

Appendix

1. *Assessing the significance of the observed differences in response between treatment and control samples, for each gene.*

In a single experiment, with observations x_1, x_2, \dots, x_k from the treatment group and y_1, y_2, \dots, y_l from the control group, a standard procedure for testing the significance of a difference in response is to compute a t -statistic (“Student”, 1908). Assuming a common variance for the x - and y -observations, the statistic can be expressed as

$$t = \sqrt{\frac{kl}{k+l}} \left\{ \frac{\bar{x} - \bar{y}}{\hat{\sigma}} \right\},$$

where

$$\bar{x} = k^{-1} \sum_{j=1}^k x_j, \quad \bar{y} = l^{-1} \sum_{j=1}^l y_j$$

and

$$\hat{\sigma}^2 = \frac{1}{k+l-2} \left\{ \sum_{j=1}^k (x_j - \bar{x})^2 + \sum_{j=1}^l (y_j - \bar{y})^2 \right\}.$$

The value of t is then compared to the t -distribution t_{k+l-2} with $k+l-2$ degrees of freedom, and is considered ‘significant’ if unusually large in absolute value.

False positives can occur either because (by chance) the x -observations are on average rather larger (or smaller) than the y -observations, or because (by chance) both the x -observations and the y -observations are tightly grouped. Thus, in the extreme case in which all k of the x -values were equal and all l of the y -values were equal, $\hat{\sigma}$ would take the value 0, and any difference between \bar{x} and \bar{y} would be judged to be significant, because then $|t| = \infty$. When screening large numbers of experiments for significant treatment effects by using $\bar{x} - \bar{y}$ as a measure of the difference in response, false positives of the first variety are an unavoidable fact of life, but those of the second variety can be reduced when the individual experiments are all of experimentally similar nature, as is the case in microarray analyses.

Suppose, then, that the overall experiment consists of N similar sub-experiments, the i 'th of which yields observations $x_{i1}, x_{i2}, \dots, x_{ik_i}$ and $y_{i1}, y_{i2}, \dots, y_{il_i}$. The idea is to suppose that there is some weak similarity between the random components of the observations in the different sub-experiments, inasmuch as the variances $\sigma_1^2, \sigma_2^2, \dots, \sigma_N^2$ underlying the data obtained in the N sub-experiments are ‘comparable’; in the sense that they can be well described as a random sample from some probability distribution, taken

independently of the mean values. Note that this already implies that the data may need to be pre-transformed, if a relationship between mean and variance is apparent; we use an appropriately chosen power transformation to achieve this. Then information about the distribution of the variances, derived from all N sub-experiments, can be used in making the estimate of the variance appropriate to each individual sub-experiment, reducing the occurrence of false positives arising from inaccurately estimating the σ_i^2 's.

We therefore use a Bayesian analogue of the two sample t -test in each of the N sub-experiments, derived on the basis of the assumptions that:

- A1. The values of μ_i (the sample weighted average of the mean of an observation), δ_i (a measure of the treatment effect, equal to 0 if there is none) and σ_i^2 are sampled independently, μ_i and δ_i from the flat, 'uninformative' improper prior density, and mv/σ_i^2 from the chi-squared χ_m^2 distribution, where the model parameters m and v are to be estimated; the larger the value of m , the more concentrated is the distribution of σ_i^2 around the value v .
- A2. Conditional on the values of μ_i , δ_i and σ_i^2 , $x_{i1}, x_{i2}, \dots, x_{ik_i}$ is a random sample of size k_i from the Normal distribution with mean $\mu_i + \delta_i/k_i$ and variance σ_i^2 , and $y_{i1}, y_{i2}, \dots, y_{il_i}$ is an independent random sample of size l_i from the Normal distribution with mean $\mu_i - \delta_i/l_i$ and variance σ_i^2 ; we suppose that both k_i and l_i are at least 2.

Then, if the parameters m and v are known, the procedure is standard. The normal likelihood coupled with the choice of 'conjugate' prior distribution leads, after integrating out the parameters μ_i and σ_i^2 , to a t -distribution t_{ν_i} for $(\delta_i - \Delta_i)/C_i$, where

$$\nu_i = k_i + l_i + m - 2, \quad \Delta_i = \left\{ \frac{k_i l_i}{k_i + l_i} \right\} (\bar{x}_i - \bar{y}_i)$$

and

$$C_i^2 = \frac{k_i l_i}{k_i + l_i} \frac{s_i^2}{\nu_i},$$

with

$$s_i^2 = s_{xi}^2 + s_{yi}^2 + mv$$

and

$$s_{xi}^2 = \sum_{j=1}^{k_i} (x_{ij} - \bar{x}_i)^2; \quad s_{yi}^2 = \sum_{j=1}^{l_i} (y_{ij} - \bar{y}_i)^2.$$

Hence δ_i can be considered to be 'significantly' different from 0 if the value of $|\Delta_i|/C_i$ is unusually large by comparison with the t_{ν_i} distribution.

Note that, if $m = 0$, this procedure results in the usual two sample t -statistic. The information about the distribution of the variances σ_i^2 derived from all N sub-experiments is seen to be formally equivalent to having m further observations, which contribute a total of mv to the residual sum of squares, thus in effect ‘shrinking’ the raw estimate of σ_i^2 towards v ; the larger the value of m , the more pronounced the shrinkage. Note also that m need not be an integer.

To estimate suitable values of m and v , we use the observed values s_{xi}^2 and s_{yi}^2 , $1 \leq i \leq N$. If mv/σ_i^2 has the χ_m^2 distribution, and if $k_i = k$ is constant in i , it follows that the s_{xi}^2 are then a random sample from the distribution whose probability density function is

$$f(y) = c(m, k)(mv)^{m/2}y^{(k-3)/2}/(mv + y)^{(m+k-1)/2}$$

in $y > 0$, where the constant $c(m, k)$ is such that f integrates to 1; and similarly for the s_{yi}^2 values, if $l_i = l$ is constant in i . Thus, in particular, if, as in many of our experiments, $k = l = 3$, it follows that the sums of squares are sampled from the distribution giving probability

$$F(a, b) = \int_a^b f(y) dy = \left\{1 + \frac{a}{mv}\right\}^{-m/2} - \left\{1 + \frac{b}{mv}\right\}^{-m/2}$$

to any interval $[a, b]$, for $0 \leq a < b \leq \infty$. This allows m and v to be estimated, for instance by choosing them to best fit the probabilities of s intervals $(a_0, a_1), (a_1, a_2), \dots, (a_{s-1}, a_s)$, where $0 = a_0 < a_1 < \dots < a_s = \infty$ are appropriately chosen, to the relative frequencies with which the s_{xi}^2 values actually belong to these intervals, by using a minimum chi-squared criterion. The model fit was typically found to be very good; Supplementary Figure 1 shows the superposition of the function $F(t, \infty)$ and the cumulative curve $S_x(t)$ defined by

$$S_x(t) = \frac{1}{N} \#\{i : s_{xi}^2 > t\}$$

for the *dmec48* treatment data.

In some of our experiments, other values of k and l were encountered. Theoretically, procedures such as maximum likelihood could be used to estimate m and v , though the log-likelihood functions are not particularly amenable. Instead, in order to maintain the simplicity of the above approach, which can be accomplished using a spread sheet, we preferred to use the fact that, if $m + k > 3$, then

$$\begin{aligned} & \int_{a_j}^{a_{j+1}} y^{-(k-3)/2} f(y) dy \\ &= c(m, k)(mv)^{-(k-3)/2} \left(\left\{1 + \frac{a_j}{mv}\right\}^{-(m+k-3)/2} - \left\{1 + \frac{a_{j+1}}{mv}\right\}^{-(m+k-3)/2} \right), \end{aligned}$$

or, equivalently,

$$\frac{\int_{a_j}^{a_{j+1}} y^{-(k-3)/2} f(y) dy}{\int_0^\infty y^{-(k-3)/2} f(y) dy} = \left\{1 + \frac{a_j}{mv}\right\}^{-(m+k-3)/2} - \left\{1 + \frac{a_{j+1}}{mv}\right\}^{-(m+k-3)/2}.$$

These theoretical values can then be fitted in similar fashion, by choice of m and v , to the s empirical weighted frequencies

$$\frac{\sum_{i:a_j \leq s_{xi}^2 < a_{j+1}} (s_{xi}^2)^{-(k-3)/2}}{\sum_{i=1}^N (s_{xi}^2)^{-(k-3)/2}}, \quad 0 \leq j \leq s-1.$$

In our application, we only needed this variant for $k = l = 2$.

The analysis leading to the Bayesian t -test was made on the assumption of having a common variance for the x - and y -values within each sub-experiment. We actually used the above estimation procedure separately for the s_{xi}^2 's and the s_{yi}^2 's, and found that whereas the m -values so obtained were reasonably similar, the values v_x and v_y were at times substantially different. We therefore modified our procedure to accomodate this, taking v to be the average of v_x and v_y , and using a Bayesian t -test for variances known to be in a given proportion: Assumption A1 remains as before, with m also taken to be the average of m_x and m_y , and A2 is replaced by the assumption

A2'. Conditional on the values of μ_i , δ_i and σ_i^2 , $x_{i1}, x_{i2}, \dots, x_{ik_i}$ is a random sample of size k_i from the Normal distribution with mean $\mu_i + \alpha_x \delta_i / k_i$ and variance $\alpha_x \sigma_i^2$, and $y_{i1}, y_{i2}, \dots, y_{il_i}$ is an independent random sample of size l_i from the Normal distribution with mean $\mu_i - \alpha_y \delta_i / l_i$ and variance $\alpha_y \sigma_i^2$;

we take $\alpha_x = v_x/v$ and $\alpha_y = v_y/v$. This has the effect of changing some of the formulae defining the test statistic slightly: we now have

$$\Delta_i = \frac{k_i l_i}{\alpha_x l_i + \alpha_y k_i} (\bar{x}_i - \bar{y}_i), \quad C_i^2 = \frac{k_i l_i}{\alpha_x l_i + \alpha_y k_i} \frac{s_i^2}{\nu_i}$$

and

$$s_i^2 = \frac{s_{xi}^2}{\alpha_x} + \frac{s_{yi}^2}{\alpha_y} + mv;$$

the degrees of freedom ν_i remain unchanged. The fits to the empirical s_{xi}^2 and s_{yi}^2 distributions obtained under these assumptions are illustrated by the superposition of $S_x(\alpha_x t)$, $S_y(\alpha_y t)$ and $F(t, \infty)$ for the *dmyc48* treatment and control data in Supplementary Figure 2.

To check the assumption that the ratio $\sigma_{xi}^2/\sigma_{yi}^2$ of the true variances has the same value α_x/α_y for each i , we computed the sample variance of z_i , $1 \leq i \leq N$, where $z_i =$

$\log_e s_{x_i}^2 - \log_e s_{y_i}^2$. Under the assumption that the ratio is fixed, and if $k = 3$, the z_i 's are a random sample from a translate of the difference of two independent random variables with Gumbel distributions, and thus have underlying variance $2\pi^2/8 \approx 2.5$. We obtained values of around 3.5 for these sample variances, indicating that a model with variances $\sigma_{x_i}^2$ and $\sigma_{y_i}^2$ sampled *independently* as in Assumption A.1 might better fit the data. The consequences for our procedure would only be to replace each s_i^2/ν_i by a value 'shrunk' somewhat closer to v , and would not materially affect our choices of interesting genes.

2. Estimating the conservation probability of a given 6-mer.

The model is as follows. For any given gene, there is a probability f that the 6-mer under consideration is essential to its functioning, in which case it will appear in the immediate upstream region in both species. With probability $1 - f$, its appearance is by chance; the conditional probability of it appearing in both species is then pp' , where p is the probability that the 6-mer appears by chance in a given species, and p' is the conditional probability that it then appears in the other species also. The value of p' could lie anywhere between p and 1, the smaller values corresponding to longer periods of evolutionary divergence between the two species. Thus the probability of the 6-mer appearing in both species is $f + (1 - f)pp'$, and in just one of them is $(1 - f)2p(1 - p')$.

The conservation probability p_c itself is here defined to be the probability that the 6-mer appears in the second species, given that it appears in the first: thus

$$p_c = \frac{f + (1 - f)pp'}{f + (1 - f)p}.$$

This can be rewritten as

$$\begin{aligned} p_c &= \frac{f + (1 - f)pp'}{f + (1 - f)pp' + (1 - f)p(1 - p')} \\ &= \frac{1}{1 + (1 - q)/2q} = \frac{2q}{1 + q}, \end{aligned}$$

where q is the probability that the 6-mer appears in both species, given that it appears in at least one of them. If b denotes the number of genes in which the 6-mer appears in both species, and T denotes the total number in which it appears in at least one species, then q is naturally estimated by b/T ; however, to protect against chance overestimates, we prefer to use the conservative estimate

$$\hat{q} = \frac{1}{T + 1} \left\{ b + 2 - 2\sqrt{1 + b(1 - b/T)} \right\},$$

which is about two standard deviations smaller if both b and T are moderately large, giving

$$\hat{p}_c = \frac{2 \left\{ b + 2 - 2\sqrt{1 + b(1 - b/T)} \right\}}{T + b + 3 - 2\sqrt{1 + b(1 - b/T)}}.$$

3. Tree-based classification.

We used a tree-based classification algorithm, CART [Breiman *et al.* (1984); Venables & Ripley (2002, pp. 251–266)], to detect 6-mers that appear more often immediately upstream of genes influenced by Myc than immediately upstream of genes uninfluenced by Myc. The presence or absence of each of the $4^6 = 4'096$ possible 6-mers was used as covariate information, on the basis of which each gene was to be classified as influenced or uninfluenced by Myc. Algorithms such as CART are most effective if many classification rules can be constructed under slightly differing conditions, and the outcomes ‘averaged’ (Ripley 1996, pp. 65–66). Since the sets of genes influenced by Myc in the different experiments were relatively small (between 50 and 400) compared with those not influenced by Myc, we achieved this by comparing the set of influenced genes with randomly selected subsets of similar size drawn from the set of around 3'500 uninfluenced genes. The 6-mer CACGTG was consistently present as the most informative predictor for being influenced by Myc. There was evidence also for the 8-mers CACGTGtt, CACGTGcg, aaCACGTG and cgCACGTG being particularly interesting.

References

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- B. D. Ripley (1996) Pattern Recognition and Neural Networks. Cambridge University Press.
- “Student” (W.S. Gosset) (1908) The probable error of a mean. Biometrika 6, 1–25.
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Supplementary Methods

Oligonucleotide sequences for in vitro synthesis of dsRNA

Each primer contained a 5' T7 RNA polymerase binding site (TAATACGACTCACTATAGGGAGA) followed by the sequences specific for the targeted genes. The specific primer sequences were as follows: *dmyc* forward: 5'-CCGGCTCTGATAG-3', reverse: 5'-TGCTCATCATGGA-3'; *gfp* forward: 5'-TGAGCAAGGGCGAGG-3', reverse: 5'-GCGGCGGTCACGAAC-3'; *cyclinE* forward: 5'-ACGCTGTTCTGGTCTGGATT-3', reverse: 5'-AAGCTGAGCGAGGAAAATGA-3'; *dmnt*: forward: 5'-CAGCGGGCAGTCCATC-3', reverse: 5'-GCCGTGGGCGTGATTA-3'.

Oligonucleotides for chromatin immunoprecipitation

Fragment "E" (+36 to +136); forward: 5' GGTCGTGCCGTACCGTATTC, reverse: 5' CGCTTAACTGGCTTCTTGCG. Fragment "U" (-1107 to -1022); forward: 5' CTCGAGCTCATTGTTCCG; reverse: 5' GAAAACCTACTCCGACTGGCC.

