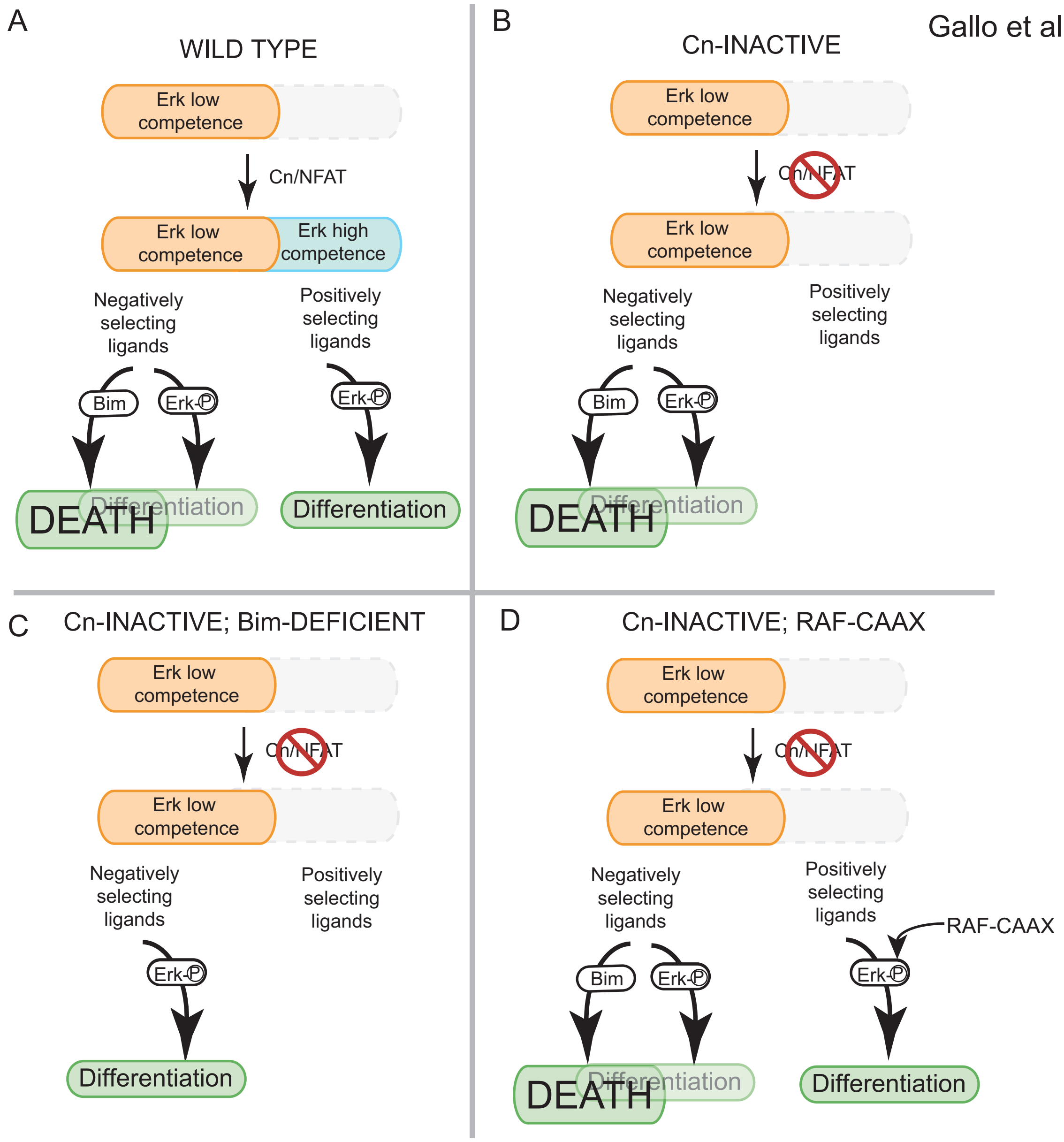
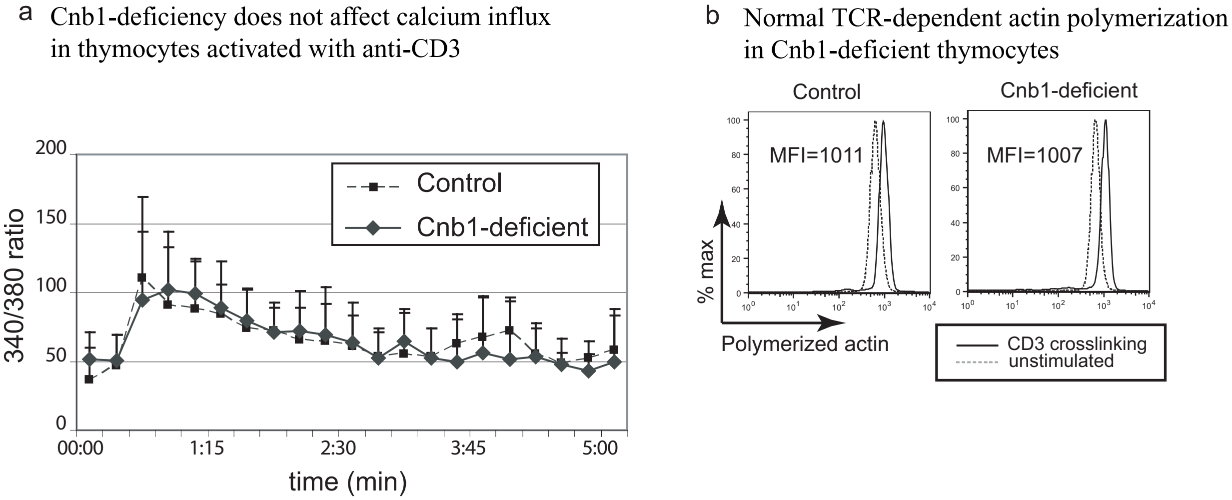
Gallo et al., Sup. Fig.1



Supplementary Figure 1

Calcineurin is required for development of cellular competency for activation of Erk in response to positive selecting signals.

DP thymocytes transition from a state in which they are unable to efficiently activate Erk, the “Erk low competence” state, to a state in which they are competent to activate Erk in response to positively selecting signals, the “Erk high competence” state. Development of the “Erk high competence” population requires calcineurin and NFAT (Cn/NFAT) activity. A) In wild-type thymocytes, negatively selecting signals activate both the Erk pathway and the Bim pathway. Bim induces death by apoptosis, which is dominat over differentiation. Positively selecting ligands activate the Erk pathway but do not activate Bim, resulting in differentiation. B) In the absence of Cn/NFAT activity, thymocytes are blocked in the “Erk low competence” state. In this state, they fail to activate Erk in response to positive selecting ligands; however they are still able to respond to negatively selecting signals by activating the Erk and Bim pathway. C) When apoptosis is circumvented by deletion of Bim, thymocytes that are blocked in the “Erk low competency” state are allowed to differentiate in response to negatively selecting ligands. D) Differentiation of thymocytes that are blocked in the “Erk low competency” state can be partially rescued by transgenic expression of constitutively active Raf-1 mutant.



a Cnb1-deficiency does not affect calcium influx in thymocytes activated with anti-CD3

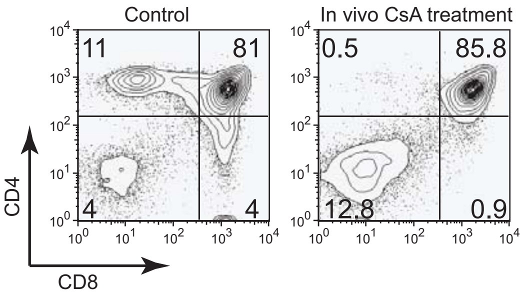
b Normal TCR-dependent actin polymerization in Cnb1-deficient thymocytes

Supplementary Figure 2

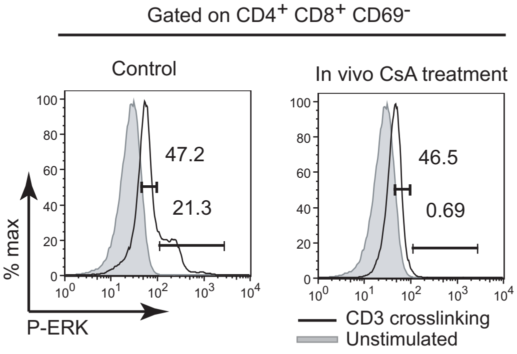
Normal TCR-dependent calcium flux and actin polymerization in Cnb1-deficient thymocytes.

Thymocytes were pulsed for 30 min with 5μg/ml of fura-2-AM (Molecular Probes) at 37^{o}C, washed once and then allowed to fall on anti-CD3ε (20ug/ml) coated chambers. The instant when the cell touched the plate was considered time zero. At the end of the observation period, fluorophore conjugated anti-CD4 and anti-CD8 antibodies were added to the chamber without dislocating the cells. Only thymocytes that stained positive for CD4 and CD8 were used for analysis. The ratio of the fura-2 emission at 510 nm resulting from 340 nm and 380 nm excitation was determined to quantify the relative intracellular calcium concentration. Data acquisition and analysis were done in Metamorph (Universal Imaging) (n=5, mean + s.d.).b) Actin polymerization in Cnb1-deficient and control DP thymocytes after 5 min of CD3ε crosslinking as assayed by FITC-phalloidin staining (Molecular Probes). MFI, Median fluorescence intensity.

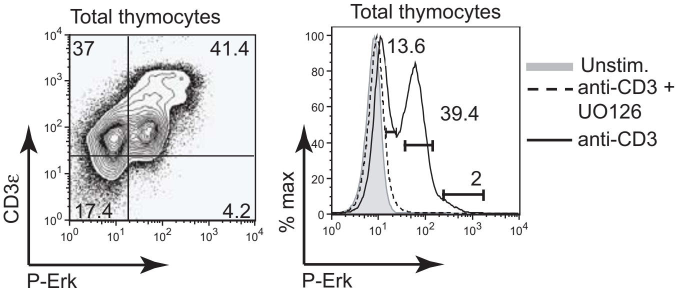
a Long term CsA treatment in vivo blocks the development of CD4$^+$ and CD8$^+$ single positive cells



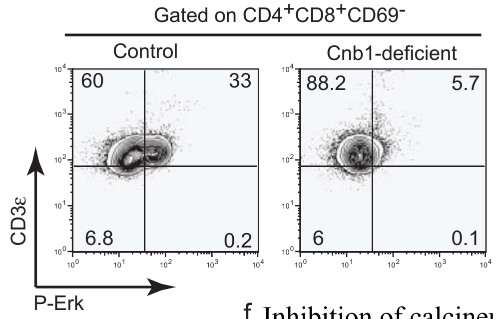
b Long term CsA treatment in vivo blocks the development of Erk competency



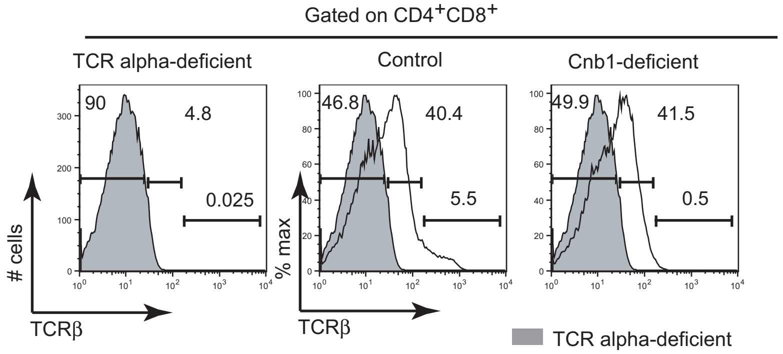
c Discrete populations with different levels of Erk phosphorylation can be observed in stimulated control thymocytes



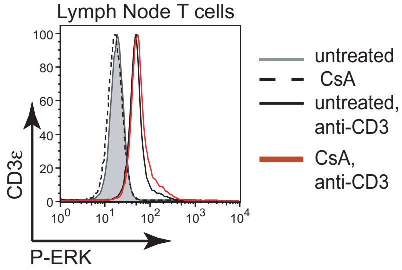
d The absence of the P-Erk high population in CD4$^+$CD8$^+$CD69$^-$ Cnb1-deficient thymocytes is not due to lower levels of CD3ε expression.



e Normal TCRβ expression and in Cnb1-deficient thymocytes



f Inhibition of calcineurin activity has no effect on Erk phosphorylation in peripheral T cells

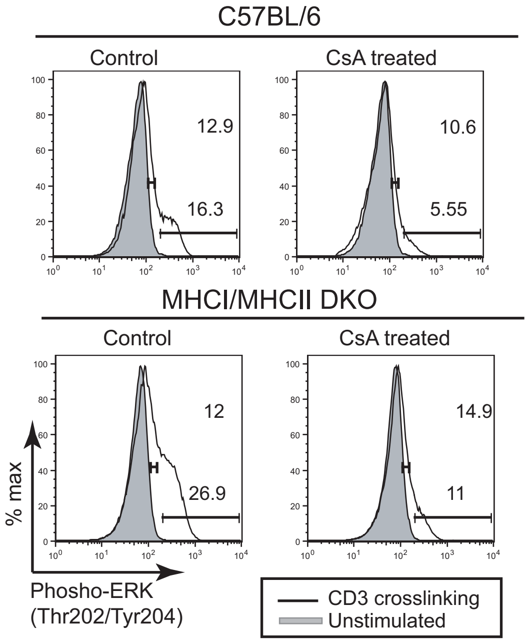


Supplementary Figure 3

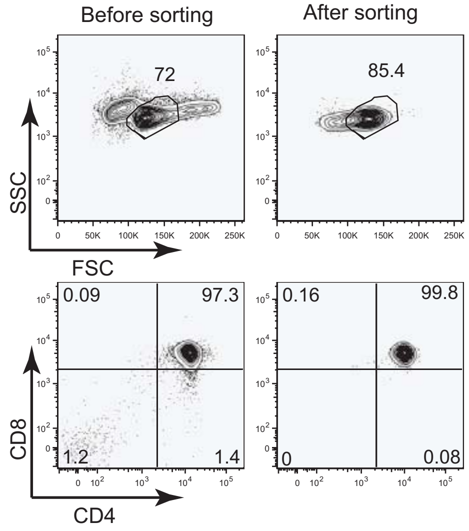
Effects of long term calcineurin inhibition on positive selection and Erk phoshorylation

a) Mice were treated with CsA (30mg/Kg/day, i.p.) for 10 days or left untreated. CsA treatment completely blocks development of single positive thymocytes. b) Erk phosphorylation was assayed by intracellular staining and flow cytometry upon CD3ε crosslinking (2 min) in thymocytes from CsA treated and control mice. CsA treatment blocks the development of the “high Erk competence” thymocyte population. c) Erk phosphorylation in Cnb1-deficient and control thymocytes was assayed as in b. The MEK inhibitor UO126 (10μM) shows specificity of the staining. The levels of cross-linked CD3ε were measured with an anti-goat antibody, which recognizes the antibody used for crosslinking. Three peaks of Erk phosphorylation were observed in control thymocytes, the highest of which corresponds to positively selected SP thymocytes, which also express higher levels of CD3ε. d) The absence of the P-Erk high population in Cnb1-deficient CD4$^+$CD8$^+$CD69$^-$ thymocytes is not due to lower levels of CD3ε crosslinking. e) The percentage of DP TCRβ^{int} pre-selection thymocytes is not affected by Cnb1-deficiency. f) Inhibition of calcineurin activity has no effect on peripheral T cells Erk phosphorylation.

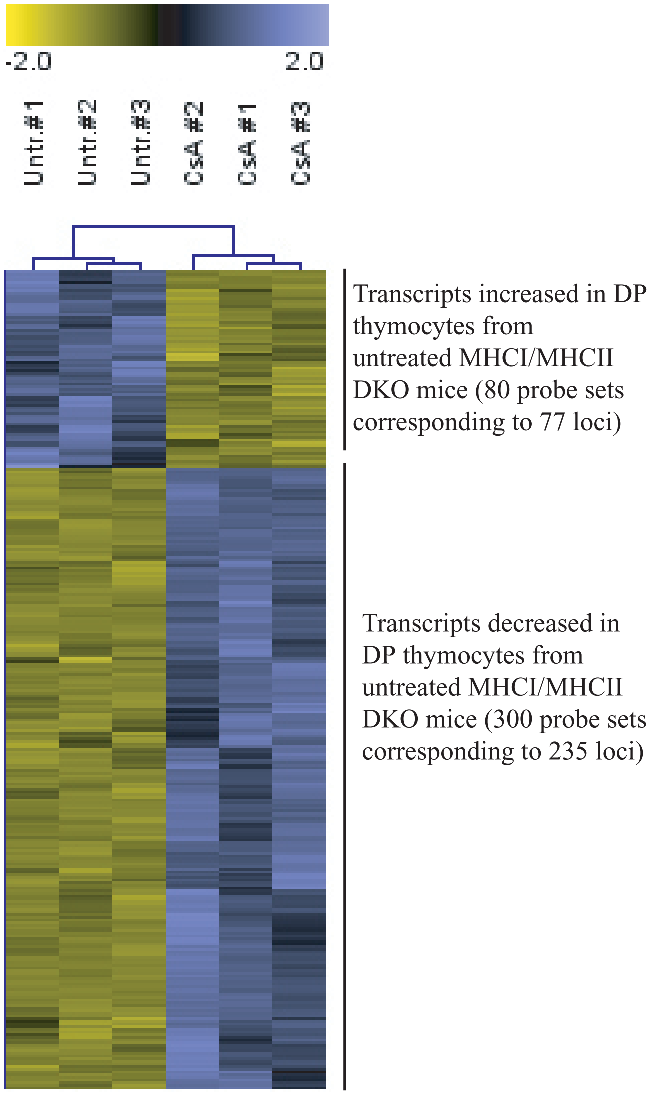
a Canonical MHC-TCR interaction is not required for development of Erk competency



b Purity of thymocytes used for microarray analysis

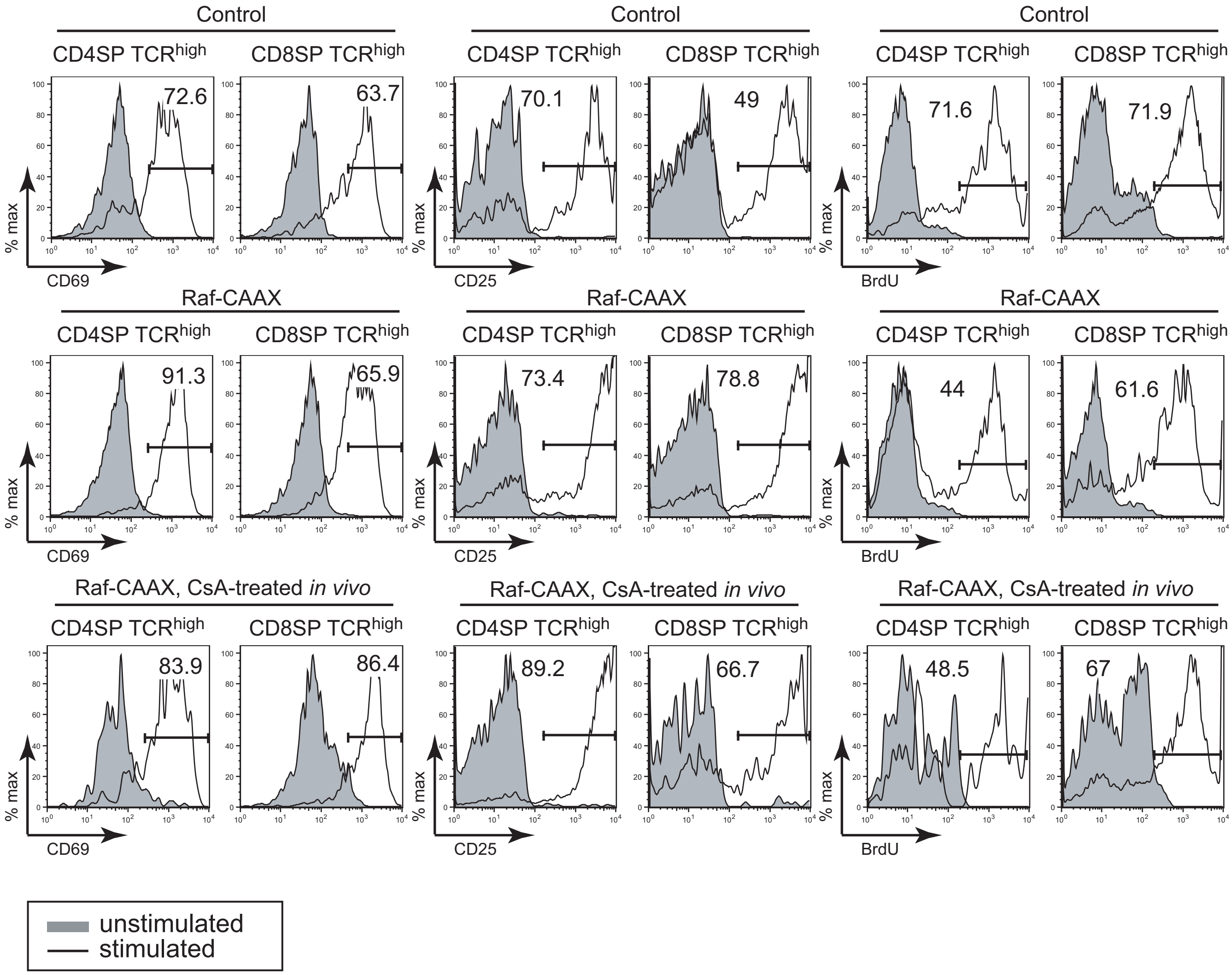


c Color-coded signal intensity of probe sets significantly changed in DP thymocytes sorted from MHCI/MHCII DKO mice treated or not with CsA; experiment clustering according to all probe sets also shown.



