Supplementary Table 3: The Correlation Coefficients between each of the significantly changed genes (313 probe sets), as identified by SAM ≥2 fold and 0% FDR), and each of the significantly changed transcription factors. The gradient of colors highlights increasing CC values (yellow: 0.9400-0.9499, light orange: 0.9500-0.9599, orange: 0.9600-0.9699, dark orange: 0.9700-0/9799, red ≥0.9800).

Probe Set ID	Gene Title	Gene Symbol	Esrrg	Arid5b	Klf13	Lhx6	Jun *	Nab2	E2f8
1415776_at	aldehyde dehydrogenase family 3, subfamily A2	Aldh3a2	0.9748	-0.9634	-0.9228	0.8629	0.7977	-0.8831	0.7803
1415777_at	pancreatic lipase related protein 1	Pnliprp1	0.9057	-0.9105	-0.8867	0.8916	0.7315	-0.7676	0.7045
1415802_at	solute carrier family 16 (monocarboxylic acid trans	Slc16a1	0.8330	-0.8556	-0.8437	0.9147	0.8821	-0.7719	0.8309
1415904_at	lipoprotein lipase	Lpl	0.9216	-0.9309	-0.9533	0.9192	0.8503	-0.7842	0.7772
1415932_x_at	ATPase, class II, type 9A	Atp9a	0.9706	-0.9702	-0.9300	0.9011	0.8022	-0.8219	0.7799
1415965_at	stearoyl-Coenzyme A desaturase 1	Scd1	0.8493	-0.8324	-0.8991	0.8383	0.8630	-0.6922	0.7252
1416023_at	stearoyl-Coenzyme A desaturase 1	Fabp3	0.9021	-0.9401	-0.9150	0.9144	0.7989	-0.8574	0.8782
1416066_at	CD9 antigen	Cd9	0.7587	-0.8161	-0.8594	0.8993	0.8382	-0.6810	0.8619
1416101_a_at	histone cluster 1, H1c	Hist1h1c	0.8337	-0.8811	-0.9238	0.9429	0.8906	-0.7754	0.8330
1416308_at	UDP-glucose dehydrogenase	Ugdh	0.8781	-0.8945	-0.8987	0.8075	0.8542	-0.7684	0.6868
1416488_at	cyclin G2	Ccng2	0.9130	-0.9140	-0.8708	0.8693	0.9140	-0.8644	0.7810
1416590_a_at	RAB34, member of RAS oncogene family	Rab34	0.8809	-0.9333	-0.8586	0.8541	0.6708	-0.7100	0.7102
1416591_at	RAB34, member of RAS oncogene family	Rab34	0.9296	-0.9515	-0.8972	0.8861	0.7236	-0.8011	0.8015
1416632_at	malic enzyme 1, NADP(+)-dependent, cytosolic ///	Mod1	0.9813	-0.9276	-0.8866	0.8403	0.8147	-0.8604	0.7608
1416896_at	ribosomal protein S6 kinase polypeptide 1	Rps6ka1	0.8818	-0.8741	-0.8337	0.8594	0.7396	-0.7593	0.7649
1416930_at	lymphocyte antigen 6 complex, locus D	Ly6d	0.9601	-0.9386	-0.9449	0.8940	0.8694	-0.7916	0.7225
1417008_at	carnitine acetyltransferase	Crat	0.9541	-0.9336	-0.9104	0.8663	0.8289	-0.8085	0.7987
1417017_at	cytochrome P450, family 17, subfamily a, polypept	Cyp17a1	-0.7635	0.8507	0.9248	-0.9483	-0.7058	0.6754	-0.6350
1417177_at	galactokinase 1	Galk1	0.9783	-0.9631	-0.9108	0.8647	0.8400	-0.8444	0.8115
1417268_at	CD14 antigen	Cd14	0.8088	-0.7491	-0.7775	0.6949	0.8149	-0.6077	0.6971
1417273_at	pyruvate dehydrogenase kinase, isoenzyme 4	Pdk4	0.9257	-0.9474	-0.9180	0.9424	0.8187	-0.8430	0.8433
1417336_a_at	synaptotagmin-like 4	Sytl4	0.9228	-0.9326	-0.8870	0.8107	0.7529	-0.7038	0.5537
1417409_at	Jun oncogene	Jun	0.8690	-0.8536	-0.8866	0.8594	0.9721	-0.7317	0.6423
1417449_at	acyl-CoA thioesterase 8	Acot8	0.9761	-0.9410	-0.8729	0.8158	0.7487	-0.8546	0.8107
1417629_at	proline dehydrogenase	Prodh	-0.8163	0.7943	0.8396	-0.8524	-0.8157	0.6632	-0.8167
1417761_at	apolipoprotein A-IV	Apoa4	-0.9760	0.9730	0.8853	-0.8107	-0.7422	0.9027	-0.6803
1417785_at	phospholipase A1 member A	Pla1a	-0.9323	0.9208	0.9013	-0.8976	-0.8421	0.8496	-0.8782
1417860_a_at	spondin 2, extracellular matrix protein	Spon2	0.8641	-0.9121	-0.8910	0.8754	0.8433	-0.8141	0.8026
1417867_at	complement factor D (adipsin)	Cfd	0.8664	-0.8936	-0.9025	0.8398	0.7005	-0.7552	0.7927
1417879_at	neuron derived neurotrophic factor	Nenf	0.8721	-0.8625	-0.8600	0.7770	0.6628	-0.7279	0.7600
1417883_at	glutathione S-transferase, theta 2	Gstt2	0.9104	-0.9012	-0.9289	0.8532	0.7447	-0.7821	0.7046

1417900_a_at	very low density lipoprotein receptor	Vldlr	0.9616	-0.9423	-0.9401	0.8481	0.8141	-0.8075	0.6945
1417930_at	Ngfi-A binding protein 2	Nab2	-0.8830	0.8820	0.8300	-0.7809	-0.6804	1.0000	-0.6918
1417963_at	phospholipid transfer protein	Pltp	0.9663	-0.9529	-0.9266	0.8866	0.8595	-0.8445	0.7892
1418013_at	camello-like 1	Cml1	-0.9670	0.9390	0.8487	-0.7617	-0.7344	0.9170	-0.6958
1418050_at	glycosylphosphatidylinositol specific phospholipas	Gpld1	-0.8653	0.8473	0.8999	-0.8796	-0.8416	0.6771	-0.7400
1418073_at	acyl-CoA thioesterase 9	Acot9	0.9287	-0.9333	-0.9685	0.8974	0.9020	-0.8097	0.6729
