Zfp64	A_52_P626780	BC004695	zinc finger protein 64	1.085	77.44	0.81316	24933	P	-1.223	0.51	0.00875	319
1300012G16Rik	A_52_P370311	NM_023625	RIKEN cDNA 1300012G16 gene	1.084	83.36	0.93906	34503	P	-1.356	0.51	0.00591	109
Adam10	A_51_P406115	NM_007399	a disintegrin and metallopeptidase doma	1.084	77.44	0.81904	25358	P	1.108	11.33	0.19231	4781
Atp5j2	A_51_P224216	NM_020582	ATP synthase, H+ transporting, mitochon	1.084	77.44	0.8711	21254	M	1.006	42.43	0.90021	12075
Chd4	A_52_P298043	NM_145979	chromodomain helicase DNA binding pro	1.084	79.26	0.85201	27871	P	1.201	2.04	0.01485	638
Chordc1	A_52_P637199	NM_025844	cysteine and histidine-rich domain (CHOR	1.084	82.34	0.89913	30930	P	-1.012	49.48	0.94037	12484
Ddx18	A_51_P235291	NM_025860	DEAD (Asp-Glu-Ala-Asp) box polypeptide	1.084	81.02	0.86362	28437	P	1.01	42.43	0.90417	12135
Dnajc2	A_52_P533198	NM_009584	DnaJ (Hsp40) homolog, subfamily C, mem	1.084	81.02	0.88204	29796	P	-1.073	30.75	0.26817	5918
Dock7	A_51_P141110	NM_026082	dedicator of cytokinesis 7	1.084	81.02	0.88339	29869	P	1.259	1.62	0.01974	840
Hnf4a	A_52_P69656	NM_008261	hepatic nuclear factor 4, alpha	1.084		0.91937	20654	A	1.184	6.98	0.14014	3857
Psma2	A_51_P415945	NM_008944	proteasome (prosome, macropain) subun	1.084	81.02	0.89008	30251	P	1.081	13.58	0.16704	4331
Sparc	A_52_P101852	NM_009242	secreted acidic cysteine rich glycoprotein	1.084	81.02	0.88993	30242	P	1.359	2.04	0.04945	1828
4933434E20Rik	A_52_P467128	NM_027500	RIKEN cDNA 4933434E20 gene	1.083	77.44	0.82564	25730	P	1.11	16.2	0.33018	6665
Baz1b	A_51_P463828	NM_011714	bromodomain adjacent to zinc finger do	1.083	81.02	0.85727	28093	P	1.185	3.01	0.02439	1004
Chuk	A_51_P223475	NM_007700	conserved helix-loop-helix ubiquitous kin	1.083	77.44	0.8256	25724	P	1.084	13.58	0.15353	4103
D4Ertd22e	A_51_P503696	NM_001025608	DNA segment, Chr 4, ERATO Doi 22, expre	1.083	82.34	0.915	32488	P	-1.032	45.68	0.54024	8949
Fbxw9	A_51_P155556	BC002276	F-box and WD-40 domain protein 9	1.083	81.02	0.88181	29776	P	1.202	2.53	0.02195	932
Ikbkap	A_51_P114878	NM_026079	inhibitor of kappa light polypeptide enha	1.083	77.44	0.82196	25488	P	1.22	3.82	0.06242	2207
Mbnl1	A_52_P228437	AK088871	muscleblind-like 1 (Drosophila)	1.083	81.02	0.85689	28090	P	1.069	25.31	0.51223	8694
Nubp2	A_51_P490171	NM_011956	nucleotide binding protein 2	1.083	81.02	0.86052	28257	P	-1.099	8.32	0.07062	2412
Ptp4a2	A_52_P585448	NM_008974	protein tyrosine phosphatase 4a2	1.083	79.26	0.85451	27976	P	1.035	36.07	0.73073	10577
Sgta	A_51_P346104	NM_024499	small glutamine-rich tetratricopeptide re	1.083	82.34	0.89647	30732	P	-1.191	1.18	0.01663	718
Snap25	A_52_P286421	NM_011428	synaptosomal-associated protein 25	1.083	82.34	0.92017	23614	M	1.247	3.82	0.0971	3040
Usp14	A_52_P276248	NM_021522	ubiquitin specific peptidase 14	1.083	81.02	0.86423	28457	P	1.193	3.82	0.05026	1858

3110002H16Rik	A_52_P112931	NM_029623	RIKEN cDNA 3110002H16 gene	1.082	82.34	0.90549	31475	P	1.172	4.63	0.05574	2022
8430419L09Rik	A_52_P116628	BC079676	RIKEN cDNA 8430419L09 gene	1.082	81.02	0.87291	29113	P	-1.497	0	0.00584	11
Als2	A_51_P180061	NM_028717	amyotrophic lateral sclerosis 2 (juvenile) l	1.082	81.02	0.84434	23873	M	1.175	3.82	0.03882	1462
Aspn	A_51_P142813	NM_025711	asporin	1.082	81.02	0.87464	29213	P	1.021	38.4	0.69959	10314
Bri3	A_51_P126643	NM_018772	brain protein I3	1.082	82.34	0.8965	30737	P	-1.324	0.51	0.00627	140
Cdca8	A_52_P463220	AK031571	cell division cycle associated 8	1.082	82.34	0.89289	28533	M	1.12	8.32	0.0794	2641
Eea1	A_51_P224617	NM_001001932	early endosome antigen 1	1.082	81.02	0.87933	29624	P	1.002	42.43	0.98357	12895
Gbe1	A_51_P273684	NM_028803	glucan (1,4-alpha-), branching enzyme 1	1.082	72.2	0.89158	24337	M	1.145	3.82	0.02595	1069
Heyl	A_52_P337259	NM_013905	hairy/enhancer-of-split related with YRPV	1.082	81.02	0.83384	24753	M	1.04	30.75	0.46638	8171
Hmbs	A_51_P155361	NM_013551	hydroxymethylbilane synthase	1.082	84.22	0.85614	26324	P	1.043	33.49	0.634	9756
Immt	A_51_P485556	NM_029673	inner membrane protein, mitochondrial	1.082	72.2	0.78867	23339	P	1.07	25.31	0.46231	8136
Mars2	A_51_P396385	NM_175439	methionine-tRNA synthetase 2 (mitochon	1.082	81.02	0.86362	28438	P	-1.091	11.33	0.09402	2981
Usmg5	A_51_P181365	NM_023211	upregulated during skeletal muscle growt	1.082	72.2	0.78638	23153	P	-1.023	47.92	0.63446	9758
2610033H07Rik	A_51_P246705	NM_029278	nucleolar protein 14	1.081	82.34	0.91173	32132	P	1.069	13.58	0.15566	4142
Ap1m1	A_51_P190805	NM_007456	adaptor-related protein complex AP-1, mu	1.081	83.36	0.93538	34232	P	1.069	16.2	0.21835	5174
Atp5c1	A_51_P378087	NM_020615	ATP synthase, H+ transporting, mitochonc	1.081	72.2	0.84973	22297	M	1.106	13.58	0.23923	5472
Cebpa	A_52_P168567	NM_007678	CCAAT/enhancer binding protein (C/EBP),	1.081	84.22	0.96215	36657	P	1.039	28.13	0.43876	7910
Csnk2b	A_51_P373379	NM_009975	casein kinase 2, beta polypeptide	1.081	82.34	0.91547	32636	P	1.067	19.02	0.27939	6086
Ech1	A_51_P421846	NM_016772	enoyl coenzyme A hydratase 1, peroxison	1.081	81.02	0.88647	30056	P	1.056	22.1	0.35022	6877
Eif2s2	A_52_P107354	NM_026030	eukaryotic translation initiation factor 2, s	1.081	82.34	0.90996	31938	P	-1.056	45.68	0.69683	10292
Gabpb1	A_52_P331701	NM_207669	GA repeat binding protein, beta 1	1.081	72.2	0.78777	23248	P	1.084	13.58	0.21375	5094
Lgi2	A_52_P446364	AK122570	leucine-rich repeat LGI family, member 2	1.081	82.34	0.91013	31973	P	1.027	33.49	0.5401	8947
Lpxn	A_51_P419147	NM_134152	leupaxin	1.081	84.22	0.96604	37125	P	1.077	19.02	0.35337	6930
Ndufv1	A_51_P364339	NM_133666	NADH dehydrogenase (ubiquinone) flavo	1.081	79.26	0.85089	27773	P	1.035	30.75	0.47895	8299
Pex19	A_51_P427177	NM_023041	peroxisome biogenesis factor 19	1.081	77.44	0.81427	25000	P	1.084	11.33	0.13417	3752
Prkcc	A_51_P290290	NM_011102	protein kinase C, gamma	1.081	79.26	0.83927	27064	P	1.063	22.1	0.30678	6400
Smarcd3	A_51_P423880	NM_025891	SWI/SNF related, matrix associated, actin	1.081	79.26	0.83534	26730	P	1.035	36.07	0.73541	10639
Tbc1d8	A_51_P448005	NM_018775	TBC1 domain family, member 8	1.081	79.26	0.83817	26991	P	-1.197	1.1	0.01654	709
Tbx6	A_51_P105991	NM_011538	T-box 6	1.081	81.02	0.8711	28993	P	-1.002	49.48	0.9753	12789
Unc13b	A_52_P1005171	AK161056	unc-13 homolog B (C. elegans)	1.081	81.02	0.88461	29969	P	1.002	42.43	0.96667	12716
Wisp1	A_51_P220343	NM_018865	WNT1 inducible signaling pathway protei	1.081	79.26	0.83388	26423	P	-1.038	43.75	0.41184	7631
Acadvl	A_51_P518340	NM_017366	acyl-Coenzyme A dehydrogenase, very lo	1.08	69.29	0.7874	23222	P	1.05	22.1	0.31396	6510
Atp6v1d	A_51_P393598	NM_023721	ATPase, H+ transporting, lysosomal V1 su	1.08	81.02	0.90781	22829	M	1.197	5.75	0.12525	3608
Dhcr7	A_51_P290986	NM_007856	7-dehydrocholesterol reductase	1.08	82.34	0.89818	30822	P	-1.021	49.48	0.90809	12179
Dhx29	A_52_P250278	NM_172594	DEAH (Asp-Glu-Ala-His) box polypeptide 2	1.08	82.34	0.91243	32233	P	-1.087	22.1	0.18331	4633
Gnat2	A_51_P359411	NM_008141	guanine nucleotide binding protein, alpha	1.08	82.34	0.90914	31804	P	1.122	6.98	0.05167	1902
Meis1	A_52_P670612	NM_010789	myeloid ecotropic viral integration site 1	1.08	77.44	0.80959	24675	P	1.149	11.33	0.24826	5621
Phf21a	A_52_P505357	AK089411	PHD finger protein 21A	1.08		0.94102	29571	A	1.074	16.2	0.23039	5357
Reck	A_51_P271887	NM_016678	reversion-inducing-cysteine-rich protein v	1.08	82.34	0.90095	31049	P	-1.287	0.51	0.00627	150
Rgs5	A_51_P354934	AK028765	regulator of G-protein signaling 5	1.08	81.02	0.86744	28698	P	1.081	13.58	0.17145	4403
Tpr	A_51_P221802	NM_133780	translocated promoter region	1.08	81.02	0.86511	28523	P	-1.056	33.49	0.23223	5383
1200009I06Rik	A_51_P204486	NM_028807	RIKEN cDNA 1200009I06 gene	1.079	84.22	0.9617	36613	P	-1.015	49.48	0.84594	11569
Cdc34	A_52_P661496	XM_982476	cell division cycle 34 homolog (S. cerevisi	1.079	81.02	0.8816	27910	M	1.095	13.58	0.19532	4824
Cyp4a14	A_51_P238576	NM_007822	cytochrome P450, family 4, subfamily a, p	1.079	82.34	0.90152	31102	P	1.143	5.75	0.06192	2187
Fgf6	A_52_P155536	NM_010204	fibroblast growth factor 6	1.079	83.36	0.8666	27100	M	1.126	5.75	0.03957	1506
Fkhl18	A_51_P296249	NM_010226	forkhead-like 18 (Drosophila)	1.079	77.44	0.82996	26060	P	1.003	42.43	0.96107	12674
Git1	A_52_P165059	NM_001004144	G protein-coupled receptor kinase-intera	1.079	81.02	0.8659	28561	P	-1.026	46.3	0.53961	8935
Lman2	A_52_P112651	NM_025828	lectin, mannose-binding 2	1.079	79.26	0.8356	26807	P	-1.134	6.98	0.09995	3103
Net1	A_52_P421499	AK020636	neuroepithelial cell transforming gene 1	1.079	82.34	0.82983	24522	P	-1.003	49.48	0.97829	12827
Phox2b	A_51_P494491	NM_008888	paired-like homeobox 2b	1.079	83.95	0.95727	36105	P	1.061	25.31	0.4022	7537
Pitpnc1	A_52_P1028214	AK171340	phosphatidylinositol transfer protein, cyt	1.079	82.34	0.90781	27435	M	1.012	42.43	0.84131	11534
Polr2e	A_52_P973604	BC045521	polymerase (RNA) II (DNA directed) polyp	1.079	81.02	0.87382	29150	P	1.061	16.2	0.20332	4943
Prdx2	A_52_P893440	NM_011563	peroxiredoxin 2	1.079	82.34	0.91866	32929	P	-1.12	9.71	0.10985	3262

1110007L15Rik	A_52_P488200	NM_026269	RIKEN cDNA 1110007L15 gene	1.078	82.34	0.92451	33419	P	1.024	38.4	0.77123	10936
AU016693	A_52_P152240	NM_178686	coiled-coil domain containing 100	1.078	79.26	0.84699	27553	P	1.015	40.63	0.73869	10671
D8Ertd354e	A_51_P467751	NM_029884	heparan-alpha-glucosaminide N-acetyltra	1.078	82.34	0.89827	30838	P	-1.212	0.92	0.0153	654
Dpp8	A_52_P481202	NM_028906	dipeptidylpeptidase 8	1.078	81.02	0.86086	28270	P	1.05	25.31	0.38497	7338
Nup37	A_51_P351009	NM_028334	nucleoporin 37	1.078	82.34	0.8968	30765	P	1.067	19.02	0.26029	5814
Sipa1l2	A_52_P26318	BC072593	signal-induced proliferation-associated 1	1.078	81.02	0.86175	28340	P	1.035	30.75	0.50083	8588
Sp100	A_51_P255016	XM_976918	nuclear antigen Sp100	1.078	81.02	0.82885	24456	M	-1.061	30.75	0.2043	4956
Supt16h	A_51_P280532	NM_033618	suppressor of Ty 16 homolog (S. cerevisia	1.078	77.44	0.81482	25067	P	-1.04	45.05	0.57286	9209
Thrb	A_52_P265108	NM_009380	thyroid hormone receptor beta	1.078	81.02	0.90137	29118	P	1.022	36.07	0.6048	9488
4930533K18Rik	A_52_P305841	AK017042	RIKEN cDNA 4930533K18 gene	1.077		0.9138	20589	A	1.161	8.32	0.15167	4060
5430411K18Rik	A_52_P630571	XM_973419	RIKEN cDNA 5430411K18 gene	1.077	81.02	0.86856	28790	P	1.074	16.2	0.18898	4708
Copa	A_52_P272519	NM_009938	coatomer protein complex subunit alpha	1.077	81.02	0.88869	30175	P	1.252	3.01	0.04563	1712
Gabarapl2	A_52_P2015	NM_026693	gamma-aminobutyric acid (GABA-A) recep	1.077	81.02	0.88592	30016	P	1.355	1.62	0.0338	1308
Mod1	A_51_P186601	M29546	malic enzyme, supernatant	1.077	81.02	0.8754	29311	P	1.065	19.02	0.23298	5397
Pex1	A_52_P682456	AK082305	peroxisome biogenesis factor 1	1.077	81.02	0.89192	30408	P	-1.059	36.07	0.29561	6280
Rhoj	A_52_P592466	NM_023275	ras homolog gene family, member J	1.077	82.34	0.90804	31663	P	1.112	8.32	0.06488	2281
Skiv2l2	A_51_P476711	NM_028151	superkiller viralicidic activity 2-like 2 (S. ce	1.077	77.44	0.81686	25213	P	-1.045	43.75	0.46161	8121
Tbce	A_51_P351137	NM_178337	tubulin-specific chaperone e	1.077	82.34	0.90474	31417	P	1.1	11.33	0.12036	3501
Tpd52	A_52_P151853	NM_001025262	tumor protein D52	1.077	83.36	0.93304	34038	P	1.368	0.24	0.00619	119
Atp13a2	A_51_P507942	NM_029097	ATPase type 13A2	1.076	83.36	0.92446	33400	P	-1.02	48.7	0.68852	10224
Casp3	A_51_P382618	U49929	caspase 3	1.076	82.34	0.90137	31074	P	-1.038	47.43	0.74234	10706
D10Ertd438e	A_52_P266909	XM_992169		1.076	79.26	0.83817	26990	P	-1.117	9.71	0.10441	3194
Ikbkb	A_52_P64364	NM_010546	inhibitor of kappaB kinase beta	1.076	81.02	0.87678	29372	P	1.073	16.2	0.17362	4437
Lrrk1	A_52_P212686	NM_146191	leucine-rich repeat kinase 1	1.076	83.36	0.91949	30573	M	-1.078	25.31	0.19852	4875
Nfx1	A_51_P376765	NM_023739	nuclear transcription factor, X-box binding	1.076	82.34	0.90474	31419	P	1.07	25.31	0.49593	8517
P4ha2	A_52_P663413	NM_011031	procollagen-proline, 2-oxoglutarate 4-diox	1.076	81.02	0.88376	29892	P	1.026	33.49	0.55596	9074
Pole4	A_51_P465043	NM_025882	polymerase (DNA-directed), epsilon 4 (p1	1.076	81.02	0.86523	28534	P	-1.224	1.18	0.02331	980
Vps13d	A_52_P963388	AK035276	vacuolar protein sorting 13 D (yeast)	1.076	79.26	0.93538	24054	M	1.029	33.49	0.51806	8748
Wtip	A_52_P481686	NM_207212	WT1-interacting protein	1.076	79.26	0.83288	26319	P	1.033	30.75	0.44065	7927
1810034K20Rik	A_51_P102652	NM_023397	RIKEN cDNA 1810034K20 gene	1.075	81.02	0.87673	29368	P	-1.098	11.33	0.09709	3038
Cab39	A_51_P230934	NM_133781	calcium binding protein 39	1.075	79.26	0.85443	27970	P	1.05	28.13	0.47441	8247
Carm1	A_52_P119883	NM_021531	coactivator-associated arginine methyltra	1.075	79.26	0.84505	25557	P	1.022	38.4	0.66683	10018
D15Ertd621e	A_52_P100506	NM_145959	DNA segment, Chr 15, ERATO Doi 621, exp	1.075	75.14	0.81473	25051	P	1.078	16.2	0.23633	5442
Edg5	A_51_P499871	NM_010333	endothelial differentiation, sphingolipid G	1.075		0.94912	18401	A	1.008	42.43	0.85207	11613
Gpr126	A_52_P414645	NM_001002268	G protein-coupled receptor 126	1.075	84.4	0.97049	37480	P	1.05	28.13	0.44509	7962
Mmaa	A_51_P270364	NM_133823	methylmalonic aciduria (cobalamin defici	1.075	79.26	0.83967	27102	P	1.006	42.43	0.92631	12360
Nfatc4	A_52_P342159	NM_023699	nuclear factor of activated T-cells, cytopla	1.075	83.95	0.95723	36104	P	-1.085	22.1	0.17545	4488
Nup188	A_51_P421041	U89435	nucleoporin 188	1.075		0.90522	22560	A	-1.074	19.02	0.1233	3565
Oaz2	A_52_P90289	NM_010952	ornithine decarboxylase antizyme 2	1.075	79.26	0.83448	26513	P	-1.013	49.48	0.77199	10939
Pkd2	A_52_P234729	NM_008861	polycystic kidney disease 2	1.075	82.34	0.9349	24258	M	-1.046	42.43	0.37807	7256
Rnf44	A_52_P536000	AK129290	ring finger protein 44	1.075	77.44	0.83198	26199	P	-1.385	0.51	0.00584	69
Suclg1	A_51_P491227	NM_019879	succinate-CoA ligase, GDP-forming, alpha	1.075	81.02	0.8711	28996	P	1.139	5.75	0.05307	1957
Trim44	A_52_P468821	NM_020267	tripartite motif-containing 44	1.075	81.02	0.8701	28891	P	1.116	6.98	0.05288	1945
Txndc5	A_52_P535561	NM_145367	thioredoxin domain containing 5	1.075	79.26	0.84326	27288	P	1.017	38.4	0.70466	10354
1700006J14Rik	A_51_P422223	NM_177313	RIKEN cDNA 1700006J14 gene	1.074	75.14	0.81013	24703	P	1.027	33.49	0.54758	9003
3110045G13Rik	A_51_P409583	AK042308	RIKEN cDNA 3110045G13 gene	1.074		0.9493	18412	A	-1.022	48.39	0.68076	10139
Atp1b1	A_51_P151484	NM_009721	ATPase, Na+/K+ transporting, beta 1 poly	1.074	77.44	0.82688	25843	P	1.297	0.66	0.00662	194
Dab2ip	A_52_P622471	NM_001001602	disabled homolog 2 (Drosophila) interacti	1.074	81.02	0.85901	28162	P	-1.039	45.05	0.53168	8856
Dgkq	A_51_P329869	NM_199011	diacylglycerol kinase, theta	1.074	82.34	0.9045	31390	P	1.013	42.43	0.88079	11867
Eif5	A_52_P336080	AK051980	eukaryotic translation initiation factor 5	1.074	82.34	0.8952	30667	P	1.153	3.46	0.02405	1001
Hbp1	A_52_P39247	NM_153198	high mobility group box transcription fact	1.074	79.26	0.85257	27909	P	-1.049	42.43	0.3622	7052
Hist2h3c1	A_51_P359462	NM_178216	histone cluster 2, H3c1	1.074	82.34	0.95092	30208	P	1.186	3.82	0.03829	1455
Nvl	A_51_P232954	NM_026171	nuclear VCP-like	1.074	83.36	0.92982	33741	P	1.087	11.33	0.11002	3264

Rab11b	A_52_P160257	NM_008997	RAB11B, member RAS oncogene family	1.074	79.26	0.83817	26978	P	1.183	4.63	0.05681	2054
Rab40b	A_51_P211471	NM_139147	Rab40b, member RAS oncogene family	1.074	83.36	0.89672	28805	M	1.03	36.07	0.63989	9810
Rer1	A_51_P512002	NM_026395	RER1 retention in endoplasmic reticulum	1.074	82.34	0.91789	23461	M	-1.022	47.92	0.63181	9734
Ube3a	A_52_P625244	NM_011668	ubiquitin protein ligase E3A	1.074	75.14	0.81287	24899	P	-1.037	44.4	0.44362	7952
Zfp319	A_52_P195327	AK148655	zinc finger protein 319	1.074	79.26	0.85693	28091	M	1.027	36.07	0.61035	9532
1110002E23Rik	A_52_P533825	NM_025365	RIKEN cDNA 1110002E23 gene	1.073	77.44	0.83448	26519	P	1.077	16.2	0.19046	4738
5730469M10Rik	A_51_P394354	NM_027464	RIKEN cDNA 5730469M10 gene	1.073	81.02	0.89241	30439	P	1.066	25.31	0.47428	8246
BC017133	A_52_P529013	NM_146169	poly(A) binding protein interacting protei	1.073	81.02	0.89059	30273	P	1.118	11.33	0.22719	5317
Cox8a	A_52_P528726	NM_007750	cytochrome c oxidase, subunit VIIIa	1.073	79.26	0.90199	22555	M	1.153	4.63	0.03601	1388
Fgfr4	A_51_P408100	NM_008011	fibroblast growth factor receptor 4	1.073	83.36	0.9372	34353	P	-1.17	1.32	0.02114	899
Ranbp5	A_52_P235569	NM_023579	RAN binding protein 5	1.073	81.02	0.86681	28657	P	-1.001	49.48	0.98495	12917
Rbm8a	A_52_P355014	NM_025875	RNA binding motif protein 8a	1.073	82.34	0.92283	33277	P	-1.091	22.1	0.19597	4836
Sds	A_51_P249335	NM_145565	serine dehydratase	1.073	81.02	0.84995	24188	M	1.116	8.32	0.07384	2506
Tnfrsf13b	A_51_P106269	NM_021349	tumor necrosis factor receptor superfami	1.073	81.02	0.86489	26993	M	1.03	36.07	0.64368	9826
Tnpo1	A_52_P420308	BC058670	transportin 1	1.073	81.02	0.90847	22864	M	1.056	22.1	0.31099	6472
2700046G09Rik	A_52_P324656	AK035700	RIKEN cDNA 2700046G09 gene	1.072	77.44	0.8236	25643	P	-1.112	8.32	0.07436	2513
Abi1	A_52_P157274	NM_001077190	abl-interactor 1	1.072	81.02	0.86362	28432	P	1.124	8.32	0.10705	3220
Alms1	A_52_P568651	NM_145223	Alstrom syndrome 1 homolog (human)	1.072	83.36	0.93319	34083	P	1.123	6.98	0.06254	2210
Cdc27	A_52_P376841	XM_903097	cell division cycle 27 homolog (S. cerevisia	1.072	79.26	0.9036	22652	M	1.122	9.71	0.17232	4409
Fmo3	A_51_P269404	NM_008030	flavin containing monooxygenase 3	1.072		0.96101	18705	A	1.041	25.31	0.34982	6872
Klk6	A_51_P258570	NM_011177	kallikrein related-peptidase 6	1.072		0.9584	18717	A	-1.376	0.66	0.0322	1265
Rnf168	A_52_P425706	NM_027355	ring fnger protein 168	1.072	82.34	0.9065	31548	P	1.121	8.32	0.10712	3222
Sart3	A_51_P212023	NM_016926	squamous cell carcinoma antigen recogni	1.072	83.95	0.95916	36312	P	1.088	11.33	0.10757	3228
Spata7	A_52_P134680	AK045704	spermatogenesis associated 7	1.072	83.36	0.93764	34394	P	1.222	1.62	0.01251	505
Trerf1	A_52_P457967	NM_172622	transcriptional regulating factor 1	1.072	81.02	0.87202	29083	P	1.02	40.63	0.76223	10876
2510003E04Rik	A_51_P296975	AK035659	RIKEN cDNA 2510003E04 gene	1.071	82.34	0.91805	32801	P	1.092	11.33	0.10258	3162
Gria3	A_52_P68221	NM_016886	glutamate receptor, ionotropic, AMPA3 (a	1.071	83.36	0.93874	34473	P	1.017	40.63	0.76026	10861
Hemgn	A_52_P311276	NM_053149	hemogen	1.071	84.22	0.96415	36814	P	1.085	13.58	0.15833	4188
Ilf3	A_52_P508355	NM_010561	interleukin enhancer binding factor 3	1.071	82.34	0.89331	30518	P	1.042	30.75	0.49593	8518
Jag1	A_52_P634090	NM_013822	jagged 1	1.071	82.34	0.91325	32372	P	1.16	11.33	0.28508	6147
Psmd7	A_52_P676913	NM_010817	proteasome (prosome, macropain) 26S su	1.071	82.34	0.91426	32442	P	1.134	6.98	0.05982	2148
Serpinh1	A_51_P287069	NM_009825	serine (or cysteine) peptidase inhibitor, cl	1.071	79.26	0.8698	27287	P	1.186	4.63	0.06763	2353
Sox9	A_51_P451606	NM_011448	SRY-box containing gene 9	1.071	81.02	0.86105	28300	P	1.091	13.58	0.15575	4143
2700008B19Rik	A_52_P1077588	XM_902919	RIKEN cDNA 2700008B19 gene	1.07	83.36	0.94226	34728	P	1.05	28.13	0.50027	8584
Adamts9	A_51_P479390	AK007436	a disintegrin-like and metallopeptidase (r	1.07	83.36	0.92526	33465	P	-1.131	4.63	0.05972	2141
Ankrd28	A_52_P37890	AK088541	ankyrin repeat domain 28	1.07	81.02	0.87504	29257	P	1.134	8.32	0.1097	3259
Ash2l	A_52_P571591	NM_011791	ash2 (absent, small, or homeotic)-like (Dr	1.07	82.34	0.89818	30819	P	1.069	16.2	0.17482	4475
Ddit4	A_51_P245796	NM_029083	DNA-damage-inducible transcript 4	1.07	81.02	0.90804	22846	M	-1.202	1.1	0.01778	753
Dtymk	A_51_P405766	NM_023136	deoxythymidylate kinase	1.07	81.02	0.87933	29623	P	1.054	22.1	0.26817	5916
E130306D19Rik	A_52_P143671	NM_001013377	RIKEN cDNA E130306D19 gene	1.07		0.95454	18577	A	1.02	40.63	0.73795	10662
Gtf2f1	A_51_P193669	NM_133801	general transcription factor IIF, polypeptic	1.07	75.14	0.82593	25742	P	1.016	40.63	0.72187	10511
Hspa4	A_52_P617817	NM_008300	heat shock protein 4	1.07	82.34	0.894	30583	P	1.091	19.02	0.42425	7768
Mcpt6	A_52_P254155	NM_010781	mast cell protease 6	1.07	79.26	0.84917	27702	M	-1.063	28.13	0.19059	4744
Mfap2	A_51_P227502	NM_008546	microfibrillar-associated protein 2	1.07	83.36	0.93855	34441	P	-1.061	40.63	0.37785	7253
Mt2	A_51_P246317	NM_008630	metallothionein 2	1.07	83.36	0.94951	24838	M	1.048	30.75	0.59505	9396
Odz2	A_52_P47660	NM_011856	odd Oz/ten-m homolog 2 (Drosophila)	1.07	82.34	0.91097	32045	P	1.006	42.43	0.95177	12601
Pip5k1b	A_51_P441979	NM_008847	phosphatidylinositol-4-phosphate 5-kinas	1.07	82.34	0.91011	31968	P	1.121	9.71	0.16079	4226
Snapc4	A_51_P349036	NM_172339	small nuclear RNA activating complex, po	1.07	83.95	0.95282	35788	P	1.053	22.1	0.25544	5735
Tgm2	A_51_P182796	NM_009373	transglutaminase 2, C polypeptide	1.07	81.02	0.8682	28754	P	1.102	16.2	0.30765	6409
Vapa	A_51_P361788	NM_013933	vesicle-associated membrane protein, ass	1.07	83.36	0.93916	24439	M	1.045	25.31	0.3817	7300
Vps54	A_52_P258501	AK084305	vacuolar protein sorting 54 (yeast)	1.07	82.34	0.90295	31251	P	1.022	38.4	0.74374	10742
1110001J03Rik	A_51_P406077	NM_025363	RIKEN cDNA 1110001J03 gene	1.069	83.36	0.9349	34189	P	1.172	3.82	0.04432	1653
2310066E14Rik	A_51_P310447	BC079880	RIKEN cDNA 2310066E14 gene	1.069	82.34	0.92201	33201	P	1.215	1.32	0.00977	358

3230401D17Rik	A_51_P451808	NM_025699	RIKEN cDNA 3230401D17 gene	1.069	77.44	0.83461	26600	P	1.019	42.43	0.87731	11832
AI553587	A_52_P657759	NM_178909	expressed sequence AI553587	1.069	82.34	0.9185	32879	P	1.094	13.58	0.17534	4487
Bmp4	A_51_P383741	NM_007554	bone morphogenetic protein 4	1.069	81.02	0.87362	29149	P	1.035	33.49	0.62917	9709
D0H4S114	A_52_P507790	AK051015	DNA segment, human D4S114	1.069	82.34	0.90966	31912	P	1.041	28.13	0.41635	7702
Flnc	A_51_P349844	BC060276	filamin C, gamma (actin binding protein 2	1.069	75.14	0.85639	24513	M	-1.014	49.48	0.83937	11526
Fmn1	A_51_P349912	NM_010230	formin 1	1.069	77.44	0.87681	27661	M	-1.046	38.4	0.281	6100
Hras1	A_51_P357664	NM_008284	Harvey rat sarcoma virus oncogene 1	1.069	81.02	0.87296	29116	P	1.004	42.43	0.93433	12422
Loh11cr2a	A_51_P502661	NM_172767	loss of heterozygosity, 11, chromosomal r	1.069	81.02	0.8711	28966	P	1.097	9.71	0.09218	2949
Ndufb7	A_51_P519276	NM_025843	NADH dehydrogenase (ubiquinone) 1 bet	1.069	81.02	0.88529	29985	P	1.027	38.4	0.72705	10535
Palm	A_52_P325444	NM_023128	paralemmin	1.069	82.34	0.91866	32922	P	1.044	28.13	0.45026	7994
Pkn3	A_52_P96040	NM_153805	protein kinase N3	1.069	81.02	0.88957	30226	M	-1.042	42.43	0.33926	6768
Rab28	A_51_P198045	AK012286	RAB28, member RAS oncogene family	1.069	82.34	0.89932	30951	P	-1.02	49.22	0.72823	10550
Trappc6b	A_51_P432354	NM_030057	trafficking protein particle complex 6B	1.069	81.02	0.8782	29500	P	1.048	22.1	0.2837	6127
0610013E23Rik	A_51_P148494	NM_029788	RIKEN cDNA 0610013E23 gene	1.068	81.02	0.8925	30448	P	1.081	13.58	0.15653	4154
Arid1b	A_52_P289256	XM_139711	AT rich interactive domain 1B (Swi1 like)	1.068	83.36	0.93688	34317	P	1.207	3.01	0.03143	1240
Atp5b	A_52_P328078	NM_016774	ATP synthase, H+ transporting mitochond	1.068	79.26	0.84266	27250	P	-1.06	42.43	0.45184	8012
B130050I23Rik	A_51_P436861	AK009699	RIKEN cDNA B130050I23 gene	1.068	81.02	0.86944	28854	P	1.089	13.58	0.21629	5132
Bat3	A_52_P130185	NM_057171	HLA-B-associated transcript 3	1.068	77.44	0.83815	26956	P	1.131	6.98	0.06159	2183
D17Wsu104e	A_51_P123920	NM_080837	DNA segment, Chr 17, Wayne State Unive	1.068	82.34	0.89822	30828	P	-1.094	30.75	0.34242	6794
Mthfd1l	A_52_P167278	NM_172308	methylenetetrahydrofolate dehydrogenas	1.068	79.26	0.89905	28960	P	1.276	2.04	0.03085	1216
Nckap1	A_51_P114606	NM_016965	NCK-associated protein 1	1.068	81.02	0.87616	29342	P	1.112	9.71	0.12552	3616
Ppp1r12c	A_51_P208410	AK144691	protein phosphatase 1, regulatory (inhibit	1.068	82.34	0.90431	31382	P	-1.073	36.07	0.34952	6864
Psma3	A_51_P391542	NM_011184	proteasome (prosome, macropain) subun	1.068	82.34	0.91645	32706	P	1.009	42.43	0.9162	12227
Ptplb	A_51_P377489	AF169286	protein tyrosine phosphatase-like (proline	1.068	82.34	0.90191	31157	P	-1.208	0.75	0.01141	462
Rpl15	A_52_P12346	NM_025586	ribosomal protein L15	1.068	77.44	0.90152	22519	M	1.016	42.43	0.83699	11507
Slc2a4	A_51_P217498	NM_009204	solute carrier family 2 (facilitated glucose	1.068	82.34	0.89679	30763	P	1.061	16.2	0.19792	4865
Smox	A_52_P430194	AK087437	spermine oxidase	1.068	84.22	0.9617	36617	P	-1.112	11.33	0.1152	3385
Usp47	A_51_P357368	NM_133758	ubiquitin specific peptidase 47	1.068	81.02	0.86471	28494	P	1.087	11.33	0.11939	3478
Anapc10	A_52_P495471	NM_026904	anaphase promoting complex subunit 10	1.067	81.02	0.86758	28721	M	-1.171	1.62	0.03004	1196
Anxa2	A_51_P165342	NM_007585	annexin A2	1.067	84.52	0.97889	38415	P	1.117	11.33	0.24087	5502
Cyp51	A_52_P636752	NM_020010	cytochrome P450, family 51	1.067	82.34	0.91861	32915	P	-1.171	11.33	0.25112	5663
Ebf1	A_51_P188054	NM_007897	early B-cell factor 1	1.067	82.34	0.91525	32564	P	1.095	16.2	0.35426	6945
Hmox2	A_52_P477819	NM_010443	heme oxygenase (decycling) 2	1.067	82.34	0.90095	31055	P	-1.128	9.71	0.1399	3845
Jph2	A_52_P142143	AK157145	junctophilin 2	1.067	82.34	0.89658	30757	M	1.158	4.63	0.04799	1793
Pde8b	A_52_P185579	AK034510	phosphodiesterase 8B	1.067	84.56	0.93314	31533	M	1.048	22.1	0.26885	5931
Ppp3cb	A_52_P457382	AK135203	protein phosphatase 3, catalytic subunit,	1.067	81.02	0.87536	29288	P	1.016	40.63	0.77595	10955
Prpf4	A_51_P193852	NM_027297	PRP4 pre-mRNA processing factor 4 homo	1.067	77.44	0.83487	26688	P	1.138	8.32	0.09339	2975
Rbmxrt	A_51_P447714	NM_009033	RNA binding motif protein, X chromosom	1.067	81.02	0.87048	28930	P	1.075	16.2	0.19537	4828
Susd2	A_52_P488666	NM_027890	sushi domain containing 2	1.067	82.34	0.91251	32276	P	1.302	9.71	0.36194	7041
Tnfrsf19	A_52_P7593	BC030062	tumor necrosis factor receptor superfami	1.067		0.95822	18704	A	1.047	28.13	0.411	7617
Uchl5	A_51_P122238	NM_019562	ubiquitin carboxyl-terminal esterase L5	1.067	82.34	0.91005	31941	P	1.194	3.82	0.05457	1995
A430005L14Rik	A_51_P221535	NM_175287	RIKEN cDNA A430005L14 gene	1.066	83.36	0.92998	33785	P	-1.003	49.48	0.94555	12534
Arf6	A_52_P93969	NM_007481	ADP-ribosylation factor 6	1.066	81.02	0.86387	28447	P	1.07	19.02	0.26008	5808
Atrn	A_52_P406419	NM_009730	attractin	1.066	83.36	0.93319	34084	P	1.149	4.63	0.04467	1664
Btbd14b	A_52_P938109	NM_025788	BTB (POZ) domain containing 14B	1.066	84.56	0.89472	26901	M	1.048	25.31	0.33154	6695
Cdc37	A_51_P425749	NM_016742	cell division cycle 37 homolog (S. cerevisia	1.066	81.02	0.88647	30054	P	-1.224	2.53	0.08911	2871
Cdx1	A_51_P318999	NM_009880	caudal type homeo box 1	1.066		0.95728	18671	A	-1.08	13.58	0.10236	3159
Cstf2	A_51_P119460	NM_133196	cleavage stimulation factor, 3' pre-RNA su	1.066	82.34	0.89921	30942	P	1.243	2.53	0.03104	1225
Gclc	A_51_P365019	NM_010295	glutamate-cysteine ligase, catalytic subun	1.066	77.44	0.84365	27323	P	-1.018	49.48	0.74374	10744
Gmnn	A_51_P166155	NM_020567	geminin	1.066	82.34	0.89294	30491	P	-1.04	44.4	0.45877	8089
Hspa8	A_51_P170371	NM_031165	heat shock protein 8	1.066	83.36	0.94607	24696	M	1.086	13.58	0.19897	4883
Kcnq1	A_52_P618494	AK142427		1.066	81.02	0.88901	30195	M	1.04	36.07	0.73205	10595
Mtus1	A_52_P202895	NM_001005863	mitochondrial tumor suppressor 1	1.066	82.34	0.91836	32866	P	1.047	30.75	0.54405	8977

Nsfl1c	A_51_P237766	NM_198326	NSFL1 (p97) cofactor (p47)	1.066	81.02	0.88234	29819	P	1.014	40.63	0.75566	10830
Prkcsh	A_51_P520690	NM_008925	protein kinase C substrate 80K-H	1.066	83.95	0.95304	35793	P	1.02	40.63	0.75804	10854
Psmc3	A_51_P280971	NM_008948	proteasome (prosome, macropain) 26S su	1.066	83.36	0.93985	34556	P	1.003	42.43	0.95029	12590
Statip1	A_51_P465871	NM_021448	elongation protein 2 homolog (S. cerevisi	1.066	83.36	0.9252	33457	P	1.167	4.63	0.05026	1860
Wdr43	A_52_P8174	AK152321	WD repeat domain 43	1.066	82.34	0.92084	33125	P	-1.017	49.48	0.8033	11200
Zfp445	A_52_P375016	NM_173364	zinc finger protein 445	1.066	82.34	0.90935	31831	P	1.213	4.63	0.07904	2632
Anp32a	A_51_P399071	NM_009672	acidic (leucine-rich) nuclear phosphoprot	1.065	77.44	0.84186	27216	P	1.016	42.43	0.84626	11577
Ascl1	A_51_P437327	NM_008553	achaete-scute complex homolog-like 1 (D	1.065	83.95	0.88295	27983	P	1.066	16.2	0.21503	5124
Cxxc5	A_51_P234788	NM_133687	CXXC finger 5	1.065	82.34	0.90352	31324	P	1.073	16.2	0.18151	4605
Gng5	A_52_P678261	NM_010318	guanine nucleotide binding protein (G pro	1.065	82.34	0.91813	32841	P	1.025	36.07	0.6184	9615
Ndufs7	A_51_P364671	NM_029272	NADH dehydrogenase (ubiquinone) Fe-S p	1.065	83.95	0.94621	35096	P	-1.128	4.63	0.06279	2225
Pcbd1	A_51_P139320	NM_025273	pterin 4 alpha carbinolamine dehydratase	1.065	79.26	0.87767	25626	P	1.047	25.31	0.32054	6572
Pik3cd	A_51_P142320	U86587	phosphatidylinositol 3-kinase catalytic de	1.065	83.36	0.88099	27880	M	1.045	28.13	0.49171	8465
Stk25	A_51_P170326	AK005289	serine/threonine kinase 25 (yeast)	1.065	82.34	0.91141	32093	P	1	49.48	0.99773	13031
Tbc1d22a	A_51_P416397	NM_145476	TBC1 domain family, member 22a	1.065	83.36	0.93874	34488	P	1.006	42.43	0.91857	12254
6030443O07Rik	A_52_P465714	AK031688	RIKEN cDNA 6030443O07 gene	1.064	83.95	0.94728	35194	P	1.145	9.71	0.18469	4650
Bnip3l	A_52_P13612	NM_009761	BCL2/adenovirus E1B interacting protein	1.064	81.02	0.88679	30075	P	1.139	9.71	0.19142	4758
Ctla2a	A_51_P180747	NM_007796	cytotoxic T lymphocyte-associated protei	1.064	82.34	0.91949	32986	P	1.074	19.02	0.30682	6402
Ftsj1	A_51_P426559	NM_133991	FtsJ homolog 1 (E. coli)	1.064	82.34	0.91983	33019	P	-1.017	49.47	0.71961	10496
Gdap10	A_51_P267587	BC052902	ganglioside-induced differentiation-assoc	1.064	79.26	0.85622	28056	P	1.123	8.32	0.08632	2807
Lphn1	A_51_P427264	NM_181039	latrophilin 1	1.064	83.95	0.9493	35376	P	1.138	13.58	0.38962	7393
Mgmt	A_52_P325621	ENSMUST00000081510	O-6-methylguanine-DNA methyltransfera	1.064	82.34	0.90924	31815	P	1.1	8.32	0.06274	2222
Mrps25	A_51_P121325	NM_025578	mitochondrial ribosomal protein S25	1.064	81.02	0.87501	29256	P	-1.064	28.13	0.188	4696
Rab40c	A_52_P1638	NM_139154	Rab40c, member RAS oncogene family	1.064	81.02	0.8711	27355	M	-1.023	47.43	0.59587	9407
Stab1	A_52_P380399	NM_138672	stabilin 1	1.064	79.26	0.87454	25451	M	-1.041	43.15	0.40008	7511
Ubtf	A_52_P281879	NM_011551	upstream binding transcription factor, RN	1.064	84.56	0.94241	27391	M	1.04	33.49	0.59085	9337
2310039E09Rik	A_51_P378029	NM_026509	RIKEN cDNA 2310039E09 gene	1.063	82.34	0.91577	25570	M	-1.029	45.68	0.52201	8766
2810407C02Rik	A_52_P445969	NM_001040396	RIKEN cDNA 2810407C02 gene	1.063	81.02	0.88204	29794	P	1.014	42.43	0.88161	11874
Bri3bp	A_52_P561236	NM_029752	Bri3 binding protein	1.063	83.36	0.94748	29957	M	1.003	42.43	0.9604	12664
Gltscr2	A_52_P405265	NM_133831	glioma tumor suppressor candidate regio	1.063	81.02	0.86904	28844	P	-1.063	30.75	0.19241	4784
Pbx1	A_52_P543460	NM_183355	pre B-cell leukemia transcription factor 1	1.063	81.02	0.86821	28766	P	1.017	42.43	0.89323	11995
Rac1	A_51_P513254	NM_009007	RAS-related C3 botulinum substrate 1	1.063	83.95	0.95341	25007	M	1.229	1.62	0.01352	575
Rps4x	A_51_P267995	NM_009094	ribosomal protein S4, X-linked	1.063	83.36	0.94195	24538	M	1.005	42.43	0.97683	12813
Sephs1	A_51_P214343	NM_175400	selenophosphate synthetase 1	1.063	81.02	0.86821	28768	P	-1.079	22.1	0.14484	3943
Sox21	A_52_P406411	NM_145464	SRY-box containing gene 21	1.063	81.02	0.89165	30373	P	-1.08	25.31	0.17971	4571
Ss18	A_52_P67964	NM_009280	synovial sarcoma translocation, Chromos	1.063	83.36	0.88794	26246	P	1.258	3.01	0.05047	1865
Ttrap	A_52_P56768	NM_019551	Traf and Tnf receptor associated protein	1.063	79.26	0.86435	28466	P	1.111	6.98	0.05981	2143
Ube2d2	A_51_P426458	NM_019912	ubiquitin-conjugating enzyme E2D 2	1.063	82.34	0.91108	32069	P	1.061	19.02	0.23395	5410
1300018I17Rik	A_51_P454234	AK154409	RIKEN cDNA 1300018I17 gene	1.062	84.4	0.97013	37413	P	1.123	9.71	0.12889	3677
2900073G15Rik	A_51_P150480	NM_026064	RIKEN cDNA 2900073G15 gene	1.062	83.36	0.92665	33561	P	1.247	11.33	0.41573	7689
Heph	A_52_P498219	NM_181273	hephaestin	1.062	84.52	0.97707	38204	P	-1.012	49.48	0.78638	11060
Mdfi	A_51_P368012	NM_010783	MyoD family inhibitor	1.062	84.22	0.90183	29158	M	-1.162	3.01	0.04735	1768
Nf2	A_52_P124665	AK161134		1.062		0.95967	18767	A	1.06	19.02	0.25181	5676
Psma5	A_51_P257960	NM_011967	proteasome (prosome, macropain) subun	1.062	83.36	0.93627	34294	P	1.097	13.58	0.2114	5058
Qrsl1	A_51_P243930	BC070459	glutaminyl-tRNA synthase (glutamine-hyd	1.062	82.34	0.91994	33024	P	1.007	42.43	0.91864	12260
Rab5c	A_51_P486479	NM_024456	RAB5C, member RAS oncogene family	1.062	79.26	0.86155	28330	P	1.132	5.75	0.04256	1600
Sirt3	A_51_P477179	NM_022433	sirtuin 3 (silent mating type information r	1.062	81.02	0.89219	30422	P	1.045	30.75	0.57782	9246
St3gal4	A_52_P316474	NM_009178	ST3 beta-galactoside alpha-2,3-sialyltrans	1.062	84.22	0.96101	36485	P	1.071	16.2	0.21488	5117
Stc1	A_51_P233334	NM_009285	stanniocalcin 1	1.062	61.79	0.92263	26036	M	1.015	40.63	0.7612	10868
Zfp451	A_52_P337471	AK122541	zinc finger protein 451	1.062	81.02	0.87701	29393	P	1.067	19.02	0.29693	6291
Cct7	A_51_P197259	NM_007638	chaperonin subunit 7 (eta)	1.061	83.36	0.92998	33816	P	1.085	22.1	0.49722	8546
Coq3	A_51_P378336	NM_172687	coenzyme Q3 homolog, methyltransferas	1.061	82.34	0.93087	29090	M	1.053	19.02	0.38082	6751
Pdlim7	A_51_P506284	NM_026131	PDZ and LIM domain 7	1.061	81.02	0.8698	28861	P	1.018	40.63	0.71304	10427

Ppat	A_51_P296905	XM_896000	phosphoribosyl pyrophosphate amidotrar	1.061	83.36	0.93277	34011	P	-1.014	49.48	0.89907	12058
Rabac1	A_51_P374383	NM_010261	Rab acceptor 1 (prenylated)	1.061	82.34	0.93688	24343	M	-1.075	38.4	0.42733	7794
2310061F22Rik	A_51_P133575	NM_153775	RIKEN cDNA 2310061F22 gene	1.06	79.26	0.86492	28515	P	-1.075	25.31	0.19127	4754
5730406M06Rik	A_52_P80548	XM_884719	RIKEN cDNA 5730406M06 gene	1.06	83.36	0.929	33696	P	-1.077	42.43	0.54441	8978
5730488B01Rik	A_51_P281878	AK017710	RIKEN cDNA 5730488B01 gene	1.06		0.92602	23805	A	1.048	25.31	0.31238	6483
Asb16	A_52_P326468	NM_148953	ankyrin repeat and SOCS box-containing 1	1.06	82.34	0.89165	26583	M	1.078	25.31	0.52369	8784
Calu	A_52_P541157	NM_007594	calumenin	1.06	83.36	0.93488	34180	P	1.12	8.32	0.08927	2874
Ciapin1	A_51_P492125	NM_134141	cytokine induced apoptosis inhibitor 1	1.06	82.34	0.90335	31283	P	1.028	33.49	0.56677	9179
Ece1	A_51_P466423	AK047359	endothelin converting enzyme 1	1.06	83.36	0.9394	34520	P	1.149	9.71	0.22657	5300
Gle1l	A_52_P476421	AK145748	GLE1 RNA export mediator-like (yeast	1.06	81.02	0.87975	29634	P	1.1	16.2	0.28682	6183
Mccc2	A_51_P211880	NM_030026	methylcrotonoyl-Coenzyme A carboxylase	1.06	83.95	0.95176	35717	P	-1.145	3.46	0.04454	1659
Plaa	A_52_P373782	NM_172695	phospholipase A2, activating protein	1.06	79.26	0.86758	28705	P	1.073	16.2	0.20419	4954
Rpo1-2	A_52_P271685	AK052672	RNA polymerase 1-2	1.06		0.95139	27714	A	1.142	6.98	0.08032	2669
Smap1	A_51_P249821	AK006817	stromal membrane-associated protein 1	1.06	81.02	0.89072	30284	P	1.084	22.1	0.48248	8351
Ube2i	A_52_P269595	BC037635	ubiquitin-conjugating enzyme E2I	1.06	83.36	0.92159	33170	P	1.201	5.75	0.12478	3594
Xist	A_51_P145453	L04961	inactive X specific transcripts	1.06		0.97952	14837	A	1.09	11.33	0.10452	3196
1110032A13Rik	A_51_P155303	NM_199197	RIKEN cDNA 1110032A13 gene	1.059	82.34	0.9036	31337	P	-1.296	0.51	0.01044	398
Abcf2	A_52_P445828	NM_013853	ATP-binding cassette, sub-family F (GCN2(	1.059	82.34	0.90781	31658	P	-1.013	49.48	0.79791	11156
Arhgap4	A_51_P339822	NM_138630	Rho GTPase activating protein 4	1.059	82.34	0.9186	32893	P	-1.07	33.49	0.28469	6142
Col4a3bp	A_52_P115638	NM_023420	procollagen, type IV, alpha 3 (Goodpastur	1.059	83.95	0.94296	34824	P	1.166	6.98	0.09163	2932
Ctbs	A_51_P255082	NM_028836	chitobiase, di-N-acetyl-	1.059	81.02	0.88098	29710	P	1.175	3.46	0.03017	1205
Dld	A_51_P184282	U73445	dihydrolipoamide dehydrogenase	1.059	82.34	0.91548	32649	P	1.081	13.58	0.16821	4345
Frap1	A_51_P282179	NM_020009	FK506 binding protein 12-rapamycin asso	1.059	81.02	0.89368	30562	P	1.038	28.13	0.37128	7186
Glipr2	A_51_P517843	NM_027450	GLI pathogenesis-related 2	1.059	84.4	0.9704	37455	P	-1.154	3.46	0.05545	2019
Ldb1	A_51_P384756	NM_010697	LIM domain binding 1	1.059	81.02	0.88412	29910	P	1.046	25.31	0.32188	6583
ORF63	A_52_P404942	NM_144854	open reading frame 63	1.059		0.98014	14845	A	-1.014	49.48	0.80625	11243
Rims2	A_51_P321847	NM_053271	regulating synaptic membrane exocytosis	1.059	82.34	0.92007	33036	P	1.155	6.98	0.08255	2715
Snrpd3	A_51_P176681	NM_026095	small nuclear ribonucleoprotein D3	1.059	83.36	0.92665	33569	P	1.039	30.75	0.48617	8397
Sos1	A_52_P341339	NM_009231	Son of sevenless homolog 1 (Drosophila)	1.059	81.02	0.89158	30345	P	1.076	19.02	0.32824	6652
Syngr1	A_51_P270733	NM_009303	synaptogyrin 1	1.059	82.34	0.90299	31266	P	-1.05	43.15	0.45351	8034
Tmem23	A_51_P421958	NM_144792	sphingomyelin synthase 1	1.059	81.02	0.87896	29553	P	1.044	28.13	0.37813	7260
Zcchc8	A_52_P589112	NM_027494	zinc finger, CCHC domain containing 8	1.059	83.36	0.92127	33143	P	1.039	28.13	0.38299	7317
4833442J19Rik	A_52_P263673	NM_177101	RIKEN cDNA 4833442J19 gene	1.058	84.22	0.9617	36603	P	1.01	42.43	0.85878	11674
Adss	A_51_P361099	NM_007422	adenylosuccinate synthetase, non muscle	1.058	83.36	0.93599	34271	P	1.169	2.53	0.01753	750
Akap8l	A_51_P277524	NM_017476	A kinase (PRKA) anchor protein 8-like	1.058	84.22	0.95973	36354	P	-1.015	49.48	0.77933	10982
Arl6ip4	A_51_P454666	NM_144509	ADP-ribosylation factor-like 6 interacting	1.058	81.02	0.89351	30547	P	1.035	36.07	0.71571	10449
Atp2c1	A_52_P397722	NM_175025	ATPase, Ca++-sequestering	1.058	81.02	0.8861	30034	P	1.132	8.32	0.09617	3014
Cat	A_52_P679769	NM_009804	catalase	1.058	84.4	0.97483	37993	P	1.113	8.32	0.07344	2495
Cltc	A_52_P67485	AK049578	clathrin, heavy polypeptide (Hc)	1.058	83.36	0.92283	33259	P	1.213	2.53	0.02095	895
D2Bwg1335e	A_51_P406334	NM_026828	DNA segment, Chr 2, Brigham & Women's	1.058	82.34	0.90871	31751	P	-1.16	1.58	0.02245	948
Dscr3	A_51_P508191	NM_007834	Down syndrome critical region gene 3	1.058	83.36	0.931	33920	P	-1.165	2.04	0.03454	1324
Paox	A_51_P180617	NM_153783	polyamine oxidase (exo-N4-amino)	1.058	83.36	0.92279	33258	P	1.108	9.71	0.1024	3161
Rab38	A_52_P21595	NM_028238	Rab38, member of RAS oncogene family	1.058	83.36	0.93345	34109	P	1.02	38.4	0.71751	10467
Scoc	A_51_P466886	NM_019708	short coiled-coil protein	1.058	82.34	0.90935	31822	P	1.052	28.13	0.48143	8323
Ube3b	A_51_P205740	NM_054093	ubiquitin protein ligase E3B	1.058	82.34	0.90911	31800	P	1.06	16.2	0.19195	4767
1110005A23Rik	A_52_P789023	NM_025364	RIKEN cDNA 1110005A23 gene	1.057	82.34	0.91252	32282	P	1.197	3.46	0.04387	1642
5730405I09Rik	A_52_P512807	XM_974899	cyclin Y	1.057	79.26	0.8726	29106	P	-1.041	44.4	0.48701	8407
BC038156	A_52_P144286	NM_177768	cDNA sequence BC038156	1.057	82.34	0.90781	31631	P	1.107	9.71	0.08446	2767
BC068171	A_51_P469633	NM_001030307	dyskeratosis congenita 1, dyskerin homol	1.057	82.34	0.89958	30964	P	1.154	3.82	0.03496	1339
Cdh3	A_51_P433237	NM_007665	cadherin 3	1.057	83.95	0.90191	27286	M	1.091	19.02	0.43314	7875
Crb3	A_51_P328089	NM_177638	crumbs homolog 3 (Drosophila)	1.057	83.36	0.92592	33528	P	-1.173	1.32	0.0225	957
D10Bwg1379e	A_52_P49042	NM_001033258	DNA segment, Chr 10, Brigham & Womer	1.057	83.36	0.92446	33408	P	-1.134	3.82	0.04561	1711
Gnao1	A_52_P205031	M36778	guanine nucleotide binding protein, alpha	1.057	82.34	0.88598	28122	M	1.136	11.33	0.22295	5259

Nedd8	A_51_P416869	NM_008683	neural precursor cell expressed, developn	1.057	82.34	0.90011	30998	P	1.03	33.49	0.58673	9311
Nrbf2	A_52_P956153	AK086152	nuclear receptor binding factor 2	1.057	82.34	0.91371	32410	P	-1.011	49.48	0.86776	11739
Pold4	A_51_P455906	NM_027196	polymerase (DNA-directed), delta 4	1.057	83.36	0.92336	33342	P	-1.026	46.85	0.59305	9365
Ppp4r1	A_51_P163867	NM_146081	protein phosphatase 4, regulatory subuni	1.057	79.26	0.87149	29045	P	1.087	13.58	0.16545	4304
Snx3	A_51_P427444	NM_017472	sorting nexin 3	1.057	81.02	0.89035	30262	P	1.227	2.53	0.03017	1206
Xylt2	A_52_P94811	NM_145828	xylosyltransferase II	1.057	83.36	0.92072	33115	P	1.061	19.02	0.21927	5195
Zhx3	A_52_P321325	AK161741	zinc fingers and homeoboxes 3	1.057	83.36	0.92988	33761	P	1.132	9.71	0.15006	4038
2010209O12Rik	A_51_P295389	BC047275	RIKEN cDNA 2010209O12 gene	1.056	82.34	0.91821	32863	P	-1.003	49.48	0.95177	12602
Cdv3	A_51_P343556	NM_175565	carnitine deficiency-associated gene expr	1.056	81.02	0.89337	30535	P	1.081	13.58	0.14993	4037
Epc1	A_51_P452003	NM_027497	enhancer of polycomb homolog 1 (Drosop	1.056	81.02	0.88759	30112	P	1.113	8.32	0.08015	2663
Fgf1	A_52_P538673	NM_010197	fibroblast growth factor 1	1.056	84.52	0.9191	25805	M	1.04	33.49	0.65314	9903
Gna11	A_51_P498004	NM_010301	guanine nucleotide binding protein, alpha	1.056	79.26	0.87526	29274	P	1.061	22.1	0.30397	6367
Gpsn2	A_51_P278550	NM_134118	glycoprotein, synaptic 2	1.056	82.34	0.91813	32839	P	1.087	13.58	0.18565	4661
Jarid2	A_52_P370203	NM_021878	jumonji, AT rich interactive domain 2	1.056	83.95	0.95609	35980	P	-1.072	36.07	0.36333	7063
Mapkapk2	A_51_P118902	NM_008551	MAP kinase-activated protein kinase 2	1.056	83.95	0.94483	34975	P	1.117	13.58	0.34283	6798
Rabif	A_51_P188237	NM_145510	RAB interacting factor	1.056	83.36	0.9238	33371	P	1.167	5.75	0.07882	2626
Rock2	A_51_P320444	NM_009072	Rho-associated coiled-coil containing prot	1.056	82.34	0.91949	33005	P	-1.034	45.05	0.49155	8454
Rraga	A_51_P226417	NM_178376	Ras-related GTP binding A	1.056	83.36	0.94449	24649	M	1.023	40.63	0.7768	10967
Sec61a2	A_52_P652164	NM_021305	Sec61, alpha subunit 2 (S. cerevisiae)	1.056	82.34	0.9089	31767	P	1.01	42.43	0.82054	11366
Tcfe2a	A_51_P394471	NM_011548	transcription factor E2a	1.056	83.36	0.92346	33344	P	1.123	8.32	0.08375	2742
Ttc13	A_51_P494622	AK144842	tetratricopeptide repeat domain 13	1.056	82.34	0.90726	31587	P	1.132	9.71	0.16097	4235
BC010304	A_52_P415365	AK172909	cDNA sequence BC010304	1.055	82.34	0.9118	32160	P	1.113	9.71	0.15366	4110
Cdc2a	A_52_P339954	NM_007659	cell division cycle 2 homolog A (S. pombe	1.055		0.98109	14883	A	-1.071	28.13	0.21458	5108
Cebpb	A_52_P605846	NM_009883	CCAAT/enhancer binding protein (C/EBP),	1.055	81.02	0.89958	27148	M	1.106	13.58	0.23035	5356
Fgfr1	A_51_P109469	NM_010206	fibroblast growth factor receptor 1	1.055	82.34	0.90548	31474	P	1.12	8.32	0.08145	2691
Fosl2	A_52_P484903	NM_008037	fos-like antigen 2	1.055	84.56	0.98238	39040	P	1.09	22.1	0.50927	8666
Ltf	A_51_P188141	NM_008522	lactotransferrin	1.055	84.56	0.98278	39104	P	-1.035	45.05	0.52627	8809
Msrb3	A_52_P121491	NM_177092	methionine sulfoxide reductase B3	1.055	81.02	0.89235	30433	P	-1.017	49.48	0.74343	10736
Snrpa	A_51_P389978	NM_015782	small nuclear ribonucleoprotein polypept	1.055	83.36	0.94098	34642	P	-1.124	6.98	0.07463	2521
Tgds	A_51_P251402	NM_029578	TDP-glucose 4,6-dehydratase	1.055	81.02	0.89727	30780	P	1.07	19.02	0.28158	6109
Vbp1	A_51_P475076	NM_011692	von Hippel-Lindau binding protein 1	1.055	83.36	0.94241	24562	M	1.12	8.32	0.06712	2343
1600012H06Rik	A_52_P394385	NM_026451	RIKEN cDNA 1600012H06 gene	1.054	83.36	0.93314	34052	P	1.115	5.75	0.04456	1661
6330442E10Rik	A_52_P220783	NM_178745	RIKEN cDNA 6330442E10 gene	1.054	83.36	0.96546	33948	P	1.106	22.1	0.50543	8640
Apoa1bp	A_51_P109939	NM_144897	apolipoprotein A-I binding protein	1.054	82.34	0.90191	31156	P	-1.269	0.75	0.0184	782
Dap3	A_52_P292882	AK032275	death associated protein 3	1.054	83.36	0.93053	33879	P	1.189	3.01	0.02147	903
Fndc3a	A_52_P995657	AK037863	fibronectin type III domain containing 3a	1.054	83.36	0.93874	34479	P	1.084	13.58	0.20699	5008
Htf9c	A_51_P387648	NM_008307	HpaII tiny fragments locus 9c	1.054	83.95	0.9516	35696	P	-1.277	0.51	0.00972	354
Mug1	A_51_P182631	NM_008645	murinoglobulin 1	1.054	83.36	0.92427	33392	P	1.14	5.75	0.04567	1714
Pcyt1a	A_52_P308881	AK163685	phosphate cytidylyltransferase 1, choline,	1.054	81.02	0.88557	30008	P	1.237	2.04	0.01723	741
Pkp4	A_51_P251245	NM_026361	plakophilin 4	1.054	82.34	0.91041	31992	P	1.071	30.75	0.66138	9981
Rpo1-1	A_51_P112557	NM_009085	RNA polymerase 1-1	1.054	82.34	0.91891	32937	P	1.005	42.43	0.91419	12211
Rsu1	A_51_P258671	NM_009105	Ras suppressor protein 1	1.054	83.36	0.93739	34382	P	1.261	1.62	0.0204	873
Wnt8b	A_51_P433887	NM_011720	wingless related MMTV integration site 8l	1.054	79.26	0.8816	29744	P	-1.007	49.48	0.91088	12199
Zfp647	A_51_P469252	NM_172817	zinc finger protein 647	1.054	82.34	0.91013	31972	P	-1.001	49.48	0.97561	12799
Acadsb	A_51_P435068	NM_025826	acyl-Coenzyme A dehydrogenase, short/b	1.053	83.36	0.92551	33503	P	-1.003	49.48	0.95687	12636
BC021611	A_51_P296090	NM_144932	cDNA sequence BC021611	1.053	84.4	0.9731	37771	P	-1.019	49	0.70868	10398
Calcr	A_52_P554768	NM_007588	calcitonin receptor	1.053	84.56	0.93986	32025	M	-1.049	40.63	0.33104	6688
D830012I24Rik	A_52_P282448	AK052864	RIKEN cDNA D830012I24 gene	1.053	81.02	0.88895	30193	P	1.074	16.2	0.18061	4588
Fmnl2	A_51_P222936	AK080318	formin-like 2	1.053	75.14	0.9191	28333	P	1.094	9.71	0.07882	2625
Kcnd1	A_51_P236053	NM_008423	potassium voltage-gated channel, Shal-re	1.053	81.02	0.89084	30290	P	-1.061	42.43	0.44623	7977
Lrrc4b	A_52_P467545	NM_198250	leucine rich repeat containing 4B	1.053		0.96703	19063	A	-1.218	0.75	0.01458	617
Nr4a3	A_51_P128397	NM_015743	nuclear receptor subfamily 4, group A, me	1.053		0.98109	14896	A	-1.074	40.63	0.48342	8364
Nt5c2	A_52_P598930	AK038326	5'-nucleotidase, cytosolic II	1.053	82.34	0.91171	32126	P	-1.091	22.1	0.20501	4968

Nucb2	A_51_P193336	NM_016773	nucleobindin 2	1.053	83.95	0.95466	35853	P	-1.056	38.4	0.33747	6754
Prdm4	A_52_P461722	NM_181650	PR domain containing 4	1.053	83.36	0.92998	33812	P	1.039	30.75	0.56342	9145
Prkaca	A_52_P138656	NM_008854	protein kinase, cAMP dependent, catalyti	1.053	83.36	0.94977	24842	M	1.204	3.82	0.05213	1921
Rasa1	A_52_P252872	AK042801	RAS p21 protein activator 1	1.053	82.34	0.91805	30432	M	1.132	6.98	0.06612	2325
Refbp2	A_52_P171659	AK047216	RIKEN cDNA B930036N10 gene	1.053	82.34	0.90924	31817	P	-1.027	46.3	0.53695	8909
Slc25a3	A_52_P486063	AK028313	solute carrier family 25 (mitochondrial ca	1.053	84.4	0.97186	37603	P	1.12	13.58	0.34879	6854
Smu1	A_52_P461552	NM_021535	smu-1 suppressor of mec-8 and unc-52 h	1.053	83.36	0.93304	34037	P	-1.006	49.48	0.91966	12269
Sp3	A_51_P112662	NM_001018042	trans-acting transcription factor 3	1.053	81.02	0.92949	24015	M	1.109	8.32	0.08005	2655
Tor1b	A_52_P466788	NM_133673	torsin family 1, member B	1.053	83.36	0.939	34501	P	1.038	28.13	0.43111	7845
Ufd1l	A_51_P328963	NM_011672	ubiquitin fusion degradation 1 like	1.053	81.02	0.89796	30804	P	-1.056	43.15	0.50748	8655
Atp5g1	A_51_P183292	NM_007506	ATP synthase, H+ transporting, mitochon	1.052	82.34	0.90362	31352	P	1.025	40.63	0.78773	11068
Cacna2d1	A_52_P160543	NM_009784	calcium channel, voltage-dependent, alph	1.052	83.36	0.92608	33544	P	1.23	2.53	0.02989	1192
Cacng7	A_51_P327675	NM_133189	calcium channel, voltage-dependent, gam	1.052		0.93314	26888	A	1.02	42.43	0.80574	10173
Ep300	A_51_P304029	AK040384	E1A binding protein p300	1.052		0.968	34140	A	1.117	11.33	0.17381	4442
F12	A_51_P184949	NM_021489	coagulation factor XII (Hageman factor)	1.052		0.94291	24485	A	1.045	28.13	0.38962	7392
Hdac10	A_52_P577361	NM_199198	histone deacetylase 10	1.052	84.22	0.96163	36534	P	-1.011	49.48	0.84549	11566
Il1f6	A_51_P504194	NM_019450	interleukin 1 family, member 6	1.052	79.26	0.93031	26676	M	-1.043	45.05	0.58997	9334
Pms2	A_51_P234174	NM_008886	postmeiotic segregation increased 2 (S. ce	1.052	83.95	0.94702	35160	P	-1.057	30.75	0.2124	5082
Rhoc	A_51_P282508	NM_007484	ras homolog gene family, member C	1.052	83.36	0.94502	24666	M	-1.044	42.43	0.33251	6707
Riok1	A_51_P498242	NM_024242	RIO kinase 1 (yeast)	1.052	82.34	0.91614	32704	P	1.047	25.31	0.34799	6850
Rps6kb1	A_52_P372321	NM_028259	ribosomal protein S6 kinase, polypeptide	1.052		0.93766	24275	A	1.051	30.75	0.59157	9345
Tex2	A_52_P394539	NM_198292	testis expressed gene 2	1.052	77.44	0.92645	28789	P	1.149	13.58	0.38944	7391
Tsg101	A_52_P401824	NM_021884	tumor susceptibility gene 101	1.052	82.34	0.90457	31397	P	1.193	3.46	0.0353	1363
2310047M15Rik	A_52_P56394	DV058987	RIKEN cDNA 2310047M15 gene	1.051	79.26	0.88855	30168	P	1.081	13.58	0.19663	4847
5730509K17Rik	A_52_P249856	NM_172274	RIKEN cDNA 5730509K17 gene	1.051	83.36	0.94006	34563	P	1.09	11.33	0.13135	3696
Bzw2	A_51_P174681	NM_025840	basic leucine zipper and W2 domains 2	1.051	84.22	0.95609	36016	P	1.007	42.43	0.90387	12129
C530030K21Rik	A_52_P336345	AK083002	RIKEN cDNA C530030K21 gene	1.051	84.22	0.95676	36061	P	1.156	6.98	0.08929	2875
Cnot1	A_52_P22365	BC058249	CCR4-NOT transcription complex, subunit	1.051	83.95	0.94234	34759	P	1.042	28.13	0.3817	7294
E2f5	A_51_P292906	X86925	E2F transcription factor 5	1.051	82.34	0.91525	32595	P	1.115	16.2	0.34861	6853
Thsd1	A_52_P22001	AK049636	thrombospondin, type I, domain 1	1.051	84.4	0.96857	37339	M	-1.006	49.48	0.97752	12818
Timp2	A_52_P540219	NM_011594	tissue inhibitor of metalloproteinase 2	1.051	82.34	0.91076	32014	P	1.187	9.71	0.25464	5731
Tnfsf5ip1	A_52_P403352	NM_134138	tumor necrosis factor superfamily, memb	1.051	83.95	0.94764	35238	P	1.197	3.01	0.02439	1010
Casp7	A_52_P260114	NM_007611	caspase 7	1.05	83.36	0.91805	30427	M	-1.068	28.13	0.19811	4868
Ccdc12	A_52_P386408	NM_028312	coiled-coil domain containing 12	1.05	83.36	0.92255	33246	P	1.073	13.58	0.15669	4160
Coil	A_51_P483839	NM_016706	coilin	1.05	81.02	0.89165	30383	P	1.087	13.58	0.17971	4573
E130016E03Rik	A_51_P190361	AK078439	RIKEN cDNA E130016E03 gene	1.05	83.36	0.92948	33719	P	1.043	25.31	0.32626	6632
Hhip	A_52_P249826	NM_020259	Hedgehog-interacting protein	1.05	83.95	0.95213	35748	P	-1.049	38.4	0.2903	6213
Mlstd2	A_52_P112791	AK012966	male sterility domain containing 2	1.05	81.02	0.9207	30680	P	-1.05	43.75	0.54441	8979
Pnpt1	A_51_P453343	NM_027869	polyribonucleotide nucleotidyltransferase	1.05	83.36	0.92744	33618	P	1.241	2.04	0.02042	875
Rpp14	A_51_P167273	NM_025938	ribonuclease P 14 subunit (human)	1.05	82.34	0.91141	32092	P	1.055	28.13	0.57455	9224
Ryk	A_52_P544017	NM_013649	receptor-like tyrosine kinase	1.05	83.36	0.93967	34546	P	1.217	9.71	0.32279	6590
Spag5	A_52_P131891	NM_017407	sperm associated antigen 5	1.05	83.36	0.94205	32195	M	1.079	19.02	0.2939	6268
Zfp629	A_52_P172199	NM_177226	zinc finger protein 629	1.05	83.36	0.9329	34013	P	-1.169	3.46	0.07031	2402
Aadac	A_51_P394115	NM_023383	arylacetamide deacetylase (esterase)	1.049		0.98366	29247	A	1.193	3.46	0.03344	1303
Abcc5	A_52_P628117	NM_176839	ATP-binding cassette, sub-family C (CFTR/	1.049	84.22	0.96163	36577	P	1.003	42.43	0.96083	12671
Col4a2	A_51_P491350	NM_009932	procollagen, type IV, alpha 2	1.049	83.95	0.95123	35597	P	1.04	33.49	0.66384	9996
Crip2	A_51_P314397	NM_024223	cysteine rich protein 2	1.049	82.34	0.91949	33001	P	-1.064	30.75	0.22129	5226
Dgkz	A_51_P505156	NM_138306	diacylglycerol kinase zeta	1.049	83.36	0.92784	33655	P	1.008	42.43	0.86776	11737
H2-Ab1	A_52_P683598	NM_207105	histocompatibility 2, class II antigen A, be	1.049	84.4	0.97197	37633	P	1.036	40.63	0.85824	11665
Ihh	A_52_P403398	AK090147	Indian hedgehog	1.049	82.34	0.91716	32748	M	1.064	19.02	0.2924	6243
Loh12cr1	A_51_P498947	NM_026371	loss of heterozygosity, 12, chromosomal r	1.049	82.34	0.909	31781	P	-1.113	19.02	0.22619	5288
Numb	A_51_P325071	NM_010949	numb gene homolog (Drosophila)	1.049	82.34	0.90966	31876	P	-1.053	40.63	0.3354	6736
Ppie	A_51_P354433	NM_019489	peptidylprolyl isomerase E (cyclophilin E)	1.049	84.22	0.95791	36169	P	1.073	13.58	0.15413	4119