Supplementary Figure 4

Canonical MHC-TCR interaction is not required for development of the "Erk high competence" population. a) Comparison of phosho-Erk staining after CD3ε cross-linking (2 min) in $CD4^{+}CD8^{+}$ DP $CD69^{-}$ thymocytes from untreated and CsA-treated MHCI/MHCII double deficient mice (DKO) and age-matched C57BL/6 controls. Development of the "Erk high competence" population is observed even in the absence of canonical MHC-TCR interaction and it is inhibited by long term in vivo CsA treatment. b) Analysis by flow citometry of sorted DP thymocytes used for microarray analysis c) Experiment clustering and color-coded signal intensity of probe sets whose expression is significantly changed n DP thymocytes sorted from CsA-treated and untreated MHCI/MHCII DKO mice. Probe sets were considered significantly chaged if all these conditions were satisfied: 100% change call in all 9-pairwise comparisons in GCOS, abslute signal log ratio $\geq$1, and significant call by one-way ANOVA with p$\leq$0.01.

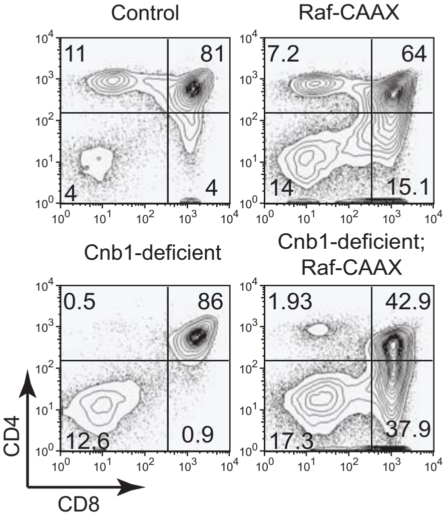


Supplementary Figure 5

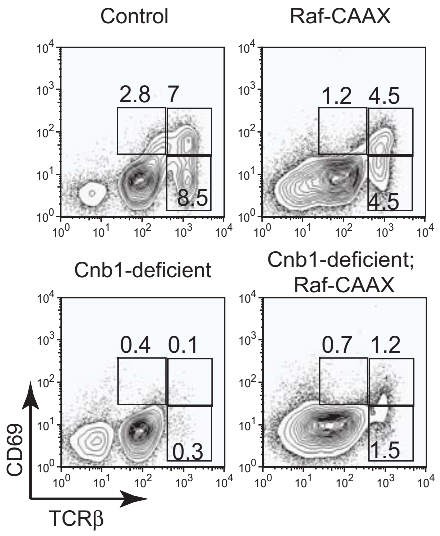
Single Positive thymocytes that develop in CsA-treated Raf-CAAX can functionally respond to TCR stimulation

Total thymocytes from mice of the indicated genotype were stimulated with anti-CD3 and anti-CD28 (note that the stimulation was performed in the absence of CsA for all samples). Thymocytes were analyzed by flow cytometry for upregulation of activation markers CD69 and CD25 (48 hours) and BrdU incorporation (68hours). For BrdU staining cells were pulsed with BrdU (10mM) for the last 18 hours of stimulation. Because of the absence of CD4SP and CD8SP in wild type mice treated with CsA, these cells could not be analyzed.

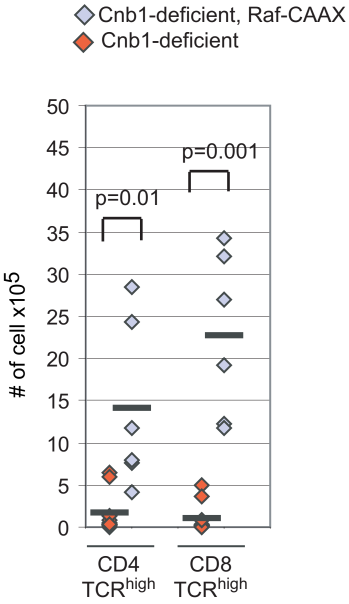
a Active Raf rescues development of CD4+ and CD8+ single positive Cnb1-deficient thymocytes



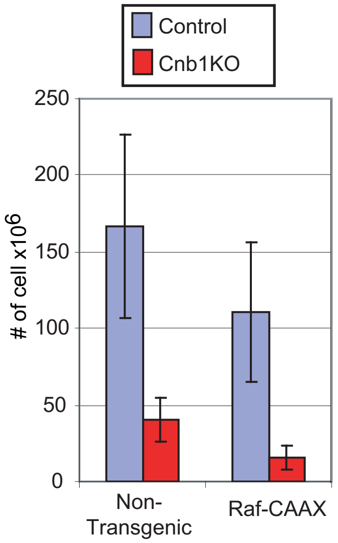
b Active Raf rescues upregulation of CD69 and TCRβ in Cnb1-deficient thymocytes



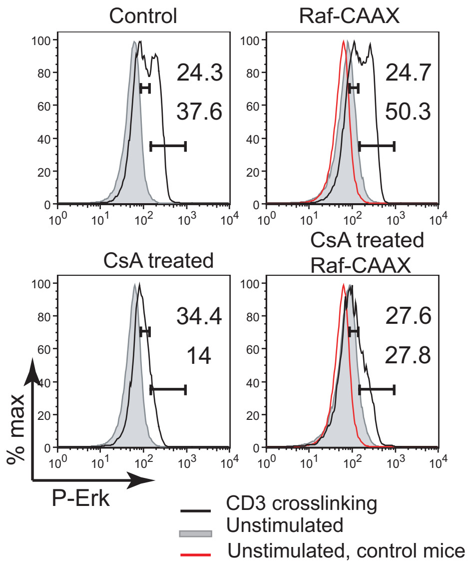
c Absolute numbers of CD4 SP and CD8SP in Raf-CAAX; Cnb1-deficient mice and control mice



d Active Raf does not rescue normal thymocyte cell number in Cnb1-deficient mice

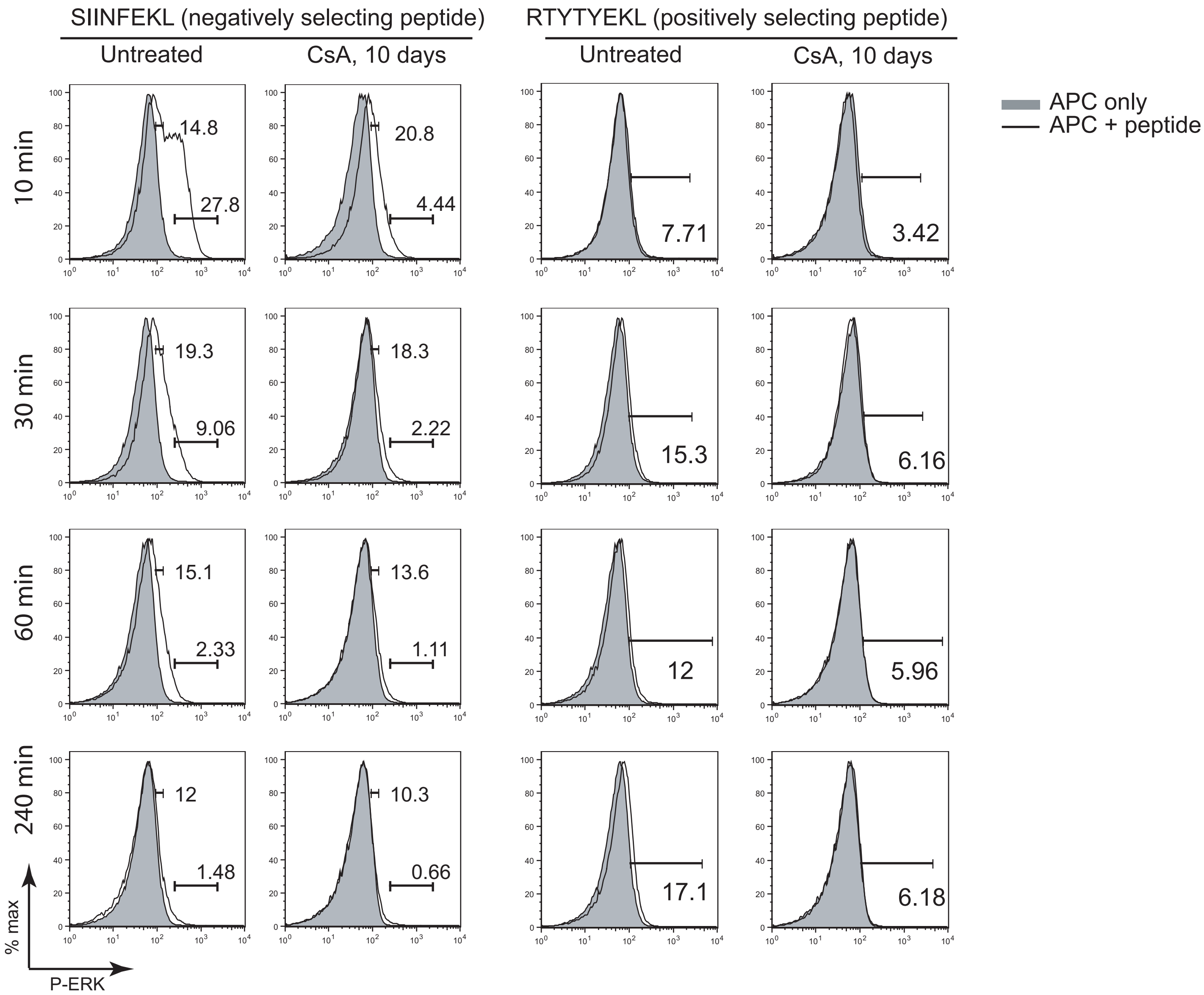


e The RAF-CAAX transgene does not restore normal Erk phosphorylation in thymocytes from CsA-treated mice



Supplementary Figure 6

The RAF-CAAX transgene partially rescues positive selection in Cnb1-defiecient mice. Cnb1-deficient thymocytes expressing the RAF-CAAX transgene and control mice were analyzed for CD4, CD8, TCRβ and CD69 expression a) The RAF-CAAX transgene partiallly rescues development of Cnb1-deficient CD4 and CD8 SP thymocytes. b) The RAF-CAAX transgene rescues upregulation ofTCRβ and CD69 in Cnb1-deficient thymocytes. c) Absolute numbers of TCR^{high} CD4 and TCR^{high} CD8 SP thymocytes in mice of indicated genotype (n≥6, bar shows average). d) Absolute thymocyte numbers in mice of indicated genotype (n≥6, mean ± s.d.). e) Phosho-Erk staining after CD3ε cross-linking (2 min) in CD4^{+}CD8^{+} thymocytes from untreated and CsA-treated (30mg/Kg/day,14 days) RAF-CAAX and control mice. Development of the "Erk high competency" population is not rescued by the RAF-CAAX transgene; basal levels of Erk phosphorylation appear increased.



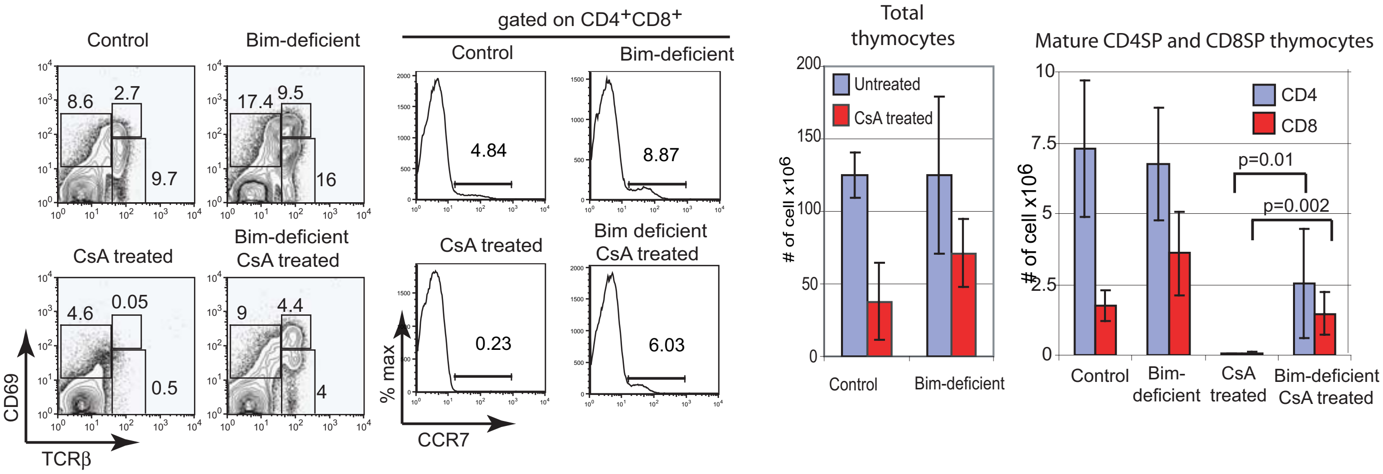
Supplementary Figure 7

Thymocytes that develop in CsA-treated OTI TAP^0 mice phoshorylate Erk in response to negative selecting but not positively selecting ligands.
Thymocytes from CsA-treated OT-I TAP^0 mice and untreated controls were stimulated with T2-H-2K^b antigen presenting cells (APC) pulsed with SIINFEKL or RYTYTYEKL. Erk phosphorylation was analyzed at the indicated time points by flow cytometry as described in experimental procedures.

a Bim-deficiency unveils upregulationof CD69 and TCRβ in the absence of calcineurin activity

b Bim deficiency unveils upregulation of CCR7 even in the absence of calcineurin activity

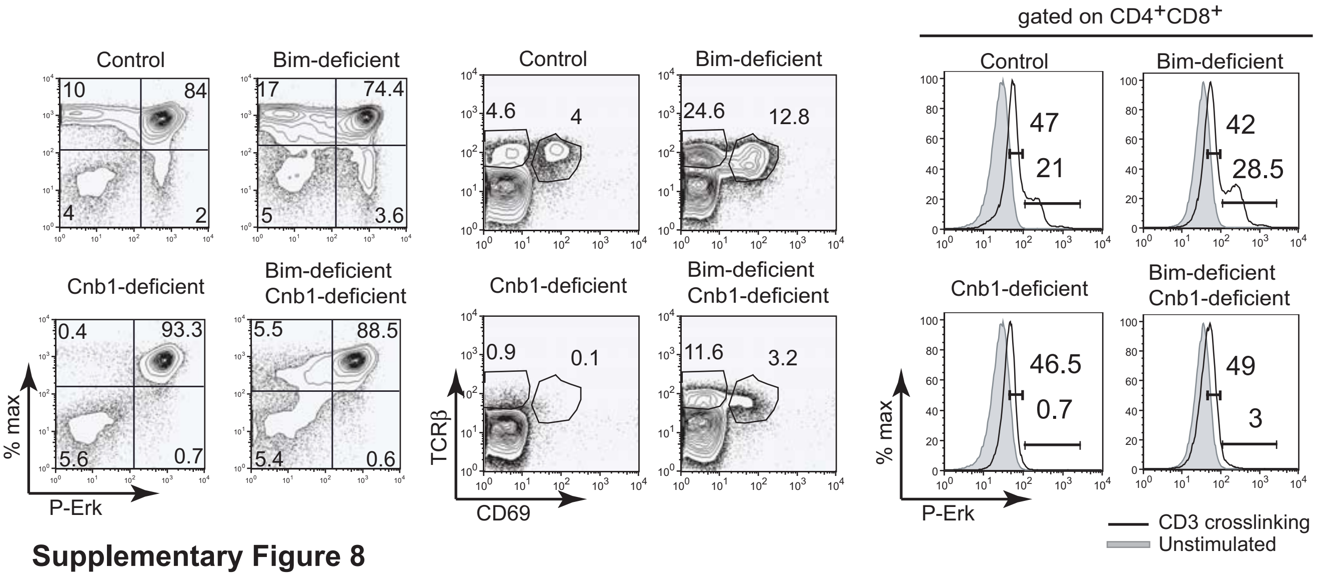
c Absolute numbers of total thymocytes and mature CD4SP and CD8SP



d CD4+and CD8+ SP development in Bim-deficient; Cnb1-deficient mice

e Upregulation of CD69 and TCRβ in Bim-deficient; Cnb1-deficient thymocytes

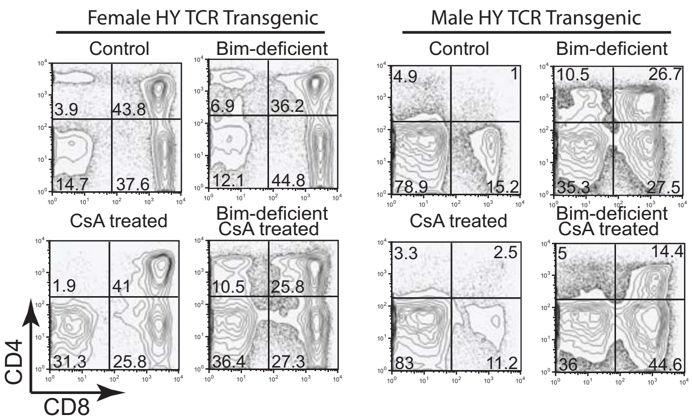
f Bim-deficiency does not rescue development of the "Erk high competence" population



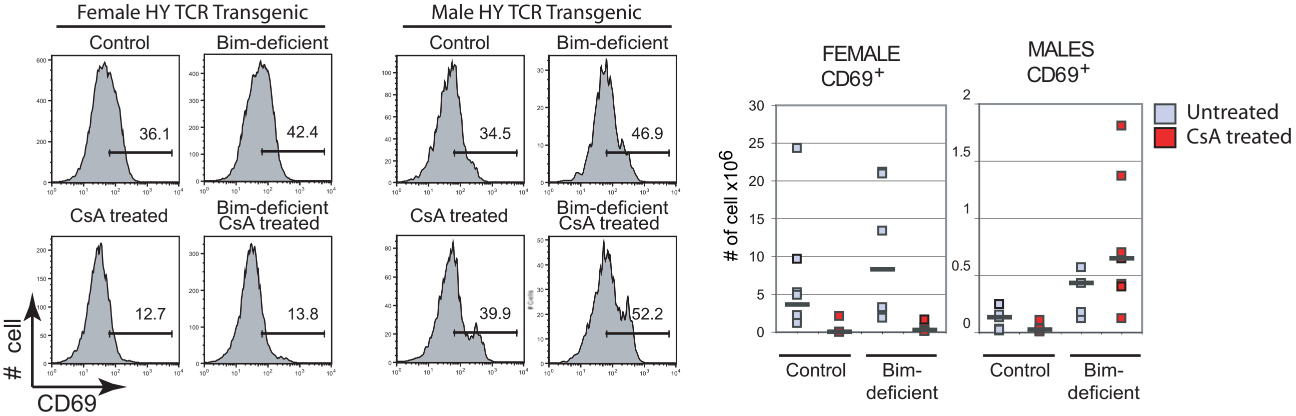
Supplementary Figure 8

Bim-deficiency unveils positive selection in the absence of calcineurin activity and results in development of auto-reactive thymocytes.
Control and Bim-deficient mice were treated with CsA (30mg/Kg/day, i.p.) for 14 days or left untreated. a) Levels of CD69 and TCRβ on developing thymocytes as measured by flow cytometry. b) CCR7 expression on DP thymocytes as analyzed by flow cytometry. c) Absolute numbers of total thympcytes and CD4SP and CD8SP thymocytes in Bim-deficient mice, treated or not with CsA (n=5, mean ± s.d.) d)Thymocytes from mice of the indicated genotype were analyzed for CD4 and CD8 expression. e) Thymocytes from mice of the indicated genotype were analyzed for CD69 and TCRβ expression. f) Comparison of phosho-Erk staining after CD3ε cross-linking (2 min) in CD4$^+$CD8$^+$ thymocytes from mice of the indicated genotype. Development of the Erk high competency is not rescued by Bim-deficiency.