1418123_at	unc-119 homolog (C. elegans)	Unc119	0.9149	-0.9285	-0.9009	0.8604	0.7429	-0.7835	0.8149
1418181_at	protein tyrosine phosphatase 4a3	Ptp4a3	0.8793	-0.8950	-0.8934	0.9172	0.8236	-0.7084	0.7945
1418210_at	profilin 2	Pfn2	0.9223	-0.9089	-0.9142	0.8436	0.8941	-0.8011	0.7731
1418213_at	keratin 23	Krt23	0.8842	-0.8745	-0.9291	0.8889	0.8853	-0.6915	0.6773
1418321_at	dodecenoyl-Coenzyme A delta isomerase (3,2 trar	Dci	0.9638	-0.9451	-0.9045	0.8633	0.8679	-0.8361	0.8283
1418328_at	carnitine palmitoyltransferase 1b, muscle /// cholin	Cpt1b /// Chkb-cpt1	0.8935	-0.8855	-0.8950	0.8231	0.8964	-0.7590	0.6623
1418438_at	fatty acid binding protein 2, intestinal	Fabp2	0.9672	-0.9646	-0.9284	0.9003	0.8144	-0.8428	0.8295
1418486_at	vanin 1	Vnn1	0.9832	-0.9450	-0.8904	0.8327	0.8237	-0.8761	0.7983
1418652_at	chemokine (C-X-C motif) ligand 9	Cxcl9	0.6628	-0.7395	-0.8131	0.8159	0.8901	-0.6231	0.5968
1418653_at	cytochrome P450, family 2, subfamily c, polypeptic	Cyp2c50	-0.8103	0.7866	0.8713	-0.8523	-0.7703	0.7348	-0.7017
1418654_at	hydroxyacid oxidase (glycolate oxidase) 3	Hao3	0.8178	-0.7725	-0.7775	0.7085	0.6678	-0.5597	0.5800
1418808_at	retinol dehydrogenase 5	Rdh5	-0.9641	0.9552	0.8863	-0.8290	-0.8221	0.8438	-0.7331
1418833_at	alanine-glyoxylate aminotransferase	Agxt	-0.9442	0.8904	0.8007	-0.7571	-0.6913	0.9305	-0.7747
1418949_at	growth differentiation factor 15	Gdf15	0.7602	-0.7997	-0.8395	0.8078	0.9149	-0.7032	0.6945
1418989_at	cathepsin E	Ctse	0.9295	-0.9594	-0.9502	0.9403	0.8754	-0.8390	0.8070
1419091_a_at	annexin A2	Anxa2	0.8814	-0.8955	-0.8661	0.8926	0.7453	-0.7362	0.6996
1419103_a_at	abhydrolase domain containing 6	Abhd6	0.9581	-0.9196	-0.8833	0.8328	0.7811	-0.8386	0.7966
1419104_at	abhydrolase domain containing 6	Abhd6	0.9288	-0.8635	-0.8273	0.7307	0.6338	-0.8146	0.6358
1419173_at	aminoacylase 1	Acy1	-0.9164	0.9269	0.9043	-0.9248	-0.8846	0.8166	-0.8458
1419349_a_at	cytochrome P450, family 2, subfamily d, polypeptic	Cyp2d9	0.8742	-0.9315	-0.9125	0.9256	0.8686	-0.8096	0.7275
1419365_at	peroxisomal biogenesis factor 11a	Pex11a	0.9736	-0.9498	-0.9206	0.8625	0.8427	-0.8629	0.7879
1419382_a_at	dehydrogenase/reductase (SDR family) member 4	Dhrs4	0.9404	-0.9323	-0.9090	0.8763	0.7734	-0.8564	0.8231
1419435_at	aldehyde oxidase 1	Aox1	0.9398	-0.9449	-0.9404	0.9158	0.8577	-0.9123	0.8164
1419491_at	defensin beta 1	Defb1	0.8870	-0.9014	-0.9095	0.8882	0.8638	-0.7782	0.6728
1419492_s_at	defensin beta 1	Defb1	0.7757	-0.8053	-0.8232	0.8355	0.9188	-0.7094	0.7352
1419504_at	monoacylglycerol O-acyltransferase 1 /// similar to	Mogat1 /// LOC100	0.9575	-0.9545	-0.9474	0.9327	0.8834	-0.8201	0.7687
1419559_at	cytochrome P450, family 4, subfamily f, polypeptid	Cyp4f14	-0.9415	0.9710	0.9769	-0.9348	-0.8669	0.8417	-0.7260
1419573_a_at	lectin, galactose binding, soluble 1	Lgals1	0.9485	-0.9277	-0.9131	0.8581	0.8045	-0.7470	0.7361
1419738_a_at	tropomyosin 2, beta	Tpm2	0.9403	-0.9105	-0.9097	0.8409	0.8148	-0.7879	0.7091
1419857_at	---	---	-0.8748	0.8606	0.9086	-0.8843	-0.8207	0.7461	-0.7653
1420405_at	solute carrier organic anion transporter family, mer	Slco1a4	-0.8405	0.8300	0.8848	-0.8839	-0.8707	0.6823	-0.7996
1420541_at	retinol dehydrogenase 16	Rdh16	0.9635	-0.9222	-0.8068	0.7473	0.7899	-0.8080	0.7285

1420603_s_at	retinoic acid early transcript 1, alpha /// retinoic aci	Raet1a /// Raet1b /	0.8207	-0.7894	-0.7836	0.6553	0.6390	-0.5873	0.4390
1420657_at	uncoupling protein 3 (mitochondrial, proton carrier)	Ucp3	0.7445	-0.7761	-0.8316	0.8758	0.6613	-0.6249	0.6399
1420722_at	elongation of very long chain fatty acids (FEN1/Elo	Elovl3	0.9015	-0.9070	-0.8453	0.7809	0.7286	-0.7558	0.6039
1420836_at	solute carrier family 25, member 30	Slc25a30	0.8548	-0.8043	-0.7897	0.7641	0.6720	-0.7466	0.7865
1420973_at	AT rich interactive domain 5B (Mrf1 like) /// similar	Arid5b /// LOC1000	-0.9656	1.0000	0.9559	-0.9165	-0.8147	0.8820	-0.7324
1421011_at	hydroxysteroid (17-beta) dehydrogenase 11	Hsd17b11	0.9449	-0.9628	-0.9446	0.9481	0.8438	-0.8491	0.8166
1421116_a_at	reticulon 4	Rtn4	0.9532	-0.9392	-0.9102	0.8086	0.8048	-0.7971	0.6731