Scarb2	A_51_P180362	NM_007644	scavenger receptor class B, member 2	1.049	83.36	0.92642	33553	P	-1.032	46.3	0.60696	9503
Sh3bp4	A_51_P322871	NM_133816	SH3-domain binding protein 4	1.049	83.36	0.93689	34322	P	1.058	22.1	0.3689	7151
Tcerg1	A_51_P414481	NM_001039474	transcription elongation regulator 1 (CA1	1.049	81.02	0.89757	30794	P	1.083	22.1	0.48526	8385
Th1l	A_51_P126817	NM_020580	TH1-like homolog (Drosophila)	1.049	82.34	0.9118	32179	P	1.081	13.58	0.13407	3746
Timm23	A_51_P511623	NM_016897	translocase of inner mitochondrial memb	1.049	83.36	0.93349	34112	P	-1.119	9.71	0.12177	3541
Wdr32	A_51_P252328	NM_153167	WD repeat domain 32	1.049	82.34	0.9191	32950	P	-1.193	3.46	0.09978	3100
Zfp160	A_51_P369796	NM_145483	zinc finger protein 160	1.049	82.34	0.9191	32963	P	-1.084	22.1	0.15283	4085
2210009G21Rik	A_51_P271828	NM_028834	RIKEN cDNA 2210009G21 gene	1.048	83.36	0.93189	33971	P	1.001	42.43	0.98826	12968
Alad	A_51_P512072	NM_008525	aminolevulinate, delta-, dehydratase	1.048	83.36	0.92998	33795	P	1.017	40.63	0.73049	10576
Alas2	A_51_P327451	NM_009653	aminolevulinic acid synthase 2, erythroid	1.048	84.22	0.96489	36909	P	-1.192	1.18	0.02177	912
BC013529	A_51_P183469	AK046650	cDNA sequence BC013529	1.048	79.26	0.96369	25378	M	1.039	33.49	0.6704	10054
Bmp6	A_52_P468441	NM_007556	bone morphogenetic protein 6	1.048	83.95	0.94373	34892	M	1.091	11.33	0.13456	3755
Cog8	A_51_P259750	AK155400	predicted gene, ENSMUSG00000074106	1.048	82.34	0.91097	32049	P	-1.026	46.3	0.53181	8863
Fxyd7	A_51_P379698	NM_022007	FXYD domain-containing ion transport reg	1.048	84.22	0.96166	36593	P	-1.064	36.07	0.32647	6634
Hagh	A_51_P127469	NM_024284	hydroxyacyl glutathione hydrolase	1.048	83.36	0.92283	33289	P	1.009	42.43	0.8934	11996
Ipo9	A_51_P149983	NM_153774	importin 9	1.048	84.4	0.97197	37638	P	-1.326	0.51	0.00591	108
Litaf	A_51_P267239	NM_019980	LPS-induced TN factor	1.048	83.36	0.93021	33840	P	1.144	9.71	0.16808	4341
Mgea6	A_52_P471088	NM_146034	meningioma expressed antigen 6 (coiled-	1.048	83.36	0.93314	34065	P	1.162	6.98	0.10264	3165
Nbn	A_52_P298548	NM_013752	nibrin	1.048	83.95	0.94291	34795	P	-1.035	45.05	0.49717	8543
Psmd8	A_51_P149325	NM_026545	proteasome (prosome, macropain) 26S su	1.048	83.95	0.94728	35196	P	-1.037	45.05	0.49465	8500
Rbp4	A_51_P374752	NM_011255	retinol binding protein 4, plasma	1.048	82.34	0.96281	28298	M	1.309	1.62	0.02536	1047
Tacc1	A_51_P331409	NM_177089	transforming, acidic coiled-coil containing	1.048	82.34	0.91011	31952	M	1.081	13.58	0.15685	4164
Tgfa	A_52_P555423	NM_031199	transforming growth factor alpha	1.048	82.34	0.94148	29723	M	1.109	8.32	0.06492	2282
Zfp191	A_51_P188749	AK088914	zinc finger protein 191	1.048	82.34	0.91219	32214	P	-1.017	49.48	0.81045	11285
Als2cl	A_51_P360678	NM_146228	ALS2 C-terminal like	1.047	83.36	0.93144	29125	M	-1.077	30.75	0.26803	5913
C130022K22Rik	A_52_P459552	NM_172730	RIKEN cDNA C130022K22 gene	1.047	82.34	0.9087	31739	P	1.006	42.43	0.92601	12356
Clta	A_51_P197321	NM_016760	clathrin, light polypeptide (Lca)	1.047	82.34	0.94373	24616	M	1.117	9.71	0.11894	3465
Csrp2bp	A_51_P259358	NM_181417	cysteine and glycine-rich protein 2 bindin	1.047	83.95	0.94386	34930	P	-1.081	19.02	0.13147	3698
Ctdsp2	A_52_P432685	NM_146012	CTD (carboxy-terminal domain, RNA poly	1.047	84.22	0.96163	36569	P	1.091	11.33	0.12581	3626
Golga3	A_52_P140497	AK077389	golgi autoantigen, golgin subfamily a, 3	1.047	82.34	0.92057	33097	P	-1.073	22.1	0.13338	3735
Gpr125	A_51_P462102	BC052391	G protein-coupled receptor 125	1.047	81.02	0.9065	31547	P	-1.199	0.92	0.01372	579
Irs1	A_52_P175242	AK141842	insulin receptor substrate 1	1.047	84.22	0.95592	35937	P	-1.096	19.02	0.16182	4258
Mmp23	A_51_P502132	NM_011985	matrix metallopeptidase 23	1.047	82.34	0.91483	32470	P	-1.146	2.04	0.03019	1207
Neurl	A_52_P339011	NM_021360	neuralized-like homolog (Drosophila)	1.047	83.95	0.9529	35790	P	-1.005	49.48	0.91365	12208
Nkiras1	A_52_P52982	NM_023526	NFKB inhibitor interacting Ras-like protei	1.047	83.95	0.94234	34747	P	-1.134	3.46	0.04256	1599
Nono	A_51_P296292	NM_023144	non-POU-domain-containing, octamer bi	1.047	82.34	0.94226	24545	M	1.067	19.02	0.25033	5649
Rpl41	A_52_P295201	NM_018860	ribosomal protein L41	1.047	84.22	0.9639	25483	M	-1.141	6.98	0.1064	3209
Slc9a3r2	A_52_P241676	NM_023449	solute carrier family 9 (sodium/hydrogen	1.047	82.34	0.91249	32247	P	1.008	42.43	0.91179	12203
Tmcc1	A_52_P674386	AK087243	transmembrane and coiled coil domains 1	1.047	84.22	0.95609	35954	P	1.048	25.31	0.37334	7206
Trim54	A_51_P181175	NM_021447	tripartite motif-containing 54	1.047	84.56	0.92595	28771	M	1.07	13.58	0.15879	4195
2700038N03Rik	A_51_P278034	NM_027356	RIKEN cDNA 2700038N03 gene	1.046	83.95	0.94989	35425	P	1.027	33.49	0.56904	9192
5630401D06Rik	A_51_P294113	AK032988	chromodomain helicase DNA binding pro	1.046	83.36	0.93804	34408	P	1.03	38.4	0.76438	10889
C330023M02Rik	A_51_P272563	NM_172722	RIKEN cDNA C330023M02 gene	1.046	82.34	0.92057	33073	P	-1.01	49.48	0.84323	11546
Cbr1	A_52_P447375	U31966	carbonyl reductase 1	1.046	82.34	0.9089	31763	P	-1.083	19.02	0.1217	3539
Epha1	A_51_P214269	NM_023580	Eph receptor A1	1.046	83.95	0.94999	35432	P	1.078	22.1	0.43136	7847
Gtf2b	A_51_P502054	NM_145546	general transcription factor IIB	1.046	84.22	0.96279	36706	P	-1.017	49.48	0.85969	11678
Hnrpk	A_52_P401423	NM_025279	heterogeneous nuclear ribonucleoprotei	1.046	83.36	0.93859	34446	P	1.244	1.62	0.01643	702
Map3k3	A_51_P100565	ENSMUST00000100328	mitogen activated protein kinase kinase k	1.046	84.22	0.96208	36651	P	1.1	11.33	0.1605	4224
Ppp6c	A_52_P204440	AK046859	protein phosphatase 6, catalytic subunit	1.046	84.22	0.93314	31541	P	-1.02	49.48	0.8701	11759
Ptpra	A_51_P382194	NM_008980	protein tyrosine phosphatase, receptor ty	1.046	83.95	0.94054	34609	P	1.14	5.75	0.04595	1726
1200014M14Rik	A_52_P365226	AK089013	RIKEN cDNA 1200014M14 gene	1.045	84.4	0.97329	37794	P	-1.143	3.01	0.03657	1404
2310047K21Rik	A_51_P445912	AK009882	RIKEN cDNA 2310047K21 gene	1.045	84.22	0.95839	36235	P	1.045	30.75	0.54146	8959
2810001G20Rik	A_52_P81630	AK012631	RIKEN cDNA 2810001G20 gene	1.045	83.95	0.9493	35364	P	1.037	33.49	0.60832	9508

Anxa3	A_51_P451032	NM_013470	annexin A3	1.045	84.4	0.96743	37238	P	-1.037	43.75	0.40226	7539
Cish	A_51_P470715	NM_009895	cytokine inducible SH2-containing proteir	1.045	84.52	0.97769	38266	P	1.447	3.46	0.14235	3891
Cul1	A_51_P335509	NM_012042	cullin 1	1.045	82.34	0.91548	32648	P	-1.061	42.43	0.47675	8276
Cul3	A_51_P188655	AF129738	cullin 3	1.045	82.34	0.91986	33022	P	1.209	2.04	0.01492	639
Dhx35	A_51_P185563	NM_145742	DEAH (Asp-Glu-Ala-His) box polypeptide 3	1.045	84.4	0.97167	37595	P	1.084	13.58	0.18008	4577
E330039K12Rik	A_51_P158189	NM_172917	RIKEN cDNA E330039K12 gene	1.045		0.95184	24882	A	-1.123	8.32	0.11077	3285
Eif1ay	A_51_P237514	NM_025437	eukaryotic translation initiation factor 1A,	1.045	83.95	0.94576	35047	P	1.038	30.75	0.52163	8764
Foxk1	A_52_P471583	NM_199068	forkhead box K1	1.045	82.34	0.92023	33050	P	1.119	9.71	0.11657	3411
Hes7	A_52_P488908	NM_033041	hairy and enhancer of split 7 (Drosophila)	1.045	83.36	0.92544	33487	M	1.1	11.33	0.17399	4452
Klhl9	A_52_P567839	NM_172871	kelch-like 9 (Drosophila)	1.045	83.36	0.93319	34079	P	1.048	36.07	0.74866	10779
Mdh2	A_51_P384879	NM_008617	malate dehydrogenase 2, NAD (mitochon	1.045	82.34	0.92243	28527	P	1.148	4.63	0.03941	1497
Pfas	A_52_P599624	AK133932	phosphoribosylformylglycinamidine synth	1.045	83.36	0.92427	33389	P	1.033	36.07	0.71002	10399
Prkcdbp	A_51_P180974	NM_028444	protein kinase C, delta binding protein	1.045	83.95	0.94484	34993	P	-1.042	44.4	0.53168	8859
Ptk2	A_52_P359381	NM_007982	PTK2 protein tyrosine kinase 2	1.045	82.34	0.92158	33162	P	1.098	9.71	0.097	3035
Rap1b	A_51_P476579	XM_985042	RAS related protein 1b	1.045	83.95	0.95791	25219	M	1.274	2.53	0.03761	1434
Rpl32	A_52_P573161	NM_172086	ribosomal protein L32	1.045	84.22	0.96279	25450	M	-1.072	40.63	0.45852	8082
Sh3bp5	A_52_P305307	NM_011894	SH3-domain binding protein 5 (BTK-assoc	1.045	84.22	0.96426	36823	P	1.006	42.43	0.96012	12657
Slc27a6	A_51_P211616	AK028699	solute carrier family 27 (fatty acid transpo	1.045		0.98354	14988	A	1.084	16.2	0.26246	5846
Wbscr22	A_51_P456590	NM_025375	Williams Beuren syndrome chromosome	1.045	83.36	0.92998	33775	P	1.028	36.07	0.62852	9702
Zfp532	A_52_P342131	NM_207255	zinc finger protein 532	1.045	83.36	0.92327	33314	P	1.166	8.32	0.17262	4421
Cdk7	A_51_P193563	NM_009874	cyclin-dependent kinase 7 (homolog of Xe	1.044	83.95	0.94904	35326	P	1.087	11.33	0.12	3494
Dnajb12	A_52_P92302	AK089427	DnaJ (Hsp40) homolog, subfamily B, mem	1.044	83.95	0.95466	35850	P	-1.304	0.51	0.00627	167
Drg2	A_51_P118742	NM_021354	developmentally regulated GTP binding p	1.044	81.02	0.9087	31744	P	-1.02	49.47	0.76438	10888
Eml2	A_51_P428013	AK005562	echinoderm microtubule associated prote	1.044	81.02	0.95624	27971	M	-1.148	3.82	0.05775	2080
Rap1gds1	A_52_P199169	AK052125	RAP1, GTP-GDP dissociation stimulator 1	1.044		0.97483	19286	A	-1.039	46.3	0.65369	9907
Smarcd2	A_51_P184197	NM_031878	SWI/SNF related, matrix associated, actin	1.044	83.36	0.95193	24962	M	1.013	42.43	0.83652	11501
Timeless	A_52_P379531	NM_011589	timeless homolog (Drosophila)	1.044	82.34	0.96239	33717	M	1.011	42.43	0.81133	11289
Tln1	A_51_P446865	NM_011602	talin 1	1.044	84.22	0.96504	36984	P	1.028	33.49	0.53218	8866
Ube3c	A_52_P314201	NM_133907	ubiquitin protein ligase E3C	1.044	83.36	0.93135	33943	P	1.075	19.02	0.32714	6643
0610012G03Rik	A_51_P417279	AK002600	RIKEN cDNA 0610012G03 gene	1.043	84.22	0.95609	35960	P	1.053	22.1	0.28112	6103
2600009E05Rik	A_52_P84447	NM_029832	RIKEN cDNA 2600009E05 gene	1.043	83.95	0.95123	35586	P	-1.223	2.53	0.08211	2706
9330129D05Rik	A_51_P384113	AK033963	RIKEN cDNA 9330129D05 gene	1.043	84.4	0.96778	37272	P	-1.264	0.51	0.00731	250
Cdo1	A_51_P489452	NM_033037	cysteine dioxygenase 1, cytosolic	1.043	83.95	0.95055	35482	P	1.153	6.98	0.08984	2893
Centg3	A_51_P410112	NM_139153	centaurin, gamma 3	1.043	83.36	0.93862	34456	P	1.061	22.1	0.32914	6657
D2Ertd435e	A_52_P550491	NM_153387	DNA segment, Chr 2, ERATO Doi 435, expi	1.043	83.36	0.93702	34348	P	1.14	6.98	0.08095	2684
Dnajb1	A_52_P171663	NM_018808	DnaJ (Hsp40) homolog, subfamily B, mem	1.043	84.56	0.98182	38974	P	1.088	13.58	0.22647	5298
Efnb1	A_51_P388478	NM_010110	ephrin B1	1.043	82.34	0.91818	32854	P	1.062	28.13	0.52549	8804
Hibadh	A_51_P165165	NM_145567	3-hydroxyisobutyrate dehydrogenase	1.043	82.34	0.92017	33042	P	-1.193	1.18	0.0225	953
Mpv17	A_51_P150802	NM_008622	Mpv17 transgene, kidney disease mutant	1.043	83.36	0.93294	34022	P	1.129	5.75	0.04588	1722
Pitpnm2	A_52_P548399	NM_011256	phosphatidylinositol transfer protein, mei	1.043		0.97483	19295	A	1.084	13.58	0.14193	3886
Plod3	A_51_P372172	NM_011962	procollagen-lysine, 2-oxoglutarate 5-dioxy	1.043	83.36	0.92462	33424	P	-1.045	43.75	0.48278	8354
Ppt1	A_52_P473866	AK153316	palmitoyl-protein thioesterase 1	1.043	83.95	0.9416	34685	P	-1.012	49.48	0.77958	10985
Pum2	A_52_P138598	AK141682	pumilio 2 (Drosophila)	1.043	83.36	0.92998	33778	P	1.112	6.98	0.05389	1974
Tef	A_52_P485573	NM_153484	thyrotroph embryonic factor	1.043	84.22	0.96099	36478	P	-1.085	44.4	0.70134	10334
U2af1l4	A_51_P509140	NM_170760	U2 small nuclear RNA auxiliary factor 1-lik	1.043	84.22	0.96489	36908	P	1.01	42.43	0.84595	11571
Yes1	A_52_P309068	AK031316	Yamaguchi sarcoma viral (v-yes) oncogene	1.043	84.56	0.94301	32323	M	1.094	13.58	0.24023	5490
Zfp101	A_51_P184796	NM_009542	zinc finger protein 101	1.043	84.22	0.96279	36705	P	-1.072	28.13	0.19532	4826
2700029M09Rik	A_51_P450518	BC042740	RIKEN cDNA 2700029M09 gene	1.042	83.36	0.92998	33800	P	1.042	33.49	0.67189	10068
Actr10	A_51_P341324	NM_019785	ARP10 actin-related protein 10 homolog (	1.042	82.34	0.9493	24822	M	-1.299	1.18	0.06339	2246
Actr1a	A_51_P509760	NM_016860	ARP1 actin-related protein 1 homolog A (	1.042	83.36	0.93702	34346	P	1.141	8.32	0.1097	3260
Atp5k	A_51_P301289	NM_007507	ATP synthase, H+ transporting, mitochonc	1.042	84.22	0.95676	36072	P	-1.045	45.68	0.64396	9830
BC038286	A_51_P174415	NM_170755	cDNA sequence BC038286	1.042	84.22	0.95883	30671	P	1.02	42.43	0.84229	11538
Clcn7	A_52_P105015	NM_011930	chloride channel 7	1.042	84.22	0.95568	35903	P	-1.447	0	0.00584	23

Dkk1	A_52_P508391	NM_010051	dickkopf homolog 1 (Xenopus laevis)	1.042	83.36	0.97791	28943	M	-1.022	48.39	0.66667	10014
Eif3s10	A_52_P524895	NM_010123	eukaryotic translation initiation factor 3, s	1.042	82.34	0.91805	32832	P	1.059	22.1	0.296	6283
Omg	A_51_P255832	NM_019409	oligodendrocyte myelin glycoprotein	1.042	84.4	0.97482	37922	P	-1.026	47.92	0.6878	10218
Rhobtb3	A_52_P413280	NM_028493	Rho-related BTB domain containing 3	1.042	83.36	0.93023	33846	P	1.074	11.33	0.12441	3587
Rpl36al	A_51_P209444	NM_025589	ribosomal protein L36a-like	1.042	84.22	0.96504	25556	M	-1.156	5.75	0.11265	3329
Tlx1	A_52_P58359	NM_021901	T-cell leukemia, homeobox 1	1.042	83.36	0.9283	33679	P	-1.168	3.46	0.06913	2378
2410014A08Rik	A_52_P223571	NM_175403	RIKEN cDNA 2410014A08 gene	1.041	82.34	0.92327	33324	P	1.079	16.2	0.19954	4893
4933428G09Rik	A_51_P459340	NM_025755	RIKEN cDNA 4933428G09 gene	1.041	83.36	0.93702	34347	P	1.012	42.43	0.88231	11883
Lancl1	A_51_P142175	NM_021295	LanC (bacterial lantibiotic synthetase com	1.041	83.36	0.9348	34169	P	1.008	42.43	0.88007	11860
Pdcd10	A_51_P496814	NM_019745	programmed cell death 10	1.041	83.95	0.94904	35323	P	-1.044	43.75	0.47086	8214
Pfdn1	A_52_P456059	NM_026027	prefoldin 1	1.041	84.22	0.95871	36293	P	1.041	30.75	0.56143	9125
Thpo	A_51_P385086	NM_009379	thrombopoietin	1.041	83.95	0.94386	34908	P	-1.316	0.51	0.01458	616
0610031J06Rik	A_51_P437717	NM_020003	RIKEN cDNA 0610031J06 gene	1.04	83.36	0.9348	34171	P	1.037	30.75	0.45372	8035
Arid5a	A_52_P350512	NM_145996	AT rich interactive domain 5A (Mrf1 like)	1.04	84.52	0.97618	38103	M	1.105	11.33	0.16577	4307
Arl2	A_52_P122696	NM_019722	ADP-ribosylation factor-like 2	1.04	84.4	0.96634	37134	P	1.051	33.49	0.6808	10140
Cables2	A_51_P141610	BC052789	Cdk5 and Abl enzyme substrate 2	1.04	83.95	0.9526	35774	P	1.094	16.2	0.25544	5734
Crk	A_52_P618807	NM_133656	v-crk sarcoma virus CT10 oncogene homo	1.04	82.34	0.9256	33517	P	-1.029	47.43	0.64519	9845
Dgcr2	A_52_P392178	AK042786	DiGeorge syndrome critical region gene 2	1.04	84.4	0.96705	37210	P	1.058	22.1	0.35507	6959
Dnajc7	A_51_P449956	NM_019795	DnaJ (Hsp40) homolog, subfamily C, mem	1.04	83.36	0.93855	34439	P	1.069	16.2	0.21497	5120
Fkbp9	A_52_P37681	NM_012056	FK506 binding protein 9	1.04	82.34	0.92546	33492	P	1.223	2.53	0.0267	1090
Nfyb	A_52_P239707	NM_010914	nuclear transcription factor-Y beta	1.04	82.34	0.92175	33175	P	1.031	36.07	0.68088	10142
Notch4	A_51_P195875	NM_010929	Notch gene homolog 4 (Drosophila)	1.04	84.4	0.97112	37529	P	1.099	11.33	0.13968	3841
Nup50	A_51_P411297	NM_016714	nucleoporin 50	1.04	84.22	0.96101	36483	P	-1.028	47.43	0.65822	9956
Rab14	A_51_P269434	NM_026697	RAB14, member RAS oncogene family	1.04	83.95	0.94425	34949	P	1.132	8.32	0.0904	2904
Rps27l	A_51_P246903	NM_026467	ribosomal protein S27-like	1.04	82.34	0.94484	32492	P	-1.203	1.32	0.02905	1169
Slc4a2	A_51_P172542	NM_009207	solute carrier family 4 (anion exchanger),	1.04	83.95	0.94613	35077	P	1.115	6.98	0.05307	1959
Vps4a	A_51_P383629	NM_126165	vacuolar protein sorting 4a (yeast)	1.04	82.34	0.92551	33506	P	-1.035	44.4	0.45312	8026
2210018M11Rik	A_52_P197261	XM_897432		1.039	84.4	0.97371	37854	P	-1.03	45.05	0.49171	8461
2610205E22Rik	A_51_P176517	NM_170592	RIKEN cDNA 2610205E22 gene	1.039	84.22	0.96276	36701	P	-1.166	3.82	0.0737	2502
Atic	A_51_P222436	NM_026195	5-aminoimidazole-4-carboxamide ribonuc	1.039	83.36	0.93689	34328	P	1.096	8.32	0.06925	2382
Bad	A_51_P419364	NM_007522	Bcl-associated death promoter	1.039	84.22	0.96039	36433	P	-1.275	0.56	0.0141	592
C230096C10Rik	A_52_P662216	NM_146157	RIKEN cDNA C230096C10 gene	1.039	83.95	0.96271	25443	M	1.088	11.33	0.1399	3850
D8Ertd738e	A_51_P391668	NM_001007571	DNA segment, Chr 8, ERATO Doi 738, expr	1.039	84.22	0.96096	36469	P	-1.044	45.05	0.58463	9296
Elovl5	A_52_P676944	NM_134255	ELOVL family member 5, elongation of lor	1.039	84.4	0.97538	25957	M	1.09	9.71	0.09627	3016
Foxd1	A_51_P237783	NM_008242	forkhead box D1	1.039	84.56	0.96558	33966	M	1.068	13.58	0.15235	4075
Hnrpd	A_52_P466887	NM_001077265	heterogeneous nuclear ribonucleoprotein	1.039	83.95	0.94519	35038	P	1.094	13.58	0.19654	4844
Ndufc2	A_51_P357459	NM_024220	NADH dehydrogenase (ubiquinone) 1, sub	1.039	82.34	0.9547	25050	M	1.135	13.58	0.33933	6770
Pqlc2	A_51_P306892	NM_145384	PQ loop repeat containing 2	1.039	82.34	0.92082	33124	P	-1.169	3.46	0.06956	2386
Prdm15	A_52_P262118	AK144820	PR domain containing 15	1.039	84.22	0.9312	31416	P	-1.107	22.1	0.2573	5769
Psmd2	A_52_P163978	NM_134101	proteasome (prosome, macropain) 26S su	1.039	83.95	0.94329	34863	P	1.104	8.32	0.07039	2408
Smndc1	A_51_P225179	NM_172429	survival motor neuron domain containing	1.039	84.22	0.96853	25702	M	1.093	19.02	0.37685	7240
Sympk	A_51_P183275	AK146894	symplekin	1.039	84.4	0.96776	37250	P	1.041	28.13	0.38751	7368
Zfp259	A_52_P282068	NM_011752	zinc finger protein 259	1.039	83.95	0.95054	35481	P	1.002	42.43	0.97618	12809
Dhdds	A_52_P27271	NM_026144	dehydrodolichyl diphosphate synthase	1.038	84.22	0.9639	36802	P	1.004	42.43	0.93005	12388
Dnajb6	A_51_P117439	NM_011847	DnaJ (Hsp40) homolog, subfamily B, mem	1.038	83.95	0.94823	35287	P	1.099	11.33	0.1508	4051
Drg1	A_51_P453948	NM_007879	developmentally regulated GTP binding p	1.038	83.95	0.95123	35589	P	1.202	3.46	0.0403	1538
Fgf2	A_51_P399845	NM_008006	fibroblast growth factor 2	1.038	84.56	0.95733	33333	M	1.127	4.63	0.03714	1413
Itm2c	A_51_P267370	NM_022417	integral membrane protein 2C	1.038	83.95	0.94234	34755	P	-1.073	25.31	0.1612	4239
Pde4a	A_52_P600760	BC044786	phosphodiesterase 4A, cAMP specific	1.038		0.98706	15063	A	-1.017	49.48	0.77661	10964
Ppp2r5e	A_51_P369478	AK014554	protein phosphatase 2, regulatory subuni	1.038	83.36	0.9362	34277	P	1.067	22.1	0.35296	6922
Rpl28	A_51_P339103	NM_009081	ribosomal protein L28	1.038	84.22	0.9689	25711	M	1.025	38.4	0.7194	10490
Sfrs8	A_51_P199624	NM_172276	splicing factor, arginine/serine-rich 8	1.038	83.95	0.94326	34859	P	-1.058	38.4	0.35084	6886
Tigd2	A_51_P393078	XM_144820	tigger transposable element derived 2	1.038	83.95	0.94294	34814	P	-1.019	49.47	0.75231	10806

Traf6	A_52_P529306	AK051130	Tnf receptor-associated factor 6	1.038		0.96863	25667	A	1.052	25.31	0.35244	6909
Uvrag	A_52_P153265	AK020590	UV radiation resistance associated gene	1.038	84.4	0.97217	37700	P	-1.075	33.49	0.33283	6713
Wdr35	A_51_P324442	NM_172470	WD repeat domain 35	1.038	82.34	0.92852	33684	P	1.06	25.31	0.40275	7543
5730407K14Rik	A_51_P323521	NM_133924	sorting nexin family member 21	1.037	84.22	0.95733	36121	P	-1.007	49.48	0.90263	12117
A530089I17Rik	A_51_P405985	NM_133999	RIKEN cDNA A530089I17 gene	1.037	84.22	0.95446	35844	P	-1.01	49.48	0.87739	11836
Brca1	A_52_P18267	NM_009764	breast cancer 1	1.037	82.34	0.967	28458	M	1.008	42.43	0.88251	11887
Cd34	A_51_P204740	NM_133654	CD34 antigen	1.037	84.52	0.97425	37884	P	-1.079	36.07	0.41288	7652
Dnaja4	A_51_P308549	NM_021422	DnaJ (Hsp40) homolog, subfamily A, mem	1.037	84.22	0.96303	36758	P	-1.007	49.48	0.90387	12130
Eif2ak1	A_52_P681727	AK020887	eukaryotic translation initiation factor 2 a	1.037	72.2	0.9617	28193	M	-1.033	46.85	0.65458	9915
Eif3s6ip	A_51_P173086	NM_145139	eukaryotic translation initiation factor 3,	1.037	83.95	0.9493	35360	P	-1.384	0.51	0.00627	145
Letmd1	A_51_P486512	NM_134093	LETM1 domain containing 1	1.037	84.22	0.96487	25521	M	1.026	40.63	0.83898	11514
Psap	A_52_P508089	NM_011179	prosaposin	1.037	84.22	0.96769	25666	M	1.045	28.13	0.4115	7621
Rufy2	A_52_P174456	NM_027425	RUN and FYVE domain-containing 2	1.037	84.22	0.95444	35842	P	-1.073	36.07	0.37699	7242
Sf3a1	A_52_P569178	AK030115	splicing factor 3a, subunit 1	1.037	84.22	0.96362	36785	P	1.066	16.2	0.19537	4827
Sufu	A_52_P340811	BC048168	suppressor of fused homolog (Drosophila	1.037	84.4	0.97114	37536	P	-1.015	49.48	0.80996	11278
Wnt5a	A_51_P162272	NM_009524	wingless-related MMTV integration site 5	1.037		0.95176	27804	A	1.044	25.31	0.33454	6732
Wnt5b	A_51_P137991	NM_009525	wingless-related MMTV integration site 5	1.037	82.34	0.92751	33639	P	-1.049	43.15	0.45669	8064
2510049I19Rik	A_52_P482124	NM_026455	RIKEN cDNA 2510049I19 gene	1.036	83.36	0.95996	33525	P	1.073	22.1	0.43177	7855
Acp6	A_51_P444335	NM_019800	acid phosphatase 6, lysophosphatidic	1.036	83.95	0.95045	35465	P	1.153	5.75	0.05291	1951
Adcyap1	A_52_P425667	NM_009625	adenylate cyclase activating polypeptide	1.036	84.56	0.98771	39569	P	1.131	22.1	0.56295	9133
AU019823	A_52_P106391	NM_212449	expressed sequence AU019823	1.036	83.95	0.94706	35162	P	1.171	9.71	0.20959	5038
BC031181	A_51_P107090	NM_001001181	cDNA sequence BC031181	1.036	79.26	0.95799	30609	P	1.202	3.46	0.04342	1627
Bin1	A_52_P384956	NM_009668	bridging integrator 1	1.036	84.22	0.95676	36054	P	1.048	22.1	0.28618	6173
Casp6	A_51_P215922	NM_009811	caspase 6	1.036	84.4	0.96492	36918	P	-1.045	46.3	0.69989	10316
Eif4g2	A_51_P347907	NM_013507	eukaryotic translation initiation factor 4,	1.036	82.34	0.93314	34049	P	1.116	8.32	0.09166	2934
Glrx2	A_51_P483928	NM_001038592	glutaredoxin 2 (thioltransferase)	1.036	84.22	0.95823	36210	P	-1.261	0.51	0.0108	421
Habp4	A_52_P421249	NM_019986	hyaluronic acid binding protein 4	1.036	84.4	0.96421	36819	P	1.058	22.1	0.35274	6918
Incenp	A_51_P264064	NM_016692	inner centromere protein	1.036	84.56	0.97889	38405	P	1.094	9.71	0.08211	2707
Pou2f3	A_51_P337156	NM_011139	POU domain, class 2, transcription factor	1.036	84.56	0.98109	31942	M	-1.08	28.13	0.25067	5653
Prkch	A_51_P355852	NM_008856	protein kinase C, eta	1.036	84.4	0.96778	37265	P	-1.127	11.33	0.17257	4416
Rbbp7	A_51_P114385	NM_009031	retinoblastoma binding protein 7	1.036	84.22	0.95755	36148	P	1.184	3.01	0.02177	913
Slc35c2	A_51_P158425	NM_144893	solute carrier family 35, member C2	1.036	83.95	0.95094	35550	P	-1.023	47.92	0.65987	9971
Snrpg	A_51_P200134	NM_026506	small nuclear ribonucleoprotein polypept	1.036	84.22	0.96696	25637	M	1.015	42.43	0.79013	11092
Tmod3	A_52_P188782	AK082971	tropomodulin 3	1.036	84.22	0.9584	36250	P	-1.148	8.32	0.14137	3870
1110001A07Rik	A_51_P237512	NM_025377	RIKEN cDNA 1110001A07 gene	1.035	84.22	0.95768	36155	P	1.091	13.58	0.17475	4466
2310035C23Rik	A_51_P231768	NM_173187	RIKEN cDNA 2310035C23 gene	1.035	83.95	0.95254	35765	P	1.099	11.33	0.16821	4347
Armcx3	A_52_P423380	NM_027870	armadillo repeat containing, X-linked 3	1.035	83.36	0.93859	34445	P	-1.157	8.32	0.15225	4070
Bex2	A_51_P237668	NM_009749	brain expressed X-linked 2	1.035	83.95	0.96219	25430	M	-1.022	49.39	0.78303	11032
Bmpr1a	A_52_P17146	NM_009758	bone morphogenetic protein receptor, ty	1.035	84.22	0.95609	36004	P	1.074	25.31	0.49251	8474
C1qbp	A_51_P466162	NM_007573	complement component 1, q subcompon	1.035	83.95	0.9493	35356	P	1.094	11.33	0.11364	3350
Cfl1	A_52_P477720	NM_007687	cofilin 1, non-muscle	1.035	84.52	0.97615	38089	P	1.18	3.82	0.04181	1580
Exosc6	A_52_P195922	NM_028274	exosome component 6	1.035	84.4	0.97154	37575	P	1.022	40.63	0.80819	11264
Fxyd1	A_51_P287001	NM_019503	FXYD domain-containing ion transport reg	1.035	84.4	0.97007	37404	P	-1.14	3.82	0.05066	1873
Gpbar1	A_51_P175311	NM_174985	G protein-coupled bile acid receptor 1	1.035	83.36	0.94271	34771	P	-1.179	4.63	0.11254	3326
Hnrpa0	A_52_P625431	AK019388	heterogeneous nuclear ribonucleoprotei	1.035	84.56	0.95275	30318	M	1.099	9.71	0.11104	3294
Irak3	A_52_P644273	NM_028679	interleukin-1 receptor-associated kinase	1.035	84.22	0.95637	36046	P	-1.074	30.75	0.28281	6117
Katnal1	A_52_P365528	NM_153572	katanin p60 subunit A-like 1	1.035	83.95	0.94651	35115	P	-1.042	43.15	0.39354	7443
Ldlr	A_52_P427024	NM_010700	low density lipoprotein receptor	1.035	84.22	0.96837	25700	M	1.025	42.43	0.87887	11849
Pip5k3	A_52_P166653	NM_011086	phosphatidylinositol-3-phosphate/phosp	1.035	77.44	0.95861	30648	P	1.048	28.13	0.49834	8565
Rhov	A_51_P439584	NM_145530	ras homolog gene family, member V	1.035	83.95	0.95046	35476	P	1.075	16.2	0.2199	5210
Tmem9	A_51_P359237	NM_025439	transmembrane protein 9	1.035	84.4	0.9648	36854	P	-1.066	28.13	0.19463	4813
Arid4b	A_51_P341821	AK080967	AT rich interactive domain 4B (Rbp1 like)	1.034	84.4	0.96096	28125	M	1.273	1.62	0.02358	989
Atp6ap1	A_51_P447988	NM_018794	ATPase, H+ transporting, lysosomal acces	1.034	83.95	0.95332	35798	P	1.153	5.75	0.06513	2289

Cacng4	A_51_P494875	AJ272045	calcium channel, voltage-dependent, gam	1.034	83.36	0.93874	34486	P	1.111	8.32	0.07623	2560
Dusp6	A_51_P502614	NM_026268	dual specificity phosphatase 6	1.034	83.95	0.96421	25493	M	1.202	3.82	0.06285	2230
Flot2	A_51_P228232	NM_008028	flotillin 2	1.034	84.22	0.95569	35927	P	1.16	11.33	0.3151	6524
H2afy	A_52_P179238	BC006955	H2A histone family, member Y	1.034	84.22	0.96163	36573	P	1.056	25.31	0.3658	7109
Kif3b	A_51_P279050	NM_008444	kinesin family member 3B	1.034	84.22	0.95916	36311	P	-1.106	6.98	0.06516	2292
Mpo	A_51_P317460	NM_010824	myeloperoxidase	1.034	83.95	0.9452	35041	P	1.016	40.63	0.77949	10984
Nol5a	A_51_P187902	NM_024193	nucleolar protein 5A	1.034	84.4	0.9703	37432	P	-1.352	0.51	0.00584	56
Polg	A_51_P468294	NM_017462	polymerase (DNA directed), gamma	1.034	83.95	0.94728	35176	P	1.09	9.71	0.08772	2834
Prdx1	A_51_P353183	NM_011034	peroxiredoxin 1	1.034	84.52	0.97808	38311	P	1.04	33.49	0.63197	9738
Stoml2	A_51_P380685	NM_023231	stomatin (Epb7.2)-like 2	1.034	84.56	0.98036	38530	P	1.086	9.71	0.09094	2920
Tcn2	A_51_P128491	NM_015749	transcobalamin 2	1.034	84.22	0.95609	35958	P	1.051	28.13	0.54667	8996
Tox	A_52_P258211	AK051947	thymocyte selection-associated HMG box	1.034	83.95	0.97161	25713	M	-1.409	0.51	0.00584	98
2700078K21Rik	A_51_P156800	NM_028308	RIKEN cDNA 2700078K21 gene	1.033	84.4	0.97194	37610	P	1.008	42.43	0.86042	11683
6530406A20Rik	A_51_P249516	AK087211	RIKEN cDNA 6530406A20 gene	1.033	84.4	0.97209	37679	P	1.01	42.43	0.83055	11462
Aldh4a1	A_52_P123230	NM_175438	aldehyde dehydrogenase 4 family, memb	1.033	83.36	0.94301	34842	P	1.081	19.02	0.35274	6912
Cdkn2d	A_51_P122356	NM_009878	cyclin-dependent kinase inhibitor 2D (p1	1.033	84.52	0.97634	38130	P	-1.01	49.48	0.8444	11559
Lass5	A_51_P481546	NM_028015	longevity assurance homolog 5 (S. cerevis	1.033	84.22	0.9552	35872	P	1.065	22.1	0.34708	6839
Nasp	A_51_P281255	NM_016777	nuclear autoantigenic sperm protein (hist	1.033	83.95	0.94662	35126	P	1.042	28.13	0.36779	7134
Nfib	A_51_P304412	NM_008687	nuclear factor I/B	1.033	84.22	0.96281	36735	P	1.035	30.75	0.45852	8085
Osbpl6	A_52_P359958	NM_145525	oxysterol binding protein-like 6	1.033	83.36	0.93965	34537	P	-1.063	36.07	0.32152	6580
Polr3c	A_52_P309008	AK016716	polymerase (RNA) III (DNA directed) poly	1.033	84.22	0.95569	35909	P	1.057	25.31	0.41996	7729
Rab19	A_51_P414126	NM_011226	RAB19, member RAS oncogene family	1.033	84.4	0.96703	37199	P	1.008	42.43	0.89842	12051
Rab24	A_51_P320401	NM_009000	RAB24, member RAS oncogene family	1.033	84.4	0.97138	37565	P	-1.025	48.39	0.70839	10394
Zfp287	A_51_P489702	NM_133208	zinc finger protein 287	1.033		0.98815	15122	A	1.008	42.43	0.9162	12225
1110005A03Rik	A_51_P114591	NM_028865	RIKEN cDNA 1110005A03 gene	1.032	83.95	0.9493	35355	P	1.112	8.32	0.06274	2220
4933407K13Rik	A_52_P287507	AK036260	RIKEN cDNA 4933407K13 gene	1.032	83.95	0.94748	35220	P	-1.035	43.75	0.41427	7668
Arih1	A_52_P239616	AK083466		1.032	84.56	0.9834	39143	P	1.12	5.75	0.04247	1595
Bmp10	A_51_P293830	NM_009756	bone morphogenetic protein 10	1.032	82.34	0.96421	28297	M	-1.039	44.4	0.47093	8215
C730034F03Rik	A_52_P28955	NM_176900	RIKEN cDNA C730034F03 gene	1.032	84.56	0.98413	39197	P	-1.151	4.63	0.08432	2759
Commd5	A_51_P430485	NM_025536	COMM domain containing 5	1.032	83.95	0.94976	35419	P	-1.142	2.53	0.03097	1220
Golgb1	A_51_P387952	AK015226	golgi autoantigen, golgin subfamily b, ma	1.032	84.52	0.97255	37740	M	-1.113	11.33	0.1174	3427
Hes2	A_51_P303308	NM_008236	hairy and enhancer of split 2 (Drosophila)	1.032	83.36	0.94335	34866	P	1.107	6.98	0.05876	2099
Msn	A_51_P115197	NM_010833	moesin	1.032	84.4	0.96778	37262	P	1.037	33.49	0.59894	9441
Slc22a8	A_51_P127527	NM_031194	solute carrier family 22 (organic anion tra	1.032	84.56	0.95861	30661	M	-1.026	46.3	0.53846	8921
Stat6	A_51_P452382	NM_009284	signal transducer and activator of transcri	1.032	84.4	0.97024	37423	P	1.056	19.02	0.22821	5332
Tbx2	A_52_P318532	NM_009324	T-box 2	1.032	84.22	0.96163	36572	P	1.001	42.43	0.97964	12840
Tlk2	A_52_P451888	NM_011903	tousled-like kinase 2 (Arabidopsis)	1.032	83.36	0.94603	35060	P	1.129	4.63	0.03654	1403
Tmeff1	A_51_P222381	NM_021436	transmembrane protein with EGF-like an	1.032	84.56	0.98789	39585	P	1.025	36.07	0.6265	9686
Alg3	A_51_P155501	NM_145939	asparagine-linked glycosylation 3 homolo	1.031	83.95	0.9493	35388	P	1.063	22.1	0.36585	7111
Ccnl2	A_52_P625745	AK048244	cyclin L2	1.031	84.52	0.97247	37739	P	1.232	8.32	0.2522	5685
D930017K21Rik	A_52_P163201	XM_988017	RIKEN cDNA D930017K21 gene	1.031	84.22	0.94883	32766	M	1.11	9.71	0.13943	3837
Ddx17	A_52_P272693	NM_199079	DEAD (Asp-Glu-Ala-Asp) box polypeptide	1.031	84.56	0.97883	38384	P	1.131	13.58	0.31612	6539
Dhrsx	A_51_P102867	NM_001033326	dehydrogenase/reductase (SDR family) X	1.031	83.95	0.94944	35398	P	-1.066	42.43	0.50522	8627
Epb4.1	A_52_P397313	AK019923	erythrocyte protein band 4.1	1.031	84.4	0.96857	37335	P	1.07	16.2	0.22856	5337
Hspb1	A_52_P404533	NM_013560	heat shock protein 1	1.031	84.52	0.97767	38246	P	-1.103	8.32	0.07486	2528
Igsf10	A_51_P155843	XM_887155	immunoglobulin superfamily, member 10	1.031	84.22	0.96045	36436	P	1.087	16.2	0.29193	6235
Jag2	A_51_P451338	NM_010588	jagged 2	1.031	84.4	0.96369	36793	P	1.102	9.71	0.08446	2770
Lcp1	A_51_P275302	NM_008879	lymphocyte cytosolic protein 1	1.031	84.56	0.97889	38409	P	-1.091	38.4	0.50239	8608
Nt5c3	A_52_P77837	NM_026004	5'-nucleotidase, cytosolic III	1.031	84.22	0.95861	36283	P	1.086	25.31	0.39055	6837
Nup107	A_52_P284814	NM_134010	nucleoporin 107	1.031	84.4	0.96573	37064	P	1.013	42.43	0.78278	11028
Pik3ca	A_52_P265002	NM_008839	phosphatidylinositol 3-kinase, catalytic, a	1.031	84.4	0.9648	36852	P	1.106	11.33	0.14256	3896
Sema3d	A_52_P649623	NM_028882	sema domain, immunoglobulin domain (I	1.031		0.9833	29235	A	1.139	8.32	0.10129	3131
1810053B23Rik	A_52_P236288	AK007854	RIKEN cDNA 1810053B23 gene	1.03	84.4	0.97186	34313	M	1.013	42.43	0.81548	11329

Abcb6	A_51_P161342	NM_023732	ATP-binding cassette, sub-family B (MDR/	1.03	84.56	0.97879	38375	P	-1.046	43.15	0.39811	7500
Bach1	A_52_P412465	NM_007520	BTB and CNC homology 1	1.03	84.4	0.96489	36892	P	1.103	11.33	0.13742	3800
Bcl2	A_52_P438280	AK077913	B-cell leukemia/lymphoma 2	1.03	84.52	0.97699	38181	P	1.001	42.43	0.98176	12875
Cnih	A_51_P399625	NM_009919	cornichon homolog (Drosophila)	1.03	84.22	0.96837	25699	M	1.041	28.13	0.43844	7907
Depdc5	A_52_P425813	NM_177786	DEP domain containing 5	1.03	83.36	0.96474	31003	M	1.04	28.13	0.3643	7078
Grinl1a	A_51_P183853	NM_178602	glutamate receptor, ionotropic, N-methyl	1.03	84.52	0.98036	26142	M	1.17	6.98	0.10589	3207
Leprot	A_51_P394690	NM_175036	leptin receptor overlapping transcript	1.03	84.56	0.97926	38432	P	1.061	19.02	0.25689	5763
Pap	A_51_P169671	NM_011036	pancreatitis-associated protein	1.03	79.26	0.9929	32507	P	-1.702	0.51	0.02745	1115
Pdcd6	A_51_P431903	NM_011051	programmed cell death 6	1.03	84.4	0.96328	36772	P	-1.081	28.13	0.21983	5203
Rgmb	A_52_P620154	AK028583	RGM domain family, member B	1.03	84.56	0.98905	39843	P	-1.122	16.2	0.19898	4884
Ube2l3	A_52_P284162	NM_009456	ubiquitin-conjugating enzyme E2L 3	1.03	84.4	0.97194	37608	P	1.174	3.01	0.02196	933
Uqcrb	A_51_P472671	NM_026219	ubiquinol-cytochrome c reductase bindin	1.03	84.52	0.97577	38043	P	1.091	11.33	0.11899	3468
Wbp4	A_51_P334604	NM_018765	WW domain binding protein 4	1.03	84.4	0.96967	37390	P	1.235	1.58	0.01123	431
2610019P18Rik	A_52_P161400	NM_178612	RIKEN cDNA 2610019P18 gene	1.029	83.36	0.94783	35252	P	1.049	19.02	0.25455	5730
4932417H02Rik	A_51_P131480	AK016530	RIKEN cDNA 4932417H02 gene	1.029	84.22	0.98946	26528	M	1.008	42.43	0.88033	11865
AA987161	A_51_P223737	XM_981751	expressed sequence AA987161	1.029	84.4	0.96629	37132	P	1.11	16.2	0.36615	7117
Ide	A_51_P299644	NM_031156	insulin degrading enzyme	1.029	84.4	0.96549	37019	P	1.05	25.31	0.36027	7021
Ltbp4	A_51_P403536	NM_175641	latent transforming growth factor beta bi	1.029	84.52	0.9731	37772	P	1.065	22.1	0.41166	7628
Mef2d	A_52_P334052	AK141270	myocyte enhancer factor 2D	1.029	84.4	0.97042	37461	P	1.071	19.02	0.27641	6048
Msc	A_52_P594410	NM_010827	musculin	1.029	83.95	0.96279	30915	M	1.002	42.43	0.97374	12773
Ppic	A_51_P161086	NM_008908	peptidylprolyl isomerase C	1.029	84.56	0.98238	39037	P	1.142	8.32	0.14174	3877
Ptx3	A_51_P374726	NM_008987	pentraxin related gene	1.029	83.95	0.96257	30893	M	1.099	8.32	0.07361	2500
Rab17	A_51_P382214	NM_008998	RAB17, member RAS oncogene family	1.029	75.14	0.96549	28378	M	1.057	22.1	0.32196	6585
Serpini1	A_52_P220573	NM_009250	serine (or cysteine) peptidase inhibitor, cl	1.029	84.4	0.96703	37194	P	1.097	8.32	0.07034	2405
Ssr3	A_52_P357858	NM_026155	signal sequence receptor, gamma	1.029	84.4	0.97483	25937	M	1.275	2.53	0.0487	1815
Tbc1d7	A_51_P425737	NM_025935	TBC1 domain family, member 7	1.029	83.95	0.95102	35559	P	1.094	9.71	0.10456	3198
Vtn	A_51_P109840	NM_011707	vitronectin	1.029	84.56	0.98482	39252	P	1.048	22.1	0.28627	6178
Zfp426	A_51_P473240	NM_146221	zinc finger protein 426	1.029	84.22	0.95967	36350	P	-1.248	3.01	0.11669	3415
2410104I19Rik	A_51_P177583	NM_028364	RIKEN cDNA 2410104I19 gene	1.028	84.4	0.97197	37636	P	-1.054	42.43	0.3919	7418
Anp32e	A_52_P125350	NM_023210	acidic (leucine-rich) nuclear phosphoprot	1.028	84.22	0.95967	36346	P	1.097	16.2	0.30072	6329
Apeh	A_51_P407977	NM_146226	acylpeptide hydrolase	1.028	84.22	0.96244	36680	P	1.033	33.49	0.55872	9093
Cyb561d2	A_51_P103509	NM_019720	cytochrome b-561 domain containing 2	1.028	84.22	0.95937	36326	P	1.003	42.43	0.96288	12694
D130095D21Rik	A_52_P1180575	AK084110	RIKEN cDNA D130095D21 gene	1.028	84.4	0.9648	36857	M	-1.002	49.48	0.96621	12714
Dnttip1	A_51_P500424	NM_133763	deoxynucleotidyltransferase, terminal, int	1.028	84.52	0.97449	37899	P	1.025	38.4	0.69138	10248
Dusp18	A_52_P493795	NM_173745	dual specificity phosphatase 18	1.028	84.56	0.97883	38385	P	-1.067	36.07	0.31286	6491
Fosb	A_51_P138378	NM_008036	FBJ osteosarcoma oncogene B	1.028	84.56	0.98663	26421	M	1.138	9.71	0.15486	4125
Ifng	A_51_P220976	NM_008337	interferon gamma	1.028		0.98503	19608	A	-1.275	0.66	0.01692	732
Kcnd3	A_51_P104290	NM_019931	potassium voltage-gated channel, Shal-re	1.028	82.34	0.97987	29031	M	1.042	28.13	0.3631	7061
Mtdh	A_51_P195622	AK035302	Metadherin	1.028	83.95	0.95254	35768	P	1.017	40.63	0.79807	11160
Nfatc2	A_52_P73436	AK081853	nuclear factor of activated T-cells, cytopla	1.028	84.56	0.98123	38822	P	1.052	19.02	0.25011	5641
Nsd1	A_52_P287576	AK036308		1.028	84.22	0.96115	36496	P	1.025	38.4	0.70529	10365
Nxf1	A_51_P356229	NM_016813	nuclear RNA export factor 1 homolog (S.	1.028	84.56	0.97961	38486	P	-1.308	0.51	0.00977	356
Psmd1	A_52_P49727	NM_027357	proteasome (prosome, macropain) 26S su	1.028	84.4	0.96973	37392	P	1.183	4.63	0.06153	2182
Pxmp4	A_52_P625683	NM_021534	peroxisomal membrane protein 4	1.028	84.56	0.98078	38597	P	-1.054	36.07	0.25967	5805
Rab7	A_51_P136883	NM_009005	RAB7, member RAS oncogene family	1.028	84.56	0.98078	26186	M	1.193	6.98	0.14358	3915
Sox2	A_52_P307739	NM_011443	SRY-box containing gene 2	1.028	81.02	0.9617	30845	M	1.134	4.63	0.03749	1430
Spag7	A_51_P335583	NM_172561	sperm associated antigen 7	1.028	84.22	0.95861	36279	P	-1.017	49.48	0.77026	10932
Zfp36l2	A_51_P406265	NM_001001806	zinc finger protein 36, C3H type-like 2	1.028	83.36	0.96495	33898	M	1.181	3.82	0.03814	1449
2310065K24Rik	A_52_P128356	NM_028221	RIKEN cDNA 2310065K24 gene	1.027	84.56	0.98078	38604	P	-1.164	2.04	0.03542	1373
Aip	A_51_P205737	NM_016666	aryl-hydrocarbon receptor-interacting pr	1.027	84.4	0.96415	36815	P	1.043	25.31	0.34661	6832
Crebbp	A_51_P448224	S66385	CREB binding protein	1.027	84.22	0.95967	36345	P	1.024	40.63	0.80573	11230
Ctso	A_52_P317043	NM_177662	cathepsin O	1.027	84.56	0.97828	38331	P	-1.008	49.48	0.88304	11896
Gab2	A_51_P194613	NM_010248	growth factor receptor bound protein 2-a	1.027		0.9735	25858	A	1.073	13.58	0.12865	3671

Itgb1	A_51_P286527	NM_010578	integrin beta 1 (fibronectin receptor beta	1.027	84.4	0.97197	37626	P	1.048	33.49	0.67849	10123
Itgb4	A_52_P143287	NM_001005608	integrin beta 4	1.027	84.56	0.98654	39390	P	1.01	42.43	0.87093	11763
Mapk8ip1	A_52_P349477	AK053819	mitogen activated protein kinase 8 intera	1.027	82.34	0.97772	34689	P	-1.022	48.7	0.69895	10307
Matn4	A_51_P264934	NM_013592	matrilin 4	1.027	83.95	0.95478	35861	M	-1.137	3.01	0.03657	1405
Mrpl10	A_51_P384640	NM_026154	mitochondrial ribosomal protein L10	1.027	84.4	0.96487	36884	P	1.029	33.49	0.49722	8545
Mrpl2	A_51_P517138	NM_025302	mitochondrial ribosomal protein L2	1.027	84.4	0.96549	37030	P	1.056	25.31	0.38834	7379
Nradd	A_51_P405227	NM_026012	neurotrophin receptor associated death c	1.026	84.4	0.96696	37166	P	-1.059	33.49	0.24984	5637
Nrarp	A_51_P504354	NM_025980	Notch-regulated ankyrin repeat protein	1.026	84.52	0.97483	37990	P	-1.008	49.48	0.92381	12331
Pon3	A_51_P256665	NM_173006	paraoxonase 3	1.026	84.52	0.97221	37728	P	1.098	11.33	0.12728	3649
Ptpn9	A_52_P132407	AK086096	protein tyrosine phosphatase, non-recept	1.026	84.4	0.97038	37443	P	1.216	1.62	0.01293	561
Rab7l1	A_51_P377004	NM_144875	RAB7, member RAS oncogene family-like	1.026	84.52	0.97199	37646	P	1.093	11.33	0.11684	3417
Sort1	A_51_P517145	NM_019972	sortilin 1	1.026	84.4	0.9696	37376	P	-1.189	1.32	0.02536	1048
Ube1x	A_52_P616047	NM_009457	ubiquitin-activating enzyme E1, Chr X	1.026	84.22	0.9617	36619	P	1.042	30.75	0.51573	8729
2310002F09Rik	A_52_P415836	AK009091	RIKEN cDNA 2310002F09 gene	1.025	84.56	0.98238	32047	M	-1.042	44.4	0.52163	8763
2310007F21Rik	A_51_P268343	NM_025857	RIKEN cDNA 2310007F21 gene	1.025	84.22	0.9617	36618	P	-1.019	49	0.70255	10340
2310036O22Rik	A_51_P286321	NM_026760	RIKEN cDNA 2310036O22 gene	1.025	83.95	0.9583	36228	P	-1.008	49.48	0.872	11786
B3galnt2	A_51_P158120	NM_178640	UDP-GalNAc:betaGlcNAc beta 1,3-galacto	1.025	84.22	0.96163	36562	P	1	49.48	0.99892	13052
Cck	A_52_P539124	BC028487	cholecystokinin	1.025	84.22	0.96779	31242	M	1.01	42.43	0.82952	11445
Dirc2	A_51_P416059	NM_153550	disrupted in renal carcinoma 2 (human)	1.025	84.4	0.96696	37167	M	1.132	6.98	0.07266	2458
Jund1	A_51_P357744	NM_010592	Jun proto-oncogene related gene d1	1.025	84.56	0.98815	26488	M	-1.012	49.48	0.8733	11788
Kcnk1	A_52_P642488	NM_008430	potassium channel, subfamily K, member	1.025	84.52	0.97699	28928	M	1.092	9.71	0.07717	2576
Maff	A_52_P608322	NM_010755	v-maf musculoaponeurotic fibrosarcoma	1.025	81.02	0.98951	32413	P	1.088	11.33	0.11855	3452
Mpdz	A_51_P414948	NM_010820	multiple PDZ domain protein	1.025	84.56	0.97874	38365	P	1.011	42.43	0.81601	11336
Mrpl20	A_51_P413698	NM_025570	mitochondrial ribosomal protein L20	1.025	84.52	0.97197	37628	P	-1.103	16.2	0.16248	4266
Pdha1	A_52_P581435	NM_008810	pyruvate dehydrogenase E1 alpha 1	1.025	84.52	0.97217	37703	P	-1.02	49	0.69292	10265
Tax1bp1	A_51_P403277	NM_025816	Tax1 (human T-cell leukemia virus type I)	1.025	84.56	0.98078	38637	P	1.049	30.75	0.5827	9283
Tpt1	A_52_P667098	NM_009429	tumor protein, translationally-controlled	1.025	84.4	0.97577	25968	M	1.155	6.98	0.11932	3472
Usp8	A_51_P382718	NM_019729	ubiquitin specific peptidase 8	1.025	84.4	0.97049	37496	P	1.072	16.2	0.21734	5158
Aebp2	A_52_P23212	NM_009637	AE binding protein 2	1.024	84.52	0.97618	38111	P	1.051	22.1	0.28555	6158
D030070L09Rik	A_51_P272206	NM_172625	RIKEN cDNA D030070L09 gene	1.024	84.52	0.97492	38009	P	-1.048	40.63	0.29697	6292
F7	A_51_P484054	NM_010172	coagulation factor VII	1.024	84.56	0.97452	31567	M	1.035	30.75	0.44179	7934
Jarid1b	A_52_P584874	NM_152895	jumonji, AT rich interactive domain 1B (R	1.024	84.56	0.98413	39209	P	-1.221	0.56	0.00985	370
Ndufb10	A_51_P516615	NM_026684	NADH dehydrogenase (ubiquinone) 1 bet	1.024	84.22	0.96163	36529	P	1.05	25.31	0.32455	6609
Parp11	A_51_P452227	NM_181402	poly (ADP-ribose) polymerase family, mer	1.024	84.22	0.9648	36872	P	1.117	5.75	0.04581	1716
Phyh	A_51_P276063	NM_010726	phytanoyl-CoA hydroxylase	1.024	84.52	0.97197	37630	P	-1.07	40.63	0.46285	8138
Pitpnm1	A_51_P103000	NM_008851	phosphatidylinositol membrane-associate	1.024	84.56	0.98187	38987	P	1.059	19.02	0.20743	5018
Tagln3	A_52_P265938	NM_019754	transgelin 3	1.024	84.56	0.97956	38468	P	1.059	22.1	0.32455	6611
Wdr36	A_51_P140819	BC069869	WD repeat domain 36	1.024	84.22	0.96489	36906	P	1.054	25.31	0.43834	7906
2310061I04Rik	A_52_P180565	BC100355	RIKEN cDNA 2310061I04 gene	1.023	84.4	0.97013	37415	P	-1.086	16.2	0.11192	3315
Car3	A_52_P639461	AK075630	carbonic anhydrase 3	1.023	84.56	0.98064	38562	M	-1.385	2.04	0.16039	4222
Clns1a	A_51_P114854	NM_023671	chloride channel, nucleotide-sensitive, 1A	1.023	84.52	0.9761	38087	P	1.007	42.43	0.90748	12165
D16Bwg1543e	A_52_P399717	AK149652	DNA segment, Chr 16, Brigham & Wome	1.023	84.56	0.97748	38230	P	-1.279	0.51	0.00731	243
Kcnc3	A_52_P337326	NM_008422	potassium voltage gated channel, Shaw-r	1.023	84.22	0.96504	36994	P	-1.044	42.43	0.33795	6758
Prepl	A_52_P230793	AK013363	prolyl endopeptidase-like	1.023	84.22	0.96495	36937	P	1.053	19.02	0.23721	5450
Rem1	A_52_P674374	NM_009047	rad and gem related GTP binding protein	1.023	84.4	0.96634	37138	P	1.068	13.58	0.14542	3950
Usp12	A_51_P467573	NM_011669	ubiquitin specific peptidase 12	1.023	84.4	0.96895	37352	P	1.23	2.53	0.03158	1241
2010002N04Rik	A_51_P156857	NM_134133	RIKEN cDNA 2010002N04 gene	1.022	84.52	0.97358	37841	P	1.12	8.32	0.09446	2989
2610008E11Rik	A_52_P161087	NM_001004362	RIKEN cDNA 2610008E11 gene	1.022	84.52	0.97483	37946	P	1.078	19.02	0.30377	6361
Add1	A_51_P282404	NM_013457	adducin 1 (alpha)	1.022	84.4	0.96696	37175	P	1.13	9.71	0.1534	4095
Atp7a	A_51_P473179	AK033254	ATPase, Cu++ transporting, alpha polypep	1.022	84.22	0.96573	37065	P	1.09	13.58	0.19142	4759
Cd86	A_51_P174723	NM_019388	CD86 antigen	1.022	84.56	0.98946	39918	P	-1.056	40.63	0.36655	7120
Cog4	A_52_P54235	AK040321	component of oligomeric golgi complex 4	1.022	84.56	0.97949	29009	M	-1.02	49	0.70719	10386
Nme2	A_51_P517988	NM_001077529	expressed in non-metastatic cells 2, prote	1.022	84.52	0.97958	26114	M	1.078	19.02	0.35632	6972

Slc27a1	A_51_P117477	NM_011977	solute carrier family 27 (fatty acid transpo	1.022	84.56	0.98765	39533	P	-1.034	44.4	0.45191	8013
Spg20	A_51_P394269	AK129171	spastic paraplegia 20, spartin (Troyer sync	1.022	79.26	0.97889	31795	P	1.223	1.62	0.01293	562
Tpd52l1	A_51_P482503	NM_009413	tumor protein D52-like 1	1.022	84.56	0.97987	38496	P	1.178	5.75	0.08441	2764
Tubgcp6	A_51_P444069	AK052293	tubulin, gamma complex associated prote	1.022	84.4	0.96762	37241	P	-1.073	25.31	0.16909	4370
Zfp511	A_51_P156263	BC065404	zinc finger protein 511	1.022	84.56	0.97818	38328	P	-1.012	49.48	0.80819	11258
4921511H13Rik	A_52_P370453	AK017495	RIKEN cDNA 4921511H13 gene	1.021	84.56	0.97767	38244	M	1.069	11.33	0.31283	6034
4930422G04Rik	A_51_P294161	BC030185	RIKEN cDNA 4930422G04 gene	1.021	84.56	0.98644	39362	P	-1.157	1.62	0.02439	1013
BC057627	A_52_P273161	NM_198631	cDNA sequence BC057627	1.021	84.52	0.97577	38046	P	1.106	16.2	0.37093	7181
Btrc	A_52_P98674	NM_009771	beta-transducin repeat containing protein	1.021	84.52	0.97218	37716	P	-1.007	49.48	0.94108	12491
Cul4b	A_51_P120948	NM_028288	cullin 4B	1.021	84.52	0.97345	37828	P	-1.005	49.48	0.9506	12591
Eaf1	A_51_P419959	NM_028932	ELL associated factor 1	1.021	83.95	0.98173	35016	P	1.337	1.17	0.01496	643
Lsm5	A_51_P336790	NM_025520	LSM5 homolog, U6 small nuclear RNA ass	1.021	84.56	0.98769	39539	P	-1.088	19.02	0.14582	3960
Mllt3	A_52_P530665	NM_027326	myeloid/lymphoid or mixed lineage-leuke	1.021	84.56	0.98109	38709	P	1.067	25.31	0.47276	8223
Nedd4	A_51_P295022	NM_010890	neural precursor cell expressed, develop	1.021	83.36	0.97345	34436	P	1.258	2.53	0.03188	1257
Nr2c2	A_51_P368265	NM_011630	nuclear receptor subfamily 2, group C, me	1.021	84.4	0.97143	37567	P	1.091	16.2	0.25778	5783
Pgam1	A_51_P342669	NM_023418	phosphoglycerate mutase 1	1.021	84.56	0.98413	26354	M	1.018	40.63	0.78568	11053
Ptprs	A_52_P90747	NM_011218	protein tyrosine phosphatase, receptor ty	1.021	83.36	0.97435	34477	M	1.11	8.32	0.0655	2299
Rnf41	A_52_P48398	NM_026259	ring finger protein 41	1.021	84.52	0.9735	37836	P	1.039	33.49	0.5912	9340
Vamp8	A_52_P279152	NM_016794	vesicle-associated membrane protein 8	1.021	84.56	0.98562	39331	P	1.009	42.43	0.88504	11924
Zfml	A_52_P543391	NM_008717	zinc finger, matrin-like	1.021	84.56	0.98064	38575	P	-1.177	2.53	0.04505	1672
1500003O03Rik	A_52_P608024	NM_019769	RIKEN cDNA 1500003O03 gene	1.02	84.56	0.98109	38743	P	1.141	6.98	0.08605	2793
Adcy3	A_51_P484671	NM_138305	adenylate cyclase 3	1.02	84.4	0.96965	37385	M	1.137	4.63	0.03224	1266
B230308N11Rik	A_52_P67958	AK083707	RIKEN cDNA B230308N11 gene	1.02	84.56	0.98946	39907	M	1.073	22.1	0.37146	7188
C730036D15Rik	A_51_P213515	NM_145368	RIKEN cDNA C730036D15 gene	1.02	79.26	0.98815	32314	M	1.01	42.43	0.83494	11493
Csf2rb1	A_52_P492939	NM_007780	colony stimulating factor 2 receptor, beta	1.02		0.98187	26259	A	1.104	9.71	0.10198	3150
Grik5	A_51_P428754	NM_008168	glutamate receptor, ionotropic, kainate 5	1.02	84.56	0.98663	39413	P	1.032	30.75	0.48401	8379
Itga8	A_52_P658911	NM_001001309	integrin alpha 8	1.02	84.22	0.97699	31659	M	-1.018	49.48	0.80093	11185
Map2k4	A_51_P471440	NM_009157	mitogen activated protein kinase kinase 4	1.02	84.52	0.97483	37997	P	-1.033	45.05	0.48068	8313
Papd4	A_51_P325374	NM_133905	PAP associated domain containing 4	1.02	84.4	0.97275	37747	P	1.155	3.01	0.02156	906
Pbx2	A_52_P339182	NM_017463	pre B-cell leukemia transcription factor 2	1.02	84.56	0.97889	38400	P	1.088	9.71	0.08811	2846
Psma7	A_51_P233603	NM_011969	proteasome (prosome, macropain) subun	1.02	84.56	0.97801	38292	P	1.02	40.63	0.8236	11397
Tceb1	A_51_P172872	NM_026456	transcription elongation factor B (SIII), po	1.02	84.52	0.97286	37758	P	1.02	38.4	0.69683	10287
Trps1	A_51_P513032	AK078617	trichorhinophalangeal syndrome I (huma	1.02	84.56	0.98165	38927	P	1.035	30.75	0.46431	8156
Vgll1	A_51_P214360	NM_133251	vestigial like 1 homolog (Drosophila)	1.02	84.56	0.98165	38934	P	1.018	38.4	0.70082	10325
A230051G13Rik	A_52_P608460	NM_173785	RIKEN cDNA A230051G13 gene	1.019	84.52	0.97543	38030	P	-1.234	1.1	0.02119	900
A630042L21Rik	A_52_P431965	NM_134134	RIKEN cDNA A630042L21 gene	1.019	84.56	0.98815	39750	P	-1.077	22.1	0.15824	4183
Bag3	A_51_P371174	NM_013863	Bcl2-associated athanogene 3	1.019	84.56	0.98078	38629	P	1.085	11.33	0.11809	3439
Capza1	A_52_P401345	NM_009797	capping protein (actin filament) muscle Z-	1.019	84.56	0.98214	39009	P	1.099	9.71	0.07994	2654
Cyp2d10	A_52_P527775	NM_010005	cytochrome P450, family 2, subfamily d, p	1.019	84.4	0.97211	37693	P	-1.019	49	0.70575	10373
D930036F22Rik	A_51_P430002	NM_177171	HEAT repeat containing 5A	1.019	84.56	0.97874	38368	P	-1.019	48.39	0.65026	9884
Eltd1	A_51_P480328	NM_133222	EGF, latrophilin seven transmembrane do	1.019	84.56	0.97862	38350	P	1.056	30.75	0.5959	9410
Eno1	A_52_P349939	NM_023119	enolase 1, alpha non-neuron	1.019	84.56	0.98815	39641	P	1.02	40.63	0.74347	10737
Med28	A_52_P362245	NM_025895	mediator of RNA polymerase II transcripti	1.019	84.56	0.97769	38261	P	1.09	11.33	0.12623	3637
Ndst1	A_51_P189142	NM_008306	N-deacetylase/N-sulfotransferase (hepara	1.019	84.4	0.97061	37500	P	1.105	11.33	0.16286	4271
Ndst2	A_51_P377390	NM_010811	N-deacetylase/N-sulfotransferase (hepara	1.019	84.56	0.97879	38380	P	-1.245	0.51	0.00726	232
Nek7	A_51_P295442	NM_021605	NIMA (never in mitosis gene a)-related ex	1.019	84.56	0.98558	26388	M	1.02	38.4	0.66052	9977
Rbm18	A_52_P59544	AK036220	RNA binding motif protein 18	1.019	84.56	0.97949	38446	P	1.171	3.01	0.02195	931
Sirt2	A_51_P110068	NM_022432	sirtuin 2 (silent mating type information r	1.019	84.52	0.97485	38002	P	-1.085	16.2	0.10964	3256
Tnrc6c	A_51_P321563	AK147471	trinucleotide repeat containing 6C	1.019	84.56	0.98147	38849	P	1.012	42.43	0.88148	11873
Ube2a	A_52_P139093	NM_019668	ubiquitin-conjugating enzyme E2A, RAD6	1.019	84.52	0.97618	38106	P	1.071	22.1	0.37588	7233
1810033M07Rik	A_51_P321290	AK007800	endoplasmic reticulum protein 27	1.018		0.98896	19740	A	-1.204	0.66	0.0108	423
Arhgap23	A_51_P310307	AK016967	RIKEN cDNA 4933428G20 gene	1.018	84.4	0.97769	34679	M	-1.078	30.75	0.2897	6207
Cdan1	A_52_P219913	AK157271	congenital dyserythropoietic anemia, typ	1.018	84.56	0.98279	39112	P	-1.156	3.82	0.07277	2466

Dnajc13	A_52_P250590	XM_135146	DnaJ (Hsp40) homolog, subfamily C, mem	1.018	84.56	0.98109	38793	P	1.145	9.71	0.17475	4471
Nup88	A_51_P237945	NM_172394	nucleoporin 88	1.018	84.56	0.98184	38980	P	1.123	8.32	0.08652	2814
Osbpl9	A_52_P194763	NM_173350	oxysterol binding protein-like 9	1.018	84.56	0.98687	39447	P	-1.073	22.1	0.14328	3908
Ranbp3	A_51_P146250	AK154201	RAN binding protein 3	1.018	84.56	0.98815	39727	P	1.122	11.33	0.24299	5539
Tap2	A_52_P86176	NM_011530	transporter 2, ATP-binding cassette, sub-f	1.018	84.52	0.97483	37979	P	1.046	28.13	0.40974	7605
Tes	A_52_P74441	NM_011570	testis derived transcript	1.018	84.56	0.98078	38594	P	1.157	8.32	0.17685	4511
Zmynd19	A_51_P390387	AK086718	zinc finger, MYND domain containing 19	1.018	84.52	0.97679	38158	P	1.078	13.58	0.1352	3765
1110014N23Rik	A_51_P340604	AK003717	RIKEN cDNA 1110014N23 gene	1.017	84.56	0.99106	40197	P	-1.156	1.18	0.01985	848
4932442K08Rik	A_52_P537852	NM_024203	RIKEN cDNA 4932442K08 gene	1.017	84.56	0.98437	39233	P	1.048	25.31	0.3867	7359
Actr2	A_51_P303906	NM_146243	ARP2 actin-related protein 2 homolog (ye	1.017	84.56	0.98898	26535	M	1.103	11.33	0.1258	3623
Arcn1	A_52_P593318	AK031385	archain 1	1.017	84.56	0.98202	39003	P	1.032	33.49	0.59505	9395
Atp11b	A_51_P146505	NM_029570	ATPase, Class VI, type 11B	1.017	84.56	0.98294	26330	M	1.071	19.02	0.25165	5670
Cdh15	A_51_P481930	NM_007662	cadherin 15	1.017	84.56	0.97618	34606	M	-1.055	43.15	0.50737	8654
Col16a1	A_52_P556933	NM_028266	procollagen, type XVI, alpha 1	1.017	84.56	0.98264	32099	M	-1.034	45.68	0.5823	9278
Ebag9	A_51_P420045	NM_019480	estrogen receptor-binding fragment-asso	1.017	84.52	0.97651	38148	P	-1.021	48.39	0.6503	9886
Elavl1	A_52_P118640	NM_010485	ELAV (embryonic lethal, abnormal vision,	1.017	84.56	0.97987	38497	P	1.122	4.63	0.03732	1420
Fbxo31	A_51_P356283	NM_133765	F-box protein 31	1.017	84.56	0.97883	38386	P	1.093	11.33	0.11078	3287
Fzd2	A_51_P404077	NM_020510	frizzled homolog 2 (Drosophila)	1.017	83.95	0.98229	32040	M	1.108	8.32	0.0795	2646
Glt8d1	A_51_P152155	NM_029626	glycosyltransferase 8 domain containing 1	1.017	84.56	0.97861	38345	P	1.171	5.75	0.09593	3012
Mrps34	A_51_P443702	NM_023260	mitochondrial ribosomal protein S34	1.017	84.56	0.98238	39041	P	1.043	25.31	0.35529	6960
Nnt	A_52_P395228	NM_008710	nicotinamide nucleotide transhydrogenas	1.017	84.56	0.99004	26590	M	1.127	4.63	0.03502	1344
Ppp5c	A_51_P307243	NM_011155	protein phosphatase 5, catalytic subunit	1.017	84.56	0.9788	38382	P	1.008	42.43	0.89972	12063
Tubgcp3	A_51_P201773	NM_198031	tubulin, gamma complex associated prote	1.017	84.52	0.97543	38027	P	-1.027	47.43	0.6544	9914
B2m	A_52_P105594	AK086184	beta-2 microglobulin	1.016	84.56	0.9824	39052	P	-1.191	19.02	0.38732	7365
BC023814	A_51_P221739	NM_153562	cDNA sequence BC023814	1.016	84.56	0.98789	26469	M	1.1	13.58	0.26812	5915
Got2	A_51_P175871	NM_010325	glutamate oxaloacetate transaminase 2, r	1.016	84.56	0.98078	38625	P	1.133	6.98	0.05867	2096
Gsta3	A_51_P503625	NM_001077353	glutathione S-transferase, alpha 3	1.016	84.56	0.99678	40948	P	-1.179	8.32	0.19688	4849
Hnrpa1	A_51_P400784	NM_001039129	heterogeneous nuclear ribonucleoprotein	1.016	84.56	0.98815	26475	M	1.07	22.1	0.3878	7370
Laptm4a	A_52_P572284	NM_008640	lysosomal-associated protein transmemb	1.016	84.52	0.98229	26301	M	1.188	5.75	0.09699	3031
Mllt7	A_51_P200875	NM_018789	myeloid/lymphoid or mixed lineage-leuke	1.016	84.56	0.98765	26417	M	1.048	22.1	0.28573	6162
Pa2g4	A_52_P365896	NM_011119	proliferation-associated 2G4	1.016	84.56	0.98023	38522	P	1.097	13.58	0.19014	4725
Ppp1cc	A_52_P540434	NM_013636	protein phosphatase 1, catalytic subunit,	1.016	84.56	0.97828	38333	P	1.163	3.82	0.03847	1460
Ralgps2	A_51_P115817	NM_023884	Ral GEF with PH domain and SH3 binding	1.016	84.56	0.98231	39033	P	1.053	22.1	0.28839	6194
Rhobtb2	A_52_P525287	AK122354	Rho-related BTB domain containing 2	1.016	84.56	0.99149	40275	M	1.09	9.71	0.09804	3064
Sec24b	A_52_P191537	XM_916502	SEC24 related gene family, member B (S.	1.016	83.95	0.98654	32221	P	1.09	13.58	0.21205	5073
Tbc1d17	A_52_P655084	NM_001042655	TBC1 domain family, member 17	1.016	84.56	0.98078	38606	P	1.075	16.2	0.22977	5347
4632411B12Rik	A_51_P262943	NM_172652	RIKEN cDNA 4632411B12 gene	1.015	84.56	0.98815	39752	P	1.001	42.43	0.99312	13000
4833420G17Rik	A_51_P429572	NM_026127	RIKEN cDNA 4833420G17 gene	1.015	84.52	0.97862	38349	P	1.063	19.02	0.25181	5673
Ap3s1	A_51_P246962	NM_009681	adaptor-related protein complex 3, sigma	1.015	84.52	0.98436	26367	M	1.131	9.71	0.16966	4379
B230117O15Rik	A_51_P365044	AK020978	RIKEN cDNA B230117O15 gene	1.015	84.56	0.98964	40029	M	1.193	3.82	0.04898	1819
Bat1a	A_52_P635776	NM_019693	HLA-B-associated transcript 1A	1.015	84.56	0.98123	38829	P	1.106	9.71	0.1233	3566
Cyld	A_51_P300001	NM_173369	cylindromatosis (turban tumor syndrome	1.015	84.56	0.9795	38460	P	1.103	9.71	0.11653	3407
Dhx38	A_51_P169588	NM_178380	DEAH (Asp-Glu-Ala-His) box polypeptide 3	1.015		0.98413	29258	A	-1.027	45.68	0.51083	8677
Fadd	A_51_P382925	NM_010175	Fas (TNFRSF6)-associated via death doma	1.015	84.56	0.98789	39612	P	1.035	30.75	0.51461	8717
Klk5	A_52_P108579	NM_026806	kallikrein related-peptidase 5	1.015		0.99427	15248	A	-1.229	2.53	0.08819	2851
Mmp14	A_51_P216303	NM_008608	matrix metallopeptidase 14 (membrane-i	1.015	84.56	0.98256	39090	P	1.027	36.07	0.58113	9264
Slc38a4	A_52_P12403	NM_027052	solute carrier family 38, member 4	1.015	84.56	0.98541	39310	P	-1.082	33.49	0.35983	7011
Ssr4	A_52_P546090	NM_009279	signal sequence receptor, delta	1.015	84.52	0.98352	26342	M	-1.166	4.63	0.0908	2913
Wdtc1	A_51_P395050	NM_199306	WD and tetratricopeptide repeats 1	1.015		0.98654	26395	A	1.021	38.4	0.65684	9944
B230339M05Rik	A_51_P247098	XM_902776	RIKEN cDNA B230339M05 gene	1.014	84.56	0.98482	39261	M	1.032	33.49	0.63223	9740
Bax	A_52_P254541	NM_007527	Bcl2-associated X protein	1.014	84.56	0.98815	39711	P	1.142	4.63	0.03574	1384
BC013481	A_51_P293489	NM_139065	cDNA sequence BC013481	1.014	84.56	0.98815	39736	P	1.258	4.63	0.11507	3382
Ddef2	A_51_P427080	NM_001004364	development and differentiation enhanci	1.014	84.56	0.98815	39726	P	-1.108	25.31	0.29873	6301

