

## **SUPPLEMENTARY DATA FOR**

### ***Arf* induces p53-dependent and independent anti-proliferative genes**

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## **TABLE OF CONTENT**

- (I) STATISTICAL ANALYSIS**
- (II) TABLES**
  - Table1: Genes selected from Affymetrix GeneChip<sup>®</sup> arrays**
  - Table2: Genes selected from cDNA microarrays**
- (III) REFERENCES**

## (I) STATISTICAL ANALYSIS:

### Analysis of paired Affymetrix GeneChip<sup>®</sup> arrays

The statistical analysis of the Affymetrix GeneChip<sup>®</sup> array expression data that identified the gene clusters consists of the following steps.

**1. Data preprocessing.** The expression data consisted of the values of the signal, detection call, and detection p-value computed for the probe sets by the Affymetrix Gene Suite v.5 program (See Appendices C to E, <sup>1</sup>). The signal intensity value of a probe set reflects the abundance of the gene in the sample. Hence if the detection call designates a probe set as absent, the actual value of signal is not meaningful. For this reason, the signal value of a probe set was truncated from below by setting it to zero if the corresponding detection call was absent.

**2. Expression modeling and gene selection.** Three pairs of arrays at each time point were created to mimic the experimental to control ratio (Cy5 to Cy3) using zinc-induced NIH3T3 cells lacking *Arf* as control. Let  $(X_{gkj}, X'_{gkj})$  be the pair of pre-processed signal values for gene  $g$  at time point  $k$  in sample  $j$ , with  $X'$  denoting the signal value in the control sample,  $g=1,2,\dots,G$  (total number of probe sets on a chip),  $j=1,2,3$ , and  $k=1,2,3,4$  (corresponding to 0, 2, 4, 8 hours) The expression of gene/probe  $g$  in the *Arf*-induced sample relative to the control sample is defined by the difference

$W_{gkj} = X_{gkj} - X'_{gkj}$ . The effect of *Arf*-induction is represented by the variation of  $W$  across the time points, leading to the following ANOVA model of gene expression:

$$W_{gkj} = \mu_g + \mu_{gk} + \mu_{gkj}, \quad j = 1,2,3, \quad k = 1,2,3,4$$

where  $\bar{\mu}_g$  is the overall mean, and  $\bar{\mu}_{gk}$  represents the systematic variation of gene  $g$ 's expression over time after *Arf* induction, which is the main effect of interest. The above model was fitted for every gene/probe and each ANOVA p-value was recorded. Gene selection was then guided by the least statistical significance of the known genes *Mdm2*, *Btg2*, *Cip1*, and *Arf* on the pathway. *Cip1* had the largest p-value of 0.0173 among the five genes, thus all genes/probes with ANOVA p-value less than or equal to 0.0173 were selected (deemed as potentially being regulated by *Arf*).

**3. Supervised clustering.** Genes/probes selected in Step 2 were further organized into clusters according to their expression patterns across the time points. In contrast to unsupervised clustering, the supervised approach clusters the genes/probes around core genes, one core per cluster, and runs sequentially. Beginning with the known genes *Mdm2*, *Btg2*, *Cip1*, and *Arf*, *Mdm2* was first used as a core gene. All selected genes/probes that have similar or opposite expression pattern to *Mdm2*, as judged by the absolute value of Pearson correlation coefficient greater than or equal to 0.9, were put into Cluster 1 with Cluster 1a (1b) containing genes/probes positively (negatively) correlated with *Mdm2*. *Btg2* and *Cip1* were clustered with *Mdm2* in Cluster 1a. Next *Arf* was used as a core to produce Clusters 2a and 2b in the same way. Next, among the selected but not clustered genes/probes, the one with the smallest ANOVA p-value was used as a core, producing Clusters 3a and 3b. Finally, the remaining selected probes were put into Cluster 4.

## Analysis of cDNA expression arrays

**1. Data transformation.** To reduce the influence of extraneous values in the Cy3 and Cy5 intensities, a logarithm transformation is applied to all the channel intensity values. The resulting data are called *raw log intensity values*.

**2. Normalization of the log intensity values.** For normalization we modified the approach proposed by Wolfinger and colleagues<sup>2</sup>. The purpose (and goal) of “normalization” is to identify and eliminate systematic variations in the raw log intensity values that may confound the effect of time on the changes of gene expression levels. This requires (a) identify sources of such systematic variations, and (b) eliminate them via a proper statistical model. For (a), it largely depends on the technology (such as the chip printer, scanner, dye labeling, etc.) that generated the intensity data and the design of the microarray experiment. Based on our understanding of the devices and this microarray experiment, we modeled two sources of variation for (a): Time (0, 2, 4, 8 hours) and Grid (1 through 16; each chip consists of 16 grids). For (b), an Analysis of Variance (ANOVA) model was used. Let  $\log Cy5_{tgi}$  denote the raw log intensity value of the Cy5 channel of spot (gene)  $j$  on chip  $i$ , Grid  $g$ , and at Time  $t$ . Here  $g=1,2,\dots,16$  corresponds to 16 grids on each chip;  $t=0,2,4,8$  corresponds to the first 4 time points;  $i = 1,2,\dots,12$  corresponds to the 12 chips in the four time points (3 per time point since the time course experiment was done in triplicates.) . The statistical model says that the variations in the raw log Cy5 intensity can be decomposed into the normalized log Cy5 intensity (*norm log Cy5*) plus variations due to Time and Grid:

$$\log Cy5_{tgi} = \text{norm log Cy5}_{tgi} + \square + Time_t + Grid_g + (TG)_{tg},$$
$$t = 0,2,4,8; g = 1,\dots,16; i = 1,\dots,12$$

Here  $\bar{\mu}$  is the overall average, and  $Time_t, Grid_g, (TG)_{ig}$  are quantities representing the systematic variations due to Time and Grid. To account for intra-grid correlation (spots in the same grid were printed by the same pin) the Grid effect was regarded as a random effect. These quantities were estimated based on the raw logCy5 data using the statistical analysis software SAS. In certain sense these quantities are special averages. For example,  $\bar{\mu}$  is the average of all the raw log Cy5 values of all valid spots on all arrays. The mathematical forms of the other quantities are more complicated. The normalized log Cy5 intensities are the raw log Cy5 intensities minus the estimated quantities, that is,

$$norm \log Cy5_{tgi} = \log Cy5_{tgi} - \bar{\mu} - Time_t - Grid_g - (TG)_{ig},$$

$$t = 0,2,4,8; g = 1,\dots,16; i = 1,\dots,12$$

The normalization of the Cy3 channel intensities is done in exactly the same way using the raw log Cy3 values.

**3. Cy5-to-Cy3 ratio after normalization.** The *log Cy5 to Cy3 normalized intensity ratios* are computed by

$$norm \log R_{tgi} = norm \log Cy5_{tgi} - norm \log Cy3_{tgi}, \quad t = 0,2,4,8; g = 1,\dots,16; i = 1,\dots,12.$$

Because the normalized intensities are on a log scale, the differences give the ratios on a log scale. These log normalized intensity ratios are used to rank, select, and cluster genes in subsequent steps. In the report files containing the gene clusters, these normalized intensity ratios are transformed back to the original scale, with values less (greater) than 1 indicating down (up) regulation relative to the “control” sample (i.e., sample labeled with the Cy3 dye).

**4. Significance-Guided selection of genes.** To select the genes whose expression levels change significantly across the four time points, the variation in the log normalized

intensities of gene (spot)  $j$  is modeled as an overall mean  $\mu_j$  plus the effect of Time and a normally distributed random error:

$$\text{norm log } R_{tgi} = \mu_j + \text{Time}_t + \epsilon_{tgi}, \quad t = 0,2,4,8; \quad g = 1,\dots,16; \quad i = 1,\dots,12.$$

Here  $\mu_j$ ,  $\text{Time}_t$  are statistical parameters representing the overall mean and the Time effect respectively.

For each gene the above model is computed, along with the F statistic testing for the Time effect, again using SAS. The stronger the time effect, the more significantly does the gene's expression level change over time. Therefore the genes are selected according to the p-values of their F statistics. The gene selection was guided by the least statistical significance of several genes known to be in the Arf/p53/Mdm2 pathway (*Mdm2*, *Cip1*, *Btg2*, and *Arf*). All genes with a p-value less than or equal to 0.0147 (p-value associated with *Arf*) were then selected.

**5. Clustering of selected genes.** The selected genes are grouped into clusters according to their expression patterns across the 0, 2, 4 and 8 hour time points, using essentially the same supervised clustering procedure described above. Genes in the same cluster have similar expression patterns. The sample (Pearson's) correlation coefficient is used as a similarity measure for clustering. Each cluster has a "core", which is either a known gene used as control, or a gene with an expression pattern representative of the cluster. For all but one cluster, the genes in a cluster are correlated with the core by their expression patterns with a correlation coefficient of at least 0.77.

**(II) TABLES:**

**Table 1. Genes selected from Affymetrix GeneChip<sup>®</sup> arrays in pMT-Arf and TKO cells**

All genes from the significance-guided selection from oligonucleotide GeneChip<sup>®</sup> arrays done in pMT-Arf cells were mapped on UniGene clusters to identify the mouse gene names and symbols. Those genes, which sequence could not be mapped onto UniGene Expressed Sequence Tags (ESTs) clusters or that were mapped onto clusters that did not correspond to known genes, were listed as EST. The functional classification was obtained either from the GENE ONTOLOGY<sup>™</sup> (GO) CONSORTIUM or from publications. For each gene, are listed from left to right, mean differences at all time points (mean-diff-0hr, mean-diff-2hr, mean-diff-4hr and mean-diff-8hr), correlation coefficient related to the core in each cluster, value of ANOVA F statistic (F value) and the corresponding p-value (Prob F). The cores for clustering analysis are highlighted in red. The same Oligonucleotide GeneChip<sup>®</sup> arrays were performed using total RNA isolated from *Arf/Mdm2/p53* triple knockout (TKO) mouse embryo fibroblasts (MEFs) infected with MSCV-IRES-GFP retroviruses expressing or not p19<sup>Arf</sup>. For each gene on the chip, the intensity difference between TKO MEFs expressing p19<sup>Arf</sup> or GFP alone was calculated. The data are listed in the last column and compared to genes selected from the arrays done in pMT-Arf. Those genes that are induced or down regulated in both arrays are highlighted in yellow in the last column.