1421214_at	cytidine monophospho-N-acetylneuraminic acid hy	Cmah	-0.9351	0.9679	0.9183	-0.8442	-0.7833	0.8430	-0.6115
1421422_at	RIKEN cDNA 5033411D12 gene	5033411D12Rik	0.9306	-0.9653	-0.9588	0.9129	0.8251	-0.8662	0.7862
1421425_a_at	regulator of calcineurin 2	Rcan2	0.9670	-0.9545	-0.9325	0.8598	0.8134	-0.8110	0.6835
1421430_at	RAD51-like 1 (S. cerevisiae)	Rad51l1	0.9551	-0.9595	-0.9171	0.9019	0.8410	-0.8601	0.8623
1421848_at	solute carrier family 22 (organic cation transporter)	Slc22a5	0.9515	-0.9141	-0.8627	0.7834	0.6668	-0.8463	0.7324
1421878_at	mitogen-activated protein kinase 9	Mapk9	0.8997	-0.9554	-0.9609	0.8720	0.7492	-0.8301	0.6580
1422076_at	acyl-CoA thioesterase 4	Acot4	0.8473	-0.7955	-0.7555	0.6836	0.5604	-0.7083	0.7404
1422146_at	sema domain, seven thrombospondin repeats (typ	Sema5b	0.8699	-0.8712	-0.8804	0.8139	0.7572	-0.6345	0.6907
1422147_a_at	phospholipase A2, group VI	Pla2g6	0.8827	-0.8791	-0.9057	0.8875	0.7688	-0.7409	0.7991
1422262_a_at	LIM homeobox protein 6	Lhx6	0.8367	-0.9165	-0.9624	1.0000	0.8521	-0.7809	0.6987
1422438_at	epoxide hydrolase 1, microsomal	Ephx1	0.8995	-0.9176	-0.9242	0.9146	0.8298	-0.8126	0.8654
1422445_at	integrin alpha 6	Itga6	0.8818	-0.9125	-0.8796	0.8368	0.7053	-0.7344	0.7229
1422701_at	zeta-chain (TCR) associated protein kinase	Zap70	-0.9245	0.9614	0.9466	-0.8795	-0.7670	0.9405	-0.6621
1422811_at	solute carrier family 27 (fatty acid transporter), mer	Slc27a1	0.9654	-0.9554	-0.9487	0.9075	0.8571	-0.7955	0.6893
1422815_at	complement component 9	C9	-0.9526	0.9196	0.7840	-0.7160	-0.6433	0.8889	-0.7205
1422906_at	ATP-binding cassette, sub-family G (WHITE), men	Abcg2	0.9631	-0.9723	-0.9424	0.9344	0.8849	-0.8638	0.8007
1422943_a_at	heat shock protein 1	Hspb1	0.8805	-0.9073	-0.8605	0.8907	0.8076	-0.8515	0.9267
1422996_at	acyl-CoA thioesterase 2	Acot2	0.9490	-0.9377	-0.9257	0.8632	0.8122	-0.7865	0.6912
1422997_s_at	acyl-CoA thioesterase 1 /// acyl-CoA thioesterase	Acot1 /// Acot2 /// L	0.9574	-0.9459	-0.9250	0.8920	0.8324	-0.8468	0.8454
1423017_a_at	interleukin 1 receptor antagonist	Il1rn	0.8464	-0.8280	-0.8831	0.8262	0.7852	-0.6248	0.6728
1423166_at	CD36 antigen	Cd36	0.9601	-0.9563	-0.9389	0.8921	0.8803	-0.8160	0.8035
1423186_at	T-cell lymphoma invasion and metastasis 2	Tiam2	-0.9111	0.9022	0.8512	-0.7723	-0.6882	0.9120	-0.7058
1423266_at	RIKEN cDNA 2810405K02 gene	2810405K02Rik	0.9404	-0.9298	-0.9079	0.8434	0.7363	-0.8402	0.7667
1423308_at	trans-golgi network protein /// hypothetical protein	Tgoln1 /// LOC100	0.9297	-0.9223	-0.9098	0.9011	0.8819	-0.8006	0.8308
1423447_at	caseinolytic peptidase X (E.coli)	Clpx	0.8169	-0.8242	-0.8084	0.7825	0.9028	-0.7979	0.6635
1423669_at	collagen, type I, alpha 1	Col1a1	0.8525	-0.8671	-0.8996	0.8218	0.7356	-0.7661	0.6394
1423844_s_at	cystathionine beta-synthase	Cbs	-0.9150	0.8589	0.7832	-0.7509	-0.6388	0.8440	-0.7943
1424118_a_at	SPC25, NDC80 kinetochore complex component,	Spc25	0.9230	-0.9408	-0.9221	0.9004	0.8343	-0.8394	0.8384
1424133_at	transmembrane protein 98	Tmem98	0.9660	-0.9314	-0.9110	0.8250	0.8159	-0.7793	0.6816
1424167_a_at	phosphomannomutase 1	Pmm1	0.9490	-0.9496	-0.9216	0.8755	0.8411	-0.8153	0.8389
1424245_at	carboxylesterase 2 /// similar to Carboxylesterase	Ces2 /// LOC6677	0.8672	-0.7931	-0.7886	0.6720	0.8402	-0.6520	0.4541

1424273_at	cytochrome P450, family 2, subfamily c, polypeptid	Cyp2c70	-0.9412	0.9262	0.8218	-0.7804	-0.6620	0.8730	-0.6986
1424282_at	PET112-like (yeast)	Pet112l	0.9026	-0.8838	-0.8942	0.8589	0.8552	-0.6625	0.7095
1424352_at	cytochrome P450, family 4, subfamily a, polypeptid	Cyp4a12b /// Cyp4	0.8253	-0.8771	-0.8525	0.9037	0.8305	-0.7973	0.7880
1424367_a_at	homer homolog 2 (Drosophila)	Homer2	-0.9040	0.9565	0.9706	-0.9581	-0.8514	0.7689	-0.7360
1424401_at	aldehyde dehydrogenase 1 family, member L1	Aldh1l1	-0.8875	0.8661	0.9016	-0.8188	-0.7527	0.8070	-0.7277
1424715_at	retinol saturase (all trans retinol 13,14 reductase)	Retsat	0.9258	-0.9217	-0.8905	0.8748	0.8353	-0.8485	0.8512
1424716_at	retinol saturase (all trans retinol 13,14 reductase)	Retsat	0.9467	-0.9534	-0.9479	0.9365	0.8894	-0.8529	0.8187
1424790_at	solute carrier family 25, member 42	Slc25a42	0.8848	-0.8784	-0.8343	0.8642	0.7324	-0.8820	0.8365