Gfm1	A_52_P311185	AK018125	G elongation factor, mitochondrial 1	1.014	84.56	0.98137	38836	P	1.131	5.75	0.04629	1733
Gtf2i	A_52_P442585	NM_010365	general transcription factor II I	1.014	84.56	0.98256	39087	P	1.096	11.33	0.13338	3733
Mcam	A_52_P268206	NM_023061	melanoma cell adhesion molecule	1.014	84.56	0.98906	39859	P	1.114	16.2	0.34927	6863
Nupl1	A_52_P594532	AK129134	nucleoporin like 1	1.014	84.56	0.98123	38824	P	-1.086	11.33	0.08915	2872
Pex14	A_51_P309534	NM_019781	peroxisomal biogenesis factor 14	1.014	84.56	0.99064	40126	P	1.001	42.43	0.98717	12951
Sox12	A_51_P322450	NM_011438	SRY-box containing gene 12	1.014	84.56	0.9862	39357	P	1.134	6.98	0.06654	2335
Zfp364	A_52_P292232	NM_026406	zinc finger protein 364	1.014	84.56	0.98815	39753	P	1.117	16.2	0.34405	6811
1300003B13Rik	A_52_P149200	NM_198003	RIKEN cDNA 1300003B13 gene	1.013	84.56	0.98654	39400	P	1.005	42.43	0.93782	12458
4933434I06Rik	A_51_P131164	BC099519	RIKEN cDNA 4933434I06 gene	1.013	84.56	0.99348	40531	P	1.003	42.43	0.94191	12499
Calm1	A_52_P224104	NM_009790	calmodulin 1	1.013	84.56	0.9824	39062	P	1.161	4.63	0.04674	1740
Ccar1	A_52_P188026	BC051052	cell division cycle and apoptosis regulator	1.013	84.56	0.98815	39676	P	-1.022	48.7	0.70857	10397
Cd151	A_51_P343252	NM_009842	CD151 antigen	1.013	84.56	0.98815	39713	P	1.053	25.31	0.36387	7069
Celsr2	A_51_P285027	NM_017392	cadherin EGF LAG seven-pass G-type rece	1.013	84.56	0.98109	38749	P	1.023	38.4	0.66248	9991
Cnnm2	A_51_P281586	NM_033569	cyclin M2	1.013	84.56	0.98815	39689	P	-1.032	45.05	0.49031	8436
Csnk1a1	A_52_P339722	NM_146087	casein kinase 1, alpha 1	1.013	84.56	0.98149	38876	P	1.228	3.46	0.06135	2177
Ftsj3	A_51_P449935	NM_025310	FtsJ homolog 3 (E. coli)	1.013	84.56	0.98818	39755	P	1.039	30.75	0.53803	8919
Plekhc1	A_51_P135832	NM_146054	pleckstrin homology domain containing, f	1.013	84.56	0.98165	38938	P	1.025	38.4	0.71936	10488
Pom121	A_51_P191393	NM_148932	nuclear pore membrane protein 121	1.013	84.56	0.98238	39039	M	-1.04	46.3	0.66021	9974
Ppp1r9b	A_51_P402484	NM_172261	protein phosphatase 1, regulatory subuni	1.013	84.56	0.98815	39675	P	1.175	4.63	0.04963	1833
Psmd11	A_52_P370353	NM_178616	proteasome (prosome, macropain) 26S su	1.013	84.56	0.98149	38870	P	-1.171	1.58	0.02589	1065
Rpl14	A_51_P232858	NM_025974	ribosomal protein L14	1.013	84.56	0.98815	39694	P	1.168	8.32	0.19727	4854
Tpm3	A_52_P661033	NM_022314	tropomyosin 3, gamma	1.013	84.56	0.99004	26588	M	1.364	2.04	0.05481	2000
Ube2g2	A_51_P248441	NM_019803	ubiquitin-conjugating enzyme E2G 2	1.013	84.56	0.98815	39671	P	1.065	16.2	0.18052	4583
1700037H04Rik	A_51_P221641	NM_026091	RIKEN cDNA 1700037H04 gene	1.012	84.56	0.98968	40037	P	1.05	22.1	0.26817	5921
2500002L14Rik	A_51_P143915	NM_025607	RIKEN cDNA 2500002L14 gene	1.012	84.56	0.98363	39159	P	1.057	19.02	0.21313	5085
Apoa5	A_51_P259930	NM_080434	apolipoprotein A-V	1.012	84.56	0.98482	32165	M	-1.048	43.75	0.47905	8301
Arfip2	A_51_P326425	NM_029802	ADP-ribosylation factor interacting protei	1.012	84.56	0.98765	39517	P	-1.021	47.92	0.62122	9634
Emd	A_51_P216147	NM_007927	emerin	1.012	84.56	0.99094	26610	M	1.014	42.43	0.79549	11141
Polr2b	A_51_P509881	NM_153798	polymerase (RNA) II (DNA directed) polyp	1.012	84.56	0.9862	39355	P	-1.008	49.48	0.87731	11834
Rabl3	A_51_P120615	NM_001042499	RAB, member of RAS oncogene family-like	1.012	84.56	0.98697	39469	P	1.079	19.02	0.36876	7146
Supt6h	A_51_P405693	NM_009297	suppressor of Ty 6 homolog (S. cerevisiae	1.012	84.56	0.98946	26566	M	1.144	8.32	0.13843	3807
Ush1c	A_52_P431843	NM_153677	Usher syndrome 1C homolog (human)	1.012	84.56	0.9888	39808	P	-1.036	46.3	0.6394	9804
2610204K14Rik	A_52_P330766	NM_025997	RIKEN cDNA 2610204K14 gene	1.011	84.56	0.98951	26576	M	1.122	9.71	0.15327	4092
9430028L06Rik	A_52_P375970	BC075677	RIKEN cDNA 9430028L06 gene	1.011	84.56	0.99275	40419	P	1.008	42.43	0.90778	12171
Aldh1b1	A_51_P510418	NM_028270	aldehyde dehydrogenase 1 family, memb	1.011	84.56	0.9929	40472	P	1.04	33.49	0.65619	9939
Arfgef2	A_52_P290725	XM_130646	ADP-ribosylation factor guanine nucleotic	1.011	84.56	0.98716	39489	P	-1.153	6.98	0.11794	3436
Copb2	A_51_P243857	NM_015827	coatomer protein complex, subunit beta 2	1.011	84.56	0.98481	39250	P	1.06	19.02	0.25769	5780
Gfpt1	A_51_P175841	NM_013528	glutamine fructose-6-phosphate transam	1.011	84.56	0.98706	39478	P	1.058	25.31	0.48248	8348
Gtpbp5	A_51_P486906	NM_181424	GTP binding protein 5	1.011	84.56	0.98413	39184	P	1.108	9.71	0.11254	3325
Hadha	A_52_P193029	NM_178878	hydroxyacyl-Coenzyme A dehydrogenase/	1.011	84.56	0.98541	39311	P	-1.229	0.92	0.01754	751
Mobk1b	A_51_P168524	NM_145571	MOB1, Mps One Binder kinase activator-l	1.011	84.56	0.98815	39714	P	-1.094	33.49	0.44001	7923
Rad21	A_52_P39237	NM_009009	RAD21 homolog (S. pombe)	1.011	84.56	0.98951	40008	P	1.013	42.43	0.83975	11527
Rest	A_51_P348456	NM_011263	RE1-silencing transcription factor	1.011	84.56	0.98946	35407	P	1.103	13.58	0.26101	5836
Rnf14	A_51_P145533	NM_020012	ring finger protein 14	1.011	84.56	0.98896	26532	M	1.155	3.82	0.02675	1092
Tnni1	A_51_P435704	NM_021467	troponin I, skeletal, slow 1	1.011	84.56	0.98558	35188	M	1.103	11.33	0.17232	4408
Ube2v1	A_52_P484081	NM_023230	ubiquitin-conjugating enzyme E2 variant 1	1.011	84.56	0.98976	40044	P	-1.058	36.07	0.25196	5679
2310051F07Rik	A_51_P166107	AK075904	RIKEN cDNA 2310051F07 gene	1.01	84.56	0.99148	40257	P	1.123	8.32	0.07314	2479
Dnajb10	A_51_P439612	NM_020266	DnaJ (Hsp40) homolog, subfamily B, mem	1.01	84.56	0.98951	39958	P	-1.067	36.07	0.34897	6861
Metap1	A_51_P102503	NM_175224	methionyl aminopeptidase 1	1.01	84.56	0.98815	39632	P	1.032	33.49	0.60547	9494
Paip1	A_52_P212284	NM_145457	polyadenylate binding protein-interacting	1.01	84.56	0.99401	40565	P	1.145	3.82	0.02692	1097
Slc30a6	A_51_P512157	NM_144798	solute carrier family 30 (zinc transporter),	1.01	84.56	0.98895	39824	P	1.067	19.02	0.2702	5960
Stx5a	A_52_P309973	NM_019829	syntaxin 5A	1.01	84.56	0.99192	40322	P	1.123	9.71	0.11387	3360
Usp52	A_52_P113100	AK034635	ubiquitin specific peptidase 52	1.01	84.56	0.99427	40630	P	1.046	28.13	0.48168	8326

1500011H22Rik	A_51_P252784	NM_026883	RIKEN cDNA 1500011H22 gene	1.009	84.56	0.98765	39532	P	1.05	25.31	0.35908	6994
2810403A07Rik	A_52_P395290	NM_028814	RIKEN cDNA 2810403A07 gene	1.009	84.56	0.98815	39684	P	1.176	13.58	0.42726	7792
4432406C05Rik	A_51_P435027	NM_025708	transmembrane protein 186	1.009	84.56	0.9883	39761	P	1.142	6.98	0.07798	2607
5730449L18Rik	A_51_P184024	NM_025677	RIKEN cDNA 5730449L18 gene	1.009	84.56	0.98687	39452	P	1.032	33.49	0.50539	8636
Daam2	A_52_P390241	NM_001008231	dishevelled associated activator of morph	1.009	84.56	0.98964	40021	P	1.084	13.58	0.15255	4077
Emp1	A_52_P120037	NM_010128	epithelial membrane protein 1	1.009	84.56	0.99395	40554	P	1.079	11.33	0.10313	3175
Erg	A_52_P499821	AK078113	avian erythroblastosis virus E-26 (v-ets) o	1.009	84.56	0.99151	40283	P	1.03	30.75	0.48471	8382
Glb1	A_52_P659925	NM_009752	galactosidase, beta 1	1.009	84.56	0.98951	40007	P	-1.025	47.92	0.64455	9841
Hspb2	A_51_P322138	NM_024441	heat shock protein 2	1.009	84.56	0.98793	39621	P	-1.052	38.4	0.27516	6027
Map2k5	A_52_P279319	NM_011840	mitogen activated protein kinase kinase 5	1.009	84.56	0.99054	40109	P	1.034	30.75	0.49233	8471
Pax2	A_51_P375526	NM_011037	paired box gene 2	1.009	84.56	0.98895	39823	P	-1.043	42.43	0.33167	6698
Ralb	A_52_P253004	NM_022327	v-ral simian leukemia viral oncogene hom	1.009	84.56	0.99017	26594	M	-1.016	49.48	0.73988	10685
Taf6l	A_52_P231658	NM_146092	TAF6-like RNA polymerase II, p300/CBP-as	1.009	84.56	0.98951	39950	P	-1.101	11.33	0.10562	3204
Thrap2	A_52_P352024	AK088795	thyroid hormone receptor associated pro	1.009	84.56	0.99151	40282	P	1.064	19.02	0.30472	6382
Ube1c	A_51_P341978	NM_011666	ubiquitin-activating enzyme E1C	1.009	84.56	0.98993	40047	P	1.123	9.71	0.16167	4249
9130011J15Rik	A_51_P414529	NM_172396	RIKEN cDNA 9130011J15 gene	1.008	84.56	0.99102	26617	M	-1.056	43.15	0.50004	8579
Arfrp1	A_52_P153497	NM_029702	ADP-ribosylation factor related protein 1	1.008	84.56	0.99148	40259	P	-1.067	38.4	0.37807	7255
Crat	A_51_P440807	NM_007760	carnitine acetyltransferase	1.008	84.56	0.991	40167	P	-1.045	43.15	0.39163	7414
Dnajc10	A_52_P63336	NM_024181	DnaJ (Hsp40) homolog, subfamily C, mem	1.008	84.56	0.99288	40445	P	1.173	5.75	0.08375	2747
Dnajc9	A_52_P446171	NM_134081	DnaJ (Hsp40) homolog, subfamily C, mem	1.008	84.56	0.99106	40188	P	-1.078	22.1	0.14687	3980
Fxc1	A_52_P464268	NM_019502	fractured callus expressed transcript 1	1.008	84.56	0.98789	39613	P	1.166	4.63	0.05886	2100
Ina	A_52_P366860	NM_146100	internexin neuronal intermediate filamen	1.008	84.56	0.99054	40108	P	-1.064	33.49	0.24299	5540
Lrrc1	A_52_P189977	NM_172528	leucine rich repeat containing 1	1.008	84.56	0.9925	40359	P	1.107	9.71	0.10534	3201
Nr2f6	A_51_P184353	NM_010150	nuclear receptor subfamily 2, group F, me	1.008	84.56	0.99192	26653	M	1.215	2.53	0.01985	844
Ppp2r2d	A_51_P497061	NM_026391	protein phosphatase 2, regulatory subuni	1.008	84.56	0.98951	40002	P	-1.228	0.56	0.01017	382
Rabggta	A_51_P481832	NM_019519	Rab geranylgeranyl transferase, a subunit	1.008	84.56	0.99141	40208	P	1.029	33.49	0.57198	9207
Srp72	A_51_P165770	NM_025691	signal recognition particle 72	1.008	84.56	0.99141	40217	P	1.057	19.02	0.22218	5239
St7l	A_52_P198916	NM_153091	suppression of tumorigenicity 7-like	1.008	84.56	0.98951	39938	P	1.003	42.43	0.96749	12722
1110002L01Rik	A_52_P60773	AK035515	RIKEN cDNA 1110002L01 gene	1.007	84.56	0.99004	40065	P	1.192	3.01	0.02803	1136
1110004F10Rik	A_51_P287030	NM_019772	RIKEN cDNA 1110004F10 gene	1.007	84.56	0.99427	40608	P	1.1	16.2	0.36141	7033
Adk	A_51_P130666	NM_134079	adenosine kinase	1.007	84.56	0.99347	26685	M	1.123	4.63	0.03904	1471
Cdk9	A_51_P190667	NM_130860	cyclin-dependent kinase 9 (CDC2-related	1.007	84.56	0.98951	39985	P	1.048	25.31	0.37353	7212
D5Ertd585e	A_51_P179953	NM_027922	DNA segment, Chr 5, ERATO Doi 585, expr	1.007	84.56	0.99148	40252	P	-1.179	1.62	0.03537	1370
Eif4ebp2	A_51_P135654	NM_010124	eukaryotic translation initiation factor 4E	1.007	84.56	0.99106	40194	P	1.018	40.63	0.74137	10697
Gabpb2	A_51_P455694	NM_172512	GA repeat binding protein, beta 2	1.007	83.95	0.99427	29535	M	-1.003	49.48	0.97713	12815
Hba-x	A_51_P204053	NM_010405	hemoglobin X, alpha-like embryonic chair	1.007		0.99405	23306	A	1.075	16.2	0.26561	5888
Hbs1l	A_52_P530979	BC085235	Hbs1-like (S. cerevisiae)	1.007	84.56	0.99214	40349	M	-1.009	49.48	0.93013	12389
Hectd1	A_52_P421728	XM_974905	HECT domain containing 1	1.007	84.56	0.99138	40206	P	1.166	6.98	0.09335	2973
Invs	A_52_P333117	AK020257	inversin	1.007		0.99532	19880	A	-1.044	43.75	0.47546	8265
Mrpl44	A_52_P668030	AK156814	mitochondrial ribosomal protein L44	1.007	84.56	0.99428	40684	P	1.235	1.62	0.01603	691
Scarf2	A_51_P294402	NM_153790	scavenger receptor class F, member 2	1.007	84.56	0.98964	40033	P	1.053	22.1	0.31989	6566
Slc25a22	A_51_P447329	NM_026646	solute carrier family 25 (mitochondrial ca	1.007	84.56	0.99155	40290	P	-1.026	47.92	0.68107	10147
Slc9a1	A_52_P466081	NM_016981	solute carrier family 9 (sodium/hydrogen	1.007	84.56	0.99532	40791	P	1.027	33.49	0.56462	9159
Tnrc5	A_51_P498403	NM_028065	trinucleotide repeat containing 5	1.007	84.56	0.99146	40221	P	1.027	33.49	0.52476	8794
5033414D02Rik	A_51_P351238	NM_026362	RIKEN cDNA 5033414D02 gene	1.006	84.56	0.99275	40404	P	1.067	16.2	0.20349	4948
5730470L24Rik	A_51_P145300	AK012679	RIKEN cDNA 5730470L24 gene	1.006	84.56	0.99538	40810	P	-1.123	4.63	0.05148	1893
BC053440	A_51_P489086	XM_134209	cDNA sequence BC053440	1.006	84.56	0.99192	40315	P	1.185	8.32	0.21889	5186
Cdh5	A_51_P309056	NM_009868	cadherin 5	1.006	84.56	0.99532	40769	P	-1.025	48.7	0.74287	10717
Cdk2ap1	A_51_P411007	NM_013812	CDK2 (cyclin-dependent kinase 2)-associa	1.006	84.56	0.99268	40387	P	1.061	19.02	0.27485	6024
Cox5a	A_51_P335900	NM_007747	cytochrome c oxidase, subunit Va	1.006	84.56	0.99147	40244	P	1.002	42.43	0.98495	12925
D10Bwg1364e	A_51_P401717	NM_145421	DNA segment, Chr 10, Brigham & Womer	1.006	84.56	0.99146	40233	P	-1.161	4.63	0.09166	2933
Iqgap1	A_52_P630828	NM_016721	IQ motif containing GTPase activating pro	1.006	84.56	0.99389	40550	P	1.312	1.32	0.01962	838
Ly6e	A_51_P148814	NM_008529	lymphocyte antigen 6 complex, locus E	1.006	84.56	0.99401	29530	M	1.038	30.75	0.50642	8644

Onecut2	A_52_P1164839	NM_194268	one cut domain, family member 2	1.006	84.56	0.99427	40605	P	-1.194	5.75	0.16545	4300
Prpf31	A_51_P340704	NM_027328	PRP31 pre-mRNA processing factor 31 ho	1.006	84.56	0.99286	40434	P	1.065	16.2	0.19032	4732
Snx26	A_52_P524761	NM_178252	sorting nexin 26	1.006	84.56	0.99106	40183	M	-1.331	0.51	0.00645	180
Ssb	A_51_P119055	NM_009278	Sjogren syndrome antigen B	1.006	84.56	0.99192	40337	P	1.093	13.58	0.17626	4503
Timp3	A_51_P463765	NM_011595	tissue inhibitor of metalloproteinase 3	1.006	84.56	0.99612	26735	M	-1.078	25.31	0.19126	4752
Trip6	A_51_P121058	NM_011639	thyroid hormone receptor interactor 6	1.006	84.56	0.99395	40553	P	1.049	22.1	0.28597	6170
U2af1	A_51_P364786	NM_024187	U2 small nuclear ribonucleoprotein auxili	1.006	84.56	0.99401	40561	P	1.06	19.02	0.25587	5741
Znrf1	A_52_P312116	AK078819	zinc and ring finger 1	1.006	84.56	0.99427	40618	P	-1.098	13.58	0.11208	3320
BC030336	A_52_P655948	AK148546	cDNA sequence BC030336	1.005	84.56	0.99155	40295	P	1.029	36.07	0.60929	9518
Lrsam1	A_52_P112139	NM_199302	leucine rich repeat and sterile alpha moti	1.005	84.56	0.99466	40723	P	1.013	42.43	0.7879	11072
Lsm6	A_52_P422755	NM_030145	LSM6 homolog, U6 small nuclear RNA ass	1.005	84.56	0.99275	40414	P	1.035	36.07	0.72886	10563
Nap1l4	A_52_P634822	NM_008672	nucleosome assembly protein 1-like 4	1.005	84.56	0.99428	40660	P	1.049	25.31	0.36196	7045
Ncoa1	A_51_P502888	NM_010881	nuclear receptor coactivator 1	1.005	84.56	0.99268	40384	P	1.032	33.49	0.57623	9238
Npc1	A_52_P410979	AK170880	Niemann Pick type C1	1.005	75.14	0.99614	26732	M	1.063	22.1	0.31612	6537
Pros1	A_51_P393426	NM_011173	protein S (alpha)	1.005	84.56	0.99401	40576	P	1.099	22.1	0.52827	8823
Pttg1ip	A_51_P173100	NM_145925	pituitary tumor-transforming 1 interactin	1.005	84.56	0.99427	40646	P	1.036	28.13	0.41501	7681
Rhot2	A_52_P535346	NM_145999	ras homolog gene family, member T2	1.005	84.56	0.99457	40715	P	-1.402	0	0.00584	24
Surb7	A_51_P396708	NM_025315	SRB7 (suppressor of RNA polymerase B) h	1.005	84.56	0.99678	40953	P	1.029	33.49	0.52263	8773
Yars	A_51_P248674	NM_134151	tyrosyl-tRNA synthetase	1.005	84.56	0.99288	40443	P	1.011	42.43	0.80573	11228
4933404O12Rik	A_51_P257122	AK016656	RIKEN cDNA 4933404O12 gene	1.004	75.14	0.99532	29547	M	1.029	33.49	0.56159	9128
Adck2	A_52_P222967	NM_178873	aarF domain containing kinase 2	1.004	84.56	0.99635	40919	P	1.186	5.75	0.08313	2731
Fdft1	A_51_P485946	NM_010191	farnesyl diphosphate farnesyl transferase	1.004	84.56	0.99554	40821	P	-1.117	28.13	0.38669	7355
Gsn	A_51_P241465	NM_146120	gelsolin	1.004	84.56	0.99532	40766	P	1.142	9.71	0.22646	5296
Lcn2	A_51_P510156	NM_008491	lipocalin 2	1.004	84.56	0.99748	41024	P	-1.087	28.13	0.27428	6019
Ppm1a	A_51_P335303	NM_008910	protein phosphatase 1A, magnesium dep	1.004	84.56	0.99614	40896	P	1.128	8.32	0.09477	2995
Ptchd1	A_51_P375771	XM_142262	patched domain containing 1	1.004	84.56	0.99686	40986	P	1.038	36.07	0.75256	10808
Rab9	A_52_P214678	NM_019773	RAB9, member RAS oncogene family	1.004	84.56	0.99608	40882	P	-1.025	48.7	0.72866	10558
Retn	A_52_P55972	NM_022984	resistin	1.004		0.99836	15316	A	1.075	16.2	0.22643	5294
Sh2d3c	A_51_P464761	NM_013781	SH2 domain containing 3C	1.004	84.56	0.99686	40971	P	1.051	22.1	0.27618	6047
Tmc6	A_52_P119972	NM_181321	transmembrane channel-like gene family	1.004	79.26	0.99614	29560	M	1.008	42.43	0.91419	12212
Tmem19	A_51_P392090	NM_133683	transmembrane protein 19	1.004	84.56	0.99348	40532	P	1.041	28.13	0.43181	7856
Usp42	A_51_P199057	NM_029749	ubiquitin specific peptidase 42	1.004	84.56	0.99614	40899	P	1.025	38.4	0.72417	10517
Arf3	A_51_P200068	NM_007478	ADP-ribosylation factor 3	1.003	84.56	0.99705	26754	M	1.116	8.32	0.08291	2723
C78339	A_51_P155550	AK090371	expressed sequence C78339	1.003	84.56	0.99428	40688	P	1.117	8.32	0.0711	2416
C79407	A_51_P294346	AK035117	expressed sequence C79407	1.003	84.56	0.99648	40935	P	-1.063	40.63	0.41596	7695
Cln3	A_52_P130982	BC047120	ceroid lipofuscinosis, neuronal 3, juvenile	1.003	84.56	0.99532	40802	P	1.152	4.63	0.04968	1842
Espn	A_52_P469345	NM_207687	espin	1.003	84.56	0.99606	40873	P	1.02	38.4	0.70731	10387
Foxd4	A_51_P443584	NM_008022	forkhead box D4	1.003		0.99864	15323	A	1.035	28.13	0.41191	7635
Irs3	A_51_P174158	NM_010571	insulin receptor substrate 3	1.003		0.99686	26747	A	-1.027	48.39	0.74264	10712
Lypla1	A_52_P8227	NM_008866	lysophospholipase 1	1.003	84.56	0.99614	40887	P	1.13	6.98	0.06328	2239
Nfkb2	A_51_P454217	NM_019408	nuclear factor of kappa light polypeptide	1.003	84.56	0.99614	40894	P	1.091	9.71	0.08963	2880
Ppfia1	A_51_P424603	AK037102	protein tyrosine phosphatase, receptor ty	1.003	84.22	0.99857	26779	M	1.136	9.71	0.18854	4704
Pqlc1	A_52_P96939	AK019858	PQ loop repeat containing 1	1.003		0.99785	23354	A	1.03	33.49	0.53852	8923
Rad17	A_51_P464633	NM_011233	RAD17 homolog (S. pombe)	1.003	84.56	0.9975	41055	P	1.133	6.98	0.06787	2359
Safb2	A_51_P332559	NM_001029979	scaffold attachment factor B2	1.003	84.56	0.99686	40970	P	-1.173	2.53	0.05055	1868
Ube2j2	A_51_P416919	NM_021402	ubiquitin-conjugating enzyme E2, J2 hom	1.003	84.56	0.99555	40824	P	1.066	19.02	0.30199	6340
A630051L19Rik	A_52_P685821	AK042002	RIKEN cDNA D730040F13 gene	1.002	84.56	0.99735	41013	P	1.04	30.75	0.49804	8558
Armcx2	A_51_P356512	NM_026139	armadillo repeat containing, X-linked 2	1.002	84.56	0.99686	40990	P	1.358	1.32	0.02595	1070
C130032J12Rik	A_51_P328645	NM_178684	RIKEN cDNA C130032J12 gene	1.002	84.56	0.99783	41108	P	1.179	3.82	0.03602	1396
Cct6b	A_51_P392040	NM_009839	chaperonin subunit 6b (zeta)	1.002	84.56	0.99748	41035	P	-1.292	0.51	0.01203	486
Cradd	A_51_P242265	NM_009950	CASP2 and RIPK1 domain containing adap	1.002	84.56	0.99857	41216	P	1.078	13.58	0.17711	4518
Mbl1	A_51_P373619	NM_010775	mannose binding lectin (A)	1.002	83.36	0.99685	35648	M	1.063	25.31	0.44217	7938
Nid1	A_51_P339943	NM_010917	nidogen 1	1.002	84.56	0.99785	26769	M	-1.048	43.15	0.461	8117

Nudcd3	A_52_P105164	NM_173748	NudC domain containing 3	1.002	84.56	0.99752	41074	P	1.081	11.33	0.12642	3641
Olig2	A_51_P367451	NM_016967	oligodendrocyte transcription factor 2	1.002		0.9993	15330	A	1.179	2.04	0.01467	626
Pnp	A_51_P488888	NM_013632	purine-nucleoside phosphorylase	1.002	84.56	0.9986	41242	P	-1.023	47.43	0.59887	9438
Sulf1	A_51_P142744	NM_172294	sulfatase 1	1.002	84.56	0.99857	41224	P	1.057	22.1	0.3306	6680
1600002K03Rik	A_51_P519570	NM_027207	RIKEN cDNA 1600002K03 gene	1.001	84.56	0.99912	41287	P	1.195	5.75	0.1174	3426
Btbd1	A_51_P242345	NM_146193	BTB (POZ) domain containing 1	1.001	84.56	0.99785	41151	P	-1.025	46.3	0.5433	8973
Cald1	A_51_P357573	NM_145575	caldesmon 1	1.001	84.56	0.99843	41198	P	-1.098	36.07	0.49986	8577
Dstn	A_51_P459350	NM_019771	destrin	1.001	84.56	0.99903	41271	P	-1.429	0.51	0.00584	40
Dyrk1a	A_52_P225969	AK047845	dual-specificity tyrosine-(Y)-phosphorylat	1.001	84.56	0.9984	41175	P	1.205	3.46	0.04727	1766
Ercc3	A_51_P366024	NM_133658	excision repair cross-complementing rode	1.001	84.56	0.99785	41144	P	1.074	19.02	0.29109	6221
Gpam	A_52_P11388	NM_008149	glycerol-3-phosphate acyltransferase, mit	1.001		0.99887	26786	A	-1.376	0.51	0.00584	93
Gpr27	A_51_P260167	NM_008158	G protein-coupled receptor 27	1.001	84.56	0.99785	41129	P	1.058	22.1	0.31081	6465
Hmgn2	A_52_P149864	NM_016957	high mobility group nucleosomal binding	1.001	84.56	0.99871	26782	M	-1.066	28.13	0.19298	4792
Purb	A_51_P468381	NM_011221	purine rich element binding protein B	1.001	84.56	0.9988	41246	P	-1.059	38.4	0.35592	6964
Rnpepl1	A_51_P220407	NM_181405	arginyl aminopeptidase (aminopeptidase	1.001	84.56	0.99944	41292	P	-1.013	49.48	0.86156	11690
6330407G11Rik	A_51_P237575	NM_023423	RIKEN cDNA 6330407G11 gene	1	83.95	0.99959	41331	P	1.199	4.63	0.07156	2425
Arfgap3	A_52_P439874	AK018680	ADP-ribosylation factor GTPase activating	1	83.95	0.99966	41334	P	1.002	42.43	0.96617	12713
Becn1	A_51_P489337	NM_019584	beclin 1 (coiled-coil, myosin-like BCL2-inte	1	83.95	0.99994	41355	P	1.053	22.1	0.31627	6544
Id1	A_51_P385786	NM_010495	inhibitor of DNA binding 1	1	82.34	0.99994	32647	P	1.035	38.4	0.776	10959
Idh2	A_51_P331507	NM_173011	isocitrate dehydrogenase 2 (NADP+), mitc	1	83.95	0.99972	41326	P	1.029	36.07	0.64171	9816
Map4k5	A_52_P57057	AK052373	mitogen-activated protein kinase kinase k	1	83.95	0.99994	41352	P	1.174	3.82	0.04432	1654
Mcm5	A_51_P190111	NM_008566	minichromosome maintenance deficient	1	84.56	0.99994	41375	P	-1.08	25.31	0.18213	4611
Pdcl	A_52_P670909	NM_026176	phosducin-like	1	84.56	0.99992	41370	P	-1.123	6.98	0.07542	2546
Rbm16	A_51_P143576	AK054357	RNA binding motif protein 16	1	84.56	0.99972	41299	P	1.013	42.43	0.80422	11211
Rbms2	A_52_P49096	NM_001039080	RNA binding motif, single stranded intera	1	83.95	0.99944	41307	P	-1.02	49.39	0.74646	10757
Rchy1	A_51_P374305	NM_026557	ring finger and CHY zinc finger domain co	1	84.56	0.99994	41369	P	1.113	8.32	0.07272	2461
Rpn1	A_52_P656634	NM_133933	ribophorin I	1	84.56	0.99994	41393	M	1.097	13.58	0.19113	4750
Slc7a8	A_51_P112734	NM_016972	solute carrier family 7 (cationic amino aci	1	83.95	0.99994	26796	M	1.105	13.58	0.24916	5633
Smad2	A_52_P397280	NM_010754	MAD homolog 2 (Drosophila)	1	83.95	0.99994	41396	P	1.104	13.58	0.20422	4955
Snx11	A_52_P253557	AK037747	sorting nexin 11	1	84.56	0.99994	41346	P	1.068	19.02	0.29228	6239
Taz	A_51_P107282	NM_181516	tafazzin	1	84.56	0.99983	41337	P	1.03	33.49	0.53987	8943
Tusc3	A_52_P515347	NM_030254	tumor suppressor candidate 3	1	84.56	0.99994	26795	M	1.035	33.49	0.6577	9950
Zfp260	A_52_P649721	NM_011981	zinc finger protein 260	1	84.56	0.99994	41345	P	-1.11	13.58	0.13916	3834
Zw10	A_51_P137007	NM_012039	ZW10 homolog (Drosophila), centromere,	1	84.56	0.99992	41400	P	1.024	33.49	0.56342	9138
4933417E01Rik	A_51_P449824	NM_028954	RIKEN cDNA 4933417E01 gene	-1.001	83.95	0.9984	41191	P	-1.006	49.48	0.90099	12102
Fahd1	A_51_P389421	NM_023480	fumarylacetoacetate hydrolase domain co	-1.001	83.95	0.99947	41309	P	1.032	30.75	0.50522	8634
Fstl3	A_52_P14851	NM_031380	follistatin-like 3	-1.001	83.95	0.9991	41291	P	1.005	42.43	0.93483	12429
G6pc3	A_51_P430555	NM_175935	glucose 6 phosphatase, catalytic, 3	-1.001	83.95	0.9991	41266	P	-1.04	43.15	0.38401	7329
Wdr48	A_52_P467046	NM_026236	WD repeat domain 48	-1.001	83.95	0.9993	41283	P	-1.015	49.48	0.74425	10746
Actn4	A_51_P394788	NM_021895	actinin alpha 4	-1.002	83.95	0.99857	26777	M	-1.193	1.1	0.01603	690
Arpc5l	A_51_P180108	NM_028809	actin related protein 2/3 complex, subuni	-1.002	83.95	0.99645	40936	P	1.077	16.2	0.24444	5567
Ccndbp1	A_51_P154469	NM_010761	cyclin D-type binding-protein 1	-1.002	83.95	0.9981	26771	M	1.183	3.82	0.03732	1423
Elovl1	A_51_P120305	NM_001039176	elongation of very long chain fatty acids (	-1.002	83.95	0.99614	40904	P	1.094	13.58	0.17257	4418
Gdf5	A_51_P415675	NM_008109	growth differentiation factor 5	-1.002	83.95	0.99752	41072	M	1.008	42.43	0.89707	12031
Notch2	A_51_P216397	NM_010928	Notch gene homolog 2 (Drosophila)	-1.002	84.4	0.99783	32623	M	-1.066	28.13	0.1884	4702
Rfxank	A_52_P484838	NM_011266	regulatory factor X-associated ankyrin-co	-1.002	83.95	0.9975	41046	P	-1.018	49.39	0.7247	10519
Rnh1	A_51_P463497	NM_145135	ribonuclease/angiogenin inhibitor 1	-1.002	83.95	0.99785	41149	P	1.033	33.49	0.5705	9197
Zfyve21	A_51_P396917	NM_026752	zinc finger, FYVE domain containing 21	-1.002	83.95	0.99827	41163	P	-1.223	1.32	0.0391	1477
Mcm2	A_51_P158210	NM_008564	minichromosome maintenance deficient	-1.003	83.95	0.99785	41139	P	-1.032	46.3	0.68212	9360
Nars	A_51_P315555	NM_027350	asparaginyl-tRNA synthetase	-1.003	83.95	0.99718	41004	P	1.072	19.02	0.263	5852
Pfdn4	A_51_P423791	NM_001013369	prefoldin 4	-1.003	83.95	0.99614	40897	P	1.078	16.2	0.25423	5728
Tmed3	A_51_P284244	NM_025360	transmembrane emp24 domain containi	-1.003	83.95	0.99783	26766	M	1.031	36.07	0.71608	10455
Arrdc2	A_51_P417651	NM_027560	arrestin domain containing 2	-1.004	83.36	0.99348	40499	P	1.017	38.4	0.69931	10310

BC057552	A_52_P412543	NM_172502	cDNA sequence BC057552	-1.004	83.95	0.99532	40798	P	-1.357	0.51	0.00584	95
H2afx	A_51_P245275	NM_010436	H2A histone family, member X	-1.004	83.95	0.99428	40694	P	-1.237	0.51	0.00877	320
Homer3	A_51_P466613	NM_011984	homer homolog 3 (Drosophila)	-1.004	83.95	0.99718	41006	P	-1.006	49.48	0.90778	12172
Irf2bp1	A_52_P381953	NM_178757	interferon regulatory factor 2 binding pro	-1.004	83.95	0.99686	40982	P	1.157	9.71	0.21223	5077
Kpna1	A_51_P256682	NM_008465	karyopherin (importin) alpha 1	-1.004	83.36	0.99427	40606	P	1.036	36.07	0.7313	10580
Mfhas1	A_51_P494825	BC082308	malignant fibrous histiocytoma amplified	-1.004	83.36	0.9938	40542	P	1.111	16.2	0.34387	6808
Pdgfrb	A_51_P150964	NM_008809	platelet derived growth factor receptor, b	-1.004	83.95	0.99532	40775	P	1.019	38.4	0.6685	10029
Cldn13	A_51_P469568	NM_020504	claudin 13	-1.005		0.99566	23331	A	-1.05	44.4	0.59052	9335
Eif3s4	A_51_P489229	NM_016876	eukaryotic translation initiation factor 3, s	-1.005	83.95	0.99532	40774	P	1.026	38.4	0.69769	10301
Hsd11b2	A_51_P410205	NM_008289	hydroxysteroid 11-beta dehydrogenase 2	-1.005	81.02	0.9929	35544	M	-1.017	49.48	0.81394	11319
0610010K06Rik	A_51_P288522	NM_027861	RIKEN cDNA 0610010K06 gene	-1.006	83.36	0.99149	40269	P	1.142	4.63	0.03815	1450
BC002230	A_51_P213592	XM_484171	cDNA sequence BC002230	-1.006	83.36	0.99348	40521	P	-1.001	49.48	0.98929	12980
Fkbpl	A_51_P515452	NM_019873	FK506 binding protein-like	-1.006	83.95	0.9944	40710	P	1.067	13.58	0.15856	4191
Foxp3	A_51_P401096	NM_054039	forkhead box P3	-1.006	83.36	0.99395	40555	M	1.08	13.58	0.17322	4427
Gimap6	A_51_P407227	NM_153175	GTPase, IMAP family member 6	-1.006	83.95	0.99455	40714	P	-1.03	48.39	0.73795	10658
Map2k2	A_51_P439626	NM_023138	mitogen activated protein kinase kinase 2	-1.006	83.36	0.9925	40360	P	-1.171	5.75	0.12271	3554
Pde8a	A_52_P391000	NM_008803	phosphodiesterase 8A	-1.006	83.95	0.99428	32548	P	-1.006	49.48	0.93029	12390
Rhof	A_51_P288802	ENSMUST00000031401	ras homolog gene family, member f	-1.006	83.36	0.99146	32454	M	-1.015	49.48	0.83616	11497
Tnk2	A_51_P386189	NM_016788	tyrosine kinase, non-receptor, 2	-1.006	83.36	0.99147	40246	P	1.114	16.2	0.34141	6785
Zfyve1	A_51_P181746	NM_183154	zinc finger, FYVE domain containing 1	-1.006	83.36	0.99155	40288	P	-1.062	30.75	0.2185	5179
2610206B13Rik	A_51_P135939	NM_026047	RIKEN cDNA 2610206B13 gene	-1.007	83.36	0.99275	40396	P	-1.048	42.43	0.3817	7299
2700038C09Rik	A_51_P299266	NM_025598	RIKEN cDNA 2700038C09 gene	-1.007	83.36	0.99348	40522	P	1.007	42.43	0.90099	12094
2900009J20Rik	A_51_P491835	AK013507	RIKEN cDNA 2900009J20 gene	-1.007	83.95	0.99518	40749	P	-1.096	19.02	0.17513	4481
Chchd2	A_52_P20354	NM_024166	coiled-coil-helix-coiled-coil-helix domain c	-1.007	83.36	0.99192	26649	M	1.031	30.75	0.45532	8051
Ppap2b	A_51_P503433	NM_080555	phosphatidic acid phosphatase type 2B	-1.007	83.36	0.991	40157	P	1.278	3.82	0.12025	3498
Sf3b1	A_52_P220190	NM_031179	splicing factor 3b, subunit 1	-1.007	83.36	0.99401	40581	P	1.047	25.31	0.32154	6581
9130404D14Rik	A_51_P429040	NM_146119	RIKEN cDNA 9130404D14 gene	-1.008	83.36	0.99268	40383	P	1.015	42.43	0.83133	11472
Atxn7l2	A_52_P287195	NM_175183	ataxin 7-like 2	-1.008	83.36	0.98946	39927	P	-1.013	49.48	0.81226	11298
E430014L09Rik	A_51_P107752	AK033357	RIKEN cDNA E430014L09 gene	-1.008	82.34	0.99156	35494	M	-1.158	2.04	0.03162	1244
Fbxw5	A_52_P563942	NM_013908	F-box and WD-40 domain protein 5	-1.008	83.36	0.98933	39894	P	-1.104	13.58	0.12406	3582
Fscn1	A_51_P366061	NM_007984	fascin homolog 1, actin bundling protein (	-1.008	83.36	0.99427	40627	P	-1.001	49.48	0.98667	12945
Kif3a	A_51_P473907	NM_008443	kinesin family member 3A	-1.008	83.36	0.99141	40215	P	1.134	4.63	0.0382	1452
Pgk2	A_51_P125487	NM_031190	phosphoglycerate kinase 2	-1.008	84.56	0.99275	35526	M	1.146	3.46	0.02494	1032
Tnip1	A_51_P327261	NM_021327	TNFAIP3 interacting protein 1	-1.008	83.95	0.99427	40651	P	1.036	28.13	0.41471	7676
Tsc2	A_51_P345714	NM_011647	tuberous sclerosis 2	-1.008	83.36	0.99348	40504	P	1.09	13.58	0.21503	5122
Zcchc9	A_51_P187231	NM_145453	zinc finger, CCHC domain containing 9	-1.008	83.36	0.98951	39961	P	1.135	9.71	0.16039	4223
2310004I03Rik	A_51_P457397	AK009140	dipeptidylpeptidase 8	-1.009	83.36	0.98687	39446	P	-1.069	33.49	0.25635	5748
Ddr1	A_51_P161582	L57509	discoidin domain receptor family, membe	-1.009	83.36	0.99428	26705	M	1.081	9.71	0.09637	3024
Mafk	A_51_P306183	NM_010757	v-maf musculoaponeurotic fibrosarcoma	-1.009	83.36	0.98964	40025	P	1.083	13.58	0.15413	4117
Nup205	A_51_P177062	AK014419	nucleoporin 205	-1.009	61.79	0.99192	26635	M	1.008	42.43	0.91901	12267
Pank4	A_51_P457054	NM_172990	pantothenate kinase 4	-1.009	83.36	0.99149	40274	P	-1.453	0.51	0.00584	48
Prdm10	A_52_P331056	XM_983233	PR domain containing 10	-1.009	83.36	0.98686	39434	M	-1.009	49.48	0.87463	11804
Psmb6	A_52_P199375	NM_008946	proteasome (prosome, macropain) subun	-1.009	83.36	0.99344	40492	P	-1.067	36.07	0.32279	6592
Rtn4ip1	A_52_P172283	NM_130892	reticulon 4 interacting protein 1	-1.009	83.36	0.98993	40048	P	-1.051	40.63	0.36214	7049
S100a11	A_51_P155643	NM_016740	S100 calcium binding protein A11 (calgizz	-1.009	84.56	0.9925	32483	P	-1.063	40.63	0.39613	7475
Sardh	A_51_P492676	NM_138665	sarcosine dehydrogenase	-1.009	83.36	0.9929	40455	P	-1.053	43.15	0.47292	8227
Thap11	A_51_P480881	NM_021513	THAP domain containing 11	-1.009	83.36	0.9909	40153	P	-1.048	38.4	0.28489	6144
Unc50	A_51_P474509	NM_026123	unc-50 homolog (C. elegans)	-1.009	83.36	0.99181	26644	M	1.003	42.43	0.97155	12761
1110008B24Rik	A_51_P153787	NM_028632	FCF1 small subunit (SSU) processome con	-1.01	83.36	0.98951	39951	P	-1.013	49.48	0.83098	11471
2310016E02Rik	A_52_P316697	NM_024460	RIKEN cDNA 2310016E02 gene	-1.01	83.36	0.98789	39594	P	-1.254	0.51	0.00707	223
Casp8ap2	A_51_P517096	NM_011997	caspase 8 associated protein 2	-1.01	83.36	0.98815	39633	P	-1.022	47.43	0.59497	9393
Edg8	A_51_P480169	NM_053190	endothelial differentiation, sphingolipid G	-1.01		0.99614	15287	A	1.1	8.32	0.06764	2356
Hoxa5	A_51_P310821	NM_010453	homeo box A5	-1.01	83.36	0.99275	40412	P	1.078	13.58	0.18589	4667

Polr3d	A_51_P223458	NM_025945	polymerase (RNA) III (DNA directed) poly	-1.01	83.36	0.98883	39813	P	1.059	19.02	0.22162	5236
Prdm1	A_51_P338746	NM_007548	PR domain containing 1, with ZNF domair	-1.01	83.36	0.98663	39411	P	-1.09	22.1	0.17752	4525
Pum1	A_51_P423219	NM_030722	pumilio 1 (Drosophila)	-1.01	83.36	0.99274	26671	M	1.299	1.62	0.02638	1086
Slc40a1	A_51_P389988	NM_016917	solute carrier family 40 (iron-regulated tr	-1.01	82.34	0.98526	39293	P	1.175	4.63	0.05019	1855
Cgrrf1	A_51_P331462	NM_026832	cell growth regulator with ring finger dom	-1.011	83.36	0.98815	39652	P	-1.022	47.92	0.62539	9676
Creld1	A_51_P205545	NM_133930	cysteine-rich with EGF-like domains 1	-1.011	83.36	0.98896	39825	P	1.028	36.07	0.6899	10240
Man2a1	A_51_P324923	NM_008549	mannosidase 2, alpha 1	-1.011	82.34	0.98482	39270	P	1.061	22.1	0.33029	6669
Npas2	A_52_P534749	NM_008719	neuronal PAS domain protein 2	-1.011	84.56	0.98845	32356	M	1.149	11.33	0.26736	5907
Ruvbl2	A_51_P133198	NM_011304	RuvB-like protein 2	-1.011	83.36	0.9862	39353	P	1.021	38.4	0.68208	10154
Tm4sf1	A_51_P240614	NM_008536	transmembrane 4 superfamily member 1	-1.011	83.36	0.98825	39759	P	1.027	42.43	0.91646	12234
0610025P10Rik	A_51_P211822	NM_001013414	RIKEN cDNA 0610025P10 gene	-1.012	83.36	0.9925	40371	P	1.097	13.58	0.24312	5552
2500003M10Rik	A_52_P510647	NM_023215	RIKEN cDNA 2500003M10 gene	-1.012	82.34	0.98164	38915	P	1.046	36.07	0.7617	10871
Ap1gbp1	A_51_P245546	NM_194341	AP1 gamma subunit binding protein 1	-1.012	83.36	0.98789	39605	P	1.14	16.2	0.40566	7572
Ces3	A_51_P375969	NM_053200	carboxylesterase 3	-1.012	83.95	0.99538	40812	P	1.247	1.17	0.00957	344
Il6st	A_51_P473888	NM_010560	interleukin 6 signal transducer	-1.012	83.36	0.98687	39453	P	1.072	16.2	0.19865	4879
Pecr	A_51_P291749	NM_023523	peroxisomal trans-2-enoyl-CoA reductase	-1.012	82.34	0.98219	39016	P	1.04	30.75	0.46325	8143
Repin1	A_52_P221887	NM_175099	replication initiator 1	-1.012	83.36	0.98815	39728	P	1.067	16.2	0.18425	4641
Stambp	A_51_P278103	NM_024239	Stam binding protein	-1.012	83.36	0.98779	39575	P	1.139	3.82	0.02803	1138
1810055E12Rik	A_51_P464149	NM_026437	RIKEN cDNA 1810055E12 gene	-1.013	83.36	0.98509	39290	P	1.08	22.1	0.41732	7713
6330503K22Rik	A_52_P344160	NM_182995	RIKEN cDNA 6330503K22 gene	-1.013	82.34	0.98078	38621	P	-1.04	43.15	0.35968	7002
Fastk	A_51_P348764	NM_023229	Fas-activated serine/threonine kinase	-1.013	83.36	0.98815	39720	P	-1.071	22.1	0.13774	3802
Hap1	A_51_P516728	NM_010404	huntingtin-associated protein 1	-1.013	83.36	0.99283	26677	M	1.224	5.75	0.13661	3779
Tbxa2r	A_52_P55772	NM_009325	thromboxane A2 receptor	-1.013	83.36	0.99148	40261	P	1.26	2.53	0.03311	1296
Usp10	A_51_P280200	NM_009462	ubiquitin specific peptidase 10	-1.013	83.36	0.98946	39922	P	-1.109	6.98	0.06217	2198
Wdr23	A_51_P275395	NM_133734	WD repeat domain 23	-1.013	83.36	0.98765	39524	P	1.142	5.75	0.06049	2162
Appbp1	A_51_P200838	NM_144931	amyloid beta precursor protein binding pı	-1.014	82.34	0.98078	38610	P	1.01	42.43	0.82749	11431
Arf2	A_51_P123345	NM_007477	ADP-ribosylation factor 2	-1.014	82.34	0.98173	38957	P	-1.035	46.3	0.60637	9497
Hells	A_51_P351970	NM_008234	helicase, lymphoid specific	-1.014	83.36	0.9925	40374	P	-1.049	36.07	0.26081	5832
Usp1	A_51_P381657	NM_146144	ubiquitin specific peptdiase 1	-1.014	83.36	0.9867	39430	P	-1.073	36.07	0.38438	7331
2310004I24Rik	A_52_P293724	NM_025510	RIKEN cDNA 2310004I24 gene	-1.015	83.36	0.98815	39630	P	1.03	33.49	0.51359	8705
Asb6	A_51_P478610	NM_133346	ankyrin repeat and SOCS box-containing ı	-1.015	83.36	0.98946	39906	P	1.022	38.4	0.70073	10323
Pira2	A_52_P506407	NM_011089	paired-Ig-like receptor A1	-1.015	82.34	0.9826	39091	P	-1.113	9.71	0.1018	3141
Rabgef1	A_51_P109923	NM_019983	RAB guanine nucleotide exchange factor (	-1.015	82.34	0.98109	38797	P	-1.012	49.48	0.79572	11144
Tnfaip2	A_51_P364485	NM_009396	tumor necrosis factor, alpha-induced prot	-1.015	82.34	0.98165	38944	P	1.012	42.43	0.80411	11210
Tufm	A_51_P165617	NM_172745	Tu translation elongation factor, mitochor	-1.015	82.34	0.98326	39140	P	1.041	28.13	0.38865	7383
Wnt11	A_51_P503131	NM_009519	wingless-related MMTV integration site 1	-1.015	82.34	0.98244	39068	P	-1.098	25.31	0.27059	5964
Bcl11b	A_51_P171772	NM_021399	B-cell leukemia/lymphoma 11B	-1.016	81.02	0.98078	31904	M	-1.087	13.58	0.10259	3163
Eif3s2	A_51_P519189	NM_018799	eukaryotic translation initiation factor 3, ș	-1.016	83.36	0.98951	39957	P	1.023	38.4	0.71117	10414
Grhpr	A_51_P427432	NM_080289	glyoxylate reductase/hydroxypyruvate rec	-1.016	82.34	0.98109	38695	P	1.008	42.43	0.8781	11841
Rabl5	A_51_P495077	NM_026073	RAB, member of RAS oncogene family-like	-1.016	83.36	0.98687	39455	P	1.088	11.33	0.11794	3435
Scap	A_52_P485971	NM_001001144	SREBF chaperone	-1.016	83.36	0.98815	39707	P	-1.36	0.51	0.00619	127
Scnm1	A_51_P284597	NM_027013	sodium channel modifier 1	-1.016	83.36	0.98733	39497	P	-1.338	0.51	0.00697	214
Wdr3	A_51_P112445	NM_175552	WD repeat domain 3	-1.016	82.34	0.97772	38280	P	1.044	28.13	0.42912	7817
0610010K14Rik	A_51_P349951	NM_026757	RIKEN cDNA 0610010K14 gene	-1.017	82.34	0.98109	38701	P	-1.065	36.07	0.33033	6673
Atp7b	A_51_P510997	NM_007511	ATPase, Cu++ transporting, beta polypept	-1.017	82.34	0.98014	38520	P	1.038	28.13	0.3643	7077
Slc35a1	A_51_P514421	NM_011895	solute carrier family 35 (CMP-sialic acid tr	-1.017	82.34	0.97483	37949	P	1.007	42.43	0.89086	11977
Taldo1	A_51_P401958	NM_011528	transaldolase 1	-1.017	82.34	0.98413	26357	M	1.078	19.02	0.35758	6984
Ypel3	A_52_P326808	NM_026875	yippee-like 3 (Drosophila)	-1.017	82.34	0.98109	38752	P	1.1	16.2	0.36407	7073
2610529C04Rik	A_52_P79385	NM_025952	RIKEN cDNA 2610529C04 gene	-1.018	82.34	0.97879	38371	P	1.11	9.71	0.10041	3108
BC003940	A_51_P176138	BC052229	cDNA sequence BC003940	-1.018	82.34	0.97307	37768	P	-1.037	45.05	0.4998	8576
Eef1e1	A_51_P164420	NM_025380	eukaryotic translation elongation factor 1	-1.018	82.34	0.97921	38429	P	1.064	28.13	0.59776	9434
Gadd45a	A_51_P296608	NM_007836	growth arrest and DNA-damage-inducible	-1.018	83.36	0.98906	39868	P	-1.064	25.31	0.1631	4272
Mcart1	A_52_P169901	NM_001009949	mitochondrial carrier triple repeat 1	-1.018	82.34	0.97889	38411	P	1.15	3.46	0.02523	1044

Pafah1b3	A_51_P267024	NM_008776	platelet-activating factor acetylhydrolase,	-1.018	82.34	0.98165	38930	P	1.143	5.75	0.04454	1660
Armcx1	A_51_P496001	NM_030066	armadillo repeat containing, X-linked 1	-1.019	82.34	0.97483	37976	P	-1.02	49.48	0.85836	11666
Dhrs7	A_51_P312437	NM_025522	dehydrogenase/reductase (SDR family) m	-1.019	82.34	0.98413	39188	P	1.055	25.31	0.43222	7859
Etfb	A_51_P155212	NM_026695	electron transferring flavoprotein, beta p	-1.019	83.36	0.98771	39552	P	1.117	8.32	0.09215	2944
Lsm4	A_51_P116487	NM_015816	LSM4 homolog, U6 small nuclear RNA ass	-1.019	83.36	0.98765	39504	P	-1.37	0.51	0.00584	81
Mybbp1a	A_51_P332627	NM_016776	MYB binding protein (P160) 1a	-1.019	82.34	0.97577	38048	P	-1.03	46.85	0.61023	9528
Ntan1	A_52_P566579	NM_010946	N-terminal Asn amidase	-1.019	82.34	0.97808	38300	P	1.119	11.33	0.19597	4837
Txnrd1	A_51_P320614	NM_001042523	thioredoxin reductase 1	-1.019	82.34	0.98561	26390	M	1.084	13.58	0.17869	4549
2810405J04Rik	A_51_P353173	NM_133747	RIKEN cDNA 2810405J04 gene	-1.02	82.34	0.98078	26166	M	1.193	3.82	0.0484	1807
6720489N17Rik	A_51_P306446	AK033958	RIKEN cDNA 6720489N17 gene	-1.02	82.34	0.97707	38199	P	1.08	16.2	0.21823	5170
Gcn5l2	A_51_P312528	NM_020004	GCN5 general control of amino acid synth	-1.02	82.34	0.97842	38340	P	-1.067	30.75	0.21237	5081
Mrg2	A_52_P575691	NM_008627	myeloid ecotropic viral integration site-re	-1.02	82.34	0.97577	38051	P	1.066	13.58	0.15513	4137
Pcbp1	A_52_P241129	NM_011865	poly(rC) binding protein 1	-1.02	82.34	0.98183	26275	M	1.065	30.75	0.71908	10473
Ppp2r4	A_52_P477919	NM_138748	protein phosphatase 2A, regulatory subu	-1.02	82.34	0.98123	38821	P	-1.113	4.63	0.05285	1944
Slit1	A_51_P101388	NM_015748	slit homolog 1 (Drosophila)	-1.02	82.34	0.97386	37869	P	-1.019	49.39	0.73901	10680
Strn3	A_52_P140604	NM_052973	striatin, calmodulin binding protein 3	-1.02	82.34	0.97921	26096	M	1.113	9.71	0.11836	3445
1300001I01Rik	A_51_P354272	AK154925	RIKEN cDNA 1300001I01 gene	-1.021	82.34	0.97807	38295	P	1.105	9.71	0.08656	2815
1700021F05Rik	A_51_P349825	NM_026411	RIKEN cDNA 1700021F05 gene	-1.021	82.34	0.98436	39221	P	-1.101	19.02	0.18161	4607
2410018C17Rik	A_51_P440522	NM_178390	RIKEN cDNA 2410018C17 gene	-1.021	82.34	0.98036	38538	P	1.085	16.2	0.31012	6449
AI929863	A_51_P142989	XM_920647	RIKEN cDNA 2810487A22 gene	-1.021	82.34	0.98105	38665	P	1.082	11.33	0.11265	3331
Cndp2	A_51_P449048	NM_023149	CNDP dipeptidase 2 (metallopeptidase M	-1.021	82.34	0.97013	37416	P	-1.03	47.43	0.6527	9897
Elmod2	A_51_P184806	NM_178736	ELMO domain containing 2	-1.021	81.02	0.96549	37020	P	1.058	19.02	0.24817	5620
Hif1a	A_51_P387608	NM_010431	hypoxia inducible factor 1, alpha subunit	-1.021	82.34	0.98078	26174	M	-1.097	36.07	0.45503	8049
Slc2a1	A_51_P464738	NM_011400	solute carrier family 2 (facilitated glucose	-1.021	82.34	0.97194	37614	P	-1.262	0.66	0.01567	672
Twist2	A_51_P165504	NM_007855	twist homolog 2 (Drosophila)	-1.021	82.34	0.98322	39135	P	1.117	6.98	0.04969	1843
Wbp11	A_51_P448987	NM_021714	WW domain binding protein 11	-1.021	82.34	0.98109	38745	P	1.022	40.63	0.84229	11539
Wbp2	A_51_P358940	NM_016852	WW domain binding protein 2	-1.021	83.36	0.98706	39482	P	1.072	13.58	0.15101	4054
Dctn6	A_51_P357085	NM_011722	dynactin 6	-1.022	82.34	0.96774	37248	P	1.091	13.58	0.16435	4284
Fbl	A_51_P349142	NM_007991	fibrillarin	-1.022	82.34	0.98149	38880	P	1.117	9.71	0.1484	4014
Hdac3	A_51_P483089	NM_010411	histone deacetylase 3	-1.022	82.34	0.9733	37799	P	1.088	9.71	0.08963	2886
Mgrn1	A_51_P442402	NM_029657	mahogunin, ring finger 1	-1.022	82.34	0.98109	38726	P	-1.003	49.48	0.96902	12736
Pqbp1	A_51_P135322	NM_019478	polyglutamine binding protein 1	-1.022	82.34	0.97601	38073	P	-1.055	36.07	0.25338	5705
Rabl4	A_51_P474422	NM_025931	RAB, member of RAS oncogene family-lik	-1.022	82.34	0.98173	38970	P	1.022	38.4	0.65581	9929
Sf3a2	A_51_P389785	NM_013651	splicing factor 3a, subunit 2	-1.022	82.34	0.98118	38811	P	1.054	19.02	0.23333	5405
Tbl3	A_52_P510771	NM_145396	transducin (beta)-like 3	-1.022	82.34	0.97042	37460	P	1.01	42.43	0.86371	11715
Atoh1	A_51_P383704	NM_007500	atonal homolog 1 (Drosophila)	-1.024	81.02	0.96973	31330	M	1.195	8.32	0.23778	5458
Bag5	A_51_P216315	NM_027404	BCL2-associated athanogene 5	-1.024	82.34	0.97199	37642	P	-1.009	49.48	0.9219	12281
Edg6	A_51_P307944	NM_010102	endothelial differentiation, G-protein-cou	-1.024	81.02	0.9688	31292	M	-1.044	45.68	0.64784	9864
Gas6	A_51_P172054	NM_019521	growth arrest specific 6	-1.024	82.34	0.98636	26403	M	1.352	3.82	0.13472	3761
Hsdl1	A_51_P396297	NM_175185	hydroxysteroid dehydrogenase like 1	-1.024	82.34	0.97483	37944	P	-1.03	46.3	0.56138	9124
Leprel2	A_51_P149699	NM_013534	leprecan-like 2	-1.024	82.34	0.98157	38906	P	-1.017	49	0.69502	10278
Rab4a	A_51_P282883	NM_009003	RAB4A, member RAS oncogene family	-1.024	82.34	0.98165	38917	P	1.045	25.31	0.30885	6427
Sez6l2	A_51_P369154	NM_144926	seizure related 6 homolog like 2	-1.024	75.14	0.98547	29308	M	1.031	36.07	0.64243	9821
Snai2	A_51_P305547	NM_011415	snail homolog 2 (Drosophila)	-1.024	82.34	0.98109	38753	P	-1.027	46.3	0.52827	8822
2210013K02Rik	A_51_P168745	NM_023712	RIKEN cDNA 2210013K02 gene	-1.025	82.34	0.97964	38490	P	-1.057	33.49	0.21655	5148
BC012278	A_51_P417861	NM_146231	cDNA sequence BC012278	-1.025	82.34	0.96647	37146	P	1.036	30.75	0.53265	8870
Gatm	A_51_P461319	NM_025961	glycine amidinotransferase (L-arginine:gly	-1.025	79.26	0.98109	31984	P	1.094	19.02	0.36527	7102
Mal2	A_51_P353252	NM_178920	mal, T-cell differentiation protein 2	-1.025	82.34	0.97949	38452	P	-1.035	46.85	0.69459	10274
Ndufs3	A_51_P395014	NM_026688	NADH dehydrogenase (ubiquinone) Fe-S	-1.025	82.34	0.98163	26256	M	1.093	13.58	0.18638	4676
Psme1	A_51_P101196	NM_011189	proteasome (prosome, macropain) 28 su	-1.025	82.34	0.97391	37871	P	-1.181	4.63	0.11894	3466
1190005P17Rik	A_52_P139478	NM_025431	RIKEN cDNA 1190005P17 gene	-1.026	82.34	0.98127	38832	P	1	42.43	0.99465	13011
Fkbp8	A_51_P220739	NM_010223	FK506 binding protein 8	-1.026	81.02	0.95942	36340	P	-1.129	3.01	0.03429	1318
Mrps18a	A_51_P275083	NM_026768	mitochondrial ribosomal protein S18A	-1.026	81.02	0.95883	36299	P	1.094	8.32	0.07325	2484

Plxnd1	A_52_P472319	AK147513	plexin D1	-1.026	82.34	0.97111	37523	P	-1.067	36.07	0.34986	6873
Rabl2a	A_52_P554007	NM_026817	RAB, member of RAS oncogene family-like	-1.026	82.34	0.96876	37346	P	1.059	25.31	0.39743	7493
Rph3al	A_52_P396401	NM_029548	rabphilin 3A-like (without C2 domains)	-1.026	82.34	0.96778	37257	P	-1.035	46.85	0.65776	9953
Sfrs16	A_52_P19016	NM_016680	splicing factor, arginine/serine-rich 16 (su	-1.026	82.34	0.9824	39043	P	-1.05	38.4	0.29524	6277
5830454D03Rik	A_51_P176387	AK077784	RIKEN cDNA 5830454D03 gene	-1.027	81.02	0.96369	36789	P	1.17	8.32	0.19014	4723
Adipoq	A_51_P458451	NM_009605	adiponectin, C1Q and collagen domain co	-1.027	81.02	0.95593	35942	P	1.036	30.75	0.48668	8404
BC057593	A_52_P391058	NM_001045559	RIKEN cDNA C920016K16 gene	-1.027	81.02	0.95986	36380	P	-1.158	3.01	0.04817	1801
D10Wsu52e	A_51_P223720	NM_145422	DNA segment, Chr 10, Wayne State Unive	-1.027	82.34	0.97328	37789	P	-1.093	25.31	0.26714	5905
Gstm5	A_51_P260169	NM_010360	glutathione S-transferase, mu 5	-1.027	81.02	0.96115	36490	P	-1.155	1.58	0.02236	944
Ntn1	A_51_P147123	NM_008744	netrin 1	-1.027	79.26	0.97419	28777	M	1.03	33.49	0.53987	8945
Rpl18	A_52_P436621	NM_009077	ribosomal protein L18	-1.027	82.34	0.97644	26000	M	-1.152	8.32	0.14104	3864
Srf	A_51_P100289	NM_020493	serum response factor	-1.027	82.34	0.98413	39182	P	1.017	40.63	0.71389	10437
Top3a	A_51_P203451	NM_009410	topoisomerase (DNA) III alpha	-1.027	82.34	0.97199	37647	P	1.097	9.71	0.11075	3282
Traf2	A_51_P270819	NM_009422	Tnf receptor-associated factor 2	-1.027	82.34	0.96778	37253	P	-1.091	11.33	0.08772	2833
Zfp598	A_51_P329855	NM_183149	zinc finger protein 598	-1.027	81.02	0.96504	36980	P	1.003	42.43	0.94339	12514
Adamts16	A_52_P424231	NM_172053	a disintegrin-like and metallopetidase (rep	-1.028	79.26	0.95928	33477	M	1.003	42.43	0.94253	12506
Dpm2	A_52_P80444	NM_010073	dolichol-phosphate (beta-D) mannosyltra	-1.028	81.02	0.96099	36480	P	-1.019	49.39	0.735	10626
Eif3s9	A_52_P414692	NM_133916	eukaryotic translation initiation factor 3, s	-1.028	81.02	0.9618	36640	P	-1.108	6.98	0.06763	2354
Evl	A_51_P433467	NM_007965	Ena-vasodilator stimulated phosphoprote	-1.028	82.34	0.98078	26182	M	1.188	2.53	0.01584	684
Gpsm1	A_51_P386585	NM_153410	G-protein signalling modulator 1 (AGS3-lik	-1.028	81.02	0.96103	36486	P	-1.004	49.48	0.96283	12689
Pnrc1	A_52_P619820	NM_001033225	proline-rich nuclear receptor coactivator 1	-1.028	79.26	0.97194	28696	M	1.369	0.35	0.00731	246
Ptdss1	A_51_P442053	NM_008959	phosphatidylserine synthase 1	-1.028	82.34	0.97964	38491	P	-1.045	43.15	0.41566	7683
Rplp2	A_52_P134382	NM_026020	ribosomal protein, large P2	-1.028	82.34	0.98109	26206	M	1.042	30.75	0.55731	9084
Echs1	A_51_P409039	NM_053119	enoyl Coenzyme A hydratase, short chain,	-1.029	82.34	0.97862	26073	M	1.042	30.75	0.49031	8435
Mcrs1	A_52_P682450	NM_016766	microspherule protein 1	-1.029	82.34	0.97618	38102	P	1.034	33.49	0.58051	9261
Mrpl24	A_51_P203597	NM_026591	mitochondrial ribosomal protein L24	-1.029	84.22	0.97767	28956	M	1.024	40.63	0.81995	11355
Pex6	A_52_P656565	NM_145488	peroxisomal biogenesis factor 6	-1.029	82.34	0.97197	37629	P	-1.017	49.48	0.88711	11933
Rhbdf1	A_52_P141322	NM_010117	rhomboid family 1 (Drosophila)	-1.029	82.34	0.96558	37049	P	1.103	8.32	0.07728	2579
Sf3b2	A_51_P280158	NM_030109	splicing factor 3b, subunit 2	-1.029	82.34	0.97035	37438	P	1.093	13.58	0.20389	4950
Sri	A_51_P489313	NM_025618	sorcin	-1.029	81.02	0.96091	36460	P	-1.032	45.68	0.54981	9020
Gm587	A_52_P269445	NM_001009950	gene model 587, (NCBI)	-1.03	82.34	0.97925	38430	P	1.069	28.13	0.61361	9562
Wdr45	A_51_P139069	NM_172372	WD repeat domain 45	-1.03	82.34	0.98078	38618	P	-1.101	8.32	0.07021	2401
6330409N04Rik	A_51_P468742	NM_025697	RIKEN cDNA 6330409N04 gene	-1.031	81.02	0.95609	36021	P	1.028	36.07	0.616	9588
AA673488	A_51_P218833	AK164438	expressed sequence AA673488	-1.031	81.02	0.96442	36829	P	1.004	42.43	0.94212	12501
Copb1	A_51_P160113	NM_033370	coatomer protein complex, subunit beta 1	-1.031	81.02	0.96163	36539	P	1.156	5.75	0.0571	2062
Eomes	A_51_P332309	NM_010136	eomesodermin homolog (Xenopus laevis)	-1.031	82.34	0.98037	31866	M	1.138	3.82	0.02835	1155
Lgals3bp	A_51_P359636	NM_011150	lectin, galactoside-binding, soluble, 3 bind	-1.031	82.34	0.98202	26292	M	-1.219	1.62	0.05496	2005
Lrp6	A_51_P169401	NM_008514	low density lipoprotein receptor-related p	-1.031	82.34	0.97767	38252	P	1.124	16.2	0.44678	7979
Usp5	A_51_P450632	NM_013700	ubiquitin specific peptidase 5 (isopeptidas	-1.031	81.02	0.96482	36876	P	1.157	3.82	0.03242	1274
Adsl	A_51_P269320	NM_009634	adenylosuccinate lyase 1	-1.032	81.02	0.96549	37027	P	1.077	16.2	0.24779	5612
BC021438	A_51_P112644	NM_145416	cDNA sequence BC021438	-1.032	81.02	0.95914	36309	P	-1.034	43.75	0.41266	7646
Bhlhb2	A_51_P272553	NM_011498	basic helix-loop-helix domain containing,	-1.032	81.02	0.9648	36875	P	-1.059	42.43	0.47734	8285
Cdh1	A_51_P137336	NM_009864	cadherin 1	-1.032	81.02	0.9615	36517	P	1.289	1.17	0.01251	516
Lgals9	A_51_P500813	NM_010708	lectin, galactose binding, soluble 9	-1.032	82.34	0.98238	39036	P	1.041	28.13	0.38851	7380
Oatl1	A_51_P429284	NM_172478	TBC1 domain family, member 25	-1.032	79.26	0.94301	34841	P	1	49.48	0.99824	13040
Thtpa	A_52_P674357	NM_153083	thiamine triphosphatase	-1.032	81.02	0.95071	35499	P	-1.229	0.56	0.02396	892
Ubtd1	A_51_P369371	NM_145500	ubiquitin domain containing 1	-1.032	82.34	0.97329	37793	P	-1.088	28.13	0.26315	5855
Bcap31	A_51_P440399	NM_012060	B-cell receptor-associated protein 31	-1.033	81.02	0.96143	36514	P	1.139	6.98	0.06242	2209
Gypc	A_51_P191199	NM_001048207	glycophorin C	-1.033	81.02	0.96504	36954	P	1.094	11.33	0.15511	4136
Nrl	A_52_P620355	NM_008736	neural retina leucine zipper gene	-1.033		0.98094	19461	A	1.081	11.33	0.11932	3471
Coro1b	A_51_P109888	NM_011778	coronin, actin binding protein 1B	-1.034	79.26	0.9371	34352	P	-1.048	42.43	0.39103	7409
Eif5a	A_51_P120201	NM_181582	eukaryotic translation initiation factor 5A	-1.034	81.02	0.95986	36370	P	1.11	11.33	0.21662	5151
Ftcd	A_51_P413740	NM_080845	formiminotransferase cyclodeaminase	-1.034		0.97199	22693	A	-1.035	47.43	0.73658	10646