Cluster 1a	GA number	Symbol	Mouse gene name	known or inferred function	mean-diff-0hr	mean-diff-2hr	mean-diff-4hr	mean-diff-8hr	FValue	ProbF	Correlation (positive)	Cluster No.	diff-TKO (Arf-GFP) 72hrs
	AW124153	Sox4	SRY-box containing gene 4	transcription factor	183	287	281	796	6.4848	0.0155	0.9942	1a	390.3
	X04748	Igl-5	immunoglobulin lambda chain 5	antibody	36	0	0	200	9.3006	0.0055	0.9586	1a	-19.2
	M64292	Btg2	B-cell translocation gene 2, anti-proliferative	anti-proliferation	261	1012	1593	2872	15.1686	0.0012	0.9228	1a	80
	D78382	Tob1	Transducer of ErbB-2.1	anti-proliferation	272	293	137	753	12.2768	0.0023	0.9314	1a	485.8
	AF012923	Wig1	Wild-type p53-induced gene 1	anti-proliferation	810	539	621	2474	19.1204	0.0005	0.9754	1a	-184.4
	X95504	Zac1	Zinc finger protein	anti-proliferation	233	270	407	654	13.9420	0.0015	0.9607	1a	66.5

		regulator of apoptosis and cell cycle arrest										
AF064071	Apaf1	Apoptotic protease activating factor 1	apoptosis	-32	-42	62	301	11.4800	0.0029	0.9801	1a	6.8
L22472	Bax	Bcl2-associated X protein	apoptosis	-55	385	242	1316	10.4186	0.0039	0.9658	1a	9.1
L35049	Bcl2l	Bcl2-like	apoptosis	83	23	110	668	6.7246	0.0141	0.9910	1a	195.9
	Tnfrsf6	Tumor necrosis factor receptor superfamily, member 6	apoptosis	0	13	104	442	16.6316	0.0008	0.9936	1a	69.9
AI849928	Ccnd1	Cyclin D1	cell cycle regulation	-502	-339	-187	886	9.3356	0.0054	0.9964	1a	-841
L49507	Ccng	Cyclin G	cell cycle regulation	344	183	359	1692	21.6284	0.0003	0.9885	1a	115.8
AF005886	Ccni	Cyclin I	cell cycle regulation	29	10	14	149	13.6014	0.0017	0.9747	1a	38
AW048937	Cdkn1a	Cyclin-dependent kinase inhibitor 1A (P21)	cell cycle regulation	455	1232	2221	5539	16.9572	0.0008	0.9792	1a	-33
U09507	Cdkn1a	Cyclin-dependent kinase inhibitor 1A (P21)	cell cycle regulation	219	724	1773	2962	6.2255	0.0173	0.9056	1a	-78.9
AJ222580	Gtse1	G two S phase expressed protein 1	cell cycle regulation	-116	-297	337	2250	17.7396	0.0007	0.9878	1a	137.2
X66449	S100a6	S100 calcium binding protein A6 (calcyclin)	cell cycle regulation	-13015	-9046	-4445	12223	7.6010	0.0100	0.9806	1a	-10778.2
AJ006590	Mcm3ap	Minichromosome maintenance deficient (S. cerevisiae) 3-associated protein	DNA primase	130	65	124	478	7.9221	0.0088	0.9808	1a	-22
AI853875	Zrfp1-pending	Zinc ring finger protein 1	endosome/lysosome associate protein	-121	-92	22	177	6.6727	0.0144	0.9378	1a	211.8
U16163	P4ha2	Procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha II polypeptide	enzyme	354	449	654	1376	7.7514	0.0094	0.9887	1a	-58.9
AF007267	Pmm1	Phosphomannomutase 1	enzyme/mannose metabolism	0	0	0	884	89.1047	0.0000	0.9923	1a	-105.5
AI840339	Rnase4	Ribonuclease, RNase A family 4	enzyme/ribonuclease	-86	-30	-36	275	16.6923	0.0008	0.9948	1a	144.7
AJ010108	Ak1	Adenylate kinase 1	enzyme/synthesis, equilibration and regulation of adenine nucleotides	514	840	652	1812	6.4017	0.0161	0.9752	1a	-22
X63023	Cyp3a13	Cytochrome P450, steroid inducible 3a13	enzyme/metabolism and detoxification	-31	9	32	123	6.9874	0.0126	0.9565	1a	39.4
U22324	Fgfr1	Fibroblast growth factor receptor 1	growth factor receptor	43	363	106	966	7.5232	0.0103	0.9407	1a	143.5
AV097950	Ftl1	Ferritin light chain 1	iron storage protein	-12	-43	389	783	8.2707	0.0078	0.9116	1a	35.9
AV232610	Hps1	Hermansky-Pudlak syndrome 1 homolog (human)	lysosome organization and biogenesis	18	-19	70	250	12.0968	0.0024	0.9703	1a	-111.3
M29464	Pdgfa	Platelet derived growth factor, alpha	mitogen	-98	410	492	1508	6.7801	0.0137	0.9566	1a	-643
M34896	Evi2	Ecotropic viral integration site 2	oncogene	85	89	305	556	7.3113	0.0111	0.9332	1a	-22.4



AI853375	Mdm2	Transformed mouse 3T3 cell double minute 2	oncogene/E3 ligase	233	611	1163	6781	50.1939	0.0000	1 (core for cluster 1a and 1b)	1a	-15.2
D89821	Arhd	Ras homolog D (RhoD)	signal transduction	24	-1	128	645	10.6767	0.0036	0.9942	1a	107.4
AF107848	Gnas	GNAS (guanine nucleotide binding protein, alpha stimulating) complex locus	signal transduction	-1444	2206	185	7018	10.5304	0.0038	0.9239	1a	-478.8
AF036907	Lat	Linker for activation of T cells	signal transduction	-19	-17	76	239	8.5406	0.0071	0.9657	1a	-31.4
AI849218	Mark3	MAP/microtubule affinity-regulating kinase 3	signal transduction	91	-10	11	350	9.1198	0.0058	0.9361	1a	-12.1
D31842	Ptpn14	Protein tyrosine phosphatase, non-receptor type 14	signal transduction	25	-114	4	290	7.2423	0.0114	0.9251	1a	77
D83484	Ptpre	Protein tyrosine phosphatase, receptor type, E	signal transduction	10	-110	78	309	8.0067	0.0086	0.9149	1a	90.1
AF050182	Per3	Period homolog 3 (Drosophila)	signal transduction/rythmic behavior	-87	-175	-71	266	6.4614	0.0157	0.9715	1a	-97.8
AW124839	Gabarap	Gamma-aminobutyric acid receptor associated protein	targeting and clustering of GABA(A) receptors	900	1488	1247	3101	9.8378	0.0046	0.9767	1a	1053.3
U85259	Esrra	Estrogen related receptor, alpha	transcription factor	109	193	78	1029	21.6008	0.0003	0.9816	1a	-70.9
M74516	Gabpb1	GA repeat binding protein, beta 1	transcription factor	10	50	101	431	8.5436	0.0071	0.9975	1a	61.7
AI836082	Gtf3c1	General transcription factor III C 1	transcription factor	-58	60	-20	715	20.6738	0.0004	0.9866	1a	-28.2
AW047899	Nfkb2	Nuclear factor of kappa light polypeptide gene enhancer in B-cells 2, p49/p100	transcription factor	-66	-8	188	380	29.5613	0.0001	0.9027	1a	291.2
X55316	Nfyb	Nuclear transcription factor-Y beta	transcription factor	51	113	82	291	8.8494	0.0064	0.9768	1a	29.4
U78103	Eed	Embryonic ectoderm development	transcription regulation	111	78	4	402	9.3608	0.0054	0.9277	1a	71.9
X99915	Hmga2	High mobility group AT-hook 2	transcription regulation	-91	-182	773	2534	34.6194	0.0001	0.9697	1a	-2314.1
AI835963	Pias3	Protein inhibitor of activated STAT 3	transcription repression	-13	85	-44	324	22.8860	0.0003	0.9238	1a	18.5
AF034080	Pias3	Protein inhibitor of activated STAT 3	transcription repression	28	35	-1	177	6.7148	0.0141	0.9537	1a	-67.8
U60020	Abcb2	ATP-binding cassette, sub-family B (MDR/TAP), member 2	transporter	60	88	85	598	21.2314	0.0004	0.9956	1a	40.2
AW120725	Ubl3	Ubiquitin-like 3	ubiquitin like protein	90	65	16	253	6.9142	0.0130	0.9107	1a	50.5
AF069954	Gng3lg	G protein gamma 3 linked gene		-13	-85	12	225	6.4888	0.0155	0.9577	1a	118.1
AW048336	Trim11	Tripartite motif protein 11		140	113	238	1024	12.4022	0.0022	0.9971	1a	68.1
AI848518	Zfp385	Zinc finger protein 385		-319	24	250	1902	50.2096	0.0000	0.9926	1a	-76.1
AA763368		EST, Moderately		218	310	451	1589	29.2197	0.0001	0.9996	1a	151.9