Oligonucleotides used for in vitro mutagenesis of the nnp1-promoter

ΔE -box 5'-ACATCGAACGGCA**AGAATTCCGGT**CGTGCCGTAC-3'; $\Delta Flank$ 5'-ATCGAACGGCC**CCACGTGATG**TCGTGCCG-3'; and $\Delta E - 40$ 5'-GTCATTTTCAGTA**ACACGTGCG**CATTTAGAGCTGTT-3'. The construct ΔE -320 was made by the insertion of a DNA adaptor into ΔE -box, the adaptor was formed by hybridisation of the following oligo-sequences: 5'-CTAGCA**ACACGTGCG**-3' and 5'-TCGAG**CGCACGTGTT**-3'. Sequences in bold contain (or replace, in the case of ΔE -box) the decameric E-box sequence.

Construction of the CG5033 and CG4364 reporters

Promoter sequences from -322 to +61 relative to the transcription start site of *CG5033* (E-box at +21, ATG at +56) and from -561 to +131 relative to the transcription start site of *CG4364* (E-box at -421, ATG at +133), respectively, were fused to the firefly luciferase ORF. In the ΔE -box mutant, the sequence "CACGTG" was replaced by "GAATTC". The following oligonucleotides were used: *CG5033*-upstream: 5'-GTAGAGATCTGAATTT**CGCTG**AAAATGGTTCGTTG-3'; *CG5033*-downstream: 5'-ATGTT**CCAT**GGGGTCAATTTTGAGGTA-3'; *CG5033*- ΔE box: 5'-ATCGCTATCGCTGACTGCA**AGAATTCCGCCG**CGTTAGTTTTGTTTTTACC-3'; *CG4364*-upstream: 5'-CCCCAGATCTTCAAGAACACGACACAAG-3'; *CG4364*-downstream: 5'-CCAAC**CAT**GGTGCCGGTTTATGAAAATG-3'; the sequences printed in bold indicate the beginnings of the luciferase ORF and the mutated E-box, respectively.

Polytene chromosome staining

Salivary glands of wandering 3rd instar larvae were dissected in PBS and fixed in 3.7 % formaldehyde solution for 3 min. Squashing was performed in a solution containing 3.7 % formaldehyde and 45 % acetic acid, according to Ashburner (1989). *Drosophila* – a laboratory manual (Cold Spring Harbor Laboratory Press). Slides were blocked in PBS containing 5 % BSA and 30 % FCS. Primary antibodies rat monoclonal anti-HA (Roche Applied Science), or mouse monoclonal anti RNA Polymerase II phosphorylated on CTD-Serine 2 (Covance MMS-129R, clone H5) were diluted 1:200 in blocking solution (5% BSA & 30% FCS in PBS) and incubated overnight at 4° C. Secondary antibodies Texas Red-conjugated anti- rat or FITC-conjugated anti mouse (Jackson ImmunoResearch Laboratories) were diluted 1:300 in blocking solution together with DAPI at 1 µg/ml for 2 h at room temperature. Fluorescence was visualized using a Zeiss Microscope.

Supplementary Legends

Supplementary Figures 1 and 2. For description see mathematical appendix.

Supplementary Figure 3: Positions of E-boxes relative to transcription start sites in genes that are bound by dMyc in DamID assays (**bound**; Orian et al. 2003), up-regulated after dMyc over-expression *in vivo* in our experiments (**up**), and in different combinations of these two gene lists. The X-axis is labeled as in Fig. 3.

Supplementary Figure 4. Localization of dMyc and RNA Pol II(0) on larval polytene chromosomes. Chromosomes of control larvae (**A**) or larvae expressing HA-tagged dMyc in the fat body (**B**) were stained with antibodies against the HA-epitope (*green*), RNA PolII(0) (*red*) and with Hoechst 33258 to reveal DNA (*blue*). Arrows indicate some prominent sites of colocalization of dMyc and PolII(0) (*yellow*). Genotypes of the flies are: “*y w dpp-GAL4 / +*” (**A**) and “*y w; UAS-HA-dMyc / dpp-GAL4*”. Magnification: 40 x.

Supplementary Figure 5. Normalized luciferase activities of dMyc target reporter constructs. Plasmids expressing the firefly luciferase ORF under the control of the wild-type or E-box deleted *CG5033* promoter (**A**) or the *CG4364* promoter (**B**) were co-transfected with *gfp* or *dmyc* double-stranded RNAs as indicated. Firefly luciferase activities were normalized to the co-transfected *Renilla* luciferase activities expressed under the control of the constitutive *tubulin* promoter. The experiments were carried out in triplicate (as described in Materials & Methods) and the error bars indicate the standard deviations.

Supplementary Figure 6. Distribution of consensus E-boxes amongst vertebrate Myc targets. A collection of 1697 potential Myc targets was obtained from the “c-Myc cancer gene” web page (<http://www.myc-cancer-gene.org/>; 2). The subsequent analysis was restricted to the 145 genes shown to be **activated** by c-Myc in **human** cells and whose status as **direct** Myc targets was supported by at least one line of evidence (gel shift, foot print, chromatin immunoprecipitation, ability to be activated by a MycER fusion protein in the presence of cycloheximide). To analyse the promoters of these genes, the sequences of 1871 human promoters (from –499 to +100 relative to the transcription start site) were obtained from the curated “eukaryotic promoter database (EPD)” at the Swiss

Institute for Bioinformatics (ISB/SIB, <http://www.epd.isb-sib.ch/>; 1); this list contained 68 of the 145 Myc target genes described above. Twenty-two of these 68 genes (35%) contained at least one consensus E-box (17 genes with 1 E-box, 4 genes with 2 E-boxes, 1 gene with 3 E-boxes). For comparison, amongst 1526 human promoters from the EPD which have not (yet) been proposed to be Myc targets in any species, only 14% harbored a consensus E-box.

Supplementary Table 1: Number of genes with significantly altered expression in the different experimental situations. Gene lists are explained in Materials and Methods.

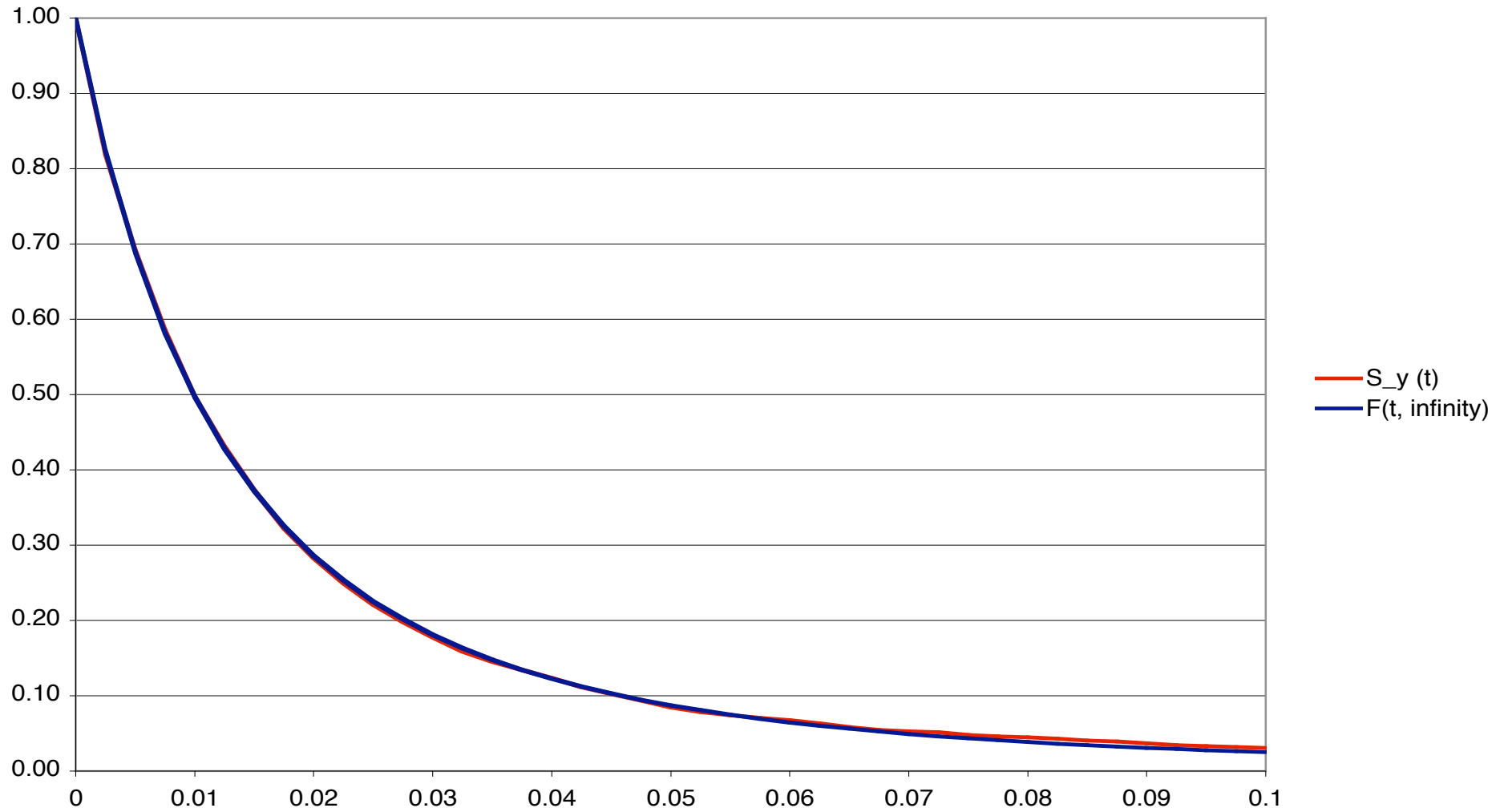
Supplementary Table 2: List of significant dMyc targets common to all three time points after *dmyc* RNAi. Columns labeled *6 h*, *12 h*, *48 h* show their expression ratios at the indicated time points, as determined by a comparison of *dmyc* RNAi microarrays with the corresponding *gfp* RNAi controls; all shown genes are down-regulated at all time points. *qRT-PCR*, expression ratios of selected genes as determined by quantitative real-time PCR of *dmyc* RNAi samples compared to *gfp* RNAi treated controls (averages and standard deviations of biologically independent triplicates). Column *E-box* shows position of E-boxes (where present) relative to transcription start site, in nucleotides. *Known* marks genes that have previously been identified as potential Myc targets in vertebrates (**V**) or *Drosophila* (**D**).

Supplementary Table 3: List of all genes that are significantly affected in any of the microarray experiments. *E-boxes*, positions of E-boxes relative to transcription start sites; **yellow** marks genes with an E-box between +1 and +100. *Affymetrix*, name of Affymetrix features corresponding to the indicated gene; wherever a single gene is represented by more than one Affymetrix feature, the 2nd and subsequent occurrences of the gene name are left blank. Column *R*, ratio of gene expression in the experiment versus control. Column *D* indicates direction of change – **U** is up-regulated, **D** is down-regulated, as compared to control. Column *S* indicates significant genes; **S**, differentially expressed with $p < 0.001$. Genes are marked in color in the experiments where they are significantly affected and their expression ratio is > 1.5 -fold; **green** fields indicate down-regulation, **red** fields up-regulation, as compared to control.

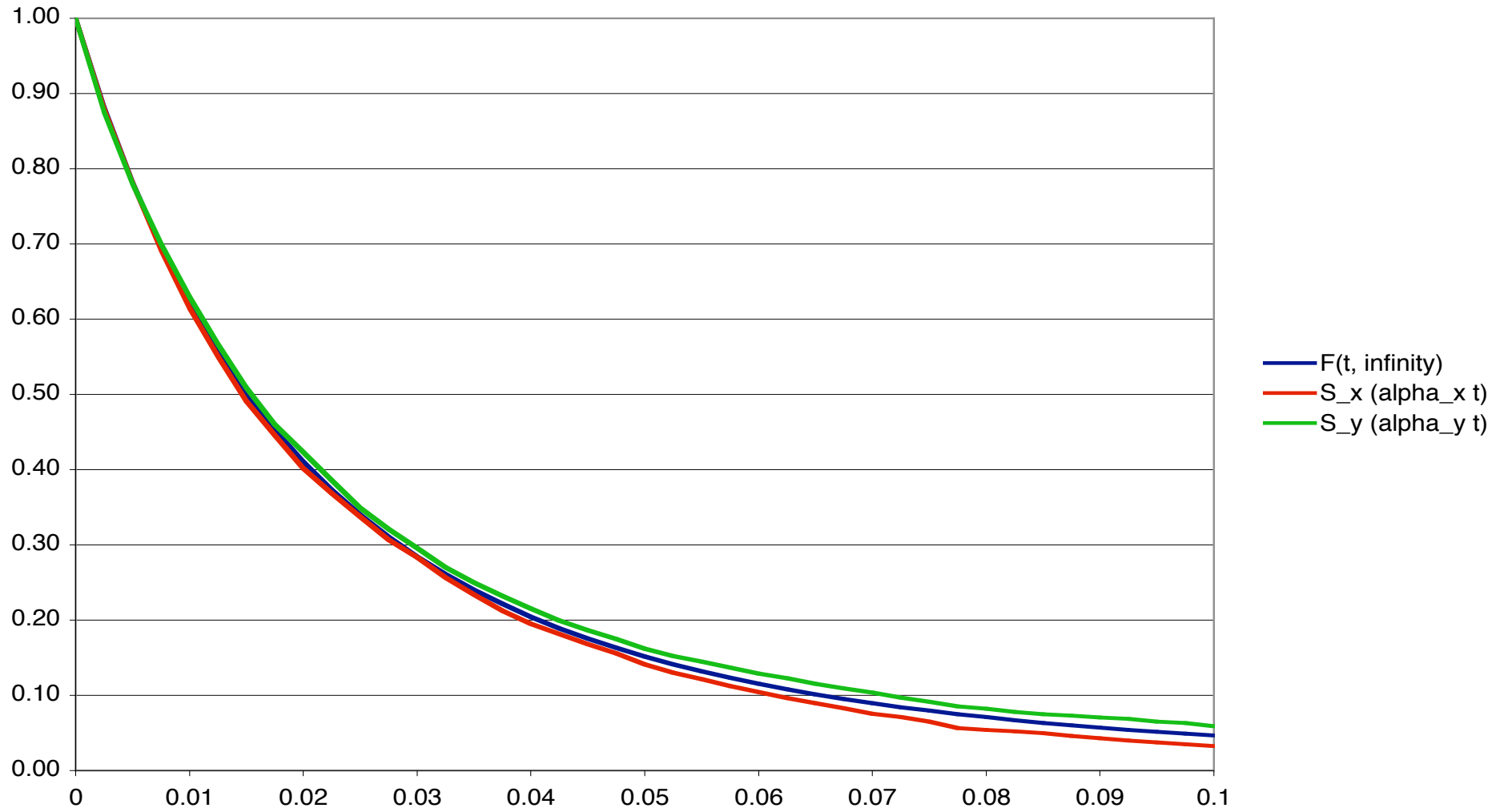
Supplementary References

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2. **Zeller, K. I., A. G. Jegga, B. J. Aronow, K. A. O'Donnell, and C. V. Dang.** 2003. An integrated database of genes responsive to the Myc oncogenic transcription factor: identification of direct genomic targets. *Genome Biol* **4**:R69.