1424826_s_at	metastasis suppressor 1	Mtss1	-0.9087	0.9367	0.9592	-0.9477	-0.9090	0.7460	-0.7064
1424835_at	glutathione S-transferase, mu 4	Gstm4	0.9534	-0.9266	-0.8678	0.7958	0.7378	-0.8140	0.7695
1424869_at	dehydrogenase/reductase (SDR family) member 7	Dhrs7b /// LOC100	0.9458	-0.9187	-0.9225	0.8676	0.8440	-0.7662	0.6511
1424904_at	RIKEN cDNA 1300010F03 gene	1300010F03Rik	0.9674	-0.9244	-0.8733	0.7856	0.7110	-0.8003	0.6728
1424934_at	UDP glucuronosyltransferase 2 family, polypeptide	Ugt2b1	-0.9688	0.9768	0.9519	-0.8859	-0.8574	0.8576	-0.7194
1424943_at	cytochrome P450, family 4, subfamily a, polypeptid	Cyp4a31	0.9187	-0.9321	-0.9125	0.8966	0.7602	-0.8351	0.7511
1425028_a_at	tropomyosin 2, beta	Tpm2	0.9629	-0.9322	-0.9134	0.8576	0.8538	-0.8296	0.7254
1425109_at	solute carrier family 44, member 3	Slc44a3	0.7893	-0.8690	-0.8715	0.9119	0.6712	-0.7593	0.8487
1425120_x_at	RIKEN cDNA 1810023F06 gene	1810023F06Rik	0.6932	-0.6626	-0.7246	0.6565	0.6431	-0.4366	0.5489
1425409_at	cholinergic receptor, nicotinic, alpha polypeptide 2	Chrna2	0.9170	-0.8472	-0.8037	0.7808	0.7557	-0.8145	0.8461
1425623_a_at	cystathionine beta-synthase	Cbs	-0.9328	0.8910	0.8402	-0.7980	-0.6901	0.8777	-0.7731
1425751_at	cDNA sequence BC014805	BC014805	-0.8574	0.8936	0.9256	-0.9172	-0.8477	0.7437	-0.7727
1425752_at	cDNA sequence BC014805	BC014805	-0.8429	0.8808	0.9038	-0.8855	-0.8483	0.7015	-0.7458
1425948_a_at	solute carrier family 25, member 30	Slc25a30	0.8561	-0.8008	-0.8193	0.7656	0.6633	-0.6992	0.6966
1425964_x_at	heat shock protein 1	Hspb1	0.8550	-0.8918	-0.8363	0.8664	0.7336	-0.8354	0.9473
1426146_a_at	choline phosphotransferase 1	Chpt1	0.9564	-0.9634	-0.9128	0.8832	0.7911	-0.8838	0.7974
1426389_at	calcium/calmodulin-dependent protein kinase ID	Camk1d	-0.8915	0.8404	0.8679	-0.8341	-0.8129	0.8210	-0.7759
1426452_a_at	RAB30, member RAS oncogene family	Rab30	0.9378	-0.9024	-0.8725	0.8589	0.8353	-0.8936	0.8581
1426785_s_at	monoglyceride lipase	Mgll	0.9344	-0.9166	-0.8899	0.8255	0.6875	-0.8503	0.7961
1426857_a_at	hydroxysteroid dehydrogenase like 2	Hsdl2	0.9787	-0.9557	-0.9343	0.8877	0.8286	-0.8935	0.7874
1426989_at	calsyntenin 3	Clstn3	0.9258	-0.9243	-0.9197	0.8551	0.7359	-0.7536	0.7321
1427005_at	polo-like kinase 2 (Drosophila)	Plk2	0.6930	-0.6751	-0.7886	0.7954	0.7741	-0.4658	0.4888
1427126_at	heat shock protein 1B	Hspa1b	0.8210	-0.8663	-0.8006	0.8773	0.6981	-0.7821	0.6703
1427347_s_at	tubulin, beta 2a	Tubb2a	0.8096	-0.8313	-0.7955	0.8428	0.8882	-0.7678	0.7743
1427472_a_at	complement component 8, beta subunit	C8b	-0.9278	0.8777	0.7369	-0.6408	-0.6073	0.8889	-0.6102
1427604_a_at	ATPase, class II, type 9A	Atp9a	0.9386	-0.9354	-0.9391	0.9018	0.8213	-0.7578	0.7518
1427631_x_at	major urinary protein 3	Mup3	-0.9292	0.9314	0.9466	-0.8871	-0.7987	0.9175	-0.6863
1427943_at	acylphosphatase 2, muscle type	Acyp2	0.8739	-0.8736	-0.8954	0.9008	0.7751	-0.7631	0.7923
1427981_a_at	cysteine sulfinic acid decarboxylase	Csad	0.8526	-0.8816	-0.8778	0.8784	0.7550	-0.8106	0.9141
1428083_at	RIKEN cDNA 2310043N10 gene	2310043N10Rik	0.9250	-0.9522	-0.9510	0.8835	0.7751	-0.7868	0.7346

1428176_at	endothelial differentiation, sphingolipid G-protein-c	Edg5	0.8390	-0.8342	-0.8797	0.7814	0.7702	-0.7043	0.7229
1428372_at	suppression of tumorigenicity 5	St5	0.9026	-0.9089	-0.9092	0.9392	0.9144	-0.8074	0.7773
1428512_at	basic helix-loop-helix domain containing, class B9	Bhlhb9	0.9110	-0.9192	-0.9312	0.8717	0.7317	-0.7700	0.7107
1428559_at	3-ketodihydrosphingosine reductase	Kdsr	0.9160	-0.8978	-0.9261	0.8244	0.8348	-0.7663	0.6984
1428739_at	RIKEN cDNA 2310040A07 gene	2310040A07Rik	-0.9608	0.9320	0.8286	-0.7474	-0.7444	0.7910	-0.7512
1428803_at	acyl-CoA thioesterase 6	Acot6	0.8961	-0.9201	-0.9364	0.8921	0.7948	-0.8192	0.8040
1429154_at	solute carrier family 35, member F2 /// similar to Sc	Slc35f2 /// LOC100	0.9013	-0.8737	-0.8285	0.8390	0.8434	-0.7812	0.7899
1429212_a_at	leucine rich repeat containing 51	Lrrc51	0.9074	-0.8855	-0.8877	0.8949	0.8401	-0.7368	0.7233
1429399_at	ring finger protein 125	Rnf125	0.8820	-0.8838	-0.9273	0.8869	0.9409	-0.7700	0.6504