G6pd2	A_51_P353735	NM_019468	glucose-6-phosphate dehydrogenase 2	-1.034	81.02	0.96005	36416	P	1.08	22.1	0.43031	7827
Pou3f2	A_51_P487010	NM_008899	POU domain, class 3, transcription factor	-1.034	81.02	0.94347	32365	M	1.02	38.4	0.67749	10109
Rheb	A_51_P322334	NM_053075	RAS-homolog enriched in brain	-1.034	82.34	0.97199	37656	P	1.073	13.58	0.15393	4115
2610003J06Rik	A_51_P434776	NM_028101	RIKEN cDNA 2610003J06 gene	-1.035	81.02	0.95215	35749	P	1.016	42.43	0.81758	11342
6620401K05Rik	A_51_P104527	NM_172774	RIKEN cDNA 6620401K05 gene	-1.035	82.34	0.97364	37848	P	1.087	9.71	0.09324	2967
Foxo1	A_51_P138044	NM_019739	forkhead box O1	-1.035	81.02	0.95046	35475	P	1.04	30.75	0.54239	8966
Gnpnat1	A_51_P219542	NM_019425	glucosamine-phosphate N-acetyltransfera	-1.035	81.02	0.96415	25492	M	-1.207	0.75	0.01266	533
Gt(ROSA)26Sor	A_51_P426919	U83174	gene trap ROSA 26, Philippe Soriano	-1.035	81.02	0.94583	35052	P	-1.001	49.48	0.99031	12988
Myef2	A_51_P281844	AK129336	myelin basic protein expression factor 2,	-1.035	81.02	0.96219	25431	M	-1.019	49	0.69769	10300
Psma6	A_51_P428364	NM_011968	proteasome (prosome, macropain) subun	-1.035	81.02	0.94665	35135	P	1.001	42.43	0.97774	12820
Stra13	A_52_P124429	NM_016665	stimulated by retinoic acid 13	-1.035	81.02	0.96005	36401	P	-1.117	8.32	0.09447	2990
AI480556	A_52_P79038	NM_001008422	expressed sequence AI480556	-1.036	82.34	0.97371	37852	P	1.004	42.43	0.95685	12635
Ap2s1	A_52_P128095	NM_198613	adaptor-related protein complex 2, sigma	-1.036	81.02	0.96163	36548	P	1.096	11.33	0.11575	3392
Capn10	A_51_P370252	NM_011796	calpain 10	-1.036	81.02	0.96573	37060	P	-1.047	40.63	0.30774	6413
Chst10	A_51_P445562	NM_145142	carbohydrate sulfotransferase 10	-1.036	81.02	0.95139	35629	P	1.03	33.49	0.50642	8646
Eif2b3	A_51_P322056	AK047344	eukaryotic translation initiation factor 2B,	-1.036	81.02	0.94357	34879	P	1.104	16.2	0.38315	7318
Grina	A_51_P200083	NM_023168	glutamate receptor, ionotropic, N-methyl	-1.036	81.02	0.95609	35977	P	-1.065	30.75	0.21892	5188
Lass2	A_51_P517381	NM_029789	longevity assurance homolog 2 (S. cerevis	-1.036	79.26	0.93023	33849	P	1.092	16.2	0.29335	6260
Mgat2	A_51_P150521	NM_146035	mannoside acetylglucosaminyltransferase	-1.036	79.26	0.93621	34286	P	1.02	38.4	0.67914	10131
Nrg3	A_51_P177071	NM_008734	neuregulin 3	-1.036	81.02	0.96573	37076	P	1.016	42.43	0.81115	11288
S100a6	A_51_P281089	NM_011313	S100 calcium binding protein A6 (calcycli	-1.036	83.36	0.9879	39615	P	1.022	40.63	0.82428	11403
Tmed1	A_51_P221852	NM_010744	transmembrane emp24 domain containi	-1.036	81.02	0.94301	34840	P	1.035	30.75	0.47523	8262
Usp22	A_52_P413623	NM_001004143	ubiquitin specific peptidase 22	-1.036	81.02	0.95609	36014	P	1.241	2.53	0.0263	1083
Usp28	A_51_P216595	NM_175482	ubiquitin specific peptidase 28	-1.036	82.34	0.97227	37734	P	1.192	2.53	0.01945	818
1810009K13Rik	A_51_P494122	NM_025462	RIKEN cDNA 1810009K13 gene	-1.037	82.34	0.97483	37962	P	-1.13	9.71	0.13197	3710
2610029I01Rik	A_51_P358243	AK154853	RIKEN cDNA 2610029I01 gene	-1.037	81.02	0.95861	36282	P	-1.13	5.75	0.0768	2569
4833408C14Rik	A_51_P118664	AK014663	RIKEN cDNA 4833408C14 gene	-1.037	81.02	0.95657	36051	P	1.058	25.31	0.45693	8070
Adrm1	A_51_P214631	NM_019822	adhesion regulating molecule 1	-1.037	82.34	0.98109	38804	P	-1.006	49.48	0.93057	12394
Brms1	A_51_P154997	NM_134155	breast cancer metastasis-suppressor 1	-1.037	81.02	0.95129	35602	P	-1.275	0.51	0.0067	211
Foxf1a	A_51_P262111	NM_010426	forkhead box F1a	-1.037	81.02	0.9516	30256	M	-1.062	38.4	0.33584	6743
Glis2	A_51_P366986	NM_031184	GLIS family zinc finger 2	-1.037	79.26	0.93621	34278	P	1.013	42.43	0.83037	11455
Hsd3b4	A_51_P352005	NM_008294	hydroxy-delta-5-steroid dehydrogenase, 3	-1.037	79.26	0.93998	29652	M	-1.037	44.4	0.44272	7942
Mapk14	A_51_P325343	NM_011951	mitogen activated protein kinase 14	-1.037	81.02	0.95609	35952	P	1.087	9.71	0.08145	2694
Nr1h2	A_51_P400203	NM_009473	nuclear receptor subfamily 1, group H, m	-1.037	79.26	0.93985	34555	P	1.01	42.43	0.82462	11407
Pold2	A_51_P342707	NM_008894	polymerase (DNA directed), delta 2, regul	-1.037	81.02	0.96163	36558	P	1.053	22.1	0.25373	5714
Ranbp9	A_51_P106191	NM_019930	RAN binding protein 9	-1.037	81.02	0.9493	35378	P	1.131	6.98	0.07325	2486
Relb	A_51_P389751	NM_009046	avian reticuloendotheliosis viral (v-rel) on	-1.037	81.02	0.94386	34912	P	-1.087	30.75	0.34111	6780
Xrcc1	A_51_P343900	NM_009532	X-ray repair complementing defective rep	-1.037	82.34	0.96703	37190	P	-1.01	49.48	0.83258	11481
Aurka	A_51_P150912	NM_011497	aurora kinase A	-1.038	79.26	0.93727	34370	P	1.032	30.75	0.47319	8229
Fkrp	A_51_P259879	NM_173430	fukutin related protein	-1.038	81.02	0.9493	35354	P	1.052	28.13	0.50522	8631
Gpaa1	A_51_P273203	NM_010331	GPI anchor attachment protein 1	-1.038	81.02	0.95184	35725	P	-1.051	40.63	0.30954	6435
Igfbp2	A_51_P423308	NM_008342	insulin-like growth factor binding protein	-1.038	79.26	0.93456	34162	P	-1.007	49.48	0.89368	12000
Ube2s	A_51_P188782	NM_133777	ubiquitin-conjugating enzyme E2S	-1.038	81.02	0.94976	35420	P	-1.166	1.62	0.02966	1180
Usp39	A_52_P150565	NM_138592	ubiquitin specific peptidase 39	-1.038	81.02	0.95713	36093	P	-1.094	19.02	0.17322	4428
Polr2j	A_51_P326086	NM_011293	polymerase (RNA) II (DNA directed) polyp	-1.04	81.02	0.9666	37148	P	-1.004	49.48	0.95699	12637
Slc25a1	A_51_P350922	NM_153150	solute carrier family 25 (mitochondrial ca	-1.04	82.34	0.97218	37720	P	1.004	42.43	0.9352	12434
Smarcb1	A_51_P284898	NM_011418	SWI/SNF related, matrix associated, actin	-1.04	81.02	0.95122	35574	P	-1.075	16.2	0.11714	3423
Txn1	A_51_P424499	NM_011660	thioredoxin 1	-1.04	75.14	0.96004	33537	P	-1.056	42.43	0.45574	8054
2810453I06Rik	A_52_P652878	NM_026050	RIKEN cDNA 2810453I06 gene	-1.041	81.02	0.9493	35372	P	1.137	5.75	0.04332	1623
5430432M24Rik	A_52_P684050	NM_028666	RIKEN cDNA 5430432M24 gene	-1.041	81.02	0.96091	36462	P	1.134	9.71	0.14826	4012
Btbd12	A_51_P490296	NM_177472	BTB (POZ) domain containing 12	-1.041	81.02	0.95129	35601	P	1.025	33.49	0.551	9041
Myoc	A_51_P375558	NM_010865	myocilin	-1.041	81.02	0.93965	34542	M	1.101	8.32	0.0728	2475
Srm	A_51_P300709	NM_009272	spermidine synthase	-1.041	81.02	0.96573	37086	P	-1.048	40.63	0.30493	6385

Tmed9	A_51_P262878	NM_026211	transmembrane emp24 protein transport	-1.041	79.26	0.95676	25164	M	1.048	25.31	0.38611	7345
Trpm7	A_51_P501396	NM_021450	transient receptor potential cation chann	-1.041	81.02	0.94783	35269	P	-1.135	9.71	0.13857	3811
Ube1dc1	A_51_P403693	NM_025692	ubiquitin-activating enzyme E1-domain co	-1.041	81.02	0.9516	35689	P	-1.056	43.15	0.51178	8689
1110038F14Rik	A_51_P121447	NM_054099	RIKEN cDNA 1110038F14 gene	-1.042	81.02	0.95088	35517	P	-1.081	30.75	0.30108	6338
1700019E19Rik	A_51_P376883	NM_029601	RIKEN cDNA 1700019E19 gene	-1.042	81.02	0.9617	36599	P	-1.018	49.39	0.73148	10583
Akap11	A_52_P244964	XM_001002157	A kinase (PRKA) anchor protein 11	-1.042	81.02	0.95838	25245	M	1.106	13.58	0.22126	5223
Cxcl5	A_52_P295432	NM_009141	chemokine (C-X-C motif) ligand 5	-1.042		0.98815	26461	A	-1.082	30.75	0.27226	5988
Dkk2	A_51_P241068	NM_020265	dickkopf homolog 2 (Xenopus laevis)	-1.042	81.02	0.96335	36775	M	1.223	2.53	0.02114	898
Ext1	A_51_P416689	NM_010162	exostoses (multiple) 1	-1.042	79.26	0.92159	33167	P	1.062	16.2	0.20651	4991
Haghl	A_51_P292073	NM_026897	hydroxyacylglutathione hydrolase-like	-1.042	81.02	0.95799	36196	P	1.045	33.49	0.66607	10010
Hdac5	A_51_P278893	NM_001077696	histone deacetylase 5	-1.042	81.02	0.94729	35205	P	-1.139	4.63	0.06694	2342
Id3	A_51_P380178	NM_008321	inhibitor of DNA binding 3	-1.042	81.02	0.96489	36907	P	-1.005	49.48	0.9227	12294
Lrfn4	A_51_P467953	NM_153388	leucine rich repeat and fibronectin type II	-1.042	82.34	0.97719	38212	P	-1.235	0.51	0.00802	294
Myl6	A_51_P243727	NM_010860	myosin, light polypeptide 6, alkali, smootl	-1.042	77.44	0.94912	24812	M	-1.087	19.02	0.14717	3984
Srebf1	A_51_P401921	NM_011480	sterol regulatory element binding factor 1	-1.042	82.34	0.96814	37320	P	-1.03	46.85	0.60107	9462
Ap4s1	A_51_P198273	NM_021710	adaptor-related protein complex AP-4, sig	-1.043	81.02	0.93953	34527	P	-1.138	3.01	0.03728	1417
BC051227	A_51_P483311	NM_183170	cDNA sequence BC051227	-1.043	81.02	0.95392	35825	P	-1.293	1.18	0.06177	2185
Epn1	A_52_P323074	NM_010147	epsin 1	-1.043	77.44	0.93023	29037	M	1.105	6.98	0.05545	2021
Ggnbp2	A_51_P225630	NM_153144	gametogenetin binding protein 2	-1.043	79.26	0.93771	34397	P	1.146	3.82	0.03237	1270
Mlf2	A_51_P361563	NM_145385	myeloid leukemia factor 2	-1.043	81.02	0.94751	35226	P	1.142	9.71	0.18428	4645
Yaf2	A_51_P292754	NM_024189	YY1 associated factor 2	-1.043	81.02	0.93874	34494	P	1.034	30.75	0.42824	7802
4930404N11Rik	A_51_P279898	AK008872	RIKEN cDNA 4930404N11 gene	-1.044	72.2	0.96115	25237	M	1.037	28.13	0.38996	7395
AA407659	A_52_P205789	NM_175352	expressed sequence AA407659	-1.044	77.44	0.909	31780	P	-1.025	47.43	0.61332	9553
Dcps	A_51_P275953	NM_027030	decapping enzyme, scavenger	-1.044	79.26	0.93724	34362	P	1.018	40.63	0.71063	10406
Ddx47	A_51_P491470	NM_026360	DEAD (Asp-Glu-Ala-Asp) box polypeptide	-1.044	81.02	0.94506	35023	P	1.073	16.2	0.23295	5396
Fnta	A_51_P112116	NM_008033	farnesyltransferase, CAAX box, alpha	-1.044	79.26	0.93087	33911	P	1.134	5.75	0.04387	1643
Rkhd1	A_52_P568165	NM_198615	ring finger (C3HC4 type) and KH domain c	-1.044	79.26	0.92592	33526	P	-1.18	1.58	0.0291	1172
Wnt7b	A_52_P231691	NM_009528	wingless-related MMTV integration site 7	-1.044	77.44	0.91079	32019	P	1.099	11.33	0.14687	3979
2210409B22Rik	A_52_P281747	AK151977	solute carrier family 44, member 1	-1.045	79.26	0.92446	33410	P	1.029	38.4	0.72867	10561
Cmas	A_51_P343309	NM_009908	cytidine monophospho-N-acetylneuramir	-1.045	79.26	0.93771	34395	P	-1.058	42.43	0.44002	7925
Irf7	A_51_P421876	NM_016850	interferon regulatory factor 7	-1.045	81.02	0.94234	34740	P	1.111	6.98	0.05028	1862
Pdxp	A_52_P609120	NM_020271	pyridoxal (pyridoxine, vitamin B6) phosph	-1.045	81.02	0.95043	35457	P	1.075	13.58	0.16382	4281
Polr2d	A_51_P419571	NM_027101	polymerase (RNA) II (DNA directed) polyp	-1.045	81.02	0.9493	35394	P	-1.016	49.48	0.88843	11947
Prx	A_52_P315837	NM_019412	periaxin	-1.045	75.14	0.90625	31523	P	-1.123	4.63	0.04938	1824
Trim33	A_51_P478279	NM_053170	tripartite motif protein 33	-1.045	77.44	0.91354	32384	P	-1.267	0.51	0.0067	204
Ube2g1	A_52_P626232	NM_025985	ubiquitin-conjugating enzyme E2G 1 (UBC	-1.045	79.26	0.93633	34297	P	-1.07	36.07	0.37664	7238
2310022A10Rik	A_51_P507172	NM_175107	RIKEN cDNA 2310022A10 gene	-1.046	81.02	0.96078	36457	P	1.107	9.71	0.10041	3113
Arpc1a	A_51_P191586	NM_019767	actin related protein 2/3 complex, subuni	-1.046	77.44	0.90634	31532	P	-1.062	30.75	0.21221	5076
Banf1	A_51_P314019	NM_001038231	barrier to autointegration factor 1	-1.046	81.02	0.95839	36239	P	1.009	42.43	0.9227	12297
Gpr56	A_52_P317393	NM_018882	G protein-coupled receptor 56	-1.046	77.44	0.96798	31262	P	1.116	8.32	0.09171	2938
Npat	A_51_P463784	XM_146900	nuclear protein in the AT region	-1.046	81.02	0.9503	35446	P	-1.004	49.48	0.94882	12570
Pcnp	A_51_P210877	NM_001024622	PEST proteolytic signal containing nuclear	-1.046	79.26	0.9493	24831	M	1.093	22.1	0.49651	8533
Zfp623	A_51_P162760	NM_030199	zinc finger protein 623	-1.046	81.02	0.95158	35670	P	1.02	36.07	0.82493	10285
Arf5	A_51_P381801	NM_007480	ADP-ribosylation factor 5	-1.047	77.44	0.91045	31997	P	1.092	11.33	0.13414	3750
Entpd7	A_52_P297741	NM_053103	ectonucleoside triphosphate diphosphoh	-1.047	79.26	0.92948	33720	P	-1.148	3.01	0.03793	1438
Ifitm3	A_51_P128876	NM_025378	interferon induced transmembrane prote	-1.047	81.02	0.94841	35290	P	1.061	28.13	0.59991	9448
Mtmr6	A_51_P205481	NM_144843	myotubularin related protein 6	-1.047	79.26	0.92949	26800	M	-1.144	13.58	0.22891	5341
Ogfr	A_52_P272217	NM_031373	opioid growth factor receptor	-1.047	79.26	0.91949	32984	P	-1.06	33.49	0.24127	5519
Pacs1	A_52_P417620	NM_153129	phosphofurin acidic cluster sorting protei	-1.047	81.02	0.9617	36621	P	1.019	38.4	0.67146	10065
Pdia5	A_52_P297642	NM_028295	protein disulfide isomerase associated 5	-1.047	81.02	0.95123	35582	P	-1.001	49.48	0.98918	12976
Tars	A_51_P479052	NM_033074	threonyl-tRNA synthetase	-1.047	79.26	0.91813	32837	P	1.064	16.2	0.16799	4338
D14Ertd449e	A_51_P222453	NM_025311	DNA segment, Chr 14, ERATO Doi 449, exp	-1.048	81.02	0.95676	36068	P	1.055	22.1	0.32456	6612
Phlda1	A_51_P195958	NM_009344	pleckstrin homology-like domain, family A	-1.048	81.02	0.968	37315	P	1.208	6.98	0.16996	4382

Taf12	A_51_P202014	NM_025579	TAF12 RNA polymerase II, TATA box bindir	-1.048	81.02	0.94386	34920	P	1.067	28.13	0.56114	9119
Arl2bp	A_51_P396752	NM_024191	ADP-ribosylation factor-like 2 binding pro	-1.049	77.44	0.90638	31534	P	1.079	16.2	0.26234	5845
Ifngr1	A_51_P391445	NM_010511	interferon gamma receptor 1	-1.049	79.26	0.95262	24987	M	1.053	28.13	0.46065	8113
Jmjd3	A_51_P122017	NM_001017426	jumonji domain containing 3	-1.049		0.93495	26957	A	1.104	5.75	0.05215	1924
Lrch4	A_52_P38964	AK131167	mSin3A-binding protein	-1.049	81.02	0.96634	37133	P	1	42.43	0.99863	13042
Acat1	A_51_P319449	NM_144784	acetyl-Coenzyme A acetyltransferase 1	-1.05	79.26	0.93757	34387	P	-1.051	42.43	0.40041	7519
Arhgdia	A_52_P419405	NM_133796	Rho GDP dissociation inhibitor (GDI) alpha	-1.05	81.02	0.96143	36511	P	-1.044	43.75	0.45157	8010
Bccip	A_51_P443475	NM_025392	BRCA2 and CDKN1A interacting protein	-1.05	79.26	0.91841	32876	P	1.027	36.07	0.6737	10085
Bsg	A_51_P329441	NM_009768	basigin	-1.05	79.26	0.91577	32664	P	-1.191	1.18	0.01749	748
Itlna	A_51_P147987	NM_010584	intelectin a	-1.05	83.95	0.99427	35590	P	1.056	22.1	0.28574	6165
Mrpl12	A_51_P143142	NM_027204	mitochondrial ribosomal protein L12	-1.05	77.44	0.89437	30614	P	-1.039	44.4	0.49414	8488
Mrpl37	A_51_P256304	NM_025500	mitochondrial ribosomal protein L37	-1.05	77.44	0.90445	31388	P	-1.121	11.33	0.14657	3976
Mrpl53	A_51_P385635	NM_026744	mitochondrial ribosomal protein L53	-1.05	79.26	0.91144	32104	P	1.031	30.75	0.47895	8300
Pnrc2	A_51_P225506	NM_026383	proline-rich nuclear receptor coactivator	-1.05	81.02	0.96876	25706	M	1.123	13.58	0.28325	6123
Tacstd2	A_51_P257938	NM_020047	tumor-associated calcium signal transduc	-1.05	77.44	0.90804	31674	P	1.067	16.2	0.21165	5063
2010004M13Rik	A_51_P333831	AK008102	RIKEN cDNA 2010004M13 gene	-1.052	79.26	0.93291	34021	P	-1.078	22.1	0.15924	4199
Adcy8	A_51_P303061	NM_009623	adenylate cyclase 8	-1.052	77.44	0.9138	28013	M	1.051	33.49	0.70826	10392
D11Bwg0434e	A_51_P127915	NM_173742	DNA segment, Chr 11, Brigham & Womer	-1.052	81.02	0.95569	25087	M	-1.061	33.49	0.24666	5601
Ehd4	A_51_P455807	NM_133838	EH-domain containing 4	-1.052	79.26	0.91813	32842	P	-1.073	28.13	0.21936	5198
Rfc2	A_52_P981680	NM_020022	replication factor C (activator 1) 2	-1.052	79.26	0.9353	34216	P	1.055	22.1	0.29293	6253
Rhog	A_52_P263068	NM_019566	ras homolog gene family, member G	-1.052	81.02	0.94783	35254	P	1.064	13.58	0.16269	4267
Stub1	A_51_P101635	NM_019719	STIP1 homology and U-Box containing pro	-1.052	79.26	0.91249	32259	P	-1.126	11.33	0.16273	4269
Tm9sf4	A_52_P198993	NM_133847	transmembrane 9 superfamily protein me	-1.052	81.02	0.95728	36110	P	1.105	8.32	0.06325	2237
2410004B18Rik	A_51_P325592	NM_025555	RIKEN cDNA 2410004B18 gene	-1.053	79.26	0.91363	32393	P	1.038	30.75	0.52265	8774
2510012J08Rik	A_52_P482849	XM_618787	RIKEN cDNA 2510012J08 gene	-1.053	77.44	0.9078	31615	P	1.088	9.71	0.08255	2714
4930570C03Rik	A_52_P528505	NM_026353	RIKEN cDNA 4930570C03 gene	-1.053	79.26	0.90919	31810	P	-1.053	36.07	0.2418	5527
Edg3	A_51_P137523	NM_010101	endothelial differentiation, sphingolipid G	-1.053	77.44	0.91462	30180	M	-1.03	48.7	0.79126	11102
Golga7	A_51_P478942	NM_020585	golgi autoantigen, golgin subfamily a, 7	-1.053	77.44	0.90577	31493	P	-1.118	9.71	0.11507	3380
Guca1a	A_51_P207751	NM_008189	guanylate cyclase activator 1a (retina)	-1.053	79.26	0.90966	31907	P	1.005	42.43	0.93138	12399
H1f0	A_52_P550932	NM_008197	H1 histone family, member 0	-1.053	79.26	0.9207	33109	P	1.083	16.2	0.24738	5608
Hnrph1	A_51_P299195	NM_021510	heterogeneous nuclear ribonucleoprotein	-1.053	79.26	0.91249	32248	P	1.11	11.33	0.21523	5126
Mark2	A_51_P414779	NM_007928	MAP/microtubule affinity-regulating kinas	-1.053	77.44	0.90331	31280	P	1.004	42.43	0.94788	12564
3300001P08Rik	A_51_P133737	NM_026313	RIKEN cDNA 3300001P08 gene	-1.054	81.02	0.96731	25657	M	1.159	8.32	0.14256	3895
Dvl2	A_51_P113106	NM_007888	dishevelled 2, dsh homolog (Drosophila)	-1.054	79.26	0.93874	34487	P	1.075	19.02	0.28325	6124
Gpr81	A_51_P294059	NM_175520	G protein-coupled receptor 81	-1.054	77.44	0.89924	30945	P	1.013	42.43	0.80819	11257
Ilkap	A_52_P464193	NM_023343	integrin-linked kinase-associated serine/t	-1.054	77.44	0.89324	30515	P	1.004	42.43	0.9532	12608
Pdlim3	A_52_P579531	NM_016798	PDZ and LIM domain 3	-1.054	77.44	0.89651	30745	P	1.013	42.43	0.82045	11363
Per1	A_52_P79889	NM_011065	period homolog 1 (Drosophila)	-1.054	82.34	0.9703	37431	P	-1.025	47.43	0.62776	9696
Trf	A_51_P362638	NM_133977	transferrin	-1.054	81.02	0.96115	36489	P	1.006	42.43	0.9231	12320
Zfp263	A_51_P272360	NM_148924	zinc finger protein 263	-1.054	79.26	0.92446	33405	P	1.087	19.02	0.44179	7935
Add3	A_51_P223144	NM_013758	adducin 3 (gamma)	-1.055	75.14	0.88417	29920	P	1.064	22.1	0.38233	7308
Casp1	A_51_P142861	NM_009807	caspase 1	-1.055	83.36	0.98883	39814	P	1.087	13.58	0.16632	4324
Hoxa7	A_51_P509263	NM_010455	homeo box A7	-1.055	81.02	0.95055	35483	P	1.115	8.32	0.08344	2736
Igfbp7	A_51_P472292	NM_008048	insulin-like growth factor binding protein	-1.055	77.44	0.9057	31488	P	-1.348	0.51	0.00584	105
Mmp24	A_51_P450376	AJ010262	matrix metallopeptidase 24	-1.055	77.44	0.89176	28465	M	-1.155	3.46	0.05456	1994
Rai12	A_51_P127777	NM_018740	retinoic acid induced 12	-1.055	79.26	0.93621	34291	P	1.058	22.1	0.29246	6245
Slc33a1	A_52_P551903	NM_015728	solute carrier family 33 (acetyl-CoA transp	-1.055	79.26	0.90873	31754	P	1.038	28.13	0.39224	7423
Slc39a7	A_51_P174016	NM_008202	solute carrier family 39 (zinc transporter),	-1.055	69.29	0.94635	27564	M	1.045	30.75	0.50433	8625
Alox12b	A_52_P316765	NM_009659	arachidonate 12-lipoxygenase, 12R type	-1.056		0.95466	21937	A	1.058	25.31	0.48382	8375
Arfgef1	A_52_P513439	XM_975420	ADP-ribosylation factor guanine nucleotic	-1.056	79.26	0.91409	32427	P	1.33	0.75	0.00932	340
Dpysl3	A_51_P115441	NM_009468	dihydropyrimidinase-like 3	-1.056	81.02	0.96956	37375	P	-1.213	0.75	0.0122	492
Pitpna	A_51_P466371	NM_008850	phosphatidylinositol transfer protein, alpl	-1.056	77.44	0.90087	31034	P	1.046	28.13	0.47406	8235
Ranbp1	A_51_P142465	NM_011239	RAN binding protein 1	-1.056	77.44	0.93023	24084	M	1.017	40.63	0.76551	10898

Trim23	A_51_P333292	NM_030731	tripartite motif protein 23	-1.056	79.26	0.91716	32741	P	1.083	13.58	0.13993	3854
Zfpm1	A_51_P360840	NM_009569	zinc finger protein, multitype 1	-1.056	81.02	0.96155	36524	P	1.103	9.71	0.10957	3255
Aadacl1	A_51_P369862	NM_178772	arylacetamide deacetylase-like 1	-1.057	79.26	0.90488	29423	P	1.022	38.4	0.67763	10115
Arhgap21	A_51_P481418	BC076629	Rho GTPase activating protein 21	-1.057	77.44	0.88709	30098	P	1.025	38.4	0.71415	10439
Csnk1d	A_51_P359813	NM_027874	casein kinase 1, delta	-1.057	79.26	0.92091	33130	P	1.072	22.1	0.37192	7195
Prkab1	A_52_P505346	NM_031869	protein kinase, AMP-activated, beta 1 nor	-1.057	75.14	0.87124	29005	P	1.084	13.58	0.18233	4615
Rxrg	A_51_P513311	NM_009107	retinoid X receptor gamma	-1.057	81.02	0.95921	33474	P	-1.325	0.51	0.00654	189
0610007P14Rik	A_51_P400375	NM_021446	RIKEN cDNA 0610007P14 gene	-1.058	79.26	0.93596	24313	M	-1.075	43.15	0.58699	9315
Chchd4	A_51_P254234	NM_133928	coiled-coil-helix-coiled-coil-helix domain	-1.058	77.44	0.90781	31630	P	-1.149	3.01	0.04289	1613
Fance	A_51_P476851	AK172283	Fanconi anemia, complementation group	-1.058	77.44	0.90474	31420	P	-1.081	25.31	0.18289	4623
Kif20a	A_51_P133137	NM_009004	kinesin family member 20A	-1.058	77.44	0.90285	31245	P	1.064	19.02	0.2458	5581
Prkci	A_51_P406671	NM_008857	protein kinase C, iota	-1.058	77.44	0.89303	30502	P	1.064	25.31	0.49414	8487
Sfrs9	A_51_P336691	NM_025573	splicing factor, arginine/serine rich 9	-1.058	77.44	0.90234	31211	P	1.112	9.71	0.12384	3577
Tubg1	A_51_P499864	NM_134024	tubulin, gamma 1	-1.058	77.44	0.905	31433	P	1.074	13.58	0.15044	4044
Zfp275	A_51_P286792	NM_031494	zinc finger protein 275	-1.058	75.14	0.9	27175	P	1.075	19.02	0.3303	6672
Adfp	A_51_P258150	NM_007408	adipose differentiation related protein	-1.059	77.44	0.90653	31552	P	-1.021	49	0.71493	10441
Cideb	A_52_P512365	NM_009894	cell death-inducing DNA fragmentation fa	-1.059	81.02	0.95073	35508	P	1.078	16.2	0.19554	4830
Foxh1	A_51_P203138	NM_007989	forkhead box H1	-1.059	77.44	0.90633	31529	P	1.131	4.63	0.09718	2771
Grasp	A_51_P425642	NM_019518	GRP1 (general receptor for phosphoinosit	-1.059	79.26	0.9348	34175	P	1.034	28.13	0.42446	7773
Il4i1	A_52_P410449	NM_010215	interleukin 4 induced 1	-1.059	79.26	0.91605	32697	P	-1.325	0.51	0.00584	75
Sf3a3	A_51_P297165	BC092058	splicing factor 3a, subunit 3	-1.059	77.44	0.888	30142	P	-1.04	43.75	0.45157	8008
2210412D01Rik	A_51_P293059	NM_133722	RIKEN cDNA 2210412D01 gene	-1.06	79.26	0.90183	29165	P	-1.032	46.3	0.60769	9506
8430406I07Rik	A_51_P187697	NM_028984	RIKEN cDNA 8430406I07 gene	-1.06	79.26	0.92592	33530	P	-1.16	2.04	0.03538	1371
A630047E20Rik	A_51_P213172	NM_173032	RIKEN cDNA A630047E20 gene	-1.06	77.44	0.88349	29879	P	-1.269	0.51	0.00985	367
Cdk5rap1	A_51_P193524	NM_025876	CDK5 regulatory subunit associated prote	-1.06	81.02	0.9493	35370	P	-1.07	33.49	0.30954	6436
Cops6	A_52_P667177	NM_012002	COP9 (constitutive photomorphogenic) h	-1.06	79.26	0.92552	33514	P	1.577	0.24	0.00731	264
Fbln5	A_51_P186703	AK090129		-1.06	79.26	0.91011	31964	P	-1.035	49.22	0.84081	11530
Glud1	A_51_P376258	NM_008133	glutamate dehydrogenase 1	-1.06	79.26	0.9386	34451	P	1.055	30.75	0.58844	9324
Hyal2	A_51_P284577	NM_010489	hyaluronoglucosaminidase 2	-1.06	75.14	0.86744	28687	P	-1.032	45.68	0.5077	8657
Rbm5	A_51_P234025	NM_148930	RNA binding motif protein 5	-1.06	75.14	0.86668	28633	P	1.199	2.04	0.0146	620
Sdhd	A_51_P260871	NM_025848	succinate dehydrogenase complex, subun	-1.06	77.44	0.8984	30850	P	1.135	5.75	0.04387	1644
Spata13	A_52_P305279	AK151394	spermatogenesis associated 13	-1.06	79.26	0.92592	33531	P	1.035	30.75	0.46843	8190
1810011O16Rik	A_51_P282424	NM_025456	E2F-associated phosphoprotein	-1.062	79.26	0.93689	34333	P	1.01	42.43	0.92526	12345
Casp2	A_51_P296448	NM_007610	caspase 2	-1.062	75.14	0.91577	23373	M	1.124	6.98	0.0585	2094
Cdc42ep1	A_52_P573255	NM_027219	CDC42 effector protein (Rho GTPase bind	-1.062	79.26	0.91144	32101	P	1.053	19.02	0.23298	5400
Cops3	A_51_P328014	NM_011991	COP9 (constitutive photomorphogenic) h	-1.062	79.26	0.91591	32674	P	1.103	9.71	0.09379	2979
Exoc7	A_51_P273754	NM_016857	exocyst complex component 7	-1.062	77.44	0.89919	30937	P	-1.087	33.49	0.38157	7292
Foxf2	A_51_P248865	NM_010225	forkhead box F2	-1.062	81.02	0.96778	37271	P	1.057	19.02	0.22683	5312
Tegt	A_52_P59579	NM_026669	testis enhanced gene transcript	-1.062	77.44	0.91861	23516	M	1.224	2.04	0.0155	660
AU022870	A_51_P395293	NM_177682	expressed sequence AU022870	-1.063	75.14	0.87393	29179	P	1.008	42.43	0.9013	12107
Dna2l	A_51_P190425	AK129051	DNA2 DNA replication helicase 2-like (yea	-1.063	81.02	0.94304	34849	P	-1.027	47.92	0.66534	10005
Dnajc12	A_51_P442284	NM_013888	DnaJ (Hsp40) homolog, subfamily C, mem	-1.063	75.14	0.8711	28985	P	-1.018	49.48	0.8159	11335
Etv4	A_51_P230382	NM_008815	ets variant gene 4 (E1A enhancer binding	-1.063	77.44	0.88378	29896	P	-1.069	28.13	0.20244	4936
Gak	A_51_P176185	NM_153569	cyclin G associated kinase	-1.063	79.26	0.93884	24434	M	1.175	8.32	0.1601	4217
Ilf2	A_51_P200633	AK161126	interleukin enhancer binding factor 2	-1.063	79.26	0.93938	34518	P	1.087	19.02	0.37939	7273
Rgl2	A_51_P460890	NM_009059	ral guanine nucleotide dissociation stimul	-1.063	79.26	0.92283	33272	P	1.026	36.07	0.61152	9545
Timp4	A_51_P355427	NM_080639	tissue inhibitor of metalloproteinase 4	-1.063	72.2	0.84699	27552	P	-1.003	49.48	0.94988	12588
2610307O08Rik	A_51_P240801	BC046640	RIKEN cDNA 2610307O08 gene	-1.064	81.02	0.94783	35267	P	-1.187	1.32	0.02229	940
Casc3	A_51_P513211	NM_138660	cancer susceptibility candidate 3	-1.064	77.44	0.89958	30967	P	1.105	13.58	0.26523	5876
D230005D02Rik	A_52_P529374	NM_172813	RIKEN cDNA D230005D02 gene	-1.064	79.26	0.92998	33788	P	1.042	28.13	0.37178	7189
Esam1	A_51_P448325	NM_027102	endothelial cell-specific adhesion molecu	-1.064	77.44	0.88617	30035	P	-1.197	1.18	0.0196	831
Ipo13	A_51_P365482	NM_146152	importin 13	-1.064	81.02	0.95045	35464	P	-1.063	36.07	0.27555	6033
Lipc	A_51_P263993	NM_008280	lipase, hepatic	-1.064	77.44	0.87048	27324	M	-1.056	42.43	0.40357	7551

Lrrc20	A_52_P77204	NM_153542	leucine rich repeat containing 20	-1.064	77.44	0.887	30090	P	1.134	5.75	0.04505	1676
Ppp1r14b	A_52_P262883	NM_008889	protein phosphatase 1, regulatory (inhibit	-1.064	75.14	0.86143	28312	P	-1.042	42.43	0.35648	6973
Senp3	A_52_P574398	NM_030702	SUMO/sentrin specific peptidase 3	-1.064	79.26	0.91529	32606	P	1.075	13.58	0.16092	4228
Zdhhc4	A_51_P248381	NM_028379	zinc finger, DHHC domain containing 4	-1.064	75.14	0.85302	27919	P	1.05	28.13	0.50017	8583
Ebf2	A_51_P386562	NM_010095	early B-cell factor 2	-1.065	79.26	0.95573	33182	P	-1.022	48.7	0.70665	10380
Gpr108	A_51_P185135	NM_030084	G protein-coupled receptor 108	-1.065	75.14	0.85763	28102	P	-1.056	36.07	0.26817	5924
Lrrk2	A_51_P290788	NM_025730	leucine-rich repeat kinase 2	-1.065	81.02	0.95102	35567	P	-1.03	45.68	0.52201	8767
Nudt3	A_51_P440657	NM_019837	nudix (nucleotide diphosphate linked moi	-1.065	77.44	0.89826	30832	P	1.11	13.58	0.2635	5864
Pigq	A_51_P232107	NM_011822	phosphatidylinositol glycan anchor biosyr	-1.065	75.14	0.84866	27652	P	1.02	38.4	0.65247	9896
Plxnb1	A_51_P281734	NM_172775	plexin B1	-1.065	79.26	0.92546	33490	P	1.057	22.1	0.31375	6504
Pou2f2	A_51_P166728	NM_011138	POU domain, class 2, transcription factor	-1.065	69.29	0.86821	25121	M	1.106	8.32	0.07038	2407
Tcfap2c	A_51_P418820	NM_009335	transcription factor AP-2, gamma	-1.065	81.02	0.95609	36000	P	-1.044	43.15	0.39637	7484
Topbp1	A_51_P302651	NM_176979	topoisomerase (DNA) II beta binding prot	-1.065	77.44	0.89303	30501	P	-1.013	49.48	0.79928	11172
2310037I24Rik	A_51_P246146	NM_133714	RIKEN cDNA 2310037I24 gene	-1.066	72.2	0.85127	26012	P	1.096	16.2	0.32529	6617
Atp6v0d1	A_51_P361201	NM_013477	ATPase, H+ transporting, lysosomal V0 su	-1.066	77.44	0.89375	30567	P	1.126	8.32	0.08819	2848
Cdipt	A_51_P408471	NM_026638	CDP-diacylglycerol--inositol 3-phosphatid	-1.066	79.26	0.9312	24127	M	1.025	36.07	0.61141	9544
Eif2b4	A_52_P425589	NM_010122	eukaryotic translation initiation factor 2B,	-1.066	75.14	0.85944	28206	P	-1.108	13.58	0.15344	4101
Golga2	A_51_P326609	BC011407	golgi autoantigen, golgin subfamily a, 2	-1.066	79.26	0.9118	32172	P	1.008	42.43	0.86391	11717
Idh3b	A_51_P130110	NM_130884	isocitrate dehydrogenase 3 (NAD+) beta	-1.066	75.14	0.86575	28556	P	1.031	36.07	0.63605	9770
Nol1	A_51_P258078	NM_138747	nucleolar protein 1	-1.066	81.02	0.94613	35085	P	-1.15	3.46	0.05135	1886
Nr6a1	A_52_P122664	NM_010264	nuclear receptor subfamily 6, group A, me	-1.066	79.26	0.91504	32498	P	-1.169	2.53	0.04772	1782
Pex11b	A_52_P666257	NM_011069	peroxisomal biogenesis factor 11b	-1.066	77.44	0.92701	23925	M	1.072	19.02	0.2865	6181
Ppp2r1a	A_51_P365578	NM_016891	protein phosphatase 2 (formerly 2A), regu	-1.066	69.29	0.83525	26715	P	1.117	9.71	0.12758	3654
Rarsl	A_51_P422781	NM_181406	arginyl-tRNA synthetase 2, mitochondrial	-1.066	79.26	0.90935	31834	P	-1.15	3.01	0.04376	1636
BC003993	A_51_P327642	NM_030560	cDNA sequence BC003993	-1.067	72.2	0.83927	27063	P	1.127	9.71	0.12865	3672
Cno	A_51_P390522	NM_133724	cappuccino	-1.067	81.02	0.94281	34782	P	1.013	42.43	0.79225	11115
Kifc3	A_52_P10195	NM_010631	kinesin family member C3	-1.067	69.29	0.83164	26185	P	-1.113	8.32	0.08301	2728
Maged2	A_51_P121635	NM_030700	melanoma antigen, family D, 2	-1.067	77.44	0.88971	30230	P	1.051	22.1	0.30204	6341
S100a13	A_51_P269852	NM_009113	S100 calcium binding protein A13	-1.067	79.26	0.92998	33786	P	1.04	30.75	0.47947	8305
Zfp637	A_51_P123795	NM_177684	zinc finger protein 637	-1.067	77.44	0.88688	30079	P	-1.026	45.05	0.66255	9237
4930453N24Rik	A_51_P311621	AK002578	RIKEN cDNA 4930453N24 gene	-1.068	77.44	0.9036	31334	P	-1.071	30.75	0.25067	5652
Arhgap8	A_52_P145482	NM_146061	Rho GTPase activating protein 8	-1.068	75.14	0.8701	28893	M	-1.187	3.01	0.07543	2549
D10Wsu102e	A_52_P140663	NM_026579	DNA segment, Chr 10, Wayne State Unive	-1.068	81.02	0.95755	36147	P	-1.041	44.4	0.48193	8337
Glis3	A_52_P546200	NM_175459	GLIS family zinc finger 3	-1.068	79.26	0.92982	33738	M	1.081	11.33	0.0996	3096
Hiat1	A_52_P49827	AK041662	hippocampus abundant gene transcript 1	-1.068	77.44	0.90436	27430	M	-1.044	42.43	0.35507	6958
Nit1	A_52_P322467	AK032189	nitrilase 1	-1.068	79.26	0.915	32490	P	1.02	38.4	0.65609	9934
Lims1	A_52_P222725	NM_026148	LIM and senescent cell antigen-like doma	-1.07	77.44	0.88236	29823	P	1.168	9.71	0.24127	5516
Lrig2	A_52_P228491	NM_001025067	leucine-rich repeats and immunoglobulin	-1.07	75.14	0.84373	27326	P	-1.139	2.53	0.0338	1309
Med19	A_51_P172842	NM_025885	mediator of RNA polymerase II transcripti	-1.07	75.14	0.84866	27656	P	-1.095	16.2	0.14403	3923
Ppan	A_51_P189985	NM_145610	peter pan homolog (Drosophila)	-1.07	79.26	0.93874	34471	P	-1.039	45.05	0.52508	8797
Pura	A_51_P155574	NM_008989	purine rich element binding protein A	-1.07	77.44	0.89061	30275	P	-1.066	33.49	0.28622	6175
Rap2c	A_51_P189425	NM_172413	RAP2C, member of RAS oncogene family	-1.07	75.14	0.85102	27785	P	1.081	11.33	0.11852	3449
Siah1a	A_52_P343641	NM_009172	seven in absentia 1A	-1.07	72.2	0.82935	25996	P	1.001	42.43	0.97964	12839
Smad7	A_51_P403636	NM_001042660	MAD homolog 7 (Drosophila)	-1.07	75.14	0.85886	28154	P	1.103	11.33	0.13666	3782
Snx1	A_51_P159673	NM_019727	sorting nexin 1	-1.07	77.44	0.88438	29933	P	-1.07	30.75	0.23044	5358
Suv420h2	A_51_P253094	NM_146177	suppressor of variegation 4-20 homolog 2	-1.07	77.44	0.87678	29377	P	1.021	38.4	0.68976	10237
Tubgcp2	A_51_P226932	NM_133755	tubulin, gamma complex associated prote	-1.07	77.44	0.90191	31174	P	1.05	25.31	0.36039	7028
Wrnip1	A_51_P432520	NM_030215	Werner helicase interacting protein 1	-1.07	75.14	0.86527	28537	P	-1.218	0.92	0.01685	727
1500003O22Rik	A_51_P293530	NM_025897	RIKEN cDNA 1500003O22 gene	-1.071	77.44	0.90537	31469	P	1.105	11.33	0.13573	3768
Aldh3b1	A_51_P506356	NM_026316	aldehyde dehydrogenase 3 family, memb	-1.071	79.26	0.91605	32691	P	1.04	28.13	0.39761	7498
BC018242	A_51_P427603	NM_144935	cDNA sequence BC018242	-1.071	81.02	0.94373	34890	P	1.032	33.49	0.53617	8902
Cdc5l	A_51_P429046	NM_152810	cell division cycle 5-like (S. pombe)	-1.071	77.44	0.91818	23489	M	1.045	30.75	0.51213	8692
Dera	A_51_P512820	NM_172733	2-deoxyribose-5-phosphate aldolase hom	-1.071	81.02	0.94613	35078	P	-1.034	45.68	0.58614	9307

Fbxo4	A_51_P490257	NM_134099	F-box protein 4	-1.071	75.14	0.86619	28573	P	1.24	2.53	0.02803	1135
Map3k9	A_51_P300867	NM_177395	mitogen-activated protein kinase kinase k	-1.071	81.02	0.94778	35250	M	1.077	16.2	0.20496	4965
Nr4a2	A_52_P494622	NM_013613	nuclear receptor subfamily 4, group A, me	-1.071	82.34	0.97958	38474	P	1.343	1.32	0.02005	859
Sart1	A_51_P178124	NM_016882	squamous cell carcinoma antigen recogni	-1.071	79.26	0.94226	34726	P	1.075	13.58	0.1464	3969
Wbp1	A_51_P160372	NM_016757	WW domain binding protein 1	-1.071	75.14	0.85127	27825	P	-1.046	40.63	0.30561	6389
Zfp71-rs1	A_51_P460398	BC016248	zinc finger protein 71, related sequence 1	-1.071	77.44	0.87802	29487	P	-1.086	19.02	0.14189	3882
Zmpste24	A_52_P483680	AK079998	zinc metallopeptidase, STE24 homolog (S.	-1.071	79.26	0.94234	34751	P	1.08	19.02	0.31247	6484
2900026A02Rik	A_51_P411728	NM_172884	RIKEN cDNA 2900026A02 gene	-1.072	79.26	0.92977	33728	P	-1.304	0.51	0.00707	221
Clstn3	A_51_P114094	NM_153508	calsyntenin 3	-1.072	77.44	0.90152	31089	P	1.077	11.33	0.12604	3629
Kctd15	A_51_P331805	NM_146188	potassium channel tetramerisation doma	-1.072	77.44	0.90137	31072	P	1.015	42.43	0.9336	12419
Mapre3	A_52_P278448	NM_133350	microtubule-associated protein, RP/EB fa	-1.072	79.26	0.93702	34345	P	1.06	22.1	0.28871	6197
Psen2	A_51_P384033	NM_011183	presenilin 2	-1.072	79.26	0.90966	31879	P	1.084	13.58	0.14633	3968
Smyd2	A_51_P320105	NM_026796	SET and MYND domain containing 2	-1.072	79.26	0.91601	32681	P	-1.122	13.58	0.1945	4812
Tbrg1	A_51_P186531	NM_025289	transforming growth factor beta regulate	-1.072	75.14	0.85831	28137	P	-1.053	42.43	0.4311	7843
Arpc5	A_52_P58041	NM_026369	actin related protein 2/3 complex, subuni	-1.073	75.14	0.86155	28329	P	1.067	16.2	0.1945	4806
Ccrk	A_52_P48723	NM_053180	cell cycle related kinase	-1.073	79.26	0.9186	32909	P	-1.032	45.05	0.49046	8445
Chkb	A_51_P159771	NM_007692	choline kinase beta	-1.073	77.44	0.90565	31480	P	1.045	33.49	0.6704	10051
Gemin6	A_52_P190745	NM_026053	gem (nuclear organelle) associated protei	-1.073	79.26	0.92364	33360	P	-1.043	43.75	0.43307	7872
Med8	A_51_P376313	NM_173719	mediator of RNA polymerase II transcripti	-1.073	79.26	0.91949	33002	P	1.049	28.13	0.42451	7776
Tmc4	A_52_P219415	NM_181820	transmembrane channel-like gene family	-1.073	77.44	0.89984	30975	P	-1.151	4.63	0.08811	2845
3100004P22Rik	A_51_P202003	NM_133693	RIKEN cDNA 3100004P22 gene	-1.074	79.26	0.93304	34046	P	-1.048	43.75	0.49288	8476
6530401D17Rik	A_51_P346815	NM_029541	RIKEN cDNA 6530401D17 gene	-1.074	75.14	0.85975	28221	P	-1.115	6.98	0.06385	2252
C230069N13	A_52_P274610	AK082618	hypothetical protein C230069N13	-1.074		0.9735	14679	A	-1.034	45.68	0.57352	9215
Cyp2b9	A_51_P467076	NM_010000	cytochrome P450, family 2, subfamily b, p	-1.074		0.9824	26250	A	1.102	8.32	0.0728	2476
D130060J10Rik	A_52_P553408	AK051620	RIKEN cDNA D130060J10 gene	-1.074	69.29	0.81296	24903	P	1.025	40.63	0.81226	11300
Hnrpf	A_51_P305997	NM_133834	heterogeneous nuclear ribonucleoprotein	-1.074	69.29	0.8833	21715	M	1.137	9.71	0.17942	4558
Katna1	A_51_P493857	NM_011835	katanin p60 (ATPase-containing) subunit A	-1.074	72.2	0.82885	25965	P	1.025	38.4	0.70331	10343
Nbr1	A_51_P248234	NM_008676	neighbor of Brca1 gene 1	-1.074	72.2	0.89149	22027	M	1.084	13.58	0.20155	4920
Nup153	A_51_P455886	NM_175749	nucleoporin 153	-1.074	79.26	0.91097	32055	P	1.037	33.49	0.61927	9618
Plvap	A_51_P414653	NM_032398	plasmalemma vesicle associated protein	-1.074	79.26	0.91784	32771	P	-1.003	49.48	0.946	12552
Ptcd1	A_52_P227065	AV132191	pentatricopeptide repeat domain 1	-1.074	79.26	0.94006	24468	M	1.056	28.13	0.5827	9286
Tm7sf2	A_52_P35064	NM_028454	transmembrane 7 superfamily member 2	-1.074	79.26	0.92194	33192	P	1.098	9.71	0.08948	2877
Top3b	A_51_P179082	NM_011624	topoisomerase (DNA) III beta	-1.074	77.44	0.8965	30736	P	-1.2	0.92	0.01444	606
Tpd52l2	A_51_P125157	NM_025482	tumor protein D52-like 2	-1.074	77.44	0.88592	30017	P	1.021	40.63	0.74332	10731
Zcchc10	A_51_P514675	NM_026479	zinc finger, CCHC domain containing 10	-1.074	72.2	0.81943	25383	P	1.222	2.53	0.02206	937
1700052K11Rik	A_51_P134262	NM_028539	RIKEN cDNA 1700052K11 gene	-1.075	77.44	0.9053	31466	P	-1.022	48.39	0.66444	10000
2600003E23Rik	A_51_P291210	NM_027373	actin filament associated protein 1	-1.075	75.14	0.84183	27199	P	1.015	42.43	0.91804	12250
Ctbp1	A_51_P482023	NM_013502	C-terminal binding protein 1	-1.075	79.26	0.91171	32129	P	-1.037	44.4	0.46016	8098
Hdac1	A_51_P507380	U80780	histone deacetylase 1	-1.075	79.26	0.92701	33578	P	1.068	22.1	0.43876	7911
Mpz	A_51_P321235	NM_008623	myelin protein zero	-1.075	79.26	0.91249	32260	P	-1.07	30.75	0.234	5414
Rrm1	A_51_P502082	NM_009103	ribonucleotide reductase M1	-1.075	77.44	0.90781	31653	P	1.021	38.4	0.67264	10077
Sumo3	A_51_P424448	NM_019929	SMT3 suppressor of mif two 3 homolog 3	-1.075	72.2	0.88895	21941	M	-1.071	22.1	0.13945	3840
Wasf3	A_51_P320125	NM_145155	WAS protein family, member 3	-1.075		0.92289	20932	A	-1.017	49.48	0.79133	11106
2610524G07Rik	A_51_P505339	NM_025596	PRELI domain containing 1	-1.076	79.26	0.91317	32352	P	1.099	11.33	0.13462	3759
Bnip3	A_51_P155234	NM_009760	BCL2/adenovirus E1B interacting protein	-1.076	75.14	0.84866	27660	P	1.002	42.43	0.96955	12742
E430029J22Rik	A_52_P483799	NM_001033384	RIKEN cDNA E030037K03 gene	-1.076		0.95861	18617	A	1.08	16.2	0.25519	5732
Mettl1	A_51_P499103	NM_010792	methyltransferase-like 1	-1.076	77.44	0.90346	31308	P	-1.05	42.43	0.3868	7360
Rbm4	A_51_P432802	NM_009032	RNA binding motif protein 4	-1.076	75.14	0.86859	28798	P	1.148	6.98	0.07509	2537
Slc35a2	A_51_P162238	NM_078484	solute carrier family 35 (UDP-galactose tr	-1.076	72.2	0.82776	25874	P	1.048	28.13	0.49605	8524
3930401K13Rik	A_51_P133052	NM_001079814	RIKEN cDNA 3930401K13 gene	-1.078	75.14	0.85886	28153	P	1.141	5.75	0.04508	1695
Cd72	A_52_P14600	AK144191	CD72 antigen	-1.078	77.44	0.89949	30961	P	-1.059	36.07	0.25658	5760
Ercc1	A_51_P390397	NM_007948	excision repair cross-complementing rode	-1.078	75.14	0.86435	28467	P	1.042	28.13	0.37996	7278
Fus	A_52_P320032	NM_139149	fusion, derived from t(12;16) malignant li	-1.078	77.44	0.88527	29983	P	1.272	3.46	0.07267	2459

Morf4l2	A_51_P416387	NM_019768	mortality factor 4 like 2	-1.078	79.26	0.94386	24637	M	1.031	36.07	0.65605	9932
Pkd1	A_51_P249127	NM_013630	polycystic kidney disease 1 homolog	-1.078	79.26	0.92504	33448	P	1.096	16.2	0.26679	5898
Rere	A_52_P421149	XM_204015	arginine glutamic acid dipeptide (RE) repe	-1.078	75.14	0.85793	28126	P	1.246	4.63	0.12137	3529
Rnase6	A_51_P104608	NM_030098	ribonuclease, RNase A family, 6	-1.078	72.2	0.83384	26412	P	-1.035	45.05	0.51724	8735
Thoc3	A_52_P869802	NM_028597	THO complex 3	-1.078	75.14	0.86821	28778	P	1.042	28.13	0.37618	7235
Trim28	A_51_P323299	NM_011588	tripartite motif protein 28	-1.078	75.14	0.85886	28155	P	-1.117	5.75	0.06325	2236
Unc5b	A_51_P294535	NM_029770	unc-5 homolog B (C. elegans)	-1.078	81.02	0.95102	35566	P	1.071	22.1	0.39381	7449
Aamp	A_52_P624362	NM_146110	angio-associated migratory protein	-1.079	75.14	0.85763	28107	P	1.051	28.13	0.46854	8191
Arpc4	A_52_P185485	NM_026552	actin related protein 2/3 complex, subuni	-1.079	77.44	0.87879	27761	P	1.117	9.71	0.13386	3739
Fbn2	A_51_P103850	NM_010181	fibrillin 2	-1.079	69.29	0.80242	24171	P	1.096	11.33	0.11709	3419
Ktn1	A_51_P233059	NM_008477	kinectin 1	-1.079	79.26	0.83558	24941	P	1.075	19.02	0.3317	6699
Mast3	A_52_P631591	BC024265	microtubule associated serine/threonine	-1.079	79.26	0.91097	32037	P	-1.016	49.48	0.80996	11279
Ptgis	A_51_P372819	NM_008968	prostaglandin I2 (prostacyclin) synthase	-1.079	79.26	0.91011	31963	P	1.081	13.58	0.1508	4049
Terf1	A_51_P482464	NM_009352	telomeric repeat binding factor 1	-1.079	79.26	0.94102	34653	P	1.025	36.07	0.59423	9378
Trappc4	A_52_P641172	NM_021789	trafficking protein particle complex 4	-1.079	75.14	0.86901	28839	P	1.039	28.13	0.42405	7764
Eif2b1	A_51_P394339	NM_145371	eukaryotic translation initiation factor 2B,	-1.08	77.44	0.89084	30291	P	-1.013	49.48	0.82319	11395
Fjx1	A_51_P355589	NM_010218	four jointed box 1 (Drosophila)	-1.08		0.92998	21034	A	1.045	28.13	0.46074	8115
Igf2r	A_51_P125467	NM_010515	insulin-like growth factor 2 receptor	-1.08	75.14	0.89289	22133	M	1.092	9.71	0.09557	3007
Ikbke	A_51_P222280	NM_019777	inhibitor of kappaB kinase epsilon	-1.08	72.2	0.81591	25161	P	-1.163	2.53	0.03749	1428
Lama5	A_51_P411061	XM_203796	laminin, alpha 5	-1.08	75.14	0.84631	27509	P	-1.023	47.92	0.65501	9918
Ncstn	A_51_P396643	NM_021607	nicastrin	-1.08	72.2	0.80911	24650	P	1.207	3.46	0.04595	1724
Ssfa2	A_52_P637829	NM_080558	sperm specific antigen 2	-1.08	69.29	0.80342	24318	P	-1.017	48.7	0.67749	10110
Tmed4	A_51_P291682	NM_134020	transmembrane emp24 protein transport	-1.08	75.14	0.90015	22467	M	1.171	3.82	0.03927	1488
2610209M04Rik	A_51_P346884	NM_025665	RIKEN cDNA 2610209M04 gene	-1.081	72.2	0.87933	21552	M	-1.061	33.49	0.25007	5639
9130005N14Rik	A_51_P303180	NM_026667	RIKEN cDNA 9130005N14 gene	-1.081	75.14	0.83762	26911	P	-1.046	40.63	0.31612	6536
Casp9	A_52_P663602	NM_015733	caspase 9	-1.081	77.44	0.88047	29672	P	-1.283	0.56	0.01291	558
Ccne1	A_52_P796682	NM_007633	cyclin E1	-1.081	69.29	0.79617	23884	P	-1.02	49.47	0.75244	10807
Ifrd1	A_51_P367060	NM_013562	interferon-related developmental regulat	-1.081	79.26	0.92907	24004	M	1.166	3.82	0.03516	1352
Pvrl1	A_52_P28651	NM_021424	poliovirus receptor-related 1	-1.081	79.26	0.92446	33415	P	-1.034	45.68	0.5599	9105
Rfx1	A_52_P523480	NM_009055	regulatory factor X, 1 (influences HLA clas	-1.081	75.14	0.85452	27985	P	1.106	11.33	0.18632	4675
Rras	A_52_P635182	NM_009101	Harvey rat sarcoma oncogene, subgroup I	-1.081	77.44	0.88982	30234	P	1.106	8.32	0.07176	2427
Sec61g	A_51_P204390	NM_011343	SEC61, gamma subunit	-1.081	75.14	0.90191	22547	M	-1.094	16.2	0.12116	3523
2700081O15Rik	A_52_P496628	NM_175381	RIKEN cDNA 2700081O15 gene	-1.082	69.29	0.78621	23142	P	-1.043	42.43	0.35691	6977
2810012G03Rik	A_51_P121432	NM_175104	RIKEN cDNA 2810012G03 gene	-1.082	75.14	0.85831	28140	P	1.01	42.43	0.9007	12082
2810021B07Rik	A_51_P293706	NM_025479	RIKEN cDNA 2810021B07 gene	-1.082	72.2	0.82538	25715	P	1.05	25.31	0.38883	7385
Bmp8a	A_51_P213266	NM_007558	bone morphogenetic protein 8a	-1.082	79.26	0.91525	22894	M	-1.006	49.48	0.91451	12215
Btbd2	A_51_P424054	XM_001000710	BTB (POZ) domain containing 2	-1.082	79.26	0.91716	32740	P	-1.067	36.07	0.29981	6314
Cog6	A_51_P298486	NM_026225	component of oligomeric golgi complex 6	-1.082	84.56	0.931	31404	P	1.502	0.66	0.01874	790
Gstm6	A_52_P415996	NM_008184	glutathione S-transferase, mu 6	-1.082	79.26	0.93689	34325	M	1.003	42.43	0.96229	12684
Kntc2	A_51_P191649	NM_023294	NDC80 homolog, kinetochore complex co	-1.082	77.44	0.87149	29040	P	1.164	6.98	0.10991	3263
Mocs2	A_52_P674309	NM_013826	molybdenum cofactor synthesis 2	-1.082	77.44	0.87776	29458	P	1.059	19.02	0.21877	5185
Rab27b	A_52_P120719	NM_030554	RAB27b, member RAS oncogene family	-1.082	81.02	0.95092	35540	P	1.056	19.02	0.23454	5420
Sav1	A_52_P652094	NM_022028	salvador homolog 1 (Drosophila)	-1.082	72.2	0.8321	26221	P	1.083	16.2	0.25746	5771
Serhl	A_51_P200277	NM_023475	serine hydrolase-like	-1.082	79.26	0.91079	32022	P	1.019	40.63	0.72658	10532
Ccdc9	A_52_P265811	NM_172297	coiled-coil domain containing 9	-1.083	77.44	0.88996	30244	P	1.078	16.2	0.1951	4818
Paip2	A_51_P514647	NM_026420	polyadenylate-binding protein-interacting	-1.083	72.2	0.88189	21659	M	1.144	22.1	0.60487	9492
Plekhg2	A_51_P178022	NM_138752	pleckstrin homology domain containing, f	-1.083	79.26	0.91788	32778	P	-1.358	0.51	0.00584	62
Reps1	A_52_P527842	NM_009048	RalBP1 associated Eps domain containing	-1.083	65.79	0.78014	22764	P	1.133	9.71	0.17468	4464
Zfp161	A_52_P59931	NM_009547	zinc finger protein 161	-1.083	79.26	0.92457	23845	M	1.064	16.2	0.18807	4700
Zswim1	A_51_P232474	NM_028028	zinc finger, SWIM domain containing 1	-1.083	77.44	0.88647	30060	P	1.069	25.31	0.45852	8083
2810482I07Rik	A_51_P476357	AV024949	RIKEN cDNA 2810482I07 gene	-1.085	72.2	0.81031	24720	P	1.01	42.43	0.87139	11769
5730557L09Rik	A_52_P86774	AK077727	RIKEN cDNA 5730557L09 gene	-1.085	77.44	0.87717	29408	P	1.035	38.4	0.81197	11294
5830416A07Rik	A_51_P121359	NM_001029993	RIKEN cDNA 5830416A07 gene	-1.085	69.29	0.79472	23798	P	-1.028	46.85	0.62002	9622

Cyp2b13	A_52_P289091	NM_007813	cytochrome P450, family 2, subfamily b, p	-1.085	75.14	0.85981	28222	P	1.098	9.71	0.07728	2580
Ggta1	A_51_P349988	NM_010283	glycoprotein galactosyltransferase alpha 1	-1.085	77.44	0.88774	30127	P	1.026	36.07	0.64071	9813
Ing1	A_52_P598	NM_011919	inhibitor of growth family, member 1	-1.085	77.44	0.8844	29945	P	1.111	11.33	0.17232	4410
Ppp1ca	A_51_P509389	NM_031868	protein phosphatase 1, catalytic subunit,	-1.085	77.44	0.88459	29965	P	1.041	25.31	0.35169	6905
Sp1	A_51_P256919	NM_013672	trans-acting transcription factor 1	-1.085	72.2	0.80746	24544	P	-1.035	47.43	0.72221	10513
Tm9sf2	A_51_P143901	NM_080556	transmembrane 9 superfamily member 2	-1.085	69.29	0.86488	20978	M	1.207	3.01	0.03553	1375
Acads	A_52_P367745	NM_007383	acyl-Coenzyme A dehydrogenase, short cl	-1.086	72.2	0.82214	24105	M	-1.045	42.43	0.35416	6938
Arhgap1	A_51_P412010	NM_146124	Rho GTPase activating protein 1	-1.086	69.29	0.78046	22789	P	1.005	42.43	0.92273	12308
Fbs1	A_52_P617619	XM_284344	fibrosin 1	-1.086	77.44	0.90577	31499	P	-1.081	38.4	0.44322	7948
Fli1	A_52_P821	NM_008026	Friend leukemia integration 1	-1.086	79.26	0.93941	34522	P	1.017	40.63	0.7477	10768
Hpgd	A_51_P458781	NM_008278	hydroxyprostaglandin dehydrogenase 15	-1.086	79.26	0.92458	33423	P	1.091	11.33	0.14653	3974
Ociad1	A_52_P17369	NM_023429	OCIA domain containing 1	-1.086	77.44	0.89289	30470	P	1.047	28.13	0.42795	7801
Snapc5	A_51_P244061	NM_183316	small nuclear RNA activating complex, po	-1.086	75.14	0.84726	27565	P	-1.075	36.07	0.37807	7258
1500032L24Rik	A_51_P501815	NM_026914	RIKEN cDNA 1500032L24 gene	-1.087	75.14	0.86568	28553	P	-1.035	45.68	0.58445	9295
B3gat2	A_52_P236755	NM_172124	beta-1,3-glucuronyltransferase 2 (glucuro	-1.087	79.26	0.92753	33642	M	1.048	25.31	0.31012	6448
Clu	A_51_P367720	NM_013492	clusterin	-1.087	79.26	0.92998	33811	P	1.153	9.71	0.18763	4692
Col4a1	A_51_P124254	NM_009931	procollagen, type IV, alpha 1	-1.087	75.14	0.84821	27607	P	1.119	9.71	0.13857	3810
Ddx3x	A_51_P290018	XM_981517	DEAD/H (Asp-Glu-Ala-Asp/His) box polype	-1.087	77.44	0.91805	23478	M	1.067	30.75	0.67318	10081
Ezh1	A_52_P237871	NM_007970	enhancer of zeste homolog 1 (Drosophila	-1.087	72.2	0.81586	25142	P	-1.021	49	0.73045	10575
Hivep1	A_51_P436002	NM_007772	human immunodeficiency virus type I enh	-1.087	69.29	0.78992	23440	P	1.253	2.53	0.04001	1527
Trim13	A_52_P17788	NM_023233	tripartite motif protein 13	-1.087	77.44	0.90177	31124	P	1.077	13.58	0.18414	4639
Tst	A_51_P430082	NM_009437	thiosulfate sulfurtransferase, mitochondr	-1.087	77.44	0.90726	31588	P	-1.103	5.75	0.05826	2088
Ube1l	A_51_P316816	NM_023738	ubiquitin-activating enzyme E1-like	-1.087	75.14	0.85581	28030	P	1.087	11.33	0.12123	3525
Wnt10b	A_51_P304643	NM_011718	wingless related MMTV integration site 1	-1.087		0.87604	21258	A	1.119	25.31	0.63989	9808
0610039J04Rik	A_51_P342271	NM_001035123	SET domain containing 6	-1.088	77.44	0.9	30990	P	-1.25	1.18	0.03799	1439
Ap4m1	A_51_P393067	NM_021392	adaptor-related protein complex AP-4, mu	-1.088	77.44	0.9089	31764	P	-1.095	11.33	0.08551	2784
D14Ertd231e	A_51_P491051	NM_153414	DNA segment, Chr 14, ERATO Doi 231, exp	-1.088	75.14	0.86072	28267	P	-1.046	43.15	0.43325	7880
Farp2	A_51_P425254	NM_145519	FERM, RhoGEF and pleckstrin domain pro	-1.088	72.2	0.79472	23803	P	1.032	33.49	0.53134	8849
Fhl3	A_51_P310635	NM_010213	four and a half LIM domains 3	-1.088	65.79	0.79372	22314	M	1.006	42.43	0.8996	12060
Gtf2f2	A_51_P192817	NM_026816	general transcription factor IIF, polypeptid	-1.088	77.44	0.89285	30461	P	-1.004	49.48	0.94908	12576
Safb	A_51_P236287	AK087504	scaffold attachment factor B	-1.088	75.14	0.83244	26257	P	1.081	16.2	0.26219	5842
Timm44	A_51_P143470	NM_011592	translocase of inner mitochondrial memb	-1.088	72.2	0.87464	21380	M	-1.06	36.07	0.267	5900
Anxa7	A_52_P397385	AK032013	annexin A7	-1.089	69.29	0.77962	22727	P	1.028	33.49	0.5599	9108
Arpc2	A_51_P152199	NM_029711	actin related protein 2/3 complex, subuni	-1.089	75.14	0.85089	27774	P	-1.037	45.68	0.60991	9525
Grb2	A_51_P198411	NM_008163	growth factor receptor bound protein 2	-1.089	77.44	0.91974	23596	M	1.094	11.33	0.11298	3336
Pou6f1	A_51_P348857	NM_010127	POU domain, class 6, transcription factor	-1.089	72.2	0.8321	26226	P	-1.036	45.05	0.49722	8544
Pter	A_51_P251069	NM_008961	phosphotriesterase related	-1.089	81.02	0.96001	36389	P	-1.028	47.43	0.64576	9853
Rae1	A_52_P524463	BC060072	RAE1 RNA export 1 homolog (S. pombe)	-1.089	75.14	0.8144	22029	M	-1.059	38.4	0.30257	6345
Ropn1l	A_51_P150763	NM_145852	ropporin 1-like	-1.089	65.79	0.75767	21506	P	1.117	8.32	0.08594	2790
Scarf1	A_52_P95544	NM_001004157	scavenger receptor class F, member 1	-1.089	75.14	0.85089	27771	P	-1.111	4.63	0.05188	1912
Sptlc1	A_51_P345593	NM_009269	serine palmitoyltransferase, long chain ba	-1.089	72.2	0.80251	24195	P	-1.024	48.39	0.67108	10060
Actg1	A_52_P72237	NM_009609	actin, gamma, cytoplasmic 1	-1.091	79.26	0.93066	33893	P	1.219	1.62	0.01251	530
Il1rapl1	A_51_P497833	ENSMUST00000078875	interleukin 1 receptor accessory protein-l	-1.091		0.87529	29278	A	1.042	28.13	0.36715	7129
Ndufs1	A_51_P273817	AK017924	NADH dehydrogenase (ubiquinone) Fe-S	-1.091	72.2	0.82983	26051	M	1.034	33.49	0.61518	9579
Pgr	A_52_P413840	AK036862	progesterone receptor	-1.091		0.96573	14501	A	1.117	6.98	0.04898	1818
Rab39b	A_51_P356620	NM_175122	RAB39B, member RAS oncogene family	-1.091	75.14	0.85249	27891	P	-1.081	22.1	0.14794	4001
S100a9	A_51_P402943	NM_009114	S100 calcium binding protein A9 (calgranu	-1.091	75.14	0.86523	28531	P	1.057	25.31	0.41573	7688
Adam15	A_51_P291815	NM_001037722	a disintegrin and metallopeptidase domai	-1.092	77.44	0.90457	31398	P	-1.146	3.01	0.04131	1560
Amfr	A_51_P435809	NM_011787	autocrine motility factor receptor	-1.092	77.44	0.92253	23745	M	1.135	6.98	0.0712	2418
D930017J03Rik	A_52_P16973	AK081934	RIKEN cDNA D930017J03 gene	-1.092	75.14	0.85949	28211	P	-1.105	11.33	0.11595	3396
Zfhx1a	A_52_P546635	NM_011546	zinc finger E-box binding homeobox 1	-1.092	75.14	0.86304	28374	P	1.071	25.31	0.51568	8723
Zfp592	A_52_P372142	NM_178707	zinc finger protein 592	-1.092	75.14	0.87052	28940	P	-1.142	4.63	0.07656	2565
1110012D08Rik	A_52_P384314	NM_178066	RIKEN cDNA 1110012D08 gene	-1.093	77.44	0.90075	31026	P	1.153	6.98	0.11595	3395