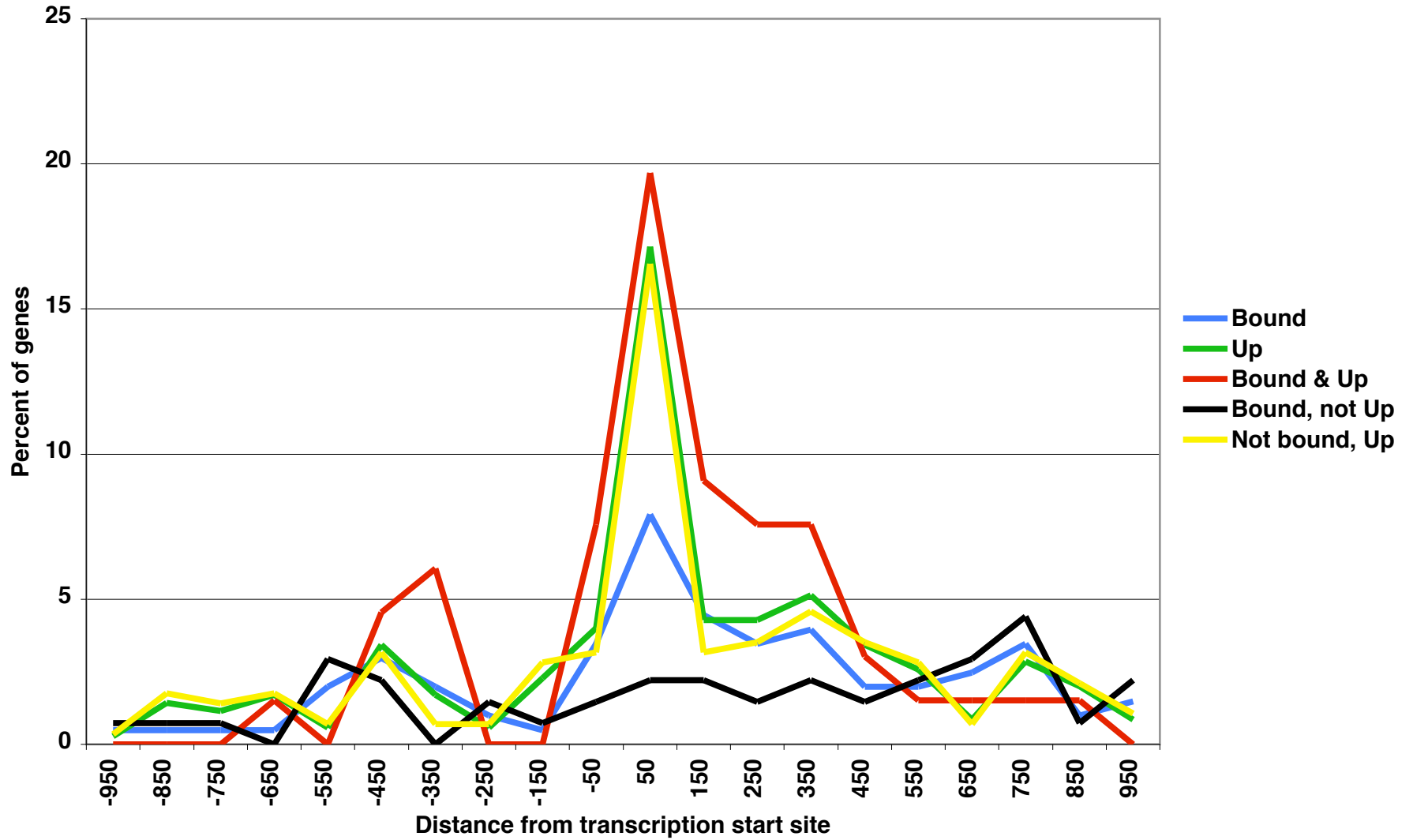
Supplementary Figure 1

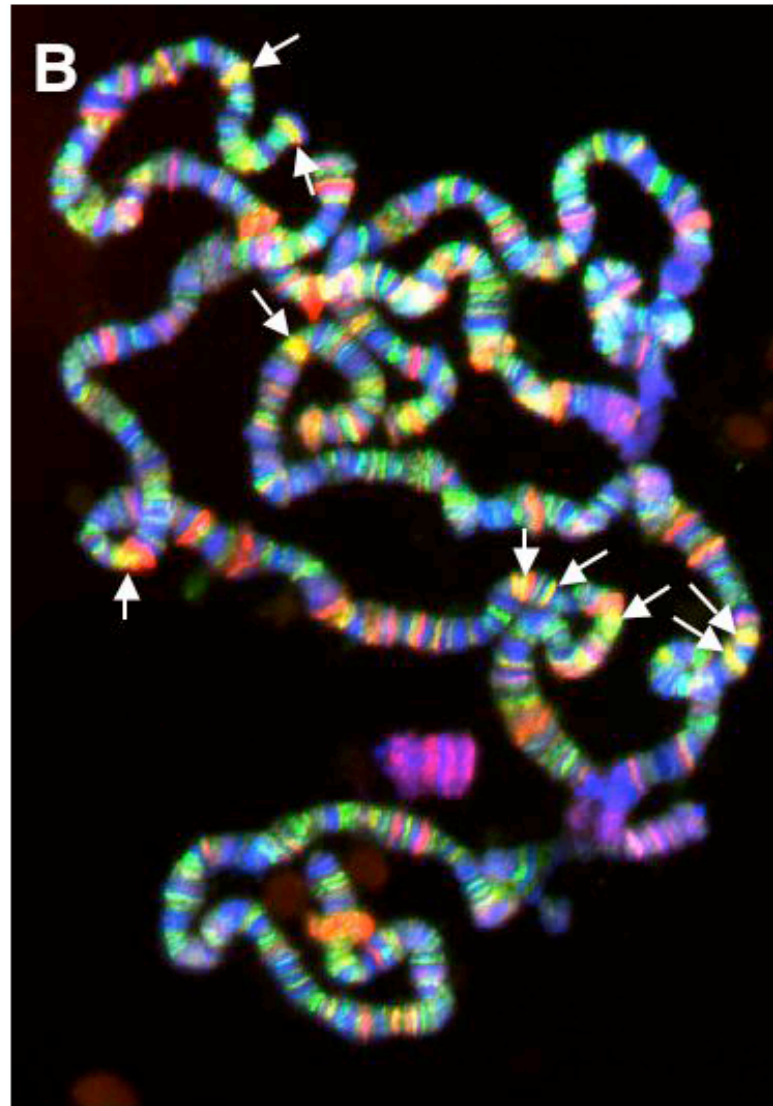
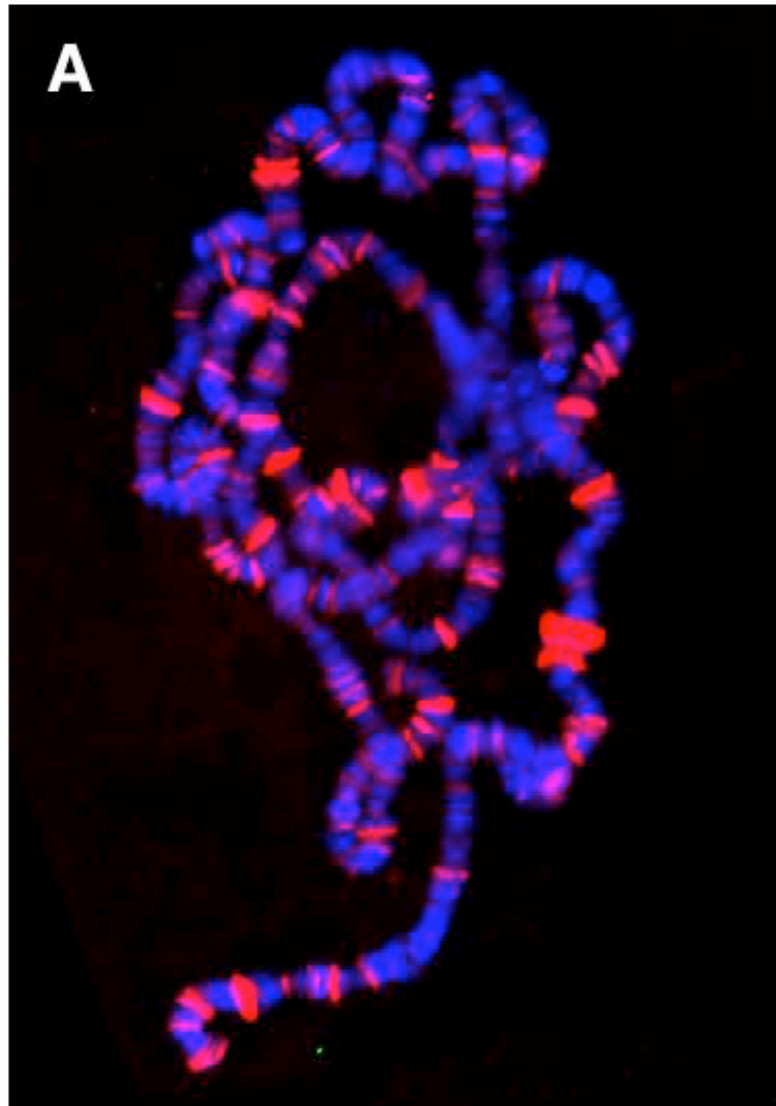


Supplementary Figure 2

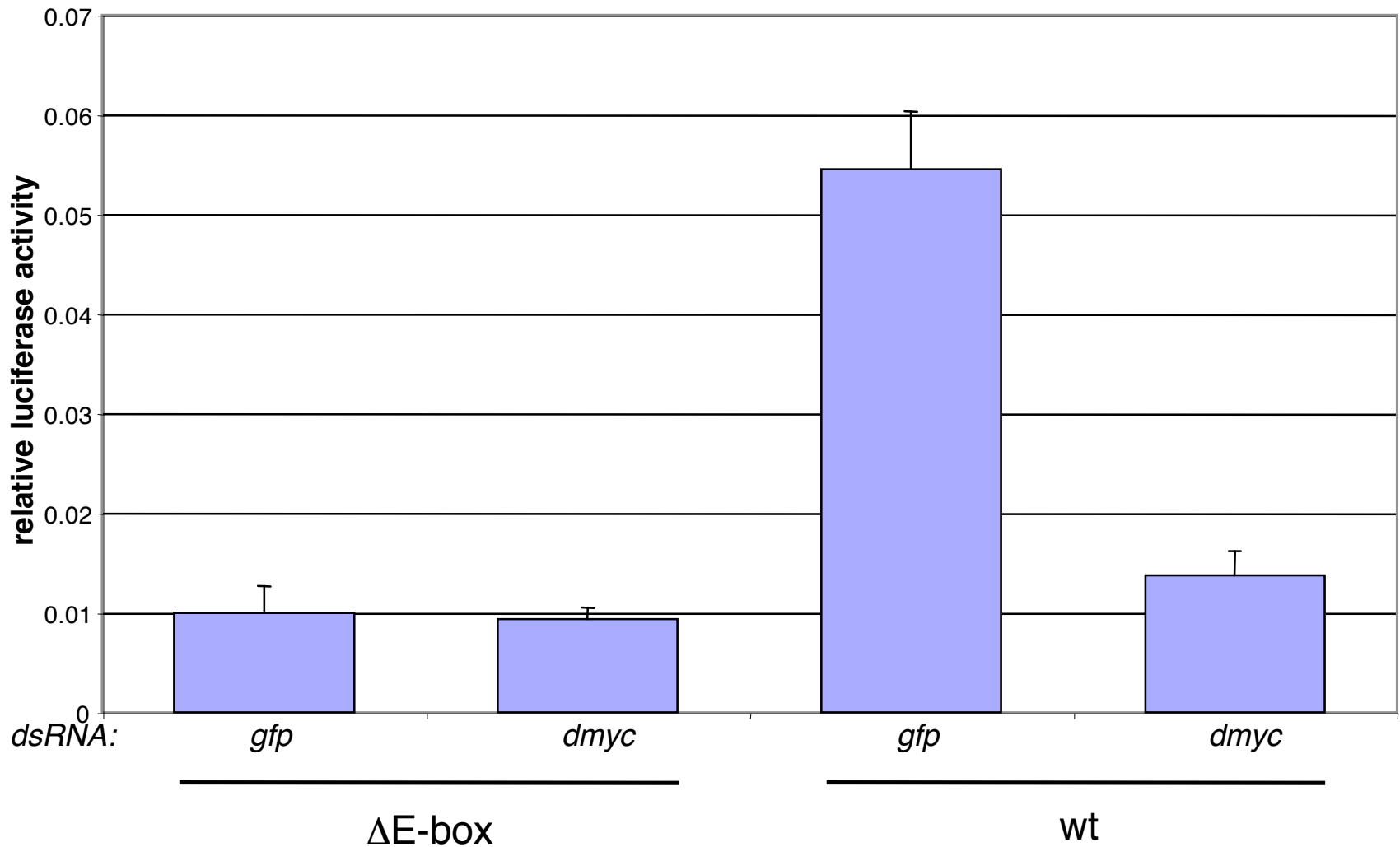


Supplementary Figure 3



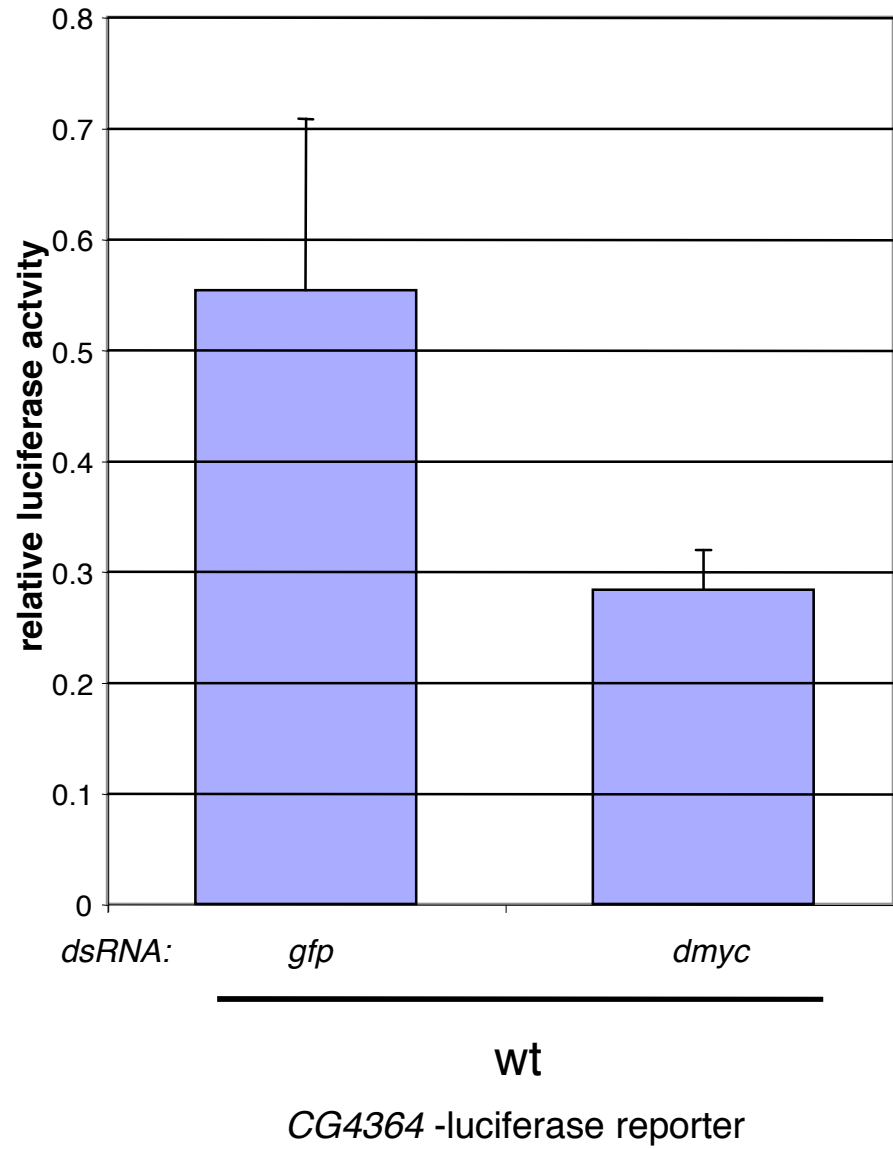


Supplementary Figure 4.