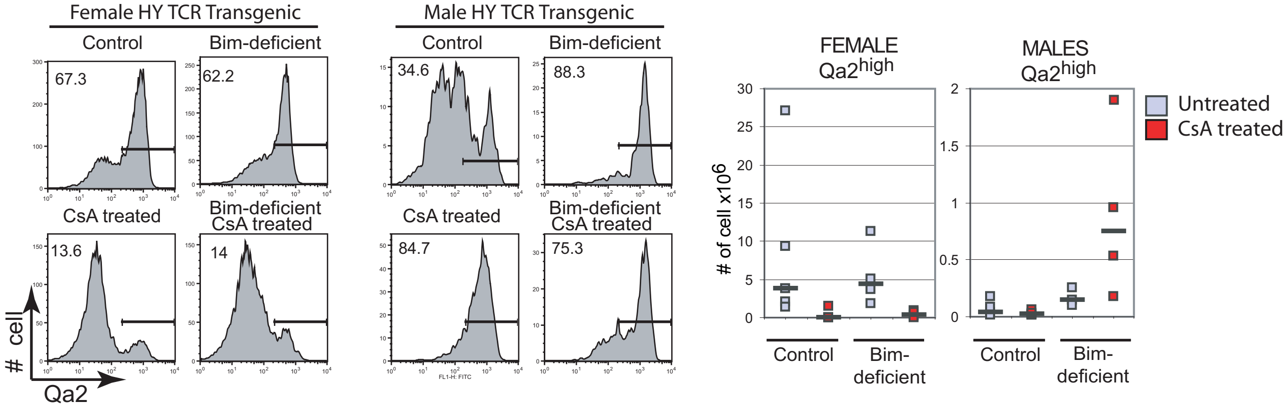
a Inhibition of calcineurin activity by CsA inhibits positive selection in Bim-deficient female but not in Bim-deficient male mice.



b Inhibition of calcineurin activity by CsA blocks CD69 upregulation in Bim-deficient HY transgenic female mice but not in Bim-deficient HY transgenic male mice



c Inhibition of calcineurin activity by CsA blocks Qa2 upregulation in Bim-deficient HY transgenic female mice but not in Bim-deficient HY transgenic male mice



Supplementary Figure 9

Bim-deficiency unveils "positive selection" by negative selecting ligands in the absence of calcineurin activity. Control and Bim-deficient HY transgenic male and female mice were treated with CsA (30mg/Kg/day, i.p.) for 14 days or left untreated. a) Expression of CD4 and CD8 in mice of indicated genotype. CsA treatment results in accumulation of CD8ISP in HY mice. b) Levels of CD69 were measured by flow cytometry on HY$^+$ CD8$^+$ thymocytes. CsA blocks CD69 upregulation in Bim-deficient females but not in Bim-deficient males. n≥4, bar indicates median value b) Levels of Qa2 were measured by flow cytometry on HY$^+$ CD8SP thymocytes. CsA blocks Qa2 upregulation in Bim-deficient females but not in Bim-deficient males. n≥4, bar indicates median value.

Supplementary Table 1. Probe sets ID, gene name, Entrez Gene ID, signal, signal log ratio and change calls for probe sets differentially expressed in DP thymocytes sorted from untreated and CsA-treated MHCI/II DKO mice

					SIGNAL			SIGNAL			pValue	U1_vs_C 1	U1_vs_C 1	U1_vs_C 2	U1_vs_C 2	U1_vs_C 3	U1_vs_C 3	U2_vs_C 1	U2_vs_C 1	U2_vs_C 2	U2_vs_C 2	U2_vs_C 3	U2_vs_C 3	U3_vs_C 1	U3_vs_C 1	U3_vs_C 2	U3_vs_C 2	U3_vs_C 3	U3_vs_C 3
Probe set ID	**Gene Name**	**Entrez Gene ID**	**Average log ratio**	**GO Biological Process**	**Untreated #1**	**Untreated #2**	**Untreated #3**	**CsA treated #1**	**CsA treated #2**	**CsA treated #3**	**one-way ANOVA**	**log ratio**	**change call**	**log ratio**	**change call**	**log ratio**	**change call**	**log ratio**	**change call**	**log ratio**	**change call**	**log ratio**	**change call**	**log ratio**	**change call**	**log ratio**	**change call**	**log ratio**	**change call**
1443865_at	Gabra2	14395	1.56	ion transport	1300.5	1403.1	1530.7	614.4	370.4	465.2	6.76E-04	1.25	I	1.68	I	1.55	I	1.14	I	1.75	I	1.6	I	1.34	I	2	I	1.76	I
1446247_at	Adamts18	208936	1.53	proteolysis	2916.2	2542.6	2945.5	1273.5	760.8	1280	0.0014046	1.54	I	2.13	I	1.47	I	1.33	I	1.83	I	1.31	I	1.28	I	1.67	I	1.23	I
1451683_x_at	H2-D1	14964	1.5	antigen processing and presentation o	329.7	388.3	406.1	139.8	136.4	206.4	0.0027415	1.94	I	1.65	I	1.37	I	1.51	I	1.2	I	1.06	I	1.75	I	1.77	I	1.29	I
1455785_at	Kcna1	16485	1.47	ion transport	1283.6	1110	947.5	364.7	432.3	381.5	0.0019009	1.69	I	1.61	I	1.38	I	1.52	I	1.49	I	1.6	I	1.19	I	1.36	I	1.4	I
1444345_at			1.4		3166.8	2479.7	3352.6	1241.8	899.7	1614.9	0.0065353	1.29	I	1.95	I	1.17	I	0.85	I	1.55	I	0.59	I	1.57	I	2.16	I	1.5	I
1459675_at			1.39		1285.6	1421.6	1548.8	529.9	397.6	551.6	5.03E-04	1.28	I	1.76	I	1.29	I	1.02	I	1.59	I	1.28	I	1.1	I	1.71	I	1.5	I
1444841_at			1.34		1458	1107.6	1353.3	529.5	610.8	542	0.002221	1.58	I	1.63	I	1.48	I	1.2	I	1.24	I	1.12	I	1.18	I	1.2	I	1.42	I
1427181_at	D18Ertd653e	52662	1.33		514.5	604.6	543.3	265.4	337.2	173.6	0.0055387	1.12	I	0.92	I	1.44	I	1.35	I	1.57	I	1.54	I	1.55	I	1.32	I	1.13	I
1442845_at	C130075A20Rik	320395	1.31		1695	1507.7	1343	659.6	475.7	513.4	0.0011423	1.22	I	1.61	I	1.13	I	1.12	I	1.72	I	1.2	I	1.11	I	1.71	I	0.95	I
1449158_at	Kcnk2	16526	1.3	ion transport	1344.9	1560.4	1348.6	483.5	564.1	612.2	4.26E-04	1.46	I	1.07	I	0.83	I	1.6	I	1.42	I	1.27	I	1.58	I	1.38	I	1.1	I
1445837_at			1.29		7220.7	8056.8	7964.4	3540	2681	4405.9	0.001728	1.16	I	1.52	I	0.99	I	1.32	I	1.59	I	1.08	I	1.17	I	1.65	I	1.11	I
1446643_at	5330409N07Rik	319766	1.27		4440.2	4395.7	4006.8	2093.9	1502.8	1801.5	3.47E-04	1.2	I	1.76	I	1.28	I	1.16	I	1.73	I	1.16	I	0.85	I	1.42	I	0.91	I
1435145_at	Cadm2	239857	1.26	cell-cell adhesion	654.9	801.1	841.5	308.9	327.6	114.3	0.0043561	0.78	I	0.58	I	1.7	I	0.97	I	1.04	I	2.05	I	1	I	1.01	I	2.17	I
1446537_at			1.24		2847.7	3296.4	3978.8	1531.5	1275	1279.8	0.0040638	0.9	I	0.97	I	1.09	I	1.12	I	1.29	I	1.45	I	1.3	I	1.46	I	1.56	I
1422834_at	Kcnd2	16508	1.24	ion transport	3111.1	3169.6	2617.3	1179.9	1118.4	1123.5	4.91E-04	1.21	I	1.14	I	1.41	I	1.29	I	1.2	I	1.38	I	1.17	I	1.13	I	1.2	I
1422223_at	Grin2b	14812	1.24	synaptic transmission	1827.6	1899.3	1688	1033.6	648.8	1065.2	0.0038195	1.26	I	1.63	I	1.25	I	1.19	I	1.6	I	1.1	I	0.9	I	1.25	I	1	I
1460214_at	Pcp4	18546	1.23		9103.8	7006.3	7948	3741.9	4016.2	3998.6	0.0025975	1.67	I	1.39	I	1.15	I	1.14	I	0.93	I	0.8	I	1.61	I	1.31	I	1.06	I
1458167_at			1.23		2467.8	2897.1	2769.2	1654	680.9	1396.8	0.009891	0.59	I	1.7	I	0.59	I	1.02	I	1.89	I	0.87	I	1.07	I	2.16	I	1.21	I
1438452_at	Nebl	74103	1.23	transport	1420.3	1273.8	1028.3	598.8	445.3	470.1	0.0040212	1.12	I	1.37	I	1.61	I	1.01	I	1.25	I	1.48	I	0.9	I	1.04	I	1.29	I
1421692_at			1.23	ion transport	1147.1	1552.5	1167.3	665.8	519.7	670.5	0.0089184	1.14	I	1.52	I	1	I	1.34	I	1.4	I	1.26	I	1.08	I	1.45	I	0.92	I
1457898_at			1.2		3332.4	3058.3	3991.8	1502.2	1290.2	1819.3	0.0037174	1.26	I	1.33	I	0.91	I	1.15	I	1.28	I	0.81	I	1.35	I	1.6	I	1.13	I
1425382_a_at	Aqp4	11829	1.2	water transport	2634.9	2318.3	2096.1	1211.2	812.9	955.4	0.0022425	0.97	I	1.7	I	1.37	I	0.87	I	1.49	I	1.27	I	0.79	I	1.27	I	1.07	I
1456119_at	Grm5	108071	1.19	G-protein coupled receptor activity	1354	1325.6	1273.8	768.2	537.1	366.1	0.0030605	0.94	I	1.05	I	1.27	I	1.04	I	1.17	I	1.39	I	1.13	I	1.27	I	1.44	I
1451280_at	Arpp21	74100	1.19		2633.3	2426.6	2554.4	1075.9	1001	1254.4	1.21E-04	1.27	I	1.34	I	1.24	I	1.1	I	1.17	I	1.16	I	1.06	I	1.41	I	1	I
1446212_at			1.19		1969.6	2081.5	2552.4	1230.9	990.3	873.7	0.0048537	0.71	I	1.12	I	1.11	I	0.96	I	1.19	I	1.27	I	1.23	I	1.53	I	1.62	I
1443127_at	9630021D06Rik	319926	1.19		2538.5	3402.3	2843.5	1640.4	1093.7	1495	0.0072722	0.55	I	1.44	I	0.83	I	0.99	I	1.75	I	1.08	I	0.91	I	1.88	I	1.24	I
1421941_at	Camk4	12326	1.19	protein amino acid phosphorylation	2915.4	2657	2599.3	1403.5	1213.9	993.7	5.79E-04	1.14	I	1.38	I	1.5	I	0.96	I	1.4	I	1.44	I	0.76	I	1.04	I	1.1	I
1458123_at	9630002A11Rik	319588	1.18		1983.2	2343.9	2218.5	1002.5	829.4	1149.7	0.0010724	1.3	I	1.42	I	0.82	I	1.09	I	1.67	I	0.88	I	1.11	I	1.39	I	0.92	I
1449634_a_at	Anks1b	544718	1.18		5618.5	4585.2	4466.8	1908.4	2042.7	1649.4	0.0014004	1.38	I	1.41	I	1.24	I	1.07	I	1.14	I	1.21	I	1.02	I	1.03	I	1.11	I
1443101_at	Grid2	14804	1.18	ion transport	506.7	595.6	464.7	288.9	138.7	201.8	0.0058005	0.74	I	1.12	I	1.36	I	1.33	I	1.49	I	1.46	I	0.56	I	1.4	I	1.15	I
1427580_a_at	Rian	75745	1.18		1862.2	1680.6	1751.8	1030.8	809.4	772.3	7.53E-04	1.09	I	1.27	I	0.97	I	1.16	I	1.24	I	1.13	I	1.21	I	1.3	I	1.24	I
1433788_at	Nrxn3	18191	1.17	synaptogenesis	2241.7	2748.3	3180	1275.1	1422.4	967.7	0.0076782	0.96	I	0.95	I	1.41	I	1.02	I	0.97	I	1.43	I	1.2	I	1.12	I	1.51	I
1424400_a_at	Aldh1l1	107747	1.17	biosynthetic process	1750.7	1394.1	1570.3	764.5	682.2	728.7	0.0013165	1.36	I	1.42	I	1.46	I	0.92	I	1.01	I	0.98	I	1.08	I	1.09	I	1.24	I
1458830_at	Fgf14	14169	1.16		1774.2	2257.5	2665.4	973.3	933	906.3	0.0074234	0.75	I	0.89	I	0.87	I	1.22	I	1.37	I	1.25	I	1.35	I	1.34	I	1.36	I
1417885_at	Mapt	17762	1.16	microtubule cytoskeleton organization	2401.3	2246.8	2206.4	1160.7	597.2	1313.5	0.0050389	0.77	I	1.52	I	0.93	I	0.82	I	1.59	I	1.05	I	1.07	I	1.69	I	1	I