		similar to Y247_HUMAN HYPOTHETICAL PROTEIN KIAA0247 [H.sapiens]										
AI848801		EST, Moderately similar to katanin p60 (ATPase-containing) subunit A1		-15	8	24	168	6.4500	0.0158	0.9971	1a	17.1
AI842938		EST, Highly similar to T00361 hypothetical protein KIAA0678 [H.sapiens]		-79	-46	-48	74	6.4426	0.0158	0.9889	1a	88.9
AI836109		EST		-30	74	-8	484	7.1945	0.0116	0.9772	1a	-86.2
AW049897		EST		28	44	74	292	7.4704	0.0105	0.9994	1a	-47.3
AI850638		EST		-308	260	164	885	12.9129	0.0020	0.9001	1a	-187.5
AW124900		EST		-16	-3	33	384	19.7084	0.0005	0.9997	1a	-69.5
AV232292		EST		-16	-43	-7	156	6.6199	0.0147	0.9852	1a	2.6
AW045710		EST		-22	7	58	309	13.9548	0.0015	0.9952	1a	-29.6
AI849135		EST		99	-16	309	1114	40.4179	0.0000	0.9805	1a	26.4
AI843231		EST		-3	257	70	559	14.7612	0.0013	0.9016	1a	-137.2
AW120683		EST		569	980	567	1901	9.2255	0.0056	0.9395	1a	-477
AW046661		EST		-41	-46	-4	134	9.5664	0.0050	0.9911	1a	21.7
AW123514		EST		-100	-88	-114	388	17.4661	0.0007	0.9879	1a	-72.1
AA727410		EST		-109	-23	225	568	8.5968	0.0070	0.9345	1a	-107.5
AI552922		EST		8	-110	23	456	12.0101	0.0025	0.9695	1a	-31.1
AI838663		EST		153	309	236	668	6.5290	0.0152	0.9676	1a	333.1
AI843359		EST		728	799	720	1044	6.3740	0.0163	0.9589	1a	1289.4
<b>Cluster 1b</b>												
<b>GA number</b>	<b>Symbol</b>	<b>Mouse gene name</b>	<b>known or inferred function</b>	<b>mean-diff-0hr</b>	<b>mean-diff-2hr</b>	<b>mean-diff-4hr</b>	<b>mean-diff-8hr</b>	<b>FValue</b>	<b>ProbF</b>	<b>Correlation (negative)</b>	<b>Cluster No.</b>	<b>diff-TKO (Arf-GFP) 72hrs</b>
AI847609	Ndufv2	NADH dehydrogenase (ubiquinone) flavoprotein 2	electron transfer	160	-258	-141	-737	6.6522	0.0145	-0.9107	1b	-311.1
AI842808	Ndufb5	NADH dehydrogenase (ubiquinone) 1 beta subcomplex 5	electron transfer	1907	2005	1508	64	6.8430	0.0134	-0.9879	1b	-1246.3
D90374	Apex	Apurinic/apyrimidinic endonuclease	enzyme/DNA repair	-549	-782	-795	-1145	8.0592	0.0084	-0.9289	1b	600.3
U95053	Gelm	Glutamate-cysteine ligase, modifier subunit	enzyme/glutathione biosynthesis	18	-91	103	-712	7.5144	0.0103	-0.9549	1b	-307.7
M33934	Impdh2	Inosine 5'-phosphate dehydrogenase 2	enzyme/guanine nucleotide biosynthesis	-538	-826	-958	-2194	13.6919	0.0016	-0.9916	1b	-879.7
AW048997	Psma5	Proteasome (prosome, macropain) subunit, alpha type 5	enzyme/peptidase (ubiquitin-dependent protein degradation)	-273	-300	-154	-1067	8.8438	0.0064	-0.9651	1b	-664.2
AB003304	Psmb5	Proteasome (prosome, macropain) subunit, beta type 5	enzyme/peptidase (ubiquitin-dependent protein degradation)	-170	-289	-508	-992	15.0141	0.0012	-0.9630	1b	323.5

AB025048	Prps1	Phosphoribosyl pyrophosphate synthetase 1	enzyme/purine biosynthesis	-62	-113	-446	-1081	8.0823	0.0083	-0.9677	1b	21.5
AB003502	Gspt1	G1 to phase transition 1	GTPase/G1 to S phase transition control	-162	-504	-812	-2865	13.3984	0.0017	-0.9952	1b	-1104.2
AA870675	Atp5c1	ATP synthase, H+ transporting, mitochondrial F1 complex, gamma polypeptide 1	hydrogen-transporting ATP synthase	262	-196	-632	-1657	17.2449	0.0007	-0.9433	1b	-614.5
AI846849	Mrps18b	Mrps18b	mitochondrial ribosomal protein	16	-109	-235	-541	18.2688	0.0006	-0.9492	1b	405.3
X80232	Silg41	Silica-induced gene 41	mRNA splicing	94	7	-14	-657	10.9069	0.0034	-0.9983	1b	-731.7
U11274	Hnrpd	Heterogeneous nuclear ribonucleoprotein D	mRNA stability control	150	-126	-254	-1531	7.1498	0.0119	-0.9933	1b	-495.6
AA656541	Cpr2-pending	Cell cycle progression 2 protein	positive control of cell proliferation	-84	-184	-84	-406	6.6075	0.0148	-0.9391	1b	-41.3
U53208	Dnajc2	DnaJ (Hsp40) homolog, subfamily C, member 2	protein folding	52	177	34	-330	7.5797	0.0100	-0.9572	1b	-260.7
AA656775	Rrr-pending	Regulator for ribosome resistance homolog (S. cerevisiae)	ribosome biogenesis regulation	26	-204	-488	-1189	9.1021	0.0059	-0.9593	1b	281.2
Z22593	Fbl	Fibrillarlin	rRNA processing	-359	-118	-194	-1795	10.0127	0.0044	-0.9750	1b	173.7
U58885	Sh3d2b	SH3 domain protein 2B	signal transduction	99	-53	134	-375	6.9765	0.0127	-0.9178	1b	248.3
X99644	Trim28	Tripartite motif protein 28	transcription regulation	-698	731	-1032	-3880	6.3876	0.0162	-0.9251	1b	-1749.5
U19891	Cebpars1	CCAAT/enhancer binding protein alpha (C/EBP), related sequence 1	transcriptional regulation	44	-97	-193	-468	9.0875	0.0059	-0.9403	1b	94.7
U63387	Cbx4 Chromobox homolog 4 (Drosophila Pc class)	Chromobox homolog 4 (Drosophila Pc class)	transcriptional repressor	107	100	-79	-387	7.0559	0.0123	-0.9641	1b	192.5
AI854811	No1	Nucleolar protein 1, 120 kDa	transformation	-216	-283	-534	-1277	12.1911	0.0024	-0.9863	1b	2.6
AI839280	tsg101	tumor susceptibility gene 101	tumorigenesis	56	-41	163	-485	6.6387	0.0146	-0.9267	1b	116.4
AI838527	Ifrd2	Interferon-related developmental regulator 2		-333	-259	-342	-752	14.1284	0.0015	-0.9828	1b	-116.8
AW121930		EST		105	-675	-863	-2205	6.3991	0.0161	-0.9415	1b	-148
AI415065		EST		-143	1994	65	-4373	11.7193	0.0027	-0.9272	1b	-630.4
AA863928		EST		-228	-107	-328	-1187	8.3485	0.0076	-0.9878	1b	-11.1
AW045742		EST		-232	213	-327	-1722	8.3462	0.0076	-0.9616	1b	-400.7
AI846545		EST		-109	-379	-209	-961	11.1989	0.0031	-0.9585	1b	1906.3
AI837302		EST		-441	-600	-656	-2004	17.7745	0.0007	-0.9989	1b	-942.2
AW121164		EST		126	285	86	-708	7.0768	0.0122	-0.9808	1b	-328.7
AI850801		EST		499	176	101	-353	7.1669	0.0118	-0.9191	1b	-423.7