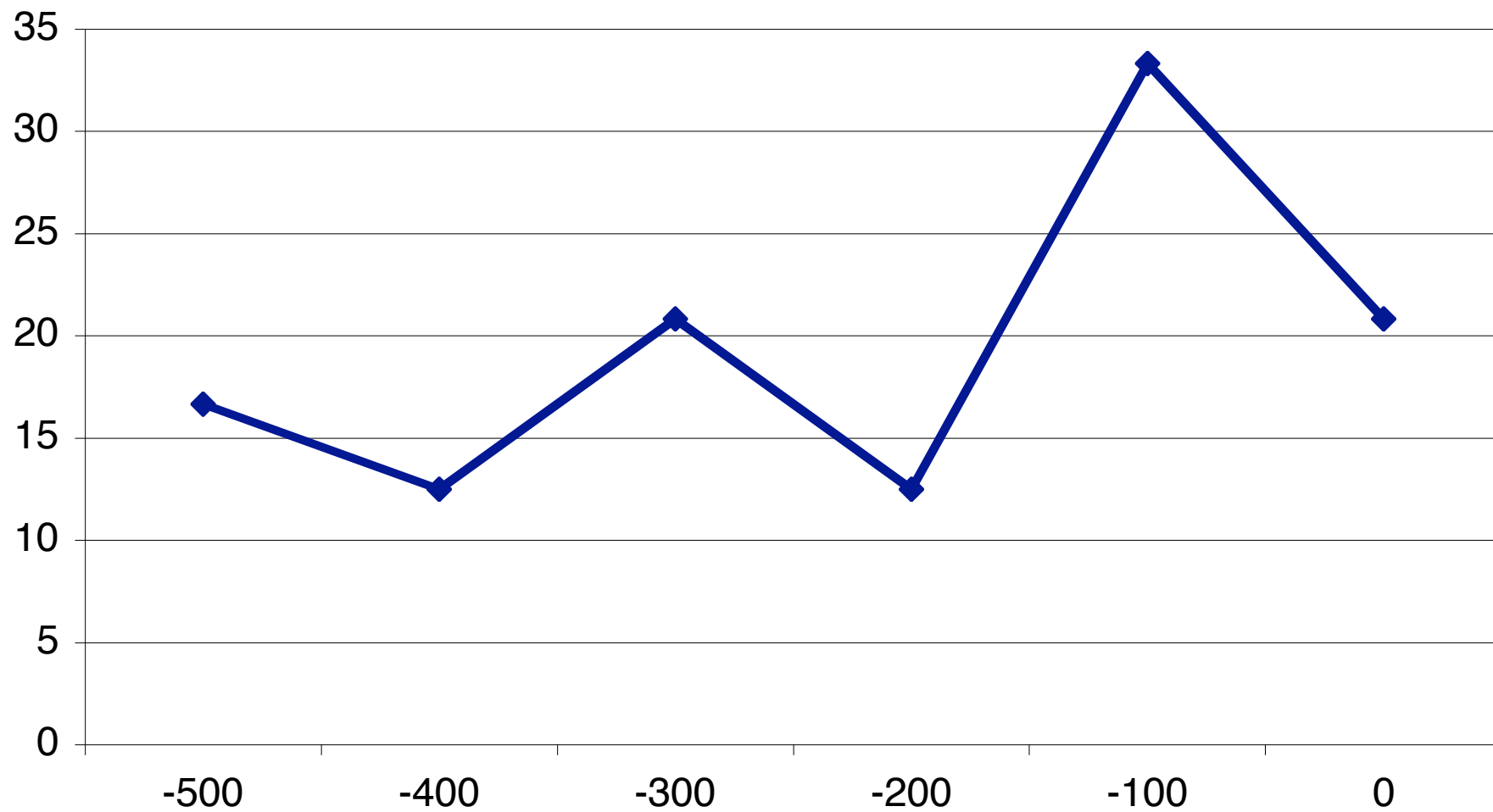
CG5033 -luciferase reporter

Supplementary Figure 5A



Supplementary Figure 5B

Distribution of E-boxes in c-Myc target promoters



Supplementary Figure 6

	Down	Up
dMyc6	373	14
dMyc12	246	7
dMyc48	53	35
cyclin E	10	22
GOF	104	165
LOF	12	19

Supplementary Table 1

Supplementary Table 2

Gene	6 h	12 h	48 h	qRT-PCR	E-box	Notes	Known
<i>Nucleolar function / ribosome biogenesis</i>							
nnp-1	1.7	2.4	2.5	1.9 ± 0.2	29	rRNA processing	
pit	1.7	2.4	2.2			RNA helicase	D, V
nop56	1.6	2.5	2.5	2.1 ± 0.2	29	snRNP	D, V
fib	1.8	3.5	2.8	2.4 ± 0.1	26, 834	35S primary transcript processing	D, V
nopp140	2.3	2.5	1.9		48, 385	nucleologenesis	D, V
CG6712	2.6	3.7	2.8	1.6 ± 0.4	46	RNA binding	D, V
CG8939	1.8	2.7	2.0		15	rRNA processing	
CG1542	2.1	2.3	2.0		78	processing of 27S pre-rRNA	D
nop5	1.7	2.7	2.6	2.5 ± 0.6	-509, -9	rRNA processing	D
CG5728	1.9	2.4	1.7		31, 789	rRNA processing	D
CG4364	1.8	2.3	2.2		-421	structural ribosome constituent	D
<i>Protein synthesis</i>							
NHP2	2.1	2.5	2.3		41	NHP2 Ribosomal protein L7AE	
CG1381	1.6	2.3	2.1		29	Ribosomal protein L10	D
hoi-polloi	1.6	3.4	2.0	1.6 ± 0.4	-15	snRNP	
<i>RNA binding / mRNA processing</i>							
CG4038	1.8	2.6	2.3		36	snRNP	
rrp46	2.2	2.1	2.2			mRNA processing	D
<i>Other</i>							
CG10341	1.5	2.3	1.7		17	defense response	D
CG11660	2.3	2.1	2.0		224	protein kinase activity	
CG6751	1.7	2.2	2.0		-641, 29	TFIID complex	
CG5033	1.6	2.2	1.8		21	transcription factor activity	D, V
FK506-bp1	1.7	1.9	1.7		-114, 216	protein folding	D, V
l(2)09851	1.7	2.3	1.7		35, 830	peroxisome targeting sequence binding	
<i>Unknown</i>							
CG7845	2.9	3.5	2.0		-697, 24		D
CG10805	2.1	2.7	2.0		-13		D
CG9799	1.8	2.1	1.8		6, 44		
CG30349	1.8	2.7	2.1		90, 236		
CG15019	2.0	2.0	1.7		-85, 936		
CG1785	1.9	2.4	2.1		-454, 19		D
CG11604	2.4	3.7	2.7		416		D
CG1234	2.0	3.0	2.2				D

Supplementary Table 3

Gene	E-boxes				Affymetrix	dmyc6			dmyc12			dmyc48			cycE			GOF			LOF		
	1st	2nd	3rd	4th		R	D	S	R	D	S	R	D	S	R	D	S	R	D	S	R	D	S
Signaling / protein phosphorylation & dephosphorylation																							
Fps85D					143164_at	1.3	D		1.0	D		1.3	U		1.1	U		2.1	D	S	1.1	U	
CG10522					148666_at	1.4	D		1.2	U		1.0	U		1.1	D		2.1	D	S	1.2	U	
SAK					144123_at	1.1	D		1.1	U		1.2	U		1.8	D		2.1	D	S	1.2	U	
CG17090					142812_at	1.3	U		1.1	U		1.1	D					1.0	D		1.2	U	
					151694_at	1.0	U		1.1	U		1.0	D		1.4	D		1.2	D		1.6	U	S
auxillin	-186				153829_at	2.0	D	S	1.4	D	S	1.1	U		1.5	D		1.0	U		1.4	U	
Pak	639	810			153976_at	1.9	D	S	1.1	D		1.1	U		1.3	D		1.2	U		1.1	U	
put					154591_at	1.8	D	S	1.2	D		1.2	U		1.0	U		1.6	D		1.1	U	
CaMKII					142793_at	1.8	D		1.6	D								1.3	U		1.3	U	
					151686_s_at	1.8	D	S	1.5	D	S	1.0	D		1.1	D		1.2	U		1.1	U	
CkII&bgr					143092_at	1.7	D	S	1.4	D	S	1.2	D		1.1	D		1.0	D		1.1	U	
CG14217					153995_at	1.7	D	S	1.2	U		1.1	U		1.1	D		1.1	D		1.1	U	
Plkk1					143050_at																		
					151762_s_at	1.2	U		1.8	D	S	1.3	D					1.2	D		1.1	U	
Btk29A	118				141857_at	1.0	D		1.0	D		1.0	U		1.0	U					1.1	U	
					142240_at				1.7	D	S										1.0	U	
					153920_at	2.4	D	S	1.1	U		1.1	U		1.5	D		1.3	D		1.1	D	
Caki					143719_at	1.2	U		1.7	D	S	1.0	D					1.7	U		1.4	U	
					143857_at	1.1	U		1.1	D		1.0	D		1.2	D		1.3	U		1.4	U	
					150327_at																		
CG7597					141597_at	1.5	D		1.6	D	S	1.1	D		1.4	D		1.1	D		1.1	D	
Brd	-193				143088_at													2.5	D	S	1.1	D	
fng	-922				143664_at	1.1	D		1.4	U		2.2	U	S	1.3	U		1.8	D	S	1.0	D	
sno					152069_at	1.7	D	S	1.5	D		1.1	U		1.2	D		1.4	U		1.2	U	
Cbl					143910_at	1.1	D		1.2	D		1.0	U		1.4	D		2.5	D	S	1.1	U	
					148403_at																		
spi					143573_at	1.3	U	S	1.2	U		1.3	U		1.1	D		1.8	D	S	1.5	U	S
msh					151799_at	1.3	D	S	1.7	D	S	1.3	D		1.1	D		1.5	U		1.2	D	
Pi3K59F	177				142299_at																		
					151517_at	1.4	D		1.2	D		1.4	U		1.3	U		2.4	D	S	1.1	U	
Pi3K68D					142750_at	1.1	D		1.1	U		1.1	U		1.3	D		2.2	U	S	1.2	U	
					151675_s_at	1.4	D		1.2	U		1.2	U		1.3	D		1.0	D		1.2	U	
sno	707				154678_at	2.0	D	S	1.2	D		1.0	U		1.0	D		1.2	U		1.2	U	
Socs36E					146427_at	1.6	U	S	1.2	D		1.1	D										
Stam					153478_at	1.6	D	S	1.1	U		1.3	U		1.2	D					1.1	D	

				151756_at	1.6 D S	1.2 D		1.2 U		1.0 D		1.1 U		1.1 U	
CG1846				142224_at	1.1 D	1.0 D		1.2 U				1.4 U		1.1 U	
				151500_at	1.6 D S	1.2 D		1.1 D		1.9 D		1.1 U		1.1 U	
Smg5				154083_at	1.6 D S	1.1 D		1.1 D		1.1 U		1.1 U		1.1 U	
CG8707				152663_at	1.6 D S	1.0 U		1.0 U		1.0 U		1.2 U		1.2 D	
CG31012				150911_at											
				151904_at	1.5 D S	1.3 D		1.1 D		1.6 D		1.1 D		1.1 D	
CG18600	30			153805_at	1.8 D S	2.5 D S		1.8 D		1.3 D		1.8 U		1.6 D	
CG8461	3			142771_at	1.9 D	1.9 D S		1.3 D		1.1 D		1.5 U		1.1 D	
spri				144808_at	1.1 U	1.9 D S		1.0 U						1.2 D	
				144809_at	1.1 D	1.2 D		1.2 D		1.2 D		1.3 U		1.4 U	
				144810_at											
				144812_at											
				151411_at											
CG31150				142109_at										1.1 D	
				143021_at	1.2 U	1.8 D S		1.2 U							
				149982_at	1.4 D	1.2 D		1.0 D							
				152020_at	1.0 U	1.1 U		1.5 U S		1.0 U					
CG7515				148349_at											
				148350_at										1.5 U	
				148351_at		1.7 D S								1.3 U	
				153125_at	1.1 D	1.0 D				1.0 U				1.2 U	
CG16807				148891_at		1.7 D S		1.3 D				1.7 D		1.2 U	
CG8981	168			142887_at	1.2 D	1.2 U		1.0 U				1.3 D		1.1 U	
				147046_at		1.4 D								1.0 D	
				151710_at	1.6 D	1.6 D S		1.1 D				2.0 D		1.1 U	
CG11660	224			142720_at	2.3 D S	2.1 D S		2.0 D S		1.5 D		2.2 U		1.5 D	
CG8801				141995_at											
				142696_at	1.0 D	1.5 D S		2.0 D S		1.4 U		1.2 U		1.3 D	S
CG17272				150278_at	1.1 D	1.2 U		1.1 U		1.3 D		2.6 U S		1.1 D	
CG11859	-58			150571_at	2.9 D S	2.0 D S		1.3 D		1.1 U		2.5 U S		1.3 D	
Ptpmeg	113			153778_at	1.1 D	1.1 D		1.3 D		1.2 D		2.0 U S		1.2 U	
CG2199	-868			154599_at	1.8 D S	1.6 D S		1.4 D		1.3 D		1.8 U S		1.2 D	
RhoGDI				153882_at	1.3 D	1.1 D		1.0 U		1.3 D		1.8 U S		1.0 U	
Transcription factors / co-factors															
H				142797_at	1.5 D S	1.1 D		1.1 U		1.1 U		1.1 U		1.0 U	
				151688_s_at	2.0 D S	1.1 D		1.1 D		1.4 D		1.1 D		1.3 U	
m4	-570			143251_at								1.9 U S		1.4 U	

HLHm3	585			143248_at															1.8 U S	1.2 U
Trl				142876_at	1.5 D S	1.5 D S	1.0 D	1.8 D											1.6 D	1.4 U
				148766_at																
				151706_s_at	1.1 D	1.0 D	1.1 U	1.7 D											1.7 D S	1.3 U
Scm				143335_at	1.9 D S	1.1 D	1.0 D	1.5 D											1.3 D	1.0 U
trx				143384_at	1.1 D	1.0 D	1.0 D	1.2 D											3.4 D S	1.3 U
Arc70				150989_at	1.3 D	1.0 D	1.0 U	1.4 D											1.3 U	1.2 U
				153799_at	2.0 D S	1.3 D	1.3 U	1.1 U											1.1 U	1.0 U
tou				152868_at	1.1 D	1.3 D	1.0 U	1.6 D											1.8 D S	1.1 U
dom	-499			142280_at	1.3 D	2.0 D S	1.4 D	1.2 D											1.1 U	1.0 U
				151511_r_at	2.4 D S	1.3 D	1.4 D	1.2 D											1.5 U	1.3 U
Sin3A	906			141716_at	2.2 D S	1.2 D	1.3 U	1.4 D											1.3 D	1.2 U
Mio				154826_at	1.6 D S	1.4 D	1.0 U	1.0 U											1.2 U	1.1 U
ftz-f1				151259_at																
				154699_at	1.9 D S	1.2 D	1.2 U	1.5 D												1.5 U
Hr39				155094_at	1.9 D S	1.1 D	1.3 U	1.0 D											1.1 D	1.1 U
NFAT	-391			153719_at	1.0 U	1.9 D S	1.0 U	1.3 D											1.2 U	1.3 U
mbl				143809_at															2.8 D S	1.6 U
				147360_at																
sina				153438_at	1.8 D	1.1 D	1.2 U	1.0 D											2.4 D S	1.0 U
sd				143337_at	1.2 D	1.5 D S	1.2 D												1.4 D	1.2 U
Adf1				153659_at	1.7 D S	1.1 U	1.1 U	1.2 D											1.8 U	1.1 U
shn				152896_at	1.3 D	1.1 U	1.3 U	1.1 D											3.4 D S	1.3 U
Mad				143670_at	2.0 D S	1.2 D	1.4 U	1.3 U											1.4 D	1.2 U
srp				141687_at	1.7 D S	1.1 D	1.3 U	1.3 D												
exd				153499_at	2.3 D S	1.1 U	1.5 U	1.5 D											1.3 D	1.1 U
kn				143207_at															2.7 D S	1.1 U
ttk				153259_s_at	1.7 D	1.1 D	1.1 U	1.0 U											1.0 U	1.6 U
				154445_at	2.9 D S	1.1 U													1.0 D	1.2 U
CrebA				143003_at	1.1 U	1.1 D	1.1 D	1.4 D											1.1 D	1.6 U S
				151748_at	1.7 D S	1.2 D	1.1 U	1.5 D											1.3 D	1.8 U
dm				143126_at	2.6 D S			1.2 D											1.3 D	
emc				153703_at	1.5 D S	1.2 D	1.3 U	1.7 D											1.1 D	1.0 U
corto	179			152846_at															2.4 D S	1.3 U
psq				154654_at	1.4 D	1.1 D	1.4 U	1.1 U											2.4 D S	1.2 U
Ada2S				154266_at	1.3 D	1.1 D	1.2 U	1.0 U											2.0 D S	1.1 U
crol				143920_at	1.3 U	1.5 D S	1.2 D												2.0 D S	1.2 U
XNP				143015_at	1.2 U	1.1 U	1.1 U	1.5 D											1.8 D S	1.0 U