1455436_at	Diras2	68203	1.15	small GTPase mediated signalling	7291.6	7170.7	6040	2996	3203.2	3204.4	7.94E-04	1.26	I	1.18	I	1.27	I	1.28	I	1.17	I	1.12	I	1.09	I	1.04	I	0.94	I
1450486_a_at	Oprl1	18389	1.13	G-protein coupled receptor protein signaling	1414.1	1319.6	1469	568.5	617.8	524.1	8.53E-05	1.18	I	1.17	I	1.36	I	0.95	I	0.97	I	1.24	I	1.08	I	1.04	I	1.2	I
1440112_at	Lrrtm3	216028	1.13		3196.7	3329.1	3704.4	1505.9	1488.9	1720.8	4.09E-04	1.24	I	1.21	I	0.89	I	1.07	I	1.31	I	0.85	I	1.25	I	1.37	I	0.94	I
1421225_a_at	Slc4a4	54403	1.13	sodium ion transport	1700.6	1944.8	1814	908	1157.3	684.2	0.004196	1.22	I	0.87	I	1.56	I	1.11	I	0.87	I	1.37	I	1.07	I	0.69	I	1.38	I
1445268_at			1.12		2351.1	2167.9	2430.1	1329.5	1212.4	762.5	0.0030395	0.95	I	0.97	I	1.45	I	0.87	I	1.03	I	1.53	I	0.8	I	0.95	I	1.49	I
1433110_at	5830474E16Rik	76094	1.12		19342	26182.3	21199.8	11113.6	9072.1	10189.2	0.0046821	0.89	I	1.18	I	1.02	I	1.03	I	1.43	I	1.27	I	0.89	I	1.26	I	1.1	I
1459457_at	Camk2d	108058	1.11	protein amino acid phosphorylation	4924.2	4841	3986.5	1831.1	2240.2	2101.1	0.0014394	1.28	I	1.17	I	1.2	I	1.14	I	1.13	I	1.1	I	1.09	I	0.88	I	0.96	I
1445473_at	Diras2	68203	1.11	small GTPase mediated signal transduction	3540.5	3968.8	3317.1	1492.3	1389.6	1278.3	3.80E-04	0.92	I	0.95	I	1.35	I	1.08	I	1.24	I	1.46	I	0.77	I	0.97	I	1.21	I
1433066_at	6330510M09Rik	76158	1.11		3145.8	4013.6	3405.8	1743.8	1657.6	1425.8	0.0022182	0.94	I	0.83	I	1.03	I	1.35	I	1.16	I	1.32	I	0.93	I	1.2	I	1.23	I
1447745_at	Aqp4	11829	1.1	water transport	2442	2098.3	2258.6	1058	1126.2	871.8	5.67E-04	0.87	I	1.24	I	1.47	I	0.56	I	1.16	I	1.21	I	0.75	I	1.31	I	1.33	I
1436999_at	5033414K04Rik	98496	1.1		1749.1	1329.3	1537.5	664.5	626.9	585.6	0.0017753	1.15	I	1.15	I	1.14	I	0.93	I	1.14	I	1.16	I	1.01	I	1.07	I	1.12	I
1427123_s_at	Copg2as2	54158	1.1		2622.7	2482.1	3091.6	1493.2	1126.5	937.4	0.0032761	0.75	I	1.32	I	1.35	I	0.85	I	0.94	I	1.06	I	1.13	I	1.2	I	1.27	I
1427426_at	Kcnq5	226922	1.09	ion transport	1993.7	2660.7	2222.6	1260.8	1137.6	1040.4	0.0050946	0.67	I	0.85	I	1.22	I	1.11	I	1.21	I	1.5	I	1.02	I	0.99	I	1.26	I
1418177_at	Gabrg2	14406	1.09	gamma-aminobutyric acid signaling pathway	1907.4	1785.7	2260.1	1070.3	823.4	1049.2	0.0035116	1.2	I	1.15	I	0.99	I	1.16	I	1.13	I	0.84	I	1.31	I	1.16	I	0.88	I
1433325_at	9330154F10Rik	77554	1.08		2571	2498.4	2236.3	1245.3	1015	1425.9	0.0015212	0.96	I	1.28	I	0.96	I	0.93	I	1.35	I	0.82	I	1.02	I	1.37	I	1.04	I
1450070_s_at	Pak1	18479	1.07	protein amino acid phosphorylation	2617.2	2782.3	2241.3	1150.1	1105.4	1249.3	0.0011381	1.09	I	1.16	I	1.11	I	1.22	I	1.25	I	1.2	I	0.79	I	0.77	I	1	I
1449507_a_at	Cd47	16423	1.07	cell adhesion	3577.4	3598.1	4023.3	1835.3	1812.6	1826.5	1.95E-04	1.06	I	0.96	I	1.19	I	1	I	0.96	I	1.1	I	1.21	I	0.94	I	1.25	I
1444499_at			1.07		2858.6	3022.7	2194.3	774.9	914.5	1208.9	0.0036926	1.09	I	1.21	I	1.26	I	1.25	I	1.09	I	1.23	I	0.88	I	0.84	I	0.82	I
1425918_at	Egln3	112407	1.07	apoptosis	3792	4048.7	4518.7	2082.1	1868.9	2338.4	0.0013131	0.95	I	1.05	I	0.82	I	1.02	I	1.07	I	0.8	I	1.33	I	1.43	I	1.13	I
1452779_at	3110006E14Rik	76980	1.05	protein modification process	1775.2	1912.8	1463.2	663.3	1067.2	710.6	0.0080245	1.33	I	0.63	I	1.28	I	1.07	I	0.84	I	1.36	I	1.1	I	0.68	I	1.15	I
1451917_a_at	Dclk1	13175	1.05	protein amino acid phosphorylation	1615.4	1417.7	1529.4	889.9	715.6	797.8	7.01E-04	0.84	I	1.05	I	1.36	I	0.67	I	1.07	I	1.25	I	0.81	I	0.9	I	1.51	I
1435940_at	AI836758	99719	1.05		2448.4	2397.6	2516.8	1209.3	1393.5	1121.4	1.56E-04	1	I	0.91	I	1.17	I	1.03	I	0.89	I	0.97	I	1.14	I	1.09	I	1.22	I
1417428_at	Gng3	14704	1.05	G-protein coupled receptor protein signaling pathway	2706.5	2499.7	3028.7	1049.8	1463.6	1243.1	0.0015612	1.36	I	0.99	I	1.14	I	1.24	I	0.82	I	0.95	I	1.15	I	0.79	I	1.04	I
1436513_at	Tanc2	77097	1.04	regulation of transcription, DNA-dependent	2345.5	2158.5	2583.7	1138.7	1079.8	1323.8	0.00118	0.88	I	0.97	I	0.99	I	0.99	I	1	I	0.96	I	1.12	I	1.25	I	1.21	I
1427763_a_at	Copg2as2	54158	1.04	protein amino acid phosphorylation	3211.9	2792.9	1945.7	1373.9	1131.3	1122.8	0.0050505	1.05	I	1.23	I	1.54	I	0.96	I	1.17	I	1.25	I	0.47	I	0.79	I	0.94	I
1435026_at	Spock2	94214	1.03	synaptogenesis	2560.2	2201.2	2539.9	1109.2	1265.5	1581.1	0.0035338	1.13	I	0.88	I	0.72	I	1.24	I	0.94	I	0.75	I	1.61	I	1.13	I	0.91	I
1428573_at	Chn2	69993	1.03	signal transduction	1846.2	1146.4	1169.5	788.2	597.5	747.9	0.0010109	1.25	I	1.36	I	1.06	I	0.83	I	1.01	I	0.81	I	1.11	I	1.02	I	0.8	I
1427247_at	D3Bwg0562e	229791	1.03		3902	3817.4	3051	1752.9	1658.6	1320.2	0.0025959	1.17	I	0.91	I	1.19	I	1.14	I	0.87	I	1.26	I	0.96	I	0.79	I	0.99	I
1420833_at	Vamp2	22318	1.03	vesicle-mediated transport	2809.9	1841.5	2400.9	1061.8	1009.8	1042.3	0.0095148	1.38	I	1.59	I	1.29	I	0.64	I	0.9	I	0.51	I	0.86	I	1.06	I	1	I
1420286_at			1.03		2478.6	2174	2143.7	1195.7	1089.6	1347.4	0.0012746	1.11	I	1.05	I	1	I	1.03	I	1.16	I	0.88	I	1.06	I	1.19	I	0.83	I
1452981_at	Cntn1	12805	1.02	DNA methylation	5217.3	5923	5151.7	2908	2962.6	2222.6	0.0013443	0.94	I	0.87	I	1.26	I	1.06	I	0.95	I	1.43	I	0.82	I	0.71	I	1.16	I
1435305_at	Ntrk2	18212	1.02	receptor protein tyrosine kinase signaling pathway	2694.2	2582.9	1994.2	1271.5	1063.9	1187.1	0.0051758	1.18	I	1.25	I	1.24	I	0.99	I	1.14	I	1.1	I	0.68	I	0.83	I	0.8	I
1433662_s_at	Timp2	21858	1.02	negative regulation of cell proliferation	2470.8	2121.7	2161.3	1128	1166.9	947.6	8.28E-04	1.24	I	1.02	I	1.07	I	1.12	I	0.85	I	1.11	I	0.98	I	0.9	I	0.9	I
1431858_at	4930480K15Rik	78800	1.02		1171.5	1166.4	1277.6	632.8	568	656.7	1.99E-04	0.72	I	1.07	I	0.92	I	0.82	I	1.07	I	1.04	I	0.99	I	1.08	I	1.44	I
1428187_at	Cd47	16423	1.02	cell adhesion	5429.1	5848.5	5332.8	3052.1	2857.4	2382.2	4.01E-04	0.79	I	0.84	I	1.12	I	0.92	I	0.97	I	1.28	I	0.98	I	1.06	I	1.22	I
1457973_at	Pcdh9	211712	1.01	homophilic cell adhesion	5629.1	7641.5	6049.8	2807.8	3137.1	2973.3	0.005021	0.8	I	0.82	I	0.74	I	1.25	I	1.09	I	1.14	I	1.12	I	1.14	I	0.97	I
1439036_a_at	Atp1b1	11931	1.01	ion transport	4890.2	5415.4	4122.7	2707.3	1701.2	2447.3	0.0063285	0.68	I	1.4	I	0.91	I	0.86	I	1.58	I	1.02	I	0.62	I	1.28	I	0.74	I
1436260_at	Cacna1e	12290	1.01	ion transport	2074.7	1901	1828	1259.8	1144.8	1293.4	0.001221	1.12	I	0.96	I	0.97	I	1.29	I	0.89	I	1.16	I	0.97	I	0.78	I	0.91	I
1422823_at	Eps8	13860	1.01	proteolysis	1432.2	1996.9	1600.2	605.7	798.5	635.4	0.0049778	1.02	I	0.66	I	0.85	I	1.22	I	1.05	I	1.3	I	1.05	I	0.88	I	1.05	I
1459317_at	Ank2	109676	1	apoptosis	2705.8	2078	2199.9	1427.1	773.5	1017.2	0.0097608	0.77	I	1.18	I	0.9	I	0.47	I	1.25	I	1.03	I	0.71	I	1.55	I	1.18	I
1459288_at	Kcnd2	16508	1	ion transport	2453.5	2614.6	2980.5	1224.7	1171.5	1389	0.0010971	0.46	I	0.88	I	0.87	I	0.85	I	1.23	I	1.06	I	1.02	I	1.41	I	1.23	I
1445234_at	C130030K03Rik	320644	1		1799.5	2071.1	1875.1	1088.9	997.5	935.7	6.01E-04	0.66	I	0.89	I	1.12	I	0.84	I	1.05	I	1.33	I	0.94	I	1.1	I	1.1	I
1439412_at	Arpp21	74100	1		21414	20041.1	16249.8	9107.3	8557.6	11893.3	0.0072287	1.36	I	1.37	I	0.91	I	1.12	I	1.23	I	0.77	I	0.86	I	0.97	I	0.44	I
1438305_at	Rims1	116837	1	positive regulation of synaptic vesicle fusion	2921.5	2565.3	2943.8	1453.8	1137.7	1331.8	6.08E-04	1.02	I	1.32	I	0.89	I	0.89	I	1.18	I	0.72	I	0.94	I	1.24	I	0.78	I
1419554_at	Cd47	16423	1	cell adhesion	12291.1	10360.7	9182	5485.4	6052.1	6314.7	0.0076788	1.16	I	1.16	I	1.13	I	0.99	I	1.03	I	1.04	I	0.85	I	0.78	I	0.84	I