AW121447		EST		-475	193	-556	-2322	27.1923	0.0002	-0.9506	1b	-179.4
AI642184		EST		-101	-79	-194	-372	7.0399	0.0124	-0.9589	1b	324.3
AI844034		EST		224	345	164	-239	7.3891	0.0108	-0.9630	1b	-241.5
AA869927		EST		58	60	-199	-725	6.2218	0.0174	-0.9742	1b	-206.7
AW046160		EST		584	388	79	-1127	8.6779	0.0068	-0.9888	1b	-232.7
AI850953		EST		448	289	286	-294	7.8513	0.0091	-0.9888	1b	148.5
AW121031		EST		-1667	-414	-1159	-3639	8.3884	0.0075	-0.9065	1b	-623.1
AW049564		EST		1229	824	799	-293	7.5393	0.0102	-0.9773	1b	303.8
<b>Cluster 2a</b>												
GA number	Symbol	Mouse gene name	known or inferred function	mean-diff-0hr	mean-diff-2hr	mean-diff-4hr	mean-diff-8hr	FValue	ProbF	Correlation (positive)	Cluster number	diff-TKO (Arf-GFP) 72hrs
X77585	Txn1	Thioredoxin 1	anti-oxidant	-8168	-3997	-5529	-10	8.2709	0.0078	0.9274	2a	-4371.6
AF044336	Cdkn2a	<b>Cyclin-dependent kinase inhibitor 2A</b>	<b>cell cycle regulation</b>	<b>1940</b>	<b>16399</b>	<b>20892</b>	<b>32073</b>	<b>21.8486</b>	<b>0.0003</b>	<b>1(core for cluster2a and 2b)</b>	2a	<b>27408.5</b>
U19860	Gas7	Growth arrest specific 7	growth arrest	-156	-42	-46	35	9.7262	0.0048	0.9841	2a	82.1
AW050287	Wdr6	WD repeat domain 6		-268	-152	0	0	6.4856	0.0155	0.9182	2a	-196.9
AI835847		EST, Highly similar to NUMM MOUSE NADH-UBIQUINONE OXIDOREDUCTASE 13 KD-A SUBUNIT [M.musculus]		-229	12	108	250	8.4141	0.0074	0.9966	2a	-371.8
AW060827		EST		-47	86	112	221	7.9893	0.0086	0.9986	2a	284
AA266298		EST		-118	129	295	422	6.3658	0.0163	0.9863	2a	158.4
AI853019		EST		-192	-82	-41	0	13.4628	0.0017	0.9843	2a	-233
<b>Cluster 2b</b>												
GA number	Symbol	Mouse gene name	known or inferred function	mean-diff-0hr	mean-diff-2hr	mean-diff-4hr	mean-diff-8hr	FValue	ProbF	Correlation (negative)	Cluster No.	diff-TKO (Arf-GFP) 72hrs
X60980	Tk1	Thymidine kinase 1	enzyme/nucleic acid metabolism	405	-401	-450	-1255	10.1695	0.0042	-0.9901	2b	-376.5
D12780	Amd1	S-adenosylmethionine decarboxylase 1	enzyme/spermidine biosynthesis	1281	695	-187	-882	13.4695	0.0017	-0.9657	2b	-488.6
Z23077	Amd2	S-adenosylmethionine decarboxylase 2	enzyme/spermidine biosynthesis	1427	805	169	-740	6.4136	0.0160	-0.9769	2b	-1076.1
U14172	Eif3	Eukaryotic translation initiation factor 3	protein synthesis	220	-287	-234	-510	7.8371	0.0091	-0.9658	2b	347.6
AB004305	Ap3d	Adaptor-related protein complex AP-3, delta subunit	protein trafficking	785	392	327	134	10.3194	0.0040	-0.9895	2b	-206.3
U10119	Vps4b	Vacuolar protein sorting 4b (yeast)	protein trafficking	140	35	-16	-108	9.0235	0.0060	-0.9978	2b	246.1
AB024303	Uble1a	Ubiquitin-like 1 (sentrin) activating enzyme E1A	SUMO-1 activating enzyme subunit	123	-70	-200	-423	14.1065	0.0015	-0.9896	2b	-85.1
X56561	Hoxd8	homeo box D8	transcriptional regulation	436	213	212	-2	9.4221	0.0053	-0.9876	2b	-106.9
AA688834	Rnpc2	RNA-binding region (RNP1, RRM) containing 2	transcriptional regulation	242	41	-114	-86	12.6039	0.0021	-0.9025	2b	-11.2
U35142	Rbbp7	Retinoblastoma binding protein 7	transcriptional repressor	844	528	-426	-1191	16.1221	0.0009	-0.9354	2b	214.7

AA799042		EST, Similar to 60S ribosomal protein L30 isolog		-292	-486	-558	-718	7.7913	0.0093	-0.9996	2b	-67.4
AI844089		EST		474	-90	54	-359	10.2599	0.0041	-0.9488	2b	1404.2
AI845321		EST		251	128	-128	-352	14.1135	0.0015	-0.9513	2b	630.5
AW125164		EST		218	22	-428	-662	8.8240	0.0064	-0.9426	2b	-218.5
AA177826		EST		262	64	97	0	6.7619	0.0138	-0.9462	2b	-23.3
<b>Cluster 3a</b>												
GA number	Symbol	Mouse gene name	known or inferred function	mean-diff-0hr	mean-diff-2hr	mean-diff-4hr	mean-diff-8hr	FValue	ProbF	correlation (positive)	Cluster No.	diff-TKO (Arf-GFP) 72hrs
AI847314	Anapc5	Anaphase-promoting complex subunit 5	cell cycle control	-809	1095	-71	464	19.1681	0.0005	0.9489	3a	-1026.8
AI840979	Suclg1	Succinate-CoA ligase, GDP-forming, alpha subunit	enzyme/citric acid cycle	-296	395	58	-203	10.5620	0.0037	0.9063	3a	170.6
AB013469	Pscd2	Pleckstrin homology, Sec7 and coiled/coiled domains 2	signal transduction	-15	340	219	251	6.4629	0.0157	0.9707	3a	66.5
X12761	Jun	Jun oncogene	transcription factor	-156	692	78	8	6.5169	0.0153	0.9073	3a	-176.9
AJ249987	Taf10	TAF10 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 30 kDa	transcription factor	-179	467	173	76	8.4863	0.0072	0.9879	3a	734.2
AI172920		EST, Similar to thyroid hormone receptor-associated protein, 150 kDa subunit		-240	213	21	0	21.2938	0.0004	1 (core for cluster3a and 3b)	3a	136.8
AW123404		EST		-708	9	-243	-401	10.5941	0.0037	0.9852	3a	-205.3
<b>Cluster 3b</b>												
GA number	Symbol	Mouse gene name	known or inferred function	mean-diff-0hr	mean-diff-2hr	mean-diff-4hr	mean-diff-8hr	FValue	ProbF	Correlation (negative)	Cluster No.	diff-TKO (Arf-GFP) 72hrs
Y00208	Hoxa5	Homeo box A5	transcription factor	272	-12	-10	104	9.6753	0.0049	-0.9061	3b	260.8
AW212708		EST		104	-122	-75	-16	12.2362	0.0023	-0.9688	3b	-32.7
<b>Cluster 4</b>												
GA number	Symbol	Mouse gene name	known or inferred function	mean-diff-0hr	mean-diff-2hr	mean-diff-4hr	mean-diff-8hr	FValue	ProbF		Cluster No.	diff-TKO (Arf-GFP) 72hrs
AF077003	Cd2ap	CD2-associated protein	adaptor protein	16	-149	44	-8	10.3802	0.0039		4	37.2
U49112	Pdcd6	Programmed cell death 6	apoptosis	72	187	12	-64	6.5805	0.0149		4	-109.9
AB014464	Cd164	CD164 antigen	cell adhesion	1673	1670	-155	110	7.1013	0.0121		4	1377.4
M31131	Cdh2	Cadherin 2	cell adhesion	55	-172	23	-26	10.4765	0.0038		4	461.1
U83903	Tnfr1	Tumor necrosis factor induced protein 6	cell adhesion	0	43	7	0	16.3806	0.0009		4	18.3
AI849615	Gas5	Growth arrest specific 5	cell cycle arrest	-587	1030	-1767	-2188	10.6915	0.0036		4	-735.1
J04633	Hsp86-1	Heat shock protein, 86 kDa 1	chaperone	-4068	1864	1060	-2240	7.1818	0.0117		4	1376.8
X70058	Scya7	Small inducible cytokine A7	chemokine	299	1212	2924	380	7.7330	0.0095		4	1412.1
U88539	Supt5h	Suppressor of Ty 5 homolog (S. cerevisiae)	chromatin structural protein	-192	188	-76	-269	9.0792	0.0059		4	96.7

AB013912	Ruvbl2	RuvB-like protein 2	DNA helicase/homologous recombination and DNA double-strand break repair	-259	131	136	-587	8.0548	0.0084		4	-54.5
AF061516	Vamp4	Vesicle-associated membrane protein 4	docking or fusion of synaptic vesicles	133	-32	-6	98	6.7482	0.0139		4	158.8
AI850362	Uck2-pending	Uridine-cytidine kinase 2	enzyme	-1846	-1052	-1107	-2394	12.9525	0.0019		4	-2281.3
AI843232	Oxct	3-oxoacid CoA transferase	enzyme/ energy production	-309	122	-340	-468	7.3918	0.0108		4	-120.6
AV080704	Gamt	Guanidinoacetate methyltransferase	enzyme/creatine biosynthesis	144	-3	187	334	8.8148	0.0065		4	-18.5
AV276715	Aldh3a2	Aldehyde dehydrogenase family 3, subfamily A2	enzyme/lipid metabolism	8	-74	16	81	7.7606	0.0094		4	63
X78445	Cyp1b1	Cytochrome P450, 1b1, benz[a]anthracene inducible	enzyme/metabolism and detoxification	235	13	0	0	10.1748	0.0042		4	581.9
Z67748	Srm	Spermidine synthase	enzyme/polyamine biosynthesis	-2042	-1464	-1702	-2457	9.8636	0.0046		4	-785.4
AW047978	Prss25	Protease, serine, 25	enzyme/protease	-241	140	-285	-182	19.3813	0.0005		4	346.4
AF077330	Ube1c	Ubiquitin-activating enzyme E1C	enzyme/protein modification	148	-52	-135	78	7.4024	0.0107		4	486.7
AF064749	Col6a3	Procollagen, type VI, alpha 3	extracellular matrix	844	4849	2175	1258	12.0051	0.0025		4	-1900
AI836140	Eplin-pending	Epithelial protein lost in neoplasm	focal adhesion	70	542	706	524	7.8320	0.0091		4	-1070.7
X04725	Ins1	insulin I	growth factor	164	-150	345	728	10.7866	0.0035		4	-49.2
AV334115	Immt	Inner membrane protein, mitochondrial	inner mitochondrial membrane protein	293	-145	83	460	8.1586	0.0081		4	-20.1
U04710	Igf2r	Insulin-like growth factor 2 receptor	lysosomal enzyme sorting	144	200	22	0	13.1687	0.0018		4	212.6
AB016490	Jtb	Jumping translocation breakpoint	membrane protein	-551	476	-611	-1554	28.5383	0.0001		4	108.5
AW046919	Mprs17	Mitochondrial ribosomal protein S17	mitochondrial ribosomal protein	10	459	-46	-520	8.3761	0.0075		4	-155.7
U83902	Mad211	MAD2 (mitotic arrest deficient, homolog)-like 1 (yeast)	mitotic spindle checkpoint control	96	96	-566	-605	7.8386	0.0091		4	-211.8
AV013428	Cryab	Crystallin, alpha B	molecular chaperone	0	-10	-238	-3	9.0360	0.0060		4	120.6
U86090	Kif5b	Kinesin family member 5B	moter protein	405	-93	80	-123	9.4351	0.0053		4	-33
X98511	Sfrs2	Splicing factor, arginine/serine-rich 2 (SC-35)	mRNA processing	-2402	383	-2522	-6304	11.2242	0.0031		4	-2806.1
AA693246	U2af1	U2 small nuclear ribonucleoprotein auxiliary factor (U2AF),35 kDa	mRNA processing	-70	400	-797	-1344	9.5149	0.0051		4	1371.2
AI226368	Hnrpdl	Heterogeneous nuclear ribonucleoprotein D-like	mRNA processing	-271	-164	-930	-1539	7.5851	0.0100		4	-491.6
AI839880	Bruno14	Bruno-like 4, RNA binding protein	mRNA splicing	0	0	71	0	19.1173	0.0005		4	124.4