CG9305			142244_at	2.1 D S			1.3 D	1.1 U	1.1 U	1.1 D	
CG7839	12		141506_at	2.1 D S				1.0 U	1.7 U	1.1 D	
osa			153971_at	2.0 D S	1.2 U		1.2 U	1.2 D	1.2 D	1.1 D	
Hcf			141291_at	1.8 D S	1.2 D		1.1 U	1.6 D	1.3 D	1.1 U	
lolal			153811_at	1.8 D S	1.1 D		1.1 U	1.2 D	1.3 U	1.3 D	
NK7.1			142439_at	1.7 D S	1.1 U		1.5 U	1.2 U			
			151571_at					1.1 U		1.1 U	
crp	483		143223_at	1.7 D S	1.4 D		1.3 U	1.1 D	1.2 D	1.4 U	
CG3847			153252_at	1.7 D S	1.1 D		1.0 D	1.0 D	1.3 U	1.4 D	
CG3995			155052_at	1.7 D S	1.3 D		1.1 U	1.1 U	1.6 U	1.1 U	
CG2608	-488		153949_at	1.7 D S	1.2 D		1.1 U	1.0 U	1.3 U	1.0 U	
CG9200			154028_at	1.7 D S	1.3 D		1.2 U	1.2 D	1.2 U	1.1 U	
su(Hw)	541		153859_at	1.7 D S	1.0 U		1.1 U	1.1 D	1.8 D	1.1 U	
MRG15			154132_at	1.6 D S	1.2 D		1.3 U	1.3 D	1.1 D	1.1 U	
kis	-299		141644_at	1.6 D S	1.1 D		1.1 U	1.3 D	1.2 D	1.2 U	
			145517_at	1.2 D	1.0 U				1.5 D	2.1 U S	
			145519_at								
Sas10	11		152191_at	1.9 D S	2.3 D S			1.1 U	2.0 U	1.3 D	
CG12050	-14		154526_at	1.6 D S	1.9 D S		1.4 D	1.2 U	1.7 U	1.4 D	
CG6854	79		154401_at	1.8 D S	1.8 D S		1.4 D	1.2 D	1.6 U	1.0 D	
bic	48		153308_at	2.0 D S	1.8 D S		1.0 U	1.2 U	1.0 D	1.2 D	
pont			153627_at	1.3 D S	1.7 D S		1.4 D	1.1 D	1.4 U	1.2 D	
Smr			144015_at	1.2 D	1.7 D S		1.3 D	1.2 D	1.2 D	1.2 U	
CG32133			142630_at								
			148738_at	1.5 D	1.7 D S		1.4 D		1.1 D	1.1 U	
l(3)mbt			141950_at								
			142550_at	1.5 D	1.6 D S		1.1 D	1.4 D	1.0 U	1.4 U	
bel			149514_at	1.0 U	1.6 D S		1.3 D	1.5 D	1.1 U	1.0 U	
CG3711			144357_at	1.0 D	1.5 D S		1.1 D		1.4 D	1.4 U	
CG8319			149571_at	1.4 D	1.5 D S		1.0 U	1.0 D	1.1 U	1.3 D	
Max	429		153406_at	1.4 D	1.1 U		1.2 D	1.3 D	2.7 U S	1.1 U	
CG5033	21		154156_at	1.6 D S	2.2 D S	1.8 D S	1.2 D		1.8 U S	1.3 D	
Protein modification / protein degradation / ubiquitination / protein folding											
Su(dx)	864		142800_at	1.7 D S	1.0 U		1.5 U	1.3 D	1.3 U	1.0 U	
			151689_s_at	1.2 D	1.2 D		1.1 U	1.4 D	1.1 D	1.0 U	
Nmt			153290_at	1.1 U	1.1 D		1.1 U	1.2 D	1.7 U S	1.1 D	
Hsc70-5			153311_at	2.2 D S	1.4 D		1.1 D	1.0 U	1.0 D	1.2 D	
Hsp68			143197_at	1.0 U	1.2 D		1.4 U	8.8 U S	1.9 U S	1.4 U	

Roe1				153163_at	1.0 U	1.6 D S	1.3 D	1.9 D	1.0 D	1.1 D
Ubi-p63E				143399_at	1.1 D	1.1 D	1.0 D	1.1 U	1.6 D S	1.0 D
eff				143638_at	1.5 D S	1.1 U	1.4 U	1.0 D	1.2 U	1.1 D
ago				148159_at	1.0 D	1.8 D S	1.3 D	1.4 D	1.2 D	1.1 U
CG7288	480			142850_at						
				151701_s_at	1.1 D	1.0 U	1.1 U	1.3 D	1.1 U	1.2 U
				151702_r_at					4.3 D S	1.3 U
CG4165	-928			154700_at	1.5 D	2.0 D S	1.1 U	1.6 D	1.0 U	1.3 D
CG32479				142762_at	1.2 U	1.4 D S	1.2 D		1.1 D	1.1 D
				147948_at	1.2 D	1.8 D S	1.3 D	1.6 D	1.4 D	1.1 U
				151677_at	1.6 D S	1.1 D	1.4 U	1.1 U	1.2 U	1.1 D
FK506-bp1	-114	216		154545_at	1.7 D S	1.9 D S	1.7 D S	1.0 D	1.4 U	1.3 D
Tbp-1				152417_at	1.0 D	1.0 D	1.1 D	1.3 D	2.2 D S	1.1 U
CG3033				152024_at	1.6 D S	1.2 U	1.1 U	1.1 D		1.4 U
Trp1				143663_at	1.3 D	1.1 U	1.4 U	1.2 U	2.2 D S	1.3 U
CG9455	627	645		146701_at	1.5 U S	1.1 U	1.1 D	1.4 D		
ApepP				153980_at	1.5 U S	1.1 D	1.0 D	1.1 D	1.4 U	1.1 U
CG10460				147497_at	1.1 D	1.8 U S	1.1 U	1.3 U	1.1 U	1.1 D
Kaz1				144142_at	1.1 D	1.2 U	2.8 U S	1.1 D		
CG13283				146385_at	1.2 D	1.0 U	2.4 U S	1.9 U		
Cys	530			142095_at						
				142969_at	1.1 D	1.3 U	2.3 U S	1.4 U	1.5 U	1.1 D
CG4398				147309_at			1.9 U S	3.3 U S		
Psa				141811_at	1.2 D	1.1 U	1.2 U	1.0 D	2.1 D S	1.1 D
sda				152119_at	1.4 D	1.1 D	1.2 U	2.8 U S	2.0 D S	1.0 U
Fpps	-600			153220_at	1.1 U	1.0 D	1.4 U	1.7 U	1.9 D S	1.0 D
CG2947	499			141203_at	2.2 D S	1.3 D	1.0 D	1.1 D	1.2 U	1.2 D
CG11357				142460_at	1.1 U	1.1 D	1.0 D	1.2 D	1.2 D	1.1 D
				151577_at	2.0 D S	1.0 U	1.4 U	1.0 U	1.2 U	1.2 U
PNGase				146663_at	1.9 D S	1.1 D	1.3 U	1.3 D	1.1 U	1.1 D
CG18177				141205_at	1.7 D S	1.3 D	1.2 U	1.0 D	1.4 U	1.2 D
CG6357				153233_at	1.6 D S	1.2 U	2.0 U S	1.5 U	2.0 U	1.1 U
olf186-F	852			141803_at	1.6 D S	1.0 U	1.5 U	1.0 U	1.0 D	1.0 D
CG10576	773			154529_at	1.6 D S	1.4 D S	1.2 D	1.3 D	1.1 D	1.2 D
CG11261				154496_at	1.5 D S	1.1 D	1.1 U	1.3 U		
Tequila				141527_at	1.1 D	1.2 U	1.6 U S	1.0 U		
				148446_at	1.2 U	1.2 D	1.5 U S	1.6 D		1.3 U
				153070_at	1.5 D S	1.1 U	1.5 U	1.2 D	1.7 D	1.0 D

CG2911	-663			149343_at	1.5 D S	1.0 U		1.2 U	1.1 D			1.1 U
Ogt				153888_at	1.5 D S	1.1 D		1.2 U	1.1 U	1.1 U		1.0 U
CG16840	-414			146218_at	1.7 D S	2.4 D S		1.7 D	1.2 D	1.9 U		1.4 D
CG12202	101			141774_at	1.4 D	1.9 D S		1.6 D	1.5 D	1.5 U		1.3 U
CG10565	441			154210_at	1.6 D S	1.8 D S		1.3 D	1.0 U	1.6 U		1.2 D
CG5358	655			149600_at	1.2 D	1.7 D S		1.5 D		1.1 D		1.1 D
REG				155140_at	1.4 D S	1.6 D S		1.3 D	1.1 D	1.2 U		1.1 D
CG12582				149266_at	1.2 D	1.6 D S		1.1 D				1.1 U
				152253_at	1.0 D	1.0 D		1.2 U	1.1 D	1.1 U		1.1 U
Trap1				155020_at	1.0 D	1.6 D S		1.1 U	1.1 U	1.6 U		1.1 D
CG6554				154448_at	1.7 D S	1.6 D S		1.3 D	1.4 D	1.2 U		1.1 D
CG11989				153956_at	1.2 D	1.5 D S	1.6 D S	1.2 D		1.4 U		1.1 D
und				151903_at	1.4 D S	1.7 D S	1.5 D S	1.0 U		1.4 U		1.1 D
CG6563	55			154690_at	2.4 D S	2.5 D S		1.8 D	1.2 D	2.9 U S		1.8 D S
CG4826				152851_at	1.1 D	1.1 U		1.6 U	1.1 D	2.8 U S		
GlcAT-S				152665_at	1.9 D S	1.1 D		1.2 U	1.1 D	2.3 U S		1.1 U
CG7182				153998_at	1.9 D S	1.6 D S		1.4 D	1.0 U	1.9 U S		1.1 D
Channels / transport												
Fbp1				143158_at						1.0 U		3.4 D S
Csat				144045_at	1.7 U S	1.0 D		1.3 U	1.4 D	1.4 D		1.2 U
CG5594				147816_at	1.1 D	1.5 D S		1.1 D				
				152231_at	1.5 D	1.1 D		1.5 U	1.1 D			
Mpcp				144140_at	1.6 D S	1.3 D		1.0 D	1.2 D	1.1 U		1.4 D
CG3071	11	942		155028_at	1.9 D S	1.8 D S		1.6 D	1.1 D	2.4 U S		1.2 D
CG11147				145844_at	1.5 U S							
CG13688				145539_at	1.5 U S	1.1 U		1.1 D	1.1 U			1.3 U
CG4330				153453_at		1.1 D		1.7 U S	1.3 U			1.3 U
CG8468				143046_at	1.1 U	1.3 D		1.1 D	1.2 D	1.5 D		1.2 U
				151760_at	1.3 D	1.1 D		1.0 U	1.0 U	2.0 D S		1.1 U
mnd				143268_at	2.2 D S	1.4 D S		1.1 U	1.3 D	1.6 U		1.4 D
CG6070	-252			152204_at	2.0 D S	1.2 D		1.1 U	1.1 D			1.1 U
CG16753				155163_at	1.9 D S	1.4 D		1.4 D	1.4 U	1.1 U		1.1 U
CG10960				153366_at	1.9 D S	1.1 U		1.2 U	1.5 U	1.5 U		1.0 U
CG8029	-807			153649_at	1.9 D S	1.2 D		1.0 U	1.1 D	1.0 D		1.1 D
hoe1				145791_at	1.8 D S	1.1 D		1.1 U	2.0 U			
				145792_at								
				151864_at	1.0 U	1.1 U						
CG2162				154920_at	1.8 D S	1.0 D		1.0 U	1.1 U	1.3 U		1.1 U

CG13384				141633_at	1.8 D S	1.2 D		1.4 U		1.2 D		1.3 U		1.3 U
Ent2	87			152416_at	1.7 D S	1.3 D S		1.2 D		1.3 D		1.1 D		1.0 D
CG5789	93			154494_at	1.7 D S	1.2 D		1.2 U		1.2 D		1.8 U		1.3 D
CG11092	876			153989_at	1.7 D S	1.2 D		1.3 U		1.3 U		1.2 D		1.0 D
sesB				141933_at	1.1 U	1.0 U		1.1 U		1.1 D		1.2 U		1.2 D
				142494_at	1.7 D S	1.2 D		1.0 U		1.0 D		1.0 D		1.1 D
CG7255	-808			141761_at	1.6 D S	1.0 D		1.2 U		1.0 D				
CG6454	-762			154732_at	1.6 D S	1.3 D		1.1 U		1.3 D		1.0 U		1.1 U
Nup358				155002_at	1.6 D S	1.2 D		1.2 U		1.1 U		1.0 D		1.0 D
CG3164				145511_at	1.6 D S	1.1 U		1.2 U		1.2 D		1.1 D		1.0 D
CG9330				149061_at	1.6 D S	1.3 D		1.1 U		1.1 D		1.2 U		1.2 U
Fatp				141619_at	1.5 D S	1.0 U		1.4 U		1.0 D		1.3 D		1.4 U
CG12295	-627			141545_at	1.3 D	2.3 D S		1.9 D		1.6 D				
CG6565				153542_at	1.5 D S	2.0 D S		1.2 U		1.2 D		1.2 U		1.1 D
CG7686				154018_at	1.4 D S	1.7 D S		1.4 D		1.1 D		1.4 U		1.4 D
CG6756				146265_at	2.0 D S	1.5 D S		1.3 D		1.0 U		1.4 U		1.1 D
CG9281	28	799		153481_at	1.3 D S	1.5 D S		1.5 D		1.0 U		1.2 U		1.3 D
CG30394	602			147617_at	1.3 D	1.0 D		1.2 U		1.1 D		1.1 U		1.2 U
				147618_at	1.2 U	1.5 D S		1.2 D		1.3 D		1.5 D		1.1 U
Tom40				144654_at	1.2 D	1.7 D S		1.7 D S		1.7 D		1.8 U		1.0 D
mge				141387_at	1.4 D S	1.4 D S		1.6 D S		1.4 D		1.5 U		1.0 D
bys	-47	23		153812_at	1.5 D S					1.0 D		2.2 U S		1.3 D
CG6574	-387			149652_at	1.3 D	1.6 D		1.0 U		1.1 U		2.1 U S		1.1 U
CG13610	123			141731_at	1.0 D	1.2 U		1.1 D		1.2 D		2.0 U S		1.2 D
CG6712	46			154160_at	2.6 D S	3.7 D S		2.8 D S		1.4 D		2.0 U S		2.0 D S
CG17723	181			154124_at	1.2 U	1.0 U		1.2 D		1.3 D		1.9 U S		1.1 U
CG2691	36			154451_at	2.1 D S	2.4 D S		1.7 D		1.0 U		1.8 U S		1.2 D
CG7627				142113_at										
				143031_at	1.1 D	1.2 D		1.1 D		1.3 D		1.8 U S		1.1 D
Metabolism / catabolism														
Pgi				152515_at	1.0 U	1.1 U		1.0 D		1.2 D		1.7 D S		1.0 U
Pepck				143299_at	1.0 D	1.1 U		1.9 U		1.1 U		4.0 D S		3.0 U S
Prat	387			154976_at	1.7 D S	1.5 D		1.2 D		1.2 D		1.5 U		1.0 U
ade2	-460	32		153122_at	1.3 D	1.5 D S		1.2 D		1.0 U		1.7 U		1.1 D
Jafrac1				153359_at	1.3 U S	1.1 U		1.0 U		1.0 U		2.0 D S		1.1 D
r-l	58	370		155103_at						1.1 D		3.4 U S		1.2 D
CG8005				148379_at	1.8 D S	2.1 D S		1.4 D		1.5 D				
dnk	143	677		143954_at	1.1 D	1.0 U		1.0 U		1.2 D		2.0 D S		1.1 U