					SIGNAL			SIGNAL			pValue	U1_vs_C 1	U1_vs_C 1	U1_vs_C 2	U1_vs_C 2	U1_vs_C 3	U1_vs_C 3	U2_vs_C 1	U2_vs_C 1	U2_vs_C 2	U2_vs_C 2	U2_vs_C 3	U2_vs_C 3	U3_vs_C 1	U3_vs_C 1	U3_vs_C 2	U3_vs_C 2	U3_vs_C 3	U3_vs_C 3
Probe set ID	Gene Name	Entrez Gene ID	Average log ratio	GO Biological Process	Untreated #1	Untreated #2	Untreated #3	CsA treated #1	CsA treated #2	CsA treated #3	one-way ANOVA	log ratio	change call	log ratio	change call	log ratio	change call	log ratio	change call	log ratio	change call	log ratio	change call	log ratio	change call	log ratio	change call	log ratio	change call
1415810_at	Uhrf1	18140	-4.4	DNA repair	305.3	149.6	159.8	4073.8	6187.6	3228.3	0.0082272	-3.87	D	-4.51	D	-3.58	D	-4.46	D	-4.88	D	-4.2	D	-4.67	D	-5.16	D	-4.27	D
1424046_at	Bub1	12235	-5.8	protein amino acid phosphorylation	16.7	20	2.3	521.8	768.1	768.5	0.0012195	-4.71	D	-5.42	D	-4.79	D	-4.69	D	-5.34	D	-4.09	D	-7.91	D	-8.05	D	-7.16	D
1430811_a_at	Nuf2	66977	-5.17	cell cycle	17.6	23.7	20.4	895.3	1228	786.9	0.0020201	-5.06	D	-5.45	D	-5.54	D	-5.12	D	-5.33	D	-4.95	D	-4.8	D	-5.21	D	-5.11	D
1416120_at	Rrm2	20135	-5.01	DNA replication	39.6	299.7	60.7	2636.5	2318.6	1924.3	6.28E-04	-6.65	D	-6.62	D	-6.62	D	-3.16	D	-2.71	D	-3.14	D	-5.44	D	-5.46	D	-5.33	D
1419513_a_at	Ect2	13605	-4.94	regulation of progression through cell cycle	2.9	52.2	19.8	1024.9	1290	787.8	0.0022838	-7.27	D	-7.99	D	-6.14	D	-3.36	D	-4.05	D	-2.31	D	-4.75	D	-4.82	D	-3.78	D
1435306_a_at	Kif11	16551	-4.93	microtubule-based process	195.4	231	101.8	4471.7	6511.2	5780.8	8.25E-04	-4.42	D	-5.05	D	-4.84	D	-4.32	D	-4.86	D	-4.65	D	-5.06	D	-5.73	D	-5.45	D
1452314_at	Kif11	16551	-4.7	microtubule-based process	107.7	107.1	9.6	2019.5	2084.8	1481.4	7.71E-04	-3.94	D	-4.01	D	-3.55	D	-4.09	D	-4.29	D	-3.73	D	-6.36	D	-6.66	D	-5.63	D
1416251_at	Mcm6	17219	-4.69	DNA replication	23.5	212.6	19	2025.1	1626.7	1422.5	0.0010316	-5.74	D	-5.67	D	-5.54	D	-3.02	D	-2.57	D	-2.41	D	-6.07	D	-5.79	D	-5.39	D
1447363_s_at	Bub1b	12236	-4.64	protein amino acid phosphorylation	32.2	10.6	14	440.4	537.1	453	1.24E-04	-4.31	D	-4.13	D	-3.78	D	-5.22	D	-6	D	-4.98	D	-4.19	D	-4.69	D	-4.45	D
1455990_at	Kif23	71819	-4.63	microtubule-based movement	32.6	102.3	68.1	1352.5	1194.9	1235.4	2.03E-05	-5.34	D	-5.3	D	-5.2	D	-3.91	D	-3.64	D	-3.72	D	-4.72	D	-4.94	D	-4.89	D
1416076_at	Ccnb1	12429	-4.55	regulation of progression through cell cycle	70	15.3	104.3	1558.5	1077.5	1226.3	0.0010644	-4.04	D	-4.29	D	-3.82	D	-5.98	D	-6.05	D	-5.76	D	-3.65	D	-3.9	D	-3.42	D
1433893_s_at	Spag5	54141	-4.51	proteolysis	23.9	16.6	17.7	505.4	456	560.2	8.57E-05	-4.09	D	-4.36	D	-4.76	D	-4.41	D	-4.92	D	-5.11	D	-4.01	D	-4.29	D	-4.64	D
1415811_at	Uhrf1	18140	-4.49	DNA repair	39.7	111.7	43.8	1145.6	1309.7	1204	2.71E-05	-4.87	D	-5.51	D	-4.78	D	-3.74	D	-3.78	D	-3.65	D	-4.64	D	-4.77	D	-4.67	D
1436847_s_at	Cdca8	52276	-4.44	cell cycle	103.3	110.9	52.2	1998.7	1910.8	1830.2	3.95E-06	-4.17	D	-4.06	D	-3.86	D	-4.02	D	-3.83	D	-4.03	D	-5.79	D	-5.08	D	-5.11	D
1426653_at	Mcm3	17215	-4.34	DNA replication	131.6	30.8	14.9	1332.1	1381.6	1657.9	2.04E-04	-3.5	D	-3.41	D	-3.68	D	-4.46	D	-4.78	D	-5.09	D	-4.29	D	-4.59	D	-5.3	D
1437370_at	Sgol2	68549	-4.3	cell cycle	19.2	24.8	80.4	724.3	874.5	692.5	2.63E-04	-4.72	D	-4.72	D	-4.79	D	-5.04	D	-5.03	D	-5	D	-3.3	D	-3.12	D	-2.98	D
1448226_at	Rrm2	20135	-4.28	DNA replication	33.8	129.2	136.3	1953.6	2213.1	1199.3	0.0052517	-5.65	D	-5.73	D	-4.78	D	-3.84	D	-4.02	D	-2.91	D	-3.79	D	-4.07	D	-3.73	D
1452315_at	Kif11	16551	-4.28	microtubule-based process	6.7	155.7	151.8	2041.1	1766	1306.2	0.0018972	-6.67	D	-6.66	D	-5.38	D	-3.54	D	-3.27	D	-2.78	D	-3.94	D	-3.43	D	-2.84	D
1429172_a_at	Ncapg	54392	-4.25		121.8	23.1	114.2	1689.1	1681.4	1423.5	8.33E-05	-3.81	D	-3.75	D	-3.45	D	-5.64	D	-5.53	D	-5.2	D	-3.78	D	-3.92	D	-3.14	D
1427707_a_at			-4.22		42.5	161.8	122.8	1752.2	2061.5	2143.4	1.12E-04	-5.14	D	-5.34	D	-5.16	D	-3.28	D	-3.48	D	-3.51	D	-3.9	D	-4.15	D	-3.99	D
1434789_at	Depdc1b	218581	-4.2	signal transduction	34.3	112.3	80.8	1422	1641.6	1297.8	1.81E-04	-5.88	D	-5.85	D	-5.37	D	-2.93	D	-3.14	D	-3.27	D	-3.7	D	-3.93	D	-3.75	D
1441520_at	Aspm	12316	-4.13	cell cycle	99.1	10.9	144.9	1256.4	1083.6	936.7	5.55E-04	-3.54	D	-3.25	D	-3.15	D	-6.73	D	-6.56	D	-6.12	D	-2.76	D	-2.53	D	-2.51	D
1448777_at	Mcm2	17216	-4.12	DNA replication	48	34.9	104.3	965.5	1055	957.6	1.62E-05	-3.91	D	-4.04	D	-4.27	D	-4.92	D	-4.96	D	-4.95	D	-3.55	D	-3.66	D	-2.86	D
1424105_a_at	Pttg1	30939	-4.08	DNA metabolic process	80.2	29.5	97	1734.4	1178.1	1662.9	0.0011623	-3.93	D	-3.64	D	-3.67	D	-5.47	D	-4.69	D	-5.12	D	-3.77	D	-3.06	D	-3.41	D
1455980_a_at	Gas2l3	237436	-4.06	cell cycle arrest	180.8	11.9	10.9	757.8	542.3	795.8	0.0028911	-1.79	D	-1.86	D	-1.98	D	-5.39	D	-4.77	D	-4.85	D	-5.61	D	-5.09	D	-5.24	D
1437251_at	Cdca2	108912	-4.03	cell cycle	56.8	137	133.1	2546.7	1725	2040.6	0.0011573	-5.41	D	-4.03	D	-5.49	D	-3.66	D	-3.35	D	-3.45	D	-3.55	D	-3.29	D	-4.07	D
1418027_at	Exo1	26909	-4.02	DNA repair	14.5	36	157.3	892.4	756.8	860.9	2.22E-04	-5.77	D	-5.47	D	-5.38	D	-4.42	D	-4.25	D	-4.37	D	-2.07	D	-2.54	D	-1.92	D
1434437_x_at	Rrm2	20135	-4.01	DNA replication	162.3	154.6	98.9	2203	2642.7	1991.3	3.75E-04	-3.83	D	-4.12	D	-3.63	D	-3.52	D	-3.91	D	-3.5	D	-4.45	D	-4.88	D	-4.22	D
1435005_at	Cenpe	229841	-4	microtubule-based movement	19.1	16.1	7.5	489.8	457.2	374.3	2.48E-04	-3.64	D	-3.97	D	-4.07	D	-3.54	D	-4.3	D	-4.24	D	-3.39	D	-4.42	D	-4.43	D
1420028_s_at	LOC671904	17215	-3.98	DNA replication	188.6	64.6	21.4	797.1	796.6	999.4	7.78E-04	-2.17	D	-1.94	D	-2.13	D	-3.76	D	-3.58	D	-3.86	D	-6.51	D	-5.25	D	-6.64	D
1440924_at	Kcnq5	226922	-3.98	microtubule-based movement	27.4	81.8	10.3	721.6	716.9	302.9	0.0037278	-4.59	D	-4.01	D	-3.28	D	-3.23	D	-2.96	D	-2.03	D	-5.93	D	-5.06	D	-4.71	D
1421546_a_at	Racgap1	26934	-3.97	cytokinesis	122.9	189.8	16.6	1102.3	875.6	1262.4	0.0013971	-3.4	D	-3.17	D	-3.2	D	-2.7	D	-2.6	D	-2.38	D	-6.63	D	-5.96	D	-5.71	D
1436808_x_at	Mcm5	17218	-3.97	DNA replication	84.6	104.8	67.8	1624.3	1614.4	1680.5	2.97E-07	-3.89	D	-3.6	D	-3.63	D	-4.22	D	-4.19	D	-3.59	D	-4.23	D	-4.18	D	-4.2	D
1452459_at	Aspm	12316	-3.96	cell cycle	23	101.6	194.7	1423.9	1605.4	1246.9	3.27E-04	-5.5	D	-5.5	D	-5.07	D	-3.53	D	-3.78	D	-3.29	D	-2.98	D	-3.2	D	-2.83	D
1419943_s_at	Ccnb1	268697	-3.95	regulation of progression through cell cycle	18.4	30.8	133.1	798.6	782.1	706	1.10E-04	-4.92	D	-5.15	D	-4.33	D	-4.27	D	-5.58	D	-3.73	D	-2.64	D	-2.85	D	-2.07	D
1430193_at	Casc5	677208	-3.91		238.6	143.2	116.5	1954.4	2992.8	1620.4	0.0081811	-3.24	D	-4.1	D	-3.01	D	-3.56	D	-4.47	D	-3.55	D	-4.19	D	-4.9	D	-4.17	D
1418317_at	Lhx2	16870	-3.9	transcription	44.7	23.7	43.2	528.4	495.6	397.1	4.02E-04	-3.03	D	-3.4	D	-3.36	D	-4.04	D	-4.45	D	-3.69	D	-4.21	D	-5.01	D	-3.94	D
1429658_a_at	Smc2	14211	-3.86	DNA metabolic process	285.6	296.9	274.7	4230.5	4036.8	4279.4	7.93E-07	-3.86	D	-3.68	D	-3.85	D	-3.97	D	-3.91	D	-4.01	D	-3.85	D	-3.76	D	-3.82	D
1417450_a_at	Tacc3	21335	-3.83	regulation of progression through cell cycle	19.4	118.3	8.3	663.4	466.8	437.2	0.0039114	-5.19	D	-4.43	D	-4.94	D	-2.34	D	-1.79	D	-1.68	D	-4.82	D	-4.55	D	-4.75	D
1448201_at	Sfrp2	20319	-3.83	somitogenesis	126.4	10.9	31.8	588.1	605.2	536.7	2.23E-04	-1.87	D	-2.18	D	-1.98	D	-5.2	D	-5.58	D	-4.95	D	-4.52	D	-4.49	D	-3.71	D
1424128_x_at	Aurkb	20877	-3.81	DNA methylation	81.8	23.3	32.2	630.1	534.5	503.9	2.67E-04	-2.33	D	-2.35	D	-2.36	D	-4.24	D	-4.49	D	-4.48	D	-4.56	D	-5.16	D	-4.36	D
1422513_at	Ccnf	12449	-3.79	regulation of progression through cell cycle	195.1	35.1	11	625.4	901.6	860	0.0023068	-2.07	D	-2.07	D	-2.39	D	-3.93	D	-4.65	D	-5.42	D	-4.18	D	-4.6	D	-4.79	D
1452534_a_at	Hmgb2	433785	-3.79	DNA replication	330.9	402.5	526.4	6344.1	6725.8	5369.9	1.49E-04	-4.16	D	-4.31	D	-3.7	D	-3.59	D	-3.78	D	-3.28	D	-3.82	D	-4.07	D	-3.38	D
1450842_a_at	Cenpa	12615	-3.77	nucleosome assembly	85.4	36.9	173.6	1072.1	1177.5	1249.4	8.14E-05	-3.2	D	-2.64	D	-2.76	D	-5.02	D	-5.72	D	-5.27	D	-3.21	D	-3.31	D	-2.77	D
1449171_at	Ttk	22137	-3.75	protein amino acid phosphorylation	155.7	8.5	68.5	776.8	823.3	905.6	1.85E-04	-2.02	D	-2.31	D	-1.69	D	-6.87	D	-5.31	D	-5.21	D	-3.59	D	-3.37	D	-3.38	D
1453107_s_at	4933413G19Rik	14235	-3.75	regulation of cell growth	139.2	11.3	17.2	663.3	729.6	584.4	5.21E-04	-2.19	D	-1.67	D	-1.36	D	-5.45	D	-4.38	D	-4.27	D	-5.04	D	-4.62	D	-4.75	D
1460314_s_at	Hist1h3a	15077	-3.64	nucleosome assembly	2108.5	1588.1	1396	21167.8	18636.1	26692.2	0.0010176	-3.27	D	-3.08	D	-3.53	D	-3.66	D	-3.48	D	-3.98	D	-3.87	D	-3.64	D	-4.23	D
1450157_a_at	Hmmr	15366	-3.6		44.8	22.2	14.9	355.9	488.8	494.5	8.16E-04	-2.7	D	-3.1	D	-2.87	D	-3.58	D	-3.56	D	-3.87	D	-4.18	D	-4.12	D	-4.41	D
1417911_at	Ccna2	12428	-3.56	regulation of progression through cell cycle	289.7	312.5	169.6	6326.1	6414.8	4975.4	2.70E-04	-3.74	D	-3.69	D	-3.3	D	-3.51	D	-3.5	D	-3.14	D	-3.85	D	-3.75	D	-3.56	D
1454694_a_at	Top2a	21973	-3.56	DNA metabolic process	236.3	254.2	111.3	2754.5	3025.9	2435.8	1.35E-04	-3.38	D	-3.52	D	-3.03	D	-2.84	D	-3.2	D	-2.67	D	-4.53	D	-4.64	D	-4.22	D
1424118_a_at	Spc25	66442	-3.54	cell cycle	28.5	248.4	173.5	1160.3	1272.7	1037.4	4.26E-04	-5.13	D	-5.18	D	-4.82	D	-2.8	D	-3.13	D	-2.84	D	-2.7	D	-2.89	D	-2.39	D
1428481_s_at	Cdca8	52276	-3.5	cell cycle	20.1	146.8	139.5	1133	1070.9	969.5	1.09E-04	-5.01	D	-4.82	D	-4.97	D	-3.08	D	-3.07	D	-3.09	D	-2.45	D	-2.46	D	-2.58	D
1436654_at	5830483C08Rik	209334	-3.49	DNA repair	26.7	104.1	28	716.7	385.6	624.9	0.0068489	-4.73	D	-3.81	D	-3.67	D	-2.69	D	-1.84	D	-2.45	D	-4.72	D	-3.64	D	-3.82	D
1452040_a_at	Cdca3	14793	-3.47	ubiquitin cycle	32.3	9.6	185.2	625.4	679.7	597.6	7.50E-04	-4.08	D	-3.72	D	-4.29	D	-4.64	D	-4.67	D	-4.9	D	-1.56	D	-1.61	D	-1.77	D
1441757_at	1190002F15Rik	381822	-3.46		278.5	284.7	367	2398.1	2937.5	2876.7	1.49E-04	-3.28	D	-3.72	D	-3.42	D	-3.28	D	-3.95	D	-3.57	D	-3.11	D	-3.43	D	-3.36	D
1458374_at	C79407	217653	-3.45		297.1	377.2	378.8	4348.3	3895.2	3160.9	5.75E-04	-3.45	D	-3.43	D	-3.29	D	-3.52	D	-3.38	D	-3.4	D	-3.66	D	-3.42	D	-3.51	D
1426817_at	LOC638774	17345	-3.42	meiosis	332.7	178.3	169.5	2796	2675.5	2929.7	9.12E-06	-2.78	D	-2.89	D	-2.81	D	-4.02	D	-4.12	D	-4.05	D	-3.38	D	-3.52	D	-3.21	D
1448635_at	Smc2	14211	-3.42	DNA metabolic process	335.7	306.9	347.6	3284.2	3836.7	2709.9	8.25E-04	-3.5	D	-3.51	D	-3.18	D	-3.43	D	-3.55	D	-3.1	D	-3.62	D	-3.73	D	-3.19	D
1452954_at	Ube2c	68612	-3.41	cytokinesis	169.7	222.2	232.2	2819.9	2679.1	2449.2	2.42E-05	-3.51	D	-4.02	D	-3.6	D	-3.04	D	-3.54	D	-2.9	D	-3.38	D	-3.49	D	-3.19	D
1417910_at	Ccna2	12428	-3.4	regulation of progression through cell cycle	188.1	296.3	204.2	1718.1	1474.1	1437.4	1.54E-04	-3.79	D	-3.3	D	-3.5	D	-2.96	D	-2.62	D	-2.78	D	-3.95	D	-3.93	D	-3.8	D
1429499_at	Fbxo5	67141	-3.38	mitotic metaphase	747.6	584.6	491.2	4936.3	7592.2	5595.3	0.0024768	-3.24	D	-3.82	D	-2.96	D	-3.21	D	-3.91	D	-3.37	D	-3.17	D	-3.77	D	-2.93	D
1452540_a_at	Hist1h2bc	319179	-3.37	nucleosome assembly	4249.6	3421.2	2080.9	34406.8	26826.4	41139.4	0.0017951	-2.95	D	-2.62	D	-3.35	D	-3.39	D	-3.03	D	-3.68	D	-3.76	D	-3.42	D	-4.12	D
1419153_at	2810417H13Rik	68026	-3.35		751.3	528.5	930.1	7428.2	6911.9	6871.3	7.70E-06	-3.6	D	-3.47	D	-3.26	D	-3.71	D	-3.67	D	-3.39	D	-3.03	D	-2.94	D	-3.04	D
1438852_x_at	Mcm6	17219	-3.27	DNA replication	86.1	61.1	39.2	750.4	913.2	648.7	8.22E-04	-2.63	D	-3.09	D	-2.87	D	-2.98	D	-3.55	D	-3.04	D	-3.83	D	-3.91	D	-3.49	D
1438009_at	RP23-480B19.10	665433	-3.26	nucleosome assembly	141.3	271.6	289.7	2080	2394.9	2122.8	5.59E-05	-3.7	D	-3.78	D	-3.7	D	-2.99	D	-3.17	D	-3.05	D	-2.89	D	-3.06	D	-3.04	D
1437313_x_at	Hmgb2	678110	-3.17	DNA replication	275.5	331.8	256.8	2499.5	2511.5	1936.1	4.47E-04	-3.65	D	-3.47	D	-3.13	D	-2.49	D	-2.48	D	-2.14	D	-3.98	D	-3.93	D	-3.24	D
1416309_at	Nusap1	108907	-3.15	mitotic sister chromatid segregation	187	274.9	190.5	1875.9	2373.9	1706.1	9.47E-04	-3.1	D	-3.69	D	-2.91	D	-2.76	D	-3.22	D	-2.55	D	-3.31	D	-3.6	D	-3.2	D
1416123_at	Ccnd2	12444	-3.11	regulation of progression through cell cycle	4006.1	1738	1373.2	17096.7	23101.5	17354.4	0.0013838	-2.25	D	-2.76	D	-2.21	D	-3.12	D	-3.54	D	-3.07	D	-3.58	D	-3.93	D	-3.5	D
1417939_at	Rad51ap1	19362	-3.11	double-strand break repair via homologous recombination	73.4	26.3	141.3	764.3	426.6	679.4	0.0070488	-3.32	D	-2.63	D	-3.2	D	-4.99	D	-4.05	D	-4.78	D	-1.94	D	-1.25	D	-1.81	D
1458447_at	Cenpf	108000	-3.07	G2 phase of mitotic cell cycle	33.3	97.2	172.3	721.7	943.1	910.6	6.89E-04	-3.78	D	-4.73	D	-4.59	D	-2.92	D	-3.06	D	-2.6	D	-1.95	D	-2.04	D	-1.94	D
1429660_s_at	Smc2	14211	-3.06	DNA metabolic process	310.1	218.9	352.9	2715.7	2512.6	1839.1	0.0015323	-3.09	D	-3.23	D	-2.68	D	-3.71	D	-3.74	D	-3.08	D	-2.8	D	-2.84	D	-2.41	D
1450920_at	Ccnb2	12442	-3.04	regulation of progression through cell cycle	28.1	163.1	257.4	984.5	1175.4	888.9	0.0012775	-4.54	D	-4.48	D	-4.85	D	-2.85	D	-3.19	D	-2	D	-1.73	D	-1.97	D	-1.73	D
1416122_at	Ccnd2	12444	-3.03	regulation of progression through cell cycle	8237.2	6416.6	3939.2	43867.3	57287.9	44064.9	7.91E-04	-2.46	D	-2.76	D	-2.54	D	-2.72	D	-3.06	D	-2.87	D	-3.43	D	-3.79	D	-3.6	D
1415945_at	Mcm5	17218	-3.02	DNA replication	299.6	121.2	177.8	1802.5	1635	1692.9	3.05E-05	-2.42	D	-2.5	D	-2.52	D	-3.62	D	-3.9	D	-3.4	D	-2.93	D	-2.94	D	-2.92	D
1448229_s_at	Ccnd2	12444	-3.01	regulation of progression through cell cycle	8955.8	5987.4	3798.6	47738.9	58307.8	47157.1	3.34E-04	-2.33	D	-2.63	D	-2.26	D	-2.94	D	-3.19	D	-2.93	D	-3.51	D	-3.86	D	-3.48	D
1448205_at	Ccnb1	12429	-3	regulation of progression through cell cycle	162.6	214.6	241.4	1888.2	2163.9	1757.2	1.44E-04	-3.49	D	-3.61	D	-3.09	D	-2.89	D	-2.97	D	-2.72	D	-2.82	D	-2.89	D	-2.54	D
1434745_at	Ccnd2	12444	-2.96	regulation of progression through cell cycle	6948.7	5871.1	5267.6	43883.1	53436.3	48635.1	1.09E-04	-2.63	D	-2.89	D	-2.76	D	-2.86	D	-3.07	D	-3	D	-3.02	D	-3.28	D	-3.16	D
1439695_a_at	Mphosph1	240641	-2.96	microtubule-based movement	11.7	178.3	189.4	568.4	767.3	553.4	0.0049697	-5.3	D	-5.81	D	-5.01	D	-2.02	D	-2.38	D	-1.82	D	-1.28	D	-2.11	D	-0.94	D
1448627_s_at	Pbk	52033	-2.96	protein amino acid phosphorylation	277.8	183.6	144.2	1837.7	2200	1490	0.0014165	-2.38	D	-3.14	D	-1.94	D	-2.94	D	-3.77	D	-2.76	D	-3.04	D	-3.8	D	-2.87	D
1415860_at	Kpna2	16647	-2.94	protein import into nucleus	511.5	249.3	368.7	2762	3372.9	2980.2	1.64E-04	-2.66	D	-2.78	D	-2.43	D	-3.31	D	-3.33	D	-2.97	D	-3.06	D	-3.1	D	-2.79	D
1448314_at	Cdc2a	12534	-2.94	protein amino acid phosphorylation	215.6	93.1	11.7	1023.5	1128.1	847.3	9.08E-04	-1.35	D	-2.04	D	-1.45	D	-3.16	D	-3.36	D	-2.66	D	-4.2	D	-4.56	D	-3.7	D
1439040_at	Cenpe	229841	-2.82	microtubule-based movement	146.5	139.2	107.6	717.6	1043.5	779.5	0.0020651	-2.72	D	-2.95	D	-2.67	D	-1.93	D	-2.8	D	-2.4	D	-3.33	D	-3.68	D	-2.93	D