		(Drosophila)										
U14648	Sfrs10	Splicing factor, arginine/serine-rich 10	mRNA splicing	208	449	-593	-1064	8.0108	0.0086		4	-268.7
AW047320	Nudel-pending	Nuclear distribution gene E-like	neuronal migration	59	158	638	286	14.1507	0.0015		4	-142.5
U81030	Tcofl1	Treacher Collins Franceschetti syndrome 1, homolog	nucleolar-cytoplasmic transport	-479	-162	-518	-795	6.2319	0.0173		4	-336.3
AV217246	Slc29a1	Solute carrier family 29 (nucleoside transporters), member 1	nucleoside transport	0	-32	90	-20	8.6600	0.0068		4	-27.4
Z50013	Hras1	Harvey rat sarcoma virus oncogene	oncogene	106	-235	-121	350	9.3218	0.0055		4	107.2
AV214912	Myo5a	Myosin Va	organelle transport	-20	-77	6	0	7.0246	0.0125		4	27.3
U97327	Cacybp	Calcyclin binding protein	protein degradation	71	-206	75	-229	8.0102	0.0086		4	36.3
AV124768	Psmb5	Proteasome (prosome, macropain) subunit, beta type 5	protein degradation	46	-103	63	138	13.1547	0.0018		4	37.8
AI838669	Psmd12	Proteasome (prosome, macropain) 26S subunit, non-ATPase, 12	protein degradation	78	53	-376	-494	8.2508	0.0079		4	-196.4
AB007139	Psmc3	Proteasome (prosome, macropain) 28 subunit, 3	protein degradation	0	897	-88	140	6.9708	0.0127		4	-153.5
AF055664	Dnaj1	DnaJ (Hsp40) homolog, subfamily A, member 1	protein folding	49	864	875	-49	12.4847	0.0022		4	456
AA919208	Hspa4	Heat shock 70 kDa protein 4	protein folding	24	-84	-44	51	7.4279	0.0106		4	79.4
U81829	Calu	Calumenin	protein folding and sorting	1089	2614	1106	207	12.9359	0.0020		4	-3
AW122165	Carm1-pending	Coactivator-associated arginine methyltransferase 1	protein methylation	-748	-69	-260	-784	6.2842	0.0169		4	-679.9
AI837110	Hrmt112	Heterogeneous nuclear ribonucleoproteins methyltransferase-like 2 (S. cerevisiae)	protein-arginine N-methyltransferase	-65	717	-836	-1004	7.3882	0.0108		4	1139.3
D73368	Erh	Enhancer of rudimentary homolog (Drosophila)	pyrimidine metabolism	-183	2386	-1659	-2093	9.2921	0.0055		4	-1183.1
D83002	Alk	Anaplastic lymphoma kinase	signal transduction	43	-213	306	332	6.7720	0.0138		4	-160.4
AF019371	Cckbr	Cholecystokinin B receptor	signal transduction	9	-132	32	176	8.6230	0.0069		4	-129.1
X70764	Emk	ELKL motif kinase	signal transduction	-75	561	-493	-710	6.4427	0.0158		4	-110.2
U34960	Gnb2	Guanine nucleotide binding	signal transduction	69	765	-537	-695	6.4716	0.0156		4	327.8

		protein, beta 2										
Z18278	Htr5a	5-hydroxytryptamine (serotonin) receptor 5A	signal transduction	35	-83	-88	248	8.4420	0.0073		4	-7.2
AF026524	Ikbkb	Inhibitor of kappaB kinase beta	signal transduction	45	-132	17	3	9.7469	0.0048		4	62.7
AJ133427	Olfir37d	olfactory receptor 37d	signal transduction	183	10	-66	198	6.9945	0.0126		4	-29.7
U42383	Ppm1g	Protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform	signal transduction	-703	48	-545	-873	6.5988	0.0148		4	-292.8
AF035644	Ptp4a2	Protein tyrosine phosphatase 4a2	signal transduction	23	1099	295	1503	16.7627	0.0008		4	545.1
AF074714	Rps6ka4	Ribosomal protein S6 kinase, 90kD, polypeptide 4	signal transduction	-1820	-517	-1256	-2233	11.0061	0.0033		4	-904.5
AF039601	Tgfr3	Transforming growth factor, beta receptor III	signal transduction	176	22	0	0	9.7958	0.0047		4	2.4
AV153952	Dgcr6	DiGeorge syndrome critical region gene 6	similar to laminin	-48	-173	62	253	6.6416	0.0145		4	-86.8
AI840995	Mtch1-pending	Mitochondrial carrier homolog 1	similar to mitochondrial carrier	-183	240	6	353	8.4867	0.0072		4	75.8
L29454	Fbn1	Fibrillin 1	structural protein of connective tissue microfibrils	127	645	-683	-1022	7.8747	0.0090		4	198.2
U60329	Psmc2	Proteasome (prosome, macropain) 28 subunit, beta	subunit of the proteasome	-89	-462	166	176	8.5218	0.0071		4	191.2
AB001489	Pigr	Polymeric immunoglobulin receptor	transcellular immunoglobulin transport	144	-159	65	107	7.9061	0.0089		4	16.8
X80508	Yap	Yes-associated protein, 65 kDa	transcription activator	-239	-114	-290	-475	6.8374	0.0134		4	-131.4
AF091234	Banp	Btg3 associated nuclear protein	transcription factor	-60	211	-335	340	10.9514	0.0033		4	217.8
M61007	Cebpb	CCAAT/enhancer binding protein (C/EBP), beta	transcription factor	691	1453	790	115	14.7087	0.0013		4	2676.3
AF059275	Hsf1	Heat shock factor 1	transcription factor	95	282	95	-56	7.9093	0.0089		4	63.3
AI852632	Litaf-pending	LPS-induced TNF-alpha factor	transcription factor	78	-34	416	566	15.9353	0.0010		4	423.1
X63190	Pea3	Polyomavirus enhancer activator 3	transcription factor	49	-33	45	178	9.3364	0.0054		4	-114.5
U66918	Shox2	Short stature homeobox 2	transcription factor	138	49	-146	-145	6.5798	0.0149		4	57.1
X94441	Tead4	TEA domain family member 4	transcription factor	74	-121	27	172	7.4158	0.0107		4	-32.5
AI842603	Yy1	YY1 transcription factor	transcription factor	40	-63	121	-128	8.6650	0.0068		4	47.2
U33626	Pml	Promyelocytic leukemia	transcription regulation	-70	-358	-59	371	17.2726	0.0007		4	Absent
M63649	Twist	Twist gene homolog, (Drosophila)	transcription regulation	-184	263	-96	-181	6.6508	0.0145		4	-55.5
X14678	Zfp36	Zinc finger protein 36	transcription regulation	42	193	0	0	6.6272	0.0146		4	5.1



U73039	Nbr1	Next to the Brca1	tumor antigen	297	70	22	118	12.1924	0.0024		4	439
AV151915	Scn1b	Sodium channel, voltage-gated, type I, beta polypeptide	voltage-gated sodium channel	286	-143	382	783	9.5652	0.0050		4	93
R75450	Cfl1	Cofilin 1, non-muscle		-1320	598	-2710	-4623	10.9164	0.0034		4	1102.2
AJ006469	Crtap	Cartilage associated protein		159	748	-24	41	6.5591	0.0151		4	-532
AI848094	Dnajc8	DnaJ (Hsp40) homolog, subfamily C, member 8		732	1081	185	-310	6.5041	0.0154		4	527.1
AI849497	Gtrgeo2			386	108	0	59	15.5877	0.0011		4	-171.7
AB028921	Nakap9	Neighbor of A-kinase anchoring protein 95		32	-46	-52	6	6.3005	0.0168		4	223.7
U37351	Pcee-	Paneth cell enhanced expression		38	-60	-238	150	7.0741	0.0122		4	-266.6
AI838337	Ptov1	Prostate tumor over expressed gene 1		51	420	76	41	8.2050	0.0080		4	171.9
AV294412		EST, Weakly similar to RL24 HUMAN 60S RIBOSOMAL PROTEIN L24 [R.norvegicus]		280	-14	401	410	7.5601	0.0101		4	-313.8
AW122429		EST, Weakly similar to procollagen-lysine 5-dioxygenase		-146	358	277	-253	11.3580	0.0030		4	-340.9
AI836625		EST, Similar to thyroid hormone receptor-associated protein, 150 kDa subunit		-328	317	-574	-822	7.4555	0.0105		4	33.5
AI844780		EST, Similar to hypothetical protein FLJ21977		-23	-96	52	44	8.4408	0.0073		4	83.3
AW124250		EST		409	1603	81	1000	6.4227	0.0159		4	-526.8
AI849432		EST		51	57	-143	-21	8.7089	0.0067		4	-43.3
AI847369		EST		186	6	56	0	6.3657	0.0163		4	-228.4
AA982208		EST		50	104	-106	23	6.3064	0.0168		4	178.8
AA940352		EST		0	206	3	0	8.3512	0.0076		4	22.7
AW125330		EST		95	22	-18	5	15.8961	0.0010		4	188.2
AW045910		EST		164	27	-57	434	12.9567	0.0019		4	0.7
AW124049		EST		256	203	370	9	8.3109	0.0077		4	15.5
AW121957		EST		-75	111	-129	54	13.5540	0.0017		4	-223.8
AW124639		EST		-19	-92	111	139	9.0386	0.0060		4	-202.8
AA030469		EST		-60	0	60	0	7.8912	0.0089		4	-38.4
AI846102		EST		-70	422	-123	-21	6.2843	0.0169		4	275.2
AI849109		EST		1	-77	11	0	7.0389	0.0124		4	-56.3
AI853616		EST		209	-17	-182	-48	8.8747	0.0063		4	519.6
AI841579		EST		40	279	768	473	14.9880	0.0012		4	130.2
AV248461		EST		413	22	-18	120	7.8802	0.0090		4	-294.2
AI849035		EST		-191	199	-449	-256	7.7835	0.0093		4	114.9
AI838149		EST		73	-357	-30	72	7.5848	0.0100		4	-29.2