Dph5	25			153752_at	1.4 D S	1.9 D S	1.4 D	1.0 U	1.6 U	1.3 D
ras				154756_at	2.2 D S	3.1 D S	1.4 D	1.2 D	1.9 U S	1.4 D
ifc				153842_at	1.5 D S	1.0 U	1.2 U	1.5 D	1.0 D	1.1 U
Inos				153296_at	1.5 U S	1.7 U S	1.0 D	1.1 D	1.2 U	1.1 D
CG32549				145298_at						1.1 D
				151352_at	1.0 U		1.3 U			
				152283_at	1.0 U	1.6 U S	1.1 U	1.6 D	1.0 D	1.0 D
Ect3				153367_at	1.1 U	1.2 U	1.7 U S	1.4 U		1.2 U
l(1)G0237				144884_at	1.2 D	1.1 U	1.1 U	1.4 D	6.9 D S	1.1 U
Tpi				152334_at					2.2 D S	1.2 D
CG3523				152126_at	1.4 D	1.0 U	1.2 U	1.1 D	1.0 D	1.5 U S
CG8839				153538_at	1.3 U S	1.1 U	1.1 U	1.3 D	1.2 U	1.5 U S
CG7351				151973_at	2.0 D S	1.1 D	1.1 U	1.2 D	1.1 U	1.1 U
Nc73EF				141810_at	1.9 D S	1.1 D	1.1 U	1.1 D	1.1 D	1.1 D
CG3045	97			152572_at	1.9 D S	1.5 D	1.2 D	1.3 D	1.3 U	1.1 U
CG11055				154767_at	1.6 D S	1.1 D	1.3 U	1.4 D	1.7 D	1.1 U
CG5191				152563_at	1.6 D S	1.0 U	1.3 U	1.3 U	1.4 U	1.1 U
CG8128				151908_at	1.6 D S	1.2 D	1.1 D	1.0 U	1.4 U	1.0 D
CG1236	-527	773		141292_at	1.6 D S	1.0 D	1.0 D	1.0 U		1.1 D
CG1753				154013_at	1.4 D	2.0 D S	1.3 D	1.1 U	1.8 U	1.3 D
CG13667				154330_at	1.6 D	1.8 D S	1.1 D	1.1 U	1.9 U	1.2 U
CG11844	906			141666_at	1.2 D	1.7 D S	1.6 D	1.2 D	1.1 U	1.2 D
CG11739				149275_at					3.8 U S	1.1 U
CG16733				149540_at					3.2 U S	1.1 U
CG6767	-336	240		148484_at	1.3 D	1.6 D S	1.1 D	1.5 D	2.5 U S	1.1 U
CG3590	-941			150041_at	1.1 D	1.0 D	1.2 D	1.3 D	2.5 U S	1.0 U
CG3902				149018_at						
				152151_at	1.2 U	1.0 U	1.0 D	1.1 U	2.4 U S	1.1 U
CG6287				151909_at					2.2 U S	1.0 D
l(2)k01209				153506_at	1.7 D	1.2 D	1.4 D	1.2 U	2.2 U S	1.7 D
CG9436				142716_at	1.2 U	1.2 U	1.1 U	1.2 D	2.1 U S	1.0 D
CG1671				141261_at	1.5 D	1.5 D	1.2 D	1.2 D	2.0 U S	1.3 D
CG11089	219			153761_at			1.5 D	1.2 D	1.9 U S	1.3 D
Lsd-2				145098_at					1.9 U S	1.0 D
CG4686				150222_at	1.1 D	1.1 U	1.1 U	1.3 D	1.8 U S	1.2 U
Cytoskeleton / cell migration / cell adhesion										
l(2)gl				153565_at	2.0 D S	1.1 D	1.2 U	1.0 U	1.8 D	1.1 U
pyd				149529_at	1.1 U	1.3 D	1.2 D	1.8 D	1.8 D	1.2 U

nop5	-509	-9		154624_at	1.7 D S	2.7 D S	2.6 D S	1.1 U		2.5 U S	1.6 D S	
Nnp-1	29			146333_at	1.7 D S	2.4 D S	2.5 D S	1.0 D		1.9 U S	1.3 D	
CG11837				154750_at	2.0 D S	2.2 D S	1.7 D	1.0 D		3.1 U S	1.3 D	
Surf6	31			143036_at	1.8 D S	1.9 D S	1.5 D	1.3 U			1.2 D	
Rs1	10			153844_at	2.1 D S	2.8 D S	1.6 D	1.0 U		2.2 U S	1.5 D	
l(1)1Bi	21			153663_at	3.0 D S		2.3 D	1.0 U		1.8 U	1.2 D	
CG5220	254			154071_at	1.8 D S	1.3 D	1.1 D	1.0 U		1.7 U	1.1 D	
Tif-IA	759			146622_at	2.1 D S	2.0 D S	1.1 D			1.3 U	1.2 D	
				146623_at	1.6 D	2.2 D S	1.4 D	1.0 U		1.2 U	1.0 U	
				153698_at	2.2 D S	1.9 D S	1.1 D	1.3 U		1.4 U	1.0 D	
CG12909	12	123		146936_at	2.2 D S	2.1 D S	1.6 D	1.2 U		2.2 U	1.3 D	
CG7911	-643	-307	15	150866_at	1.4 D S	1.6 D S	1.4 D	1.0 D		1.5 U	1.2 D	
Nop56	29			153330_at	1.6 D S	2.5 D S	2.5 D S	1.1 U		3.2 U S	1.4 D S	
CG5728	31	789		154959_at	1.9 D S	2.4 D S	1.7 D S	1.1 U		2.6 U S	1.4 D	
NHP2	41			141956_at								
				142579_at	2.0 D S	2.5 D S	2.3 D S	1.0 D		2.5 U S	1.5 D	
CG10685				146481_at	1.4 D S	1.8 D S	1.4 D	1.1 D		2.4 U S	1.3 D	
La	351			143668_at	1.9 D S	1.5 D S	1.4 D	1.1 D		2.1 U S	1.2 D	
Translation / protein synthesis												
CG6388	-1			154663_at	1.5 D S	1.7 D S	1.4 D	1.0 D		1.8 U	1.2 D	
Rpp30				152046_at	1.7 D S	1.6 D S	1.3 D	1.0 D		1.6 U	1.1 D	
Nmd3	16			153358_at	1.6 D S	1.8 D S	1.5 D	1.2 D		1.8 U	1.3 D	
pelo	-977			154677_at	2.1 D S	1.3 D	1.1 U	1.2 D		1.1 U	1.0 U	
RpS14a	223			143460_at	1.6 D S	1.2 U	1.0 D	1.6 U		1.1 U	1.1 D	
mRpL1				154580_at	1.5 D S	1.2 D	1.0 D	1.0 D		1.8 U	1.1 D	
CG8495				149586_at	1.8 D S	1.9 D S	1.6 D	1.2 U		1.0 D	1.0 U	
CG4866				147369_at	1.5 D	1.9 D S	1.5 D	1.0 U		2.3 U S	1.3 D	
eIF-4E				141629_at	1.3 D S	1.1 D	1.1 D	1.0 U		1.7 U S	1.0 D	
eIF-4G				153267_at	1.9 D S	1.4 D S	1.1 D	1.0 U		1.0 U	1.1 D	
CG8443				142634_at	1.5 D	1.9 D S	1.3 D			1.0 U	1.1 D	
				151655_at		1.0 D				1.6 U	1.0 U	
clF2				148110_i_at	1.4 U S	1.3 D S	1.2 D	1.3 D		1.1 D	1.0 U	
				148111_r_at	1.1 U	1.3 D S	1.1 D	1.5 D		1.1 U	1.0 U	
				148112_at	1.1 D	1.7 D S	1.3 D				1.0 D	
AGO2				151275_r_at								
				151276_f_at	1.0 D	1.5 D S	1.3 D	1.6 D		1.3 D	1.0 U	
				153226_at	1.1 D	1.0 D	1.1 D	1.4 D		2.6 D S	1.1 D	
CG10192				141569_at	1.7 D S	1.0 D	1.1 U	1.0 U		1.2 D	1.3 U	

EfTuM	595			142510_at	1.3 D	1.8 D S	1.7 D	1.1 D	1.5 U	1.3 D
Ef1&ggr				150815_at	1.0 U	1.5 D S	2.3 D S	1.0 U	1.3 U	1.1 D
eEF1&dgr	-276	202		153449_at	1.5 D S	1.6 D S	1.2 D	1.1 U	1.8 U S	1.1 D
Aats-arg	592			145157_at	1.7 D S	1.5 D	1.0 D	1.3 D	1.1 U	1.0 D
Aats-tyr	-804			142649_at	1.2 U	1.4 D S	1.8 D S	1.3 D	1.3 U	1.3 D
Aats-ile				154387_at	1.9 D S	1.7 D S	1.4 D	1.0 D	1.1 U	1.1 D
Aats-cys				142650_s_at	1.8 D S	1.1 D	1.1 D	1.1 U		1.1 D
CG6479				153108_at	1.5 D S	1.1 D	1.1 D	1.3 D	1.3 D	1.1 D
CG4045				153114_at	1.3 D	1.9 D S	1.3 D	1.5 D	1.1 U	1.3 D
CG4159	-204			150267_at	1.7 D S	1.7 D S	1.6 D	1.1 D	2.0 U	1.5 D
Nac&agr	-674			152402_at	1.1 D	1.2 D S	1.8 D S	1.1 D	1.0 U	1.4 D S
CG13096	-656	27		142984_at	1.3 D	1.4 D S	1.9 D S	1.2 U	2.0 U S	1.4 D
mRNA processing										
heph				150961_at						
				153488_at	1.2 D	1.4 D	1.2 D	1.3 D	2.0 D S	1.2 U
CG4266				154472_at	1.9 D S	1.1 U	1.1 U	1.1 D	1.0 U	1.1 D
hoip	-15			146098_at	1.6 D S	3.4 D S	2.0 D S	1.0 D	3.7 U S	1.7 D S
CG5931				153263_at	1.9 D S	1.1 D	1.1 D	1.1 U	1.1 D	1.1 U
Dek				153681_at	1.7 D S	1.0 U	1.1 U	1.0 U	1.3 D	1.0 D
CG6610				148261_at	1.7 D S	1.0 U	1.1 U	1.2 D	1.9 U	1.1 U
SF2				154911_at	1.5 D S	1.2 D	1.0 D	1.5 D	1.1 D	1.0 U
CG13900	155	369		147940_at	2.1 D S	2.5 D S	1.5 D	1.4 D	1.0 D	1.1 D
CG4901				146130_at	1.7 D S	1.9 D S	1.2 D	1.1 D	1.9 U S	1.1 U
cpsf				154835_at	2.0 D S	1.2 D	1.1 U	1.3 D	1.0 D	1.2 D
Pabp2				143566_i_at	1.7 D S	1.1 D	1.2 U	1.2 U	1.2 D	1.1 U
				143567_r_at						
CG1972				153639_at	1.6 D S	1.0 U	1.3 U	1.1 U		1.1 D
Rtc1	35			141535_at	1.8 D S	2.1 D S	1.5 D	1.1 D	1.4 U	1.2 D
CG30122				147452_at	1.5 D	2.1 D S	1.2 D		1.5 D	1.2 U
				154274_at	1.1 D	1.0 D	1.0 D	1.2 D	1.1 D	1.0 D
CG8414				147278_at	1.8 D S	1.9 D S	1.3 D	1.1 U	1.5 U	1.4 D
Rrp4				153140_at	1.2 D	1.8 D S	1.6 D	1.2 D	1.3 U	1.2 D
Ski6	41			146317_at	1.7 D S	1.8 D S	1.4 D	1.1 D	1.4 U	1.2 D
Rrp42				147273_at	1.3 D	1.8 D S	1.1 U	1.0 D	1.9 U	1.1 U
Rrp46				153132_at	2.2 D S	2.1 D S	2.2 D S	1.3 D	1.6 U	1.1 D
lp259				153317_at	1.1 D	1.3 D S	1.5 D S	1.2 U	1.0 D	1.2 D
Dis3	-902	-144		141818_at	1.5 D S	2.6 D S		1.2 U	2.5 U S	1.2 D
CG10214				153933_at	2.3 D S	2.0 D S	1.1 U	1.2 D	2.5 U S	1.0 U