2310043N10Rik	A_51_P234692	AK028745	RIKEN cDNA 2310043N10 gene	-1.093	75.14	0.9493	32814	P	-1.073	46.3	0.78864	11079
2700059D21Rik	A_52_P442779	NM_001007589	RIKEN cDNA 2700059D21 gene	-1.093	72.2	0.81757	25255	P	-1.065	28.13	0.18425	4640
Akt1s1	A_51_P478326	NM_026270	AKT1 substrate 1 (proline-rich)	-1.093	69.29	0.76604	21979	P	-1.08	16.2	0.11423	3373
Brd7	A_52_P311104	NM_012047	bromodomain containing 7	-1.093	72.2	0.82206	25501	P	1.064	19.02	0.31099	6473
Klk8	A_52_P216672	NM_008940	kallikrein related-peptidase 8	-1.093	79.26	0.94264	29678	M	-1.138	6.98	0.10588	3206
Lyl1	A_51_P143190	NM_008535	lymphoblastomic leukemia	-1.093	81.02	0.95683	36083	P	1.066	19.02	0.22274	5253
Rab5a	A_51_P117600	NM_025887	RAB5A, member RAS oncogene family	-1.093	65.79	0.74297	20716	P	1.243	2.04	0.01802	767
Suox	A_51_P249360	NM_173733	sulfite oxidase	-1.093	72.2	0.87575	21436	M	-1.144	2.04	0.02741	1113
Trappc6a	A_51_P485683	NM_025960	trafficking protein particle complex 6A	-1.093	69.29	0.78777	23254	P	1.127	13.58	0.36472	7086
Ttk	A_52_P110534	NM_009445	Ttk protein kinase	-1.093	72.2	0.83762	23465	M	1.045	30.75	0.50433	8624
D330037H05Rik	A_52_P452268	BC075726	RIKEN cDNA D330037H05 gene	-1.094	79.26	0.92533	33476	P	-1.201	1.1	0.01749	749
Gna-rs1	A_52_P491766	NM_008136	guanine nucleotide binding protein, relat	-1.094	72.2	0.81533	25116	P	1.017	42.43	0.84813	11591
Klhl18	A_51_P429739	NM_177771	kelch-like 18 (Drosophila)	-1.094	72.2	0.80292	24245	P	1.064	16.2	0.20496	4966
Stk11ip	A_51_P516994	NM_027886	serine/threonine kinase 11 interacting pr	-1.094	79.26	0.92998	33769	P	1.036	30.75	0.45026	7995
Tor1a	A_51_P365964	NM_144884	torsin family 1, member A (torsin A)	-1.094	72.2	0.82679	25827	P	1.14	5.75	0.05592	2032
Cherp	A_51_P519837	NM_138585	calcium homeostasis endoplasmic reticul	-1.095	79.26	0.93984	34554	P	1.073	22.1	0.40911	7600
Cyba	A_51_P131800	NM_007806	cytochrome b-245, alpha polypeptide	-1.095	79.26	0.94858	35303	P	-1.057	42.43	0.45183	8011
Dbn1	A_51_P446232	NM_019813	drebrin 1	-1.095	75.14	0.84866	27664	P	1.11	9.71	0.12387	3578
Map3k4	A_51_P495767	NM_011948	mitogen activated protein kinase kinase k	-1.095	72.2	0.80275	24232	P	-1.135	2.04	0.02978	1186
Plscr3	A_52_P8100	NM_023564	phospholipid scramblase 3	-1.095	69.29	0.81678	23809	M	1.003	42.43	0.96018	12658
Pmvk	A_51_P492408	NM_026784	phosphomevalonate kinase	-1.095	75.14	0.8365	26849	P	-1.051	43.15	0.42897	7816
Smarca5	A_52_P304881	NM_053124	SWI/SNF related, matrix associated, actin	-1.095	69.29	0.78867	23335	P	1.095	16.2	0.33375	6722
Usp16	A_51_P513424	NM_024258	ubiquitin specific peptidase 16	-1.095	69.29	0.77055	22226	P	-1.064	33.49	0.26484	5871
1810032O08Rik	A_51_P117666	BC055707	RIKEN cDNA 1810032O08 gene	-1.096	79.26	0.91725	32757	P	1.036	30.75	0.44099	7931
Abl1	A_52_P333953	NM_009594	v-abl Abelson murine leukemia oncogene	-1.096	79.26	0.91805	32827	P	1.041	28.13	0.46025	8099
Edg1	A_52_P532227	NM_007901	endothelial differentiation sphingolipid G	-1.096	72.2	0.79166	23564	P	1.116	9.71	0.12865	3674
Hspa14	A_52_P361551	NM_015765	heat shock protein 14	-1.096	77.44	0.89647	30733	P	1.014	42.43	0.80093	11188
Klf3	A_51_P492640	NM_008453	Kruppel-like factor 3 (basic)	-1.096	72.2	0.82824	25915	P	1.076	19.02	0.31099	6469
Rab33b	A_51_P502026	NM_016858	RAB33B, member of RAS oncogene family	-1.096	72.2	0.8577	20734	M	1.086	16.2	0.26942	5947
Zfp36l1	A_51_P235801	NM_007564	zinc finger protein 36, C3H type-like 1	-1.096	72.2	0.86673	21058	M	1.021	38.4	0.6857	10200
Zfp410	A_51_P369897	NM_144833	zinc finger protein 410	-1.096	72.2	0.82254	25563	P	1.06	19.02	0.23432	5416
2610002F03Rik	A_52_P199776	BC046478	RIKEN cDNA 2610002F03 gene	-1.098	72.2	0.78969	23407	P	-1.039	44.4	0.4549	8046
Cpne1	A_51_P114772	NM_170588	copine I	-1.098	75.14	0.84651	27531	P	1.18	3.82	0.04225	1589
Gstt2	A_51_P350048	NM_010361	glutathione S-transferase, theta 2	-1.098	77.44	0.90966	31874	P	1.012	42.43	0.81394	11314
Igsf9	A_52_P443701	NM_033608	immunoglobulin superfamily, member 9	-1.098	72.2	0.79286	23679	M	-1.042	43.15	0.40481	7565
Mat2a	A_51_P500344	NM_145569	methionine adenosyltransferase II, alpha	-1.098	69.29	0.84186	20178	M	1.376	0.24	0.00584	87
Nudc	A_51_P238933	NM_010948	nuclear distribution gene C homolog (Asp	-1.098	77.44	0.89084	30288	P	-1.063	28.13	0.17235	4414
Pdcd7	A_51_P487345	NM_016688	programmed cell death protein 7	-1.098	69.29	0.78154	22834	P	1.023	40.63	0.80077	11181
Ppp4c	A_51_P208394	NM_019674	protein phosphatase 4, catalytic subunit	-1.098	75.14	0.84314	27282	P	1.048	28.13	0.43068	7837
Pscd3	A_51_P488928	NM_011182	pleckstrin homology, Sec7 and coiled-coil	-1.098	65.79	0.7471	20940	P	-1.106	9.71	0.08456	2775
1110008F13Rik	A_51_P450100	NM_026124	RIKEN cDNA 1110008F13 gene	-1.099	61.79	0.72253	19821	P	-1.051	36.07	0.26234	5844
4632417K18Rik	A_51_P394802	NM_026640	RIKEN cDNA 4632417K18 gene	-1.099	77.44	0.894	30578	P	-1.059	40.63	0.3817	7297
4933403F05Rik	A_51_P216313	NM_153794	RIKEN cDNA 4933403F05 gene	-1.099	72.2	0.79257	23646	P	1.094	9.71	0.08191	2698
4933433P14Rik	A_52_P338039	NM_178613	RIKEN cDNA 4933433P14 gene	-1.099	77.44	0.90152	31100	P	-1.007	49.48	0.93505	12430
Akr1c18	A_51_P256170	NM_134066	aldo-keto reductase family 1, member C1	-1.099	77.44	0.88692	30085	P	1.103	11.33	0.13414	3749
D11Wsu99e	A_51_P146407	NM_138598	DNA segment, Chr 11, Wayne State Unive	-1.099	72.2	0.79111	23510	P	1.14	4.63	0.03749	1427
Eif2b5	A_51_P151968	NM_172265	eukaryotic translation initiation factor 2B,	-1.099	72.2	0.80925	24654	P	1.079	16.2	0.21435	5100
Gdf1	A_51_P464300	NM_008107	growth differentiation factor 1	-1.099	77.44	0.89651	30741	P	1.048	28.13	0.43434	7891
Icam2	A_51_P267754	NM_010494	intercellular adhesion molecule 2	-1.099	69.29	0.75252	21218	P	1.143	4.63	0.03429	1319
Pparbp	A_51_P324082	NM_013634	peroxisome proliferator activated recept	-1.099	69.29	0.78314	22962	P	1.006	42.43	0.92557	12347
3230401M21Rik	A_51_P299216	BC043315	WD repeat domain 90	-1.1	77.44	0.90217	31197	P	-1.229	0.56	0.01026	389
8430436F23Rik	A_51_P470205	AK018460	MOB1, Mps One Binder kinase activator-l	-1.1	79.26	0.91685	32730	P	1.106	16.2	0.40034	7518
A730098D12Rik	A_52_P472936	BC048817	RIKEN cDNA A730098D12 gene	-1.1	72.2	0.85251	20601	M	1.064	22.1	0.33754	6756

BC004022	A_51_P310773	BC004022	cDNA sequence BC004022	-1.1	65.79	0.72464	19987	P	-1.138	3.01	0.03558	1380
Cap1	A_51_P440682	NM_007598	CAP, adenylate cyclase-associated protein	-1.1	72.2	0.8182	25310	P	1.155	5.75	0.07509	2533
Dhx30	A_51_P426283	NM_133347	DEAH (Asp-Glu-Ala-His) box polypeptide 3	-1.1	79.26	0.92825	33670	P	-1.084	22.1	0.15965	4211
Nudcd2	A_51_P418339	NM_026023	NudC domain containing 2	-1.1	75.14	0.8596	28214	P	-1.006	49.48	0.90494	12145
Thoc4	A_51_P154684	NM_011568	THO complex 4	-1.1	77.44	0.89984	22453	M	1.141	4.63	0.04147	1567
Cacnb3	A_51_P259009	NM_007581	calcium channel, voltage-dependent, beta	-1.101	77.44	0.90512	31450	P	-1.217	0.75	0.01399	588
Dom3z	A_51_P267388	NM_033613	DOM-3 homolog Z (C. elegans)	-1.101	77.44	0.89472	30644	P	1.103	8.32	0.07486	2524
Entpd2	A_51_P112932	NM_009849	ectonucleoside triphosphate diphosphohy	-1.101	75.14	0.86128	28308	P	1.254	2.04	0.02453	1016
Irf2bp2	A_51_P424221	XM_284454	interferon regulatory factor 2 binding pro	-1.101	77.44	0.92106	23685	M	1.159	8.32	0.18324	4629
Pink1	A_51_P196605	NM_026880	PTEN induced putative kinase 1	-1.101	75.14	0.86362	28428	P	1.019	38.4	0.66562	10008
Snx17	A_51_P225083	NM_153680	sorting nexin 17	-1.101	75.14	0.84699	27551	P	1.075	16.2	0.24634	5597
Unc84a	A_51_P281433	NM_024451	unc-84 homolog A (C. elegans)	-1.101	72.2	0.84837	20437	M	1.235	3.01	0.03933	1490
Lgtn	A_52_P352327	NM_010709	ligatin	-1.103	72.2	0.7993	24064	P	1.012	42.43	0.82423	11400
Rab8a	A_52_P684214	NM_023126	RAB8A, member RAS oncogene family	-1.103	65.79	0.71828	19403	P	1.103	11.33	0.16339	4275
Sbds	A_51_P466875	NM_023248	Shwachman-Bodian-Diamond syndrome h	-1.103	69.29	0.77055	22235	P	1.11	6.98	0.05688	2059
AA536749	A_51_P275514	NM_012027	expressed sequence AA536749	-1.104	72.2	0.82821	25897	P	1.039	30.75	0.53437	8884
AI597479	A_52_P239292	NM_133818	expressed sequence AI597479	-1.104	72.2	0.7912	23545	P	1.081	16.2	0.28389	6133
Cbx6	A_51_P221428	NM_028763	chromobox homolog 6	-1.104	77.44	0.90032	22471	M	1.175	6.98	0.13611	3777
Chaf1b	A_51_P367310	NM_028083	chromatin assembly factor 1, subunit B (p	-1.104	69.29	0.75252	21235	P	1.103	8.32	0.06041	2160
Clic4	A_51_P127681	NM_013885	chloride intracellular channel 4 (mitochor	-1.104	69.29	0.75046	21104	P	-1.061	42.43	0.5077	8656
Dazap1	A_51_P205099	NM_133188	DAZ associated protein 1	-1.104	75.14	0.87252	29097	P	1.1	16.2	0.30384	6364
Ewsr1	A_51_P412947	NM_007968	Ewing sarcoma breakpoint region 1	-1.104	65.79	0.73228	20363	P	1.078	22.1	0.49039	8439
Oprs1	A_51_P300726	NM_011014	opioid receptor, sigma 1	-1.104	72.2	0.81925	25380	P	1.056	19.02	0.23951	5477
Rbm15b	A_51_P503194	AK075777	RNA binding motif protein 15B	-1.104	69.29	0.77113	22259	P	1.095	9.71	0.08424	2756
Rnmtl1	A_51_P401527	NM_183263	RNA methyltransferase like 1	-1.104	72.2	0.81115	24793	P	1.008	42.43	0.89972	12062
Slbp	A_51_P127615	NM_009193	stem-loop binding protein	-1.104	72.2	0.86734	21082	M	1.034	33.49	0.52445	8793
Fbxo5	A_51_P393958	NM_025995	F-box protein 5	-1.105	57.76	0.69711	18246	P	-1.308	0.51	0.00756	277
H1fx	A_52_P748854	BU511373	H1 histone family, member X	-1.105	72.2	0.79819	23996	P	-1.26	0.51	0.00707	224
Mtap	A_51_P341349	NM_024433	methylthioadenosine phosphorylase	-1.105	69.29	0.76474	21895	P	1.025	38.4	0.74275	10713
Ppp2r5d	A_51_P233396	NM_009358	protein phosphatase 2, regulatory subuni	-1.105	72.2	0.79387	23754	P	1.133	13.58	0.30041	6326
Rbm12	A_51_P276652	NM_029397	RNA binding motif protein 12	-1.105	72.2	0.79782	23986	P	1.043	28.13	0.42431	7770
Rxrb	A_52_P519689	NM_011306	retinoid X receptor beta	-1.105	72.2	0.81524	25093	P	1.006	42.43	0.90206	12111
Usp21	A_51_P346747	NM_013919	ubiquitin specific peptidase 21	-1.105	69.29	0.77135	22266	P	1.048	22.1	0.2683	5928
Zmynd11	A_52_P609965	NM_144516	zinc finger, MYND domain containing 11	-1.105	69.29	0.7737	22443	P	1.141	5.75	0.04552	1705
1700001O22Rik	A_52_P552870	AK019754	RIKEN cDNA 1700001O22 gene	-1.106	72.2	0.80341	24306	P	-1.317	0.51	0.0131	565
2310047M10Rik	A_51_P518926	AK009886	RIKEN cDNA 2310047M10 gene	-1.106	75.14	0.8411	27161	P	-1.195	1.18	0.02027	868
Bzw1	A_52_P542763	NM_025824	basic leucine zipper and W2 domains 1	-1.106	69.29	0.77253	22372	P	-1.14	3.01	0.03908	1475
Cebpg	A_52_P121675	NM_009884	CCAAT/enhancer binding protein (C/EBP),	-1.106	65.79	0.71236	19074	P	1.051	22.1	0.31694	6550
Kdelr1	A_52_P596541	NM_133950	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	-1.106	72.2	0.81447	25023	P	1.171	3.46	0.02661	1089
Lhx4	A_51_P233088	NM_010712	LIM homeobox protein 4	-1.106	72.2	0.80341	24308	P	1.074	19.02	0.32814	6649
Nr1d1	A_52_P130952	NM_145434	nuclear receptor subfamily 1, group D, me	-1.106	72.2	0.80512	24426	P	1.036	33.49	0.64844	9872
Rcn2	A_51_P165041	AF049125	reticulocalbin 2	-1.106	61.79	0.69665	18229	P	1.116	6.98	0.06119	2173
Fhl2	A_51_P140237	NM_010212	four and a half LIM domains 2	-1.107	79.26	0.93516	34206	P	1.216	2.04	0.01604	693
G6pdx	A_51_P187082	NM_008062	glucose-6-phosphate dehydrogenase X-lin	-1.107	75.14	0.83958	27099	P	1.071	11.33	0.28992	5745
Nr0b2	A_51_P265338	NM_011850	nuclear receptor subfamily 0, group B, me	-1.107	69.29	0.77073	22251	P	-1.198	0.75	0.01279	554
Polr2c	A_51_P239926	NM_009090	polymerase (RNA) II (DNA directed) polyp	-1.107	72.2	0.7918	23594	P	-1.035	44.4	0.44543	7964
Vasp	A_51_P179131	AK157021	vasodilator-stimulated phosphoprotein	-1.107	65.79	0.72307	19876	P	1.159	3.82	0.02935	1177
Wsb2	A_52_P683572	NM_021539	WD repeat and SOCS box-containing 2	-1.107	65.79	0.72729	20063	P	1.402	0.24	0.00619	118
Bmyc	A_52_P466853	NM_023326	brain expressed myelocytomatosis oncog	-1.109	72.2	0.83384	26389	P	-1.031	46.3	0.59283	9364
Psen1	A_51_P464576	NM_008943	presenilin 1	-1.109	61.79	0.68802	17820	P	1.117	11.33	0.19968	4898
Sumo2	A_51_P427906	NM_133354	SMT3 suppressor of mif two 3 homolog 2	-1.109	72.2	0.85256	20604	M	-1.12	8.32	0.08802	2840
5730453I16Rik	A_51_P283754	NM_172302	RIKEN cDNA 5730453I16 gene	-1.11	72.2	0.80436	24380	P	1.023	36.07	0.59276	9362
Actr5	A_52_P216548	AK046584	ARP5 actin-related protein 5 homolog (ye	-1.11	72.2	0.8184	22271	M	1.112	11.33	0.15498	4130

Asl	A_51_P174645	NM_133768	argininosuccinate lyase	-1.11	72.2	0.82666	25807	P	1.033	36.07	0.70131	10331
Entpd4	A_52_P582907	NM_026174	ectonucleoside triphosphate diphosphoh	-1.11	77.44	0.8938	30571	P	-1.124	6.98	0.08811	2843
Hey1	A_51_P258409	NM_010423	hairy/enhancer-of-split related with YRP	-1.11	65.79	0.73577	20480	P	1.05	28.13	0.48617	8396
Qtrt1	A_51_P314168	NM_021888	queuine tRNA-ribosyltransferase 1	-1.11	65.79	0.70918	18903	P	1.014	40.63	0.73874	10676
Rfwd3	A_52_P4698	NM_146218	ring finger and WD repeat domain 3	-1.11	72.2	0.79639	23898	P	1.212	2.53	0.01955	828
Sfrs6	A_51_P185121	AK004831	splicing factor, arginine/serine-rich 6	-1.11	72.2	0.81482	25068	P	1.305	2.53	0.04505	1674
Tyki	A_51_P400190	NM_020557	thymidylate kinase family LPS-inducible	-1.11	69.29	0.74634	20896	P	1.047	25.31	0.33257	6710
Uts2r	A_51_P292016	NM_145440	urotensin 2 receptor	-1.11	75.14	0.85928	28182	P	1.118	9.71	0.10872	3236
Amd1	A_51_P381763	Z14986	S-adenosylmethionine decarboxylase 1	-1.111	69.29	0.82265	19058	M	-1.01	49.48	0.94555	12535
B230208H17Rik	A_52_P86750	AK081397	RIKEN cDNA B230208H17 gene	-1.111	77.44	0.88878	30179	M	-1.028	46.3	0.56342	9140
Birc6	A_51_P297586	NM_007566	baculoviral IAP repeat-containing 6	-1.111	72.2	0.84605	20357	M	1.014	42.43	0.85696	11643
Dhx32	A_51_P285997	NM_133941	DEAH (Asp-Glu-Ala-His) box polypeptide	-1.111	69.29	0.76735	22051	P	1.021	40.63	0.7827	11022
Enpp4	A_51_P207934	NM_199016	ectonucleotide pyrophosphatase/phosph	-1.111	72.2	0.79812	23993	P	-1.074	38.4	0.43222	7861
Hdac7a	A_52_P435016	NM_019572	histone deacetylase 7A	-1.111	72.2	0.81015	24709	P	-1.05	42.43	0.39103	7412
Ncoa2	A_52_P335636	NM_008678	nuclear receptor coactivator 2	-1.111	57.76	0.67054	17075	P	1.038	28.13	0.36915	7156
Xab2	A_51_P392147	NM_026156	XPA binding protein 2	-1.111	72.2	0.80715	24528	P	1.041	30.75	0.48832	8424
Akap12	A_51_P342567	NM_031185	A kinase (PRKA) anchor protein (gravin) 1	-1.112	77.44	0.90581	22737	M	1.115	5.75	0.04247	1594
Atp5l	A_52_P75415	NM_013795	ATP synthase, H+ transporting, mitochon	-1.112	69.29	0.83762	19988	M	1.057	25.31	0.39973	7510
Cirbp	A_51_P272106	NM_007705	cold inducible RNA binding protein	-1.112	79.26	0.94067	24483	M	1.002	42.43	0.98749	12959
Dbi	A_51_P399697	NM_001037999	diazepam binding inhibitor	-1.112	79.26	0.93654	29411	P	1.157	9.71	0.21849	5176
Gps2	A_51_P320782	NM_019726	G protein pathway suppressor 2	-1.112	72.2	0.81518	25089	P	1.033	33.49	0.56248	9130
Gtf3c5	A_51_P105810	NM_148928	general transcription factor IIIC, polypept	-1.112	75.14	0.84587	27467	P	-1.124	3.82	0.04561	1710
Ptger1	A_51_P144303	NM_013641		-1.112		0.89165	19221	A	-1.255	0.75	0.01985	849
Rad23a	A_52_P48206	NM_009010	RAD23a homolog (S. cerevisiae)	-1.112	72.2	0.78885	23377	P	-1.01	49.48	0.89905	12056
Ak2	A_52_P68101	NM_016895	adenylate kinase 2	-1.114	69.29	0.7366	20504	P	1.188	4.63	0.0698	2394
H2afv	A_51_P472630	BC028539	H2A histone family, member V	-1.114	72.2	0.82619	25766	P	1.021	40.63	0.80165	11193
Kdelr2	A_52_P69998	NM_025841	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	-1.114	77.44	0.89818	30820	P	1.254	1.32	0.01222	495
Lrp10	A_51_P430357	NM_022993	low-density lipoprotein receptor-related	-1.114	61.79	0.67864	17388	P	1.065	16.2	0.17514	4482
Nola2	A_52_P313813	NM_026631	nucleolar protein family A, member 2	-1.114	75.14	0.84699	27549	P	1.027	36.07	0.59225	9355
Nrd1	A_52_P51783	NM_146150	nardilysin, N-arginine dibasic convertase,	-1.114	65.79	0.71509	19222	P	1.058	25.31	0.42028	7731
Pip5k2b	A_52_P307893	NM_054051	phosphatidylinositol-4-phosphate 5-kinas	-1.114	69.29	0.74985	21061	P	1.031	36.07	0.66214	9990
Plp2	A_51_P243532	NM_019755	proteolipid protein 2	-1.114	69.29	0.77139	22283	P	1.138	3.82	0.02825	1146
0610009J22Rik	A_51_P208019	NM_027859	ring finger protein 215	-1.115	77.44	0.90462	31401	P	1.134	5.75	0.04332	1621
2010311D03Rik	A_51_P236721	NM_133839	RIKEN cDNA 2010311D03 gene	-1.115	65.79	0.70849	18868	P	1.094	11.33	0.13196	3709
2410004P03Rik	A_51_P217415	XM_126830	RIKEN cDNA 2410004P03 gene	-1.115	69.29	0.78046	22793	P	-1.022	47.92	0.64396	9829
Abcf1	A_51_P107234	NM_013854	ATP-binding cassette, sub-family F (GCN2	-1.115	72.2	0.82007	25417	P	1.042	30.75	0.59553	9403
Cfi	A_51_P496905	NM_007686	complement component factor i	-1.115	79.26	0.93314	34072	P	-1.158	8.32	0.15789	4181
Egr1	A_51_P367866	NM_007913	early growth response 1	-1.115	77.44	0.9087	22876	M	1.365	3.01	0.10198	3147
Foxb1	A_52_P345229	NM_022378	forkhead box B1	-1.115		0.92778	20974	A	1.01	42.43	0.93029	12391
Gdi1	A_51_P391276	NM_010273	guanosine diphosphate (GDP) dissociatio	-1.115	72.2	0.79372	23733	P	1.213	1.62	0.01203	487
Gnb2	A_51_P140311	NM_010312	guanine nucleotide binding protein, beta	-1.115	69.29	0.73504	20449	P	1.182	11.33	0.29992	6316
Hnrpu	A_51_P324393	NM_016805	heterogeneous nuclear ribonucleoprotei	-1.115	69.29	0.74317	20729	P	1.12	8.32	0.08448	2772
Hsd17b1	A_51_P243435	NM_010475	hydroxysteroid (17-beta) dehydrogenase	-1.115	57.76	0.70619	17766	M	1.068	13.58	0.13909	3833
Robo4	A_51_P138939	NM_028783	roundabout homolog 4 (Drosophila)	-1.115	72.2	0.81981	25406	P	1.004	42.43	0.94341	12515
Ube4b	A_52_P614582	NM_022022	ubiquitination factor E4B, UFD2 homolog	-1.115	72.2	0.81096	24766	P	1.118	11.33	0.19896	4882
2210403K04Rik	A_51_P144801	AK008813	RIKEN cDNA 2210403K04 gene	-1.116	75.14	0.87933	29619	P	1.105	6.98	0.05898	2105
5133400G04Rik	A_51_P297388	NM_027733	RIKEN cDNA 5133400G04 gene	-1.116	72.2	0.80691	24509	P	-1.3	0.51	0.00636	171
Arl6ip5	A_51_P259902	NM_022992	ADP-ribosylation factor-like 6 interacting	-1.116	72.2	0.8666	21049	M	1.217	3.46	0.05374	1971
Ivd	A_52_P550069	NM_019826	isovaleryl coenzyme A dehydrogenase	-1.116	65.79	0.71658	19314	P	1.067	22.1	0.43315	7876
Rab4b	A_51_P258620	NM_029391	RAB4B, member RAS oncogene family	-1.116	61.79	0.68027	17451	P	1.053	19.02	0.24252	5532
Tsta3	A_51_P210928	NM_031201	tissue specific transplantation antigen P3	-1.116	75.14	0.85117	27811	P	-1.064	28.13	0.178	4537
Fah	A_52_P302496	NM_010176	fumarylacetoacetate hydrolase	-1.117	72.2	0.78653	23160	P	1.012	42.43	0.80843	11268
Lyn	A_51_P345422	NM_010747	Yamaguchi sarcoma viral (v-yes-1) oncoge	-1.117	79.26	0.92203	33202	P	-1.034	45.68	0.55948	9101

Nmi	A_51_P125067	NM_019401	N-myc (and STAT) interactor	-1.117	77.44	0.88448	29960	P	1.221	5.75	0.14657	3975
Ptch1	A_51_P127435	NM_008957	patched homolog 1	-1.117		0.81031	18154	A	1.006	42.43	0.90511	12149
Slc15a4	A_51_P301023	NM_133895	solute carrier family 15, member 4	-1.117	61.79	0.67001	17032	P	1.063	19.02	0.21441	5106
Slc25a19	A_51_P467006	NM_026071	solute carrier family 25 (mitochondrial th	-1.117	61.79	0.68137	17489	P	-1.087	30.75	0.32591	6625
Sos2	A_51_P371152	XM_127051	Son of sevenless homolog 2 (Drosophila)	-1.117	69.29	0.77591	22517	P	1.058	25.31	0.45679	8065
2610203E10Rik	A_52_P625277	NM_183220	RIKEN cDNA 2610203E10 gene	-1.119	75.14	0.8577	28116	P	-1.109	6.98	0.06339	2244
Alg5	A_51_P387342	NM_025442	asparagine-linked glycosylation 5 homolo	-1.119	69.29	0.81506	18678	M	1.114	11.33	0.16984	4381
Brd2	A_51_P295652	NM_001025387	bromodomain containing 2	-1.119	72.2	0.86423	20949	M	1.107	8.32	0.07863	2616
C030007I09Rik	A_52_P333487	AK046449		-1.119	69.29	0.75902	21556	P	1.02	38.4	0.71731	10464
Cd59a	A_52_P40257	NM_007652	CD59a antigen	-1.119	77.44	0.88842	30159	P	1.033	33.49	0.551	9039
Fbxo9	A_51_P312846	NM_023605	f-box protein 9	-1.119	72.2	0.86562	21006	M	1.064	19.02	0.26923	5939
Gpc4	A_52_P480532	AK020640	glypican 4	-1.119	75.14	0.86918	21173	M	-1.017	49.48	0.73205	10591
Hnrpll	A_52_P103377	BC071184	heterogeneous nuclear ribonucleoprotein	-1.119	75.14	0.86758	28713	P	1.079	13.58	0.18771	4694
Mbnl2	A_51_P494361	NM_175341	muscleblind-like 2	-1.119	57.76	0.65163	16155	P	1.042	33.49	0.63655	9776
Ssr2	A_51_P314264	NM_025448	signal sequence receptor, beta	-1.119	75.14	0.85913	26561	P	-1.058	43.15	0.49966	8573
Syngr2	A_51_P105986	NM_009304	synaptogyrin 2	-1.119	72.2	0.80842	24625	P	-1.1	16.2	0.14642	3971
5930436O19Rik	A_52_P514850	AK041816		-1.12	72.2	0.81183	24813	P	1.126	11.33	0.19142	4760
BC033915	A_51_P124467	BC063268	cDNA sequence BC033915	-1.12	77.44	0.90268	31224	P	1.013	40.63	0.76651	10911
Cggbp1	A_52_P620641	NM_178647	CGG triplet repeat binding protein 1	-1.12	65.79	0.70237	18530	P	1.076	22.1	0.44001	7921
Cnp1	A_51_P232901	NM_009923	cyclic nucleotide phosphodiesterase 1	-1.12	75.14	0.85533	28010	P	1.022	38.4	0.63989	9809
Cxxc1	A_51_P262533	NM_028868	CXXC finger 1 (PHD domain)	-1.12	72.2	0.79338	23696	P	-1.015	49.48	0.75721	10840
Lsm2	A_52_P434038	NM_030597	LSM2 homolog, U6 small nuclear RNA ass	-1.12	65.79	0.72855	20148	P	-1.003	49.48	0.94016	12478
Tbp	A_51_P461828	BC012685	TATA box binding protein	-1.12	69.29	0.76748	22078	P	1.207	3.46	0.04606	1731
Fzd5	A_52_P224125	NM_022721	frizzled homolog 5 (Drosophila)	-1.121	69.29	0.77139	22291	P	1.083	11.33	0.10199	3153
Kif2c	A_51_P135092	NM_134471	kinesin family member 2C	-1.121	65.79	0.72307	19910	P	-1.063	42.43	0.48221	8345
Ppp2r3a	A_51_P492625	AK054122	protein phosphatase 2 (formerly 2A), regu	-1.121	72.2	0.81686	25214	P	1.024	38.4	0.70351	10344
Sqrdl	A_51_P209261	NM_021507	sulfide quinone reductase-like (yeast)	-1.121	72.2	0.81362	24950	P	1.058	16.2	0.19569	4832
Stx7	A_51_P363719	NM_016797	syntaxin 7	-1.121	75.14	0.86908	21171	M	1.006	42.43	0.89971	12061
1500034J01Rik	A_52_P407854	BC093523	RIKEN cDNA 1500034J01 gene	-1.122	61.79	0.66573	16870	P	1.082	11.33	0.11809	3438
Antxr2	A_51_P142515	NM_133738	anthrax toxin receptor 2	-1.122	75.14	0.86086	28271	P	1.05	25.31	0.35425	6941
Cds1	A_51_P479696	NM_173370	CDP-diacylglycerol synthase 1	-1.122	65.79	0.71858	19442	P	1.074	22.1	0.44318	7946
D14Ertd500e	A_51_P214306	NM_145462	DNA segment, Chr 14, ERATO Doi 500, ex	-1.122	72.2	0.83461	26611	P	-1.324	0.51	0.0067	202
Hgs	A_51_P460633	NM_008244	HGF-regulated tyrosine kinase substrate	-1.122	72.2	0.80419	24361	P	1.006	42.43	0.93149	12402
Lamc1	A_51_P199354	NM_010683	laminin, gamma 1	-1.122	69.29	0.77954	22710	P	1.149	8.32	0.14179	3880
Rcn3	A_52_P223618	NM_026555	reticulocalbin 3, EF-hand calcium binding	-1.122	72.2	0.78942	23392	P	-1.061	33.49	0.25423	5726
Ubqln1	A_51_P504105	NM_152234	ubiquilin 1	-1.122	61.79	0.68577	17709	P	1.217	3.82	0.05962	2139
Wnt2b	A_52_P403173	NM_009520	wingless related MMTV integration site 2	-1.122	69.29	0.77237	22358	P	-1.02	48.39	0.6543	9912
6030468B19Rik	A_51_P371536	AK020081	RIKEN cDNA 6030468B19 gene	-1.124	75.14	0.84288	25421	M	-1.027	46.3	0.5554	9066
Atad3a	A_51_P244356	NM_179203	ATPase family, AAA domain containing 3A	-1.124	75.14	0.86489	28512	P	-1.025	47.43	0.61571	9585
Cables1	A_51_P117581	NM_022021	Cdk5 and Abl enzyme substrate 1	-1.124	69.29	0.7763	22542	P	-1.003	49.48	0.94963	12581
Cebpz	A_52_P533350	NM_001024806	CCAAT/enhancer binding protein zeta	-1.124	72.2	0.79703	23923	P	1.015	40.63	0.78484	11049
Nsun2	A_52_P365768	NM_145354	NOL1/NOP2/Sun domain family 2	-1.124	61.79	0.657	16429	P	1.006	42.43	0.92273	12316
Plcb4	A_52_P137415	NM_013829	phospholipase C, beta 4	-1.124	65.79	0.72752	20078	P	1.083	13.58	0.18501	4653
Ppp1r16a	A_52_P110157	NM_033371	protein phosphatase 1, regulatory (inhibi	-1.124	65.79	0.72456	19973	P	-1.049	44.4	0.59709	9416
Smn1	A_51_P453502	NM_011420	survival motor neuron 1	-1.124	72.2	0.83244	26258	P	-1.148	2.53	0.03732	1419
4933440N22Rik	A_51_P300054	XM_986054	RIKEN cDNA 4933440N22 gene	-1.125	72.2	0.80507	24418	P	-1.018	49.48	0.74619	10754
Amotl2	A_51_P348804	NM_019764	angiomotin like 2	-1.125	65.79	0.71259	19086	P	1.107	9.71	0.13497	3764
Atf3	A_52_P452689	NM_007498	activating transcription factor 3	-1.125	79.26	0.94006	34584	P	-1.037	48.39	0.78837	11075
Clec2d	A_51_P324690	NM_053109	C-type lectin domain family 2, member d	-1.125	75.14	0.85336	27937	P	1.005	42.43	0.92969	12386
Ddx6	A_52_P573497	NM_181324	DEAD (Asp-Glu-Ala-Asp) box polypeptide	-1.125	65.79	0.75941	17799	M	1.065	25.31	0.43044	7832
Sacm1l	A_51_P519385	NM_030692	SAC1 (suppressor of actin mutations 1, ho	-1.125	61.79	0.77781	17136	M	1.008	42.43	0.88809	11942
Wdr5	A_51_P390437	NM_080848	WD repeat domain 5	-1.125	65.79	0.71449	19186	P	-1.059	30.75	0.21086	5050
Actr3	A_51_P217535	NM_023735	ARP3 actin-related protein 3 homolog (ye	-1.126	72.2	0.84728	20405	M	1.108	11.33	0.15788	4179

Cs	A_52_P182659	NM_026444	citrate synthase	-1.126	65.79	0.71449	18155	P	-1.015	49.48	0.80495	11218
Dpf2	A_51_P372874	NM_011262	D4, zinc and double PHD fingers family 2	-1.126	72.2	0.80051	24118	P	1.042	25.31	0.34979	6871
Eml4	A_51_P117832	NM_199466	echinoderm microtubule associated prote	-1.126	65.79	0.69309	18065	P	1.095	13.58	0.23654	5444
Rab35	A_51_P354572	NM_198163	RAB35, member RAS oncogene family	-1.126	69.29	0.78077	22806	P	1.151	4.63	0.04332	1622
Rfc4	A_51_P378450	NM_145480	replication factor C (activator 1) 4	-1.126	65.79	0.68811	17839	P	1.015	42.43	0.79994	11175
Rg9mtd3	A_52_P185109	NM_027266	RNA (guanine-9-) methyltransferase dom	-1.126	72.2	0.82097	25449	P	-1.139	2.53	0.03337	1301
Syk	A_51_P444934	NM_011518	spleen tyrosine kinase	-1.126	75.14	0.84399	27343	P	-1.259	0.56	0.01073	416
Atp9a	A_52_P276840	NM_015731	ATPase, class II, type 9A	-1.127	65.79	0.7167	19320	P	-1.587	0	0.00584	25
BC038479	A_51_P104197	NM_153803	cDNA sequence BC038479	-1.127	69.29	0.78278	22923	P	1.099	13.58	0.24328	5557
Bckdk	A_51_P404413	NM_009739	branched chain ketoacid dehydrogenase l	-1.127	65.79	0.6989	18319	P	-1.169	2.04	0.03496	1338
Ccng2	A_51_P360165	NM_007635	cyclin G2	-1.127	72.2	0.80585	24460	P	-1.108	8.32	0.07566	2552
Cog3	A_51_P499153	NM_177381	component of oligomeric golgi complex 3	-1.127	65.79	0.79007	17572	M	-1.145	4.63	0.06923	2381
Ddb2	A_52_P3825	NM_028119	damage specific DNA binding protein 2	-1.127	72.2	0.81591	25146	P	1.025	40.63	0.84626	11580
Fbxl8	A_51_P120254	NM_015821	F-box and leucine-rich repeat protein 8	-1.127	75.14	0.84427	27356	P	1.04	30.75	0.56318	9135
G6pc	A_51_P462385	NM_008061	glucose-6-phosphatase, catalytic	-1.127	69.29	0.76244	21782	P	1.067	19.02	0.27923	6079
Galm	A_51_P136337	NM_176963	galactose mutarotase	-1.127	72.2	0.80281	24241	M	-1.197	1.1	0.01704	739
Hsd17b12	A_52_P243599	NM_019657	hydroxysteroid (17-beta) dehydrogenase	-1.127	69.29	0.77214	22354	P	1.023	42.43	0.8792	11852
Mirg	A_52_P277415	AK077315	miRNA containing gene	-1.127	72.2	0.82449	25681	P	1.154	9.71	0.17832	4543
Mrps7	A_51_P193302	NM_025305	mitochondrial ribosomal protein S7	-1.127	72.2	0.81287	24896	P	-1.094	22.1	0.13728	3484
Pkmyt1	A_51_P312360	ENSMUST00000024701	protein kinase, membrane associated tyro	-1.127	75.14	0.84099	27157	P	1.01	42.43	0.85616	11636
Pmpca	A_52_P504302	NM_173180	peptidase (mitochondrial processing) alph	-1.127	65.79	0.71134	19035	P	1.138	3.82	0.03188	1256
Tmem15	A_51_P284966	NM_177648	dolichol kinase	-1.127	72.2	0.79435	23770	P	-1.128	3.46	0.0419	1581
Tube1	A_52_P242194	AK039886	epsilon-tubulin 1	-1.127	81.02	0.82602	18428	M	-1.042	43.75	0.47441	8253
Ddx39	A_51_P288162	NM_197982	DEAD (Asp-Glu-Ala-Asp) box polypeptide	-1.129	69.29	0.7489	21013	P	1.045	22.1	0.30267	6347
Enpp1	A_51_P231499	NM_008813	ectonucleotide pyrophosphatase/phosph	-1.129	72.2	0.80436	24385	P	1.084	13.58	0.15718	4166
Gnmt	A_51_P419439	NM_010321	glycine N-methyltransferase	-1.129	61.79	0.64949	16077	P	1.076	13.58	0.17491	4477
Gprc5c	A_52_P405460	BC008228	G protein-coupled receptor, family C, grou	-1.129	75.14	0.85933	28188	P	-1.159	2.04	0.0353	1361
Mbd3	A_51_P398004	NM_013595	methyl-CpG binding domain protein 3	-1.129	69.29	0.76749	22079	P	-1.025	47.43	0.63197	9735
Rnf10	A_51_P202652	NM_016698	ring finger protein 10	-1.129	69.29	0.76088	21692	P	1.089	13.58	0.19032	4733
Ror2	A_51_P234365	NM_013846	receptor tyrosine kinase-like orphan recep	-1.129	79.26	0.9238	33372	P	1.022	40.63	0.8037	11205
Scyl1	A_51_P498023	NM_023912	SCY1-like 1 (S. cerevisiae)	-1.129	75.14	0.84931	27711	P	1.127	5.75	0.04017	1534
Slc25a17	A_51_P181170	NM_011399	solute carrier family 25 (mitochondrial ca	-1.129	65.79	0.71359	19131	P	1.094	11.33	0.10949	3250
Slc43a1	A_51_P362483	BC053747	solute carrier family 43, member 1	-1.129		0.84855	20244	A	-1.211	1.1	0.01933	816
Vars2l	A_52_P185639	NM_175137	valyl-tRNA synthetase 2, mitochondrial (p	-1.129	57.76	0.64092	15720	P	-1.197	1.18	0.02152	904
Vhlh	A_52_P670070	S76748	von Hippel-Lindau syndrome homolog	-1.129	61.79	0.65604	16395	P	-1.015	49.48	0.82868	11440
2810007J24Rik	A_51_P189733	NM_175250	RIKEN cDNA 2810007J24 gene	-1.13	57.76	0.62667	14761	P	1.078	19.02	0.30903	6428
6330549D23Rik	A_52_P225772	NM_175469	RIKEN cDNA 6330549D23 gene	-1.13	81.02	0.84873	24143	M	-1.039	45.05	0.5599	9106
Agpat2	A_51_P238565	NM_026212	1-acylglycerol-3-phosphate O-acyltransfer	-1.13	72.2	0.83252	26272	P	-1.193	3.46	0.09699	3032
Alg8	A_52_P651371	NM_199035	asparagine-linked glycosylation 8 homolo	-1.13	49.93	0.60581	13713	P	-1.03	46.85	0.63229	9743
Cib1	A_51_P175454	NM_011870	calcium and integrin binding 1 (calmyrin)	-1.13	69.29	0.7823	22881	P	1.015	40.63	0.73436	10622
Ddx42	A_52_P346367	NM_028074	DEAD (Asp-Glu-Ala-Asp) box polypeptide	-1.13	72.2	0.81062	24730	P	-1.091	22.1	0.20743	5020
Dffa	A_52_P586539	NM_001025296	DNA fragmentation factor, alpha subunit	-1.13	69.29	0.76568	21950	P	1.11	13.58	0.24876	5628
Hoxa10	A_51_P466285	NM_008263	homeo box A10	-1.13	79.26	0.93324	31569	M	1.065	16.2	0.17381	4446
Ier3	A_51_P286488	NM_133662	immediate early response 3	-1.13	75.14	0.88077	29704	P	1.349	6.98	0.27762	6058
Tradd	A_51_P288505	NM_001033161	TNFRSF1A-associated via death domain	-1.13	72.2	0.79136	23551	P	1.028	36.07	0.59408	9375
Zfp57	A_51_P197925	NM_001013745	zinc finger protein 57	-1.13	69.29	0.75532	20417	M	1.006	42.43	0.91179	12202
B4galt6	A_51_P122268	NM_019737	UDP-Gal:betaGlcNAc beta 1,4-galactosyltr	-1.131	69.29	0.76088	21686	P	1.149	6.98	0.08414	2751
Ccnf	A_51_P328333	NM_007634	cyclin F	-1.131	69.29	0.73731	19337	M	-1.226	0.75	0.01515	647
Cyln2	A_52_P360112	NM_009990	CAP-GLY domain containing linker protein	-1.131	75.14	0.8411	27173	P	1.034	36.07	0.68921	10230
Ski	A_51_P301508	NM_011385	Sloan-Kettering viral oncogene homolog	-1.131	65.79	0.69069	17952	P	1.08	13.58	0.13156	3701
Sln	A_51_P297498	NM_025540	sarcolipin	-1.131		0.94728	13948	A	1.045	25.31	0.31396	6511
Zfp219	A_52_P512329	NM_027248	zinc finger protein 219	-1.131	65.79	0.75215	20214	M	1.231	2.53	0.0225	956
9930021J03Rik	A_52_P671502	AK047515	RIKEN cDNA 9930021J03 gene	-1.133	65.79	0.69872	18312	P	1.019	40.63	0.71961	10494

Csf3	A_51_P317176	NM_009971	colony stimulating factor 3 (granulocyte)	-1.133	79.26	0.7823	18438	M	1.053	19.02	0.25085	5659
Nr1d2	A_52_P303891	NM_011584	nuclear receptor subfamily 1, group D, me	-1.133	69.29	0.82214	18999	M	1.105	8.32	0.0698	2393
Ppp4r2	A_52_P212887	NM_182939	protein phosphatase 4, regulatory subuni	-1.133	65.79	0.79365	17755	M	1.191	3.82	0.04689	1749
Rassf5	A_51_P275679	NM_018750	Ras association (RalGDS/AF-6) domain far	-1.133	61.79	0.67089	17094	P	1.058	28.13	0.52299	8780
Stard7	A_51_P390496	NM_139308	START domain containing 7	-1.133	61.79	0.7704	16872	M	1.167	4.63	0.05612	2035
5630401D24Rik	A_51_P125567	NM_144877	RIKEN cDNA 5630401D24 gene	-1.134	61.79	0.65421	16317	P	1.07	13.58	0.14341	3913
Akap8	A_51_P176549	NM_019774	A kinase (PRKA) anchor protein 8	-1.134	69.29	0.82282	19072	M	1.06	30.75	0.6297	9711
Cdca7	A_51_P202857	NM_025866	cell division cycle associated 7	-1.134	72.2	0.79919	24055	P	-1.325	0.51	0.00584	64
Ell	A_51_P292943	NM_007924	elongation factor RNA polymerase II	-1.134	72.2	0.83384	26400	P	1.056	19.02	0.23119	5366
Fhod1	A_51_P495379	NM_177699	formin homology 2 domain containing 1	-1.134	65.79	0.68725	17784	P	1.045	28.13	0.40407	7560
Pias1	A_51_P312166	NM_019663	protein inhibitor of activated STAT 1	-1.134	69.29	0.77853	22680	P	1.001	42.43	0.9888	12974
Qtrtd1	A_52_P392742	NM_029128	queuine tRNA-ribosyltransferase domain	-1.134	57.76	0.62794	14851	P	-1.12	9.71	0.11175	3311
1200009F10Rik	A_52_P417694	NM_027078	RIKEN cDNA 1200009F10 gene	-1.135	72.2	0.81301	24912	P	1.079	16.2	0.24038	5492
2810026P18Rik	A_52_P522166	BU509931		-1.135	61.79	0.66142	16644	P	1.005	42.43	0.9313	12396
BC017158	A_51_P304510	NM_145590	cDNA sequence BC017158	-1.135	72.2	0.83095	26107	P	1.027	38.4	0.73228	10605
Lamb1-1	A_51_P244287	NM_008482	laminin B1 subunit 1	-1.135	65.79	0.698	18268	P	-1.045	44.4	0.55422	9055
Tmpo	A_51_P328926	NM_011605	thymopoietin	-1.135	69.29	0.7491	21047	P	1.089	9.71	0.08651	2813
A530041M06Rik	A_52_P739394	AK040901	RIKEN cDNA A530041M06 gene	-1.136	49.93	0.59503	13235	P	1.083	22.1	0.4643	8151
Alas1	A_52_P129756	NM_020559	aminolevulinic acid synthase 1	-1.136	61.79	0.65572	16366	P	-1.037	45.05	0.48934	8431
Fubp3	A_51_P268297	NM_001033389	far upstream element (FUSE) binding prot	-1.136	61.79	0.75861	16417	M	-1.037	44.4	0.48664	8401
Hnrpdl	A_51_P476091	ENSMUST00000031271	heterogeneous nuclear ribonucleoprotein	-1.136	75.14	0.77148	21164	P	1.104	13.58	0.23887	5468
Hnrph2	A_51_P333885	NM_019868	heterogeneous nuclear ribonucleoprotein	-1.136	69.29	0.82279	19068	M	1.116	9.71	0.14791	4000
Igfals	A_51_P277088	NM_008340	insulin-like growth factor binding protein,	-1.136	75.14	0.85319	27927	P	1.007	42.43	0.88957	11961
Slc27a4	A_52_P61854	NM_011989	solute carrier family 27 (fatty acid transpo	-1.136	53.87	0.60358	13607	P	-1.027	45.68	0.52549	8805
Yeats4	A_51_P342227	NM_026570	YEATS domain containing 4	-1.136	61.79	0.7682	16801	M	1.188	11.33	0.32966	6658
1200011M11Rik	A_52_P238902	NM_024262	RIKEN cDNA 1200011M11 gene	-1.138	69.29	0.77253	22363	P	-1.02	49	0.71217	10419
4922503N01Rik	A_51_P342126	NM_153392	RIKEN cDNA 4922503N01 gene	-1.138	72.2	0.79613	23876	P	-1.094	22.1	0.20568	4984
5730536A07Rik	A_51_P327530	NM_026635	RIKEN cDNA 5730536A07 gene	-1.138	69.29	0.75606	21452	P	-1.094	28.13	0.30427	6376
Bmi1	A_51_P121547	NM_007552	Bmi1 polycomb ring finger oncogene	-1.138	69.29	0.74163	20677	P	1.004	42.43	0.94576	12550
Cldn5	A_51_P189814	NM_013805	claudin 5	-1.138	75.14	0.84664	27539	P	1.056	22.1	0.26935	5942
Hn1	A_51_P247157	NM_008258	hematological and neurological expressed	-1.138	72.2	0.83129	26133	P	-1.123	6.98	0.076	2553
Siah1b	A_51_P378602	NM_009173	seven in absentia 1B	-1.138	57.76	0.62767	14839	P	1.011	42.43	0.88251	11889
Traf7	A_51_P172373	NM_153792	Tnf receptor-associated factor 7	-1.138	61.79	0.6531	16264	P	1.129	11.33	0.27184	5979
Ubb	A_52_P606297	NM_011664	ubiquitin B	-1.138	72.2	0.85387	20635	M	1.079	19.02	0.31282	6487
Ythdf2	A_51_P271751	NM_145393	YTH domain family 2	-1.138	61.79	0.7522	16151	M	1.01	42.43	0.9166	12235
Adck4	A_51_P197209	NM_133770	aarF domain containing kinase 4	-1.139	65.79	0.69954	18353	P	-1.02	49	0.7056	10369
Atf4	A_52_P139727	NM_009716	activating transcription factor 4	-1.139	69.29	0.78948	23399	P	-1.049	43.15	0.46769	8186
Cacnb1	A_51_P478138	NM_031173	calcium channel, voltage-dependent, beta	-1.139	65.79	0.7332	19136	M	-1.084	28.13	0.27425	6016
Egln1	A_51_P186899	NM_053207	EGL nine homolog 1 (C. elegans)	-1.139	69.29	0.77167	22347	P	1.136	8.32	0.1313	3694
Hnrpa2b1	A_51_P419981	AF073993	heterogeneous nuclear ribonucleoprotein	-1.139	72.2	0.83448	19721	M	-1.014	49.48	0.78783	11070
Rab33a	A_52_P66226	NM_011228	RAB33A, member of RAS oncogene family	-1.139	84.56	0.89837	26865	P	1.065	19.02	0.22137	5227
Rbl1	A_51_P286665	NM_011249	retinoblastoma-like 1 (p107)	-1.139	69.29	0.7539	21315	P	1.206	3.46	0.04256	1602
Sh3bgrl2	A_52_P316933	NM_172507	SH3 domain binding glutamic acid-rich pr	-1.139	79.26	0.93324	34093	P	-1.087	30.75	0.33062	6681
Tsc22d3	A_51_P235816	AF024519	TSC22 domain family 3	-1.139	61.79	0.75588	16340	M	-1.242	5.75	0.21645	5140
Actb	A_51_P173760	NM_007393	actin, beta, cytoplasmic	-1.14	79.26	0.93538	24290	M	1.172	3.82	0.0383	1458
Bst2	A_51_P169693	NM_198095	bone marrow stromal cell antigen 2	-1.14	65.79	0.71622	19288	P	1.001	42.43	0.97325	12767
Kif22	A_51_P493467	NM_145588	kinesin family member 22	-1.14	65.79	0.721	19642	P	1.003	42.43	0.95103	12596
Ugcgl1	A_51_P236775	AK134231	UDP-glucose ceramide glucosyltransferas	-1.14	65.79	0.68448	17644	P	-1.142	3.82	0.05981	2144
1810073N04Rik	A_52_P145914	NM_024249	RIKEN cDNA 1810073N04 gene	-1.142	69.29	0.76604	21982	P	1.03	33.49	0.49675	8537
2810013P06Rik	A_51_P255373	AK077895	RIKEN cDNA 2810013P06 gene	-1.142	57.76	0.73642	15673	M	1.063	22.1	0.33807	6762
D930010J01Rik	A_52_P559957	NM_134147	RIKEN cDNA D930010J01 gene	-1.142	77.44	0.89435	30608	P	1.078	13.58	0.188	4697
Impdh2	A_51_P257898	NM_011830	inosine 5'-phosphate dehydrogenase 2	-1.142	65.79	0.68819	17840	P	-1.106	16.2	0.1765	4508
Med25	A_52_P632227	NM_029365	mediator of RNA polymerase II transcripti	-1.142	75.14	0.85187	27847	P	-1.022	47.92	0.62498	9671

Cyp2c70	A_51_P134142	NM_145499	cytochrome P450, family 2, subfamily c, p	-1.143	72.2	0.78753	21906	M	-1.036	45.05	0.49593	8519
Ninj1	A_51_P295046	NM_013610	ninjurin 1	-1.143	53.87	0.60279	13573	P	1.009	42.43	0.91797	12248
Rif1	A_51_P439711	NM_175238	Rap1 interacting factor 1 homolog (yeast)	-1.143	57.76	0.60363	13610	P	-1.096	38.4	0.5353	8891
Zfp523	A_51_P222815	NM_172617	zinc finger protein 523	-1.143	65.79	0.68868	17848	P	1.05	28.13	0.54903	9014
Azi2	A_52_P674847	NM_013727	5-azacytidine induced gene 2	-1.144	72.2	0.79778	23982	P	-1.001	49.48	0.98039	12849
Dhx9	A_51_P369683	NM_007842	DEAH (Asp-Glu-Ala-His) box polypeptide	-1.144	57.76	0.64806	14094	P	1.095	9.71	0.0789	2628
Galnt3	A_51_P380005	NM_015736	UDP-N-acetyl-alpha-D-galactosamine:pol	-1.144	77.44	0.92234	33209	P	1.083	16.2	0.22642	5292
Nes	A_51_P452323	NM_016701	nestin	-1.144	72.2	0.8435	27294	P	-1.061	28.13	0.18616	4673
Sephs2	A_51_P418765	NM_009266	selenophosphate synthetase 2	-1.144	57.76	0.61013	13957	P	-1.221	0.92	0.01571	675
Vegfa	A_52_P249424	NM_001025257	vascular endothelial growth factor A	-1.144	72.2	0.79763	23975	P	1.087	16.2	0.2306	5360
2610002J23Rik	A_52_P328116	AK164857	RIKEN cDNA 2610002J23 gene	-1.145	45.92	0.56378	11825	P	-1.12	6.98	0.07798	2606
4931406I20Rik	A_51_P152222	NM_025739	RIKEN cDNA 4931406I20 gene	-1.145	69.29	0.77678	22558	P	1.003	42.43	0.94908	12575
Frem2	A_51_P214503	NM_172862	Fras1 related extracellular matrix protein	-1.145		0.89109	26460	A	-1.004	49.48	0.93771	12457
Itih3	A_51_P367100	NM_008407	inter-alpha trypsin inhibitor, heavy chain	-1.145	61.79	0.70086	17492	M	1.013	42.43	0.79013	11090
Mfge8	A_51_P255682	NM_008594	milk fat globule-EGF factor 8 protein	-1.145	72.2	0.83817	27004	P	1.18	3.46	0.03519	1355
Nfya	A_52_P550049	BC057099	nuclear transcription factor-Y alpha	-1.145	65.79	0.72009	19557	P	1.022	38.4	0.71928	10486
Rgs19	A_51_P388984	NM_026446	regulator of G-protein signaling 19	-1.145	61.79	0.67	17028	P	-1.015	49.48	0.73696	10649
1110002B05Rik	A_52_P561936	NM_134054	RIKEN cDNA 1110002B05 gene	-1.147	65.79	0.70099	18436	P	1.04	28.13	0.45323	8028
Abcd3	A_52_P394395	NM_008991	ATP-binding cassette, sub-family D (ALD),	-1.147	69.29	0.82666	19209	M	1.214	9.71	0.29461	6272
Bcl7b	A_51_P505412	NM_009745	B-cell CLL/lymphoma 7B	-1.147	65.79	0.70407	18640	P	1.017	40.63	0.7285	10553
C330021A05Rik	A_52_P71666	NM_153082	RIKEN cDNA C330021A05 gene	-1.147	49.93	0.78248	20112	M	-1.053	42.43	0.41585	7692
Canx	A_52_P337679	NM_007597	calnexin	-1.147	72.2	0.82988	19378	M	1.144	4.63	0.04432	1655
Ggh	A_51_P439970	NM_010281	gamma-glutamyl hydrolase	-1.147	65.79	0.70103	18439	P	1.064	28.13	0.5331	8872
Gss	A_52_P358860	NM_008180	glutathione synthetase	-1.147	69.29	0.76244	21787	P	-1.377	0.51	0.00584	100
Il11	A_51_P267783	NM_008350	interleukin 11	-1.147	77.44	0.91097	32052	P	1.16	3.82	0.03814	1447
Pou3f1	A_51_P511270	NM_011141	POU domain, class 3, transcription factor	-1.147		0.93855	13704	A	1.089	9.71	0.07994	2651
Riok3	A_52_P370443	NM_024182	RIO kinase 3 (yeast)	-1.147	72.2	0.7132	17097	P	1.088	19.02	0.36214	7051
Stx6	A_52_P214891	NM_021433	syntaxin 6	-1.147	72.2	0.7944	23782	P	1.117	9.71	0.11002	3265
Cnot2	A_52_P12604	NM_001037847	CCR4-NOT transcription complex, subunit	-1.148	61.79	0.63052	15158	P	1.011	42.43	0.87447	11803
Cyyr1	A_51_P462461	NM_144853	cysteine and tyrosine-rich protein 1	-1.148		0.81778	18519	A	-1.031	45.68	0.53816	8920
Ell3	A_52_P382926	NM_145973	elongation factor RNA polymerase II-like	-1.148	72.2	0.83857	27014	P	1.001	42.43	0.98918	12978
F3	A_51_P236846	NM_010171	coagulation factor III	-1.148	75.14	0.84706	27555	P	1.142	8.32	0.1419	3885
Npdc1	A_51_P154596	NM_008721	neural proliferation, differentiation and c	-1.148	57.76	0.62552	14718	P	1.061	22.1	0.38928	7387
Odc1	A_52_P7041	NM_013614	similar to Ornithine decarboxylase (ODC)	-1.148	75.14	0.87252	29100	P	1.255	3.46	0.06064	2168
Rnf146	A_52_P183071	BC023104	ring finger protein 146	-1.148	65.79	0.72835	20136	P	1.091	19.02	0.35983	7009
Rpn2	A_52_P57651	NM_019642	ribophorin II	-1.148	69.29	0.75282	21253	P	1.06	22.1	0.29981	6312
Trim15	A_52_P233342	NM_001024134	tripartite motif protein 15	-1.148	72.2	0.84228	27228	M	-1.22	0.56	0.00977	362
Aqp2	A_51_P492298	NM_009699	aquaporin 2	-1.149	72.2	0.80242	24176	P	1.168	2.53	0.01802	766
Aup1	A_51_P165984	NM_007517	ancient ubiquitous protein	-1.149	65.79	0.70239	18533	P	1.005	42.43	0.91864	12261
Mum1l1	A_51_P418029	NM_175541	melanoma associated antigen (mutated)	-1.149	72.2	0.82765	25867	P	1.041	28.13	0.37743	7250
Nup43	A_52_P566055	NM_145706	nucleoporin 43	-1.149	69.29	0.76022	21634	P	1.035	36.07	0.66894	10034
Psmb9	A_51_P369803	NM_013585	proteosome (prosome, macropain) subur	-1.149	72.2	0.82914	25979	P	1.003	42.43	0.96286	12690
Ptdsr	A_51_P332952	NM_033398	jumonji domain containing 6	-1.149	69.29	0.74208	20695	P	1.122	6.98	0.05995	2154
Rad1	A_52_P278192	NM_011232	RAD1 homolog (S. pombe)	-1.149	72.2	0.79586	23860	P	1.146	6.98	0.07211	2439
Rnf130	A_51_P398517	NM_021540	ring finger protein 130	-1.149	57.76	0.68397	15910	P	-1.035	44.4	0.45323	8029
Srp54	A_51_P420901	NM_011899	signal recognition particle 54	-1.149	69.29	0.82559	19166	M	1.121	13.58	0.32092	6575
Tgif	A_52_P257590	NM_009372	TG interacting factor 1	-1.149	65.79	0.68139	17495	P	1.202	6.98	0.14469	3939
0610006I08Rik	A_51_P457492	NM_025791	RIKEN cDNA 0610006I08 gene	-1.151	61.79	0.66969	17014	P	-1.192	1.18	0.01896	800
Abcb11	A_51_P309338	NM_021022	ATP-binding cassette, sub-family B (MDR/	-1.151	72.2	0.80756	24555	P	1.011	42.43	0.83061	11466
Anxa4	A_51_P256344	NM_013471	annexin A4	-1.151	65.79	0.77015	19963	P	1.14	8.32	0.13739	3793
Dusp12	A_51_P134776	NM_023173	dual specificity phosphatase 12	-1.151	69.29	0.7332	20390	P	1.005	42.43	0.93769	12456
Irf2	A_51_P316523	NM_008391	interferon regulatory factor 2	-1.151	69.29	0.74447	20817	P	1.164	9.71	0.22226	5243
Luc7l	A_52_P311417	NM_025881	Luc7 homolog (S. cerevisiae)-like	-1.151	65.79	0.7114	19041	P	1.136	9.71	0.15944	4209

Parg	A_51_P413461	NM_011960	poly (ADP-ribose) glycohydrolase	-1.151	57.76	0.60729	13768	P	-1.336	0.51	0.00755	273
Rg9mtd1	A_51_P301994	NM_029092	RNA (guanine-9-) methyltransferase doma	-1.151	72.2	0.82703	25846	P	-1.02	48.39	0.66709	10020
2010317E24Rik	A_51_P472217	BC070477	RIKEN cDNA 2010317E24 gene	-1.152	75.14	0.85101	27783	P	-1.192	1.62	0.03941	1495
Asb8	A_51_P142091	NM_030121	ankyrin repeat and SOCS box-containing	-1.152	69.29	0.8011	18038	M	1.073	22.1	0.38475	7335
Bcl2l13	A_51_P255757	NM_153516	BCL2-like 13 (apoptosis facilitator)	-1.152	61.79	0.6713	17100	P	1.081	11.33	0.11652	3406
Clptm1	A_51_P332799	NM_019649	cleft lip and palate associated transmemb	-1.152	53.87	0.58634	12837	P	-1.053	40.63	0.33294	6714
Jak2	A_52_P309376	NM_008413	Janus kinase 2	-1.152	75.14	0.88121	29727	P	-1.017	49.48	0.80818	11256
Map2k3	A_51_P272817	NM_008928	mitogen activated protein kinase kinase 3	-1.152	53.87	0.57768	12388	P	1.076	16.2	0.24471	5568
Sfrs2	A_51_P262432	NM_011358	splicing factor, arginine/serine-rich 2 (SC-	-1.152	69.29	0.79483	17806	M	-1.137	3.82	0.05152	1896
Tspyl1	A_52_P658034	NM_009433	testis-specific protein, Y-encoded-like 1	-1.152	72.2	0.8365	26846	P	-1.019	49.48	0.799	11169
Zcchc3	A_51_P479132	NM_175126	zinc finger, CCHC domain containing 3	-1.152	65.79	0.73013	20264	P	1.03	36.07	0.66894	10036
1810007M14Rik	A_51_P317166	AK007365	RIKEN cDNA 1810007M14 gene	-1.153	57.76	0.59364	13149	P	1.18	9.71	0.2404	5493
2600005C20Rik	A_52_P644790	AK083675	ribosomal RNA processing 1 homolog B (	-1.153		0.82214	16470	A	1.143	9.71	0.15508	4133
Arf1	A_52_P242438	NM_007476	ADP-ribosylation factor 1	-1.153	61.79	0.73382	15618	M	1.183	3.82	0.05209	1915
BC023892	A_51_P272876	XM_135029	cDNA sequence BC023892	-1.153	72.2	0.82214	25529	P	1.084	19.02	0.37742	7248
Dazap2	A_51_P321580	NM_011873	DAZ associated protein 2	-1.153	69.29	0.82639	19184	M	1.213	5.75	0.14469	3937
Fndc3b	A_51_P202512	NM_173182	fibronectin type III domain containing 3B	-1.153	45.92	0.54522	11207	P	1.077	30.75	0.71557	10446
Fzr1	A_52_P486322	NM_019757	fizzy/cell division cycle 20 related 1 (Dros	-1.153	75.14	0.88606	30031	P	-1.068	38.4	0.3959	7470
Gnaq	A_51_P311659	AK031823		-1.153	61.79	0.66333	16714	P	1.139	8.32	0.12613	3632
H47	A_51_P323610	NM_024439	histocompatibility 47	-1.153	65.79	0.72077	19613	P	-1.072	28.13	0.20046	4911
Kctd3	A_52_P243102	NM_172650	potassium channel tetramerisation doma	-1.153	69.29	0.7414	20665	P	1.067	25.31	0.45934	8093
Mbtps1	A_51_P382588	NM_019709	membrane-bound transcription factor pe	-1.153	69.29	0.80583	18245	M	1.095	13.58	0.22294	5257
Psme3	A_51_P166762	NM_011192	proteaseome (prosome, macropain) 28 s	-1.153	57.76	0.62667	14766	P	-1.087	30.75	0.31073	6463
Slc30a7	A_52_P113207	AK039587	solute carrier family 30 (zinc transporter),	-1.153		0.9343	13599	A	-1.185	1.18	0.02003	857
Spcs2	A_51_P273843	NM_025668	signal peptidase complex subunit 2 homo	-1.153	57.76	0.71545	14603	M	1.112	11.33	0.15725	4168
Adora2a	A_51_P387348	BC110692	adenosine A2a receptor	-1.155	53.87	0.59026	12973	P	1.148	3.01	0.02253	962
Eif4g1	A_51_P384193	NM_145941	eukaryotic translation initiation factor 4,	-1.155	72.2	0.80825	24605	P	1.028	36.07	0.59488	9390
Fnbp4	A_51_P509808	NM_018828	formin binding protein 4	-1.155	61.79	0.65947	16558	P	1.159	4.63	0.0453	1703
Kbtbd2	A_51_P189151	AK028396	kelch repeat and BTB (POZ) domain conta	-1.155	61.79	0.62996	15084	P	1.096	11.33	0.17106	4400
Mycbp	A_52_P408657	NM_019660	c-myc binding protein	-1.155	65.79	0.7015	18477	P	1.015	42.43	0.8124	11306
Serf2	A_51_P145357	NM_011354	small EDRK-rich factor 2	-1.155	53.87	0.7001	13953	M	-1.017	49.48	0.75469	10821
Tbc1d10b	A_51_P233947	NM_144522	TBC1 domain family, member 10b	-1.155	69.29	0.78472	23050	P	1.037	36.07	0.71909	10482
Cdc42se1	A_51_P512591	NM_172395	CDC42 small effector 1	-1.156	49.93	0.55997	11758	P	1.034	30.75	0.47675	8279
Mat1a	A_51_P464182	NM_133653	methionine adenosyltransferase I, alpha	-1.156	65.79	0.71674	19336	P	-1.008	49.48	0.89905	12055
Mxi1	A_51_P294994	NM_001008542	Max interacting protein 1	-1.156	53.87	0.58964	12942	P	-1.05	38.4	0.27417	6015
Nit2	A_52_P448006	NM_023175	nitrilase family, member 2	-1.156	61.79	0.67001	17034	P	1.017	40.63	0.71638	10461
Rbm9	A_52_P310530	NM_053104	RNA binding motif protein 9	-1.156	57.76	0.66363	15969	P	1.106	13.58	0.23272	5392
Sec23b	A_51_P371120	NM_019787	SEC23B (S. cerevisiae)	-1.156	57.76	0.61992	14455	P	-1.078	25.31	0.17766	4527
Ubqln2	A_52_P381929	NM_018798	ubiquilin 2	-1.156	69.29	0.74909	21033	P	1.123	6.98	0.07145	2422
Cpn1	A_52_P308669	NM_030703	carboxypeptidase N, polypeptide 1	-1.157	53.87	0.56806	11984	P	-1.064	33.49	0.27	5957
Mknk2	A_52_P376135	NM_021462	MAP kinase-interacting serine/threonine	-1.157	75.14	0.70968	16944	P	-1.04	45.05	0.58166	9266
Ppm1g	A_51_P484832	NM_008014	protein phosphatase 1G (formerly 2C), m	-1.157	61.79	0.63441	15414	P	1.165	5.75	0.06576	2303
Prpf18	A_51_P148597	NM_026045	PRP18 pre-mRNA processing factor 18 ho	-1.157	53.87	0.70294	14091	M	1.553	0.24	0.0065	181
Slc1a5	A_51_P453475	NM_009201	solute carrier family 1 (neutral amino aci	-1.157	61.79	0.65034	16107	P	1.008	42.43	0.88304	11895
Smad5	A_51_P452207	NM_008541	MAD homolog 5 (Drosophila)	-1.157	61.79	0.65163	16153	P	1.015	42.43	0.85461	11626
Tenc1	A_51_P395473	NM_153533	tensin like C1 domain-containing phospha	-1.157	42.28	0.52633	10567	P	1.01	42.43	0.8449	11560
Tex261	A_51_P147654	AK170049	testis expressed gene 261	-1.157	65.79	0.72699	20051	P	1.072	16.2	0.18589	4668
Map3k7	A_52_P175952	NM_172688	mitogen activated protein kinase kinase k	-1.159	45.92	0.52764	10623	P	1.052	22.1	0.25407	5725
Mcm7	A_51_P165704	NM_008568	minichromosome maintenance deficient	-1.159	57.76	0.6013	13521	P	-1.264	0.51	0.00731	253
Srp19	A_51_P514668	NM_025527	signal recognition particle 19	-1.159	61.79	0.67216	17159	P	1.013	42.43	0.79039	11099
Trp53	A_52_P491849	NM_011640	transformation related protein 53	-1.159	61.79	0.64187	15781	P	1.04	33.49	0.61966	9619
Ube2r2	A_52_P194170	NM_026275	ubiquitin-conjugating enzyme E2R 2	-1.159	45.92	0.53453	10870	P	1.085	13.58	0.2134	5089
1110032O16Rik	A_52_P225466	BC046763	RIKEN cDNA 1110032O16 gene	-1.16	65.79	0.6926	18055	P	1.003	42.43	0.98171	12866

Bace1	A_51_P167971	NM_011792	beta-site APP cleaving enzyme 1	-1.16	61.79	0.64288	15845	P	1.01	42.43	0.82696	11429
Brd4	A_52_P494230	NM_020508	bromodomain containing 4	-1.16	69.29	0.78996	17564	M	1.022	38.4	0.74779	10773
Cd47	A_51_P221014	NM_010581	CD47 antigen (Rh-related antigen, integri	-1.16	53.87	0.57513	12255	P	1.109	13.58	0.28419	6140
Ipo4	A_51_P347823	NM_024267	importin 4	-1.16	69.29	0.74584	20878	P	-1.053	45.68	0.69459	10275
Rbm22	A_51_P195365	NM_025776	RNA binding motif protein 22	-1.16	57.76	0.58724	12871	P	1.101	8.32	0.07277	2471
Sipa1	A_52_P675381	NM_011379	signal-induced proliferation associated ge	-1.16	65.79	0.72009	19555	P	1.031	36.07	0.63382	9754
2310003C23Rik	A_51_P133445	NM_029607	RIKEN cDNA 2310003C23 gene	-1.161	45.92	0.5299	10744	P	1.041	30.75	0.48679	8405
4933435A13Rik	A_52_P495439	NM_028304	RIKEN cDNA 4933435A13 gene	-1.161	65.79	0.72307	19917	P	-1.007	49.48	0.92036	12277
Mapre1	A_51_P185509	NM_007896	microtubule-associated protein, RP/EB fa	-1.161	57.76	0.59336	13101	P	1.026	36.07	0.61001	9526
Ncoa6	A_51_P521128	NM_019825	nuclear receptor coactivator 6	-1.161	65.79	0.68798	17818	P	-1.024	48.39	0.68864	10225
Rab23	A_52_P623538	NM_008999	RAB23, member RAS oncogene family	-1.161	65.79	0.69194	18025	P	-1.078	28.13	0.22782	5331
Smad3	A_52_P352277	NM_016769	MAD homolog 3 (Drosophila)	-1.161	65.79	0.70407	18644	P	1.075	19.02	0.29151	6225
Stat2	A_51_P225808	NM_019963	signal transducer and activator of transcri	-1.161	61.79	0.64373	15879	P	1.032	36.07	0.65948	9965
Tbn	A_51_P203710	NM_022015	taube nuss	-1.161	61.79	0.66969	17017	P	-1.166	2.53	0.04039	1540
Tloc1	A_52_P537459	NM_027016	translocation protein 1	-1.161	65.79	0.68725	17783	P	1.038	30.75	0.53437	8882
0910001A06Rik	A_52_P63709	NM_144846	RIKEN cDNA 0910001A06 gene	-1.163	61.79	0.67248	17192	P	1.022	38.4	0.68308	10171
Dusp22	A_51_P231793	NM_134068	dual specificity phosphatase 22	-1.163	69.29	0.79007	23463	P	-1.027	49	0.787	11064
Gcs1	A_52_P536481	NM_020619	glucosidase 1	-1.163	49.93	0.54741	11308	P	1.059	22.1	0.29147	6224
Rab21	A_52_P78966	NM_024454	RAB21, member RAS oncogene family	-1.163	49.93	0.53653	10927	P	1.145	9.71	0.15915	4198
Spop	A_51_P330717	NM_025287	speckle-type POZ protein	-1.163	49.93	0.55231	11501	P	1.126	8.32	0.07774	2594
Tpcn2	A_51_P517952	NM_146206	two pore segment channel 2	-1.163	61.79	0.63457	15448	P	-1.031	46.85	0.64521	9847
Apba3	A_51_P285960	NM_018758	amyloid beta (A4) precursor protein-bindi	-1.164	65.79	0.68943	17898	P	1.104	19.02	0.4846	8381
BC030476	A_51_P330825	NM_173421	cDNA sequence BC030476	-1.164	72.2	0.83678	26867	P	1.126	5.75	0.05015	1853
D330050I23Rik	A_52_P6092	NM_207269	RIKEN cDNA D330050I23 gene	-1.164	65.79	0.78046	17240	M	1.319	1.58	0.02469	1021
Gcdh	A_51_P260098	U18992	glutaryl-Coenzyme A dehydrogenase	-1.164	53.87	0.66333	15945	P	-1.02	49.48	0.78373	11039
Map3k7ip1	A_51_P121466	NM_025609	mitogen-activated protein kinase kinase k	-1.164	72.2	0.79913	24047	P	-1.207	0.75	0.01141	447
BC005471	A_51_P328883	NM_145612	zinc finger protein 810	-1.166	57.76	0.58633	12836	P	-1.211	1.32	0.034	1313
Cbll1	A_52_P368244	AK051737	Casitas B-lineage lymphoma-like 1	-1.166	61.79	0.67372	17247	P	1.126	5.75	0.0403	1539
D4Wsu53e	A_51_P346715	NM_023665	DNA segment, Chr 4, Wayne State Univer	-1.166	69.29	0.79032	17581	M	1.027	42.43	0.92842	12374
Ebi3	A_51_P202633	NM_015766	Epstein-Barr virus induced gene 3	-1.166	69.29	0.7874	23218	P	1.112	8.32	0.07263	2455
Foxj2	A_52_P503181	NM_021899	forkhead box J2	-1.166	65.79	0.77458	17023	M	1.005	42.43	0.92273	12315
Hnrpl	A_51_P181571	NM_177301	heterogeneous nuclear ribonucleoprotei	-1.166	69.29	0.81427	18630	M	1.053	22.1	0.27583	6038
Lck	A_51_P141288	NM_010693	lymphocyte protein tyrosine kinase	-1.166	53.87	0.58125	12551	P	1.065	19.02	0.22	5212
Npepps	A_51_P133078	NM_008942	aminopeptidase puromycin sensitive	-1.166	53.87	0.55906	11702	P	1.014	42.43	0.91857	12256
Pla2g12a	A_51_P207550	NM_023196	phospholipase A2, group XIIA	-1.166	69.29	0.75422	21327	P	-1.142	4.63	0.06417	2260
Scamp2	A_51_P115547	NM_022813	secretory carrier membrane protein 2	-1.166	49.93	0.68148	13256	M	1.134	11.33	0.21414	5097
Srp68	A_52_P561584	NM_146032	signal recognition particle 68	-1.166	65.79	0.72059	19580	P	1.028	36.07	0.6385	9791
Tapbp	A_51_P304500	NM_001025313	TAP binding protein	-1.166	65.79	0.78035	17230	M	-1.018	49.22	0.71557	10447
Usp9x	A_52_P622391	NM_009481	ubiquitin specific peptidase 9, X chromos	-1.166	57.76	0.59094	13007	P	1.023	38.4	0.68824	10222
Zfp286	A_52_P664405	NM_138949	zinc finger protein 286	-1.166	75.14	0.8698	28867	P	-1.342	0.51	0.00627	160
Zfyve19	A_51_P372936	NM_028054	zinc finger, FYVE domain containing 19	-1.166	57.76	0.60101	13505	P	1.131	13.58	0.32695	6641
Cnn2	A_51_P427663	NM_007725	calponin 2	-1.167	72.2	0.83927	27078	P	1.267	1.58	0.01607	694
D2Ertd391e	A_51_P448881	NM_145528	DNA segment, Chr 2, ERATO Doi 391, exp	-1.167	49.93	0.54163	11064	P	1.038	30.75	0.45757	8075
Gjb1	A_51_P462422	NM_008124	gap junction membrane channel protein	-1.167	72.2	0.81499	25076	M	-1.253	3.01	0.11789	3430
Napa	A_51_P246816	NM_025898	N-ethylmaleimide sensitive fusion protei	-1.167	65.79	0.7075	18804	P	-1.124	3.01	0.03702	1409
Serf1	A_52_P85495	BC001981	predicted gene, ENSMUSG00000050599	-1.167	49.93	0.53474	10880	P	-1.159	1.32	0.01962	837
Socs5	A_52_P281033	NM_019654	suppressor of cytokine signaling 5	-1.167	65.79	0.70666	18761	P	1.013	40.63	0.76376	10883
Xbp1	A_52_P185079	NM_013842	X-box binding protein 1	-1.167	65.79	0.73227	20356	P	1.052	25.31	0.4138	7663
Anapc4	A_51_P434198	NM_024213	anaphase promoting complex subunit 4	-1.168	61.79	0.62794	14858	P	1.052	22.1	0.32441	6606
Arid3a	A_51_P485828	NM_007880	AT rich interactive domain 3A (Bright like)	-1.168	61.79	0.6718	17125	P	1.003	42.43	0.97937	12833
Dhx8	A_52_P657859	AK049586	DEAH (Asp-Glu-Ala-His) box polypeptide	-1.168	65.79	0.68139	17493	P	-1.01	49.48	0.83846	11512
Htatip	A_52_P584109	NM_178637	HIV-1 tat interactive protein, homolog (h	-1.168	49.93	0.52969	10734	P	1.05	22.1	0.28928	6203
Klhdc3	A_51_P148122	NM_027910	kelch domain containing 3	-1.168	61.79	0.66728	16916	P	1.113	6.98	0.05346	1966