AI850482		EST		-100	-9	0	0	11.5384	0.0028		4	10.2
AI848598		EST		1	-57	-9	0	6.3635	0.0163		4	-62.2
AI838655		EST		343	221	930	1415	10.3861	0.0039		4	-89.4
AW121624		EST		215	35	-121	-41	9.5815	0.0050		4	160.6
AA734444		EST		57	-145	0	26	7.3155	0.0111		4	5.9
AI846338		EST		658	342	582	6	9.0576	0.0060		4	67.6
AW123907		EST		174	0	-14	-15	8.0456	0.0085		4	31.9
AI853561		EST		106	-90	-70	63	7.2768	0.0113		4	67.2
AW123589		EST		77	94	193	22	6.8986	0.0131		4	70.1
AI847483		EST		66	-41	521	61	7.1913	0.0117		4	27.1
AW046708		EST		266	976	176	-394	20.4551	0.0004		4	508
AW124835		EST		216	1225	188	-1012	15.4154	0.0011		4	-729.5
AW125397		EST		-1174	543	-1222	-2240	6.9394	0.0129		4	-1373.5
AI648005		EST		-213	62	-309	-739	15.5757	0.0011		4	35.6
AI606257		EST		-99	75	-271	-468	7.0393	0.0124		4	84.3
AW060951		EST		-90	782	-704	-1531	37.3609	0.0000		4	-840.8
AI845106		EST		-194	355	-101	-420	6.4361	0.0159		4	252.7
AW226650		EST		-509	474	64	-954	6.3383	0.0165		4	976.2
AI852355		EST		-997	-306	-1225	-1485	10.5365	0.0037		4	-108.6
D18865		EST		9	-56	3	45	7.1141	0.0120		4	-26.3
AA833096		EST		15	-18	162	306	9.0662	0.0059		4	153.6
AI646237		EST		10	-216	-19	135	6.8136	0.0136		4	2.7
AI152353		EST		12	-64	34	147	7.0084	0.0125		4	22
AV379809		EST		238	-981	123	1048	6.3928	0.0161		4	-222
AI847054		EST		348	279	470	572	8.2309	0.0079		4	70.1

**Table 2. Genes selected from cDNA microarrays.**

All genes after significance-guided selection from cDNA microarrays were mapped on UniGene clusters to identify the mouse gene names and symbols. Those cDNA which could not be mapped onto UniGene clusters or were mapped onto clusters not corresponding to named genes were listed as Expressed Sequence Tags (ESTs). The function classification was obtained either from the GO terms (GENE ONTOLOGY™ CONSORTIUM ) or publications. Normalized cy5 to cy3 ratios at all time points (NMR0h, NMR2h, NMR4h, NMR8h), correlation coefficient related to the core in each cluster and p-value corresponding to each gene are listed. The cores for clustering analysis are highlighted in red.

GenBank	Symbol	Mouse gene name	Known or inferred function	NMR0h	NMR2h	NMR4h	NMR8h	Correlation	p-value	Cluster number
<b>Cluster 1</b>										
AA175547	stinp	stress induced protein	apoptosis	0.89	0.52	0.08	159.42	0.97273	0.00764	1
AA125367	Ptpn16	protein tyrosine phosphatase, non-receptor type 16	cell cycle regulation	2.16	1.87	2.06	7.01	0.97298	0.00998	1
W88005	Cdkn1a	Cyclin-dependent kinase inhibitor 1A (P21)	cell cycle regulation	4.08	6.37	13.72	30.79	0.99274	0.00016	1
Control	Cdkn1a	Cyclin-dependent kinase inhibitor 1A (P21)	cell cycle regulation	2.99	6.56	13.43	31.92	0.99184	0.00010	1
W16205	Btg2	B-cell translocation gene 2, anti-proliferative	cell cycle regulation	1.07	6.08	11.93	73.21	0.99333	0.00032	1
AA154848	Btg2	B-cell translocation gene 2, anti-proliferative	cell cycle regulation	0.55	6.51	8.10	52.18	0.98791	0.00129	1
AA023645	Fhl2	four and a half LIM domains 2	development/differentiation	1.77	3.07	4.08	4.52	0.77304	0.00488	1
W62931	Polk	polymerase (DNA directed) kappa	DNA synthesis/DNA repair	0.76	0.97	1.10	9.86	0.97936	0.00794	1
AA119072	Cln2	ceroid-lipofuscinosis, neuronal 2	lysosomal enzyme	2.46	4.16	2.11	6.88	0.83798	0.00048	1
W82141	Lamp1	lysosomal membrane glycoprotein 1	lysosomal protein	1.73	2.46	2.27	3.24	0.88907	0.01276	1
<b>Control</b>	<b>Mdm2</b>	<b>Transformed mouse 3T3 cell double minute 2</b>	<b>proliferation</b>	<b>1.81</b>	<b>3.25</b>	<b>12.32</b>	<b>45.48</b>	<b>1.00000</b>	<b>0.00006</b>	<b>1</b>
W85238	Litaf-pending	LPS-induced TNF-alpha factor	transcription factor	1.42	3.50	3.16	4.88	0.81854	0.00516	1
W89677	Gtf3c1	General transcription factor III C 1	transcription factor	1.12	0.91	0.03	3.70	0.86070	0.00097	1
W97853	Hoxb9	homeo box B9	transcription factor/development	1.65	2.44	1.51	4.18	0.87934	0.01102	1
AA138191	Pml	Promyelocytic leukemia	transcription regulation	0.89	2.15	2.10	4.74	0.95570	0.01205	1
AA038657	Tgif	TG interacting factor	transcription regulator	3.63	3.57	3.91	8.90	0.98446	0.00873	1
AA003214		ESTs, Weakly similar to T17286 hypothetical protein DKFZp434H0350.1 [H.sapiens]		1.09	1.91	1.34	2.94	0.87644	0.00973	1
AA030942		EST		1.59	0.78	0.27	5.39	0.90017	0.00242	1

AA062137		EST		1.31	0.40	0.08	5.17	0.90952	0.00026	1
AA120679		EST		1.31	1.15	0.58	5.10	0.92810	0.01132	1
AA153697		EST		1.41	2.14	5.59	26.80	0.99694	0.00005	1
AA145237		EST		0.99	1.22	0.08	8.18	0.93667	0.01411	1
AA166336		EST		3.16	2.87	4.26	4.50	0.80885	0.00004	1
AA105240		EST		2.91	2.44	2.44	5.59	0.94298	0.01037	1
AA111643		EST		1.09	1.57	0.93	2.79	0.87827	0.00614	1
AA119512		EST		1.33	1.19	0.09	3.59	0.81581	0.01417	1
AA061458		EST		1.49	1.55	0.07	7.21	0.90181	0.00321	1
W77518		EST		0.98	2.32	1.27	4.65	0.89840	0.01203	1
W97158		EST		2.19	4.72	4.16	6.86	0.85710	0.01275	1
W67049		EST		0.93	1.43	1.10	3.72	0.95948	0.00650	1
AA087038		EST		0.59	1.99	1.31	3.08	0.83683	0.01030	1
<b>Cluster 2</b>										
AA048952	Slc4a2	solute carrier family 4 (anion exchanger), member 2	anion transport	0.88	1.15	0.18	0.64	0.93866	0.00227	2
AA541870	Ars2-pending	Arsenate resistance protein 2	arsenate resistance	0.98	1.24	0.19	0.50	0.84706	0.01346	2
AA049376	Aamp-rs	Angio-associated migratory protein, related sequence	cell adhesion	1.39	1.49	0.08	0.94	0.90073	0.00927	2
W08451	Tob2	transducer of ERBB2, 2	cell cycle regulation	0.89	1.88	0.16	0.40	0.81724	0.01329	2
AA036170	Tob1	transducer of ErbB-2.1	cell cycle regulation	1.16	1.93	0.04	2.78	0.80210	0.00489	2
W62231	5-Sep	septin 5	cell cycle regulation	1.20	1.41	0.16	0.75	0.89598	0.00220	2
W91463	Ddef1	development and differentiation enhancing	cell motility	2.37	4.21	1.55	3.44	0.95166	0.00737	2
W97502	Isg20	interferon-stimulated protein (20 kDa)	cell proliferation and differentiation regulation	1.00	1.63	0.05	0.86	0.97298	0.01086	2
W15976	Supt6h	suppressor of Ty 6 homolog (S. cerevisiae)	chromatin modulator	0.78	1.69	0.20	0.40	0.81343	0.00710	2
AA048444	Supt6h	suppressor of Ty 6 homolog (S. cerevisiae)	chromatin regulator	0.92	1.00	0.20	0.67	0.91041	0.01221	2
AA063751	Itsn	Intersectin (SH3 domain protein 1A)	endocytosis and synaptic vesicle recycling	1.14	1.02	0.04	0.53	0.77914	0.00364	2
AA000807	Apaa-pending	N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase	enzyme/lysosomal enzyme targeting	1.05	3.73	0.14	0.84	0.83558	0.00194	2
AA059687	Siat1	Sialyltransferase 1 (beta-galactoside alpha-2,6-sialyltransferase)	enzyme/metabolism	4.10	30.06	0.10	18.51	0.89073	0.00018	2
AA030780	Peci	peroxisomal delta3, delta2-enoyl-Coenzyme A isomerase	enzyme/peroxysome	1.63	1.95	0.27	0.88	0.85727	0.01458	2
W83728	Dpm2	dolichol-phosphate (beta-D) mannosyltransferase 2	metabolism	1.26	3.06	0.25	1.57	0.95477	0.01106	2
W41928	Cpsf1	Cleavage and polyadenylation specificity factor 1	mRNA processing	1.21	1.74	0.22	0.86	0.93185	0.01159	2
AA124161	Stau1	staufer (RNA binding protein) homolog 1 (Drosophila)	mRNA transport	0.81	1.89	0.35	0.69	0.85523	0.00288	2
W64796	Epim	Epimorphin	protein trafficking	0.87	1.05	0.03	0.53	0.90567	0.00207	2
AA050765	Tgfbr3	transforming growth factor, beta receptor III	signal transduction	2.32	3.88	0.36	3.08	0.99513	0.00144	2
AA175102	Shc1	Src homology 2 domain-containing transforming protein C1	signal transduction	1.33	1.75	0.32	1.29	0.98632	0.01282	2
AA153988	Rip1	Ral-interacting protein 1	signal transduction	2.03	2.36	0.18	0.90	0.82604	0.00520	2