Csl4	246			146231_at	2.0 D S	1.9 D S	1.4 D		1.1 D		2.0 U S	1.0 U
RNA binding												
CG3335	-28			148477_at					1.1 D		3.0 U S	1.3 D
CG5589	25			142865_at	2.7 D S	2.5 D S	2.1 D		1.1 D		3.0 U S	1.5 D
Dbp73D	-712	27		141976_at								
				142656_at	2.8 D S	1.8 D S	1.7 D		1.2 D		2.5 U S	1.1 D
CG9630				152670_at	2.2 D S	3.4 D S	1.5 D		1.2 U		2.4 U S	1.6 D
CG11920	23			153152_at	3.5 D S	2.0 D S	1.2 D		1.1 D		2.4 U S	1.3 D
CG9809	32	587		149278_at	1.7 D S	2.2 D S					2.1 U S	1.1 D
CG3808	29	633		141727_at							2.1 U S	1.5 D
CG9253	16			146573_at	1.8 D S	2.6 D S	1.8 D		1.0 D		2.1 U S	1.0 U
CG11738	12			154039_at	1.4 D	2.1 D S	1.6 D S		1.1 U		2.0 U S	1.4 D
CG6937	11			150379_at	1.4 D S	1.5 D S	1.5 D		1.3 U		1.8 U S	1.3 D
mod	-457	574		154081_at	1.8 D S	1.8 D S	1.4 D		1.2 U		1.8 U S	1.5 D S
Rnp4F				154594_at	1.0 U	1.1 D	1.1 D		1.2 D		1.1 U	1.7 U S
l(2)35Df				152101_at	2.6 D S	2.5 D S	1.5 D		1.3 D		1.8 U	1.5 D
CG5800				145251_at	2.1 D S	2.2 D S	1.4 D		1.1 D		1.6 U	1.3 D
CG14230	225	345		154638_at	1.6 D S	2.0 D S	1.3 D		1.3 U		2.1 U	1.1 D
vig	-498			153593_at	1.7 D S	1.9 D S	1.3 D		1.0 D		1.3 D	1.2 D
pit				155149_at	1.7 D S	2.4 D S	2.2 D S		1.1 U		1.8 U	1.4 D
Mitochondrial function												
Cpr				141208_at	1.5 D S	1.2 D	1.1 U		1.2 D		1.0 D	1.2 U
Cyt-c-p	566			143115_at	1.1 U	1.1 D	1.1 D		1.1 D		1.9 U S	1.2 D
Marf	-920	428		153256_at	1.7 D S	1.4 D S	1.0 D		1.1 D		1.4 D	1.1 D
slgA	-160			142569_at							1.6 U	1.1 D
				151627_s_at							2.2 U S	1.0 U
Cyp6a8				141840_at								
				142189_at	1.8 U S		1.1 D		2.2 D			
CG8430				154150_at	1.1 D	1.1 U	1.1 U		1.1 D		2.6 D S	1.1 D
l(2)tid				141787_at	1.7 D S	1.3 D	1.0 D		1.1 U		1.6 U	1.1 D
CG18324				141476_at	1.7 D S	1.0 U	1.2 U		1.1 U			1.1 D
CG7943	-368			141740_at	1.6 D S	1.4 D	1.0 D		1.2 D		1.1 D	1.1 D
CG2118				153355_at	1.4 D	1.8 D S	1.1 D		1.0 D		1.2 U	1.1 D
CG5037				154662_at	1.8 D S	1.6 D S	1.3 D		1.1 U		1.2 U	1.2 D
CG6459	278			154495_at	1.2 D	1.4 D S	1.8 D S		1.3 D		1.3 U	1.2 D
Mgstl				144097_at	1.0 U	1.0 U	1.1 U		1.5 D		3.5 U S	1.0 D
CG5946				152426_at	1.3 D	1.1 U	1.0 D		1.3 D		2.8 U S	1.0 U
Nmdmc				151767_at	1.2 D	1.8 D S	1.6 D		1.1 U		2.4 U S	1.2 D

				151656_at	1.7 D S	1.3 U		1.8 U		1.3 U		1.1 D		1.1 U	
Nmda1				141915_at	1.3 D		1.1 D	1.2 U		1.0 D				1.5 U	
				142415_at	1.8 D S	1.0 U		1.2 U		1.0 D		3.4 D S		1.1 D	
Immunity / stress response															
Dox-A3				141775_at	1.5 U S	1.1 U		1.0 D		1.2 D					
PGRP-SD	134			148352_at	1.0 D		1.0 U	1.9 U S		1.7 U					
PGRP-SA				144882_at	1.2 U S	1.3 U S		1.7 U S		1.3 U					
TI				151935_at	1.6 D S	1.0 U		1.3 U		1.3 U		1.0 D		1.1 U	
CG10535	-1			153291_at	1.5 D S	1.5 D S		1.3 D		1.1 D		1.4 U		1.0 D	
Drs				143605_at	1.0 D		1.1 U	2.8 U S		1.2 U					
PHGPx				141815_at	1.6 U S	1.3 U S		1.1 U		1.3 D		1.1 D		1.0 D	
Spn27A	-712			154259_at	1.0 U		1.3 U	1.9 U S		1.2 U		1.0 U		1.1 D	
CG10341	17			152902_at	1.5 D S	2.3 D S		1.7 D S		1.2 D		2.9 U S		1.2 D	
Extracellular matrix															
LanB1				151856_at	1.2 D		1.1 U	1.8 U S		1.1 U		1.0 U		1.1 U	
Sgs8				143350_at								23.5 U S		1.1 D	
CG32354				151303_at											
				152249_at	1.2 D		1.5 U S	2.6 U							
dp				145764_at										1.9 U S	
Lcp4				143235_at								1.1 D		2.6 D S	
Lcp1				143232_at								1.3 D		1.9 D S	
Lcp2				143233_at								1.2 D		1.7 D S	
CG8502	185			141397_at								1.7 U S		1.1 U	
Apoptosis															
Ice				152941_at	1.1 D		1.2 U	1.0 U		1.4 D		1.9 D S		1.0 D	
CG7263				154947_at	1.5 D		1.6 D S	1.0 D		1.0 D		1.1 U		1.4 D	
p53	979			150416_at	1.1 U		1.1 U	1.2 U		1.1 U		2.1 U S		1.1 U	
unk				143458_at	1.3 D		1.3 D	1.1 D				2.2 D S		1.3 U	
CG14722	298			154037_at	1.9 D S		1.5 D S	1.1 D		1.1 D		1.8 U		1.3 D	
MESR4				147376_at	1.2 D		1.5 D S	1.3 D		1.5 D		1.0 U		1.3 U	
CG32130				148716_at											
				151834_at								1.9 U S		1.6 U	
Chromatin structure / general PolII transcription															
Taf4				142999_at	1.6 D S	1.2 D		1.1 U		1.4 D		1.2 D		1.2 U	
				151747_s_at	1.2 D		1.3 D	1.0 U		1.6 D		1.5 D		1.4 U	
RplI215				155027_at	1.8 D S	1.2 D		1.1 U		1.4 D		1.3 D		1.2 U	
Rpb5	536			146974_at	1.5 D S	1.7 D S		1.4 D		1.1 D		1.5 U		1.2 D	

spt4				142904_at	1.7 D S	1.1 U		1.1 U		1.1 D		1.1 U		1.1 D	
				151714_at											
Spt5				152632_at	1.0 D	1.1 U		1.1 U		1.1 D		1.7 D S		1.0 U	
E(bx)				147914_at	1.4 D	1.4 D		1.3 U				1.6 D		1.1 U	
				147915_at	1.1 U	1.3 D		1.0 U				2.2 D S		1.1 U	
				147916_at		2.6 D S						2.3 D		1.2 U	
CG6751	-641	29		154076_at	1.7 D S	2.2 D S		2.0 D S		1.0 D		2.1 U		1.3 D	
Various															
wus				154066_at				1.2 U						1.8 D S	1.0 U
l(2)37Cc				152440_at	1.2 D	1.6 D S		1.3 D		1.3 D		1.1 U		1.1 D	
l(2)09851	35	830		146653_at	1.7 D S	2.3 D S		1.7 D S		1.3 D		2.5 U S		1.3 D	
bgn				141854_at											
				142234_at	1.8 D S	2.3 D S				1.3 D		1.8 U		1.3 D	
				147811_at											
lig				155119_at	1.5 D S	1.0 D		1.0 U		1.2 D		1.0 U		1.0 D	
dah				153153_at	1.1 D	1.2 U		1.2 U		1.1 D		2.3 D S		1.1 D	
CG1994	-17			144714_at	2.3 D S			4.1 D S		1.1 D		4.0 U S		1.9 D S	
CG3091				142199_at	1.0 D	1.4 U		3.1 U S		2.5 U S					
CG32982				146070_at	1.1 U	1.0 U		1.0 U		1.2 D		2.3 D S		1.3 U	
				146071_at	1.1 U	1.3 D								1.1 U	
				152498_at	1.3 U	1.2 U		1.3 U		1.3 U				1.1 U	
Incnp				141608_at	1.1 U	1.1 U		1.1 U		1.3 D		2.2 D S		1.1 U	
sip2				145935_at	1.2 U	1.1 U		1.1 U		1.5 D		1.8 D S		1.2 U	
CG17836	-944			141483_at	1.2 U	1.2 U		1.2 U		1.1 U		1.6 D S		1.0 U	
bnb				152418_at								1.6 U		2.9 U S	
CG32767				144505_at	1.1 D	1.4 D		1.1 D				1.3 D		1.6 U S	
				144506_at											
CG31637				145906_at				1.1 D							
				154703_at	2.0 D S	1.1 U		1.6 U		1.3 U		1.5 U		1.1 D	
CG11811				152077_at	1.8 D S	1.1 D		1.1 U		1.1 D		1.0 D		1.0 D	
CG8668				154502_at	1.8 D S	1.2 D		1.2 U		1.2 D		1.2 U		1.3 U	
slim	-904			152991_at	1.7 D S	1.1 D		1.1 D		1.2 D		1.1 D		1.2 U	
Nup153				141207_at	1.6 D S	1.5 D		1.1 D		1.5 D		1.0 U		1.0 D	
CG11255				152613_at	1.6 D S	1.5 D S		1.4 D		1.3 D		1.5 U		1.0 D	
CG31224				153102_at	1.6 D S	1.1 D		1.1 U		1.2 D		1.2 D		1.1 U	
				153568_at											
yps				154807_at	1.5 D S	1.2 D		1.1 D		1.2 D		1.1 U		1.1 D	
Ngp	41			141785_at	1.8 D S	2.6 D S		1.2 D		1.1 U		1.8 U		1.3 D	

Nufip				153331_at	1.9 D S	2.5 D S	1.7 D				1.7 U			
CG13397				141346_at	1.3 D	2.4 D S	1.5 D		1.4 U					
CG10903				149471_at	1.0 D	1.8 D S	1.8 D		1.1 D		2.0 U		1.2 D	
larp				153228_at	1.6 D S	1.7 D S	1.0 D		1.2 D		1.0 U		1.0 U	
Tsp3A				144411_at	1.3 D	1.7 D S	1.2 U						1.0 U	
CG32626				151340_at	1.3 U	1.6 D S	1.0 D							
				151341_at										
				152306_at	1.5 U S	1.3 U S	1.0 D		1.1 D		1.3 D		1.2 U	
CG1662	163			152076_at	1.1 D	1.5 D S	1.5 D		1.3 D		1.4 U			
metI	385			154782_at	1.7 D S	1.5 D S	1.1 D		1.1 U		1.2 U		1.1 D	
nudC				148915_at	1.5 D S	1.5 D S	1.2 D		1.0 U		1.4 U		1.1 D	
CG4038	36			143696_at	1.8 D S	2.6 D S	2.3 D S		1.4 D		1.8 U		1.4 D	
spas	-921			154205_at	1.1 D	1.0 D	1.1 D				4.2 U S		1.2 U	
MgstI-&PSgr				146619_i_at	1.1 D	1.0 U	1.2 U		1.6 D		3.2 U S		1.2 U	
				146620_s_at	1.2 U	1.1 U	1.0 U		1.3 D		2.7 U S		1.0 D	
Acyp2	970			149974_at	1.3 D	1.1 U	1.2 U		1.2 D		2.9 U S		1.1 U	
Gip				143691_at	1.1 D	1.3 D	1.1 D		1.1 D		2.8 U S		1.1 U	
ppan	16			143634_at	2.3 D S	3.6 D S	1.3 D		1.2 U		2.8 U S		1.3 D	
lama				153774_at	1.0 D	1.1 U	1.1 U		1.3 D		2.6 U S		1.2 D	
CG1965	-57			151951_at	1.5 D	1.0 U	1.1 D		1.3 D		2.5 U S		1.1 U	
CG6697				154017_at	1.1 U	1.3 U	1.0 U		1.1 D		2.3 U S		1.1 U	
Mpp6				146574_at		1.4 D	1.4 D		1.2 D		2.3 U S		1.4 U	
pen	16			154002_at	1.9 D S	2.7 D S	1.5 D		1.0 D		1.9 U S		1.3 D	
Dgp-1				144194_at	1.2 D	1.3 D	1.2 U		2.3 D		1.8 U S		1.3 D	
Nrt				142670_at									1.4 U	
				151661_s_at	1.0 D	1.1 U	1.2 D		1.9 U		1.8 U S		1.1 U	
Uhg1	-14	336	498	151217_at							1.7 U S			
melt				143969_at							2.2 D S		1.4 U	
Cyp9f3&PSgr				149768_s_at	1.4 U S	1.1 D	1.5 U S		1.0 D		1.0 U		1.2 U	
msb1I				154597_at	1.1 D	1.1 U	1.1 D		1.0 D		2.1 D S		1.1 U	
nord	-735			147847_at										
				147849_at							1.7 D		1.9 U S	
Mys45A	5			146866_at	2.2 D S				1.1 U		1.9 U		1.4 D	
Mkrn1				149186_at	2.0 D S	1.1 D	1.1 D		1.3 D		1.4 D		1.1 U	
Mlf				155053_at	1.9 D S	1.4 D	1.1 U		1.2 D		1.3 D		1.1 D	
MESK2				147624_at										
				151859_at	1.8 D S	1.2 D	1.1 U		1.2 U		1.3 U		1.2 D	
Jhl-1	-480	-369		146935_at	1.6 D S	1.3 D	1.4 D		1.1 D		1.2 U		1.4 D	

CG2818	-982			154114_at	1.1 D		1.1 D		1.2 D		1.6 D		2.1 D S	1.1 U	
CG8561				147192_at									2.1 D S	1.1 U	
CG10191				153557_at	1.2 D		1.1 U		1.1 U		1.5 D		2.1 D S	1.2 U	
CG10722				153787_at	1.2 D		1.1 D						2.1 D S	1.2 U	
SP1173	-332			152553_at									2.0 D S	1.1 U	
CG10176				146436_at									1.7 D S	1.3 U	
CG3624				152370_at	1.3 U		1.1 U		1.4 U		3.9 U S		1.7 D S	1.0 D	
CG12159				146775_at	1.1 D		1.2 U		1.5 U		1.2 U		1.1 U	2.0 U S	
CG8483				154850_at									1.2 D	1.6 U S	
CG6896				142928_at			1.3 D								
				151721_at	2.7 D S		1.1 D		2.0 U		1.2 U			1.1 D	
CG6550				153079_at	2.4 D S						1.2 D		2.2 U	1.2 D	
CG15141				154299_at	2.1 D S		1.1 D							1.1 D	
CG10080				141651_at	2.1 D S		1.6 D		1.1 D		1.2 U		1.8 U	1.2 D	
CG6421				144100_at											
				155133_at	2.1 D S		1.8 D		1.5 D		1.4 D			1.1 D	
CG5098				142629_at	1.3 D		1.5 D		1.1 D				1.1 D	1.4 U	
				151652_at	2.0 D S		1.5 D		1.2 U		1.4 D		1.2 D	1.2 U	
CG18604				142636_at			1.2 D							1.1 U	
				151657_at	2.0 D S		1.1 D		1.6 U		1.1 D		1.1 D	1.2 U	
CG3226				153789_at	1.9 D S		1.0 U		1.2 U		1.3 U		1.2 U	1.1 U	
CG17912				142747_at											
				151671_at	1.9 D S		1.1 U							1.1 U	
CG10495	-30			153552_at	1.9 D S		1.3 D		1.1 D		1.0 U		1.4 U	1.0 U	
CG9386	177			149564_at	1.9 D S		1.3 D		1.1 U		1.2 U		1.6 U	1.0 D	
CG9047				142263_at	1.2 U		1.1 U		1.5 U		1.2 D		1.1 D	1.1 U	
				151506_at	1.9 D S		1.0 D		1.4 U		1.1 U		1.6 D	1.1 U	
CG32428				151117_at	1.3 D		1.1 D		1.5 D				1.1 D	1.2 U	
				155007_at	1.9 D S		1.4 D S		1.3 D		1.4 D		1.0 D	1.1 U	
CG13694				142106_at	1.8 D S		1.2 D		1.3 U		1.4 U				
				143010_at											
CG1575	-830	518		155108_at	1.8 D S						1.2 U				
CG11417	9	674		154171_at	1.8 D S				1.5 D						
CG4278				154440_at	1.8 D S		1.3 D		1.1 U		1.1 D		1.7 U	1.2 D	
CG4281	69			152343_at	1.8 D S		1.2 D		1.1 U		1.4 D		1.1 D	1.3 U	
CG18316				152995_at	1.8 D S		1.0 D		1.3 U		1.3 U		3.2 D S	1.6 U S	
CG7800				152374_at	1.8 D S		1.1 D		1.2 U		1.3 D		1.2 U	1.3 D	
CG7987	-243			142970_at	1.8 D S		1.5 D		1.2 U		1.2 D		1.8 U	1.1 U	