Sertad1	A_52_P217211	NM_018820	SERTA domain containing 1	-1.168	69.29	0.75654	21466	P	-1.127	16.2	0.24328	5558
Tsen54	A_51_P434953	NM_029557	tRNA splicing endonuclease 54 homolog (	-1.168	65.79	0.71197	19062	P	-1.161	3.82	0.0744	2516
4931406P16Rik	A_51_P326187	NM_172741	RIKEN cDNA 4931406P16 gene	-1.17	57.76	0.58498	12776	P	1.113	6.98	0.0571	2061
6720469N11Rik	A_52_P131812	AK032898	RIKEN cDNA 6720469N11 gene	-1.17	75.14	0.89294	30488	P	-1.092	16.2	0.11933	3477
Adnp	A_52_P55717	NM_009628	activity-dependent neuroprotective prote	-1.17	61.79	0.62641	14750	P	1.07	22.1	0.35673	6976
C1qtnf4	A_52_P633489	NM_026161	C1q and tumor necrosis factor related pro	-1.17	69.29	0.79529	23844	P	1.05	22.1	0.2529	5694
Camk2b	A_51_P318933	NM_007595	calcium/calmodulin-dependent protein ki	-1.17	65.79	0.77954	17200	M	1.063	19.02	0.22975	5345
Map4k1	A_52_P552589	NM_008279	mitogen activated protein kinase kinase k	-1.17	77.44	0.9089	31765	M	1.02	38.4	0.70084	10327
Prkx	A_51_P179864	NM_016979	protein kinase, X-linked	-1.17	57.76	0.60291	13590	P	1.061	25.31	0.4228	7756
Raly	A_51_P337246	NM_023130	hnRNP-associated with lethal yellow	-1.17	57.76	0.60208	13532	P	1.122	5.75	0.04247	1596
Rnpep	A_51_P493558	NM_145417	arginyl aminopeptidase (aminopeptidase	-1.17	61.79	0.63638	15553	P	1.069	19.02	0.2829	6118
Slc38a2	A_52_P676686	NM_175121	solute carrier family 38, member 2	-1.17	57.76	0.58964	12938	P	1.103	11.33	0.18616	4672
Tsfm	A_51_P235705	NM_025537	Ts translation elongation factor, mitochon	-1.17	65.79	0.72255	19834	P	-1.088	25.31	0.20825	5027
Zbp1	A_51_P184936	NM_021394	Z-DNA binding protein 1	-1.17	45.92	0.52072	10372	P	1.022	40.63	0.79541	11139
5730494M16Rik	A_52_P356841	NM_001004361	RIKEN cDNA 5730494M16 gene	-1.171	65.79	0.69847	18303	P	1.01	42.43	0.92211	12284
AU020206	A_51_P368171	AK049415	expressed sequence AU020206	-1.171	75.14	0.88491	29974	P	1.053	22.1	0.30737	6406
BC037393	A_52_P444785	NM_201369	cDNA sequence BC037393	-1.171	72.2	0.82265	25582	P	1.081	13.58	0.17748	4522
Csda	A_51_P311977	NM_011733	cold shock domain protein A	-1.171	61.79	0.63638	15550	P	1.126	5.75	0.04155	1570
Dhx15	A_51_P247960	AF017153	DEAH (Asp-Glu-Ala-His) box polypeptide 1	-1.171	53.87	0.56811	11999	P	-1.155	1.62	0.02519	1038
Eif4g3	A_51_P438363	NM_172703	eukaryotic translation initiation factor 4 g	-1.171	61.79	0.65572	16365	P	1.21	6.98	0.16182	4252
Nt5m	A_51_P344046	NM_134029	5',3'-nucleotidase, mitochondrial	-1.171	65.79	0.71977	19510	P	1.038	28.13	0.39381	7448
Prpf3	A_52_P672453	NM_027541	PRP3 pre-mRNA processing factor 3 homo	-1.171	42.28	0.49535	9446	P	1.231	2.53	0.0227	966
Rutbc2	A_52_P170985	NM_172718	RUN and TBC1 domain containing 2	-1.171	65.79	0.75046	16080	M	-1.039	44.4	0.48303	8361
Stat5a	A_51_P152765	NM_011488	signal transducer and activator of transcri	-1.171	57.76	0.59355	13111	P	1.031	33.49	0.61332	9551
Tbc1d20	A_52_P419437	AK082369	TBC1 domain family, member 20	-1.171	53.87	0.5664	11918	P	1.227	3.46	0.04772	1785
Hnrpab	A_52_P20966	NM_010448	heterogeneous nuclear ribonucleoprotein	-1.172	53.87	0.55252	11520	P	1.106	9.71	0.08966	2888
Hpcal1	A_52_P536735	NM_016677	hippocalcin-like 1	-1.172	57.76	0.61836	14319	P	-1.117	19.02	0.24315	5554
Ptov1	A_51_P369628	NM_133949	prostate tumor over expressed gene 1	-1.172	53.87	0.57688	12360	P	-1.154	4.63	0.08202	2704
Rab3d	A_52_P432919	NM_031874	RAB3D, member RAS oncogene family	-1.172	65.79	0.72951	20199	P	-1.025	46.3	0.55063	9033
Spcs3	A_52_P214861	AK048051	signal peptidase complex subunit 3 homo	-1.172	45.92	0.5136	10078	P	-1.098	22.1	0.19654	4843
Cant1	A_52_P85892	NM_029502	calcium activated nucleotidase 1	-1.174	49.93	0.54172	10632	M	-1.119	6.98	0.0697	2392
Cth	A_51_P431737	NM_145953	cystathionase (cystathionine gamma-lyase	-1.174	72.2	0.83732	26889	P	-1.02	48.39	0.6447	9844
Igfbp1	A_51_P447545	NM_008341	insulin-like growth factor binding protein	-1.174	69.29	0.60476	11876	M	1.124	11.33	0.20298	4942
Lars	A_52_P500488	BC052715	leucyl-tRNA synthetase	-1.174	53.87	0.56839	12012	P	-1.04	43.75	0.45489	8044
Msh6	A_51_P405565	NM_010830	mutS homolog 6 (E. coli)	-1.174	53.87	0.54946	11406	P	1.091	19.02	0.41258	7643
Nck1	A_51_P182662	NM_010878	non-catalytic region of tyrosine kinase ad	-1.174	61.79	0.6529	16244	P	1.163	6.98	0.12424	3585
Polr2a	A_51_P211810	NM_009089	polymerase (RNA) II (DNA directed) polyp	-1.174	53.87	0.57108	12095	P	-1.073	28.13	0.21612	5130
Ppp2ca	A_51_P516896	NM_019411	protein phosphatase 2 (formerly 2A), cata	-1.174	38.68	0.48167	8994	P	1.028	33.49	0.54114	8955
Ssh1	A_52_P597323	AK173144	slingshot homolog 1 (Drosophila)	-1.174	65.79	0.74794	17331	M	-1.381	0.51	0.00584	59
Arih2	A_52_P669843	NM_011790	ariadne homolog 2 (Drosophila)	-1.175	38.68	0.47761	8883	P	1.079	16.2	0.19844	4872
BC018507	A_51_P232439	BC026613	cDNA sequence BC018507	-1.175	42.28	0.48921	9213	P	1.123	8.32	0.1018	3142
Bnip2	A_52_P364922	NM_001008238	BCL2/adenovirus E1B interacting protein	-1.175	65.79	0.72009	19547	P	1.05	25.31	0.35342	6931
Cited1	A_51_P255365	NM_007709	Cbp/p300-interacting transactivator with	-1.175	65.79	0.69103	17963	P	-1.027	47.43	0.64736	9863
Phtf1	A_52_P644226	NM_013629	putative homeodomain transcription fact	-1.175	49.93	0.54582	11234	P	1.076	16.2	0.22891	5340
Slc35a3	A_52_P514317	NM_144902	solute carrier family 35 (UDP-N-acetylgluc	-1.175	57.76	0.58543	12809	P	1.012	42.43	0.92526	12343
9530058B02Rik	A_51_P106527	NM_026633	RIKEN cDNA 9530058B02 gene	-1.176	57.76	0.59713	13338	P	1.078	11.33	0.12528	3609
Apoa1	A_51_P408082	NM_009692	apolipoprotein A-I	-1.176	79.26	0.94912	35337	P	-1.058	43.15	0.53196	8865
BC067068	A_52_P7195	NM_207522	cDNA sequence BC067068	-1.176	31.88	0.47135	8618	P	-1.087	28.13	0.25778	5784
Elf1	A_52_P296382	BC053914	E74-like factor 1	-1.176	61.79	0.63583	15520	P	-1.036	45.68	0.59325	9368
Ephx2	A_51_P116940	NM_007940	epoxide hydrolase 2, cytoplasmic	-1.176	75.14	0.8861	30032	P	-1.016	49.48	0.75053	10794
Gnaz	A_52_P307761	NM_010311	guanine nucleotide binding protein, alpha	-1.176	61.79	0.63718	15579	P	1.1	8.32	0.07487	2529
Inppl1	A_51_P142334	NM_010567	inositol polyphosphate phosphatase-like 1	-1.176	65.79	0.68972	17908	P	1.036	28.13	0.40356	7550
Med9	A_51_P496400	NM_138675	mediator of RNA polymerase II transcripti	-1.176	65.79	0.69914	18344	P	-1.358	0.51	0.00643	177

Pole2	A_51_P269687	NM_011133	polymerase (DNA directed), epsilon 2 (p5	-1.176	75.14	0.87046	28926	P	-1.054	36.07	0.26935	5944
Rcl1	A_52_P241484	NM_021525	RNA terminal phosphate cyclase-like 1	-1.176	53.87	0.57961	12471	P	1.063	19.02	0.29461	6273
Rnf126	A_51_P266847	NM_144528	ring finger protein 126	-1.176	65.79	0.74163	20678	P	-1.02	48.7	0.68365	10178
Tor2a	A_52_P88773	NM_152800	torsin family 2, member A	-1.176	57.76	0.61882	14389	P	1.012	33.49	0.88024	10545
1600027N09Rik	A_51_P422691	BC085320	RIKEN cDNA 1600027N09 gene	-1.178	42.28	0.48921	9215	P	1.01	42.43	0.88429	11908
Cdc20	A_51_P361022	NM_023223	cell division cycle 20 homolog (S. cerevisia	-1.178	72.2	0.84246	27239	P	-1.421	0	0.00584	29
Cdc42ep3	A_51_P267494	NM_026514	CDC42 effector protein (Rho GTPase bind	-1.178	57.76	0.61824	14304	P	-1.085	25.31	0.21473	5110
Ddb1	A_51_P459538	NM_015735	damage specific DNA binding protein 1	-1.178	49.93	0.54352	11146	P	1.133	5.75	0.04955	1831
Drap1	A_51_P479933	NM_024176	Dr1 associated protein 1 (negative cofacto	-1.178	69.29	0.76858	22145	P	1.038	30.75	0.46339	8144
Ranbp2	A_51_P511375	NM_011240	RAN binding protein 2	-1.178	45.92	0.51541	10136	P	1.027	33.49	0.56295	9134
Rbm7	A_52_P145017	NM_144948	RNA binding motif protein 7	-1.178	69.29	0.78046	22790	P	-1.078	38.4	0.43247	7864
Smad4	A_52_P611867	NM_008540	MAD homolog 4 (Drosophila)	-1.178	65.79	0.74659	15957	M	1.205	3.01	0.02732	1107
Zdhhc14	A_51_P174081	NM_146073	zinc finger, DHHC domain containing 14	-1.178	69.29	0.76814	22113	P	1.061	22.1	0.33394	6726
Btbd9	A_51_P491437	NM_172618	BTB (POZ) domain containing 9	-1.179	61.79	0.64101	15725	P	-1.045	43.75	0.43432	7890
Mcfd2	A_51_P465232	NM_139295	multiple coagulation factor deficiency 2	-1.179	65.79	0.73228	20359	P	1.027	36.07	0.63397	9755
Nsun5	A_52_P493183	AK156651	NOL1/NOP2/Sun domain family, member	-1.179	61.79	0.64534	15920	P	-1.202	1.18	0.0183	778
Phf10	A_51_P311125	NM_024250	PHD finger protein 10	-1.179	65.79	0.71601	19277	P	1.065	22.1	0.3844	7332
Shh	A_52_P49014	NM_009170	sonic hedgehog	-1.179	61.79	0.67248	17176	P	1.055	22.1	0.35146	6900
Syncrip	A_52_P567031	NM_019796	synaptotagmin binding, cytoplasmic RNA	-1.179	45.92	0.50463	9852	P	-1.054	43.15	0.4569	8067
Zfp358	A_51_P350996	NM_080461	zinc finger protein 358	-1.179	57.76	0.59402	13175	P	1.066	19.02	0.24279	5537
Agpat5	A_51_P361286	NM_026792	1-acylglycerol-3-phosphate O-acyltransfer	-1.181	75.14	0.82598	24281	P	1.058	22.1	0.34344	6802
Ggps1	A_51_P179604	NM_010282	geranylgeranyl diphosphate synthase 1	-1.181	38.68	0.47332	8718	P	-1.013	49.48	0.94151	12496
Golph4	A_52_P279920	AK149286	golgi phosphoprotein 4	-1.181	57.76	0.60851	13853	P	1.037	28.13	0.42111	7740
Hic2	A_52_P234354	NM_178922	hypermethylated in cancer 2	-1.181	61.79	0.64982	16093	P	-1.255	0.56	0.01072	415
Hnf4g	A_52_P739999	AK136534	hepatocyte nuclear factor 4, gamma	-1.181	72.2	0.8117	24811	P	-1.008	49.48	0.9227	12298
Kif5b	A_52_P273177	NM_008448	kinesin family member 5B	-1.181	53.87	0.54622	11256	P	1.084	16.2	0.23607	5438
Pak2	A_51_P172323	NM_177326	p21 (CDKN1A)-activated kinase 2	-1.181	42.28	0.4809	8973	P	1.028	30.75	0.49171	8463
Plekha6	A_52_P430179	NM_182930	pleckstrin homology domain containing, f	-1.181	65.79	0.6922	18042	P	-1.253	0.51	0.01023	387
Rnf26	A_51_P201609	NM_153762	ring finger protein 26	-1.181	65.79	0.70795	18836	P	-1.305	0.51	0.00652	184
Scrib	A_52_P683315	NM_134089	scribbled homolog (Drosophila)	-1.181	69.29	0.7629	21823	P	-1.166	1.18	0.01922	804
Mrpl33	A_52_P336091	BC027018	mitochondrial ribosomal protein L33	-1.182	65.79	0.71367	19143	P	1.046	28.13	0.43952	7916
Nipsnap1	A_51_P214516	NM_008698	4-nitrophenylphosphatase domain and no	-1.182	61.79	0.6718	17126	P	1.014	42.43	0.80705	11248
Pigo	A_52_P462081	NM_020035	phosphatidylinositol glycan anchor biosyr	-1.182	57.76	0.61815	14282	P	1.124	6.98	0.06101	2171
Prickle1	A_51_P385370	NM_001033217	prickle like 1 (Drosophila)	-1.182	49.93	0.52286	10446	P	-1.071	28.13	0.20535	4977
Surf5	A_51_P141554	NM_011513	surfeit gene 5	-1.182	49.93	0.5415	11063	P	1.02	38.4	0.72022	10499
4930506L13Rik	A_51_P168392	NM_030188	tetratricopeptide repeat domain 30A1	-1.183	49.93	0.52271	10441	P	-1.022	49	0.72485	10522
Myo6	A_52_P565427	NM_001039546	myosin VI	-1.183	69.29	0.79338	17742	M	-1.157	9.71	0.20501	4969
Nfix	A_52_P148428	AK080940	nuclear factor I/X	-1.183	57.76	0.62064	14488	P	1.041	28.13	0.45234	8020
Rapgef2	A_51_P289912	XM_203999	Rap guanine nucleotide exchange factor (	-1.183	57.76	0.59081	13004	P	1.003	42.43	0.94341	12517
Crot	A_51_P489153	NM_023733	carnitine O-octanoyltransferase	-1.185	69.29	0.74904	21020	P	-1.037	44.4	0.48193	8333
Dhrs3	A_52_P387237	NM_011303	dehydrogenase/reductase (SDR family) m	-1.185	72.2	0.81031	24719	P	1.051	25.31	0.41166	7627
Eya2	A_51_P334209	NM_010165	eyes absent 2 homolog (Drosophila)	-1.185	65.79	0.70847	18861	M	-1.008	49.48	0.90225	12116
LOC232875	A_52_P199747	BC094341	predicted gene, EG232875	-1.185	75.14	0.8845	29961	P	-1.033	47.43	0.69502	10279
Pou5f1	A_51_P202340	NM_013633	POU domain, class 5, transcription factor	-1.185	75.14	0.88903	30197	P	1.001	42.43	0.98495	12928
Psmb10	A_52_P570266	NM_013640	proteasome (prosome, macropain) subun	-1.185	72.2	0.80802	24601	P	-1.188	1.58	0.02982	1188
Ubn1	A_52_P288444	NM_026666	ubinuclein 1	-1.185	69.29	0.7993	24065	P	1.087	11.33	0.1319	3706
1810073G14Rik	A_52_P104700	NM_026342	RIKEN cDNA 1810073G14 gene	-1.186	45.92	0.49715	9517	P	-1.07	33.49	0.30284	6351
1810074P20Rik	A_52_P153333	NM_026194	RIKEN cDNA 1810074P20 gene	-1.186	61.79	0.66999	17025	P	-1.009	49.48	0.87183	11783
Ash1l	A_52_P621271	NM_138679	ash1 (absent, small, or homeotic)-like (Dr	-1.186	53.87	0.54172	11072	P	1.02	38.4	0.66451	10001
Atf7	A_52_P294567	NM_146065	activating transcription factor 7	-1.186	65.79	0.69196	17175	M	1.015	42.43	0.83846	11511
Hoxb5	A_51_P436342	NM_008268	homeo box B5	-1.186	57.76	0.60476	13671	P	1.118	4.63	0.04002	1531
Jun	A_51_P325914	NM_010591	Jun oncogene	-1.186	61.79	0.71674	14669	M	1.01	42.43	0.85759	11652
Nat6	A_51_P268145	NM_019750	N-acetyltransferase 6	-1.186	69.29	0.77678	22557	P	1.003	42.43	0.93907	12471

Npm3	A_51_P499201	NM_008723	nucleoplasmin 3	-1.186	49.93	0.53749	10958	P	-1.174	3.01	0.06482	2274
Shb	A_52_P696044	AK145414	src homology 2 domain-containing transf	-1.186	49.93	0.52633	10575	P	-1.003	49.48	0.97164	12762
Supt5h	A_52_P15229	NM_013676	suppressor of Ty 5 homolog (S. cerevisiae	-1.186	53.87	0.55118	11472	P	-1.045	43.75	0.49465	8498
A230106M15Rik	A_51_P466828	ENSMUST00000073524	RIKEN cDNA A230106M15 gene	-1.188	61.79	0.6267	14772	P	1.129	6.98	0.05995	2155
AI428936	A_52_P147803	NM_153577	expressed sequence AI428936	-1.188	61.79	0.66247	16686	P	-1.094	33.49	0.39927	7508
BC043118	A_51_P160439	NM_174848	cDNA sequence BC043118	-1.188	69.29	0.75858	17770	M	1.106	11.33	0.19196	4772
Cbara1	A_52_P400542	AK083520	calcium binding atopy-related autoantige	-1.188		0.77488	16726	A	1.106	9.71	0.08344	2737
Cntnap4	A_52_P1107623	AK034258	contactin associated protein-like 4	-1.188	81.02	0.71449	13517	M	-1.006	49.48	0.92004	12275
D230014K01Rik	A_52_P28775	NM_172573	RIKEN cDNA D230014K01 gene	-1.188	69.29	0.78097	22810	P	1.016	40.63	0.72888	10564
Gorasp2	A_51_P173197	NM_027352	golgi reassembly stacking protein 2	-1.188	53.87	0.54835	11354	P	1.137	16.2	0.42447	7775
Hcls1	A_51_P297679	NM_008225	hematopoietic cell specific Lyn substrate	-1.188	69.29	0.78484	23064	P	-1.094	13.58	0.11655	3408
Hdh	A_51_P205943	NM_010414	Huntington disease gene homolog	-1.188	53.87	0.5752	12258	P	-1.117	6.98	0.0659	2315
Osbp	A_51_P393768	XM_148904	oxysterol binding protein	-1.188	61.79	0.70773	14254	M	-1.045	42.43	0.35274	6916
Thrap3	A_52_P115996	BC026580	thyroid hormone receptor associated pro	-1.188	61.79	0.65843	16506	P	-1.166	3.82	0.07384	2505
Zfp46	A_52_P621817	NM_009557	zinc finger protein 46	-1.188	53.87	0.56738	11968	P	1.037	30.75	0.53117	8841
D19Ertd737e	A_52_P60519	NM_029648	DNA segment, Chr 19, ERATO Doi 737, ex	-1.189	61.79	0.6618	16666	P	-1.123	5.75	0.06486	2278
Exosc7	A_52_P296048	AK085426	exosome component 7	-1.189		0.8038	15806	A	1.02	38.4	0.68914	10229
Golga5	A_52_P670037	NM_013747	golgi autoantigen, golgin subfamily a, 5	-1.189	42.28	0.47267	8707	P	1.18	3.82	0.04831	1804
Ppp2r2a	A_51_P301736	NM_028032	protein phosphatase 2 (formerly 2A), regu	-1.189	45.92	0.50308	9800	P	-1.01	49.48	0.8119	11293
Zfp326	A_52_P356853	NM_018759	zinc finger protein 326	-1.189	61.79	0.67644	17326	P	1.13	9.71	0.1288	3676
2310008M10Rik	A_52_P592951	NM_025509	RIKEN cDNA 2310008M10 gene	-1.19	69.29	0.80242	18075	M	1.01	42.43	0.90778	12176
Ddx5	A_52_P611798	NM_007840	DEAD (Asp-Glu-Ala-Asp) box polypeptide	-1.19	69.29	0.79529	17826	M	1.178	3.82	0.0408	1553
Dlgap4	A_52_P600038	NM_146128	discs, large homolog-associated protein 4	-1.19	57.76	0.59251	13043	P	-1.183	1.32	0.02492	1029
Rnf128	A_51_P268331	NM_023270	ring finger protein 128	-1.19	61.79	0.65628	16409	P	-1.041	43.75	0.4549	8048
Angpt1	A_52_P574140	NM_009640	angiopoietin 1	-1.192		0.91293	13005	A	-1.219	0.56	0.01002	376
Ehmt1	A_51_P485768	NM_172545	euchromatic histone methyltransferase 1	-1.192	65.79	0.77774	17131	M	1.02	40.63	0.76096	10866
Elf2	A_51_P496273	NM_023502	E74-like factor 2	-1.192	53.87	0.57069	12073	P	1.051	25.31	0.37536	7226
Erf	A_52_P326354	NM_010155	Ets2 repressor factor	-1.192	61.79	0.65402	16310	P	-1.009	49.48	0.89188	11982
Ifrd2	A_51_P172251	NM_025903	interferon-related developmental regulat	-1.192	69.29	0.75687	21478	P	1.095	11.33	0.12322	3561
Mtss1	A_52_P601055	AK129139	metastasis suppressor 1	-1.192	69.29	0.81943	18899	M	1.07	16.2	0.16913	4373
Nsf	A_52_P518715	NM_008740	N-ethylmaleimide sensitive fusion protei	-1.192	49.93	0.52779	10638	P	1.051	28.13	0.55557	9073
Pon1	A_51_P108659	NM_011134	paraoxonase 1	-1.192		0.68356	14586	A	1.02	38.4	0.7161	10458
Ppp1cb	A_51_P342716	NM_172707	protein phosphatase 1, catalytic subunit,	-1.192	69.29	0.82225	19032	M	-1.035	49.22	0.84595	11572
Rnps1	A_52_P41985	NM_009070	ribonucleic acid binding protein S1	-1.192	42.28	0.47073	8565	P	1.025	38.4	0.68767	10216
Rps6ka1	A_51_P150044	NM_009097	ribosomal protein S6 kinase polypeptide	-1.192	72.2	0.82276	25593	P	-1.001	49.48	0.9932	13003
Sptlc2	A_52_P59916	NM_011479	serine palmitoyltransferase, long chain b	-1.192	65.79	0.70327	18571	P	1.016	42.43	0.82109	11373
Trip11	A_51_P176265	BC025876	thyroid hormone receptor interactor 11	-1.192	45.92	0.49191	9321	P	1.201	4.63	0.06781	2358
1200014J11Rik	A_51_P101660	NM_025818	RIKEN cDNA 1200014J11 gene	-1.193	38.68	0.44699	7850	P	-1.008	49.48	0.87466	11806
Dffb	A_52_P46742	NM_007859	DNA fragmentation factor, beta subunit	-1.193	72.2	0.83933	25236	P	1.07	19.02	0.26529	5881
Hip2	A_51_P363714	NM_016786	huntingtin interacting protein 2	-1.193	45.92	0.49841	9606	P	1.027	33.49	0.56467	9163
Slc2a6	A_51_P268831	NM_172659	solute carrier family 2 (facilitated glucose	-1.193	57.76	0.59557	13266	P	-1.126	8.32	0.09995	3102
Tnrc4	A_51_P106591	NM_172434	trinucleotide repeat containing 4	-1.193	61.79	0.70185	14037	M	1.119	16.2	0.43068	7838
Unc93b1	A_52_P507382	NM_019449	unc-93 homolog B1 (C. elegans)	-1.193	53.87	0.55666	11634	P	-1.022	47.43	0.60474	9487
Zfp330	A_52_P537466	NM_145600	zinc finger protein 330	-1.193	72.2	0.85249	27896	P	1.03	33.49	0.52265	8775
2410015N17Rik	A_51_P158876	NM_023203	RIKEN cDNA 2410015N17 gene	-1.195	57.76	0.6233	14606	P	1.015	42.43	0.7827	11021
2810432D09Rik	A_51_P411130	NM_027278	RIKEN cDNA 2810432D09 gene	-1.195	61.79	0.64753	15985	P	-1.058	38.4	0.31686	6548
Etf1	A_52_P585350	AK038771	eukaryotic translation termination factor	-1.195	72.2	0.81398	24976	P	1.031	36.07	0.62622	9680
Klf1	A_51_P168630	NM_010635	Kruppel-like factor 1 (erythroid)	-1.195	75.14	0.89176	30396	M	1.039	25.31	0.3592	6996
Lrp5	A_51_P364168	NM_008513	low density lipoprotein receptor-related	-1.195	38.68	0.45903	8178	P	1.109	19.02	0.47063	8203
Ppp2r5a	A_52_P108952	NM_144880	protein phosphatase 2, regulatory subuni	-1.195	53.87	0.55427	11576	P	1.038	30.75	0.46054	8108
Slc35a4	A_51_P121412	NM_026404	solute carrier family 35, member A4	-1.195	31.88	0.43241	7426	P	-1.031	46.85	0.65026	9883
AK122209	A_52_P484118	NM_001029876	cDNA sequence AK122209	-1.196	53.87	0.54147	11062	P	1	49.48	0.99655	13023
Aprin	A_52_P24783	NM_175310	androgen-induced proliferation inhibitor	-1.196	65.79	0.70178	18495	P	-1.031	48.39	0.75016	10788

Dolpp1	A_51_P246690	NM_020329	dolichyl pyrophosphate phosphatase 1	-1.196	38.68	0.45088	7931	P	1.061	19.02	0.24577	5579
Etv1	A_51_P307979	NM_007960	ets variant gene 1	-1.196	65.79	0.70335	18588	P	-1.052	44.4	0.6265	9685
Nup54	A_52_P131584	AK014260	nucleoporin 54	-1.196	65.79	0.73835	20571	P	1.025	40.63	0.81937	11349
Rdh5	A_51_P479618	NM_134006	retinol dehydrogenase 5	-1.196	61.79	0.63777	15609	P	-1.09	22.1	0.19195	4769
Scd1	A_52_P682382	NM_009127	stearoyl-Coenzyme A desaturase 1	-1.196	57.76	0.58431	12737	P	-1.208	19.02	0.38943	7389
Sepx1	A_52_P393634	NM_013759	selenoprotein X 1	-1.196	65.79	0.68819	17843	P	1.077	11.33	0.12552	3618
Tnrc9	A_51_P465082	NM_172913	TOX high mobility group box family mem	-1.196	57.76	0.59506	13239	P	-1.153	9.71	0.18293	4624
9430015G10Rik	A_51_P462862	NM_145557	RIKEN cDNA 9430015G10 gene	-1.198	53.87	0.56988	12054	P	-1.042	43.15	0.38085	7283
Apobec3	A_52_P645410	NM_030255	apolipoprotein B editing complex 3	-1.198	61.79	0.63553	15496	P	-1.042	40.63	0.32455	6610
Dullard	A_51_P515585	NM_026017	Dullard homolog (Xenopus laevis)	-1.198	53.87	0.54946	11418	P	-1.1	19.02	0.1985	4874
Mmab	A_52_P111830	NM_029956	methylmalonic aciduria (cobalamin defici	-1.198	65.79	0.71369	19159	P	-1.032	46.85	0.63755	9780
Phf2	A_52_P686091	NM_011078	PHD finger protein 2	-1.198	57.76	0.69909	13908	M	1.054	22.1	0.34764	6843
2610020O08Rik	A_51_P159746	NM_025937	RIKEN cDNA 2610020O08 gene	-1.199	53.87	0.57961	12467	P	-1.021	48.7	0.68922	10233
Brpf3	A_52_P34420	AK147555	bromodomain and PHD finger containing,	-1.199	53.87	0.55853	11679	P	1.167	6.98	0.10051	3116
Ccl20	A_51_P408595	NM_016960	chemokine (C-C motif) ligand 20	-1.199	69.29	0.77068	22246	P	1.152	5.75	0.06761	2351
Dyx1c1	A_51_P332264	NM_026314	dyslexia susceptibility 1 candidate 1 hom	-1.199	49.93	0.52449	10513	P	1.099	9.71	0.09716	3042
Rqcd1	A_52_P110068	NM_021383	rcd1 (required for cell differentiation) hor	-1.199	42.28	0.46905	8485	P	1.098	11.33	0.15413	4118
Snx9	A_51_P371323	NM_025664	sorting nexin 9	-1.199	61.79	0.66067	16596	P	1.053	22.1	0.28542	6155
2310022B05Rik	A_52_P434556	NM_175149	RIKEN cDNA 2310022B05 gene	-1.2	72.2	0.81904	25365	P	1.035	30.75	0.45074	8002
4930503L19Rik	A_52_P515907	NM_172967	RIKEN cDNA 4930503L19 gene	-1.2	65.79	0.72951	20194	P	-1.029	45.68	0.51223	8693
Arg1	A_51_P303160	NM_007482	arginase 1, liver	-1.2	57.76	0.62335	14609	P	-1.092	33.49	0.43136	7848
Jmjd2c	A_52_P8320	AK039000	jumonji domain containing 2C	-1.2	79.26	0.77816	18255	M	1.064	19.02	0.21892	5189
Neurod1	A_52_P408391	NM_010894	neurogenic differentiation 1	-1.2	57.76	0.61575	14186	P	1.059	19.02	0.26009	5811
Ppp1r15b	A_51_P274091	BC058078	protein phosphatase 1, regulatory (inhibit	-1.2	53.87	0.54946	11412	P	1.117	8.32	0.08984	2894
Ralbp1	A_51_P260490	NM_009067	ralA binding protein 1	-1.2	61.79	0.72991	15462	M	1.023	38.4	0.75347	10812
Tacstd1	A_52_P447944	NM_008532	tumor-associated calcium signal transduc	-1.2	65.79	0.73404	20424	P	1.182	3.82	0.05265	1938
3000004C01Rik	A_52_P520466	NM_197959	RIKEN cDNA 3000004C01 gene	-1.202		0.77139	14225	A	-1.01	49.48	0.8717	11779
AU042671	A_51_P450764	AK037367	expressed sequence AU042671	-1.202	61.79	0.6618	16661	P	-1.064	28.13	0.19298	4793
Csrp2	A_51_P300337	NM_007792	cysteine and glycine-rich protein 2	-1.202	61.79	0.64229	15822	P	1.114	9.71	0.11181	3314
Cugbp1	A_51_P431558	AK033771	CUG triplet repeat, RNA binding protein 1	-1.202	57.76	0.67779	13124	M	1.077	19.02	0.31098	6467
Erh	A_52_P811874	AK078010	enhancer of rudimentary homolog (Dros	-1.202	69.29	0.75317	21291	P	-1.06	38.4	0.33584	6742
Prkcd	A_51_P460734	NM_011103	protein kinase C, delta	-1.202	53.87	0.5509	11465	P	1.05	28.13	0.49834	8563
Sdc1	A_52_P479269	NM_011519	syndecan 1	-1.202	79.26	0.93021	33839	P	-1.012	49.48	0.82002	11359
5930416I19Rik	A_52_P268549	NM_197981	RIKEN cDNA 5930416I19 gene	-1.203	61.79	0.6755	17290	P	-1.202	1.18	0.01985	845
Atp1a1	A_52_P515497	NM_144900	ATPase, Na+/K+ transporting, alpha 1 pol	-1.203	61.79	0.7216	14937	M	1.103	9.71	0.08637	2810
Cenpb	A_52_P262250	NM_007682	centromere protein B	-1.203	45.92	0.49249	9351	P	1.013	42.43	0.81133	11291
Cldn7	A_51_P165185	NM_016887	claudin 7	-1.203	42.28	0.52207	9533	P	1.013	42.43	0.81422	11322
Gab1	A_52_P417437	NM_021356	growth factor receptor bound protein 2-a	-1.203	45.92	0.49311	9365	P	1.037	28.13	0.42425	7767
Hipk1	A_52_P235929	NM_010432	homeodomain interacting protein kinase	-1.203	49.93	0.52957	10724	P	1.091	11.33	0.13896	3821
Kcnk5	A_52_P514352	NM_021542	potassium channel, subfamily K, member	-1.203	49.93	0.53228	10794	P	1.038	33.49	0.63871	9796
Parp1	A_51_P314277	NM_007415	poly (ADP-ribose) polymerase family, mer	-1.203	49.93	0.51432	10101	P	1.046	25.31	0.3489	6858
Acvr1	A_52_P352131	NM_007394	activin A receptor, type 1	-1.205	49.93	0.51819	10276	P	1.091	13.58	0.21709	5152
Cd36	A_51_P375138	L23108	CD36 antigen	-1.205	61.79	0.64241	15824	P	-1.355	0.51	0.0144	604
D130051D11Rik	A_52_P555808	AK083890	RIKEN cDNA D130051D11 gene	-1.205	61.79	0.6328	15360	P	1.123	8.32	0.07248	2452
Fzd3	A_51_P190863	NM_021458	frizzled homolog 3 (Drosophila)	-1.205	45.92	0.48882	9200	P	1.129	11.33	0.26529	5882
Hlf	A_51_P134228	NM_172563	hepatic leukemia factor	-1.205	65.79	0.70407	18638	P	1.035	30.75	0.50164	8595
Iars	A_52_P200617	NM_172015	isoleucine-tRNA synthetase	-1.205	49.93	0.51244	10031	P	1.008	42.43	0.92249	12289
Osbpl11	A_51_P223199	NM_176840	oxysterol binding protein-like 11	-1.205	38.68	0.43241	7416	P	1.081	19.02	0.30021	6319
Polr3k	A_52_P240453	NM_025901	polymerase (RNA) III (DNA directed) poly	-1.205	53.87	0.57399	12191	P	-1.08	33.49	0.34537	6824
Rrs1	A_52_P579640	NM_021511	RRS1 ribosome biogenesis regulator hom	-1.205	61.79	0.63754	15599	P	1.054	22.1	0.31544	6529
Tm9sf1	A_51_P455410	NM_028780	transmembrane 9 superfamily member 1	-1.205	38.68	0.58125	10103	M	-1.007	49.48	0.90099	12100
Tram1	A_51_P499169	NM_028173	translocating chain-associating membran	-1.205	53.87	0.63918	11847	M	1.053	28.13	0.47441	8256
4933426M11Rik	A_52_P666646	NM_178682	RIKEN cDNA 4933426M11 gene	-1.206	53.87	0.56811	11985	P	1.139	6.98	0.06114	2172

Copz2	A_52_P180310	BF100712	coatomer protein complex, subunit zeta 2	-1.206	53.87	0.57914	11898	M	-1.053	40.63	0.35931	6998
Elk1	A_52_P1028571	AK082260	ELK1, member of ETS oncogene family	-1.206	49.93	0.53335	10830	P	1.18	3.82	0.04067	1548
Hmga1	A_51_P483118	NM_016660	high mobility group AT-hook 1	-1.206	45.92	0.49187	9317	P	1.074	13.58	0.13456	3757
Maml1	A_51_P104861	NM_175334	mastermind like 1 (Drosophila)	-1.206	61.79	0.68577	17726	P	1.133	6.98	0.06967	2390
Rbpsuhl	A_52_P574759	NM_009036	recombination signal binding protein for i	-1.206	72.2	0.81652	25182	P	1.179	5.75	0.07656	2566
Sox15	A_51_P440440	NM_009235	SRY-box containing gene 15	-1.206	57.76	0.64378	14921	M	1.011	42.43	0.82646	11423
Usf2	A_52_P647919	U01663	upstream transcription factor 2	-1.206	57.76	0.60765	13803	P	-1.02	49.48	0.83204	11479
Ccbl1	A_51_P220055	NM_172404	cysteine conjugate-beta lyase 1	-1.208	42.28	0.46682	8439	P	1.09	13.58	0.20566	4983
Hipk2	A_52_P554845	NM_010433	homeodomain interacting protein kinase	-1.208	61.79	0.64225	15816	P	1.097	13.58	0.20332	4944
Igfbp5	A_52_P281702	NM_010518	insulin-like growth factor binding protein	-1.208	75.14	0.77768	18601	M	1.138	13.58	0.37353	7210
Il11ra1	A_51_P353946	NM_010549	interleukin 11 receptor, alpha chain 1	-1.208	45.92	0.49037	9243	P	1.03	38.4	0.73869	10672
Nkx6-1	A_51_P441153	NM_144955	NK6 transcription factor related, locus 1 (	-1.208	57.76	0.61013	13955	P	1.003	42.43	0.96907	12737
Pnn	A_51_P121793	NM_008891	pinin	-1.208	57.76	0.61261	14100	P	1.032	36.07	0.66863	10032
Rnf38	A_52_P469767	AK044324	ring finger protein 38	-1.208		0.90544	12780	A	-1.013	49.48	0.8769	11825
Ythdf1	A_51_P488799	NM_173761	YTH domain family 1	-1.208	45.92	0.4726	8694	P	1.084	19.02	0.41349	7662
Calr	A_51_P416419	NM_007591	calreticulin	-1.209	65.79	0.75317	16208	M	1.162	4.63	0.04831	1805
Ccnd3	A_51_P238448	NM_007632	cyclin D3	-1.209	49.93	0.52496	10541	P	-1.161	2.04	0.03176	1249
Gda	A_51_P291950	NM_010266	guanine deaminase	-1.209		0.78867	18750	A	-1.3	0.51	0.00756	285
Podxl	A_52_P380263	NM_013723	podocalyxin-like	-1.209	65.79	0.75002	21073	P	1.17	5.75	0.08811	2842
Zfp661	A_51_P105869	NM_028141	zinc finger protein 661	-1.209	61.79	0.65972	16578	P	-1.119	16.2	0.21643	5134
Cdk6	A_51_P388310	NM_009873	cyclin-dependent kinase 6	-1.211	61.79	0.66359	16759	P	1.229	3.01	0.03709	1410
Gja1	A_52_P174915	NM_010288	gap junction membrane channel protein a	-1.211	61.79	0.67019	17058	P	1.146	8.32	0.13213	3715
Pdlim1	A_52_P283426	ENSMUST00000068439	PDZ and LIM domain 1 (elfin)	-1.211	83.95	0.84753	21903	M	-1.159	2.04	0.03098	1223
Pols	A_52_P380329	NM_198600	polymerase (DNA directed) sigma	-1.211	53.87	0.54891	11381	P	1.133	11.33	0.23108	5363
Preb	A_51_P135037	AK029838	prolactin regulatory element binding	-1.211	57.76	0.60253	13556	P	1.012	42.43	0.8699	11757
Psmd3	A_51_P130427	NM_009439	proteasome (prosome, macropain) 26S su	-1.211	53.87	0.57363	11674	P	-1.047	43.15	0.4504	7996
Selenbp1	A_52_P629487	NM_009150	selenium binding protein 1	-1.211	53.87	0.54327	11130	P	-1.084	19.02	0.14642	3970
Smad1	A_51_P409260	NM_008539	MAD homolog 1 (Drosophila)	-1.211	65.79	0.72221	19767	P	1.054	22.1	0.31486	6521
Stip1	A_52_P57249	AK080936	stress-induced phosphoprotein 1	-1.211	75.14	0.86488	28509	P	1.021	40.63	0.74306	10730
2810004A10Rik	A_51_P253732	NM_027265	interleukin 17 receptor D	-1.212	49.93	0.52719	10613	P	-1.24	0.66	0.01141	452
9830124H08Rik	A_52_P277695	AK165863	RIKEN cDNA 9830124H08 gene	-1.212	42.28	0.57961	10028	M	1.229	4.63	0.08963	2887
Lfng	A_52_P187940	ENSMUST00000031555	lunatic fringe gene homolog (Drosophila)	-1.212	61.79	0.65158	16141	P	1.037	33.49	0.57465	9225
Prom2	A_52_P452667	NM_178047	prominin 2	-1.212	57.76	0.59834	13369	P	-1.116	13.58	0.15736	4169
Rcor3	A_52_P338033	AK135612	REST corepressor 3	-1.212	28.61	0.39742	6443	P	1.098	13.58	0.23218	5381
Slc35c1	A_52_P144062	NM_211358	solute carrier family 35, member C1	-1.212	45.92	0.48675	9153	M	1.068	19.02	0.25067	5651
Tpx2	A_51_P369200	NM_028109	TPX2, microtubule-associated protein hor	-1.212	65.79	0.70411	17703	M	-1.28	0.56	0.0141	591
Zzef1	A_51_P114336	AK018382	zinc finger, ZZ-type with EF hand domain	-1.212	53.87	0.55427	11577	P	1.206	1.58	0.01101	426
Capg	A_51_P273921	NM_007599	capping protein (actin filament), gelsolin-	-1.214	75.14	0.86348	28404	P	1.058	19.02	0.23607	5432
Cnot6	A_52_P544032	NM_212484	CCR4-NOT transcription complex, subunit	-1.214	31.88	0.40381	6577	P	-1.015	49.48	0.82758	11438
Pygo2	A_52_P362128	NM_026869	pygopus 2	-1.214	42.28	0.46777	8453	P	1.008	42.43	0.89905	12057
Trim11	A_52_P548940	NM_053168	tripartite motif protein 11	-1.214	53.87	0.57322	12152	P	-1.079	33.49	0.3375	6755
2310042G06Rik	A_52_P381749	NM_025531	slowmo homolog 2 (Drosophila)	-1.215	28.61	0.5486	9186	M	1.016	42.43	0.86142	11689
Cd83	A_51_P199135	NM_009856	CD83 antigen	-1.215	65.79	0.7185	19419	P	1.004	42.43	0.97816	12821
Tmcc2	A_51_P454993	NM_178874	transmembrane and coiled-coil domains	-1.215	61.79	0.69094	17957	P	1.068	16.2	0.1701	4386
Txndc4	A_52_P12001	NM_029572	thioredoxin domain containing 4 (endopla	-1.215	23.47	0.38726	6109	P	1.107	8.32	0.06459	2270
Hpn	A_51_P434483	NM_008281	hepsin	-1.217	38.68	0.43021	7343	P	-1.008	49.48	0.92316	12322
L3mbtl2	A_51_P245393	NM_145993	l(3)mbt-like 2 (Drosophila)	-1.217	57.76	0.62828	14893	P	1.099	9.71	0.09699	3034
Ogdh	A_52_P369310	NM_010956	oxoglutarate dehydrogenase (lipoamide)	-1.217	49.93	0.51076	9964	P	1.02	38.4	0.68081	10141
Usp4	A_52_P116384	NM_011678	ubiquitin specific peptidase 4 (proto-onco	-1.217	49.93	0.51147	9990	P	1.121	11.33	0.20738	5013
Aggf1	A_51_P496769	NM_025630	angiogenic factor with G patch and FHA d	-1.218	28.61	0.39281	6242	P	-1.013	49.48	0.86781	11742
Arf4	A_51_P295625	NM_007479	ADP-ribosylation factor 4	-1.218	35.45	0.55853	9442	M	1.177	3.82	0.04494	1669
Clk3	A_52_P559498	NM_007713	CDC-like kinase 3	-1.218	25.79	0.38425	6014	P	1.034	33.49	0.64956	9880
Fgl2	A_52_P266132	NM_008013	fibrinogen-like protein 2	-1.218	53.87	0.57306	12142	P	-1.057	45.68	0.71087	10409

Slc22a17	A_51_P111902	NM_021551	solute carrier family 22 (organic cation tra	-1.218	53.87	0.54628	11265	P	-1.084	30.75	0.31627	6543
Synpo	A_51_P123676	AK034012	synaptopodin	-1.218	45.92	0.4705	8549	P	-1.002	49.48	0.98199	12880
1200002N14Rik	A_51_P481482	NM_027878	RIKEN cDNA 1200002N14 gene	-1.22	72.2	0.84604	27486	P	1.081	11.33	0.1217	3537
Golga4	A_51_P112789	NM_018748	golgi autoantigen, golgin subfamily a, 4	-1.22	57.76	0.66588	12756	M	1.157	4.63	0.04747	1779
Jub	A_52_P131548	NM_010590	ajuba	-1.22	69.29	0.79639	23897	P	1.113	9.71	0.12087	3507
Slc7a10	A_51_P268193	NM_017394	solute carrier family 7 (cationic amino aci	-1.22	65.79	0.70219	18517	P	-1.289	0.56	0.01509	645
U2af2	A_51_P358908	NM_133671	U2 small nuclear ribonucleoprotein auxili	-1.22	49.93	0.5012	9678	P	1.061	19.02	0.26276	5847
Es2el	A_52_P315483	BC013711	expressed sequence 2 embryonic lethal	-1.221	45.92	0.49187	9316	P	1.04	30.75	0.48291	8358
Fbxo3	A_52_P336357	NM_212433	F-box protein 3	-1.221	42.28	0.46325	8332	P	-1.027	46.3	0.56533	9167
Galnt2	A_51_P370350	NM_139272	UDP-N-acetyl-alpha-D-galactosamine:poly	-1.221	45.92	0.48052	8958	P	1.109	6.98	0.05908	2111
Hmgcr	A_51_P507410	NM_008255	3-hydroxy-3-methylglutaryl-Coenzyme A r	-1.221	61.79	0.6451	15914	P	1.059	22.1	0.36027	7025
Ak3l1	A_51_P428582	NM_009647	adenylate kinase 3 alpha-like 1	-1.222	45.92	0.4955	9457	P	1.076	16.2	0.2722	5986
Efna1	A_51_P266683	NM_010107	ephrin A1	-1.222	61.79	0.64816	16013	P	-1.146	2.04	0.02996	1195
Fev	A_51_P518841	NM_153111	FEV (ETS oncogene family)	-1.222	61.79	0.73282	15586	M	1.008	42.43	0.89642	12017
Grn	A_52_P508750	NM_008175	granulin	-1.222	53.87	0.55958	11737	P	-1.071	28.13	0.19543	4829
Gtl2	A_51_P455997	XM_981786	GTL2, imprinted maternally expressed un	-1.222	69.29	0.82214	22470	P	1.416	3.82	0.17953	4564
Mdm2	A_52_P469842	NM_010786	transformed mouse 3T3 cell double minu	-1.222	25.79	0.37646	5781	P	1.104	8.32	0.06848	2370
R74862	A_51_P210457	NM_133790	expressed sequence R74862	-1.222	57.76	0.61846	14326	P	1.008	42.43	0.91896	12264
Sema4d	A_51_P146320	NM_013660	sema domain, immunoglobulin domain (I	-1.222	57.76	0.61652	14213	P	1.168	2.53	0.01781	757
Snrp70	A_52_P501767	BC049128	U1 small nuclear ribonucleoprotein polyp	-1.222	65.79	0.7471	20934	P	-1.01	49.48	0.882	11878
Trpv6	A_51_P479029	NM_022413	transient receptor potential cation chann	-1.222	65.79	0.7101	18949	M	-1.159	1.32	0.02084	888
1200013P24Rik	A_51_P378777	NM_029090	RIKEN cDNA 1200013P24 gene	-1.224	72.2	0.82225	25543	P	-1.013	49.48	0.8576	11653
2010305C02Rik	A_51_P328622	NM_027249	RIKEN cDNA 2010305C02 gene	-1.224	65.79	0.71608	19278	P	-1.019	49	0.69138	10249
Fos	A_52_P262219	NM_010234	FBJ osteosarcoma oncogene	-1.224	69.29	0.79166	17656	M	1.163	6.98	0.08874	2860
Frmd4b	A_51_P392350	NM_145148	FERM domain containing 4B	-1.224	53.87	0.58125	12557	P	1.061	19.02	0.20824	5026
Gars	A_52_P585475	NM_180678	glycyl-tRNA synthetase	-1.224	53.87	0.55093	11467	P	-1.027	46.85	0.61536	9583
Hspa5	A_51_P395098	NM_022310	heat shock 70kD protein 5 (glucose-regula	-1.224	42.28	0.57955	10012	M	1.1	16.2	0.32883	6656
Nudt13	A_52_P166868	BC038023	nudix (nucleoside diphosphate linked mo	-1.224	61.79	0.65256	16223	P	1.18	4.63	0.05893	2101
Prkacb	A_52_P432680	NM_011100	protein kinase, cAMP dependent, catalyti	-1.224	38.68	0.55763	9419	M	1.102	13.58	0.21849	5178
Thap4	A_51_P345110	NM_025920	THAP domain containing 4	-1.224	45.92	0.48787	9182	P	1.049	25.31	0.3972	7490
Zmynd17	A_51_P369426	AK014794	zinc finger, MYND domain containing 17	-1.224	65.79	0.70976	18931	P	1.043	28.13	0.4301	7823
1810007P19Rik	A_52_P579448	NM_172701	RIKEN cDNA 1810007P19 gene	-1.225	61.79	0.6422	15814	P	-1.291	0.51	0.00637	174
4933424B01Rik	A_51_P140607	NM_138757	RIKEN cDNA 4933424B01 gene	-1.225	35.45	0.40896	6692	P	-1.022	48.7	0.71347	10432
9330107J05Rik	A_52_P166735	AK047625	RIKEN cDNA 4930431J08 gene	-1.225	72.2	0.81663	25197	P	-1.212	1.1	0.01896	801
Clic1	A_51_P357341	NM_033444	chloride intracellular channel 1	-1.225	57.76	0.67779	13125	M	1.185	3.46	0.02811	1141
Fbxo42	A_52_P586671	NM_172518	F-box protein 42	-1.225	45.92	0.4781	8893	P	1.184	4.63	0.06285	2229
Hnrpm	A_51_P170946	NM_029804	heterogeneous nuclear ribonucleoprotein	-1.225	61.79	0.72951	15444	M	1.174	4.63	0.05931	2127
Lsp1	A_52_P63044	NM_019391	lymphocyte specific 1	-1.225	65.79	0.75819	21512	P	-1.103	22.1	0.22532	5277
Mxd4	A_52_P528996	AK040356	Max dimerization protein 4	-1.225	61.79	0.67305	17205	P	1.03	36.07	0.65501	9919
Ppid	A_52_P485700	NM_026352	peptidylprolyl isomerase D (cyclophilin D)	-1.225	45.92	0.46598	8403	P	-1.037	46.85	0.68382	10179
Tk1	A_51_P224013	NM_009387	thymidine kinase 1	-1.225	75.14	0.8666	28625	P	-1.052	38.4	0.26659	5895
Vil2	A_51_P413348	NM_009510	villin 2	-1.225	49.93	0.51518	10107	P	1.375	0.75	0.01102	427
9030624J02Rik	A_52_P421972	AK035840	RIKEN cDNA 9030624J02 gene	-1.227		0.82563	13483	A	-1.06	36.07	0.28839	6192
Ptprn	A_51_P318510	NM_008985	protein tyrosine phosphatase, receptor ty	-1.227	49.93	0.52286	10447	P	-1.027	47.43	0.66555	10006
Smarca4	A_51_P479733	NM_011417	SWI/SNF related, matrix associated, actin	-1.227	61.79	0.6857	17695	P	1.121	9.71	0.11667	3413
Ddost	A_51_P216075	NM_007838	dolichyl-di-phosphooligosaccharide-prote	-1.229	35.45	0.54396	9041	M	-1.096	11.33	0.09872	3080
Ibtk	A_52_P311491	BC060722	inhibitor of Bruton agammaglobulinemia	-1.229	45.92	0.56738	10336	M	1.133	9.71	0.1612	4238
Plekhg3	A_51_P327369	AK080928	pleckstrin homology domain containing, f	-1.229	53.87	0.5505	11452	P	1.024	36.07	0.58534	9304
Slc35b2	A_52_P427564	NM_028662	solute carrier family 35, member B2	-1.229	42.28	0.4608	8250	P	-1.032	45.68	0.52517	8799
Wdr12	A_52_P161167	NM_021312	WD repeat domain 12	-1.229	57.76	0.61005	13939	P	-1.04	43.75	0.41142	7620
Hipk3	A_52_P76829	NM_010434	homeodomain interacting protein kinase	-1.23	61.79	0.68445	17633	P	-1.008	49.48	0.92526	12346
Mcl1	A_51_P238786	NM_008562	myeloid cell leukemia sequence 1	-1.23	25.79	0.52286	8480	M	1.142	11.33	0.27207	5984
Zbtb17	A_51_P463849	NM_009541	zinc finger and BTB domain containing 17	-1.23	38.68	0.41247	6841	P	-1.152	3.82	0.06417	2261

Hps5	A_52_P669145	NM_001005247	Hermansky-Pudlak syndrome 5 homolog	-1.232	53.87	0.54294	11107	P	-1.1	9.71	0.08012	2658
M6prbp1	A_51_P223404	NM_025836	mannose-6-phosphate receptor binding p	-1.232	65.79	0.70274	18550	P	1.048	28.13	0.43976	7919
Ndnl2	A_52_P196721	AK131157	necdin-like 2	-1.232	75.14	0.90003	30997	P	-1.08	22.1	0.14879	4025
Oaz1	A_51_P104128	AK003452	ornithine decarboxylase antizyme	-1.232	45.92	0.49576	9474	P	1.065	16.2	0.19146	4762
Pml	A_51_P282799	NM_008884	promyelocytic leukemia	-1.232	65.79	0.7015	18469	P	1.129	13.58	0.35082	6882
Smyd4	A_51_P460774	NM_177009	SET and MYND domain containing 4	-1.232	53.87	0.56811	11991	P	-1.019	49.22	0.7277	10548
9430010O03Rik	A_52_P423128	NM_176849	RIKEN cDNA 9430010O03 gene	-1.233	57.76	0.68577	13406	M	1.088	28.13	0.68881	10227
Axin1	A_52_P197007	NM_009733	axin 1	-1.233	38.68	0.42411	7192	P	1.102	11.33	0.1484	4016
Bak1	A_51_P395011	NM_007523	BCL2-antagonist/killer 1	-1.233	42.28	0.44136	7673	P	1.084	11.33	0.11108	3298
Dcbld1	A_51_P483699	NM_025705	discoidin, CUB and LCCL domain containi	-1.233	57.76	0.5944	13196	P	1.037	28.13	0.42503	7777
Ddah1	A_51_P110471	NM_026993	dimethylarginine dimethylaminohydrolas	-1.233	65.79	0.74736	20960	M	-1.018	49.48	0.74235	10707
Nup210	A_51_P420037	NM_018815	nucleoporin 210	-1.233	57.76	0.62384	14635	P	-1.057	38.4	0.34421	6813
Pip5k2a	A_52_P271468	NM_008845	phosphatidylinositol-4-phosphate 5-kinas	-1.233	49.93	0.52519	10547	P	-1.032	46.3	0.60929	9517
Qars	A_52_P360756	AK161817	glutaminyl-tRNA synthetase	-1.233		0.72307	12512	A	1.044	28.13	0.47086	8213
Sec24c	A_51_P186564	NM_172596	SEC24 related gene family, member C (S.	-1.233	45.92	0.46953	8505	P	-1.189	1.18	0.01816	770
2810485I05Rik	A_51_P104125	NM_176836	RIKEN cDNA 2810485I05 gene	-1.235	45.92	0.58539	10266	M	1.012	42.43	0.80819	11259
Atp8b2	A_52_P591542	XM_283873	Atpase, class I, type 8B, member 2	-1.235	49.93	0.53279	10819	P	-1.283	0.51	0.0067	201
Foxc2	A_51_P196444	NM_013519	forkhead box C2	-1.235	61.79	0.68412	17613	P	1.094	11.33	0.12623	3638
Ihpk1	A_51_P103718	NM_013785	inositol hexaphosphate kinase 1	-1.235	57.76	0.6045	13663	P	1.05	25.31	0.41191	7634
Ptpn12	A_51_P447668	NM_011203	protein tyrosine phosphatase, non-recept	-1.235	45.92	0.49127	9275	P	-1.086	22.1	0.18898	4709
Snrpa1	A_51_P164270	NM_021336	small nuclear ribonucleoprotein polypept	-1.235	61.79	0.69105	17969	P	-1.048	43.75	0.48398	8378
Sp6	A_52_P383577	NM_031183	trans-acting transcription factor 6	-1.235	49.93	0.50667	9879	P	-1.142	4.63	0.06279	2228
Tbc1d2	A_51_P454707	AK041359	TBC1 domain family, member 2	-1.235		0.80583	19872	A	1.006	42.43	0.90792	12177
4921506J03Rik	A_51_P176783	NM_001033474	RIKEN cDNA 4921506J03 gene	-1.236	42.28	0.56518	9611	M	1.087	19.02	0.33333	6719
Arid2	A_52_P25008	NM_175251	AT rich interactive domain 2 (Arid-rfx like)	-1.236	35.45	0.39874	6481	P	1.127	9.71	0.12271	3557
Dapk3	A_51_P493285	NM_007828	death-associated kinase 3	-1.236	45.92	0.4623	8298	P	-1.013	49.48	0.79039	11098
Khdrbs1	A_52_P199058	NM_011317	KH domain containing, RNA binding, signa	-1.236	23.47	0.35282	5184	P	1.076	16.2	0.20625	4988
Rtkn	A_51_P234330	NM_133641	rhotekin	-1.236	57.76	0.637	15574	P	1.075	13.58	0.1612	4237
Sntb1	A_51_P144500	NM_016667	syntrophin, basic 1	-1.236	49.93	0.53474	10881	P	1.174	8.32	0.16598	4315
Spint1	A_52_P509886	NM_016907	serine protease inhibitor, Kunitz type 1	-1.236	38.68	0.42094	7077	P	-1.058	40.63	0.3949	7460
Agt	A_51_P323712	NM_007428	angiotensinogen (serpin peptidase inhibit	-1.238	69.29	0.76891	22154	P	-1.042	42.43	0.35034	6878
BC027382	A_52_P632691	AK134496	cDNA sequence BC027382	-1.238	49.93	0.51637	10194	P	1.006	42.43	0.92659	12367
Eed	A_51_P238643	NM_021876	embryonic ectoderm development	-1.238	57.76	0.62384	14643	P	-1.165	2.53	0.04335	1625
Gstp1	A_51_P374464	NM_013541	glutathione S-transferase, pi 1	-1.238	42.28	0.45132	7964	P	-1.204	4.63	0.15747	4173
Msh3	A_52_P491493	XM_983328	mutS homolog 3 (E. coli)	-1.238	45.92	0.54594	10787	M	1.015	42.43	0.80573	11227
Nfkbib	A_51_P259459	NM_010908	nuclear factor of kappa light chain gene e	-1.238	57.76	0.61828	14309	P	-1.014	49.48	0.7827	11025
Ssbp4	A_52_P563617	NM_133772	single stranded DNA binding protein 4	-1.238	72.2	0.84917	27700	P	1.061	19.02	0.22046	5215
Tbc1d10a	A_51_P222386	NM_134023	TBC1 domain family, member 10a	-1.238	45.92	0.47956	8932	P	1.028	33.49	0.49593	8516
Bms1l	A_51_P278950	NM_194339	BMS1 homolog, ribosome assembly prote	-1.239	72.2	0.83244	26249	P	1.008	42.43	0.87351	11794
Eif2ak3	A_51_P253642	NM_010121	eukaryotic translation initiation factor 2 a	-1.239	53.87	0.58491	12766	P	-1.072	30.75	0.263	5849
Luc7l2	A_51_P361557	NM_138680	LUC7-like 2 (S. cerevisiae)	-1.239	53.87	0.6388	11836	M	1.142	9.71	0.18425	4643
Mpzl1	A_51_P228295	NM_001001880	myelin protein zero-like 1	-1.239	49.93	0.52692	10600	P	1.051	30.75	0.60845	9509
Pcx	A_51_P480578	NM_008797	pyruvate carboxylase	-1.239	65.79	0.73775	20555	P	-1.13	3.82	0.04979	1850
4930431B09Rik	A_51_P447976	BC046309	RIKEN cDNA 4930431B09 gene	-1.241	42.28	0.44185	7701	P	-1.021	47.92	0.6382	9790
Caskin2	A_51_P354804	NM_080643	cask-interacting protein 2	-1.241	61.79	0.64847	16035	P	1.056	19.02	0.26176	5840
Gopc	A_51_P427736	NM_053187	golgi associated PDZ and coiled-coil motif	-1.241	49.93	0.50968	9921	P	-1.025	47.43	0.63229	9741
Unc119	A_51_P201638	NM_011676	unc-119 homolog (C. elegans)	-1.241	31.88	0.37646	5784	P	1.013	40.63	0.76047	10862
Elk3	A_52_P627357	NM_205536	ELK3, member of ETS oncogene family	-1.242	49.93	0.59355	10492	M	1.054	25.31	0.40887	7598
Gsr	A_51_P359625	NM_010344	glutathione reductase 1	-1.242	65.79	0.75132	16117	M	1.058	30.75	0.63515	9764
Hmgb2	A_52_P485417	NM_008252	high mobility group box 2	-1.242	65.79	0.75691	21479	P	-1.191	0.92	0.01372	578
Myo9a	A_52_P201531	AK029836	myosin IXa	-1.242	42.28	0.44353	7762	P	1.123	6.98	0.06577	2309
Pnpla2	A_52_P681771	NM_025802	patatin-like phospholipase domain contai	-1.242	38.68	0.41313	6854	P	1.11	8.32	0.06587	2311
Rce1	A_51_P108778	NM_023131	RCE1 homolog, prenyl protein peptidase	-1.242	35.45	0.39447	6323	P	1.048	28.13	0.40275	7542

Tff2	A_51_P480602	NM_009363	trefoil factor 2 (spasmolytic protein 1)	-1.242	61.79	0.77907	18667	M	-1.284	0.75	0.02005	862
Zbtb10	A_52_P325161	XM_485202	zinc finger and BTB domain containing 10	-1.242	61.79	0.66137	16641	P	-1.387	0.51	0.00584	97
0610011L14Rik	A_52_P211208	NM_026661	RIKEN cDNA 0610011L14 gene	-1.244		0.61694	12744	A	-1.035	45.05	0.50922	8664
0610030E20Rik	A_52_P297457	BC066053	RIKEN cDNA 0610030E20 gene	-1.244	61.79	0.64753	15984	P	-1.248	0.51	0.00774	292
1810031K17Rik	A_52_P428228	NM_026977	RIKEN cDNA 1810031K17 gene	-1.244	57.76	0.61187	14030	P	-1.356	0.51	0.01251	524
Cyp20a1	A_51_P370470	NM_030013	cytochrome P450, family 20, subfamily A,	-1.244	61.79	0.67883	17404	P	1.074	11.33	0.12248	3553
Dgcr8	A_52_P150999	AK044890	DiGeorge syndrome critical region gene 8	-1.244	65.79	0.72707	20059	P	1.042	33.49	0.62775	9695
Hmg20a	A_52_P228389	AK039222	high mobility group 20A	-1.244	45.92	0.49059	9251	P	1.104	13.58	0.26884	5930
Myh9	A_51_P313711	NM_022410	myosin, heavy polypeptide 9, non-muscle	-1.244	69.29	0.82279	19069	M	1.037	30.75	0.47447	8259
Peli1	A_51_P208490	AK040256		-1.244	45.92	0.49512	9438	M	1.12	16.2	0.36911	7153
Rock1	A_52_P119672	NM_009071	Rho-associated coiled-coil containing prot	-1.244	42.28	0.45319	8010	P	-1.157	1.62	0.02609	1078
Snf1lk2	A_52_P575296	NM_178710	SNF1-like kinase 2	-1.244	35.45	0.38395	6006	P	1.04	28.13	0.43432	7889
Trpc4ap	A_52_P427484	NM_019828	transient receptor potential cation chann	-1.244	45.92	0.47092	8581	P	1.075	16.2	0.22119	5222
AI837181	A_51_P244923	NM_134149	expressed sequence AI837181	-1.245	49.93	0.51941	10332	P	-1.008	49.48	0.94108	12490
Fbxo28	A_51_P445392	NM_175127	F-box protein 28	-1.245	42.28	0.43739	7549	P	-1.029	46.85	0.60412	9483
Gspt1	A_51_P440004	NM_146066	G1 to S phase transition 1	-1.245	42.28	0.45467	8044	P	-1.353	0.51	0.00584	77
Hes1	A_51_P498093	NM_008235	hairy and enhancer of split 1 (Drosophila)	-1.245	42.28	0.42844	7311	P	1.149	3.82	0.02989	1193
Nr2c1	A_52_P175116	AK053907	nuclear receptor subfamily 2, group C, me	-1.245	53.87	0.48549	8344	M	1.078	13.58	0.17335	4432
S100a10	A_51_P342871	NM_009112	S100 calcium binding protein A10 (calpac	-1.245	65.79	0.72159	19719	P	1.002	42.43	0.98778	12965
Syt13	A_52_P253044	NM_030725	synaptotagmin XIII	-1.245	69.29	0.78582	17405	M	-1.323	0.51	0.00802	296
Zfp87	A_52_P188070	AK019056	zinc finger protein 87	-1.245	57.76	0.60643	13746	P	1.1	11.33	0.15617	4152
Zhx2	A_51_P381230	NM_199449	zinc fingers and homeoboxes protein 2	-1.245	49.93	0.53833	11004	P	-1.002	49.48	0.97426	12780
Ppib	A_51_P327828	NM_011149	peptidylprolyl isomerase B	-1.247	53.87	0.5734	12157	P	1.038	30.75	0.5279	8819
Zfp131	A_51_P469288	NM_028245	zinc finger protein 131	-1.247	25.79	0.3484	5074	P	1.127	6.98	0.05437	1988
2010008E23Rik	A_52_P511431	NM_028076	RIKEN cDNA 2010008E23 gene	-1.248	49.93	0.50695	9882	P	1.058	19.02	0.26833	5929
Eif3s7	A_52_P425237	AK158344	eukaryotic translation initiation factor 3,	-1.248	61.79	0.64239	15823	P	1.182	3.82	0.03953	1499
Mrpl43	A_52_P374351	NM_053164	mitochondrial ribosomal protein L43	-1.248	53.87	0.5509	11463	P	1.007	42.43	0.92232	12287
Sfpq	A_52_P292528	NM_023603	splicing factor proline/glutamine rich (pol	-1.248	53.87	0.57878	10732	M	1.156	11.33	0.30392	6365
2610034B18Rik	A_52_P615010	NM_027420	RIKEN cDNA 2610034B18 gene	-1.25	49.93	0.53377	10856	P	-1.078	16.2	0.11418	3370
Atf6	A_52_P464346	XM_888686	activating transcription factor 6	-1.25	53.87	0.54272	11095	P	1.084	19.02	0.40873	7597
Dnajb9	A_52_P613358	NM_013760	DnaJ (Hsp40) homolog, subfamily B, mem	-1.25	57.76	0.5944	13210	P	1.103	13.58	0.21184	5071
Hnrpa3	A_51_P443482	NM_146130	heterogeneous nuclear ribonucleoprotei	-1.25	23.47	0.48755	7510	M	1.165	6.98	0.12533	3611
Mtmr1	A_52_P240934	NM_016985	myotubularin related protein 1	-1.25		0.82255	16504	A	1.021	38.4	0.72173	10508
Pdgfc	A_52_P408629	AK081347	platelet-derived growth factor, C polypep	-1.25	75.14	0.66736	13439	M	-1.022	48.7	0.70847	10395
Cadps	A_52_P121903	NM_012061	Ca<2+>dependent activator protein for se	-1.252	35.45	0.39281	6248	P	-1.006	49.48	0.89755	12037
Car9	A_52_P610923	NM_139305	carbonic anhydrase 9	-1.252	75.14	0.93862	29401	M	1.118	9.71	0.12388	3579
Cflar	A_51_P326091	BC023121	CASP8 and FADD-like apoptosis regulator	-1.252	61.79	0.72992	15473	M	1.115	8.32	0.08432	2760
2410002O22Rik	A_52_P311148	AK012141	RIKEN cDNA 2410002O22 gene	-1.253	38.68	0.42357	7149	P	1.011	42.43	0.84001	11529
5730589K01Rik	A_52_P276794	NM_023434	TOX high mobility group box family mem	-1.253	53.87	0.54639	11275	P	-1.054	38.4	0.31208	6480
BC039093	A_52_P422557	XM_131700	cDNA sequence BC039093	-1.253	49.93	0.51278	10044	P	1.124	8.32	0.07694	2574
Ddx28	A_51_P219325	NM_028038	DEAD (Asp-Glu-Ala-Asp) box polypeptide	-1.253	42.28	0.43708	7545	P	1.026	38.4	0.70782	10389
Nedd4l	A_51_P305936	NM_031881	neural precursor cell expressed, develop	-1.253	35.45	0.38794	6122	P	1.078	19.02	0.35987	7012
Nrp2	A_52_P93910	NM_001077403	neuropilin 2	-1.253	49.93	0.53669	10931	P	1.114	13.58	0.25926	5799
Sfrs2ip	A_51_P302507	NM_028148	splicing factor, arginine/serine-rich 2, inte	-1.253	38.68	0.42063	7036	P	1.146	4.63	0.03904	1463
Zfp111	A_52_P366443	NM_019940	zinc finger protein 111	-1.253	45.92	0.46319	8327	P	1.162	3.46	0.02801	1125
Ap2a2	A_52_P668488	NM_007459	adaptor protein complex AP-2, alpha 2 su	-1.255	42.28	0.45145	7972	P	-1.154	4.63	0.07828	2610
Armet	A_51_P418168	NM_029103	arginine-rich, mutated in early stage tum	-1.255	53.87	0.54821	11350	P	1.084	11.33	0.12566	3621
Bmp7	A_51_P492366	NM_007557	bone morphogenetic protein 7	-1.255	65.79	0.70134	17520	M	1.045	25.31	0.34198	6793
Dll3	A_51_P504494	NM_007866	delta-like 3 (Drosophila)	-1.255	57.76	0.60503	13691	M	1.084	9.71	0.09718	3043
Dpagt1	A_51_P422208	NM_007875	dolichyl-phosphate (UDP-N-acetylglucosa	-1.255	35.45	0.38911	6159	P	-1.31	0.51	0.00804	299
Sfrs10	A_52_P320822	BC057996	splicing factor, arginine/serine-rich 10 (tra	-1.255	49.93	0.51629	10181	P	-1.069	22.1	0.139	3822
Whsc1	A_51_P400498	BC079668	Wolf-Hirschhorn syndrome candidate 1 (	-1.255	49.93	0.53419	10863	P	-1.02	49.22	0.71731	10463
1110014L15Rik	A_52_P684066	AK003710	RIKEN cDNA 1110014L15 gene	-1.256	45.92	0.4921	9330	P	1.097	9.71	0.0808	2680