1429523_a_at	solute carrier family 39 (metal ion transporter), mei	Slc39a5	0.9655	-0.9497	-0.9266	0.8900	0.8823	-0.8227	0.8226
1429570_at	mixed lineage kinase domain-like	Mlkl	0.6880	-0.7077	-0.8279	0.8007	0.6819	-0.4832	0.4790
1429786_a_at	ZW10 interactor	Zwint	0.9627	-0.9696	-0.9174	0.8958	0.8766	-0.8570	0.7953
1429859_a_at	ADP-ribosylation factor-like 2 binding protein	Arl2bp	0.8600	-0.8747	-0.8914	0.8157	0.7220	-0.6876	0.6780
1429947_a_at	Z-DNA binding protein 1	Zbp1	0.8399	-0.8726	-0.8958	0.7906	0.8110	-0.7069	0.4189
1430307_a_at	malic enzyme 1, NADP(+)-dependent, cytosolic ///	Mod1	0.9697	-0.9309	-0.9019	0.8509	0.8448	-0.8549	0.7585
1430388_a_at	sulfatase 2	Sulf2	0.7908	-0.8498	-0.8614	0.9318	0.7780	-0.6931	0.8094
1430700_a_at	phospholipase A2, group VII (platelet-activating fac	Pla2g7	0.8592	-0.8612	-0.8472	0.8336	0.8914	-0.7385	0.6244
1430780_a_at	phosphomannomutase 1	Pmm1	0.9562	-0.9683	-0.9398	0.8830	0.8679	-0.7977	0.7503
1431056_a_at	lipoprotein lipase	Lpl	0.8904	-0.8995	-0.9343	0.8864	0.8929	-0.7468	0.7225
1431278_s_at	phospholipase A2, group VI	Pla2g6	0.8494	-0.8281	-0.8511	0.7694	0.6368	-0.6567	0.6441
1432517_a_at	nicotinamide N-methyltransferase	Nnmt	-0.9629	0.9357	0.9059	-0.8610	-0.7724	0.9214	-0.7650
1432543_a_at	Kruppel-like factor 13	Klf13	-0.9021	0.9559	1.0000	-0.9624	-0.8529	0.8300	-0.6651
1432562_at	RIKEN cDNA 1110006G14 gene	1110006G14Rik	0.8840	-0.8937	-0.9266	0.8930	0.8407	-0.7923	0.7864
1433601_at	adrenergic receptor, alpha 2a	Adra2a	0.8590	-0.8772	-0.8610	0.9117	0.8654	-0.7926	0.7656
1433691_at	protein phosphatase 1, regulatory (inhibitor) subun	Ppp1r3c	0.8019	-0.8259	-0.7806	0.7793	0.8958	-0.7389	0.6626
1433779_at	cancer susceptibility candidate 4	Casc4	0.9048	-0.9460	-0.9274	0.9430	0.8231	-0.7998	0.7572
1433898_at	---	---	0.8812	-0.8578	-0.8366	0.8436	0.7220	-0.8196	0.7981
1433924_at	---	---	0.7852	-0.8616	-0.8026	0.8475	0.6857	-0.8133	0.9103
1434036_at	metastasis suppressor 1	Mtss1	-0.9733	0.9825	0.9519	-0.9182	-0.8722	0.8899	-0.7425
1434089_at	synaptopodin	Synpo	0.8551	-0.8033	-0.8402	0.7588	0.7485	-0.6330	0.6689
1434109_at	SH3 domain binding glutamic acid-rich protein like	Sh3bgrl2	0.9289	-0.9326	-0.9223	0.8935	0.7272	-0.8655	0.8004
1434170_at	WD repeat domain 40B	Wdr40b	0.8705	-0.9221	-0.9761	0.9311	0.7807	-0.8664	0.6686
1434382_at	serine incorporator 2 /// hypothetical protein LOC1(	Serinc2 /// LOC100	0.9585	-0.9540	-0.9123	0.8772	0.7879	-0.8406	0.8521
1434465_x_at	very low density lipoprotein receptor	Vldlr	0.9387	-0.9299	-0.9377	0.8689	0.8402	-0.7617	0.7623
1434582_at	ELKS/RAB6-interacting/CAST family member 2	Erc2	0.8040	-0.8353	-0.8372	0.8190	0.7264	-0.7328	0.9023
1434599_a_at	tight junction protein 2	Tjp2	0.8474	-0.8986	-0.9507	0.9645	0.8304	-0.7599	0.6033
1434642_at	hydroxysteroid (17-beta) dehydrogenase 11	Hsd17b11	0.9143	-0.9241	-0.9053	0.8893	0.8386	-0.8311	0.8461
1434671_at	RIKEN cDNA B230337E12 gene	B230337E12Rik	0.9511	-0.9444	-0.9019	0.8950	0.7589	-0.8276	0.7734

1434897_a_at	solute carrier family 25 (mitochondrial carrier, ader	Slc25a4	0.9358	-0.9329	-0.9235	0.8879	0.8410	-0.7652	0.6603
1435084_at	RIKEN cDNA C730049O14 gene	C730049O14Rik	0.8774	-0.8971	-0.9249	0.8994	0.9474	-0.7729	0.7465
1435196_at	neurotrophic tyrosine kinase, receptor, type 2	Ntrk2	-0.8512	0.8252	0.8490	-0.8264	-0.7255	0.8608	-0.7081
1435245_at	glutaminase 2 (liver, mitochondrial)	Gls2	-0.9390	0.8996	0.7825	-0.7172	-0.6289	0.9133	-0.6751
1435254_at	plexin B1	Plxnb1	-0.9500	0.9251	0.9363	-0.9052	-0.9144	0.8374	-0.6827
1435255_at	plexin B1	Plxnb1	-0.9639	0.9463	0.8956	-0.8256	-0.7494	0.8825	-0.7279
1435275_at	cytochrome c oxidase subunit VIb polypeptide 2	Cox6b2	0.9506	-0.9391	-0.9449	0.9059	0.8975	-0.8192	0.7595
1435394_s_at	ras homolog gene family, member C	Rhoc	0.8184	-0.8442	-0.9041	0.9355	0.8673	-0.6626	0.7734
1435446_a_at	choline phosphotransferase 1	Chpt1	0.9546	-0.9691	-0.9192	0.8963	0.8666	-0.8883	0.8266
1435549_at	transient receptor potential cation channel, subfam	Trpm4	0.9351	-0.9565	-0.9224	0.8971	0.7893	-0.7860	0.7814
1435658_at	solute carrier family 27 (fatty acid transporter), mer	Slc27a1	0.9154	-0.8994	-0.8940	0.8117	0.6989	-0.7268	0.6375