AA386915	Taf12	TAF12 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 20 kDa	transcription factor	1.33	3.11	0.63	1.14	0.84502	0.01395	2
AA014382	Rarg	retinoic acid receptor, gamma	transcription factor	3.24	6.36	1.81	7.49	0.81383	0.00380	2
W55827	Nfix	Nuclear factor I/X	transcription factor	1.15	2.66	0.94	1.60	0.86541	0.01390	2
AA027381	Trim8	Tripartite motif protein 8		1.13	3.63	0.49	3.80	0.83775	0.00522	2
AA111754	Pcnx	Pecanex homolog (Drosophila)		0.79	1.93	0.07	0.19	0.77224	0.00762	2
AA175386	Cc1	coiled coil forming protein 1		1.22	0.98	0.06	0.88	0.80847	0.00300	2
W98950		ESTs, Weakly similar to P2CH_HUMAN PUTATIVE PROTEIN PHOSPHATASE 2C [H.sapiens]		1.26	1.32	0.10	0.67	0.84455	0.01335	2
W36926		EST, Weakly similar to JAK3 MOUSE TYROSINE-PROTEIN KINASE JAK3 [M.musculus]		1.39	1.71	0.14	0.97	0.92889	0.00668	2
AA073756		EST, Weakly similar to histone deacetylase mHDA1 [M.musculus]		0.41	1.53	0.06	0.42	0.85227	0.00909	2
W65797		EST, Similar to protein phosphatase 2, regulatory subunit B (B56), beta isoform,		1.06	1.63	0.30	2.24	0.79782	0.01264	2
AA064188		EST, Similar to integral inner nuclear membrane protein		1.08	1.26	0.13	0.44	0.80222	0.01236	2
AA002951		EST, Similar to conserved gene amplified in osteosarcoma		2.37	2.96	0.22	1.45	0.90447	0.01257	2
AA138311		EST, Highly similar to CBP MOUSE CREB-BINDING PROTEIN [M.musculus]		2.08	2.63	1.02	1.81	0.95690	0.00964	2
AA051577		EST		0.84	1.07	0.02	0.67	0.95727	0.01057	2
AA111232		EST		0.62	0.87	0.01	0.16	0.79003	0.00324	2
AA146510		EST		1.50	1.67	0.63	2.28	0.78006	0.00105	2
AA058079		EST		1.37	1.77	0.09	2.16	0.88636	0.00297	2
AA108369		EST		1.31	1.49	0.05	0.56	0.82606	0.00744	2
AA110246		EST		1.90	1.67	0.33	1.41	0.83180	0.00133	2
AA051151		EST		1.23	1.19	0.08	1.35	0.87196	0.00722	2
AA058098		EST		1.32	1.46	0.28	1.01	0.92421	0.01164	2
AA178026		EST		0.69	0.93	0.15	0.99	0.93025	0.01461	2
AA178628		EST		1.43	1.55	0.27	1.09	0.91859	0.00064	2
W59516		EST		1.14	1.25	0.24	0.53	0.78828	0.00499	2
AA163457		EST		0.92	1.17	0.13	1.08	0.96635	0.00485	2
AA064325		EST		1.14	1.76	0.10	0.62	0.88919	0.00602	2
W11217		EST		1.47	2.31	0.23	2.27	0.95650	0.01036	2
W09954		EST		1.41	1.95	0.23	1.86	0.96593	0.00188	2
W77046		EST		1.68	2.89	0.06	0.33	0.77390	0.01433	2
W77521		EST		0.91	1.38	0.04	0.39	0.85441	0.00231	2
AA049268		EST		0.79	1.44	0.26	1.90	0.79756	0.00563	2
AA172748		EST		0.97	0.98	0.07	0.54	0.84696	0.01383	2
W98042		EST		0.54	1.28	0.22	0.28	0.77016	0.00240	2
AA021966		EST		0.79	1.05	0.10	0.89	0.98283	0.00094	2
AA031055		EST		0.86	1.98	0.21	0.61	0.86488	0.00599	2
W62404		EST		1.78	4.74	0.93	2.60	0.91234	0.00815	2
AA124340		EST		2.73	2.40	0.12	2.54	0.85216	0.00741	2
AA033040		EST		0.47	1.58	0.07	0.47	0.86858	0.00208	2
AA058029		EST		0.54	0.90	0.04	0.29	0.88827	0.00413	2

W64239		EST		1.14	2.37	0.06	0.37	0.81061	0.00838	2
W89697		EST		1.05	1.49	0.33	0.98	0.98154	0.01053	2
W50731		EST		1.32	1.39	0.12	0.74	0.85802	0.00716	2
W99150		EST		0.94	2.57	0.06	0.70	0.87709	0.00426	2
AA124959		EST		1.05	1.26	0.10	0.64	0.89909	0.01304	2
<b>W75669</b>		<b>EST</b>		<b>0.83</b>	<b>1.40</b>	<b>0.07</b>	<b>0.99</b>	<b>1.00000</b>	<b>0.00036</b>	<b>2</b>
<b>Cluster 3</b>										
AA008925	Cdc25a	Cell division cycle 25 homolog A (S. cerevisiae)	cell cycle regulation	0.80	0.65	0.01	0.00	0.91668	0.00982	3
AA153012	Chaf1a	chromatin assembly factor 1, subunit A (p150)	chromatin assembly	0.89	0.68	0.06	0.24	0.87260	0.00506	3
AA016759	Mcmd6	Mini chromosome maintenance deficient 6 (S. cerevisiae)	DNA replication regulation	1.47	1.55	0.98	0.68	0.91619	0.01235	3
W89873	Recc1	replication factor C, 140 kDa	DNA synthesis/DNA repair	1.06	0.90	0.20	0.10	0.91059	0.00195	3
AA035902	Pold2	polymerase (DNA directed), delta 2, regulatory subunit (50 kDa)	DNA synthesis/DNA repair	1.51	2.26	0.68	0.39	0.97220	0.00524	3
AA050378	Pola2	DNA polymerase alpha 2, 68 kDa	DNA synthesis/DNA repair	1.26	1.04	0.15	0.35	0.90432	0.00215	3
AA032916	Endog	Endonuclease G	endonuclease	1.08	1.00	0.10	0.02	0.94031	0.00950	3
W34612	Tgm2	transglutaminase 2, C polypeptide	enzyme/ post-translational modification of protein	1.24	2.43	0.66	0.45	0.93638	0.01032	3
AA116513	Fasn	fatty acid synthase	enzyme/fatty acid biosynthesis	0.69	0.92	0.21	0.07	0.97726	0.00804	3
AA414662	Sps2	selenophosphate synthetase 2	enzyme/monoselenophosphate	1.16	0.79	0.02	0.14	0.85546	0.00832	3
AA050540	Gart	phosphoribosylglycinamide formyltransferase	enzyme/purin nucleotide biosynthesis	1.49	1.96	0.43	0.40	0.99607	0.00854	3
AA060483	Nolc1	Nucleolar and coiled-body phosphoprotein 1	protein shuttling	1.05	1.39	0.89	0.37	0.82276	0.01055	3
AA058302	Igf2bp3	Insulin-like growth factor 2, binding protein 3	RNA binding protein	1.34	1.46	0.21	0.25	0.98024	0.00394	3
W96860	Pp6-pending	placental protein 6	signaling	0.71	0.72	0.03	0.06	0.96531	0.00305	3
AA036322		EST	signaling/protein kinase	0.96	0.81	0.23	0.05	0.89153	0.00184	3
AA032414	Snap25bp	Synaptosomal-associated protein, 25 kDa, binding protein	synaptic neurotransmitter release	0.84	0.73	0.05	0.20	0.92321	0.01229	3
AA154152	Srf	serum response factor	transcription factor	0.55	2.04	0.41	0.12	0.84113	0.00712	3
AA003969	Pbx2	Pre B-cell leukemia transcription factor 2	transcription factor	1.29	1.17	0.04	0.48	0.91516	0.00275	3
AA032807	Foxm1	Forkhead box M1	transcription factor	0.87	1.42	0.33	0.28	0.97910	0.01444	3
AA032559	Eef2k	Eukaryotic elongation factor-2 kinase	translational control	1.47	1.15	0.05	0.50	0.86854	0.01196	3
W11545	Snx5	Sorting nexin 5	vesicle transport	1.64	1.45	0.43	0.16	0.90712	0.00486	3
AA048752	Rga	Recombination activating gene 1 gene activation		1.19	1.13	0.06	0.25	0.95248	0.00503	3
W45812		EST, Weakly similar to Z151 MOUSE ZINC FINGER PROTEIN 151 [M.musculus]		1.17	0.94	0.05	0.37	0.88205	0.00170	3
AA060321		EST		1.11	0.93	0.03	0.26	0.91364	0.00324	3
AA034616		EST		0.97	0.77	0.03	0.29	0.88008	0.01097	3
AA087204		EST		1.42	1.17	0.31	0.27	0.89908	0.00183	3
AA138018		EST		1.64	1.48	0.16	0.36	0.93783	0.01322	3
AA139205		EST		1.07	1.15	0.52	0.66	0.97923	0.00664	3
W76785		EST		2.70	2.15	0.25	0.61	0.89626	0.00337	3