Bcl10	A_52_P566867	AK080820	B-cell leukemia/lymphoma 10	-1.256	49.93	0.4726	8321	M	1.056	28.13	0.57716	9241
Cd276	A_51_P499551	NM_133983	CD276 antigen	-1.256	31.88	0.35955	5390	P	-1.279	0.66	0.01529	650
Mllt1	A_52_P227307	NM_022328	myeloid/lymphoid or mixed lineage-leuke	-1.256	42.28	0.43099	7391	P	1.135	9.71	0.18329	4632
Polr3e	A_52_P231410	AK029412	polymerase (RNA) III (DNA directed) poly	-1.256	53.87	0.5486	11375	P	-1.141	3.01	0.03904	1467
Ptpn2	A_52_P403484	BC008269	protein tyrosine phosphatase, non-recept	-1.256	61.79	0.65713	16449	P	1.067	16.2	0.197	4852
Smpd2	A_51_P234421	NM_009213	sphingomyelin phosphodiesterase 2, neut	-1.256	45.92	0.49658	9487	P	1.059	16.2	0.20222	4935
Suhw2	A_51_P486068	NM_177475	suppressor of hairy wing homolog 2 (Dros	-1.256	49.93	0.50948	9916	P	1.01	42.43	0.88445	11915
Utx	A_52_P346950	AK080370	ubiquitously transcribed tetratricopeptide	-1.256	61.79	0.64108	13255	M	1.092	13.58	0.18565	4660
Yy1	A_52_P317874	AK137406	YY1 transcription factor	-1.256	49.93	0.53797	10988	P	-1.056	36.07	0.24396	5564
2900057K09Rik	A_52_P577729	BC062943	RIKEN cDNA 2900057K09 gene	-1.258	31.88	0.36739	5555	P	1.139	9.71	0.19654	4841
4833427B12Rik	A_52_P381303	BC082565	RIKEN cDNA 4833427B12 gene	-1.258	53.87	0.57612	12310	P	-1.003	49.48	0.96579	12708
2810423A18Rik	A_51_P270635	AK013141	RIKEN cDNA 2810423A18 gene	-1.259	28.61	0.34488	5006	P	1.038	30.75	0.4582	8079
Cnot7	A_52_P410732	NM_011135	CCR4-NOT transcription complex, subunit	-1.259	42.28	0.44327	7752	P	1.019	38.4	0.67402	10089
Copg	A_52_P349694	NM_201244	coatomer protein complex, subunit gamm	-1.259	53.87	0.57878	12431	P	-1.025	48.7	0.74243	10711
Cyfip2	A_52_P359745	NM_133769	cytoplasmic FMR1 interacting protein 2	-1.259	61.79	0.72762	15370	M	-1.142	6.98	0.10735	3226
Ifnar1	A_51_P168545	NM_010508	interferon (alpha and beta) receptor 1	-1.259	20.94	0.32122	4410	P	1.014	42.43	0.80001	11177
Pitpnb	A_52_P608318	NM_019640	phosphatidylinositol transfer protein, bet	-1.259	49.93	0.50367	9831	P	1.008	42.43	0.86004	11679
Spint2	A_51_P497350	NM_011464	serine protease inhibitor, Kunitz type 2	-1.259	65.79	0.74239	15833	M	1.073	36.07	0.81259	11308
5133401N09Rik	A_52_P335609	NM_198004	RIKEN cDNA 5133401N09 gene	-1.261	28.61	0.34273	4973	P	-1.003	49.48	0.94643	12556
Ppp1r2	A_51_P221512	NM_025800	protein phosphatase 1, regulatory (inhibit	-1.261	49.93	0.5373	10947	P	1.199	2.53	0.01663	713
Rbm17	A_51_P515496	NM_152824	RNA binding motif protein 17	-1.261	28.61	0.34719	5051	P	1.086	11.33	0.09827	3071
Sdf2l1	A_51_P280446	NM_022324	stromal cell-derived factor 2-like 1	-1.261	38.68	0.51629	8275	M	-1.336	0.51	0.00623	136
Wdr26	A_52_P605296	XM_977731	WD repeat domain 26	-1.261	38.68	0.40616	6636	P	1.047	25.31	0.38151	7289
0610040J01Rik	A_51_P483617	NM_029554	RIKEN cDNA 0610040J01 gene	-1.263	72.2	0.83553	19853	M	1.085	11.33	0.12552	3617
2310028O11Rik	A_51_P486639	XM_901483	RIKEN cDNA 2310028O11 gene	-1.263	38.68	0.41125	6798	P	1.062	19.02	0.23232	5384
2810441K11Rik	A_52_P619903	NM_026798	RIKEN cDNA 2810441K11 gene	-1.263	35.45	0.37219	5660	P	1.074	19.02	0.35474	6950
Clstn1	A_52_P448205	BC053843	calsyntenin 1	-1.263	49.93	0.53335	10836	P	1.061	22.1	0.30312	6356
Ifitm2	A_51_P168459	NM_030694	interferon induced transmembrane prote	-1.263	35.45	0.38461	6023	P	-1.089	36.07	0.45311	8025
Lin28	A_52_P294305	NM_145833	lin-28 homolog (C. elegans)	-1.263	57.76	0.61205	14068	P	-1.025	47.43	0.64212	9820
Slc25a20	A_51_P344008	NM_020520	solute carrier family 25 (mitochondrial ca	-1.263	61.79	0.67249	17193	P	1.137	9.71	0.18229	4613
Tnfaip1	A_52_P52036	NM_009395	tumor necrosis factor, alpha-induced prot	-1.263	20.94	0.31692	4287	P	1.142	6.98	0.06454	2269
Strn4	A_51_P234833	NM_133789	striatin, calmodulin binding protein 4	-1.264	53.87	0.58125	12605	P	-1.031	47.92	0.74287	10714
Xpnpep1	A_51_P448427	NM_133216	X-prolyl aminopeptidase (aminopeptidase	-1.264	31.88	0.35096	5132	P	1.074	13.58	0.14949	4033
2600011C06Rik	A_52_P259425	BC010792	RNA binding motif protein 25	-1.266	57.76	0.63941	15663	P	-1.039	46.3	0.66025	9975
Phc2	A_51_P457388	NM_018774	polyhomeotic-like 2 (Drosophila)	-1.266	31.88	0.35584	5255	P	1.097	13.58	0.17832	4542
Adcy6	A_51_P243134	NM_007405	adenylate cyclase 6	-1.267	38.68	0.41329	6859	P	1.085	11.33	0.13679	3788
Man2b1	A_52_P322573	AK054315	mannosidase 2, alpha B1	-1.267	69.29	0.68443	16818	P	-1.126	3.82	0.04505	1688
Ppp1r3c	A_52_P30451	NM_016854	protein phosphatase 1, regulatory (inhibit	-1.267	53.87	0.58125	12577	P	1.064	19.02	0.23847	5464
Satb2	A_52_P536927	AK129270	special AT-rich sequence binding protein	-1.267	65.79	0.73114	20323	P	1.083	11.33	0.12367	3572
Esco2	A_51_P195034	NM_028039	establishment of cohesion 1 homolog 2 (	-1.269	72.2	0.85746	28098	P	-1.194	1.32	0.0537	1754
Gmeb2	A_51_P101228	NM_198169	glucocorticoid modulatory element bindi	-1.269	31.88	0.34902	5099	P	-1.047	42.43	0.34534	6820
Herpud1	A_51_P434101	NM_022331	homocysteine-inducible, endoplasmic ret	-1.269	28.61	0.3596	5196	P	-1.121	19.02	0.23748	5452
Mnat1	A_52_P190942	AK053621	menage a trois 1	-1.269		0.79718	15597	A	1.046	30.75	0.51573	8728
Ncoa4	A_51_P151983	NM_001033988	nuclear receptor coactivator 4	-1.271	57.76	0.64215	15803	P	1.192	5.75	0.09121	2928
Ndufs2	A_51_P393761	NM_153064	NADH dehydrogenase (ubiquinone) Fe-S	-1.271	61.79	0.65256	16217	P	-1.66	0.51	0.0146	622
Nup98	A_52_P170761	NM_022979	nucleoporin 98	-1.271	65.79	0.73698	20521	P	1.02	38.4	0.69683	10288
Polk	A_51_P363588	NM_012048	polymerase (DNA directed), kappa	-1.271	38.68	0.42029	7032	P	1.027	30.75	0.49768	8554
Spnb1	A_52_P490012	S66283	spectrin beta 1	-1.271	28.61	0.44123	6699	M	1.073	13.58	0.16133	4242
Surf6	A_52_P283119	AK164904	surfeit gene 6	-1.271	53.87	0.55923	11715	P	-1.069	28.13	0.19731	4859
Tinag	A_51_P283004	NM_012033	tubulointerstitial nephritis antigen	-1.271	61.79	0.70294	18554	P	-1.027	46.3	0.54635	8994
Ubqln4	A_51_P362161	NM_033526	ubiquilin 4	-1.271	38.68	0.41046	6753	P	1.033	36.07	0.66434	9998
4930579K19Rik	A_51_P306739	NM_175227	RIKEN cDNA 4930579K19 gene	-1.272	25.79	0.32081	4392	P	1.013	42.43	0.83006	11452
Dtnb	A_52_P136751	NM_007886	dystrobrevin, beta	-1.272	57.76	0.60523	13702	P	1.009	42.43	0.87436	11802

Rbmx	A_51_P277270	NM_011252	RNA binding motif protein, X chromosom	-1.272	35.45	0.37022	5633	P	1.009	42.43	0.85658	11640
Rybp	A_51_P279505	NM_019743	RING1 and YY1 binding protein	-1.272	61.79	0.70236	18521	P	1.094	11.33	0.14618	3966
Sf3b3	A_51_P113747	AK017529	splicing factor 3b, subunit 3	-1.272	35.45	0.37747	5845	P	-1.109	8.32	0.07214	2442
Slc12a7	A_51_P421734	NM_011390	solute carrier family 12, member 7	-1.272	61.79	0.67305	17211	P	1.035	30.75	0.43881	7913
0610011F06Rik	A_51_P443618	NM_026686	RIKEN cDNA 0610011F06 gene	-1.274	45.92	0.49273	9353	P	1.153	3.82	0.03594	1386
C030034I22Rik	A_52_P778544	AK147961	RIKEN cDNA C030034I22 gene	-1.274	57.76	0.62287	14573	P	-1.134	4.63	0.06577	2310
Ckap2	A_52_P162099	NM_001004140	cytoskeleton associated protein 2	-1.274	65.79	0.73001	20243	M	1.096	11.33	0.15354	4106
Eif3s1	A_52_P654965	BC080788	eukaryotic translation initiation factor 3, s	-1.274	49.93	0.52791	10647	P	1.048	25.31	0.31429	6518
Ppapdc1	A_51_P281593	AK144593	phosphatidic acid phosphatase type 2 dor	-1.274	25.79	0.32338	4447	P	-1.107	16.2	0.18061	4586
Scml4	A_51_P338799	NM_172938	sex comb on midleg-like 4 (Drosophila)	-1.274	53.87	0.57307	12145	P	1.051	25.31	0.35417	6939
2600014M03Rik	A_52_P65703	NM_178620	major facilitator superfamily domain cont	-1.276	38.68	0.41016	6738	P	1.067	25.31	0.53859	8924
Chaf1a	A_51_P196973	NM_013733	chromatin assembly factor 1, subunit A (p	-1.276	53.87	0.54899	11388	P	1.028	33.49	0.57292	9210
Commd7	A_52_P646705	NM_133850	COMM domain containing 7	-1.276	25.79	0.32851	4612	P	1.124	6.98	0.05931	2129
Hoxd8	A_52_P485542	NM_008276	homeo box D8	-1.276	69.29	0.78992	23435	P	1.001	42.43	0.99571	13014
Kit	A_51_P355906	NM_021099	kit oncogene	-1.276	65.79	0.72231	19783	P	-1.044	46.3	0.68259	10162
Mkln1	A_52_P459538	AK037967	muskelin 1, intracellular mediator contair	-1.276	53.87	0.5746	12223	P	1.103	13.58	0.24554	5576
Mras	A_52_P256929	NM_008624	muscle and microspikes RAS	-1.276	45.92	0.49852	9616	P	1.083	11.33	0.11656	3409
Saa2	A_51_P166886	NM_011314	serum amyloid A 2	-1.276	53.87	0.54327	10172	M	-1.024	47.43	0.59766	9430
Tmem27	A_51_P248595	NM_020626	transmembrane protein 27	-1.276	57.76	0.67557	13048	M	1.115	16.2	0.38299	7315
Cdc14b	A_51_P416660	NM_172587	CDC14 cell division cycle 14 homolog B (S	-1.277	45.92	0.47131	8614	P	1.028	36.07	0.68236	10159
Cks1b	A_51_P227004	NM_016904	CDC28 protein kinase 1b	-1.277	35.45	0.49773	7787	M	1.111	13.58	0.2948	6274
Junb	A_51_P159201	NM_008416	Jun-B oncogene	-1.277	45.92	0.55722	9410	M	1.146	8.32	0.11713	3422
Kin	A_52_P455275	NM_025280	antigenic determinant of rec-A protein	-1.277	53.87	0.59546	13260	P	1.071	13.58	0.14782	3996
Phldb2	A_52_P153700	NM_153412	pleckstrin homology-like domain, family E	-1.277	25.79	0.32383	4476	P	-1.006	49.48	0.92077	12278
Arhgef19	A_51_P442759	NM_172520	Rho guanine nucleotide exchange factor (	-1.279	35.45	0.38565	6058	P	1.038	33.49	0.59528	9400
Arl6ip2	A_51_P163834	NM_019717	ADP-ribosylation factor-like 6 interacting		-1.279	61.79	0.71119	19027	P	1.056	22.1	0.34708	6838
Csnk2a1	A_51_P397768	NM_007788	casein kinase 2, alpha 1 polypeptide	-1.279	23.47	0.30778	4107	P	1.057	19.02	0.22271	5251
Ctdsp1	A_51_P222071	NM_153088	CTD (carboxy-terminal domain, RNA polyı	-1.279	42.28	0.46206	8277	P	-1.106	38.4	0.56089	9117
Hnrpr	A_52_P451268	AK042968	heterogeneous nuclear ribonucleoprotein	-1.279	61.79	0.65889	16541	P	1.074	13.58	0.12691	3644
Mark3	A_52_P344704	NM_022801	MAP/microtubule affinity-regulating kinas	-1.279	31.88	0.34533	5016	P	-1.031	45.68	0.52295	8779
Slc6a6	A_52_P339996	NM_009320	solute carrier family 6 (neurotransmitter t	-1.279	57.76	0.65107	12209	M	-1.016	49.48	0.87436	11801
Eif2b2	A_51_P229816	NM_145445	eukaryotic translation initiation factor 2B,	-1.28	42.28	0.4306	7373	P	1.019	40.63	0.72829	10552
Fcho2	A_52_P333921	BC053718	FCH domain only 2	-1.28	42.28	0.45734	8109	P	1.077	16.2	0.26536	5883
Lrmp	A_51_P130079	NM_008511	lymphoid-restricted membrane protein	-1.28	61.79	0.66674	16897	P	-1.077	40.63	0.48187	8329
Pogz	A_51_P513449	NM_172683	pogo transposable element with ZNF dom	-1.28	45.92	0.55958	9482	M	-1.098	25.31	0.25635	5749
Rpo1-3	A_52_P1083868	AK037475		-1.28	42.28	0.43833	7581	P	-1.176	1.32	0.02221	938
Tcfec	A_52_P127925	NM_031198	transcription factor EC	-1.28	45.92	0.49455	9411	P	-1.07	25.31	0.17475	4472
Tnrc6a	A_51_P509229	NM_144925	trinucleotide repeat containing 6a	-1.28	25.79	0.32102	4398	P	1.125	16.2	0.40523	7568
Fgl1	A_52_P294510	NM_145594	fibrinogen-like protein 1	-1.282	45.92	0.51941	9899	P	1.067	19.02	0.26583	5891
Ica1	A_52_P260339	NM_010492	islet cell autoantigen 1	-1.282	49.93	0.50317	9808	P	-1.21	1.1	0.01711	740
Nktr	A_51_P246387	NM_010918	natural killer tumor recognition sequence	-1.282	38.68	0.39874	6480	P	1.196	6.98	0.17372	4440
Pcsk7	A_51_P351285	NM_008794	proprotein convertase subtilisin/kexin typ	-1.282	42.28	0.45055	7915	P	1.02	38.4	0.6993	10308
Ar	A_51_P496031	NM_013476	androgen receptor	-1.284	38.68	0.39347	6266	M	-1.075	40.63	0.52383	8785
Insm1	A_51_P140887	NM_016889	insulinoma-associated 1	-1.284	49.93	0.53335	10832	P	-1.13	13.58	0.20155	4921
Rabep2	A_51_P484959	NM_030566	rabaptin, RAB GTPase binding effector pro	-1.284	69.29	0.7823	22879	P	-1.024	48.39	0.68496	10190
Sox7	A_51_P476018	NM_011446	SRY-box containing gene 7	-1.284	42.28	0.44372	7763	P	1.036	33.49	0.61566	9584
Srrm2	A_51_P166277	NM_175229	serine/arginine repetitive matrix 2	-1.284	45.92	0.57591	9900	M	1.025	42.43	0.89068	11971
4930402E16Rik	A_52_P411025	NM_198308	RIKEN cDNA 4930402E16 gene	-1.285	57.76	0.58493	12170	M	-1.078	28.13	0.23972	5481
6030446N20Rik	A_52_P988136	AK037547	RIKEN cDNA 6030446N20 gene	-1.285	61.79	0.70894	18882	M	1.075	16.2	0.24158	5524
Gsta4	A_51_P112223	NM_010357	glutathione S-transferase, alpha 4	-1.285	81.02	0.94819	30087	P	-1.069	36.07	0.36189	7039
Tmprss6	A_51_P219266	NM_027902	transmembrane serine protease 6	-1.285	45.92	0.47426	8758	P	-1.097	22.1	0.19871	4880
Maged1	A_51_P174854	NM_019791	melanoma antigen, family D, 1	-1.287	28.61	0.46688	6939	M	1.04	28.13	0.37012	7168
Mrpl27	A_52_P180692	AK080324	mitochondrial ribosomal protein L27	-1.287	65.79	0.75046	21111	P	1.063	22.1	0.39745	7494

Slc25a28	A_52_P295533	NM_145156	solute carrier family 25, member 28	-1.287	35.45	0.38796	6132	P	-1.235	0.66	0.01251	519
Arhgdib	A_52_P515247	NM_007486	Rho, GDP dissociation inhibitor (GDI) beta	-1.289	72.2	0.84055	27121	P	-1.179	2.53	0.05247	1934
Gpsm3	A_51_P106322	NM_134116	G-protein signalling modulator 3 (AGS3-lil	-1.289	45.92	0.4813	8981	P	-1.008	49.48	0.90099	12099
Rela	A_51_P385993	NM_009045	v-rel reticuloendotheliosis viral oncogene	-1.289	42.28	0.44218	7716	P	1.08	13.58	0.15136	4057
Stat3	A_51_P201480	NM_213659	signal transducer and activator of transcri	-1.289	53.87	0.61088	13267	P	1.114	13.58	0.28389	6132
Taf13	A_51_P120608	NM_025444	TAF13 RNA polymerase II, TATA box bindir	-1.289	38.68	0.4035	6575	P	1.018	40.63	0.71909	10480
4933425L03Rik	A_52_P80567	BC057020	RIKEN cDNA 4933425L03 gene	-1.29	35.45	0.37646	5779	P	-1.056	42.43	0.46231	8135
Impa2	A_51_P299287	NM_053261	inositol (myo)-1(or 4)-monophosphatase	-1.29	53.87	0.59861	13381	P	1.048	28.13	0.4157	7684
Papola	A_52_P404096	NM_011112	poly (A) polymerase alpha	-1.29	25.79	0.31874	4354	P	1.067	19.02	0.27384	6009
Slc35e3	A_51_P459402	NM_029875	solute carrier family 35, member E3	-1.29	45.92	0.48379	9040	P	-1.046	45.05	0.60318	9479
Vcp	A_51_P109766	NM_009503	valosin containing protein	-1.29	53.87	0.5012	8402	M	1.104	8.32	0.05956	2135
Zfp422	A_52_P206762	NM_026057	zinc finger protein 422	-1.29	38.68	0.50777	8058	M	-1.035	45.68	0.54625	8991
Dmwd	A_51_P483946	NM_010058	dystrophia myotonica-containing WD repe	-1.292	49.93	0.54639	11274	P	-1.097	25.31	0.27795	6061
Gfi1	A_51_P200262	NM_010278	growth factor independent 1	-1.292	42.28	0.5306	9408	P	-1.075	36.07	0.39678	7489
H3f3a	A_51_P456237	NM_008210	H3 histone, family 3A	-1.292	69.29	0.7948	17804	M	1.221	3.46	0.05486	2002
Nfkbia	A_51_P295192	NM_010907	nuclear factor of kappa light chain gene e	-1.292	53.87	0.55224	11500	P	1.245	6.98	0.18901	4710
Sfn	A_51_P213940	NM_018754	stratifin	-1.292	72.2	0.83127	26128	P	1.015	40.63	0.76694	10913
Dll4	A_51_P384402	NM_019454	delta-like 4 (Drosophila)	-1.294	31.88	0.34633	5035	P	1.042	28.13	0.4138	7666
Mrps2	A_52_P405955	NM_080452	mitochondrial ribosomal protein S2	-1.294	20.94	0.28987	3619	P	1.064	22.1	0.35998	7018
Pah	A_51_P186547	NM_008777	phenylalanine hydroxylase	-1.294	69.29	0.80717	24534	P	1.131	16.2	0.42726	7789
Slc22a1	A_52_P229972	NM_009202	solute carrier family 22 (organic cation tra	-1.294	75.14	0.86026	26680	P	-1.041	45.05	0.53866	8929
Stard10	A_51_P191520	NM_019990	START domain containing 10	-1.294	18.5	0.2835	3497	P	-1.048	43.75	0.52383	8786
Wfs1	A_51_P216593	NM_011716	Wolfram syndrome 1 homolog (human)	-1.294	45.92	0.57311	9825	M	1.116	8.32	0.08802	2839
Apaf1	A_51_P368696	NM_001042558	apoptotic peptidase activating factor 1	-1.295	42.28	0.44996	7906	P	1.017	40.63	0.70431	10349
D030016E14Rik	A_52_P514336	NM_177240	RIKEN cDNA D030016E14 gene	-1.295	49.93	0.54468	11192	P	1.045	28.13	0.46999	8199
Sfrs4	A_52_P550780	NM_020587	splicing factor, arginine/serine-rich 4 (SRp	-1.295	25.79	0.31283	4211	P	-1.014	49.48	0.74779	10770
Stxbp4	A_51_P502957	NM_011505	syntaxin binding protein 4	-1.295	28.61	0.32293	4438	P	1.074	19.02	0.35082	6883
Trib1	A_52_P573552	NM_144549	tribbles homolog 1 (Drosophila)	-1.295	45.92	0.4726	8668	P	-1.084	22.1	0.1534	4098
4732495E13Rik	A_51_P224771	NM_172608	RIKEN cDNA 4732495E13 gene	-1.297	53.87	0.61502	11116	M	1.162	3.82	0.03553	1379
Ap4e1	A_51_P484477	XM_894489	adaptor-related protein complex AP-4, ep	-1.297	61.79	0.68969	17903	P	1.072	19.02	0.29787	6298
F730014I05Rik	A_52_P285124	AK041830	RIKEN cDNA F730014I05 gene	-1.297	45.92	0.50238	9728	P	-1.142	3.01	0.04095	1554
Oxr1	A_51_P161893	NM_130885	oxidation resistance 1	-1.297	28.61	0.32228	4430	P	-1.236	2.04	0.07846	2613
Tirap	A_52_P676956	NM_054096	toll-interleukin 1 receptor (TIR) domain-co	-1.297	53.87	0.5702	12063	P	1.163	3.46	0.02717	1105
Brwd3	A_52_P8409	AK083676	bromodomain and WD repeat domain co	-1.299	28.61	0.48069	7834	M	1.022	36.07	0.62027	9624
Mospd3	A_51_P492228	NM_030037	motile sperm domain containing 3	-1.299	28.61	0.3333	4750	P	1.01	42.43	0.87549	11814
Nxt1	A_52_P184398	NM_019761	NTF2-related export protein 1	-1.299	42.28	0.45371	8026	P	-1.028	47.43	0.64576	9854
Sh3bp1	A_51_P342906	NM_009164	SH3-domain binding protein 1	-1.299	53.87	0.58125	12555	P	-1.004	49.48	0.96884	12732
Vezf1	A_52_P45708	NM_016686	vascular endothelial zinc finger 1	-1.299	38.68	0.41313	6853	P	1.04	33.49	0.63726	9779
Zbtb24	A_52_P302108	NM_153398	zinc finger and BTB domain containing 24	-1.299	49.93	0.53141	10780	P	1.042	30.75	0.59114	9339
4921537D05Rik	A_51_P366211	AK141627	RIKEN cDNA 4921537D05 gene	-1.3	57.76	0.61423	14138	P	-1.017	49.48	0.74126	10696
Cpe	A_52_P78417	NM_013494	carboxypeptidase E	-1.3	28.61	0.45133	6586	M	1.339	0.24	0.00619	125
Lepre1	A_51_P346923	NM_019782	leprecan 1	-1.3	35.45	0.37401	5712	M	-1.021	49	0.71153	10416
Nfkbiz	A_51_P387591	NM_030612	nuclear factor of kappa light polypeptide	-1.3	57.76	0.65402	16305	P	-1.146	19.02	0.30984	6444
Pim2	A_51_P458428	NM_138606	proviral integration site 2	-1.3	49.93	0.52944	10709	P	-1.087	25.31	0.19537	4420
Rnf40	A_51_P236013	NM_172281	ring finger protein 40	-1.3	57.76	0.65596	12395	M	1.116	6.98	0.05437	1987
Rpa1	A_51_P333159	NM_026653	replication protein A1	-1.3	25.79	0.3077	4093	P	-1.157	1.58	0.02161	908
Wdr40a	A_52_P274504	AK083369	WD repeat domain 40A	-1.3	42.28	0.43048	7359	P	1.036	30.75	0.43181	7857
9130229H14Rik	A_52_P637034	BC125472	melanoma inhibitory activity 3	-1.302	23.47	0.2978	3765	P	-1.102	22.1	0.25309	5698
Arrdc1	A_52_P188018	NM_178408	arrestin domain containing 1	-1.302	28.61	0.33104	4684	P	-1.069	25.31	0.17171	4404
Faah	A_51_P386660	NM_010173	fatty acid amide hydrolase	-1.302	31.88	0.33699	4833	P	1.045	28.13	0.40641	7581
Gsto1	A_51_P155313	NM_010362	glutathione S-transferase omega 1	-1.302	72.2	0.83826	27007	P	1.206	2.53	0.02026	865
Slc25a14	A_52_P478281	AK051145	solute carrier family 25 (mitochondrial ca	-1.302		0.46206	6900	A	1.125	16.2	0.38049	7281
Tmem16f	A_52_P660158	NM_175344	transmembrane protein 16F	-1.302	42.28	0.43969	7618	P	1.096	13.58	0.23137	5371

2010005J08Rik	A_52_P199299	NM_001077661	RIKEN cDNA 2010005J08 gene	-1.304	42.28	0.44256	7736	P	1.06	22.1	0.30091	6337
Capn2	A_51_P448109	NM_009794	calpain 2	-1.304	18.5	0.27224	3227	P	1.066	22.1	0.39272	7431
Fbxo45	A_51_P447299	NM_173439	F-box protein 45	-1.304	75.14	0.90389	31368	M	1.071	19.02	0.29102	6220
Gal	A_51_P258281	NM_010253	galanin	-1.304	49.93	0.52006	10351	P	1.001	42.43	0.98302	12889
Glg1	A_52_P279759	AK050772	golgi apparatus protein 1	-1.304	31.88	0.33591	4803	P	1.071	13.58	0.13757	3801
Pmm2	A_52_P36306	NM_016881	phosphomannomutase 2	-1.304	38.68	0.41089	6768	P	1.098	11.33	0.13274	3727
Tpst2	A_51_P222153	NM_009419	protein-tyrosine sulfotransferase 2	-1.304	57.76	0.6711	12914	M	-1.054	40.63	0.33097	6684
Ctcf	A_51_P513785	NM_007794	CCCTC-binding factor	-1.305	28.61	0.32	4378	P	1.091	16.2	0.29951	6310
Glcci1	A_52_P370935	NM_178072	glucocorticoid induced transcript 1	-1.305	20.94	0.28084	3457	P	1.076	11.33	0.11836	3446
Guk1	A_51_P235878	NM_008193	guanylate kinase 1	-1.305	49.93	0.51541	10137	P	-1.034	45.05	0.47127	8219
Plcb3	A_51_P236042	NM_008874	phospholipase C, beta 3	-1.305	49.93	0.5083	9902	P	1.006	42.43	0.92493	12339
Sdc4	A_51_P323248	NM_011521	syndecan 4	-1.305	35.45	0.4719	7091	M	1.073	13.58	0.15329	4093
1110067D22Rik	A_51_P440047	NM_173752	RIKEN cDNA 1110067D22 gene	-1.307	45.92	0.49479	9422	P	1.087	11.33	0.11329	3341
Apoc4	A_51_P460332	NM_007385	apolipoprotein C-IV	-1.307	53.87	0.57878	12428	P	-1.026	47.43	0.61731	9606
Ate1	A_52_P119290	NM_001029895	arginine-tRNA-protein transferase 1	-1.307	61.79	0.698	18269	P	-1.182	0.92	0.01399	587
Chd1	A_52_P329250	NM_007690	chromodomain helicase DNA binding pro	-1.307	31.88	0.33953	4909	P	-1.027	49	0.78144	11004
Hk2	A_51_P204080	NM_013820	hexokinase 2	-1.307	69.29	0.78979	23417	P	1.076	13.58	0.13414	3747
Hoxb3	A_51_P460643	NM_001079869	homeo box B3	-1.307	42.28	0.43906	7605	P	1.084	13.58	0.15085	4052
Ikbkg	A_52_P507853	AK048446	inhibitor of kappaB kinase gamma	-1.307	35.45	0.37262	5674	P	-1.128	4.63	0.05635	2040
Khsrp	A_52_P123252	NM_010613	KH-type splicing regulatory protein	-1.307	69.29	0.80341	24310	P	1.097	13.58	0.23432	5415
BC019731	A_52_P563917	NM_144914	cDNA sequence BC019731	-1.309	38.68	0.40486	6610	P	1.013	42.43	0.81537	11327
BC043098	A_52_P178998	NM_174997	cDNA sequence BC043098	-1.309	42.28	0.51736	8308	M	1.105	9.71	0.08176	2696
Csrp1	A_52_P209184	NM_007791	cysteine and glycine-rich protein 1	-1.309	31.88	0.33582	4801	P	-1.04	43.15	0.38179	7306
1500031H01Rik	A_52_P54856	BC064081	RIKEN cDNA 1500031H01 gene	-1.311	45.92	0.47092	8591	P	1.058	13.58	0.30038	5869
1700029G01Rik	A_52_P456192	NM_025856	RIKEN cDNA 1700029G01 gene	-1.311	42.28	0.43833	7582	P	-1.034	44.4	0.45218	8017
BC020002	A_52_P483305	NM_145374	cDNA sequence BC020002	-1.311	25.79	0.31434	4233	P	1.014	42.43	0.80427	11212
Folr2	A_51_P162671	NM_008035	folate receptor 2 (fetal)	-1.311	38.68	0.41016	6742	P	-1.022	49.22	0.74976	10786
Pex26	A_52_P354306	NM_028730	peroxisome biogenesis factor 26	-1.311	35.45	0.36757	5577	P	-1.018	48.39	0.66188	9988
Ppm1l	A_51_P212515	NM_178726	protein phosphatase 1 (formerly 2C)-like	-1.311	45.92	0.50055	9664	P	-1.247	2.04	0.0794	2639
Psmb8	A_51_P345367	NM_010724	proteosome (prosome, macropain) subur	-1.311	49.93	0.53335	10845	P	1.07	16.2	0.23494	5422
Rbp1	A_52_P418791	NM_011254	retinol binding protein 1, cellular	-1.311	72.2	0.84365	27310	P	-1.188	2.53	0.05982	2150
Stat1	A_52_P70261	NM_009283	signal transducer and activator of transcri	-1.311	31.88	0.34117	4950	P	1.116	8.32	0.07833	2611
Tdg	A_52_P33287	NM_011561	thymine DNA glycosylase	-1.311	35.45	0.37895	5892	P	1.032	33.49	0.5959	9409
0610009O20Rik	A_51_P238405	BC002117	RIKEN cDNA 0610009O20 gene	-1.312		0.51328	9234	A	1.087	13.58	0.17832	4544
1110049F12Rik	A_51_P507129	NM_025411	RIKEN cDNA 1110049F12 gene	-1.312	20.94	0.41247	5649	M	1.057	28.13	0.59587	9408
Arid1a	A_51_P118671	XM_992408	AT rich interactive domain 1A (Swi1 like)	-1.312	38.68	0.40993	6733	P	1.083	16.2	0.25246	5687
Cenpa	A_51_P273979	NM_007681	centromere protein A	-1.312	61.79	0.68143	17496	P	-1.002	49.48	0.97474	12784
Cenpf	A_51_P246119	XM_899897	centromere protein F	-1.312	49.93	0.59376	12539	M	-1.094	9.71	0.07542	2548
Chst2	A_51_P258894	NM_018763	carbohydrate sulfotransferase 2	-1.312	49.93	0.55657	11627	P	-1.169	2.04	0.03953	1500
Jmjd1b	A_51_P383584	XM_619530	jumonji domain containing 1B	-1.312	31.88	0.34986	5120	P	1.039	30.75	0.55887	9096
Kdelr3	A_52_P473966	NM_134090	KDEL (Lys-Asp-Glu-Leu) endoplasmic retic	-1.312	23.47	0.29829	3776	P	1.044	30.75	0.54927	9015
Sfrp2	A_51_P520849	NM_009144	secreted frizzled-related protein 2	-1.312	49.93	0.51644	10195	P	1.075	13.58	0.14104	3863
Usf1	A_51_P233478	NM_009480	upstream transcription factor 1	-1.312	42.28	0.4305	7361	P	-1.127	8.32	0.11546	3389
A330008L17Rik	A_52_P663296	NM_175479	RIKEN cDNA A330008L17 gene	-1.314	49.93	0.52211	10413	P	1.03	33.49	0.51156	8682
Dag1	A_51_P148675	NM_010017	dystroglycan 1	-1.314	38.68	0.42304	7140	P	1.019	38.4	0.68053	10138
Def8	A_52_P29879	NM_054046	differentially expressed in FDCP 8	-1.314	35.45	0.3773	5825	P	-1.127	4.63	0.05915	2114
Eef1d	A_52_P477489	NM_029663	eukaryotic translation elongation factor 1	-1.314	49.93	0.52683	10597	P	1.091	13.58	0.21488	5118
Luzp1	A_52_P359621	NM_024452	leucine zipper protein 1	-1.314	25.79	0.31243	4199	P	1.051	25.31	0.35758	6981
Mad2l1	A_51_P230873	NM_019499	MAD2 (mitotic arrest deficient, homolog)	-1.314	42.28	0.43021	7344	P	1.002	42.43	0.98302	12888
Rhod	A_51_P452953	NM_007485	ras homolog gene family, member D	-1.314	57.76	0.6419	15788	P	1.1	8.32	0.0606	2167
Snx4	A_51_P480779	AK027953	sorting nexin 4	-1.314	57.76	0.69991	17462	M	1.071	19.02	0.27879	6073
Syp	A_51_P379428	NM_009305	synaptophysin	-1.314	53.87	0.51736	9823	P	-1.339	0.51	0.00584	66
Syvn1	A_51_P176341	NM_028769	synovial apoptosis inhibitor 1, synoviolin	-1.314	57.76	0.61828	14307	P	1.028	33.49	0.50642	8648

Tyk2	A_51_P466824	NM_018793	tyrosine kinase 2	-1.314	45.92	0.49004	9239	P	-1.02	48.39	0.65581	9925
2810429I04Rik	A_52_P502226	AK043092	RIKEN cDNA 2810429I04 gene	-1.316	38.68	0.39458	6351	P	-1.223	0.66	0.01141	442
A930028L21Rik	A_51_P406090	AK020899	RIKEN cDNA A930028L21 gene	-1.316	49.93	0.51272	10042	P	1.034	30.75	0.49288	8477
Aof2	A_51_P463321	NM_133872	amine oxidase (flavin containing) domain	-1.316	42.28	0.42411	7197	P	-1.001	49.48	0.99461	13012
Eif4e	A_52_P1035759	AK045366		-1.316	25.79	0.3116	4186	P	1.139	5.75	0.05893	2102
Ezh2	A_51_P248067	NM_007971	enhancer of zeste homolog 2 (Drosophila	-1.316	45.92	0.49177	9312	P	1.02	42.43	0.93782	12459
Foxj3	A_52_P100208	AK086875	forkhead box J3	-1.316	20.94	0.27555	3324	P	1.134	8.32	0.10934	3247
Gamt	A_51_P484869	NM_010255	guanidinoacetate methyltransferase	-1.316	53.87	0.49393	9025	P	-1.078	22.1	0.14008	3856
Irf1	A_51_P146103	NM_008390	interferon regulatory factor 1	-1.316	42.28	0.46319	8328	P	1.091	22.1	0.53618	8903
Pex5	A_52_P419007	NM_008995	peroxisome biogenesis factor 5	-1.316	18.5	0.261	3005	P	1.072	16.2	0.20908	5033
Plagl2	A_51_P35377	NM_018807	pleiomorphic adenoma gene-like 2	-1.316	49.93	0.51822	10292	P	1.048	25.31	0.36187	7038
Poldip3	A_52_P113487	AK052722	polymerase (DNA-directed), delta interact	-1.316	57.76	0.63575	15517	P	-1.027	46.85	0.57885	9252
Prpf8	A_51_P168662	NM_138659	pre-mRNA processing factor 8	-1.316	42.28	0.43969	7619	P	-1.134	2.53	0.03334	1299
Rnf6	A_52_P344116	NM_028774	ring finger protein (C3H2C3 type) 6	-1.316	61.79	0.66969	17015	P	1.027	33.49	0.53134	8852
Slc7a1	A_51_P243246	NM_007513	solute carrier family 7 (cationic amino aci	-1.316		0.47332	7987	A	1.179	4.63	0.06194	2188
Arhgef12	A_52_P390227	NM_027144	Rho guanine nucleotide exchange factor (	-1.318	16.01	0.25139	2808	P	1.155	9.71	0.19014	4724
Hrb	A_51_P191021	NM_010472	HIV-1 Rev binding protein	-1.318	31.88	0.33699	4829	P	-1.084	33.49	0.35878	6990
Myt1	A_51_P407480	NM_008665	myelin transcription factor 1	-1.318	38.68	0.49852	7833	M	1.026	33.49	0.55121	9046
Nr5a2	A_51_P514449	NM_030676	nuclear receptor subfamily 5, group A, me	-1.318	45.92	0.48412	9061	P	1.07	16.2	0.17804	4540
Rnf138	A_51_P261608	AB025011	ring finger protein 138	-1.318	28.61	0.33133	4693	P	-1.168	3.46	0.069	2377
Stk24	A_51_P221625	NM_145465	serine/threonine kinase 24 (STE20 homol	-1.318	20.94	0.4077	5512	M	1.012	42.43	0.8227	11386
Bok	A_51_P373082	AF027707	Bcl-2-related ovarian killer protein	-1.319	49.93	0.54963	11429	P	-1.053	36.07	0.27	5958
Mical1	A_51_P356760	NM_138315	microtubule associated monoxygenase, ca	-1.319	57.76	0.62303	14591	P	-1.108	8.32	0.08255	2716
Mvk	A_52_P569067	NM_023556	mevalonate kinase	-1.319	28.61	0.33032	4677	P	1.05	25.31	0.36715	7130
Pank3	A_52_P572197	NM_145962	pantothenate kinase 3	-1.319	38.68	0.39887	6484	P	1.064	19.02	0.2199	5207
Tfrc	A_52_P228236	NM_011638	transferrin receptor	-1.319	35.45	0.38726	6108	P	1.103	8.32	0.06895	2376
Zfp295	A_52_P574527	AK129313	zinc finger protein 295	-1.319	45.92	0.50247	9742	P	1.058	28.13	0.56078	9116
Acadl	A_51_P149455	NM_007381	acyl-Coenzyme A dehydrogenase, long-ch	-1.321	28.61	0.31417	4232	P	-1.05	40.63	0.31526	6528
Icam1	A_52_P613241	NM_010493	intercellular adhesion molecule	-1.321	45.92	0.47782	8889	P	1.092	11.33	0.15885	4197
Lmtk2	A_51_P103533	XM_132499	lemur tyrosine kinase 2	-1.321	49.93	0.55303	11533	P	1.07	16.2	0.23607	5431
BC024479	A_51_P321136	NM_146222	cDNA sequence BC024479	-1.323	45.92	0.47599	8824	P	1.044	33.49	0.68286	10168
Chic2	A_51_P148311	NM_028850	cysteine-rich hydrophobic domain 2	-1.323	31.88	0.34113	4945	P	1.058	22.1	0.28393	6135
D130059P03Rik	A_51_P239036	NM_177185	RIKEN cDNA D130059P03 gene	-1.323	35.45	0.36329	5469	P	1.034	30.75	0.46816	8189
Il4ra	A_51_P464478	NM_001008700	interleukin 4 receptor, alpha	-1.323	38.68	0.40156	6541	P	-1.022	48.7	0.69323	10269
Pcm1	A_51_P420698	NM_023662	pericentriolar material 1	-1.323	31.88	0.34074	4939	P	1.015	40.63	0.75358	10813
Pla2g6	A_51_P464860	NM_016915	phospholipase A2, group VI	-1.325	49.93	0.5505	11453	P	-1.091	9.71	0.07749	2586
Ppp1r3f	A_51_P264487	NM_138605	protein phosphatase 1, regulatory (inhibit	-1.325	45.92	0.49689	9495	P	1.009	42.43	0.88445	11918
Praf2	A_52_P597338	NM_138602	PRA1 domain family 2	-1.325	53.87	0.60495	13683	P	1.042	33.49	0.68661	10210
4833439L19Rik	A_51_P158007	NM_133797	RIKEN cDNA 4833439L19 gene	-1.326	49.93	0.59665	10620	M	1.079	19.02	0.29916	6303
Gusb	A_51_P211491	NM_010368	glucuronidase, beta	-1.326	42.28	0.43073	7380	P	1	49.48	0.99824	13046
Slc26a2	A_52_P83905	NM_007885	solute carrier family 26 (sulfate transporte	-1.326	45.92	0.50284	9778	M	1.118	6.98	0.05119	1881
Slc39a5	A_51_P206235	NM_028051	solute carrier family 39 (metal ion transpo	-1.326	28.61	0.31643	4277	P	1.037	30.75	0.46355	8146
Asxl2	A_51_P250433	NM_172421	additional sex combs like 2 (Drosophila)	-1.328	38.68	0.40877	6689	P	1.117	6.98	0.05149	1895
Atf1	A_52_P228079	NM_007497	activating transcription factor 1	-1.328	23.47	0.29225	3662	P	1.075	13.58	0.178	4539
Gprc5b	A_51_P173709	NM_022420	G protein-coupled receptor, family C, grou	-1.328	35.45	0.38406	6009	P	1.11	11.33	0.19654	4845
Lmo4	A_52_P330314	AK033097	LIM domain only 4	-1.328	72.2	0.87536	29289	P	-1.013	49.48	0.79287	11122
Pld1	A_52_P578359	NM_008875	phospholipase D1	-1.328	61.79	0.6933	18077	P	1.014	42.43	0.82056	11368
Prpsap1	A_52_P642109	BC029621	phosphoribosyl pyrophosphate synthetas	-1.328	31.88	0.33511	4777	P	1.062	22.1	0.30267	6346
Tead2	A_52_P39546	NM_011565	TEA domain family member 2	-1.328	38.68	0.41909	6993	P	-1.017	49.48	0.80093	11186
Cuzd1	A_51_P155465	NM_008411	CUB and zona pellucida-like domains 1	-1.33	38.68	0.51873	9881	P	-1.38	0.51	0.0146	621
Sec24d	A_51_P141274	NM_027135	SEC24 related gene family, member D (S.	-1.33	20.94	0.27031	3156	P	1.113	9.71	0.1203	3499
Sgpl1	A_51_P391695	NM_009163	sphingosine phosphate lyase 1	-1.33	25.79	0.30923	4140	P	-1.113	11.33	0.12534	3612
Srpr	A_52_P134666	NM_026130	signal recognition particle receptor ('dock	-1.33	23.47	0.27727	3372	P	1.073	19.02	0.31282	6486

Tle1	A_52_P328044	NM_011599	transducin-like enhancer of split 1, homol	-1.33	12.21	0.23742	2488	P	1.075	13.58	0.13581	3771
Vdac1	A_52_P909310	NM_011694	voltage-dependent anion channel 1	-1.33	49.93	0.57768	9959	M	-1.002	49.48	0.97546	12795
1810015A11Rik	A_51_P202244	AK032396	RIKEN cDNA 1810015A11 gene	-1.332		0.72951	10639	A	1.135	6.98	0.05982	2149
Klhl8	A_51_P402393	NM_178741	kelch-like 8 (Drosophila)	-1.332	18.5	0.25354	2875	P	-1.045	43.75	0.44191	7937
Usp36	A_51_P119016	XM_126772	ubiquitin specific peptidase 36	-1.332	42.28	0.4623	8301	P	1.05	25.31	0.35484	6952
Zfp281	A_51_P438479	NM_177643	zinc finger protein 281	-1.333	35.45	0.37569	5741	P	1.107	9.71	0.12478	3593
Aco2	A_52_P899263	AK029122	aconitase 2, mitochondrial	-1.335	42.28	0.43862	7595	M	1.018	38.4	0.6682	10026
Diap1	A_51_P427768	NM_007858	diaphanous homolog 1 (Drosophila)	-1.335	31.88	0.33527	4781	P	-1.084	28.13	0.2603	5815
Dnajb11	A_51_P188073	ENSMUST00000004574	DnaJ (Hsp40) homolog, subfamily B, mem	-1.335	25.79	0.41235	5645	M	1.539	1.58	0.06258	2213
Farsla	A_52_P323975	NM_025648	phenylalanyl-tRNA synthetase, alpha subu	-1.335	31.88	0.35263	5179	P	1.026	40.63	0.80671	11247
Slc35d1	A_52_P137331	AK037934	solute carrier family 35 (UDP-glucuronic a	-1.335	53.87	0.51294	8362	M	1.124	9.71	0.12479	3599
Txnip	A_52_P420792	NM_001009935	thioredoxin interacting protein	-1.335	49.93	0.55311	11538	P	1.314	8.32	0.33411	6730
Zfp496	A_51_P515173	NM_172941	zinc finger with KRAB and SCAN domains	-1.335	49.93	0.54476	11194	P	1.018	38.4	0.68343	10175
Adam9	A_51_P518378	NM_007404	a disintegrin and metallopeptidase domai	-1.337	28.61	0.32851	4609	P	-1.164	2.53	0.03749	1429
Csk	A_52_P397204	NM_007783	c-src tyrosine kinase	-1.337	42.28	0.51432	8226	M	1.264	3.01	0.05665	2048
Lasp1	A_52_P419298	NM_010688	LIM and SH3 protein 1	-1.337	38.68	0.40568	6623	P	1.078	19.02	0.30486	6384
Armc7	A_51_P162676	NM_177778	armadillo repeat containing 7	-1.339	49.93	0.532	10789	P	1.119	8.32	0.0744	2515
Arpc1b	A_51_P331279	NM_023142	actin related protein 2/3 complex, subuni	-1.339	45.92	0.50272	9761	P	-1.013	49.48	0.7935	11124
Capn7	A_52_P623782	NM_009796	calpain 7	-1.339	18.5	0.29034	3374	P	1.034	33.49	0.58504	9302
D16Bwg1494e	A_51_P165082	AB041601	DNA segment, Chr 16, Brigham & Womer	-1.339	49.93	0.53849	11009	P	-1.273	0.51	0.00697	217
Gale	A_51_P401193	NM_178389	galactose-4-epimerase, UDP	-1.339	42.28	0.45913	8186	P	1.175	2.53	0.01663	715
Tfdp1	A_52_P375493	AK030820	transcription factor Dp 1	-1.339	23.47	0.28718	3552	P	-1.172	2.04	0.04199	1583
1810006K21Rik	A_52_P17635	BC024923	RIKEN cDNA 1810006K21 gene	-1.34	53.87	0.59535	13257	P	1.006	42.43	0.91513	12218
5430440L12Rik	A_52_P962404	AK017417	RIKEN cDNA 5430440L12 gene	-1.34	45.92	0.47517	8802	P	1.07	22.1	0.43568	7894
Bcl2l1	A_52_P148861	NM_009743	Bcl2-like 1	-1.34	45.92	0.48772	9178	P	1.217	2.53	0.02014	864
C1galt1	A_51_P165475	NM_052993	core 1 synthase, glycoprotein-N-acetylgal	-1.34	35.45	0.37456	5727	P	-1.207	1.18	0.01986	850
Mkl1	A_51_P174894	BC050941	MKL (megakaryoblastic leukemia)/myoca	-1.34	53.87	0.58125	12604	P	-1.07	33.49	0.26561	5887
Pdgfrl	A_51_P466229	NM_026840	platelet-derived growth factor receptor-li	-1.34	18.5	0.25516	2938	P	1.008	42.43	0.8756	11817
Pdzrn3	A_52_P327176	NM_018884	PDZ domain containing RING finger 3	-1.34	38.68	0.39447	6319	P	1	49.48	0.99613	13024
Tjp2	A_52_P396042	NM_011597	tight junction protein 2	-1.34	38.68	0.41743	6952	P	-1.035	46.3	0.62481	9670
Tmem39b	A_52_P357039	NM_199305	transmembrane protein 39b	-1.34	25.79	0.29354	3689	P	-1.219	0.75	0.01152	469
Zfp313	A_51_P259378	NM_030743	zinc finger protein 313	-1.34	42.28	0.4614	8259	P	1.073	13.58	0.23519	5007
2810417H13Rik	A_52_P13448	NM_026515	RIKEN cDNA 2810417H13 gene	-1.342	61.79	0.6817	17507	P	-1.162	1.62	0.02874	1160
Fgf10	A_52_P42269	NM_008002	fibroblast growth factor 10	-1.342	69.29	0.79717	23949	P	-1.025	48.7	0.73225	10604
Gsta1	A_51_P305140	NM_008181	glutathione S-transferase, alpha 1 (Ya)	-1.342	77.44	0.92504	33453	P	1.056	19.02	0.21983	5202
Ppp2cb	A_51_P125538	NM_017374	protein phosphatase 2 (formerly 2A), cata	-1.342	35.45	0.37577	5744	P	-1.341	0.51	0.00965	351
Tjp1	A_51_P390739	NM_009386	tight junction protein 1	-1.342	31.88	0.34261	4971	P	-1.033	48.39	0.78612	11056
Map3k2	A_52_P448559	AK036364	mitogen activated protein kinase kinase k	-1.344		0.82024	10811	A	1.113	9.71	0.11089	3289
Sec63	A_52_P363203	AK090248	SEC63-like (S. cerevisiae)	-1.344	57.76	0.65823	16501	P	-1.064	33.49	0.26585	5892
Tlk1	A_51_P287272	NM_172664	tousled-like kinase 1	-1.344	25.79	0.40914	5542	M	1.073	13.58	0.16503	4294
9630030I15Rik	A_51_P167505	AK079340	RIKEN cDNA 9630030I15 gene	-1.346	49.93	0.47827	8525	P	-1.045	42.43	0.34459	6816
Cars	A_51_P374863	NM_013742	cysteinyl-tRNA synthetase	-1.346	31.88	0.33273	4729	P	-1.117	8.32	0.07967	2649
Clec2i	A_51_P182311	NM_020257	C-type lectin domain family 2, member i	-1.346	13.61	0.23063	2373	P	1.02	38.4	0.7056	10371
D930015E06Rik	A_52_P551603	NM_172681	RIKEN cDNA D930015E06 gene	-1.346	16.01	0.23887	2529	P	1.05	25.31	0.36956	7159
F11r	A_51_P458866	NM_172647	F11 receptor	-1.346	23.47	0.28614	3531	P	1.026	33.49	0.54363	8974
Por	A_51_P207921	NM_008898	P450 (cytochrome) oxidoreductase	-1.348	49.93	0.51792	10256	P	-1.017	49.47	0.73345	10613
Trp53bp2	A_51_P363564	NM_173378	transformation related protein 53 binding	-1.348	13.61	0.22953	2331	P	1.226	2.53	0.03013	1203
Cenph	A_51_P492830	NM_021886	centromere protein H	-1.35	38.68	0.41119	6794	P	1.004	42.43	0.95341	12611
Dexi	A_51_P336622	NM_021428	dexamethasone-induced transcript	-1.35	45.92	0.48031	8954	P	1.053	19.02	0.25371	5713
Jup	A_52_P401386	NM_010593	junction plakoglobin	-1.35	38.68	0.41311	6850	P	-1.235	0.75	0.01485	635
Sox4	A_51_P105178	NM_009238	SRY-box containing gene 4	-1.35	23.47	0.27834	3396	P	-1.237	0.56	0.00985	366
Naga	A_51_P117130	NM_008669	N-acetyl galactosaminidase, alpha	-1.351	16.01	0.24137	2567	P	-1.207	1.18	0.01933	811
St3gal6	A_51_P281333	NM_018784	ST3 beta-galactoside alpha-2,3-sialyltrans	-1.351	45.92	0.50253	9746	P	1.056	19.02	0.23823	5460

Stard13	A_52_P435118	NM_146258	serologically defined colon cancer antiger	-1.351	45.92	0.50196	9718	M	-1.354	0.51	0.00699	218
0610007L01Rik	A_52_P7183	BC033455	RIKEN cDNA 0610007L01 gene	-1.353	28.61	0.32995	4670	P	-1.314	0.51	0.0067	200
Cd164	A_52_P220090	NM_016898	CD164 antigen	-1.353	18.5	0.24428	2681	P	1.1	11.33	0.15494	4129
Nanog	A_51_P294233	NM_028016	Nanog homeobox	-1.353	57.76	0.65862	16534	P	1.213	3.82	0.11418	3089
Rcor1	A_52_P535052	NM_198023	REST corepressor 1	-1.353	23.47	0.30716	3917	P	1.069	16.2	0.18081	4592
5430407P10Rik	A_51_P474169	NM_144883	RIKEN cDNA 5430407P10 gene	-1.355	28.61	0.30755	4083	P	-1.073	28.13	0.19009	4721
5830434P21Rik	A_52_P686136	NM_172661	RIKEN cDNA 5830434P21 gene	-1.355	57.76	0.65846	12475	M	1.07	22.1	0.37717	7244
Rassf3	A_52_P460703	NM_138956	Ras association (RalGDS/AF-6) domain far	-1.355	42.28	0.47093	8601	P	1.208	8.32	0.21043	5046
Sfmbt1	A_52_P160518	NM_019460	Scm-like with four mbt domains 1	-1.355	28.61	0.32851	4625	P	-1.18	1.32	0.02201	935
Ctdspl	A_51_P486943	NM_133710	CTD (carboxy-terminal domain, RNA polyı	-1.357	42.28	0.45371	8019	P	-1.095	11.33	0.08536	2779
Fbxl20	A_51_P500996	NM_028149	F-box and leucine-rich repeat protein 20	-1.357	31.88	0.34944	5111	P	-1.003	49.48	0.96288	12691
Hyou1	A_52_P122830	NM_021395	hypoxia up-regulated 1	-1.357	49.93	0.60024	10721	M	1.071	22.1	0.37574	7232
Slc39a14	A_51_P282983	NM_144808	solute carrier family 39 (zinc transporter),	-1.357	23.47	0.27555	3335	P	1.116	8.32	0.08637	2808
1110021L09Rik	A_51_P369381	AK003902	RIKEN cDNA 1110021L09 gene	-1.359	38.68	0.41411	6869	P	1.042	33.49	0.67054	10056
Anxa11	A_51_P280597	NM_013469	annexin A11	-1.359	28.61	0.3104	4167	P	-1.042	43.15	0.36206	7048
Cyp2d22	A_52_P478420	AK086555	cytochrome P450, family 2, subfamily d, p	-1.359	49.93	0.56997	12057	P	1.006	42.43	0.91644	12232
Farp1	A_51_P332939	NM_134082	FERM, RhoGEF (Arhgef) and pleckstrin do	-1.359	31.88	0.35679	5273	P	1.174	11.33	0.31208	6479
Ptprn2	A_52_P50150	NM_011215	protein tyrosine phosphatase, receptor ty	-1.359	49.93	0.56811	12001	P	1.005	42.43	0.9227	12296
Tgif2	A_51_P456657	NM_173396	TGFB-induced factor 2	-1.359	45.92	0.51785	10248	P	1.038	28.13	0.40075	7526
Usp48	A_52_P175086	NM_130879	ubiquitin specific peptidase 48	-1.359	13.61	0.22589	2302	P	1.034	33.49	0.56467	9162
Hao3	A_51_P114722	NM_019545	hydroxyacid oxidase (glycolate oxidase) 3	-1.361		0.70407	9976	A	-1.084	19.02	0.12478	3598
1700049E15Rik	A_52_P794440	BY706721	RIKEN cDNA 1700049E15 gene	-1.362	31.88	0.34833	4907	M	1.025	36.07	0.60894	9512
AI931714	A_52_P203143	AK045296	expressed sequence AI931714	-1.362	49.93	0.63454	12171	M	-1.117	8.32	0.08005	2656
BC021381	A_51_P407879	NM_145382	cDNA sequence BC021381	-1.362	45.92	0.56811	9686	M	1	42.43	0.99858	13041
Has2	A_51_P213359	NM_008216	hyaluronan synthase 2	-1.362	12.21	0.21476	2118	P	1.006	42.43	0.89842	12049
Cdc2l6	A_51_P479464	AK122421	cell division cycle 2-like 6 (CDK8-like)	-1.364	31.88	0.35343	5200	P	-1.155	4.63	0.09017	2899
D17Wsu92e	A_51_P397920	NM_001033279	DNA segment, Chr 17, Wayne State Unive	-1.366	20.94	0.26612	3083	P	-1.272	0.51	0.00772	289
Mapre2	A_51_P438149	NM_153058	microtubule-associated protein, RP/EB far	-1.366	35.45	0.46053	6799	M	1.104	16.2	0.37208	7196
Serpini2	A_51_P510900	NM_026460	serine (or cysteine) peptidase inhibitor, cl	-1.366	28.61	0.32181	4420	P	1.035	40.63	0.84339	11549
Ltbr	A_51_P156274	NM_010736	lymphotoxin B receptor	-1.368	35.45	0.37262	5669	P	1.046	25.31	0.32183	6582
Plcl2	A_51_P219444	NM_013880	phospholipase C-like 2	-1.368	31.88	0.33757	4863	P	-1.002	49.48	0.97261	12764
5730446C15Rik	A_52_P102022	AK017641	RIKEN cDNA 5730446C15 gene	-1.37	42.28	0.43593	7516	M	1.022	38.4	0.65689	9947
Vkorc1l1	A_52_P96552	NM_027121	vitamin K epoxide reductase complex, sub	-1.37	13.61	0.22315	2251	P	-1.081	28.13	0.21745	5162
Ap2m1	A_52_P422976	AK141862	adaptor protein complex AP-2, mu1	-1.372	49.93	0.57024	12066	P	-1.083	19.02	0.12322	3562
2310044G17Rik	A_52_P366772	NM_173735	RIKEN cDNA 2310044G17 gene	-1.374	28.61	0.32076	4383	P	1.003	42.43	0.96229	12685
Disp2	A_52_P627068	NM_170593	dispatched homolog 2 (Drosophila)	-1.374	49.93	0.59945	10704	M	1.132	16.2	0.4549	8045
Fgf9	A_51_P497152	NM_013518	fibroblast growth factor 9	-1.374	28.61	0.30794	4115	P	1.001	42.43	0.98311	12892
Gja5	A_52_P525317	NM_008121	gap junction membrane channel protein a	-1.374	49.93	0.57439	12211	P	-1.072	33.49	0.27297	5998
Il2rb	A_51_P286496	NM_008368	interleukin 2 receptor, beta chain	-1.374	53.87	0.60112	13510	P	1.035	30.75	0.43031	7825
Adcy9	A_51_P501538	NM_009624	adenylate cyclase 9	-1.376	13.61	0.21981	2194	P	1.107	8.32	0.06396	2254
Hoxa9	A_51_P117924	NM_010456	homeo box A9	-1.376	38.68	0.41401	6867	P	1.078	11.33	0.10686	3215
Pfn1	A_51_P220993	NM_011072	profilin 1	-1.376	28.61	0.31692	4285	P	1.016	42.43	0.87812	11842
Rnf2	A_52_P149743	NM_011277	ring finger protein 2	-1.376	31.88	0.33203	4705	P	1.031	36.07	0.65133	9894
Socs4	A_51_P165424	NM_080843	suppressor of cytokine signaling 4	-1.376	53.87	0.58261	12654	P	1.005	42.43	0.93297	12408
4632419K20Rik	A_52_P644072	AK014591	RIKEN cDNA 4632419K20 gene	-1.377	49.93	0.5405	11041	P	1.132	6.98	0.07548	2551
Akr1c20	A_51_P382764	BC021607	aldo-keto reductase family 1, member C2	-1.377		0.57961	8449	A	1.042	28.13	0.38385	7323
Cotl1	A_52_P435356	NM_028071	coactosin-like 1 (Dictyostelium)	-1.377	38.68	0.41841	6976	P	-1.081	19.02	0.1399	3849
Qscn6	A_52_P302304	NM_023268	quiescin Q6	-1.377	25.79	0.29606	3720	P	-1.214	0.75	0.01251	506
Xpr1	A_52_P678117	NM_011273	xenotropic and polytropic retrovirus rece	-1.377	49.93	0.52683	10593	P	1.117	8.32	0.07115	2417
1810010M01Rik	A_51_P140429	NM_026918	RIKEN cDNA 1810010M01 gene	-1.379	45.92	0.55657	9401	M	-1.087	38.4	0.50326	8612
AI413194	A_51_P181785	AK033727	expressed sequence AI413194	-1.379	18.5	0.24282	2611	P	1.02	40.63	0.73795	10659
Myo18a	A_51_P396375	NM_011586	myosin XVIIIa	-1.379	42.28	0.47485	8794	P	-1.098	16.2	0.14307	3906
Pbx4	A_51_P428781	NM_001024954	pre-B-cell leukemia transcription factor 4	-1.379	45.92	0.50184	9700	P	1.008	42.43	0.8896	11962

Ace2	A_51_P257496	NM_027286	angiotensin I converting enzyme (peptidy	-1.381	13.61	0.24282	2512	P	-1.17	2.04	0.03454	1325
BC060631	A_51_P339824	NM_177700	cDNA sequence BC060631	-1.381	53.87	0.5816	12624	P	-1.037	46.3	0.67913	10130
Kcnj11	A_52_P402705	NM_010602	potassium inwardly rectifying channel, su	-1.381	25.79	0.29912	3831	P	-1.135	3.82	0.0482	1802
Ptch2	A_51_P410346	NM_008958	patched homolog 2	-1.381	20.94	0.24913	2774	P	1.012	42.43	0.79039	11097
Tdh	A_51_P143712	NM_021480	L-threonine dehydrogenase	-1.381	65.79	0.74536	20865	P	1.043	25.31	0.31828	6558
B230206F22Rik	A_52_P177865	AK035525	RIKEN cDNA B230206F22 gene	-1.383	45.92	0.49841	9591	P	1.135	6.98	0.08441	2762
Ccm2	A_51_P314895	NM_146014	cerebral cavernous malformation 2 homo	-1.383	12.21	0.20511	2012	P	1.035	33.49	0.64357	9822
Csnk1g1	A_51_P329733	NM_173185	casein kinase 1, gamma 1	-1.383		0.69665	11705	A	1.137	4.63	0.03516	1354
Hist1h2ab	A_52_P420466	NM_175660	histone cluster 1, H2ab	-1.383	57.76	0.39874	5350	M	1.048	22.1	0.29561	6279
Muc1	A_51_P467346	NM_013605	mucin 1, transmembrane	-1.383	53.87	0.58861	12911	P	-1.479	0	0.00584	14
Ncoa5	A_52_P223080	NM_144892	nuclear receptor coactivator 5	-1.383	25.79	0.29304	3681	P	1.038	33.49	0.6452	9846
Suclg2	A_51_P478672	NM_011507	succinate-Coenzyme A ligase, GDP-formin	-1.383	35.45	0.38735	6114	P	-1.086	19.02	0.13993	3853
Zfp397	A_51_P101086	NM_027007	zinc finger protein 397	-1.383	49.93	0.53962	11027	P	1.235	1.62	0.01469	629
Zranb1	A_51_P225048	AK010069	zinc finger, RAN-binding domain containir	-1.383	13.61	0.21523	2124	P	-1.082	38.4	0.47276	8224
3300001A09Rik	A_51_P415395	BC039571	RIKEN cDNA 3300001A09 gene	-1.385	45.92	0.52501	10544	P	-1.251	0.56	0.01026	392
Dut	A_51_P418469	NM_023595	deoxyuridine triphosphatase	-1.385	28.61	0.3288	4636	P	1.109	9.71	0.09821	3065
E130014J05Rik	A_51_P340083	NM_001040400	RIKEN cDNA E130014J05 gene	-1.385	25.79	0.30415	3997	P	-1.022	49.48	0.81576	11332
Kif11	A_52_P177802	AK050778	kinesin family member 11	-1.385	42.28	0.38628	5855	M	-1.013	49.48	0.82502	11417
Pard6b	A_52_P37123	BC025147	par-6 (partitioning defective 6) homolog b	-1.385	25.79	0.30035	3863	P	1.079	22.1	0.42379	7763
Ppm1b	A_51_P140541	BC090963	protein phosphatase 1B, magnesium depe	-1.385	20.94	0.24754	2749	P	1.188	4.63	0.06464	2272
Prkd2	A_51_P499441	NM_178900	protein kinase D2	-1.387	45.92	0.49512	9433	P	1.015	40.63	0.73659	10647
Tmem16a	A_51_P168894	NM_178642	transmembrane protein 16A	-1.387	49.93	0.5441	11164	P	1.063	25.31	0.51523	8721
Cldn15	A_51_P306710	NM_021719	claudin 15	-1.389	53.87	0.57977	12499	P	-1.058	43.75	0.57598	9235
D3Ucla1	A_51_P449765	NM_030685	DNA segment, Chr 3, University of Califor	-1.389	12.21	0.32365	3709	M	1.011	42.43	0.85452	11623
Sfrs3	A_52_P545451	AK141440	splicing factor, arginine/serine-rich 3 (SRp	-1.389	49.93	0.54594	11242	P	1.091	13.58	0.16645	4325
Lman1	A_52_P652513	NM_027400	lectin, mannose-binding, 1	-1.391	28.61	0.39646	5288	M	1.011	42.43	0.89314	11993
Osbpl1a	A_52_P19606	NM_207530	oxysterol binding protein-like 1A	-1.391	31.88	0.3356	4793	P	-1.072	33.49	0.2923	6241
Pparg	A_51_P106799	NM_011146	peroxisome proliferator activated recepto	-1.391	38.68	0.43241	7434	P	1.158	3.01	0.02124	901
Ptma	A_52_P249402	NM_008972	prothymosin alpha	-1.391	42.28	0.41871	6156	M	1.165	8.32	0.13739	3794
Rfx3	A_52_P322514	AK041120	regulatory factor X, 3 (influences HLA clas	-1.391	53.87	0.62272	14563	P	1.147	8.32	0.10782	3231
AI848100	A_52_P225722	XM_975051	expressed sequence AI848100	-1.393	18.5	0.23499	2429	P	-1.015	49.48	0.90008	12069
Habp2	A_51_P330922	NM_146101	hyaluronic acid binding protein 2	-1.393	75.14	0.66728	11881	M	1.015	42.43	0.81394	11315
Hist2h2aa1	A_52_P64609	NM_013549	histone cluster 2, H2aa1	-1.393	31.88	0.33953	4337	M	1.07	16.2	0.20345	4946
Zfp574	A_51_P243207	NM_175477	zinc finger protein 574	-1.393	31.88	0.33836	4895	P	1.05	22.1	0.28362	6126
AU024582	A_52_P165001	NM_153125	expressed sequence AU024582	-1.395	38.68	0.3981	6461	P	1.115	8.32	0.06662	2336
AW822216	A_52_P286002	NM_178884	expressed sequence AW822216	-1.395	28.61	0.31417	4231	P	1.097	16.2	0.30967	6439
Fhl1	A_51_P335000	NM_001077361	four and a half LIM domains 1	-1.395	23.47	0.36739	4674	M	-1.147	13.58	0.23691	5446
Dnalc4	A_51_P185846	NM_017470	dynein, axonemal, light chain 4	-1.397	35.45	0.39458	6342	P	1.068	19.02	0.29307	6256
Dnmt3a	A_52_P169048	NM_007872	DNA methyltransferase 3A	-1.397	18.5	0.24333	2617	P	-1.116	9.71	0.09522	3006
Son	A_52_P158782	AK034390	Son cell proliferation protein	-1.397	28.61	0.31487	4249	P	1.116	6.98	0.05502	2009
Srprb	A_51_P190262	NM_009275	signal recognition particle receptor, B sub	-1.397	31.88	0.36223	5448	P	1.054	19.02	0.2358	5428
Zfp148	A_52_P201972	AK037342	zinc finger protein 148	-1.397	38.68	0.43241	7424	P	-1.192	2.53	0.05449	1992
1110007M04Rik	A_52_P325265	NM_026742	RIKEN cDNA 1110007M04 gene	-1.399	35.45	0.38885	6154	P	1.017	40.63	0.73537	10636
Cdca3	A_51_P127195	NM_013538	cell division cycle associated 3	-1.399	65.79	0.74659	20911	P	-1.003	49.48	0.94392	12520
Nde1	A_51_P438909	NM_023317	nuclear distribution gene E homolog 1 (A	-1.399	23.47	0.27669	3353	P	-1.128	3.82	0.05056	1869
Nptx1	A_52_P109393	NM_008730	neuronal pentraxin 1	-1.399	53.87	0.64073	12401	M	1.094	11.33	0.1399	3848
Sgol1	A_51_P487999	NM_028232	shugoshin-like 1 (S. pombe)	-1.399	61.79	0.70562	18697	P	-1.045	42.43	0.36832	7142
Actn1	A_51_P347862	NM_134156	actinin, alpha 1	-1.401	42.28	0.46785	8467	P	1.014	40.63	0.76529	10895
Emilin1	A_51_P222359	NM_133918	elastin microfibril interfacer 1	-1.401	18.5	0.24021	2542	P	1.06	16.2	0.19966	4896
Peci	A_51_P394665	NM_011868	peroxisomal delta3, delta2-enoyl-Coenzyı	-1.401	12.21	0.19856	1932	P	-1.095	25.31	0.27	5959
Sec14l2	A_51_P488427	NM_144520	SEC14-like 2 (S. cerevisiae)	-1.401	49.93	0.54946	11403	P	-1.036	43.75	0.41266	7645
Carhsp1	A_52_P174386	NM_025821	calcium regulated heat stable protein 1	-1.403	45.92	0.50315	9802	P	1.004	42.43	0.96023	12661
Hars	A_52_P454361	AK077437	histidyl-tRNA synthetase	-1.403	18.5	0.23874	2528	P	1.042	30.75	0.49432	8493

Itih2	A_51_P196726	NM_010582	inter-alpha trypsin inhibitor, heavy chain	-1.403	28.61	0.32127	4413	P	1.033	33.49	0.51304	8698
Plcg2	A_51_P279163	NM_172285	phospholipase C, gamma 2	-1.403	57.76	0.67728	17343	P	-1.056	38.4	0.32015	6567
Ap3s2	A_52_P584236	NM_009682	adaptor-related protein complex 3, sigma	-1.404	18.5	0.24342	2629	P	1.11	8.32	0.07141	2419
Serpina1b	A_52_P324042	BC037008	serine (or cysteine) preptidase inhibitor, c	-1.404	45.92	0.52089	10376	P	-1.028	46.3	0.55241	9050
Socs1	A_51_P279606	NM_009896	suppressor of cytokine signaling 1	-1.404	25.79	0.28777	3566	P	1.037	30.75	0.51568	8724
Creb3l2	A_52_P343856	NM_178661	cAMP responsive element binding protei	-1.406	42.28	0.46893	8484	P	1.025	38.4	0.78055	10989
Daxx	A_51_P412835	NM_007829	Fas death domain-associated protein	-1.406	25.79	0.29875	3800	P	1.152	3.82	0.03252	1279
Zfp282	A_52_P395381	AK081854	zinc finger protein 282	-1.406	38.68	0.3991	6494	M	-1.075	28.13	0.20535	4976
Arnt	A_52_P84015	AK037762	aryl hydrocarbon receptor nuclear transl	-1.408	31.88	0.35766	5353	M	-1.131	3.82	0.05066	1872
Ccrl1	A_52_P153291	NM_145700	chemokine (C-C motif) receptor-like 1	-1.408	38.68	0.40939	6500	M	1.029	33.49	0.54853	9006
Nbl1	A_51_P244492	NM_008675	neuroblastoma, suppression of tumorige	-1.408	45.92	0.49168	9298	P	1.05	25.31	0.32705	6642
B4galt5	A_51_P324535	NM_019835	UDP-Gal:betaGlcNAc beta 1,4-galactosylt	-1.41	23.47	0.27445	3298	P	1.093	9.71	0.09788	3063
Rbm6	A_52_P298198	AK029954	RNA binding motif protein 6	-1.41		0.53923	8573	A	1.143	16.2	0.44278	7943
Sh2d4a	A_51_P454196	AK008803	SH2 domain containing 4A	-1.41	65.79	0.78314	22947	P	1.015	42.43	0.78639	11061
Ucn3	A_51_P342327	NM_031250	urocortin 3	-1.41	9.39	0.22632	2166	P	-1.386	0.66	0.03744	1426
Wnt3a	A_51_P210970	NM_009522	wingless-related MMTV integration site 3	-1.41		0.66333	8986	A	1.099	8.32	0.07057	2410
Adipor1	A_52_P522097	NM_028320	adiponectin receptor 1	-1.412	10.84	0.18422	1690	P	1.001	42.43	0.98727	12956
St5	A_51_P167746	NM_001001326	suppression of tumorigenicity 5	-1.412	25.79	0.29726	3748	P	-1.078	40.63	0.48521	8384
Lgals2	A_52_P563375	NM_025622	lectin, galactose-binding, soluble 2	-1.414	69.29	0.95228	33020	P	-1.01	49.48	0.8894	11957
Rbm14	A_51_P116616	NM_019869	RNA binding motif protein 14	-1.416	31.88	0.42597	6002	M	1.084	13.58	0.1871	4685
Wdhd1	A_52_P655890	NM_172598	WD repeat and HMG-box DNA binding pr	-1.416	28.61	0.31861	4348	P	1.035	30.75	0.48722	8412
Cckar	A_51_P307741	NM_009827	cholecystokinin A receptor	-1.418	23.47	0.31374	4070	P	-1.145	3.01	0.03732	1424
Mta2	A_51_P164207	NM_011842	metastasis-associated gene family, memb	-1.418	16.01	0.23614	2306	P	1.082	11.33	0.12616	3636
Slc7a6	A_52_P462071	NM_178798	solute carrier family 7 (cationic amino aci	-1.418	25.79	0.30258	3935	P	1.013	42.43	0.79861	11167
Zdhhc3	A_51_P258435	NM_026917	zinc finger, DHHC domain containing 3	-1.418	10.84	0.1825	1669	P	-1.02	49.48	0.78997	11089
2810037C14Rik	A_52_P453498	NM_026034	armadillo repeat containing 10	-1.42	13.61	0.20375	1986	P	1.031	38.4	0.78134	11003
Mapk3	A_51_P158628	NM_011952	mitogen activated protein kinase 3	-1.42	16.01	0.22227	2236	P	1.119	5.75	0.04276	1607
2610027C15Rik	A_52_P678056	NM_172145	RIKEN cDNA 2610027C15 gene	-1.422	28.61	0.32598	4533	P	-1.183	1.32	0.02317	976
A130010J15Rik	A_51_P414320	NM_181048	RIKEN cDNA A130010J15 gene	-1.422	13.61	0.19603	1873	P	-1.247	1.18	0.03182	1254
Car12	A_52_P646858	NM_178396	carbonic anyhydrase 12	-1.422	72.2	0.72148	17049	M	1.123	13.58	0.30236	6342
Rab26	A_52_P448870	AK043912	RAB26, member RAS oncogene family	-1.422	12.21	0.1878	1775	P	1.076	13.58	0.12661	3642
H2-T22	A_51_P432544	NM_010397	histocompatibility 2, T region locus 22	-1.425	18.5	0.23595	2452	P	-1.02	49	0.71928	10487
Rras2	A_51_P112912	NM_025846	related RAS viral (r-ras) oncogene homol	-1.425	18.5	0.2301	2351	P	-1.378	0.51	0.00989	373
BC025462	A_51_P441843	NM_145946	cDNA sequence BC025462	-1.429	38.68	0.41841	6971	P	-1.353	0.51	0.00584	74
Grip1	A_51_P494744	NM_028736	glutamate receptor interacting protein 1	-1.429	18.5	0.22953	2339	P	1.24	2.04	0.01925	806
Slc31a2	A_51_P416137	NM_025286	solute carrier family 31, member 2	-1.429	18.5	0.24155	2573	P	1.033	30.75	0.44605	7975
Ugcg	A_51_P332717	NM_011673	UDP-glucose ceramide glucosyltransferas	-1.429	31.88	0.36597	5516	P	1.05	25.31	0.38157	7291
Crabp1	A_52_P185907	NM_013496	cellular retinoic acid binding protein I	-1.431	69.29	0.82276	25592	P	-1.015	49.48	0.85206	11609
Ggt1	A_51_P468073	NM_008116	gamma-glutamyltransferase 1	-1.431	25.79	0.28781	3575	P	-1.051	42.43	0.38172	7302
Slc14a1	A_51_P343689	NM_028122	solute carrier family 14 (urea transporter)	-1.431	49.93	0.58129	12620	P	-1.042	43.75	0.46538	8163
Tpm2	A_52_P315976	NM_009416	tropomyosin 2, beta	-1.431	45.92	0.50336	9816	P	-1.165	2.53	0.04314	1616
Usp54	A_51_P351883	NM_030180	ubiquitin specific peptidase 54	-1.431	18.5	0.2301	2364	P	1.106	11.33	0.16229	4263
Rab3a	A_52_P276397	NM_009001	RAB3A, member RAS oncogene family	-1.435	38.68	0.48031	7330	M	-1.044	45.05	0.59894	9442
Foxa1	A_51_P417643	NM_008259	forkhead box A1	-1.437	28.61	0.33591	4807	M	1.094	9.71	0.09478	2996
6030408C04Rik	A_51_P461716	NM_001015099	RIKEN cDNA 6030408C04 gene	-1.439	18.5	0.23776	2503	P	-1.114	13.58	0.14794	4003
Tbcd	A_51_P392244	NM_029878	tubulin-specific chaperone d	-1.439	23.47	0.28068	3435	P	-1.013	49.48	0.86753	11735
Trib2	A_51_P103819	NM_144551	tribbles homolog 2 (Drosophila)	-1.439	57.76	0.65228	16186	P	-1.01	49.48	0.89562	12015
4121402D02Rik	A_51_P380249	NM_028722	RIKEN cDNA 4121402D02 gene	-1.441	13.61	0.19322	1854	P	1.064	25.31	0.48303	8360
Pkn2	A_52_P290629	AK083425	protein kinase N2	-1.441	16.01	0.21984	2202	P	1.069	22.1	0.39615	7478
Traf3	A_51_P469411	NM_011632	Tnf receptor-associated factor 3	-1.441	35.45	0.39458	6362	P	-1.12	16.2	0.20155	4924
Galk1	A_51_P243304	NM_016905	galactokinase 1	-1.443	53.87	0.62859	14951	P	1.049	22.1	0.26921	5937
Itga6	A_52_P324934	AK045391	integrin alpha 6	-1.443	35.45	0.37681	5813	P	-1.194	1.1	0.01672	719
Lrrc16	A_52_P635250	AK051570	leucine rich repeat containing 16	-1.443	20.94	0.24363	2652	P	1.129	9.71	0.14566	3956