1419838_s_at	Plk4	20873	-2.78	protein amino acid phosphorylation	24.9	138.4	243.4	841.1	897.1	574.5	0.0057237	-4.07	D	-4.84	D	-4.66	D	-2.2	D	-2.3	D	-2.07	D	-1.62	D	-1.83	D	-1.43	D
1433599_at	Baz1a	217578	-2.77	chromatin remodeling	199.2	367.9	106.3	1143.4	1382.7	1025.9	0.0017928	-2.6	D	-2.93	D	-2.52	D	-1.86	D	-2.22	D	-1.76	D	-3.76	D	-3.77	D	-3.47	D
1455956_x_at	Ccnd2	12444	-2.77	regulation of progression through cell cycle	10466.1	7977.7	6449.3	60833	66645.3	74602.5	1.43E-04	-2.17	D	-2.36	D	-2.36	D	-2.67	D	-2.81	D	-2.82	D	-3.11	D	-3.34	D	-3.31	D
1416299_at	Shcbp1	20419	-2.76		129.1	32.3	63.3	1008.8	868.9	1063.3	1.50E-04	-2.08	D	-2.26	D	-2.31	D	-2.34	D	-3.53	D	-2.62	D	-3.13	D	-3.25	D	-3.28	D
1422460_at	Mad2l1	56150	-2.74	mitotic sister chromatid segregation	269.2	231.7	190.2	1428.4	1787.5	1450.9	3.62E-04	-2.64	D	-3.23	D	-2.51	D	-2.52	D	-2.99	D	-2.62	D	-2.51	D	-2.94	D	-2.67	D
1436186_at	E2f8	108961	-2.73	regulation of progression through cell cycle	112	28.3	100.6	747.5	818.6	626.2	4.66E-04	-1.96	D	-2.03	D	-1.81	D	-3.7	D	-4.18	D	-4.14	D	-1.77	D	-2.47	D	-2.49	D
1439301_at	Rad51l1	19363	-2.73	DNA metabolic process	133.4	177	204.6	1120.5	1139.6	1472	7.61E-04	-2.95	D	-3.06	D	-3.49	D	-2.5	D	-2.88	D	-2.93	D	-2.23	D	-2.25	D	-2.31	D
1427161_at	Cenpf	108000	-2.72	G2 phase of mitotic cell cycle	291.6	209.8	429	2019.3	2064.8	1709.7	2.28E-04	-2.7	D	-2.74	D	-2.7	D	-3.26	D	-3.61	D	-3.07	D	-2.12	D	-2.28	D	-2.04	D
1422430_at	Fignl1	60530	-2.69		32.5	49.4	100.2	427.1	473.8	361.9	7.12E-04	-3.21	D	-3.1	D	-3.4	D	-2.76	D	-3.12	D	-2.35	D	-2.46	D	-2.13	D	-1.71	D
1416698_a_at	Cks1b	54124	-2.68	cell cycle	341.1	463	426	2939.6	2600.8	2562.3	5.24E-05	-3.09	D	-3	D	-2.9	D	-2.57	D	-2.32	D	-2.11	D	-2.88	D	-2.65	D	-2.57	D
1417458_s_at	Cks2	66197	-2.68	cytokinesis	227.6	174.5	166	1090.9	823	1147.3	0.0012292	-2.45	D	-2.14	D	-2.44	D	-3.2	D	-2.82	D	-3.15	D	-2.94	D	-2.41	D	-2.6	D
1444257_at	Prr11	270906	-2.68		115.2	49.2	203.2	708.9	704	654.1	2.93E-04	-2.58	D	-2.52	D	-2.49	D	-3.89	D	-3.36	D	-3.79	D	-1.95	D	-2.02	D	-1.56	D
1448710_at	Cxcr4	12767	-2.62	patterning of blood vessels	595.5	426.3	440.7	2495	3147.4	2934.2	2.87E-04	-2.2	D	-2.44	D	-2.35	D	-2.69	D	-2.97	D	-2.68	D	-2.62	D	-2.91	D	-2.76	D
1427275_at	Smc4	70099	-2.61	DNA metabolic process	397.9	735.6	1067.8	3584.8	3446	4357.5	8.72E-04	-3.14	D	-3.36	D	-2.92	D	-2.46	D	-2.58	D	-2.18	D	-2.17	D	-2.5	D	-2.16	D
1438434_at	Arhgap11a	228482	-2.6	signal transduction	286.4	198.8	107	1428.1	1726.2	942.6	0.0075479	-2.22	D	-2.36	D	-1.49	D	-2.91	D	-2.71	D	-1.94	D	-3.73	D	-3.27	D	-2.75	D
1458560_at	Aspm	12316	-2.6	cell cycle	142.2	176.6	106.2	1021.1	1397.8	1700.1	0.0033688	-2.77	D	-2.42	D	-2.49	D	-2.26	D	-2.83	D	-2.51	D	-2.6	D	-2.92	D	-2.57	D
1438390_s_at	Pttg1	30939	-2.57	DNA metabolic process	426.2	156.9	652.9	2728.6	2462.5	3061	4.82E-04	-2.78	D	-2.23	D	-2.75	D	-3.57	D	-3.34	D	-3.68	D	-1.76	D	-1.29	D	-1.75	D
1428104_at	Tpx2	72119	-2.55	spindle assembly	93.6	88.7	232.7	1076.9	722.8	988.3	0.0024483	-3.2	D	-2.75	D	-3.56	D	-3.21	D	-2.57	D	-3.02	D	-1.67	D	-1.24	D	-1.76	D
1439252_at			-2.54		368.1	299	512.5	2349.8	2490.7	2712	6.54E-05	-2.35	D	-2.41	D	-2.57	D	-2.71	D	-2.81	D	-3.08	D	-2.16	D	-2.14	D	-2.6	D
1441637_at	F730047E07Rik	212377	-2.54		183.2	17.2	84.1	409.6	329.8	393.8	0.0063619	-1.94	D	-1.57	D	-1.36	D	-4.25	D	-3.72	D	-3.64	D	-2.44	D	-1.87	D	-2.1	D
1417821_at	D17H6S56E-5	110956	-2.52		286.1	250.6	58.4	1361.3	1241.4	1080	6.75E-04	-2.25	D	-2.51	D	-1.74	D	-2.32	D	-2.24	D	-2.44	D	-3.09	D	-3.66	D	-2.43	D
1430127_a_at	Ccnd2	12444	-2.52	regulation of progression through cell cycle	3139.3	1891	1758.5	11570.1	13796.8	10736.2	6.48E-04	-2.1	D	-2.34	D	-1.98	D	-2.6	D	-2.91	D	-2.66	D	-2.65	D	-2.86	D	-2.61	D
1450862_at	Rad54l	19366	-2.5	DNA repair	229.2	336.6	455.3	1154.3	1542.4	1712.5	0.0031359	-2.87	D	-2.68	D	-3.04	D	-2.26	D	-2.22	D	-2.36	D	-2.16	D	-2.38	D	-2.53	D
1423774_a_at	Prc1	233406	-2.48	cytokinesis	109.6	180.4	215.4	911.1	961.6	1401	0.0043497	-2.91	D	-3.33	D	-2.91	D	-2.47	D	-2.46	D	-2.5	D	-1.93	D	-1.85	D	-1.96	D
1448519_at	Tead2	21677	-2.48	transcription	217.5	107.3	100.6	942.1	812.5	748	5.39E-04	-1.83	D	-1.89	D	-1.92	D	-2.84	D	-2.79	D	-2.63	D	-2.96	D	-2.68	D	-2.82	D
1436708_x_at	Mcm4	17217	-2.46	DNA replication	319	240.8	120.1	1182.5	1365.7	1068.7	7.12E-04	-2.08	D	-2.36	D	-1.78	D	-2.24	D	-2.39	D	-2.04	D	-3.29	D	-3.26	D	-2.66	D
1418334_at	Dbf4	27214	-2.43	DNA replication	257.8	269	286.8	1303.3	1406.3	900.8	0.0037989	-2.49	D	-2.65	D	-2.3	D	-2.63	D	-2.59	D	-2.18	D	-2.57	D	-2.55	D	-1.89	D
1452242_at	Cep55	74107	-2.42	cell cycle	141.1	108.1	138.2	802.8	954.1	781.2	2.06E-04	-2.19	D	-2.44	D	-2.02	D	-2.78	D	-2.86	D	-2.67	D	-2.47	D	-2.26	D	-2.07	D
1417457_at	Cks2	66197	-2.41	cytokinesis	150.2	120.7	218	1080.3	1028.5	657	0.005107	-2.68	D	-2.76	D	-2.07	D	-3.15	D	-2.93	D	-2.36	D	-2.08	D	-2.12	D	-1.55	D
1417541_at	Hells	15201	-2.38	urogenital system development	95.3	111.3	118.9	691.9	548.9	559.1	4.57E-04	-2.22	D	-2.49	D	-2.82	D	-2.4	D	-2.25	D	-2.5	D	-2.43	D	-2.01	D	-2.29	D
1423847_at	Ncapd2	68298	-2.37	cell cycle	358.8	233.7	351.5	1742.6	1995.6	1262.6	0.0034789	-1.92	D	-2.22	D	-1.8	D	-2.9	D	-2.97	D	-2.67	D	-2.12	D	-2.62	D	-2.14	D
1434767_at	C79407	217653	-2.37		229.2	181.2	342.9	1355.6	1511.4	1217.9	3.38E-04	-2.62	D	-2.83	D	-2.27	D	-2.48	D	-2.72	D	-2.22	D	-2.1	D	-2.32	D	-1.79	D
1458873_at	Aspm	12316	-2.36	cell cycle	176.3	157.1	273.1	1234.9	1118.6	1106.8	6.28E-05	-2.4	D	-2.28	D	-2.34	D	-2.75	D	-2.64	D	-2.54	D	-2.11	D	-2.15	D	-2.03	D
1417938_at	Rad51ap1	19362	-2.32	double-strand break repair via homologous recombination	70.8	84.3	142.2	848.2	767.7	727.7	8.14E-05	-3.03	D	-3.67	D	-2.88	D	-2.2	D	-2.14	D	-2.47	D	-1.44	D	-1.62	D	-1.47	D
1427276_at	Smc4	70099	-2.32	DNA metabolic process	973.8	1041.7	761.2	5359	5306	4868.6	1.78E-05	-2.08	D	-2.32	D	-1.81	D	-2.34	D	-2.37	D	-2.16	D	-2.6	D	-2.71	D	-2.51	D
1417947_at	Pcna	18538	-2.31	DNA replication	776.3	603.9	738.5	3782.6	3780.3	3660.7	1.34E-06	-2.28	D	-2.19	D	-2.31	D	-2.38	D	-2.49	D	-2.45	D	-2.29	D	-2.24	D	-2.12	D
1422814_at	Aspm	12316	-2.31	cell cycle	92.3	126.3	277.4	724.9	1100	741.4	0.0069164	-2.53	D	-3.31	D	-2.79	D	-2.5	D	-3.09	D	-2.7	D	-0.9	D	-1.77	D	-1.2	D
1426300_at	Alcam	11658	-2.28	cell adhesion	356.3	536.5	787.1	2082.2	2131.6	2525.8	8.52E-04	-2.81	D	-2.73	D	-2.84	D	-2.21	D	-2.09	D	-2.24	D	-1.62	D	-1.98	D	-1.98	D
1422731_at	Limd1	29806	-2.27		1694.6	957	892.2	4215.7	6917.4	5086	0.0072341	-1.42	D	-2.12	D	-1.85	D	-2.26	D	-3.01	D	-2.58	D	-2.05	D	-2.75	D	-2.43	D
1452197_at	Smc4	70099	-2.27	DNA metabolic process	996.5	991.3	777.5	4440.1	5131.9	4131.3	2.79E-04	-2.4	D	-2.48	D	-2.18	D	-2.02	D	-2.2	D	-1.79	D	-2.61	D	-2.57	D	-2.15	D
1415878_at	Rrm1	20133	-2.26	DNA replication	557.3	513.9	598.8	2133.1	2273.2	2148.9	5.57E-06	-2.39	D	-2.18	D	-2.12	D	-2.29	D	-2.41	D	-2.22	D	-2.25	D	-2.33	D	-2.19	D
1451358_a_at	Racgap1	26934	-2.24	cytokinesis	426	309.8	238.3	1589.5	1689.9	1137.8	0.0030017	-2.19	D	-2.27	D	-1.94	D	-2.25	D	-2.39	D	-1.88	D	-2.48	D	-2.63	D	-2.15	D
1432361_a_at	Cenpp	66336	-2.23		74	115.7	74	272.5	340.9	280.6	0.0012131	-2.16	D	-2.24	D	-1.99	D	-2.31	D	-1.93	D	-1.99	D	-2.37	D	-2.57	D	-2.51	D
1442134_at	Prr11	270906	-2.23		117.6	400.5	178.3	1033.7	1031.9	1085.8	7.37E-04	-2.96	D	-3.18	D	-2.89	D	-1.42	D	-1.01	D	-1.57	D	-2	D	-2.65	D	-2.42	D
1422948_s_at	Hist1h4a	319155	-2.22	nucleosome assembly	5971.7	5947	3840.2	25169.5	22071.5	24737.6	9.78E-05	-2.18	D	-1.87	D	-2.12	D	-2.08	D	-1.88	D	-2.03	D	-2.69	D	-2.46	D	-2.66	D
1456032_x_at	EG666634	51788	-2.2	nucleosome assembly	748.6	1150.1	981.3	5145	6188.7	4248.1	0.0017851	-2.26	D	-2.76	D	-1.81	D	-1.94	D	-2.26	D	-1.64	D	-2.43	D	-2.65	D	-2.08	D
1439436_x_at	Incenp	16319	-2.12	cytokinesis	244	397.5	249.5	1664.5	1615.3	1429.2	1.30E-04	-2.35	D	-2.51	D	-2.22	D	-1.85	D	-1.61	D	-1.78	D	-2.41	D	-2.1	D	-2.25	D
1452115_a_at	Plk4	20873	-2.12	protein amino acid phosphorylation	99.5	148.4	196.9	608.6	591.2	624	1.01E-04	-2.82	D	-2.68	D	-2.65	D	-2.2	D	-2.01	D	-2.08	D	-1.45	D	-1.48	D	-1.67	D
1422040_at	Sema7a	20361	-2.09	multicellular organismal development	153.6	34.3	121.4	324.7	503.1	392.5	0.0085369	-1.05	D	-1.72	D	-1.44	D	-2.89	D	-3.93	D	-3.31	D	-1.14	D	-1.65	D	-1.67	D
1418369_at	Prim1	19075	-2.08	DNA replication	178	316.1	245	1336.9	1242.3	1119	1.89E-04	-2.48	D	-2.54	D	-2.34	D	-1.94	D	-1.84	D	-1.68	D	-2.08	D	-1.96	D	-1.86	D
1419172_at	Dhfr	13361	-2.06	glycine biosynthetic process	174.6	480.7	314.6	1072	857.4	1123.2	0.0044671	-2.43	D	-2.22	D	-3.01	D	-1.74	D	-1.95	D	-2.06	D	-1.73	D	-1.47	D	-1.89	D
1422398_at	Hist1h1e	50709	-2.06	nucleosome assembly	5164.3	4573.5	3541.5	21308.2	21494.1	21796.4	4.19E-06	-1.95	D	-2.15	D	-1.9	D	-1.71	D	-2.03	D	-1.72	D	-2.27	D	-2.49	D	-2.28	D
1448127_at	Rrm1	20133	-2.06	DNA replication	1278.3	1764.6	1509.1	6014.3	5475.5	4533.9	0.0010955	-2.25	D	-2.13	D	-1.96	D	-1.82	D	-1.75	D	-1.55	D	-2.45	D	-2.43	D	-2.23	D
1438320_s_at	Mcm7	17220	-2.04	DNA replication	1203.2	1036.2	783.5	3775.7	4360	4245.3	1.35E-04	-1.81	D	-1.79	D	-1.81	D	-1.87	D	-2.04	D	-1.95	D	-2.3	D	-2.38	D	-2.44	D
1426301_at	Alcam	11658	-2.02	cell adhesion	780.1	572.2	901.4	2556.9	2949.7	2570.9	2.69E-04	-2	D	-2.1	D	-1.71	D	-2.44	D	-2.58	D	-2.13	D	-1.81	D	-1.88	D	-1.54	D
1429734_at	4632434I11Rik	74041	-2.02		50.6	275.5	258.8	922.8	786.7	666.6	0.0044808	-3.07	D	-3.51	D	-4.04	D	-1.44	D	-1.24	D	-1.47	D	-1.28	D	-1.17	D	-0.92	D
1416415_a_at	EG666634	51788	-2.01	nucleosome assembly	2181	2425.6	1933.3	10753.9	9093.1	9122.5	1.91E-04	-2.08	D	-2.08	D	-1.74	D	-1.97	D	-1.96	D	-1.66	D	-2.26	D	-2.36	D	-1.98	D
1436174_at	Atad2	70472	-2.01		172.8	195.9	215.8	1031.5	899.3	1195.2	6.09E-04	-2.61	D	-1.94	D	-2.3	D	-2.2	D	-2.01	D	-2.11	D	-1.29	D	-1.71	D	-1.95	D
1422944_a_at	Diap3	56419	-2	cellular component organization and biogenesis	122.8	166.3	168	695.9	625.7	588	1.57E-04	-2.68	D	-2.44	D	-2.37	D	-2.25	D	-2.1	D	-2.05	D	-1.54	D	-1.26	D	-1.29	D
1440633_at	Neil3	234258	-1.99	DNA repair	250.7	85.6	236.2	660.5	883.7	689.9	0.0032129	-1.59	D	-1.86	D	-1.49	D	-2.97	D	-3.16	D	-3	D	-1.15	D	-1.43	D	-1.23	D
1460247_a_at	Skp2	27401	-1.99	regulation of progression through cell cycle	1427.9	964.9	1367.8	4756.8	4940.2	4882.6	2.03E-05	-1.72	D	-1.84	D	-1.74	D	-2.07	D	-2.15	D	-2	D	-2.15	D	-2.17	D	-2.03	D
1438091_a_at	H2afz	51788	-1.97	nucleosome assembly	2543	1832.8	1277.4	6801.9	7856.1	6859.7	4.57E-04	-1.44	D	-1.65	D	-1.38	D	-1.83	D	-1.99	D	-1.82	D	-2.54	D	-2.66	D	-2.41	D
1418969_at	Skp2	27401	-1.94	regulation of progression through cell cycle	702.8	745.6	513.9	3031.2	3835.4	2263	0.006519	-1.61	D	-2.11	D	-1.52	D	-1.61	D	-2.09	D	-1.64	D	-2.16	D	-2.68	D	-2.06	D
1445298_at			-1.93		202.7	161.9	182.4	955	671.1	631.4	0.0051282	-1.98	D	-2	D	-1.3	D	-2.66	D	-2.3	D	-1.69	D	-2.13	D	-1.9	D	-1.39	D
1452036_a_at	Tmpo	21917	-1.93	regulation of transcription	965.7	909	825	3368	3089.3	3033.4	3.45E-05	-1.89	D	-2.09	D	-1.56	D	-1.79	D	-2.01	D	-1.4	D	-2.24	D	-2.38	D	-2.04	D
1438092_x_at	EG666634	51788	-1.91	nucleosome assembly	2464.9	1905.7	1393.7	6647.5	7742.6	5375.3	0.0034076	-1.72	D	-1.91	D	-1.44	D	-1.88	D	-2.03	D	-1.58	D	-2.26	D	-2.41	D	-1.99	D
1428230_at	Prkcn	75292	-1.9	protein amino acid phosphorylation	1692.8	2399.2	1325.7	5915.7	7415.9	7905.3	0.0014604	-1.65	D	-1.94	D	-2.02	D	-1.3	D	-1.64	D	-1.73	D	-2.07	D	-2.33	D	-2.38	D
1436600_at	Tox3	244579	-1.9	regulation of transcription, DNA-dependent	349	472.8	615.2	1681	2042.3	1693	7.17E-04	-1.92	D	-2.21	D	-1.94	D	-1.84	D	-2.04	D	-1.62	D	-1.73	D	-2.22	D	-1.54	D
1423775_s_at	Prc1	233406	-1.86	cytokinesis	273.7	241.4	127.5	1008.1	959.1	1360.9	0.0026179	-1.57	D	-1.31	D	-1.26	D	-1.39	D	-1.71	D	-1.72	D	-2.47	D	-2.56	D	-2.78	D
1424511_at	Aurka	20878	-1.86	mitotic cell cycle	93	319.3	221.5	855.3	634.6	701	0.004968	-2.75	D	-2.68	D	-2.63	D	-1.14	D	-0.97	D	-0.99	D	-1.9	D	-1.74	D	-1.98	D
1423393_at	Clic4	29876	-1.84	transport	3547.9	3683.2	3754.2	11386.6	15876.5	12309.2	0.0022474	-1.69	D	-2.19	D	-1.75	D	-1.63	D	-2.15	D	-1.73	D	-1.6	D	-2.11	D	-1.67	D
1424143_a_at	Cdt1	67177	-1.84	DNA replication checkpoint	268.6	306	291.6	1175.5	1003.9	1249.9	3.16E-04	-2.13	D	-1.88	D	-2.06	D	-1.67	D	-1.61	D	-1.92	D	-1.73	D	-1.64	D	-1.91	D
1437467_at	Alcam	11658	-1.84	cell adhesion	328.6	133.7	251.3	1154.2	743.6	1049.3	0.0053579	-1.47	D	-0.92	D	-1.44	D	-2.66	D	-2.21	D	-2.83	D	-1.7	D	-1.47	D	-1.89	D
1417082_at	Anp32b	67628	-1.83	S phase of mitotic cell cycle	623.9	470.1	508	1375.9	1647.2	1529.9	4.18E-04	-1.41	D	-1.5	D	-1.48	D	-2.2	D	-2.61	D	-2.35	D	-1.3	D	-1.84	D	-1.74	D
1418494_at	Ebf2	13592	-1.81	transcription	436.1	279.8	415	965.7	1203.5	989.9	0.0016833	-1.63	D	-1.94	D	-1.59	D	-1.92	D	-2.38	D	-2.09	D	-1.35	D	-1.88	D	-1.48	D
1428976_at	Tmpo	21917	-1.81	regulation of transcription	504.9	436.8	386.1	1427.4	1682.6	1263.3	0.0013182	-1.22	D	-1.66	D	-1.16	D	-1.68	D	-2.27	D	-1.75	D	-2.07	D	-2.26	D	-2.23	D
1443744_at			-1.81		4570.7	4540.4	6657.1	18222.4	19250	23663.8	0.0011224	-1.88	D	-1.93	D	-2.05	D	-1.71	D	-1.78	D	-2.03	D	-1.56	D	-1.63	D	-1.72	D
1437033_a_at	Skp2	27401	-1.8	regulation of progression through cell cycle	357.5	293.7	508.4	992.2	778.4	963.2	0.0047429	-1.65	D	-1.73	D	-1.62	D	-2.07	D	-2.14	D	-1.69	D	-1.74	D	-1.74	D	-1.79	D
1449061_a_at	Prim1	19075	-1.8	DNA replication	70.1	111.2	133.2	373.1	461.5	366.7	0.0011667	-1.87	D	-2.27	D	-2.17	D	-1.26	D	-1.63	D	-1.94	D	-1.59	D	-1.94	D	-1.53	D
1449822_at	Atoh1	11921	-1.8	neuron migration	211.3	377.7	266.6	1041	1138.8	1216.2	2.75E-04	-1.01	D	-1.51	D	-1.72	D	-1.82	D	-1.45	D	-2	D	-1.92	D	-2.21	D	-2.54	D
1423674_at	Usp1	230484	-1.79	ubiquitin-dependent protein catabolic process	1805.5	1663	1336.7	5208.5	5489.9	4232.6	0.0011376	-1.73	D	-1.7	D	-1.57	D	-1.8	D	-1.8	D	-1.64	D	-2.04	D	-2	D	-1.82	D
1421731_a_at	Fen1	14156	-1.78	DNA replication	267.2	193.4	167.3	759.1	811.3	723	1.47E-04	-1.81	D	-1.69	D	-1.29	D	-1.83	D	-1.91	D	-1.62	D	-1.94	D	-1.95	D	-2.02	D
1452114_s_at	Igfbp5	16011	-1.78	regulation of cell growth	1531.1	1671.9	2112.9	4731.7	7166.4	6213.3	0.0042721	-1.64	D	-2.32	D	-1.99	D	-1.48	D	-2.16	D	-1.79	D	-1.16	D	-1.89	D	-1.55	D
1417222_a_at	Tmem123	71929	-1.76		162.3	143.3	148	589	768.4	678.2	5.36E-04	-2.11	D	-2.24	D	-1.96	D	-1.95	D	-1.94	D	-1.28	D	-1.58	D	-1.6	D	-1.14	D