AA058191		EST		0.85	0.63	0.02	0.20	0.86751	0.00522	3
AA111051		EST		1.43	1.30	0.12	0.66	0.89620	0.00039	3
AA120279		EST		1.38	0.96	0.09	0.46	0.82003	0.00415	3
AA061958		EST		0.68	0.51	0.02	0.21	0.86076	0.00407	3
AA116572		EST		1.34	0.86	0.03	0.24	0.82240	0.00693	3
AA125243		EST		1.40	1.00	0.05	0.27	0.85865	0.00651	3
AA016346		EST		1.89	1.43	0.05	0.08	0.89129	0.00042	3
AA028460		EST		0.96	0.95	0.01	0.09	0.96199	0.00276	3
AA051330		EST		0.87	0.87	0.05	0.11	0.96489	0.01327	3
AA086931		EST		0.93	0.72	0.02	0.05	0.89960	0.00731	3
AA177368		EST		1.40	1.45	0.50	0.44	0.96619	0.00727	3
AA466758		EST		1.56	1.58	0.28	0.44	0.96703	0.00274	3
W34722		EST		1.14	0.96	0.25	0.13	0.90438	0.00144	3
W67062		EST		1.20	1.21	0.17	0.15	0.96324	0.00121	3
W90920		EST		1.15	1.27	0.07	0.15	0.98217	0.00754	3
AA008231		EST		0.90	0.61	0.02	0.09	0.84954	0.01050	3
AA008727		EST		0.91	0.85	0.03	0.14	0.94825	0.00811	3
AA118998		EST		1.78	1.47	0.26	0.11	0.90451	0.00318	3
AA118312		EST		0.87	0.51	0.03	0.10	0.80102	0.00449	3
AA119802		EST		1.32	1.26	0.56	0.13	0.88442	0.00340	3
AA124396		EST		0.98	1.67	0.21	0.10	0.98304	0.01468	3
AA542348		EST		1.48	1.98	1.20	0.47	0.83807	0.00088	3
W33415		EST		1.89	2.02	0.97	0.93	0.97973	0.01115	3
W87034		EST		1.65	1.71	0.45	0.43	0.96874	0.01412	3
AA015421		EST		1.22	0.96	0.08	0.19	0.89830	0.01267	3
AA118706		EST		0.98	0.62	0.05	0.06	0.82569	0.01232	3
W97140		EST		0.62	0.54	0.01	0.16	0.91822	0.00790	3
W97904		EST		0.65	0.80	0.39	0.20	0.93476	0.01278	3
AA087054		EST		2.02	2.07	0.73	0.35	0.94095	0.00297	3
AA109106		EST		0.06	0.26	0.05	0.00	0.82982	0.00178	3
AA139711		EST		0.79	1.07	0.13	0.05	0.99033	0.00746	3
AA437456		EST		0.89	0.57	0.17	0.15	0.79587	0.00299	3
W36781		EST		0.99	1.64	0.36	0.30	0.97869	0.00560	3
<b>W62436</b>		<b>EST</b>		<b>1.43</b>	<b>2.05</b>	<b>0.04</b>	<b>0.21</b>	<b>1.00000</b>	<b>0.00055</b>	<b>3</b>
W89239		EST		0.88	0.67	0.05	0.26	0.86720	0.00366	3
W96828		EST		1.08	0.83	0.11	0.27	0.87824	0.00711	3
AA013895		EST		1.25	0.93	0.09	0.20	0.87644	0.01387	3
AA051679		EST		1.04	1.62	0.15	0.12	0.99371	0.00987	3
AA414106		EST		0.63	0.61	0.07	0.04	0.95338	0.00955	3
<b>Cluster 4</b>										
AA003218	Kifc1	kinesin family member C1	cell cycle regulation	1.16	0.73	0.05	1.10	0.97859	0.01012	4
W13154	Rab9	RAB9, member RAS oncogene family	signal transduction	1.48	0.91	0.37	2.13	0.95481	0.00873	4
AA030294	Fzd1	frizzled homolog 1, (Drosophila)	signal transduction	0.98	0.62	0.03	0.73	0.91701	0.00322	4
W98395	Ddr1	Discoidin domain receptor family, member 1	signal transduction	1.30	0.93	0.04	1.55	0.98200	0.01161	4
W82358		EST, Weakly similar to TYROSINE-PROTEIN KINASE JAK3 [M.musculus]		1.38	0.73	0.05	1.41	0.99799	0.00094	4
W98906		EST, Weakly similar to T12543 hypothetical protein DKFZp434M154.1 [H.sapiens]		2.10	1.55	0.37	2.15	0.97770	0.01475	4
<b>W10134</b>		<b>EST</b>		<b>1.07</b>	<b>0.60</b>	<b>0.14</b>	<b>1.15</b>	<b>1.00000</b>	<b>0.00182</b>	<b>4</b>

AA177856		EST		0.57	0.16	0.07	0.83	0.92855	0.01061	4
W13043		EST		1.45	1.45	0.77	2.49	0.84048	0.01249	4
W70708		EST		0.89	0.68	0.17	1.38	0.94448	0.00423	4
AA061365		EST		1.47	1.05	0.11	2.44	0.94056	0.01264	4
W81803		EST		0.62	0.57	0.05	1.35	0.86620	0.01137	4
W91374		EST		2.00	0.89	0.02	1.63	0.96918	0.00454	4
AA137467		EST		1.40	0.72	0.04	0.66	0.77390	0.00688	4
<b>Cluster 5</b>										
AA142685	Add3	Adducin 3 (gamma)	assembly of spectrin-actin network	1.73	1.05	0.27	0.86	0.94254	0.00597	5
AA105224	Tm4sf6	transmembrane 4 superfamily member 6	cell adhesion	0.88	0.54	0.10	0.36	0.96285	0.01235	5
AA063754	Vps41	Vacuolar protein sorting 41 (yeast)	protein sorting	0.97	0.53	0.11	0.26	0.99397	0.00349	5
<b>AA138500</b>	<b>Vps4a</b>	<b>Vacuolar protein sorting protein 4a</b>	<b>protein trafficking</b>	<b>0.93</b>	<b>0.40</b>	<b>0.02</b>	<b>0.09</b>	<b>1.00000</b>	<b>0.00348</b>	<b>5</b>
AA178745	Sec61g	SEC61, gamma subunit (S. cerevisiae)	protein trafficking	2.00	0.72	0.15	0.28	0.99297	0.00835	5
AA178495	Jak2	Janus kinase 2	signal transduction	1.93	0.95	0.09	0.48	0.99077	0.00661	5
W34498	Es2el	Expressed sequence 2 embryonic lethal		2.74	1.15	0.05	0.89	0.96620	0.00758	5
AA108457		EST, Weakly similar to cytochrome P450 3A13 [M.musculus]		2.64	1.87	1.01	1.58	0.95860	0.00772	5
AA178021		EST, Similar to huntingtin interacting protein 1		0.88	0.37	0.02	0.01	0.99688	0.01223	5
AA059979		EST		1.36	0.58	0.12	0.14	0.99801	0.00440	5
AA145326		EST		2.05	0.44	0.01	0.03	0.97890	0.00049	5
AA154423		EST		0.94	0.47	0.01	0.06	0.99577	0.01430	5
<b>Cluster 6</b>										
AA047917	Itga5	integrin alpha 5 (fibronectin receptor alpha)	cell adhesion	0.97	3.12	2.17	2.74	0.47077	0.00364	6
Control		ARF	cell cycle regulation	49.56	1216.49	3226.07	2143.45	1.00000	0.01467	6
W67089	Edr2	Early development regulator 2 (homolog of polyhomeotic 2)	enzyme/endopeptidase	1.36	3.08	1.99	2.16	0.21129	0.00357	6
AA061982	Rnu22	RNA, U22 small nucleolar	rRNA processing	1.07	1.55	1.02	0.35	-0.31547	0.00062	6
AA064011	Aqp1	aquaporin 1	water transport	2.45	4.84	3.65	3.45	0.32813	0.01110	6
AA183901		EST, Similar to huntingtin interacting protein 1		1.24	2.06	2.47	2.70	0.87206	0.00145	6
W96939		EST, Similar to cortactin isoform B		1.41	2.55	2.63	3.12	0.76080	0.00309	6
W77082		EST		2.09	3.74	2.71	3.08	0.26142	0.00210	6
AA118680		EST		1.66	2.23	1.56	0.43	-0.33100	0.01070	6
W80058		EST		0.70	2.22	1.11	0.62	-0.02395	0.01151	6



### **(III) REFERENCES:**

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