Edg7	A_51_P134452	NM_022983	endothelial differentiation, lysophosphati	-1.445		0.63339	9910	A	1.06	19.02	0.25595	5744
Prkca	A_51_P118012	NM_011101	protein kinase C, alpha	-1.445	23.47	0.28619	3535	P	1.268	1.32	0.01345	573
Pyy	A_52_P366462	NM_145435	peptide YY	-1.445	18.5	0.32666	3760	M	-1.04	48.39	0.80583	11234
9530068E07Rik	A_52_P265762	NM_153117	RIKEN cDNA 9530068E07 gene	-1.447	18.5	0.22555	2277	P	1.061	25.31	0.48168	8327
Map3k1	A_51_P402193	NM_011945	mitogen activated protein kinase kinase k	-1.447	38.68	0.46984	7000	M	1.09	11.33	0.14258	3897
Shc2	A_51_P104108	BC059866	src homology 2 domain-containing transf	-1.447	23.47	0.2752	3316	P	-1.261	0.51	0.01059	407
Tbl2	A_52_P109304	NM_013763	transducin (beta)-like 2	-1.447	16.01	0.21534	2133	P	1.133	9.71	0.14583	3961
Tcp11	A_52_P75127	NM_013687	t-complex protein 11	-1.447	42.28	0.46248	8305	P	1.06	25.31	0.44567	7970
Ube2d1	A_52_P546459	NM_145420	ubiquitin-conjugating enzyme E2D 1, UBC	-1.447	12.21	0.18707	1763	P	-1.42	0.51	0.00584	30
AK129302	A_52_P1108518	AK086554	cDNA sequence AK129302	-1.449		0.41761	6130	A	-1.137	9.71	0.15517	4139
Elmo2	A_51_P199382	NM_207705	engulfment and cell motility 2, ced-12 ho	-1.449	35.45	0.38521	6047	P	1.087	16.2	0.27	5956
Onecut3	A_52_P474152	NM_139226	one cut domain, family member 3	-1.449		0.58316	12112	A	1.088	11.33	0.11364	3352
Efna2	A_51_P352850	NM_007909	ephrin A2	-1.453	25.79	0.2978	3761	P	-1.006	49.48	0.91844	12251
Pcsk2	A_51_P134045	NM_008792	proprotein convertase subtilisin/kexin typ	-1.453	20.94	0.33242	3921	M	-1.283	1.18	0.04067	1547
Dhx34	A_51_P342813	NM_027883	DEAH (Asp-Glu-Ala-His) box polypeptide	-1.456	13.61	0.18905	1784	P	1.02	38.4	0.72866	10559
Pole	A_51_P155482	NM_011132	polymerase (DNA directed), epsilon	-1.456	35.45	0.30777	3758	M	1.04	28.13	0.36745	7132
Slc35e4	A_51_P268934	NM_153142	solute carrier family 35, member E4	-1.456	20.94	0.24845	2765	P	-1.05	38.4	0.27959	6090
Hao1	A_51_P318262	NM_010403	hydroxyacid oxidase 1, liver	-1.458	16.01	0.22315	2248	P	1.086	16.2	0.23133	5370
Map2k1ip1	A_51_P173555	NM_019920	mitogen-activated protein kinase kinase 1	-1.458	72.2	0.58498	11608	P	-1.226	13.58	0.35987	7015
Phactr4	A_51_P323221	NM_175306	phosphatase and actin regulator 4	-1.458	23.47	0.28068	3436	P	1.022	42.43	0.87369	11797
Sec61a1	A_52_P489729	NM_016906	Sec61 alpha 1 subunit (S. cerevisiae)	-1.458	10.84	0.24282	2324	M	-1.242	0.51	0.00756	279
Slc22a18	A_51_P165882	NM_001042760	solute carrier family 22 (organic cation tra	-1.458	45.92	0.52692	10601	P	-1.09	25.31	0.24091	5511
Mta1	A_51_P423030	NM_054081	metastasis associated 1	-1.46	31.88	0.36169	5436	P	1.047	25.31	0.32039	6569
Agtr2	A_51_P437978	NM_007429	angiotensin II receptor, type 2	-1.462		0.62716	8069	A	1.051	22.1	0.25345	5706
Ets2	A_52_P658122	NM_011809	E26 avian leukemia oncogene 2, 3' domai	-1.462	18.5	0.32161	3669	M	1.084	19.02	0.39637	7482
Ctse	A_51_P217906	NM_007799	cathepsin E	-1.464	72.2	0.87701	29403	P	-1.143	2.53	0.03244	1278
Klf12	A_52_P617636	NM_010636	Kruppel-like factor 12	-1.464	23.47	0.2694	3146	P	1.027	33.49	0.54146	8957
P4hb	A_51_P311990	NM_011032	prolyl 4-hydroxylase, beta polypeptide	-1.464	42.28	0.52785	8641	M	1.075	22.1	0.38555	7343
Tap1	A_51_P100327	NM_013683	transporter 1, ATP-binding cassette, sub-f	-1.464	12.21	0.18646	1750	P	1.014	42.43	0.7827	11023
Rab10	A_52_P647162	AK045299	RAB10, member RAS oncogene family	-1.466	53.87	0.62996	15119	P	1.261	1.17	0.00932	341
Esrrg	A_51_P224192	NM_011935	estrogen-related receptor gamma	-1.468	31.88	0.3543	5225	P	1.089	16.2	0.2757	6036
Igfbp3	A_52_P851352	AK045003	insulin-like growth factor binding protein	-1.468	16.01	0.21773	2169	M	1.171	3.82	0.03953	1502
Cks2	A_51_P462249	NM_025415	CDC28 protein kinase regulatory subunit	-1.473	31.88	0.37271	5676	P	1.008	42.43	0.86426	11720
Lmnb1	A_51_P120717	NM_010721	lamin B1	-1.473	35.45	0.37749	5851	P	1.113	11.33	0.1683	4353
2410081M15Rik	A_51_P435817	NM_028603	RIKEN cDNA 2410081M15 gene	-1.475	35.45	0.38483	6028	P	1.088	9.71	0.09438	2984
Cdh4	A_52_P402897	AK038529	cadherin 4	-1.475	49.93	0.54875	11377	P	-1.078	16.2	0.10878	3240
Rod1	A_51_P310040	NM_144904	ROD1 regulator of differentiation 1 (S. po	-1.475	28.61	0.2777	3107	P	-1.364	0.51	0.01238	501
Trim59	A_51_P275808	NM_025863	tripartite motif-containing 59	-1.475	25.79	0.29875	3814	P	-1.028	47.43	0.66916	10043
Gp2	A_51_P268391	NM_025989	glycoprotein 2 (zymogen granule membra	-1.477	23.47	0.39447	5525	M	-1.373	0.51	0.0109	424
Ins2	A_51_P389597	NM_008387	insulin II	-1.477	72.2	0.88596	21833	M	1.04	30.75	0.52251	8771
S100a14	A_51_P419226	NM_025393	S100 calcium binding protein A14	-1.477	72.2	0.84605	27494	P	-1.176	1.58	0.02439	1009
B4galt2	A_51_P496685	NM_017377	UDP-Gal:betaGlcNAc beta 1,4- galactosylt	-1.479	18.5	0.22953	2338	P	1.045	25.31	0.36973	7160
Isg20	A_52_P448253	NM_020583	interferon-stimulated protein	-1.481	38.68	0.41521	6904	P	-1.145	3.46	0.04586	1720
Slc38a3	A_51_P139030	NM_023805	solute carrier family 38, member 3	-1.481	42.28	0.47476	8771	P	-1.009	49.48	0.87183	11781
Cuedc1	A_52_P479647	NM_198013	CUE domain containing 1	-1.484	16.01	0.21903	2191	P	-1.134	11.33	0.17361	4436
Pex11c	A_52_P573970	BC024096	peroxisomal biogenesis factor 11c	-1.484	38.68	0.41798	6962	P	1.038	30.75	0.47083	8212
Pim1	A_52_P530291	NM_008842	proviral integration site 1	-1.486	42.28	0.46016	8222	P	-1.251	0.56	0.012	485
Chrm3	A_51_P247853	NM_033269	cholinergic receptor, muscarinic 3, cardia	-1.488	5.15	0.12854	1012	P	1.001	42.43	0.98176	12877
Grtp1	A_51_P109144	NM_025768	GH regulated TBC protein 1	-1.488	6.91	0.13645	1083	P	1.003	42.43	0.95069	12593
Pnliprp2	A_51_P314669	NM_011128	pancreatic lipase-related protein 2	-1.488	16.01	0.33953	4333	M	1.02	40.63	0.7133	9594
Shc1	A_52_P384250	NM_011368	src homology 2 domain-containing transf	-1.488	16.01	0.21628	2158	P	1.053	22.1	0.27494	6026
Spr	A_51_P163958	NM_011467	sepiapterin reductase	-1.488	16.01	0.21115	2080	P	1.057	16.2	0.20441	4957
Ush2a	A_52_P649547	NM_021408	Usher syndrome 2A (autosomal recessive	-1.488	49.93	0.58078	12538	P	-1.131	6.98	0.09289	2960

D11Ertd18e	A_51_P430585	NM_026740	solute carrier family 46, member 1	-1.49	18.5	0.23776	2502	P	-1.022	47.92	0.65059	9892
Flnb	A_52_P222350	XM_990154	filamin, beta	-1.49	20.94	0.24858	2769	P	1.138	6.98	0.07798	2605
Cyb561	A_52_P681787	NM_007805	cytochrome b-561	-1.493	13.61	0.19135	1831	P	-1.21	1.58	0.03718	1415
Taf1c	A_51_P411355	NM_021441	TATA box binding protein (Tbp)-associated	-1.493	31.88	0.34533	5014	P	-1.037	44.4	0.46495	8159
Twsg1	A_52_P451378	NM_023053	twisted gastrulation homolog 1 (Drosophi	-1.493	8.15	0.24748	2320	M	1.053	33.49	0.72851	10555
Ccnd2	A_52_P514391	NM_009829	cyclin D2	-1.495	25.79	0.30959	4153	P	-1.15	2.04	0.03115	1231
Dicer1	A_51_P333060	NM_148948	Dicer1, Dcr-1 homolog (Drosophila)	-1.495	8.15	0.14625	1204	P	1.006	42.43	0.92893	12378
Fgfr1op	A_52_P147778	NM_201230	Fgfr1 oncogene partner	-1.495	13.61	0.19661	1883	P	1.055	22.1	0.32472	6614
Ptbp2	A_52_P593110	AK015056	polypyrimidine tract binding protein 2	-1.495	31.88	0.34574	5023	P	1.076	13.58	0.15575	4145
Slc20a2	A_52_P229044	NM_011394	solute carrier family 20, member 2	-1.495	10.84	0.17066	1497	P	1.001	42.43	0.99494	13013
BC024868	A_51_P127456	BC070402	cDNA sequence BC024868	-1.497	16.01	0.2154	2136	P	1.056	22.1	0.31428	6517
Myc	A_51_P102096	NM_010849	myelocytomatosis oncogene	-1.499	35.45	0.29583	3598	P	1.003	42.43	0.95315	12605
Ddx19b	A_51_P262144	NM_172284	DEAD (Asp-Glu-Ala-Asp) box polypeptide	-1.506	4.65	0.1859	1565	M	1.001	42.43	0.98495	12931
Gbp2	A_51_P203955	NM_010260	guanylate nucleotide binding protein 2	-1.506	38.68	0.4443	7781	P	-1.105	11.33	0.09767	3057
Il2ra	A_51_P118945	AF054581	interleukin 2 receptor, alpha chain	-1.508		0.59032	10020	A	1.081	16.2	0.2575	5772
Dnajc1	A_52_P690892	AK030790		-1.511	18.5	0.22953	2336	P	-1.225	3.82	0.15034	4042
Hdlbp	A_52_P303085	NM_133808	high density lipoprotein (HDL) binding pro	-1.511	6.57	0.12849	1008	P	1.146	8.32	0.11418	3372
Rnf144	A_52_P662591	NM_080563	ring finger protein 144	-1.511		0.50226	6605	A	-1.208	0.92	0.01571	674
Traf5	A_51_P473154	NM_011633	Tnf receptor-associated factor 5	-1.511	23.47	0.28891	3592	P	1.017	38.4	0.69206	10256
Anxa13	A_52_P662711	NM_027211	annexin A13	-1.513	72.2	0.86243	28360	P	1.063	19.02	0.21889	5187
Ncoa3	A_52_P477759	NM_008679	nuclear receptor coactivator 3	-1.517	13.61	0.19761	1923	P	-1.013	49.48	0.88079	11868
Ga17	A_51_P141308	NM_145380	dendritic cell protein GA17	-1.52	25.79	0.37009	4711	M	-1.03	47.92	0.7128	10426
Prdx4	A_52_P313861	AK165551	peroxiredoxin 4	-1.52	16.01	0.21816	2175	P	1.058	19.02	0.23887	5470
Prkaa1	A_52_P173344	NM_001013367	protein kinase, AMP-activated, alpha 1 ca	-1.52	16.01	0.20291	1975	P	1.017	40.63	0.74952	10783
Prrxl1	A_52_P122255	NM_001001796	paired related homeobox protein-like 1	-1.52	42.28	0.47485	8787	P	1.037	36.07	0.75138	10800
Ampd2	A_51_P479769	NM_028779	adenosine monophosphate deaminase 2	-1.522	28.61	0.32995	4669	P	-1.022	48.39	0.66018	9973
Ghr	A_52_P54106	AK034547	growth hormone receptor	-1.522	20.94	0.24428	2675	P	1.03	33.49	0.50229	8607
Gna14	A_51_P110323	NM_008137	guanine nucleotide binding protein, alpha	-1.522	28.61	0.3288	4641	P	-1.033	46.3	0.59947	9443
Elf3	A_51_P480241	NM_007921	E74-like factor 3	-1.524	42.28	0.47092	8587	P	-1.13	6.98	0.09328	2972
Cebpd	A_51_P444447	NM_007679	CCAAT/enhancer binding protein (C/EBP),	-1.527	7.45	0.13209	1049	P	1.08	13.58	0.14481	3942
Nr1h5	A_51_P226664	NM_201619	nuclear receptor subfamily 1, group H, me	-1.527	75.14	0.76926	19283	M	-1.082	25.31	0.18339	4635
Eps8l2	A_52_P257426	NM_133191	EPS8-like 2	-1.529	9.39	0.14404	1179	P	1.006	42.43	0.93782	12460
Isgf3g	A_52_P176013	NM_008394	interferon dependent positive acting tran	-1.529	20.94	0.25354	2877	P	1.142	5.75	0.05139	1889
Dctd	A_52_P301085	NM_178788	dCMP deaminase	-1.531	84.56	0.44375	5625	M	1.07	19.02	0.27795	6062
Reg3a	A_51_P267969	NM_011259	regenerating islet-derived 3 alpha	-1.531	69.29	0.8426	27245	P	1.093	16.2	0.27297	5996
2310007D09Rik	A_51_P273556	NM_027975	RIKEN cDNA 2310007D09 gene	-1.534	35.45	0.28591	3283	M	1.186	6.98	0.1508	4048
Slc7a2	A_52_P77764	NM_007514	solute carrier family 7 (cationic amino aci	-1.534	42.28	0.47247	8657	P	1.04	30.75	0.53419	8881
Tbc1d4	A_52_P939390	AK042979	TBC1 domain family, member 4	-1.534	42.28	0.4726	8312	M	1.038	28.13	0.38164	7293
Ang1	A_51_P391159	NM_007447	angiogenin, ribonuclease A family, memb	-1.536	45.92	0.52412	10485	P	-1.491	0.51	0.01199	479
Il2rg	A_51_P456952	NM_013563	interleukin 2 receptor, gamma chain	-1.536	31.88	0.38521	6046	P	-1.078	22.1	0.15934	4204
Npas3	A_52_P557459	AF168769	neuronal PAS domain protein 3	-1.536	49.93	0.49852	7001	M	1.115	8.32	0.06391	2253
Pim3	A_51_P189746	NM_145478	proviral integration site 3	-1.536	12.21	0.18354	1677	P	1.097	19.02	0.3947	7456
Rara	A_51_P389724	NM_009024	retinoic acid receptor, alpha	-1.536	18.5	0.24343	2631	P	1.07	13.58	0.16182	4251
Anln	A_51_P313896	NM_028390	anillin, actin binding protein (scraps homo	-1.538	57.76	0.34574	4155	M	-1.173	1.58	0.02707	1100
Btg1	A_51_P288193	NM_007569	B-cell translocation gene 1, anti-proliferat	-1.538	18.5	0.29726	3151	M	1.163	3.82	0.02902	1165
Onecut1	A_51_P368894	NM_008262	one cut domain, family member 1	-1.538	8.15	0.13502	1069	P	1.114	9.71	0.15194	4063
Ptpn13	A_51_P455208	NM_011204	protein tyrosine phosphatase, non-recept	-1.538	28.61	0.33753	4847	P	-1.007	49.48	0.89173	11981
Sycn	A_51_P434332	NM_026716	syncollin	-1.538	38.68	0.46111	6813	M	-1.247	0.92	0.02302	972
Ube2j1	A_51_P257107	NM_019586	ubiquitin-conjugating enzyme E2, J1	-1.538	9.39	0.14222	1159	P	1.003	42.43	0.98495	12914
Impdh1	A_52_P183038	NM_011829	inosine 5'-phosphate dehydrogenase 1	-1.543	35.45	0.41915	6995	P	-1.065	33.49	0.25544	5733
H2afy3	A_51_P487668	NM_026230	H2A histone family, member Y3	-1.546	16.01	0.21253	2095	P	-1.116	5.75	0.05734	2074
Nfs1	A_52_P252121	AK003786	nitrogen fixation gene 1 (S. cerevisiae)	-1.546	8.15	0.13335	1063	M	-1.076	22.1	0.13264	3724
Taf5l	A_51_P349662	NM_133966	TAF5-like RNA polymerase II, p300/CBP-as	-1.546	10.33	0.15622	1303	P	-1.037	43.15	0.37012	7171

Pde3a	A_51_P109060	NM_018779	phosphodiesterase 3A, cGMP inhibited	-1.548	12.21	0.29533	3171	M	-1.032	48.39	0.78083	10996
Peg3	A_51_P206037	NM_008817	paternally expressed 3	-1.548	23.47	0.28009	3424	P	1.008	42.43	0.93901	12470
Afp	A_51_P510891	NM_007423	alpha fetoprotein	-1.55		0.41673	6679	A	-1.417	0.51	0.00584	103
Slc16a1	A_51_P397367	NM_009196	solute carrier family 16 (monocarboxylic a	-1.55	65.79	0.7596	21606	P	1.022	38.4	0.7111	10412
Stau1	A_52_P65136	AK041781	staufen (RNA binding protein) homolog 1	-1.55	28.61	0.32773	4580	P	1.02	40.63	0.75728	10843
Tbx15	A_52_P648635	NM_011534	T-box 15	-1.553		0.43833	6982	A	1.109	9.71	0.09767	3053
Dtx1	A_51_P202050	NM_008052	deltex 1 homolog (Drosophila)	-1.555	45.92	0.55922	11706	P	1.042	28.13	0.39097	7407
Gata5	A_51_P213260	NM_008093	GATA binding protein 5	-1.558		0.50463	6671	A	1.059	19.02	0.22642	5293
Plagl1	A_52_P532456	BC065150	pleiomorphic adenoma gene-like 1	-1.558	4.65	0.14404	1112	P	1.105	9.71	0.08321	2733
Ctbp2	A_51_P315303	NM_009980	C-terminal binding protein 2	-1.56	6.91	0.12368	970	P	-1.094	16.2	0.11975	3490
Mcm3	A_51_P324934	AK088142	minichromosome maintenance deficient	-1.56	42.28	0.47485	8796	P	-1.063	33.49	0.26817	5919
Tcf7	A_52_P244702	NM_009331	transcription factor 7, T-cell specific	-1.56	57.76	0.6977	18259	P	1.088	11.33	0.12012	3497
Trp53bp1	A_52_P364757	NM_013735	transformation related protein 53 binding	-1.56	10.84	0.15704	1309	P	1.097	16.2	0.35391	6935
Clca1	A_52_P669035	NM_009899	chloride channel calcium activated 1	-1.562	45.92	0.51679	10204	P	1.061	16.2	0.1735	4433
Kcmf1	A_52_P545491	AK084157	potassium channel modulatory factor 1	-1.562	42.28	0.48769	9177	P	1.013	42.43	0.80093	11184
Sf3b4	A_52_P253665	XM_001001232	splicing factor 3b, subunit 4	-1.562		0.56811	6723	A	1.074	13.58	0.17007	4383
Cyp4b1	A_51_P118704	NM_007823	cytochrome P450, family 4, subfamily b, p	-1.565	23.47	0.28421	3515	P	-1.059	38.4	0.35533	6962
Stat5b	A_52_P53698	NM_011489	signal transducer and activator of transcri	-1.567	28.61	0.39711	5312	M	1.146	8.32	0.12478	3590
Crlf3	A_52_P116024	NM_018776	cytokine receptor-like factor 3	-1.57	13.61	0.18564	1718	P	-1.01	49.48	0.83055	11460
Nav1	A_51_P196087	NM_173437	neuron navigator 1	-1.57	10.84	0.16388	1414	P	-1.319	0.51	0.01026	391
Ndfip2	A_52_P141786	NM_029561	Nedd4 family interacting protein 2	-1.57	8.15	0.13206	1046	P	-1.087	22.1	0.17087	4399
Tcf7l2	A_52_P566741	NM_009333	transcription factor 7-like 2, T-cell specific	-1.572	20.94	0.26726	3103	P	1.048	25.31	0.35274	6914
Ttc7	A_51_P103209	NM_028639	tetratricopeptide repeat domain 7	-1.572	18.5	0.24137	2563	P	-1.063	36.07	0.29062	6215
Acta2	A_52_P210078	NM_007392	actin, alpha 2, smooth muscle, aorta	-1.575	42.28	0.47357	8733	P	-1.174	3.82	0.09631	3023
Aqp12	A_52_P240693	NM_177587	aquaporin 12	-1.575	31.88	0.35723	5339	P	-1.105	11.33	0.09903	3086
AW112037	A_52_P676461	AK037065	expressed sequence AW112037	-1.575	12.21	0.17312	1535	P	1.18	2.53	0.01587	686
Top2a	A_51_P252157	NM_011623	topoisomerase (DNA) II alpha	-1.575	42.28	0.50904	9912	M	-2.031	0	0.00584	21
Fras1	A_51_P383270	NM_175473	Fraser syndrome 1 homolog (human)	-1.577	49.93	0.57184	12111	P	-1.123	3.82	0.04798	1792
Jak3	A_51_P288406	NM_010589	insulin-like 3	-1.577	20.94	0.25495	2920	P	-1.045	46.85	0.74918	10782
Neurog2	A_51_P370615	NM_009718	neurogenin 2	-1.577		0.54623	7614	A	1.11	6.98	0.05792	2084
Pcyt1b	A_52_P160005	NM_211138	phosphate cytidylyltransferase 1, choline,	-1.577	20.94	0.25583	2944	P	1.115	6.98	0.06202	2195
Arhgdig	A_52_P50325	NM_008113	Rho GDP dissociation inhibitor (GDI) gam	-1.58	13.61	0.19042	1813	P	1.064	19.02	0.3034	6360
Ret	A_51_P324191	NM_009050	ret proto-oncogene	-1.58	45.92	0.51739	10212	M	1.092	9.71	0.0789	2629
Shcbp1	A_51_P204402	NM_011369	Shc SH2-domain binding protein 1	-1.58	61.79	0.71109	18003	P	1.005	42.43	0.94292	12509
Alcam	A_51_P359272	NM_009655	activated leukocyte cell adhesion molecul	-1.582	10.84	0.15792	1322	P	-1.182	1.62	0.03829	1456
D230004J03Rik	A_52_P173108	XM_886913	RIKEN cDNA D230004J03 gene	-1.582	7.45	0.12618	989	P	-1.005	49.48	0.92304	12319
D430014M15	A_51_P306949	NM_177764	predicted gene, EG269902	-1.585	12.21	0.1769	1606	P	1.027	36.07	0.65435	9913
Man1a	A_51_P287418	NM_008548	mannosidase 1, alpha	-1.585	10.84	0.24262	2222	M	-1.039	46.85	0.71798	10470
Ube2c	A_51_P451151	NM_026785	ubiquitin-conjugating enzyme E2C	-1.585	31.88	0.36867	5592	P	1.033	30.75	0.4864	8399
Cd24a	A_52_P244193	NM_009846	CD24a antigen	-1.587	23.47	0.33844	4086	M	-1.097	28.13	0.33251	6708
Slc1a3	A_51_P268697	NM_148938	solute carrier family 1 (glial high affinity g	-1.587	13.61	0.18383	1683	P	1.05	28.13	0.45348	8033
Derl3	A_51_P491667	NM_024440	Der1-like domain family, member 3	-1.592	10.33	0.15198	1254	P	-1.252	0.51	0.00697	216
Tcf3	A_52_P387724	NM_001079822	transcription factor 3	-1.592	25.79	0.32426	4492	P	1.099	8.32	0.0689	2373
Nfkb1	A_52_P582969	BC050841	nuclear factor of kappa light chain gene e	-1.595	28.61	0.35492	5246	P	1.048	22.1	0.2939	6269
Rad51c	A_51_P252519	NM_053269	Rad51 homolog c (S. cerevisiae)	-1.595	31.88	0.36771	5580	P	-1.095	11.33	0.09238	2952
Slc2a2	A_51_P185693	NM_031197	solute carrier family 2 (facilitated glucose	-1.595	31.88	0.42175	5884	M	-1.147	11.33	0.21301	5084
Wiz	A_51_P196056	NM_212438	widely-interspaced zinc finger motifs	-1.595	20.94	0.32338	3692	M	1.046	33.49	0.71087	10408
Cyp2u1	A_52_P421698	NM_027816	cytochrome P450, family 2, subfamily u, p	-1.597	18.5	0.23742	2483	P	-1.067	43.75	0.61731	9604
Hdac6	A_51_P449361	NM_010413	histone deacetylase 6	-1.6	16.01	0.20501	2007	P	-1.183	3.46	0.08658	2817
Lphn3	A_51_P121962	AK051766	latrophilin 3	-1.6	16.01	0.21534	2132	P	1.05	25.31	0.35968	7001
Plekha5	A_52_P587054	NM_144920	pleckstrin homology domain containing, f	-1.6	4.11	0.09418	698	P	-1.03	48.7	0.79156	11109
Ahcyl1	A_52_P491971	AK087454	S-adenosylhomocysteine hydrolase-like 1	-1.603	28.61	0.33775	4876	P	1.097	22.1	0.49414	8485
Mtac2d1	A_52_P448749	AK053942	membrane targeting (tandem) C2 domai	-1.603	53.87	0.63676	15571	P	2.249	0	0.00367	2

Fbxw11	A_52_P962431	AK010033	F-box and WD-40 domain protein 11	-1.605	20.94	0.26119	3013	P	1.061	22.1	0.38332	7319
C630004H02Rik	A_51_P186552	NM_175454	RIKEN cDNA C630004H02 gene	-1.608	6.91	0.11833	915	P	-1.143	8.32	0.14368	3917
Cnn1	A_51_P350817	NM_009922	calponin 1	-1.608	49.93	0.57439	12213	P	1.035	30.75	0.49912	8569
Serpinb1a	A_51_P181297	NM_025429	serine (or cysteine) peptidase inhibitor, cl	-1.608	42.28	0.49127	9273	P	1.004	42.43	0.94576	12546
Tmsb4x	A_51_P224843	NM_021278	thymosin, beta 4, X chromosome	-1.608	25.79	0.354	4368	M	-1.135	28.13	0.41266	7647
Clps	A_51_P164459	NM_025469	colipase, pancreatic	-1.61	57.76	0.6888	13512	M	1.152	13.58	0.40439	7562
Cpa1	A_52_P161237	NM_025350	carboxypeptidase A1	-1.613	45.92	0.54267	8996	M	1	42.43	0.99863	13039
P2rx1	A_52_P494081	NM_008771	purinergic receptor P2X, ligand-gated ion	-1.613	42.28	0.51595	10161	P	1.043	25.31	0.36414	7075
Rnase1	A_51_P472153	NM_011271	ribonuclease, RNase A family, 1 (pancreat	-1.613	38.68	0.47916	7309	M	1.018	42.43	0.87093	11764
Ehd1	A_51_P469008	NM_010119	EH-domain containing 1	-1.618	16.01	0.21676	2162	P	1.204	3.46	0.03913	1484
Kcnh7	A_52_P376374	AK043768	potassium voltage-gated channel, subfam	-1.618		0.5377	6142	A	1.1	9.71	0.09775	3061
Slc41a3	A_51_P442097	NM_027868	solute carrier family 41, member 3	-1.618	13.61	0.19322	1853	P	-1.117	6.98	0.07325	2489
Gls2	A_51_P169087	NM_001033264	glutaminase 2 (liver, mitochondrial)	-1.621	10.33	0.1443	1188	P	-1.225	1.58	0.04735	1773
Arhgap9	A_51_P439326	NM_146011	Rho GTPase activating protein 9	-1.623	20.94	0.26649	3098	P	1.183	3.46	0.03601	1389
2610207I05Rik	A_51_P371695	NM_001031814	RIKEN cDNA 2610207I05 gene	-1.626	23.47	0.27843	3405	P	1.009	42.43	0.90963	12189
Srd5a2l	A_51_P334730	NM_020611	steroid 5 alpha-reductase 2-like	-1.626	6.91	0.11375	878	P	-1.103	6.98	0.06217	2199
Cyp2f2	A_51_P453909	NM_007817	cytochrome P450, family 2, subfamily f, p	-1.629		0.53113	6016	A	1.072	16.2	0.25011	5642
Kcnn3	A_51_P508300	NM_080466	potassium intermediate/small conductan	-1.629	6.91	0.11112	851	P	-1.207	0.92	0.01417	596
Dmbt1	A_51_P500676	NM_007769	deleted in malignant brain tumors 1	-1.631	16.01	0.2752	2794	M	-1.413	0.51	0.00584	41
Pdgfa	A_51_P370090	NM_008808	platelet derived growth factor, alpha	-1.631	23.47	0.29875	3813	P	1.19	3.46	0.02917	1175
Gata3	A_52_P546363	NM_008091	GATA binding protein 3	-1.637	25.79	0.31995	4370	P	1.049	28.13	0.42028	7732
Ins1	A_51_P312755	NM_008386	insulin I	-1.637	57.76	0.70968	14341	M	1.02	40.63	0.79257	11121
Tpst1	A_51_P417025	NM_013837	protein-tyrosine sulfotransferase 1	-1.637	16.01	0.21095	2070	P	-1.147	3.82	0.0659	2314
Foxp1	A_52_P276792	NM_053202	forkhead box P1	-1.639	5.86	0.10304	788	P	1.074	19.02	0.35169	6902
Ube2h	A_52_P304798	NM_009459	ubiquitin-conjugating enzyme E2H	-1.639	13.61	0.2011	1963	P	1.117	8.32	0.07774	2590
Kcnn4	A_51_P389636	NM_008433	potassium intermediate/small conductan	-1.642	57.76	0.71034	18968	P	-1.089	19.02	0.15136	4058
Ptges	A_51_P312327	NM_022415	prostaglandin E synthase	-1.642	4.65	0.09071	644	P	1.005	42.43	0.97124	12759
Rbp2	A_52_P125363	NM_009034	retinol binding protein 2, cellular	-1.642	65.79	0.7642	21883	P	-1.095	22.1	0.20694	5005
Tbl1x	A_52_P260592	NM_020601	transducin (beta)-like 1 X-linked	-1.65	5.86	0.10238	775	P	1.069	16.2	0.1763	4505
St3gal1	A_51_P301804	NM_009177	ST3 beta-galactoside alpha-2,3-sialyltrans	-1.653	12.21	0.17312	1540	P	-1.017	49.22	0.704	10348
H2-K1	A_52_P50496	AK168517	histocompatibility 2, K1, K region	-1.656	28.61	0.34064	4933	P	1.032	38.4	0.77354	10950
Fkbp11	A_52_P326399	NM_024169	FK506 binding protein 11	-1.658	10.84	0.158	1324	P	-1.254	4.63	0.19298	4796
Ctla4	A_52_P184548	NM_009843	cytotoxic T-lymphocyte-associated protei	-1.661	38.68	0.49168	8128	P	-1.03	49.39	0.83458	11491
Pftk1	A_51_P367081	NM_011074	PFTAIRE protein kinase 1	-1.661	5.15	0.09201	676	P	-1.198	3.46	0.0952	3003
Mknk1	A_52_P246082	NM_021461	MAP kinase-interacting serine/threonine	-1.664	5.86	0.09691	720	P	-1.097	40.63	0.57988	9258
Clic6	A_52_P447284	NM_172469	chloride intracellular channel 6	-1.667	61.79	0.73504	20452	P	1.053	25.31	0.41073	7614
Nr3c1	A_52_P254174	NM_008173	nuclear receptor subfamily 3, group C, me	-1.672	13.61	0.19756	1907	P	1.02	38.4	0.70065	10321
Foxp2	A_51_P233753	NM_053242	forkhead box P2	-1.675	16.01	0.22111	2221	P	1.024	36.07	0.65004	9882
Srrm1	A_51_P446098	NM_016799	serine/arginine repetitive matrix 1	-1.675	28.61	0.35622	5265	P	1.119	11.33	0.24196	5528
Furin	A_51_P400107	NM_011046	furin (paired basic amino acid cleaving en	-1.678	28.61	0.38551	5033	M	-1.007	49.48	0.90778	12175
Kctd6	A_51_P297865	NM_027782	potassium channel tetramerisation doma	-1.678	9.39	0.14396	1175	P	-1.206	1.32	0.03072	1214
Cd38	A_52_P168962	NM_007646	CD38 antigen	-1.684		0.50704	5495	A	-1.024	49	0.7429	10720
Kif12	A_51_P344586	NM_010616	kinesin family member 12	-1.684	13.61	0.20291	1978	P	-1.051	42.43	0.38269	7311
Atp2a3	A_52_P262209	NM_016745	ATPase, Ca++ transporting, ubiquitous	-1.686	12.21	0.182	1650	P	1.073	16.2	0.20163	4932
Bcat2	A_52_P448266	NM_009737	branched chain aminotransferase 2, mito	-1.692	3.78	0.07413	498	P	1.038	28.13	0.4068	7585
Pnliprp1	A_51_P136781	NM_018874	pancreatic lipase related protein 1	-1.692	28.61	0.38628	5048	M	1.258	1.62	0.01925	807
AW548124	A_52_P299535	NM_134117	expressed sequence AW548124	-1.695	4.11	0.07997	552	P	1.07	19.02	0.30075	6333
Depdc6	A_52_P661503	AK170208	DEP domain containing 6	-1.695	5.15	0.16264	1241	M	1.056	16.2	0.20563	4981
1810044A24Rik	A_52_P488649	AK029106	RIKEN cDNA 1810044A24 gene	-1.698	12.21	0.18646	1741	P	1.008	42.43	0.92201	12283
Pvrl3	A_51_P125009	NM_021495	poliovirus receptor-related 3	-1.698	8.15	0.13196	1044	P	-1.213	1.1	0.01816	772
2810451A06Rik	A_51_P257743	NM_176835	RIKEN cDNA 2810451A06 gene	-1.701	5.15	0.09365	693	P	-1.058	40.63	0.3946	7454
Bcl6	A_52_P161495	NM_009744	B-cell leukemia/lymphoma 6	-1.701	5.15	0.13209	997	P	1.083	11.33	0.11714	3424
Gucy2c	A_51_P100991	NM_145067	guanylate cyclase 2c	-1.706	4.65	0.08664	602	P	-1.035	45.05	0.49043	8444

Ramp1	A_51_P348665	NM_016894	receptor (calcitonin) activity modifying pr	-1.706	10.84	0.15746	1315	P	1.017	42.43	0.82608	11422
Terf2	A_52_P427544	NM_009353	telomeric repeat binding factor 2	-1.706	5.15	0.08948	629	P	-1.06	38.4	0.36472	7089
Cel	A_51_P242205	NM_009885	carboxyl ester lipase	-1.709	25.79	0.36697	4660	M	1.131	16.2	0.39259	7426
Dscr1l1	A_52_P414464	NM_207649	Down syndrome critical region gene 1-like	-1.709	13.61	0.19661	1880	P	1.027	36.07	0.61332	9555
Pla2g2f	A_52_P114691	NM_012045	phospholipase A2, group IIF	-1.709	31.88	0.39742	6445	P	-1.071	43.15	0.56462	9160
Rad51	A_51_P148105	NM_011234	RAD51 homolog (S. cerevisiae)	-1.715	42.28	0.49899	9627	P	1.079	9.71	0.10096	3128
Cbfa2t3h	A_52_P13802	NM_009824	core-binding factor, runt domain, alpha su	-1.718	4.65	0.08664	600	P	-1.067	36.07	0.304	6373
Ggcx	A_52_P110812	NM_019802	gamma-glutamyl carboxylase	-1.718	10.84	0.1677	1467	P	-1.091	30.75	0.31396	6508
Lpgat1	A_51_P453351	NM_172266	lysophosphatidylglycerol acyltransferase	-1.724	4.65	0.0868	612	P	1.015	42.43	0.92862	12376
NP_TR6JSE50FPA	A_51_P471134	NM_203509	olfactory receptor 1372, pseudogene 1	-1.724	7.45	0.12071	928	P	1.307	3.01	0.07359	2499
Pcyox1	A_51_P508029	NM_025823	prenylcysteine oxidase 1	-1.724	3.82	0.07413	496	P	1.023	38.4	0.72507	10524
Dpysl4	A_52_P470438	NM_011993	dihydropyrimidinase-like 4	-1.727	49.93	0.58727	12881	P	1.032	30.75	0.47441	8250
Spbc25	A_51_P514700	NM_025565	SPC25, NDC80 kinetochore complex comp	-1.727	7.45	0.12332	959	P	-1.184	11.33	0.27484	6023
Ntrk2	A_51_P393454	NM_001025074	neurotrophic tyrosine kinase, receptor, ty	-1.73	6.91	0.11375	877	P	1.017	38.4	0.69072	10244
Rgs11	A_52_P209527	BC019741	regulator of G-protein signaling 11	-1.73	35.45	0.44105	7665	P	-1.038	45.68	0.57598	9232
Nisch	A_52_P472515	AK088377	nischarin	-1.733	18.5	0.25155	2817	P	-1.01	49.48	0.93323	12413
Pzp	A_51_P490323	NM_007376		-1.733		0.50317	6646	A	1.043	25.31	0.33411	6728
Exosc3	A_52_P488409	AK016397	exosome component 3	-1.751	7.45	0.11833	912	P	1.035	30.75	0.5252	8801
Bach2	A_52_P184618	NM_007521	BTB and CNC homology 2	-1.757	10.84	0.16423	1420	P	1.087	16.2	0.27611	6043
Arid3b	A_52_P454394	NM_019689	AT rich interactive domain 3B (Bright like)	-1.764	7.45	0.12327	956	P	1.066	16.2	0.20858	5029
Parp3	A_52_P480425	NM_145619	poly (ADP-ribose) polymerase family, mer	-1.767	13.61	0.20154	1964	P	-1.059	40.63	0.40595	7577
Procr	A_51_P382152	NM_011171	protein C receptor, endothelial	-1.767	28.61	0.37403	5715	P	-1.006	49.48	0.93118	12395
Cdon	A_51_P334739	NM_021339	cell adhesion molecule-related/down-reg	-1.773	6.57	0.10308	794	P	1.009	42.43	0.85083	11600
Cpb1	A_51_P391934	NM_029706	carboxypeptidase B1 (tissue)	-1.779	38.68	0.49512	7714	M	-1.263	0.51	0.01026	390
Trim25	A_52_P654161	NM_009546	tripartite motif protein 25	-1.779	13.61	0.21253	2094	P	1.168	3.46	0.0248	1027
Ankrd10	A_51_P499530	NM_133971	ankyrin repeat domain 10	-1.786	5.15	0.08759	619	P	-1.127	19.02	0.28158	6108
Itpr3	A_51_P104897	NM_080553	inositol 1,4,5-triphosphate receptor 3	-1.786	28.61	0.35908	5385	P	1.01	42.43	0.87369	11796
Nudt4	A_52_P305246	NM_027722	nudix (nucleoside diphosphate linked mo	-1.786	6.91	0.11273	870	P	1.077	13.58	0.13402	3744
Mki67	A_51_P253808	X82786	antigen identified by monoclonal antibod	-1.805	25.79	0.26149	2933	M	1.013	42.43	0.78965	11085
Hbegf	A_51_P181565	NM_010415	heparin-binding EGF-like growth factor	-1.808	38.68	0.47617	8840	P	-1.045	43.15	0.42795	7799
Camk1d	A_52_P384310	NM_177343	calcium/calmodulin-dependent protein ki	-1.812	8.15	0.13102	1035	P	1.044	28.13	0.37772	7252
Gadd45g	A_51_P315904	NM_011817	growth arrest and DNA-damage-inducible	-1.812	3.78	0.12332	884	M	-1.044	45.05	0.58195	9267
Hmgn3	A_51_P422183	BC005693	high mobility group nucleosomal binding	-1.812	10.84	0.17365	1561	P	-1.135	22.1	0.32039	6570
Ror1	A_52_P212025	AK012979	receptor tyrosine kinase-like orphan rece	-1.812	5.86	0.09691	722	P	1.052	19.02	0.24312	5550
Tbx18	A_52_P279263	NM_023814	T-box18	-1.812	6.91	0.1589	1160	P	1.084	19.02	0.33041	6675
Abcc8	A_52_P218188	NM_011510	ATP-binding cassette, sub-family C (CFTR/	-1.815	16.01	0.21981	2193	P	-1.181	3.46	0.07277	2467
Hsd17b13	A_52_P595140	NM_198030	hydroxysteroid (17-beta) dehydrogenase	-1.818	25.79	0.34172	4958	P	-1.148	3.82	0.06338	2243
Rhobtb1	A_52_P614517	XM_920622	Rho-related BTB domain containing 1	-1.818	9.39	0.16091	1252	M	-1.195	1.18	0.01893	796
Rasd1	A_52_P496726	NM_009026	RAS, dexamethasone-induced 1	-1.825	16.01	0.24343	2634	P	1.008	42.43	0.882	11875
Stch	A_52_P376804	NM_030201	stress 70 protein chaperone, microsome-	-1.825	12.21	0.18392	1684	P	1.036	36.07	0.70599	10374
Tnfrsf22	A_52_P323852	NM_023680	tumor necrosis factor receptor superfami	-1.828	3.78	0.06658	420	P	1.03	33.49	0.59744	9426
2310014D11Rik	A_51_P440923	AK009333	RIKEN cDNA 2310014D11 gene	-1.832	6.57	0.11558	854	P	-1.028	49.22	0.80404	11209
D430019H16Rik	A_52_P97699	BC058677	RIKEN cDNA D430019H16 gene	-1.832	23.47	0.30128	3891	P	-1.04	44.4	0.49423	8492
Eif4enif1	A_52_P285418	AK090363	eukaryotic translation initiation factor 4E	-1.835	42.28	0.33772	4512	M	1.081	13.58	0.18052	4581
Gstm2	A_51_P284486	NM_008183	glutathione S-transferase, mu 2	-1.852	1.87	0.05412	329	P	-1.141	3.82	0.05218	1927
Hhex	A_52_P528600	NM_008245	hematopoietically expressed homeobox	-1.859	9.39	0.1416	1145	P	1.054	22.1	0.61123	8871
Cnot8	A_51_P481293	NM_026949	CCR4-NOT transcription complex, subunit	-1.866	2.87	0.06292	387	P	1.037	30.75	0.42859	7808
Fh1	A_51_P359333	NM_010209	fumarate hydratase 1	-1.869	5.15	0.11123	820	P	-1.024	49.39	0.79758	11155
Ell2	A_51_P230507	NM_138953	elongation factor RNA polymerase II 2	-1.873	4.11	0.07465	504	P	-1.284	0.51	0.0065	182
Kctd1	A_52_P137637	XM_980194	potassium channel tetramerisation doma	-1.88	23.47	0.31447	4242	P	-1.317	0.51	0.00707	220
Rps6ka2	A_51_P320466	NM_011299	ribosomal protein S6 kinase, polypeptide	-1.88	5.15	0.09071	643	P	1.113	5.75	0.0453	1701
Pla2g1b	A_51_P280893	NM_011107	phospholipase A2, group IB, pancreas	-1.883	20.94	0.31826	3608	M	1.025	36.07	0.65871	9960
Ctrc	A_51_P384436	NM_001033875	chymotrypsin C (caldecrin)	-1.887	25.79	0.3571	4428	M	1.203	13.58	0.47683	8280

Foxm1	A_52_P28806	NM_008021	forkhead box M1	-1.901	16.01	0.23366	2414	P	1.065	28.13	0.54113	8954
Rrbp1	A_51_P164686	BC031452	ribosome binding protein 1	-1.901	4.11	0.07112	471	P	1.014	42.43	0.81873	11347
Gcnt2	A_52_P363216	NM_133219	glucosaminyl (N-acetyl) transferase 2, I-br	-1.905	1.87	0.05412	330	P	-1.243	0.56	0.01123	432
Gstm1	A_52_P415215	NM_010358	glutathione S-transferase, mu 1	-1.905	7.45	0.11833	911	P	-1.164	2.04	0.03696	1408
Eml1	A_52_P54609	AK082168	echinoderm microtubule associated prote	-1.912	18.5	0.26936	3141	P	1.013	42.43	0.84438	11557
Mtmr3	A_51_P150195	NM_028860	myotubularin related protein 3	-1.912	9.39	0.1478	1219	P	1.087	11.33	0.13593	3772
Vit	A_52_P51176	AK018949	vitrin	-1.916		0.42946	4056	A	-1.003	49.48	0.96478	12703
Stat4	A_51_P177092	NM_011487	signal transducer and activator of transcri	-1.927	4.65	0.07612	524	P	1.039	30.75	0.48206	8341
C1qa	A_51_P181451	NM_007572	complement component 1, q subcompon	-1.931	4.65	0.08156	571	P	1.058	22.1	0.28383	6128
Rhoh	A_51_P489289	BC094937	ras homolog gene family, member H	-1.931		0.27137	3076	A	1.062	19.02	0.22	5211
Satb1	A_52_P110489	AK040502	special AT-rich sequence binding protein	-1.934	10.33	0.15535	1296	P	1.009	42.43	0.92273	12309
Cdk8	A_52_P771744	AK089626	cyclin-dependent kinase 8	-1.938	2.4	0.05799	352	P	-1.182	6.98	0.18644	4678
Kras	A_51_P377237	NM_021284	v-Ki-ras2 Kirsten rat sarcoma viral oncoge	-1.938	12.21	0.1841	1640	P	-1.326	0.51	0.01625	697
Reg1	A_51_P329811	NM_009042	regenerating islet-derived 1	-1.942	18.5	0.28813	3012	M	-1.188	3.82	0.11418	3371
Bcl6b	A_51_P424959	NM_007528	B-cell CLL/lymphoma 6, member B	-1.949	1.44	0.04421	267	P	-1.113	4.63	0.05166	1901
Rel	A_51_P187461	NM_009044	reticuloendotheliosis oncogene	-1.949	31.88	0.40867	6686	P	-1.044	44.4	0.55828	9086
Ela1	A_52_P578634	NM_033612	elastase 1, pancreatic	-1.953	13.61	0.24877	2342	M	1.187	9.71	0.25769	5778
Vnn1	A_51_P424532	NM_011704	vanin 1	-1.957	49.93	0.6028	13581	P	1.17	4.63	0.05437	1990
Baiap2l1	A_52_P138096	NM_025833	BAI1-associated protein 2-like 1	-1.969	7.45	0.12526	979	P	-1.302	0.51	0.01049	403
Ccnb1	A_51_P287093	NM_172301	cyclin B1	-1.969	20.94	0.29663	3741	P	-1.272	0.75	0.01896	799
Aldoc	A_51_P425284	AK039267	aldolase 3, C isoform	-1.972	57.76	0.32734	3174	M	-1.053	38.4	0.31369	6501
Ctrl	A_51_P177491	NM_023182	chymotrypsin-like	-1.976	16.01	0.28068	2906	M	1.051	28.13	0.53134	8848
Tat	A_51_P228574	NM_146214	tyrosine aminotransferase	-1.976	5.15	0.08931	626	P	1.065	19.02	0.2311	5364
Ptf1a	A_51_P226711	NM_018809	pancreas specific transcription factor, 1a	-1.984	10.84	0.17059	1491	P	1.183	3.01	0.02595	1067
G6pc2	A_52_P498119	NM_021331	glucose-6-phosphatase, catalytic, 2	-1.988	5.86	0.14088	1020	M	-1.323	1.58	0.09269	2958
Wars	A_52_P35174	NM_011710	tryptophanyl-tRNA synthetase	-1.996	9.39	0.15268	1274	P	1.013	42.43	0.83438	11488
Pnlip	A_51_P520552	AK007357	pancreatic lipase	-2	9.39	0.1849	1487	M	1.073	16.2	0.22718	5316
Tnfaip8	A_51_P435968	NM_134131	tumor necrosis factor, alpha-induced prot	-2.012	31.88	0.41119	6773	P	-1.048	42.43	0.35632	6967
Bcas3	A_52_P311618	AK034117	breast carcinoma amplified sequence 3	-2.016		0.4035	3588	A	1.121	8.32	0.07211	2434
Rnf141	A_52_P560797	NM_025999	ring finger protein 141	-2.02	4.11	0.074	494	P	1.032	33.49	0.54705	8998
Cd9	A_51_P320626	AK038228		-2.028	42.28	0.54119	11056	P	1.041	38.4	0.82109	11374
Aqp8	A_51_P183261	NM_007474	aquaporin 8	-2.033	45.92	0.56738	11956	P	1.008	42.43	0.89842	12046
Mbc2	A_51_P334685	NM_011843	membrane bound C2 domain containing	-2.033	3.82	0.06716	425	P	-1.188	0.75	0.0131	568
Adra2a	A_51_P434567	NM_007417	adrenergic receptor, alpha 2a	-2.041	4.65	0.07612	525	P	-1.042	45.05	0.57598	9236
Akr1b7	A_51_P331288	NM_009731	aldo-keto reductase family 1, member B7	-2.041	53.87	0.67678	17330	P	1.157	9.71	0.2389	5471
Efemp1	A_51_P337412	NM_146015	epidermal growth factor-containing fibuli	-2.041	6.91	0.11992	924	P	1.1	9.71	0.08874	2863
Aurkb	A_51_P415059	NM_011496	aurora kinase B	-2.045	35.45	0.19322	1323	M	1.157	9.71	0.25838	5790
Birc5	A_51_P230103	NM_001012273	baculoviral IAP repeat-containing 5	-2.045	49.93	0.60124	13516	P	1.013	42.43	0.80819	11260
Tm4sf4	A_51_P371001	NM_145539	transmembrane 4 superfamily member 4	-2.049	7.45	0.1607	1286	P	-1.083	19.02	0.13993	3852
Mgll	A_52_P568977	AK006949	monoglyceride lipase	-2.053		0.39447	3452	A	-1.05	38.4	0.28538	6151
Ranbp17	A_52_P175046	AK046865	RAN binding protein 17	-2.062	16.01	0.24428	2680	P	-1.32	0.51	0.00903	330
BC039632	A_52_P501167	XM_620568	cDNA sequence BC039632	-2.07	8.15	0.1769	1407	M	-1.246	1.62	0.0734	2494
Cd44	A_52_P523459	NM_009851	CD44 antigen	-2.07	16.01	0.24333	2616	P	-1.023	47.92	0.63929	9801
2310040A07Rik	A_51_P497090	BC021944	RIKEN cDNA 2310040A07 gene	-2.079	6.57	0.10284	779	P	-1.044	43.15	0.37881	7263
Tff3	A_51_P456208	NM_011575	trefoil factor 3, intestinal	-2.083	57.76	0.83789	25113	P	1.019	40.63	0.71936	10489
Paxip1	A_51_P232720	NM_018878	PAX interacting (with transcription-activat	-2.092	0.77	0.03147	195	P	-1.201	2.53	0.07199	2433
Defb1	A_52_P321140	NM_007843	defensin beta 1	-2.11	6.91	0.11679	880	P	-1.292	3.82	0.19327	4798
Prss2	A_51_P418901	NM_009430	protease, serine, 2	-2.11	38.68	0.50937	8083	M	1.239	2.04	0.02003	856
Nexn	A_52_P367520	NM_199465	nexilin	-2.114	10.84	0.18955	1797	P	-1.154	2.04	0.03104	1227
1810049H19Rik	A_51_P276486	NM_001003405	RIKEN cDNA 1810049H19 gene	-2.123	45.92	0.58882	10362	M	1.294	4.63	0.14189	3884
Ctrb1	A_51_P205761	NM_025583	chymotrypsinogen B1	-2.132	23.47	0.34902	4260	M	1.318	0.75	0.00756	276
Ceacam1	A_51_P183446	NM_001039186	CEA-related cell adhesion molecule 1	-2.137	38.68	0.48031	8955	P	1.077	19.02	0.29317	6259
Tmod2	A_52_P451614	NM_001038710	tropomodulin 2	-2.137	0.55	0.0289	172	P	-1.093	42.43	0.63136	9729

Ltb4dh	A_51_P444437	NM_025968	leukotriene B4 12-hydroxydehydrogenase	-2.146	38.68	0.47838	8911	P	-1.163	2.53	0.0391	1476
Ehf	A_52_P609918	NM_007914	ets homologous factor	-2.16	25.79	0.3571	5290	P	1.02	38.4	0.68607	10204
Uhrf1	A_51_P491742	NM_010931	ubiquitin-like, containing PHD and RING fi	-2.16	35.45	0.44372	7764	P	-1.17	3.01	0.05119	1883
Traip	A_51_P254045	NM_011634	TRAF-interacting protein	-2.174	10.33	0.17353	1555	P	-1.087	25.31	0.23711	5449
Cdc6	A_52_P219473	NM_011799	cell division cycle 6 homolog (S. cerevisiae	-2.179		0.1716	1113	A	-1.138	2.53	0.03177	1250
Etv5	A_52_P631015	NM_023794	ets variant gene 5	-2.183	4.65	0.07997	545	P	1.072	22.1	0.39731	7491
Scg2	A_51_P327970	NM_009129	secretogranin II	-2.183	1.44	0.07413	476	M	-1.073	42.43	0.54474	8982
2210010C04Rik	A_51_P414661	NM_023333	RIKEN cDNA 2210010C04 gene	-2.203	28.61	0.39874	5361	M	1.19	16.2	0.49039	8438
Pycr2	A_51_P249051	NM_133705	pyrroline-5-carboxylate reductase family,	-2.203	3.82	0.06915	455	P	1.032	33.49	0.5684	9189
ORF9	A_51_P492047	NM_020622	open reading frame 9	-2.217	38.68	0.44834	7588	P	1.136	3.82	0.02902	1166
Chst3	A_52_P390944	NM_016803	carbohydrate (chondroitin 6/keratan) sulf	-2.227	12.21	0.1443	1155	P	1.036	28.13	0.42376	7762
Fosl1	A_51_P308796	NM_010235	fos-like antigen 1	-2.232	61.79	0.1691	1084	M	1.008	42.43	0.86302	11706
Elovl6	A_51_P463440	NM_130450	ELOVL family member 6, elongation of lor	-2.237	3.78	0.06245	379	P	1.192	8.32	0.2216	5234
Prss3	A_51_P394552	NM_011645	protease, serine, 3	-2.242	35.45	0.48193	7383	M	1.388	3.82	0.15044	4046
Retnla	A_51_P254817	NM_020509	resistin like alpha	-2.247	42.28	0.3531	4509	M	-1.013	49.48	0.80573	11231
Cbs	A_52_P210246	NM_144855	cystathionine beta-synthase	-2.252	1.87	0.04995	297	P	-1.092	11.33	0.09111	2925
Il10	A_51_P430766	NM_010548	interleukin 10	-2.257		0.35438	2869	A	1.011	42.43	0.82412	11398
Il6ra	A_51_P415855	NM_010559	interleukin 6 receptor, alpha	-2.262	3.82	0.06741	429	P	-1.476	0.51	0.01933	812
Slc39a4	A_51_P103222	NM_028064	solute carrier family 39 (zinc transporter),	-2.268	45.92	0.57885	12440	P	1.062	19.02	0.21655	5150
Cldn3	A_51_P157902	NM_009902	claudin 3	-2.299	5.15	0.09711	725	P	-1.343	1.1	0.05591	2031
Gpx2	A_51_P486810	NM_030677	glutathione peroxidase 2	-2.299	49.93	0.61136	14009	P	-1.116	8.32	0.08883	2866
Proc	A_51_P295967	NM_001042768	protein C	-2.299	6.57	0.10778	822	P	1.526	1.32	0.05145	1891
Atp8b1	A_51_P192329	NM_001001488	ATPase, class I, type 8B, member 1	-2.304	1.38	0.0305	192	P	-1.205	4.63	0.14846	4020
Tgtp	A_52_P676510	NM_011579	T-cell specific GTPase	-2.309	23.47	0.33231	4708	P	-1.03	46.3	0.56495	9165
Il1r1	A_51_P271503	NM_008362	interleukin 1 receptor, type I	-2.342	6.91	0.14891	1090	M	-1.113	11.33	0.12581	3625
Pvr	A_52_P225377	AK014446	poliovirus receptor	-2.347		0.33775	2671	A	1.031	40.63	0.85207	11610
Slc30a8	A_52_P529022	NM_172816	solute carrier family 30 (zinc transporter),	-2.347	1.44	0.04794	284	M	-1.866	0	0.00376	4
Ccnd1	A_51_P262766	NM_007631	cyclin D1	-2.353	0.55	0.02517	148	P	-1.131	5.75	0.07486	2527
Igf2	A_51_P516833	NM_010514	insulin-like growth factor 2	-2.353	4.65	0.08306	583	P	1.088	11.33	0.13109	3688
Nupr1	A_51_P519251	NM_019738	nuclear protein 1	-2.353	3.82	0.07471	491	M	-1.275	1.18	0.04505	1683
Rnase4	A_51_P237383	NM_021472	ribonuclease, RNase A family 4	-2.353	2.87	0.05858	355	P	-1.762	1.18	0.13679	3786
Phf13	A_52_P632397	NM_172705	PHD finger protein 13	-2.387	6.57	0.11253	864	P	-1.079	19.02	0.12129	3527
Gcgr	A_51_P211403	NM_008101	glucagon receptor	-2.404	3.82	0.07147	479	P	-1.05	44.4	0.5786	9250
Car2	A_51_P455647	NM_009801	carbonic anhydrase 2	-2.41	57.76	0.71369	19162	P	1.183	6.98	0.14811	4007
Mesp1	A_51_P341725	NM_008588	mesoderm posterior 1	-2.427	4.65	0.0868	610	P	1.065	16.2	0.17692	4512
Reg2	A_51_P333549	NM_009043	regenerating islet-derived 2	-2.445	20.94	0.32751	3785	M	-1.225	11.33	0.32279	6591
Gsta2	A_52_P458682	NM_008182	glutathione S-transferase, alpha 2 (Yc2)	-2.451	53.87	0.68523	17672	P	1.16	8.32	0.13742	3799
Hs6st2	A_52_P599317	NM_001077202	heparan sulfate 6-O-sulfotransferase 2	-2.451	10.33	0.17552	1581	P	1.12	13.58	0.27928	6081
Lef1	A_51_P501145	AK083328	lymphoid enhancer binding factor 1	-2.463	25.79	0.36978	5616	P	1.042	40.63	0.88222	11881
Nck2	A_52_P372925	NM_010879	non-catalytic region of tyrosine kinase ad	-2.481	1.44	0.03468	216	P	-1.052	38.4	0.2725	5990
Serpina3g	A_51_P326191	NM_009251	serine (or cysteine) peptidase inhibitor, cl	-2.494	4.11	0.07997	557	P	1.152	6.98	0.07543	2550
Deaf1	A_52_P545575	AK080564	deformed epidermal autoregulatory factc	-2.519	0.55	0.02244	140	P	1.006	42.43	0.905	12147
Reln	A_51_P365369	NM_011261	reelin	-2.525	18.5	0.28891	3607	P	1.087	11.33	0.12036	3500
Sfrp5	A_51_P476169	NM_018780	secreted frizzled-related sequence protei	-2.591	2.4	0.05352	318	P	1.062	19.02	0.2463	5595
Trp53inp2	A_51_P228354	NM_178111	transformation related protein 53 inducib	-2.604	5.15	0.12136	861	M	-1.529	0.51	0.01123	430
Gcnt1	A_52_P227137	NM_010265	glucosaminyl (N-acetyl) transferase 1, cor	-2.611	7.45	0.14471	1194	M	-1.03	45.68	0.50952	8669
Iapp	A_51_P119841	NM_010491	islet amyloid polypeptide	-2.632	10.33	0.19797	1674	M	-1.236	0.75	0.03814	1293
Rac2	A_51_P121891	NM_009008	RAS-related C3 botulinum substrate 2	-2.646	16.01	0.26214	3020	P	-1.342	0.51	0.00584	58
Sema4g	A_51_P331003	NM_011976	sema domain, immunoglobulin domain (I	-2.646	7.45	0.14396	1171	P	1.169	3.46	0.0268	1095
Ccl5	A_51_P485312	NM_013653	chemokine (C-C motif) ligand 5	-2.674	38.68	0.51432	10097	P	1.027	33.49	0.56342	9144
Anpep	A_52_P231184	NM_008486	alanyl (membrane) aminopeptidase	-2.681	1.21	0.02577	154	P	1.12	6.98	0.05397	1975
Abcb4	A_51_P249118	NM_008830	ATP-binding cassette, sub-family B (MDR/	-2.688	3.82	0.07147	482	P	1.001	42.43	0.99013	12987
Elmo1	A_52_P613688	NM_198093	engulfment and cell motility 1, ced-12 ho	-2.688	1.44	0.03586	225	P	-1.019	48.7	0.67396	10088

Prc1	A_51_P366931	NM_145150	protein regulator of cytokinesis 1	-2.695	4.65	0.0915	655	P	1.015	40.63	0.74339	10733
Hoxd1	A_51_P305217	NM_010467	homeo box D1	-2.747		0.29225	2088	A	1.103	11.33	0.15775	4175
Ppy	A_52_P460791	NM_008918	pancreatic polypeptide	-2.778	13.61	0.25347	2418	M	-1.291	5.75	0.23847	5463
Chga	A_51_P358316	NM_007693	chromogranin A	-2.793	20.94	0.34879	4253	M	-1.241	2.53	0.09521	3004
Plac8	A_51_P515883	NM_139198	placenta-specific 8	-2.809	53.87	0.68305	17546	P	-1.09	30.75	0.31508	6523
Pigr	A_51_P239737	NM_011082	polymeric immunoglobulin receptor	-2.899	45.92	0.60436	13648	P	-1.011	49.48	0.82193	11379
Pgf	A_51_P318381	NM_008827	placental growth factor	-2.95	1.48	0.04214	257	P	-1.003	49.48	0.97124	12758
Nkx2-2	A_51_P197718	NM_010919	NK2 transcription factor related, locus 2 (	-2.967	2.4	0.074	472	M	-1.162	2.53	0.04464	1662
Myb	A_51_P375543	NM_010848	myeloblastosis oncogene	-3.049	38.68	0.52957	10730	P	-1.056	42.43	0.47031	8200
Fxyd6	A_51_P490247	NM_022004	FXYD domain-containing ion transport reg	-3.195	1.44	0.03494	217	P	-1.487	0.51	0.01938	817
Muc2	A_51_P128320	BC034197	mucin 2	-3.215	31.88	0.37219	5462	P	1.083	11.33	0.12216	3546
Rrm2	A_51_P110689	NM_009104	ribonucleotide reductase M2	-3.215	4.65	0.10238	774	P	-1.442	0.51	0.03335	1300
Barx2	A_52_P533817	AK009185	BarH-like homeobox 2	-3.279	7.45	0.16388	1412	P	1.062	19.02	0.28627	6177
Cpb2	A_51_P262701	NM_019775	carboxypeptidase B2 (plasma)	-3.413	3.82	0.0794	537	P	1.047	28.13	0.49171	8460
Ambp	A_51_P145785	NM_007443	alpha 1 microglobulin/bikunin	-3.436	1.21	0.02713	161	P	-1.088	33.49	0.36478	7090
Xlkd1	A_52_P686785	NM_053247	extra cellular link domain-containing 1	-3.448	0	0.01582	81	P	-1.077	22.1	0.13896	3820
H2-Eb1	A_51_P393226	X52641	histocompatibility 2, class II antigen E bet	-3.831	31.88	0.45823	8144	P	1.053	25.31	0.35657	6974
Wnt4	A_51_P130475	NM_009523	wingless-related MMTV integration site 4	-3.831	0	0.01412	66	P	-1.105	6.98	0.06127	2175
Uox	A_51_P205385	NM_009474	urate oxidase	-3.861	0	0.01385	63	P	-1.062	33.49	0.246	5583
1810009J06Rik	A_51_P502075	NM_023707	RIKEN cDNA 1810009J06 gene	-3.906	9.39	0.18765	1774	P	1.336	3.01	0.08717	2826
Bmp1	A_51_P488646	NM_009755	bone morphogenetic protein 1	-3.906	3.78	0.07931	536	P	-1.092	19.02	0.17385	4449
Cd79b	A_51_P342652	NM_008339	CD79B antigen	-3.953	18.5	0.32851	4607	P	1.008	42.43	0.91867	12262
Six4	A_52_P420340	NM_011382	sine oculis-related homeobox 4 homolog	-4.405	0	0.01819	117	P	-1.218	1.18	0.02468	1018
Sez6l	A_51_P201747	BC065117	seizure related 6 homolog like	-4.525	4.11	0.11253	802	M	-2.055	0	0.00731	244
Dusp4	A_51_P347333	AK012530	dual specificity phosphatase 4	-4.566	0.77	0.02771	163	P	1.013	42.43	0.82749	11436
Tnfrsf11b	A_52_P106620	NM_008764	tumor necrosis factor receptor superfami	-4.566	0	0.01582	80	P	-1.724	0	0.00584	6
Igh-6	A_52_P358360	AK088666	immunoglobulin heavy chain 6 (heavy cha	-4.587	12.21	0.26183	3016	P	-1.114	25.31	0.30779	6416
Fxyd3	A_52_P377791	NM_008557	FXYD domain-containing ion transport reg	-4.695	1.58	0.05304	310	P	-1.169	2.04	0.03941	1496
Ddc	A_52_P63905	NM_016672	dopa decarboxylase	-5.102	0	0.01538	71	P	-1.9	0	0.00584	78
	A_51_P196590	NM_008212	hydroxyacyl-Coenzyme A dehydrogenase	-5.435	0	0.00773	27	P	-2.44	0	0.00584	79
Klf5	A_52_P54463	BC006646	Kruppel-like factor 5	-5.263	0	0.00773	28	P	1.138	6.98	0.07017	2399
2210415F13Rik	A_52_P670766	NM_027339	RIKEN cDNA 2210415F13 gene	-5.618	35.45	0.49841	9580	P	-1.015	49.48	0.81862	11345
Loxl2	A_52_P480351	XM_985144	lysyl oxidase-like 2	-5.65	0	0.00636	19	P	-1.022	47.92	0.6291	9706
Ttr	A_51_P194149	NM_013697	transthyretin	-5.747	0	0.01677	98	P	-1.122	19.02	0.24091	5508
Foxa2	A_51_P222773	NM_010446	forkhead box A2	-6.289	4.11	0.10445	805	P	-1.385	0.51	0.00584	31
Sell	A_51_P236234	NM_011346	selectin, lymphocyte	-6.757	12.21	0.14458	1162	P	-1.048	40.63	0.32191	6584
Igl-V1	A_52_P829408	AK008145	immunoglobulin lambda chain, variable 1	-6.944	13.61	0.19756	1633	M	-1.216	1.18	0.0289	1163
Retnlb	A_51_P428360	NM_023881	resistin like beta	-9.346	8.15	0.19974	1945	P	1.103	11.33	0.14486	3944
Reg4	A_52_P257758	NM_026328	regenerating islet-derived family, membe	-15.152	12.21	0.15261	1093	P	1.067	13.58	0.14723	3987
Slc14a2	A_52_P198885	NM_207651	solute carrier family 14 (urea transporter)	-15.385	0	0.00616	14	P	-1.41	1.18	0.07798	2602
Insrr	A_51_P233546	NM_011832	insulin receptor-related receptor	-29.412	0	0.00616	1	P	-1.231	0.92	0.01749	745
4930556A17Rik	A_51_P486593	XM_979591	RIKEN cDNA 4930556A17 gene					A	1.013	42.43	0.81957	11352
A630012P03Rik	A_52_P74381	AK085028	RIKEN cDNA A630012P03 gene					A	1.045	25.31	0.32115	6577
Barx1	A_51_P151493	NM_007526	BarH-like homeobox 1					A	-1.132	22.1	0.30954	6437
BC006965	A_51_P288719	BC006965	cDNA sequence BC006965					A	-1.018	48.39	0.6582	9955
Bmp8b	A_51_P411926	NM_007559	bone morphogenetic protein 8b					A	1.06	22.1	0.30567	6390
D10Ertd755e	A_52_P494580	AK080282	DNA segment, Chr 10, ERATO Doi 755, expressed					A	1.025	36.07	0.59776	9433
D230019N24Rik	A_51_P442193	AK051927	RIKEN cDNA D230019N24 gene					A	-1.091	9.71	0.0811	2685
D830007B15Rik	A_52_P33202	AK077061	RIKEN cDNA D830007B15 gene					A	1.011	42.43	0.80547	11223
Dmgdh	A_51_P273679	NM_028772	dimethylglycine dehydrogenase precursor					A	1.005	42.43	0.92557	12351
Ela2	A_51_P144551	NM_015779	elastase 2, neutrophil					A	1.01	42.43	0.9443	12524
F830002L21Rik	A_52_P1028835	AK089577	RIKEN cDNA F830002L21 gene					A	-1.002	49.48	0.96935	12740
Hand1	A_51_P342549	NM_008213	heart and neural crest derivatives expressed transcript 1					A	1.174	2.53	0.01645	703

Hoxc4	A_51_P183481	NM_013553	homeo box C4	A	1.039	30.75	0.46523	8160
Hoxd11	A_51_P112319	NM_008273	homeo box D11	A	1.03	33.49	0.55544	9070
Mds1	A_51_P437349	NM_021442	myelodysplasia syndrome 1 homolog (human)	A	1.083	11.33	0.1367	3783
Neurod6	A_51_P394997	NM_009717	neurogenic differentiation 6	A	-1.311	0.51	0.00654	190
Nkx2-5	A_51_P173285	NM_008700	NK2 transcription factor related, locus 5 (Drosophila)	A	1.03	30.75	0.49171	8467
Pcdhb9	A_51_P483878	NM_053134	protocadherin beta 9	A	-1.312	0.51	0.00584	89
Pitx1	A_52_P522255	NM_011097	paired-like homeodomain transcription factor 1	A	1.009	42.43	0.87351	11793
Serpina3a	A_51_P125779	BC063325	serine (or cysteine) peptidase inhibitor, clade A, member 3A	A	-1.027	46.85	0.60921	9515
Trpm8	A_51_P156334	NM_134252	transient receptor potential cation channel, subfamily M, member 8	A	-1.197	4.63	0.13845	3808
Ucp3	A_52_P380379	NM_009464	uncoupling protein 3 (mitochondrial, proton carrier)	A	1.046	25.31	0.304	6371
Upk1b	A_51_P113195	NM_178924	uroplakin 1B	A	-1.199	1.18	0.02003	853