1447930_at	Baz1a	217578	-1.76	chromatin remodeling	306.3	277.9	356.8	1036.4	1086.7	1100	1.46E-05	-1.57	D	-2.13	D	-1.76	D	-1.88	D	-2.43	D	-2.5	D	-0.74	D	-1.32	D	-1.52	D
1456573_x_at	Nnt	18115	-1.76	electron transport	283.4	266.9	336	1177.6	1463.6	924.8	0.0047163	-2.17	D	-1.76	D	-1.81	D	-1.97	D	-1.77	D	-1.47	D	-1.74	D	-1.63	D	-1.48	D
1438292_x_at	Adk	11534	-1.74	purine ribonucleoside salvage	501.8	369.8	160.8	1000.3	1112.5	807.1	0.0092086	-1.16	D	-1.41	D	-1.23	D	-1.39	D	-1.56	D	-1.58	D	-2.25	D	-2.62	D	-2.47	D
1439270_x_at	LOC625094	19384	-1.74	regulation of progression through cell cycle	3091.4	3100.9	2903.8	10221.2	10210.8	9170.2	4.26E-05	-1.71	D	-1.72	D	-1.65	D	-1.76	D	-1.7	D	-1.73	D	-1.83	D	-1.78	D	-1.76	D
1418366_at	Hist1h2ad	15267	-1.72	nucleosome assembly	984.2	906.1	939.5	3168.4	2374.9	3194.8	0.0018769	-1.79	D	-1.6	D	-2.08	D	-1.57	D	-1.34	D	-1.76	D	-1.82	D	-1.58	D	-1.94	D
1425050_at	Isoc1	66307	-1.72	metabolic process	1899	1508	1615.9	4825.9	6742.5	6424.4	0.0020207	-1.3	D	-1.68	D	-1.56	D	-1.63	D	-1.92	D	-1.86	D	-1.66	D	-1.89	D	-1.96	D
1452241_at	Topbp1	235559	-1.72	DNA repair	244.4	217	383.5	761.6	1063.4	761	0.006837	-1.76	D	-2.07	D	-1.77	D	-1.88	D	-2.05	D	-1.66	D	-1.37	D	-1.76	D	-1.19	D
1417420_at	Ccnd1	12443	-1.71	regulation of progression through cell cycle	632	761.8	620.5	1677.5	1970	1747.2	3.42E-04	-1.39	D	-1.63	D	-1.6	D	-1.37	D	-1.42	D	-1.34	D	-2.22	D	-2.29	D	-2.11	D
1421237_at	Tmpo	21917	-1.71	regulation of transcription	318.4	392.9	237.6	865.6	1057.9	814.2	0.002339	-1.55	D	-1.36	D	-1.52	D	-1.5	D	-1.42	D	-1.27	D	-2.19	D	-2.24	D	-2.36	D
1434410_at	BC043118	224273	-1.7		142.1	401.6	151	956	687.4	784.3	0.0075442	-2.36	D	-1.98	D	-1.71	D	-1.32	D	-0.9	D	-0.93	D	-2.32	D	-2.02	D	-1.74	D
1451782_a_at	Slc29a1	63959	-1.69	transport	838.9	985.9	655.3	3272.5	2945.5	2718.8	3.25E-04	-1.48	D	-1.47	D	-1.66	D	-1.53	D	-1.34	D	-1.3	D	-2.24	D	-2.11	D	-2.08	D
1454686_at	6430706D22Rik	381280	-1.68		353.6	350.3	409.8	1212.8	1469.2	1310	2.41E-04	-1.72	D	-1.89	D	-1.33	D	-1.98	D	-1.93	D	-1.68	D	-1.53	D	-1.82	D	-1.25	D
1416746_at	H2afx	15270	-1.67	DNA damage checkpoint	550.5	487.7	776.7	1894.3	2009.7	2120.8	2.13E-04	-1.44	D	-1.22	D	-1.89	D	-2.24	D	-1.74	D	-2.26	D	-1.54	D	-0.94	D	-1.73	D
1415829_at	Lbr	98386	-1.66	nucleic acid binding	475.7	589.3	398.1	1538.4	1827.2	1165	0.006868	-1.69	D	-2.02	D	-1.51	D	-1.4	D	-1.77	D	-1.28	D	-1.63	D	-2.13	D	-1.47	D
1434578_x_at	LOC625094	19384	-1.66	regulation of progression through cell cycle	1947.7	2538.7	1903.2	6805.6	5987	5275.8	0.0013292	-1.86	D	-1.75	D	-1.63	D	-1.68	D	-1.55	D	-1.49	D	-1.78	D	-1.7	D	-1.52	D
1438606_a_at	Clic4	29876	-1.66	transport	960.9	876.3	979.6	2940.9	3375.8	3343.8	9.15E-05	-1.59	D	-1.71	D	-1.61	D	-1.74	D	-1.85	D	-1.82	D	-1.58	D	-1.67	D	-1.38	D
1419254_at	Mthfd2	17768	-1.64	one-carbon compound metabolic process	465.3	433.4	256.3	1113.6	1049.7	999.2	7.84E-04	-1.37	D	-1.48	D	-1.55	D	-1.52	D	-1.44	D	-1.37	D	-2.09	D	-2.14	D	-1.8	D
1421951_at	Lhx1	16869	-1.64	endoderm formation	3357.1	3193.7	2787.3	7955.5	10046.4	10058.1	9.71E-04	-1.46	D	-1.78	D	-1.72	D	-1.45	D	-1.76	D	-1.83	D	-1.38	D	-1.56	D	-1.84	D
1435509_x_at	Cdk2ap1	13445	-1.64	cell cycle	2396.2	2193.5	1581	6468.4	7210.1	6180.7	3.13E-04	-1.36	D	-1.56	D	-1.34	D	-1.47	D	-1.78	D	-1.5	D	-1.84	D	-2.08	D	-1.8	D
1449207_a_at	Kif20a	19348	-1.64	transport	217.7	182.5	99.7	465.6	547.2	568.9	0.0015559	-1.44	D	-1.24	D	-1.42	D	-1.37	D	-1.6	D	-1.34	D	-2.16	D	-2.06	D	-2.1	D
1445073_at			-1.63		869.8	921.6	1210.9	2592.9	2029.5	2385.6	0.0024164	-1.85	D	-1.9	D	-1.95	D	-1.73	D	-1.55	D	-1.71	D	-1.29	D	-1.29	D	-1.42	D
1433507_a_at	Hmgn2	15331	-1.61	DNA packaging	10070.5	10225	10115.1	30536.2	32897.8	29165.7	4.52E-05	-1.67	D	-1.81	D	-1.69	D	-1.64	D	-1.68	D	-1.46	D	-1.5	D	-1.57	D	-1.43	D
1456314_x_at	Cdk2ap1	13445	-1.61	cell cycle	3045.1	1597.5	1301.9	6284	8347.9	6869.6	0.0031537	-1.24	D	-1.53	D	-1.26	D	-1.38	D	-1.67	D	-1.39	D	-1.79	D	-2.24	D	-2.01	D
1426612_at	Tipin	66131	-1.6		244.7	276.7	422.6	805.6	937.1	1133.3	0.0042235	-1.69	D	-1.84	D	-2.42	D	-1.61	D	-1.57	D	-1.58	D	-1.21	D	-1.01	D	-1.46	D
1416214_at	Mcm4	17217	-1.58	DNA replication	304.6	391.9	457.9	991.3	942	1075.7	4.73E-04	-2.06	D	-2.18	D	-2.14	D	-1.37	D	-1.35	D	-1.45	D	-1.23	D	-1.2	D	-1.28	D
1416030_a_at	Mcm7	17220	-1.57	DNA replication	302.4	193.3	311.7	914.1	952.3	818	3.44E-04	-1.49	D	-1.61	D	-1.56	D	-1.92	D	-1.91	D	-1.89	D	-1.11	D	-1.43	D	-1.17	D
1434891_at	Ptgfrn	19221	-1.57	negative regulation of protein biosynthetic process	264.3	404.4	419.1	1070.4	1351.4	898.9	0.0061471	-1.39	D	-1.63	D	-1.86	D	-1.73	D	-1.91	D	-1.55	D	-1.27	D	-1.42	D	-1.41	D
1451456_at	6430706D22Rik	381280	-1.57		313.1	240.2	251.9	714.1	903.3	603.9	0.0063954	-1.16	D	-1.76	D	-1.37	D	-1.48	D	-2.14	D	-1.55	D	-1.37	D	-1.92	D	-1.37	D
1417587_at	Timeless	21853	-1.55	morphogenesis of an epithelium	171.4	274.4	242	929	844.5	793	2.33E-04	-1.79	D	-1.86	D	-1.59	D	-1.53	D	-1.73	D	-1.42	D	-1.39	D	-1.54	D	-1.14	D
1427048_at	Smo	319757	-1.55	vasculogenesis	282.6	494.4	356.8	1098.4	1135.3	1449.4	0.0026316	-2.22	D	-2.03	D	-2.03	D	-1.11	D	-1.26	D	-1.48	D	-1.29	D	-1.19	D	-1.38	D
1438977_x_at	LOC625094	19384	-1.55	regulation of progression through cell cycle	2260.4	2058.4	2147.7	6950.4	6084.6	6060.7	1.47E-04	-1.62	D	-1.37	D	-1.34	D	-1.86	D	-1.67	D	-1.56	D	-1.67	D	-1.42	D	-1.41	D
1423675_at	Usp1	230484	-1.53	ubiquitin-dependent protein catabolic process	746.1	840	273.3	1904.8	1656.8	1595	0.0052751	-1.31	D	-1.45	D	-1.24	D	-1.21	D	-1.13	D	-0.9	D	-2.4	D	-2.15	D	-2.01	D
1427863_at	Hist1h3d	319149	-1.53	nucleosome assembly	469.7	844.2	809.1	3286.5	2607.7	2156.5	0.0048199	-2.1	D	-1.18	D	-1.46	D	-1.76	D	-1.52	D	-1.37	D	-1.92	D	-1.28	D	-1.18	D
1431430_s_at	LOC630539	630539	-1.53		781.5	762.7	674.3	2462.2	1847.7	3158.1	0.0099911	-1.54	D	-1.16	D	-1.14	D	-1.79	D	-1.55	D	-1.61	D	-1.71	D	-1.6	D	-1.63	D
1436959_x_at	Nelf	56876	-1.53		279.9	231.8	287.2	678.4	792.2	996.3	0.0041881	-1.21	D	-1.15	D	-1.23	D	-1.72	D	-1.84	D	-2.5	D	-1.17	D	-1.37	D	-1.59	D
1441677_at	Smc4	70099	-1.52	DNA metabolic process	236.5	284.3	460.8	988	759.5	1071.8	0.00609	-1.64	D	-1.07	D	-1.49	D	-1.58	D	-1.28	D	-1.8	D	-1.66	D	-1.36	D	-1.84	D
1451346_at	Mtap	66902	-1.52	nucleotide and nucleic acid metabolic process	431.7	362	374.4	1008.3	1218.4	792.1	0.007827	-1.62	D	-1.92	D	-1.16	D	-1.23	D	-2.01	D	-1.54	D	-1.35	D	-1.84	D	-1.01	D
1460354_a_at	Mrpl13	68537	-1.52	translation	228.6	205.9	172.5	628.2	563.5	528.8	3.72E-04	-1.16	D	-1.14	D	-1.23	D	-1.47	D	-1.5	D	-1.47	D	-1.63	D	-1.97	D	-2.13	D
1459388_at			-1.51		597	609.6	688.4	1770.8	1327.9	1962.6	0.0051505	-1.47	D	-1.12	D	-1.47	D	-1.7	D	-1.42	D	-1.9	D	-1.51	D	-1.21	D	-1.81	D
1426752_at	Phf17	269424	-1.5	transcription	889.5	922.7	1351.2	2261.9	3333.1	2803.6	0.0070517	-1.5	D	-1.88	D	-1.98	D	-1.28	D	-1.83	D	-1.57	D	-0.85	D	-1.41	D	-1.16	D
1421883_at	Elavl2	15569	-1.49		2349.3	1940.1	1670.9	4499.3	5505.4	4355.6	0.0024479	-1.44	D	-1.58	D	-1.48	D	-1.56	D	-1.65	D	-1.59	D	-1.29	D	-1.4	D	-1.43	D
1433569_x_at	LOC625094	19384	-1.49	regulation of progression through cell cycle	3664.2	3342.5	3176.7	8989	8691.9	8349.3	2.27E-05	-1.42	D	-1.25	D	-1.31	D	-1.61	D	-1.49	D	-1.58	D	-1.61	D	-1.57	D	-1.54	D
1456513_at	Ebf3	13593	-1.49	transcription	389.7	706.6	813.9	1968.2	1382	1674.9	0.0080285	-1.93	D	-1.36	D	-1.78	D	-1.78	D	-1.42	D	-1.92	D	-1.18	D	-0.75	D	-1.31	D
1416031_s_at	Mcm7	17220	-1.48	DNA replication	555.8	593.9	531.6	861.6	1100.4	1010.1	0.0039277	-1.03	D	-1.66	D	-1.23	D	-1.15	D	-1.63	D	-1.49	D	-1.37	D	-2.03	D	-1.77	D
1416124_at	Ccnd2	12444	-1.48	regulation of progression through cell cycle	955.3	686	931.4	4192.8	3740.8	4575.1	2.06E-04	-1.12	D	-1.22	D	-1.43	D	-1.54	D	-1.7	D	-1.8	D	-1.34	D	-1.46	D	-1.75	D
1452659_at	Dek	110052	-1.48		1900.9	2110.2	1871.1	5101.1	6000	4773.7	8.81E-04	-1.35	D	-1.65	D	-1.32	D	-1.41	D	-1.62	D	-1.24	D	-1.48	D	-1.79	D	-1.45	D
1415888_at	Hdgf	15191	-1.47	cellular process	8222.9	7812.5	5252.9	18409.8	22543.8	20313	9.18E-04	-1.09	D	-1.4	D	-1.31	D	-1.23	D	-1.45	D	-1.37	D	-1.67	D	-1.91	D	-1.76	D
1451080_at	Usp1	230484	-1.47	ubiquitin-dependent protein catabolic process	926.1	918.4	1088.9	2574.1	3126.5	2402.5	0.0015723	-1.42	D	-1.56	D	-1.43	D	-1.43	D	-1.58	D	-1.39	D	-1.5	D	-1.65	D	-1.3	D
1436193_at	Man1c1	230815	-1.46	mannose metabolic process	1796.4	1738.5	1973.8	4402.8	4276.6	4526.6	1.43E-05	-1.58	D	-1.58	D	-1.68	D	-1.34	D	-1.44	D	-1.63	D	-1.25	D	-1.21	D	-1.44	D
1438168_x_at	Ddx39	68278	-1.46	mRNA processing	342.3	513.8	519.2	1529.8	1659.9	1319.6	8.12E-04	-1.74	D	-1.73	D	-1.59	D	-1.37	D	-1.47	D	-1.44	D	-1.29	D	-1.36	D	-1.16	D
1418566_s_at	Nudcd2	52653	-1.45		847.7	984.6	743	2508.4	2859.1	2207.8	0.0011501	-1.57	D	-1.79	D	-1.28	D	-1.36	D	-1.33	D	-0.91	D	-1.63	D	-1.9	D	-1.24	D
1421882_a_at	Elavl2	15569	-1.45		2901.3	3271.2	2927.7	7511.6	9585.4	6391.5	0.0070553	-1.51	D	-1.7	D	-1.23	D	-1.27	D	-1.51	D	-1.03	D	-1.67	D	-1.84	D	-1.31	D
1422439_a_at	Cdk4	12567	-1.45	regulation of progression through cell cycle	648.3	606.8	722.1	1979.1	1769.5	1752	1.28E-04	-1.35	D	-1.2	D	-1.18	D	-1.72	D	-1.65	D	-1.55	D	-1.49	D	-1.46	D	-1.42	D
1455963_at	6332401O19Rik	319832	-1.45		469.2	468.9	323.7	1144.1	1664.4	1094.7	0.0095218	-0.74	D	-1.59	D	-0.89	D	-1.19	D	-1.74	D	-1.06	D	-1.82	D	-2.24	D	-1.76	D
1456730_x_at	Actl6a	56456	-1.44	regulation of cell growth	620.7	672.6	305.8	1852.4	1498.4	1347.8	0.0053865	-1.31	D	-1.4	D	-0.94	D	-1.33	D	-1.23	D	-1.16	D	-2.17	D	-1.92	D	-1.46	D
1421399_at	Insm1	53626	-1.43	cell differentiation	2660.6	4066	4195.2	9541.8	9550.5	9425.5	2.86E-04	-1.61	D	-1.62	D	-1.64	D	-1.36	D	-1.42	D	-1.39	D	-1.31	D	-1.37	D	-1.16	D
1444295_at	Neo1	18007	-1.42	protein amino acid phosphorylation	947.4	1026.2	729.3	2113.7	2257	2575.9	9.69E-04	-1.16	D	-1.27	D	-1.28	D	-1.19	D	-1.44	D	-1.27	D	-1.61	D	-1.83	D	-1.72	D
1455814_x_at	Ddx39	68278	-1.42	mRNA processing	603	589.8	457.7	1568.6	1658.2	1275.5	0.0015817	-1.2	D	-1.17	D	-0.92	D	-1.51	D	-1.4	D	-1.12	D	-2.02	D	-1.85	D	-1.63	D
1450428_at	Lhx1	16869	-1.41	endoderm formation	970.2	1024.6	914.8	2085.2	2822.8	2728.4	0.0025306	-1.27	D	-1.65	D	-1.48	D	-1.28	D	-1.43	D	-1.48	D	-1.2	D	-1.42	D	-1.44	D
1423520_at	Lmnb1	16906	-1.39		2068.3	2726.6	1522.7	6848.2	6684.3	5428.4	0.001757	-1.47	D	-1.52	D	-1.09	D	-1.26	D	-1.07	D	-0.9	D	-1.88	D	-1.79	D	-1.54	D
1429295_s_at	Trip13	69716	-1.39		191.1	241.1	171.6	509.9	624.9	472.9	0.0026366	-1.46	D	-1.51	D	-1.34	D	-1.13	D	-1.06	D	-0.99	D	-1.59	D	-1.98	D	-1.46	D
1420592_a_at	Anp32e	66471	-1.38		926.1	783.4	931.2	1943.1	2445.9	1883.6	0.0028077	-1.09	D	-1.26	D	-1.14	D	-1.58	D	-2.05	D	-1.55	D	-1.19	D	-1.38	D	-1.19	D
1438015_at	Dkc1	245474	-1.38	rRNA modification	658.2	581.6	402.6	1646.9	1561.6	1643.9	1.87E-04	-1.1	D	-1.34	D	-0.7	D	-1.35	D	-1.25	D	-1.35	D	-1.79	D	-1.73	D	-1.84	D
1452226_at	Rcc2	108911	-1.38	cell cycle	527.5	720	555.3	1860.2	2232.4	1438.4	0.0063336	-1.54	D	-1.73	D	-1.38	D	-1.21	D	-1.24	D	-0.95	D	-1.45	D	-1.64	D	-1.32	D
1420894_at	Tgfbr1	21812	-1.33	skeletal development	336.9	321.1	462.2	1160.1	928.6	931.9	0.0020312	-1.12	D	-1.47	D	-1.28	D	-1.53	D	-1.49	D	-1.61	D	-0.91	D	-1.42	D	-1.11	D
1416683_at	Plxnb2	140570	-1.32	multicellular organismal development	530.4	740.3	577.1	1310.1	1514.9	1405.7	7.95E-04	-1.32	D	-1.45	D	-1.57	D	-1.21	D	-1.14	D	-1.24	D	-1.18	D	-1.34	D	-1.47	D
1418367_x_at	Hist1h2ad	15267	-1.32	nucleosome assembly	2218.2	1750.1	1319.3	5867.2	4503.6	5910.7	0.0022936	-1.43	D	-1.04	D	-1.36	D	-1.33	D	-1.1	D	-1.32	D	-1.55	D	-1.2	D	-1.54	D
1450644_at	Zfp36l1	12192	-1.32	vasculogenesis	8613.9	8247.8	9336.7	21410.1	18961.8	24084.6	0.0010863	-1.36	D	-1.32	D	-1.56	D	-1.32	D	-1.27	D	-1.48	D	-1.18	D	-1.03	D	-1.38	D
1457886_at	LOC552873	552873	-1.32		588.3	752	400.9	1613.1	1171.4	1636.7	0.0080218	-1.55	D	-1.08	D	-1.42	D	-1.26	D	-0.77	D	-1.02	D	-1.93	D	-1.36	D	-1.45	D
1458514_at	AA536887	101458	-1.31		823.4	360.1	766.1	1505	1491.7	1454.9	0.004714	-1.13	D	-1	D	-1.33	D	-1.78	D	-1.61	D	-1.71	D	-1.02	D	-1.17	D	-1.04	D
1416042_s_at	Nasp	50927	-1.3	regulation of progression through cell cycle	688.1	962.3	794	2039.4	1633.7	1637.5	0.0036434	-1.52	D	-1.21	D	-1.21	D	-1.26	D	-1.25	D	-1.06	D	-1.54	D	-1.45	D	-1.24	D
1433883_at	Tpm4	326618	-1.3		1286.6	1280.1	1281.9	3432.1	4249.5	2876.1	0.0049698	-1.25	D	-1.44	D	-1.18	D	-1.31	D	-1.54	D	-1.18	D	-1.27	D	-1.47	D	-1.06	D
1437309_a_at	Rpa1	68275	-1.3	DNA replication	533.6	705.1	525	1860.1	1843.5	1446.5	0.001561	-1.61	D	-1.4	D	-1.25	D	-1.14	D	-1.19	D	-1.21	D	-1.33	D	-1.44	D	-1.16	D
1423416_at	Smarcc1	20588	-1.28	DNA packaging	3000.5	2213.4	2597.1	6266.4	6441.5	6364	8.66E-05	-1.07	D	-1.09	D	-1.33	D	-1.43	D	-1.38	D	-1.61	D	-1.15	D	-1.11	D	-1.33	D
1452287_at			-1.27		819.9	1025.9	920.9	2246.8	2270.5	2303.6	2.57E-05	-1.07	D	-0.96	D	-1.25	D	-1.47	D	-1.38	D	-1.36	D	-1.32	D	-1.33	D	-1.32	D
1416701_at	Rnd3	74194	-1.26	actin filament organization	1203.9	876.1	660.9	1978.2	2343	2379.6	0.0029035	-0.75	D	-1.03	D	-0.92	D	-1.08	D	-1.4	D	-1.16	D	-1.42	D	-1.91	D	-1.67	D
1434700_at	6030408C04Rik	217558	-1.26	protein modification process	1531.6	1467.6	1148.6	2601.7	3425.3	3143.2	0.0033996	-1.21	D	-1.56	D	-0.98	D	-0.91	D	-1.34	D	-0.81	D	-1.43	D	-1.74	D	-1.4	D
1455869_at	Camk2b	12323	-1.26	G1/S transition of mitotic cell cycle	18217.7	9469.8	10047.4	26783.6	30614.8	28309	0.0062261	-0.66	D	-0.72	D	-0.67	D	-1.53	D	-1.65	D	-1.58	D	-1.47	D	-1.59	D	-1.46	D
1428136_at	Sfrp1	20377	-1.24	somitogenesis	727.2	485	646.3	1141.5	1348	1425.1	0.0034499	-0.94	D	-1.05	D	-1.32	D	-1.34	D	-1.5	D	-1.63	D	-0.91	D	-1.14	D	-1.35	D
1437807_x_at	Ctnna1	12385	-1.24	cell adhesion	581.3	431.9	500.9	1301.2	1319.7	1330.8	5.07E-05	-1.23	D	-1.07	D	-1.03	D	-1.79	D	-1.49	D	-1.47	D	-1.21	D	-0.9	D	-0.95	D
1439463_x_at	EG434174	15289	-1.24	DNA packaging	3592.1	3273	4325.6	9384.8	8909.8	8691.6	1.46E-04	-1.22	D	-1.24	D	-1.22	D	-1.34	D	-1.35	D	-1.37	D	-1.17	D	-1.15	D	-1.11	D
1416544_at	Ezh2	14056	-1.23	transcription	1012.8	898.9	877	2158.7	2227	2090.3	2.87E-05	-1.37	D	-1.28	D	-1.11	D	-1.3	D	-1.32	D	-1.08	D	-1.3	D	-1.27	D	-1.01	D
1423564_a_at	Paics	67054	-1.23	purine nucleotide biosynthetic process	837	1085.8	668.7	2225.7	3003.3	2010.5	0.0088549	-0.82	D	-1.18	D	-0.84	D	-0.86	D	-1.2	D	-0.77	D	-1.71	D	-1.99	D	-1.71	D
1429556_at	2610024B07Rik	269987	-1.23		621.4	609.2	637	1391.2	1406.6	1660.5	5.96E-04	-1.37	D	-1.47	D	-1.56	D	-1.27	D	-1.38	D	-1.72	D	-0.68	D	-0.73	D	-0.88	D