1435666_at	microtubule associated serine/threonine kinase 3	Mast3	-0.9113	0.9113	0.9278	-0.8761	-0.7732	0.7618	-0.7737
1435893_at	very low density lipoprotein receptor	Vldlr	0.9034	-0.9037	-0.9409	0.8844	0.8967	-0.7458	0.7274
1435902_at	nudix (nucleoside diphosphate linked moiety X)-typ	Nudt18	0.8233	-0.8761	-0.9035	0.8669	0.7693	-0.7217	0.6740
1435963_at	sema domain, seven thrombospondin repeats (typ	Sema5b	0.8716	-0.8817	-0.7967	0.7947	0.6854	-0.7903	0.7825
1436038_a_at	phosphatidylinositol glycan anchor biosynthesis, cl	Pigp	0.8932	-0.8877	-0.9275	0.8863	0.7831	-0.7586	0.7611
1436186_at	E2F transcription factor 8	E2f8	0.7303	-0.7324	-0.6651	0.6987	0.6344	-0.6918	1.0000
1436313_at	SCY1-like 2 (S. cerevisiae)	Scyl2	0.9317	-0.9528	-0.9399	0.9196	0.8759	-0.8507	0.8189
1436314_at	SCY1-like 2 (S. cerevisiae)	Scyl2	0.9022	-0.9548	-0.9187	0.9289	0.7745	-0.9056	0.8391
1436504_x_at	apolipoprotein A-IV	Apoa4	-0.9819	0.9882	0.9459	-0.8851	-0.7958	0.9207	-0.7083
1436890_at	UDP-N-acteylglucosamine pyrophosphorylase 1-lik	Uap1l1	0.9379	-0.9245	-0.8725	0.8116	0.7241	-0.7914	0.7803
1436994_a_at	histone cluster 1, H1c	Hist1h1c	0.7889	-0.8325	-0.9074	0.9185	0.8748	-0.7532	0.6996
1437040_at	ethanolamine kinase 2	Etnk2	-0.9012	0.9240	0.9638	-0.9429	-0.8611	0.7594	-0.7592
1437073_x_at	---	---	0.8202	-0.7767	-0.7672	0.7568	0.6414	-0.7449	0.8286
1437455_a_at	B-cell translocation gene 1, anti-proliferative /// sim	Btg1 /// LOC10004	0.9016	-0.9124	-0.9421	0.9119	0.9173	-0.8783	0.7286
1437496_at	RIKEN cDNA 9330129D05 gene	9330129D05Rik	0.9424	-0.9282	-0.9213	0.8357	0.8335	-0.7932	0.6422
1437580_s_at	NIMA (never in mitosis gene a)-related expressed	Nek2	0.9340	-0.8772	-0.8176	0.7252	0.8397	-0.7686	0.7219
1437590_at	RIKEN cDNA 4833409A17 gene	4833409A17Rik	0.8432	-0.7898	-0.8473	0.7959	0.8304	-0.6734	0.6792
1437724_x_at	phosphatidylinositol membrane-associated 1	Pitpnm1	0.9317	-0.9330	-0.9203	0.9131	0.9330	-0.8442	0.7276
1438001_x_at	receptor accessory protein 5	Reep5	0.8114	-0.8316	-0.8351	0.7873	0.6414	-0.6636	0.8270
1438258_at	very low density lipoprotein receptor	Vldlr	0.8858	-0.9517	-0.9351	0.8730	0.8367	-0.7701	0.6638
1438310_at	---	---	0.9361	-0.9428	-0.9497	0.9299	0.8227	-0.8046	0.7808
1438448_at	otopetrin 1	Otop1	0.9455	-0.9453	-0.9340	0.9308	0.8581	-0.8084	0.7307
1438659_x_at	coiled-coil-helix-coiled-coil-helix domain containing	Chchd6	0.8848	-0.8468	-0.8478	0.7422	0.7671	-0.6916	0.6220
1438676_at	macrophage activation 2 like	Mpa2l	0.8990	-0.9212	-0.9299	0.8377	0.8458	-0.7689	0.5602
1438740_at	N-myristoyltransferase 2	Nmt2	0.9132	-0.8787	-0.8675	0.8186	0.7178	-0.8198	0.7959
1439293_at	cDNA sequence BC031353	BC031353	-0.8025	0.8446	0.9408	-0.9436	-0.8569	0.7311	-0.7377
1439478_at	acyl-CoA thioesterase 2	Acot2	0.9129	-0.9089	-0.8844	0.8635	0.8671	-0.7950	0.8454

1439795_at	G protein-coupled receptor 64	Gpr64	0.8972	-0.8711	-0.7897	0.7644	0.5928	-0.8212	0.8323
1440134_at	cytochrome P450, family 4, subfamily a, polypepti	Cyp4a31	0.9451	-0.9576	-0.9514	0.9192	0.8637	-0.8507	0.8182
1440178_x_at	zeta-chain (TCR) associated protein kinase	Zap70	-0.8929	0.9030	0.8864	-0.8084	-0.6943	0.9676	-0.5597
1441768_at	RIKEN cDNA 9430051O21 gene	9430051O21Rik	-0.9060	0.9253	0.9285	-0.8880	-0.7867	0.8493	-0.8657
1441919_x_at	carnitine acetyltransferase	Crat	0.8241	-0.7839	-0.7740	0.6700	0.6193	-0.7744	0.7751
1441971_at	---	---	0.9240	-0.9599	-0.9317	0.9129	0.8062	-0.8907	0.8734
1442331_at	---	---	-0.9603	0.9799	0.9640	-0.8936	-0.8168	0.9128	-0.6970
1442508_at	RIKEN cDNA 4933404M19 gene	4933404M19Rik	0.9277	-0.9608	-0.9541	0.9318	0.8127	-0.8275	0.8368
1443180_at	---	---	-0.9762	0.9590	0.8751	-0.8124	-0.7267	0.9193	-0.7757
1443603_at	---	---	-0.8942	0.8823	0.8811	-0.8107	-0.6588	0.8235	-0.6565
1443870_at	ATP-binding cassette, sub-family C (CFTR/MRP),	Abcc4	0.9441	-0.9293	-0.9463	0.8685	0.8500	-0.7637	0.6702
1443902_at	RIKEN cDNA 6430573F11 gene	6430573F11Rik	0.9086	-0.9144	-0.9028	0.9110	0.7988	-0.8235	0.6948
1445597_s_at	HRAS like suppressor 3	Hrasls3	0.9032	-0.9119	-0.8287	0.7148	0.7083	-0.7199	0.5934
1446284_at	metastasis suppressor 1	Mtss1	-0.8919	0.9057	0.9124	-0.9158	-0.8270	0.7601	-0.8475