CG5319				142530_at	1.0 D		1.1 D		1.1 U		1.2 D		1.0 U		1.0 U
				151609_at	1.8 D S		1.2 U		1.3 U		1.4 D		1.4 D		1.2 U
CG14210	1			145381_at	1.8 D S										
CG7670				153349_at	1.7 D S		1.0 U		1.0 U		1.1 D		1.8 D		1.1 U
CG1675				146907_at	1.7 D S		1.1 D		1.1 U		1.1 D		1.6 U		1.3 D
CG11033	-827			142996_at									1.0 D		1.2 D
				151745_at	1.7 D S		1.0 U		1.1 U		1.4 D		1.4 D		1.1 U
CG4957				141923_at											
				142449_at	1.7 D S		1.5 D		1.2 U		1.0 D		1.8 U		1.6 U
CG11279				148695_at	1.7 D S		1.4 D		1.3 D		1.0 U		2.0 U		1.3 D
CG7668				153234_at	1.7 D S		1.0 U		1.2 U		1.1 D		1.1 D		1.1 U
CG7506				151858_at	1.7 D S		1.2 D		1.4 D		1.1 U		1.1 U		1.1 D
CG11444	-352			153333_at	1.7 D S		1.3 D		1.2 D		1.1 D		1.6 U		1.2 D
CG3420				142004_at											
				142715_at	1.7 D S		1.2 D		1.0 D		1.2 D				1.0 U
CG7516	25	936		154953_at	1.7 D S		1.6 D						1.7 U		1.3 D
CG14648				142781_at	1.2 D		1.1 U		1.2 D		1.3 D		1.0 D		1.1 D
				151683_at	1.6 D S		1.1 D		1.1 D		1.0 D		1.1 D		1.0 U
CG6194	664			153901_at	1.6 D S		1.0 U		1.0 D		1.1 D		1.3 U		1.2 D
CG9795				154414_at	1.6 D S		1.4 D		1.2 D		1.1 D		1.1 U		1.4 U
CG15881				153375_at	1.6 D S		1.2 D		1.1 U		1.2 U		1.1 U		1.0 D
CG15433	48			145760_at	1.6 D S		1.5 D S		1.1 D		1.0 U		1.5 U		1.2 D
CG1416				155036_at	1.6 D S		1.2 D		1.1 U		1.4 U		1.1 U		1.2 D
CG8229				154406_at	1.5 D S		1.3 D		1.0 D		1.0 U		1.1 U		1.2 D
CG31342				149810_at	1.2 U		1.4 D		1.1 D				1.3 D		1.0 U
				154631_at	1.5 D S		1.1 D		1.4 U		1.0 D		1.1 D		1.0 U
CG1371				141706_at	1.5 D S		1.4 D S		1.0 D		1.2 D		1.3 D		1.1 D
CG9324				153490_at	1.5 D S		1.1 U		1.1 U		1.2 D		2.1 D S		1.2 D
CG7950	229	237		153139_at	1.5 D S		1.4 D S		1.5 D		1.0 D		1.2 U		1.0 U
CG17295				146028_at	1.5 D S		1.1 U		1.1 U		1.2 U		1.5 U		1.1 U
CG6181				154620_at	1.5 D S		1.1 D		1.2 U		1.3 D		1.2 D		1.1 D
CG32708				143025_at	1.5 D S		1.3 D		1.3 D		1.1 D		1.3 U		1.1 D
CG17385				147201_at	1.5 D S		1.0 D		1.0 D		1.3 D		1.3 U		1.1 D
CG9318				155059_at	1.5 D S		1.0 U		1.2 U		1.1 D		1.1 U		1.2 U
CG6833	546	892		152845_at	1.5 D S		1.0 D		1.1 D		1.4 D		1.0 U		1.1 D
CG14224	362			142855_at									1.1 D		
				151703_at	1.5 D S		1.1 D		1.0 U		1.3 D		1.2 U		1.1 U
CG7728	26			154829_at	2.2 D S		2.7 D S		1.3 D		1.0 D		1.1 U		1.3 D

CG11180	-98			153192_at	2.5 D S	2.5 D S	2.0 D		1.2 D	1.9 U	1.2 U	
CG5645	26			153460_at		2.3 D S					1.5 D	
CG2972	17			153909_at	1.6 D S	2.3 D S	1.6 D		1.1 D	1.6 U	1.2 D	
CG8368				148285_at	3.1 D S	2.3 D S	1.7 D		1.2 D	1.9 U	1.5 D	
CG10286	40			152411_at	2.3 D S	2.1 D S	1.4 D		1.0 D	1.6 U	1.3 D	
CG14788	34			141845_at								
				142203_at	1.7 D S	2.1 D S	1.7 D		1.2 D	1.7 U	1.5 D S	
CG9107				154505_at	1.5 D S	2.0 D S	1.6 D		1.0 U	2.0 U	1.2 D	
CG3735	30			154746_at	2.0 D S	2.0 D S	1.1 D		1.2 D	1.9 U	1.0 D	
CG32763	13	137		154033_at		2.0 D S	1.8 D		1.2 D	1.9 U	1.3 D	
CG2614				153768_at	1.8 D S	1.9 D S	1.1 D		1.1 U	1.6 U	1.0 U	
CG8327	11			152178_at	1.1 D	1.9 D S	1.5 D		1.3 D	1.9 U	1.5 D	
CG10189	378			152470_at	1.4 D	1.9 D S	1.3 D		1.0 D	1.4 U	1.1 D	
CG4069	30			141287_at	2.0 D S	1.9 D S	1.3 D		1.0 D		1.2 D	
CG12134	217			146915_at	1.9 D S	1.9 D S	1.4 D		1.4 D	1.6 U	1.2 D	
CG15867	-343			151423_at	1.1 U	1.8 D S					1.2 U	
CG33129				146211_at	1.0 U	1.1 D	1.0 D		1.3 D	1.1 D	1.0 U	
				146212_at	1.1 D	1.8 D S	1.2 D		1.2 D	1.2 U	1.0 D	
CG3224	212			144605_at	1.3 D	1.8 D S	1.4 D		1.1 U		1.0 U	
CG3709				145515_at	1.7 D	1.8 D S	1.4 D		1.6 D	2.0 U	1.6 D	
CG8675	230	316		153631_at	1.5 D	1.8 D S	1.0 D		1.0 U	1.9 U	1.2 D	
CG9123				142027_at								
				142782_s_at	1.7 D S	1.8 D S	1.5 D		1.0 U	1.3 U	1.0 D	
CG30497				146765_at	1.1 U	1.2 D	1.1 U		1.6 D			
				146766_at	1.0 D	1.8 D S	1.0 U					
CG9890				147737_at	1.3 D	1.7 D S			1.0 D	1.6 U	1.2 U	
CG2875	816			154029_at	1.9 D S	1.7 D S	1.4 D		1.3 D	1.6 U	1.1 D	
CG11123	-849			146739_at	1.9 D S	1.7 D S	1.1 D		1.2 D	2.0 U	1.2 D	
CG2260	7	364		154955_at	1.5 D	1.7 D S			1.0 D	1.5 U	1.1 D	
CG14543	769			150641_at	1.4 D	1.7 D S	1.4 D		1.1 U	1.5 U	1.4 D	
CG4975	745			147394_at	1.3 D	1.7 D S	1.3 D		1.2 D	1.6 U	1.2 D	
CG1074				141546_at	1.6 D S	1.7 D S	1.3 D		1.1 D	1.8 U	1.2 D	
CG12592				143043_s_at	1.1 D	1.7 D S	1.1 D		1.5 D	1.0 D	1.2 D	
				151759_s_at	1.5 D S	1.4 D S	1.0 D		1.4 D	1.1 U	1.1 U	
CG15771				142223_at	1.1 D	1.3 D	1.1 U		1.1 D	1.2 U	1.1 D	
				151499_at	1.4 D	1.7 D S	1.2 U		1.2 U	1.6 U	1.2 U	
CG8002				145362_at	1.2 U	1.7 D S	1.1 U			1.1 D	1.4 U	
CG9922				149869_at	1.4 D	1.6 D S	1.3 D		1.3 U	1.4 U	1.2 D	

l(3)s1921				142561_at	1.4 D	1.6 D S	1.3 D	1.2 D	1.6 U	1.1 U
CG5290	186	195		141652_at	1.7 D S	1.6 D S	1.4 D	1.3 U	1.2 U	1.1 D
CG12797				154566_at	1.1 D	1.5 D S	1.0 U	1.1 D	1.5 U	1.0 U
CG4364	-421			154393_at	1.8 D S	2.3 D S	2.2 D S	1.5 U	1.1 U	1.3 D
CG10805	-13			141566_at	2.1 D S	2.7 D S	2.0 D S	1.2 U	1.6 U	1.5 D
CG2982	39			154908_at		1.9 D S	1.9 D S		1.8 U	1.1 D
CG14434				144625_at	1.2 D	1.4 D S	1.8 D S	1.1 D	1.1 D	1.1 D
CG3251	-568	-172		145773_at	1.0 D	1.5 D S	1.7 D S	1.3 D		
CG7519				149182_at	1.3 D	1.6 D S	1.6 D S	1.6 D	1.5 U	1.1 D
CG5047				142738_at	1.3 D	1.4 D	1.1 D	1.3 D	5.3 U S	1.3 D
CG11563	22			150954_at	1.8 D S	3.4 D S	1.5 D	1.0 U	3.7 U S	1.3 D
CG3259				149889_at					3.2 U S	1.3 U
CG9799	6	440		141659_at	1.8 D S	2.1 D S	1.8 D S	1.0 U	3.1 U S	1.4 D
CG11604	416			153448_at	2.4 D S	3.7 D S	2.7 D S	1.2 D	3.1 U S	1.4 D
CG9246	34			155156_at	2.2 D S	2.1 D S	1.3 D	1.5 U	3.0 U S	1.1 D
CG18178	109			151938_at	2.2 D S	2.8 D S	1.6 D	1.0 D	3.0 U S	1.2 D
CG7338				154433_at	2.0 D S	2.8 D S	1.6 D	1.1 D	2.9 U S	1.6 D S
l(3)07882	45	237		153862_at	1.9 D S	1.6 D	1.7 D	1.1 U	2.9 U S	1.1 D
CG15027	-38			145101_at	2.1 D S	2.5 D S		1.1 U	2.8 U S	1.1 D
CG11880				141361_at	1.3 D	1.3 U	1.1 D	1.4 D	2.8 U S	1.2 U
CG12325	40			153712_at	2.5 D S		2.3 D S	1.2 D	2.7 U S	1.1 D
CG7137	41			153734_at	1.8 D S	1.8 D	1.4 D	1.1 D	2.6 U S	1.1 D
CG12785	19			155019_at	2.4 D S	2.5 D S	1.8 D	1.1 D	2.6 U S	1.4 D
CG7637	-726	-43		146963_at	2.0 D S	2.3 D S	1.6 D	1.0 U	2.6 U S	1.6 D
CG7006	-500	-380	28	142493_at	1.7 D S	2.1 D S	1.5 D	1.2 D	2.5 U S	1.3 D
CG5558	23	29		153877_at	2.1 D S	1.8 D	1.1 U	1.4 U	2.5 U S	1.2 D
CG7993	36			151780_at	1.2 D	1.6 D S		1.2 U	2.5 U S	
CG6724	217			146191_at	1.8 D S	1.7 D S	1.7 D	1.0 U	2.4 U S	1.2 D
CG7845	-697	24		141258_at	2.9 D S	3.5 D S	2.0 D S	1.4 D	2.4 U S	1.6 D
CG1381	29			141230_at	1.6 D S	2.3 D S	2.1 D S	1.1 U	2.4 U S	1.5 D
CG12093				142691_at	1.1 D	1.1 U	1.0 U	1.4 D	2.4 U S	1.1 D
CG4554	-6			153124_at	2.0 D S	3.1 D S		1.0 U	2.4 U S	1.3 D
CG18135				155139_at		1.1 D	1.3 U		2.3 U S	1.5 U
CG13773				152912_at	1.7 D S	2.1 D S	1.7 D	1.0 U	2.3 U S	1.2 D
CG3817				153284_at	1.5 D	1.1 D	1.2 D	1.0 U	2.3 U S	1.3 D
CG30118	424			147439_at	1.2 D	1.4 D			1.3 U	1.1 D
				152372_at	1.2 D	1.4 D			2.3 U S	1.0 D
CG30349	90	236		146843_at	1.6 D S	2.5 D S	2.0 D S	1.2 D	1.9 U S	1.5 D

				146844_at	1.8 D S	2.7 D S	2.1 D S	1.0 D		2.3 U S	1.6 D	
CG12975				149168_at	1.7 D S	2.0 D S	1.4 D	1.2 D		2.3 U S	1.2 D	
CG14701				149679_at	1.4 D	1.4 D S	1.5 D	1.5 D		2.3 U S	1.3 D	
CG10648	10			144716_at	1.3 D	4.0 D S	2.4 D S	1.5 D		2.3 U S	1.7 D	
CG15014	153			148169_at	1.5 D	1.3 D	1.3 D	1.7 D		2.3 U S	1.1 D	
CG14286				150175_at	1.4 D	1.4 D	1.0 D	1.2 D		2.3 U S	1.1 D	
CG10220	25			142621_at	1.1 D	1.2 D	1.1 U	1.2 D		1.3 D	1.1 U	
				151647_at	2.4 D S	2.8 D S	1.4 D	1.1 D		2.2 U S	1.9 D	
CG5114	14			153148_at	1.2 D	2.3 D S	1.9 D S	1.2 D		2.2 U S	1.2 D	
CG9422	-637	15		146687_at	1.1 D	1.2 D	1.1 U	1.0 D		2.2 U S	1.1 D	
CG1234				154719_at	2.0 D S	3.0 D S	2.2 D S	1.1 D		2.2 U S	1.2 D	
CG12128	33			153156_at	2.4 D S	2.5 D S	1.3 D	1.0 D		2.2 U S	1.4 D	
CG7841	-221			148805_at						2.1 U S		
CG6509				146243_at	1.4 D	1.1 D	1.0 D	1.3 D		2.1 U S	1.2 U	
CG9986				154402_at	1.3 U	1.1 U	1.0 D	1.3 D		2.0 U S	1.0 D	
CG3983	135	727		150045_at	3.3 D S	2.3 D S	1.6 D	1.2 U		2.0 U S	1.4 D	
CG14550	810			150642_at	1.2 D	1.1 D	1.0 D	1.0 D		2.0 U S	1.3 D	
CG8816	63			147104_at	1.8 D S	2.8 D S	1.5 D	1.0 D		2.0 U S	1.2 D	
CG7989	30			153875_at	1.7 D S	2.5 D S	1.5 D	1.6 D		2.0 U S	1.1 D	
CG11076	806			150993_at	2.3 D S	2.0 D S	1.6 D	1.4 D		2.0 U S	1.3 D	
CG1785	-454	19		152691_at	1.9 D S	2.4 D S	2.1 D S	1.2 D		1.9 U S	1.2 D	
CG8064	25			151766_at		2.2 D S		1.4 D		1.9 U S	1.3 D	
CG12301	-12			154570_at	1.3 D			1.1 D		1.9 U S	1.2 D	
CG3353	-946	34		150304_at	1.6 D S	2.2 D S	1.5 D	1.2 D		1.9 U S	1.2 D	
CG18166				144345_s_at	1.6 D S	2.4 D S	1.3 D	1.5 D		1.8 U S	1.1 D	