1437179_at	LOC671598	51869	-1.23	response to DNA damage stimulus	1154.4	1446.7	1020.7	2718.5	2019.3	2370.1	0.0081252	-1.46	D	-1.02	D	-1.35	D	-1.25	D	-0.9	D	-0.96	D	-1.53	D	-1.13	D	-1.47	D
1434775_at	Pard3	93742	-1.21	cell cycle	424.2	337.3	388.4	983.9	1126.4	1136.5	2.26E-04	-1.19	D	-1.1	D	-1.34	D	-1.17	D	-1.35	D	-1.15	D	-1.17	D	-1.32	D	-1.11	D
1457806_at	Dock1	330662	-1.21	electron transport	1286.9	1615.3	1188.8	2584.7	3603.8	2814.2	0.0080758	-1	D	-1.36	D	-1.21	D	-0.9	D	-1.29	D	-0.94	D	-1.16	D	-1.79	D	-1.21	D
1425263_a_at	Mbp	17196	-1.2	myelination	1130.6	1269.6	1171.9	2737.5	2889.2	2451.4	3.69E-04	-0.89	D	-1.42	D	-1.16	D	-1.07	D	-1.62	D	-1.45	D	-0.95	D	-1.31	D	-0.95	D
1415914_at	Hnrpab	15384	-1.19	epithelial to mesenchymal transition	11437	10805.5	10294	25024.4	26186	23402.4	8.75E-05	-0.97	D	-1.22	D	-1.08	D	-1.12	D	-1.29	D	-1.13	D	-1.25	D	-1.38	D	-1.24	D
1456632_at	Bcl11a	14025	-1.19	transcription	417.1	341.2	390.4	750.7	619.6	721.5	0.0023082	-1	D	-0.81	D	-1.42	D	-1.22	D	-1.7	D	-1.34	D	-0.92	D	-1.15	D	-1.18	D
1460716_a_at	Cbfb	12400	-1.19	ossification	1029.4	1231.3	867.4	2510.5	2585.9	2516.9	1.58E-04	-1.39	D	-1.26	D	-1.42	D	-1.15	D	-0.97	D	-1.16	D	-1.27	D	-1.08	D	-1.04	D
1420895_at	Tgfbr1	21812	-1.18	skeletal development	523.5	517.5	457.9	1014	1195.8	1064.5	5.23E-04	-1.02	D	-1.28	D	-1.11	D	-1.16	D	-1.66	D	-1.37	D	-0.91	D	-1.35	D	-0.77	D
1425048_a_at	Hmgb1	15289	-1.18	DNA packaging	8306.2	10784.7	10844.1	22235.2	22169	22578.3	1.28E-04	-1.4	D	-1.42	D	-1.25	D	-1.07	D	-1.06	D	-0.99	D	-1.13	D	-1.16	D	-1.1	D
1428349_s_at	Ebf3	13593	-1.17	transcription	12226.3	13305	12508.8	23343.6	25311.3	22024.2	4.18E-04	-1.17	D	-1.36	D	-1.15	D	-1	D	-1.23	D	-1	D	-1.12	D	-1.34	D	-1.14	D
1432152_at	2610109H07Rik	70433	-1.17		946.5	1173.7	891	1975	2410.1	2019.8	0.0022641	-1.09	D	-1.5	D	-1.1	D	-0.82	D	-1.12	D	-1.07	D	-1.1	D	-1.44	D	-1.27	D
1450914_at	Ppp1r14b	18938	-1.16		1215.9	1120.2	1187.9	2970	2723.4	3011.7	5.24E-05	-0.93	D	-0.72	D	-1.04	D	-1.19	D	-1.27	D	-1.41	D	-1.22	D	-1.24	D	-1.43	D
1456664_x_at	EG665008	637008	-1.16	RNA processing	3104.1	2368.4	1805.3	5435.9	5261.8	4806.6	0.0028486	-1.13	D	-1.06	D	-0.85	D	-1.2	D	-1.12	D	-0.84	D	-1.54	D	-1.45	D	-1.21	D
1456377_x_at	Limd2	632329	-1.15		603.2	714.1	453.1	1135.6	1338	1073.8	0.0057375	-1.54	D	-1.42	D	-1.15	D	-0.8	D	-1.12	D	-0.53	D	-1.08	D	-1.44	D	-1.23	D
1416105_at	Nnt	18115	-1.14	electron transport	343.4	371.8	507	836.7	994.7	1007	0.0019425	-1.16	D	-1.37	D	-1.28	D	-1.28	D	-1.45	D	-1.46	D	-0.57	D	-0.85	D	-0.81	D
1423392_at	Clic4	29876	-1.14	transport	2088.7	2193.2	1681.6	4382.4	3624.2	3900.7	0.0018613	-1.19	D	-0.88	D	-1.03	D	-1.07	D	-0.78	D	-0.88	D	-1.72	D	-1.31	D	-1.4	D
1448729_a_at	4-Sep	18952	-1.14	cell cycle	765.6	743.4	690.3	1674.4	1876.8	1940	1.91E-04	-1	D	-1.01	D	-1.11	D	-0.99	D	-1.16	D	-1.15	D	-1.22	D	-1.22	D	-1.37	D
1422946_a_at	Dnmt1	13433	-1.13	DNA methylation	583.7	736.4	655.3	1486	1629.7	1638.7	1.52E-04	-1.31	D	-1.4	D	-1.58	D	-0.8	D	-1.15	D	-1.07	D	-0.7	D	-1	D	-1.15	D
1452784_at	Itgav	16410	-1.13	angiogenesis	539.1	554.5	584.7	1350.9	1153.3	1226.6	3.20E-04	-1.35	D	-1.23	D	-1.52	D	-1.21	D	-0.93	D	-1.1	D	-1	D	-0.87	D	-0.95	D
1426208_x_at	Plagl1	22634	-1.12	positive regulation of transcription by RNA polymerase II	3591	3506.7	2879.3	7648.6	7431.8	5733.9	0.0050078	-1.09	D	-1.2	D	-0.92	D	-1.16	D	-1.15	D	-1.03	D	-1.17	D	-1.36	D	-1.03	D
1434880_at	Etv6	14011	-1.12	regulation of progression through cell cycle	1113.4	914	968.2	1769.1	2519.4	2216	0.0066163	-0.84	D	-1.34	D	-1.21	D	-0.91	D	-1.53	D	-1.26	D	-0.61	D	-1.11	D	-1.26	D
1435324_x_at	Hmgb1	15289	-1.12	DNA packaging	8716.3	7468.1	7919.6	17432.3	16921.5	16478.4	4.09E-05	-1.04	D	-1.05	D	-1.16	D	-1.16	D	-1.17	D	-1.17	D	-1.12	D	-1.11	D	-1.12	D
1455897_x_at	Hmgn1	15312	-1.12	pyrimidine dimer repair via nucleotide-excision repair	12049.2	12219.1	7839.5	22434.3	24463.2	21490.9	0.0019714	-0.88	D	-1	D	-0.83	D	-0.96	D	-1.05	D	-0.86	D	-1.52	D	-1.59	D	-1.42	D
1426885_a_at	Cdk2ap1	13445	-1.11	cell cycle	3284.5	3800.4	3559	6786	6723.5	8356.3	0.002518	-0.91	D	-1	D	-1.34	D	-1.09	D	-0.97	D	-1.42	D	-1	D	-0.97	D	-1.31	D
1418180_at	Sp1	20683	-1.1	transcription	11838.1	11461.6	11860	24401	24109.6	26847.8	1.07E-04	-1.01	D	-1.07	D	-1.34	D	-1.03	D	-1.05	D	-1.35	D	-0.88	D	-1	D	-1.14	D
1419964_s_at	Hdgf	15191	-1.1	cellular process	1268	1473.7	1568.8	3079.4	3373.4	3208.4	1.31E-04	-1.12	D	-1.2	D	-1.12	D	-1.08	D	-1.22	D	-1.13	D	-0.99	D	-1.12	D	-0.95	D
1422440_at	Cdk4	12567	-1.1	regulation of progression through cell cycle	494.6	367.5	302.8	807.2	1080.3	1031	0.0044563	-0.88	D	-1.02	D	-1.02	D	-1.26	D	-1.56	D	-1.42	D	-0.9	D	-0.89	D	-0.98	D
1454454_at			-1.09		1732.8	1571.4	2045.7	3497.6	4657.4	3423.1	0.0080085	-1.1	D	-1.53	D	-1.1	D	-0.89	D	-1.27	D	-1.02	D	-0.88	D	-1.27	D	-0.78	D
1460168_at	Sfrp1	20377	-1.09	mRNA processing	669.5	600.8	1100.9	1494.4	1721.4	1500	2.58E-04	-1.2	D	-1.49	D	-1.31	D	-1.03	D	-1.31	D	-1.13	D	-0.68	D	-0.86	D	-0.77	D
1428029_a_at	H2afv	77605	-1.08	nucleosome assembly	1133.1	769.9	969.5	1853.9	1805.8	2122	0.0025264	-0.92	D	-0.92	D	-0.93	D	-1.37	D	-1.72	D	-1.19	D	-0.96	D	-0.91	D	-0.78	D
1451356_at	Anp32e	66471	-1.08		1109.5	753.3	818.5	1576.4	1661.3	1632	0.0028963	-1.05	D	-1.16	D	-0.97	D	-1.18	D	-1.33	D	-1.05	D	-1.03	D	-1.08	D	-0.89	D
1455855_x_at	Hnrpab	15384	-1.08	epithelial to mesenchymal transition	35004.8	30388.4	30621	59583	65063.5	68981.6	4.73E-04	-0.97	D	-1.16	D	-1.07	D	-1.07	D	-1.22	D	-1.06	D	-1	D	-1.18	D	-0.99	D
1423421_at	Ankrd49	56503	-1.07	regulation of transcription, DNA-dependent	791.6	875.8	853.8	1498.3	1809.4	1348.5	0.0067224	-1.11	D	-1.31	D	-0.85	D	-0.89	D	-1.24	D	-1.1	D	-0.87	D	-1.26	D	-1	D
1424394_at	Selm	114679	-1.07		1084.4	916	808.3	1774.2	1727.6	1764	5.53E-04	-1.09	D	-0.85	D	-0.8	D	-1.1	D	-1.01	D	-1.09	D	-1.22	D	-1.2	D	-1.31	D
1438940_x_at	Hmgn1	15312	-1.07	pyrimidine dimer repair via nucleotide-excision repair	16042.1	15335.3	10767.9	30212	30974.1	28117.4	0.001075	-0.81	D	-0.93	D	-0.77	D	-0.94	D	-1.02	D	-0.96	D	-1.34	D	-1.53	D	-1.37	D
1426406_at	Setd8	67956	-1.06	chromatin modification	1379.9	1502.3	1320.9	2381.1	2781.2	3440.4	0.0094532	-0.8	D	-0.95	D	-1.14	D	-0.86	D	-1.16	D	-1.36	D	-0.84	D	-1.13	D	-1.31	D
1433519_at	Nucks1	98415	-1.06		3667.8	5483.6	4197.6	10816.4	9193.8	8876.8	0.0030314	-0.93	D	-1.33	D	-0.78	D	-0.93	D	-1.3	D	-0.77	D	-1.2	D	-1.36	D	-0.91	D
1430820_a_at	Bbx	70508	-1.05	transcription	1120.2	1016	1152	1977.4	2061.8	2129.8	9.06E-05	-0.95	D	-0.81	D	-1.11	D	-1.07	D	-1.19	D	-1.2	D	-1.03	D	-0.97	D	-1.15	D
1451920_a_at	Rfc1	19687	-1.05	DNA replication	855.8	912.3	1099.5	1671.2	1762	1821.3	7.46E-04	-1.07	D	-1.06	D	-1.31	D	-1.19	D	-1.09	D	-1.27	D	-0.77	D	-0.77	D	-0.88	D
1459838_s_at	Btbd11	74007	-1.05	regulation of transcription, DNA-dependent	331.5	302.7	387.8	609.6	735	723.9	0.0017918	-1.25	D	-1.33	D	-1.52	D	-0.89	D	-0.93	D	-1.35	D	-0.71	D	-0.65	D	-0.82	D
1429458_at	2410127L17Rik	626107	-1.04		2415.5	3026.9	3099.5	7039.8	7326.5	7637.6	8.52E-05	-1.21	D	-1.23	D	-1.25	D	-1.03	D	-1.2	D	-1.17	D	-0.66	D	-0.8	D	-0.77	D
1426514_at	4631426J05Rik	77590	-1.03	hexose biosynthetic process	1170.3	1312.7	1413.6	2696.1	2400	2507.1	3.80E-04	-1.11	D	-1.01	D	-1.24	D	-1.02	D	-1.02	D	-1	D	-0.81	D	-1.01	D	-1.02	D
1416726_s_at	Ube2s	77891	-1.02	protein modification process	1743.3	1401.4	1363.1	3673.4	3344.8	3773	2.92E-04	-1.11	D	-0.9	D	-0.97	D	-1.07	D	-0.91	D	-0.95	D	-1.16	D	-1.03	D	-1.07	D
1418512_at	Stk3	56274	-1.02	protein amino acid phosphorylation	808.4	981.8	726.9	1801.4	2609.1	2041.6	0.0064001	-1.33	D	-1.39	D	-1.28	D	-0.89	D	-0.85	D	-1.02	D	-0.83	D	-0.55	D	-1.03	D
1424768_at	Cald1	109624	-1.01	muscle contraction	1268.1	1407.2	1650.4	2444.7	3046.9	3073.4	0.0037751	-1.07	D	-1.22	D	-1.25	D	-0.85	D	-1.14	D	-1.22	D	-0.59	D	-0.87	D	-0.89	D
1427231_at	Robo1	19876	-1.01	chemotaxis	734.5	819.5	983	1644.5	1922.1	1751.7	0.0010427	-0.95	D	-1.51	D	-1.32	D	-0.68	D	-1.01	D	-0.95	D	-0.64	D	-1.1	D	-0.89	D
1422801_at	RP23-336J1.4	27041	-1	transport	2469.8	2320.8	1900.9	4769	4745.7	4501.6	2.14E-04	-1.16	D	-1.21	D	-0.94	D	-1.03	D	-1.03	D	-0.9	D	-0.93	D	-1	D	-0.8	D
1423818_a_at	Arl6ip1	54208	-1	cotranslational protein targeting to membrane	2098.3	1295.2	1593.7	3076.3	3809.9	3184.7	0.0066256	-0.68	D	-0.94	D	-0.6	D	-1.22	D	-1.48	D	-1.13	D	-0.86	D	-1.19	D	-0.86	D
1437711_x_at	EG666231	18263	-1	kidney development	3362	3786.6	2634.9	6066.4	6945.4	5726.8	0.003808	-1.01	D	-1.2	D	-0.9	D	-0.72	D	-0.89	D	-0.61	D	-1.2	D	-1.41	D	-1.09	D
1447787_x_at	Gja7	14615	-1	vasculogenesis	4468	2966.1	2234.6	6889.1	7815.8	7445.4	0.004242	-0.9	D	-0.93	D	-0.89	D	-1	D	-1	D	-0.97	D	-1.12	D	-1.22	D	-1.01	D