1446423_at	---	---	0.9377	-0.9274	-0.8948	0.8499	0.8665	-0.8703	0.8336
1447186_at	solute carrier family 6, member 16	Slc6a16	0.9406	-0.9312	-0.8759	0.7947	0.6723	-0.7656	0.5960
1447458_at	---	---	-0.9313	0.9441	0.9633	-0.8664	-0.8200	0.8385	-0.5819
1447602_x_at	sulfatase 2	Sulf2	0.6541	-0.7358	-0.7783	0.8146	0.6208	-0.5572	0.8478
1447774_x_at	RIKEN cDNA 5730469M10 gene	5730469M10Rik	0.8846	-0.8674	-0.8666	0.7970	0.7915	-0.7372	0.5693
1447845_s_at	vanin 1	Vnn1	0.9790	-0.9552	-0.9237	0.8798	0.8415	-0.8723	0.8120
1447919_x_at	NADH dehydrogenase (ubiquinone) 1, alpha/beta	Ndufab1	0.9080	-0.9321	-0.9536	0.9243	0.8184	-0.8017	0.7581
1447927_at	macrophage activation 2 like /// macrophage activa	Mpa2l /// LOC6265	0.8670	-0.8839	-0.9000	0.8194	0.9124	-0.7684	0.5701
1448188_at	uncoupling protein 2 (mitochondrial, proton carrier)	Ucp2	0.8973	-0.8537	-0.8564	0.7454	0.7230	-0.6601	0.5566
1448361_at	tetratricopeptide repeat domain 3	Ttc3	0.8956	-0.9084	-0.9294	0.8899	0.7893	-0.7576	0.8256
1448382_at	enoyl-Coenzyme A, hydratase/3-hydroxyacyl Coe	Ehhadh	0.9400	-0.9336	-0.9297	0.9064	0.9065	-0.8384	0.8269
1448694_at	Jun oncogene	Jun	0.7580	-0.7759	-0.8192	0.8449	0.9721	-0.6291	0.6266
1448700_at	G0/G1 switch gene 2	G0s2	0.7951	-0.7627	-0.7077	0.6555	0.6829	-0.6155	0.9029

1448752_at	carbonic anhydrase 2	Car2	0.9261	-0.8885	-0.8580	0.7787	0.6974	-0.7069	0.6587
1448927_at	potassium intermediate/small conductance calciu	Kcnn2	-0.9351	0.9230	0.8913	-0.8594	-0.7746	0.7314	-0.7781
1448986_x_at	---	---	0.8679	-0.8814	-0.8699	0.8636	0.7638	-0.7889	0.8199
1448989_a_at	myosin IB	Myo1b	-0.8088	0.8206	0.9100	-0.8889	-0.8039	0.6367	-0.6938
1449038_at	hydroxysteroid 11-beta dehydrogenase 1	Hsd11b1	-0.9776	0.9640	0.9204	-0.8813	-0.7859	0.8968	-0.7545
1449065_at	acyl-CoA thioesterase 1 /// similar to acyl-CoA thio	Acot1 /// LOC1000	0.9685	-0.9537	-0.9367	0.8984	0.8621	-0.8576	0.8249
1449079_s_at	ST3 beta-galactoside alpha-2,3-sialyltransferase 6	St3gal6	0.8870	-0.8797	-0.8492	0.7540	0.6100	-0.6886	0.5197
1449442_at	peroxisomal biogenesis factor 11a	Pex11a	0.9726	-0.9283	-0.8737	0.8019	0.7888	-0.8389	0.8281
1449577_x_at	tropomyosin 2, beta	Tpm2	0.9122	-0.9318	-0.9199	0.8826	0.8702	-0.7260	0.7869
1449619_s_at	Rho GTPase activating protein 9	Arhgap9	0.8682	-0.8482	-0.8544	0.7969	0.7464	-0.6649	0.6672
1449773_s_at	growth arrest and DNA-damage-inducible 45 beta	Gadd45b	0.8945	-0.9332	-0.9170	0.9016	0.7945	-0.9334	0.8030
1449945_at	peroxisome proliferative activated receptor, gamm	Ppargc1b	-0.9643	0.9771	0.8897	-0.8371	-0.7420	0.9340	-0.7277
1450018_s_at	solute carrier family 25, member 30	Slc25a30	0.8441	-0.8203	-0.8245	0.8239	0.7162	-0.7664	0.8494
1450061_at	ectodermal-neural cortex 1	Enc1	0.9278	-0.9519	-0.9189	0.8656	0.7765	-0.7670	0.6509
1450243_a_at	regulator of calcineurin 2	Rcan2	0.9317	-0.9193	-0.8203	0.8167	0.7635	-0.7885	0.8103
1450248_at	a disintegrin and metallopeptidase domain 11	Adam11	0.8869	-0.9058	-0.9582	0.9150	0.8201	-0.7530	0.6076
1450264_a_at	choline kinase alpha	Chka	0.7062	-0.7733	-0.7333	0.8245	0.8102	-0.6591	0.8474
1450391_a_at	monoglyceride lipase	Mgll	0.9711	-0.9458	-0.9086	0.8691	0.8290	-0.8997	0.8449
1450395_at	solute carrier family 22 (organic cation transporter)	Slc22a5	0.9087	-0.8760	-0.8183	0.7775	0.7224	-0.7796	0.7884
1450717_at	angiogenin, ribonuclease, RNase A family, 5	Ang	-0.8825	0.8923	0.8898	-0.8941	-0.7950	0.6839	-0.8008
1450883_a_at	CD36 antigen	Cd36	0.9572	-0.9465	-0.9352	0.8850	0.8930	-0.8013	0.7879
1450884_at	CD36 antigen	Cd36	0.9346	-0.9438	-0.9370	0.9053	0.9140	-0.7909	0.7921
1450970_at	glutamate oxaloacetate transaminase 1, soluble	Got1	-0.9195	0.8804	0.9096	-0.8404	-0.7846	0.8044	-0.7449
1450971_at	growth arrest and DNA-damage-inducible 45 beta	Gadd45b	0.9087	-0.9203	-0.9249	0.8867	0.8528	-0.9103	0.7401
1451156_s_at	very low density lipoprotein receptor	Vldlr	0.8367	-0.8779	-0.9249	0.8719	0.8234	-0.6331	0.5737
1451290_at	microtubule-associated protein 1 light chain 3 alph	Map1lc3a	0.9383	-0.9444	-0.8738	0.8625	0.7608	-0.8690	0.8831
1451421_a_at	rogdi homolog (Drosophila)	Rogdi	0.9270	-0.9453	-0.9150	0.9141	0.7629	-0.8264	0.7867
1451460_a_at	solute carrier family 22 (organic anion transporter),	Slc22a7	-0.7956	0.8083	0.9020	-0.8564	-0.7876	0.7856	-0.6088
1451488_at	RIKEN cDNA 1110028A07 gene	1110028A07Rik	0.9471	-0.9580	-0.9177	0.8584	0.7503	-0.7638	0.6808
1451681_at	cDNA sequence BC089597	BC089597	-0.9263	0.9277	0.9470	-0.9289	-0.8560	0.8233	-0.8077
1451788_at	coagulation factor XI	F11	-0.9403	0.9860	0.9645	-0.9182	-0.8439	0.8163	-0.7036
1451798_at	interleukin 1 receptor antagonist	Il1rn	0.8453	-0.8237	-0.8912	0.8469	0.8212	-0.6122	0.6170
1452050_at	calcium/calmodulin-dependent protein kinase ID	Camk1d	-0.8606	0.8938	0.9412	-0.9473	-0.7653	0.8186	-0.7564
1452416_at	interleukin 6 receptor, alpha	Il6ra	-0.8235	0.8875	0.9599	-0.9650	-0.8607	0.6776	-0.6915
1452716_at	RIKEN cDNA 5730469M10 gene	5730469M10Rik	0.9557	-0.9316	-0.9314	0.8789	0.8797	-0.7812	0.6783
1452864_at	mediator of RNA polymerase II transcription, subu	Med12l	0.8775	-0.8880	-0.8474	0.8773	0.8400	-0.7498	0.8988
1452893_s_at	RIKEN cDNA 1110065P19 gene /// RIKEN cDNA	1110065P19Rik ///	-0.9648	0.9635	0.9377	-0.8870	-0.8600	0.7973	-0.7389
1453056_at	solute carrier family 16 (monocarboxylic acid trans	Slc16a13	0.9033	-0.8846	-0.8614	0.8883	0.8576	-0.7581	0.8595

1453836_a_at	monoglyceride lipase	Mgll	0.9370	-0.9054	-0.8754	0.8102	0.6965	-0.8561	0.7999
1454078_a_at	galactose-3-O-sulfotransferase 1	Gal3st1	0.9036	-0.8675	-0.8943	0.8163	0.7901	-0.6876	0.6907
1454880_s_at	Bcl2 modifying factor	Bmf	-0.9425	0.9426	0.8488	-0.7879	-0.7541	0.7422	-0.7481
1455025_at	progestin and adipoQ receptor family member IX	Paqr9	0.8787	-0.8342	-0.8219	0.7756	0.6440	-0.6925	0.7104
1455178_at	small G protein signaling modulator 2	Sgsm2	0.8366	-0.9009	-0.9067	0.8805	0.8907	-0.8145	0.5619
1455267_at	estrogen-related receptor gamma	Esrrg	1.0000	-0.9656	-0.9021	0.8367	0.8135	-0.8830	0.7303
1455270_at	a disintegrin and metallopeptidase domain 11	Adam11	0.8115	-0.8558	-0.9400	0.9291	0.8744	-0.6573	0.6443
1455288_at	RIKEN cDNA 1110036O03 gene	1110036O03Rik	0.9432	-0.8979	-0.8405	0.7887	0.7217	-0.8830	0.8544
1455383_at	hypothetical protein C730043O17	C730043O17	-0.9481	0.9899	0.9780	-0.9511	-0.8560	0.8504	-0.7612
1455439_a_at	lectin, galactose binding, soluble 1	Lgals1	0.9555	-0.9245	-0.9042	0.8502	0.8138	-0.7472	0.6978
1455457_at	cytochrome P450, family 2, subfamily c, polypeptid	Cyp2c54	-0.8054	0.7892	0.8593	-0.8290	-0.8224	0.6964	-0.7156
1455520_at	protein phosphatase 2, regulatory subunit B (B56),	Ppp2r5c /// LOC10	0.9121	-0.8666	-0.8737	0.7695	0.7715	-0.7422	0.6700
1455936_a_at	RNA binding protein gene with multiple splicing	Rbpms	0.8372	-0.8402	-0.8429	0.8678	0.8707	-0.7193	0.7220
1456096_at	RIKEN cDNA 6430573F11 gene	6430573F11Rik	0.9222	-0.9387	-0.9049	0.9120	0.9214	-0.8351	0.7543
1456424_s_at	phospholipid transfer protein	Pltp	0.9482	-0.9315	-0.9019	0.8513	0.8741	-0.8089	0.7749
1456642_x_at	S100 calcium binding protein A10 (calpactin)	S100a10	0.9176	-0.9455	-0.8979	0.8989	0.8957	-0.7935	0.8038
1456769_at	dual specificity phosphatase 3 (vaccinia virus phos	Dusp3	0.9397	-0.9799	-0.9549	0.9268	0.7663	-0.8408	0.7674
1457213_a_at	diacylglycerol kinase, eta	Dgkh	0.8892	-0.9026	-0.8964	0.8234	0.7163	-0.7863	0.8387
1458701_at	preimplantation protein 4	Prei4	-0.9493	0.9256	0.8969	-0.8372	-0.8728	0.8439	-0.7857
1458829_at	---	---	-0.8774	0.7951	0.7716	-0.7627	-0.7540	0.8566	-0.6951
1458832_at	---	---	-0.9509	0.9273	0.8186	-0.8066	-0.7626	0.8291	-0.7693
1459361_at	---	---	-0.9401	0.8827	0.8985	-0.8000	-0.7818	0.8079	-0.6251
1459686_at	---	---	0.8605	-0.9007	-0.9061	0.8852	0.7499	-0.7202	0.5994
1459740_s_at	uncoupling protein 2 (mitochondrial, proton carrier)	Ucp2	0.8934	-0.8611	-0.8626	0.7446	0.6996	-0.7124	0.6059
1459741_x_at	uncoupling protein 2 (mitochondrial, proton carrier)	Ucp2	0.9075	-0.8773	-0.8253	0.7345	0.6818	-0.6573	0.5840
1460196_at	carbonyl reductase 1	Cbr1	0.7905	-0.8309	-0.8160	0.8738	0.7425	-0.7799	0.8538
1460251_at	Fas (TNF receptor superfamily member 6)	Fas	0.8204	-0.7938	-0.8580	0.8295	0.8653	-0.6048	0.7092

* The CC values for Jun represent the average of the CC values from each of its two significantly changed probe sets.