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SUPPLEMENTARY INFORMATION

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SUPPLEMENTARY INFORMATION-1

SUPPLEMENTARY TEXT

Section I. Generation, biological properties, and use of cell lines utilized in our microarray analysis

In order to generate the cell clones used in this study, we took advantage of the oncogenic properties of the constitutively active versions (Q63L mutants) of Rho subfamily proteins when overexpressed in rodent fibroblasts (Schuebel *et al.*, 1998). Based on this property, we transfected NIH3T3 cells with plasmids encoding the indicated versions of Rho subfamily proteins to obtain foci of transformed cells (**Fig. S1a**). Selected foci were picked, pooled, and used for the subsequent microarray experiments (**Fig. S1b**). These cell clones were considered optimal to analyze the transcriptomal changes associated to the chronic stimulation of Rho subfamily-dependent pathways, because they showed the typical hallmarks of Rho-expressing cells, including the increase in the number and thickness of stress fibers (**Fig. S1c**), the constitutive phosphorylation of the myosin light chain (MLC) (**Fig. S1d**) (Amano *et al.*, 1996), and the increased phosphorylation levels of MLC phosphatase (data not shown) (Etienne-Manneville & Hall, 2002; Jaffe & Hall, 2005; Kimura *et al.*, 1996; Nobes & Hall, 1995; Ridley & Hall, 1992). Other properties exhibited by these cells included loss of contact inhibition (**Fig. S1a**), anchorage growth independence, ability to metastasize to lungs when inoculated in nude mice through the tail vein, and tumorigenicity when injected intradermally in nude mice (data not shown) (del Peso *et al.*, 1997; Perona *et al.*, 1993; Sahai *et al.*, 1999).

To avoid the activation of genetic programs related to serum withdrawal or contact inhibition that may confound the detection of Rho-specific transcriptomal changes (Coller *et al.*, 2006), we cultured the chosen cell lines and the parental NIH3T3 cells in the presence of serum and maintained them at confluency levels lower than 70% prior to RNA extraction. These conditions were therefore different to the previous cDNA microarray work with RhoA^{Q63L}-transformed NIH3T3 cells that used samples derived from confluent and serum-starved cultures (Teramoto *et al.*, 2003). In addition, we isolated total RNAs from eight (in the case of NIH3T3 cells), seven (in the case of RhoA^{Q63L}-transformed cells) and six (in the case of RhoB^{Q63L}- and RhoC^{Q63L}-transformed cells) independent cell cultures in order to make it possible a robust statistical treatment of the data obtained. RNAs samples were finally converted into biotinylated-cRNA probes and hybridized independently to Affymetrix arrays, thus allowing the monitoring of the expression status of ≈ 12,000 mouse genes.

Section II. Comparison of the transcriptomal changes induced by Rho subfamily proteins

As indicated in the main text, the statistical analysis of our microarray data revealed two groups ("A" and "B") of Rho-regulated genes. Group "A" included those genes that were similarly regulated by the three GTPases (**Fig. 1**a). This group was the largest, since it included approximately 83.6% of all genes regulated by these GTPases. Group "B" comprised genes that, according to statistical criteria, seemed to be specifically regulated by RhoA^{Q63L} alone or shared by RhoA^{Q63L} alone (4.8% of all genes, **Fig. 1b**) or shared by RhoA^{Q63L} and RhoB^{Q63L} (5.9% of all genes, **Fig. 1c**), RhoA^{Q63L} and RhoC^{Q63L} (3.1% of all genes, **Fig. 1d**) or RhoB^{Q63L} and RhoC^{Q63L} (2.6% of all genes, **Fig. 1e**). We could not detect genes uniquely regulated by RhoB^{Q63L} or RhoC^{Q63L} GTPases (**Fig. 1**). Based on these data, we concluded that RhoA^{Q63L}, RhoB^{Q63L}, and RhoC^{Q63L} induced changes in a total number of 1,008, 950, and 924 genes, respectively (**Fig. 1**). Despite this initial classification, a more careful examination of our microarray data indicated that the segregation of the “A” and “B” groups was only a statistical effect and did not stand a solid scrutiny under more biological criteria. Thus, we observed that most “B” subset genes showed tendencies of change similar to those observed in the “A” group when compared to the parental cell line (for example, see experimental samples present in **Fig. 1b,d**). In this case, their exclusion from the latter group was only due to the fact that their expression levels did not pass the arbitrary fold change (≥1.5 fold) or P values (≤ 0.01) set forth in our statistical analysis. Alternatively, some genes were excluded from the “A” group because their expression values showed variation in some, but not all, of the RNA samples used in the analysis (i.e., **Fig. 1c**, RhoC^{Q63L} samples 1-3). When those samples were excluded, those genes showed similar expression patterns in all Rho subfamily-transformed cells (data not shown). The only exception falling outside this description is the *thrombospondin 1* gene, which was up-regulated and down-regulated by RhoA^{Q63L} and RhoB^{Q63L}, respectively. This gene did not show variations in the case of RhoC^{Q63L}-transformed cells (**Table S1**). Based on this analysis, we concluded that RhoA, RhoB and RhoC proteins induce very similar transcriptomal profiles, at least in the case of NIH3T3 cells.

Section III. Corroboration of microarray data using independent techniques

For the independent confirmation of the microarray results, we analyzed the expression of 27 of the up-regulated and 20 of the down-regulated genes in the parental and Rho-transformed cells using real-time quantitative RT-PCR analysis. This analysis confirmed that these 47 genes were indeed regulated by Rho subfamily GTPases (**Table S2**). Subsequent studies during the characterization of the RhoA^{Q63L}-dependent transcriptome corroborated the differential expression of 10 extra genes (**Fig. S5**). However, we found that the fold changes obtained for the analyzed transcripts were usually higher in the RT-PCR analysis than in the microarray experiments (compare **Tables S1** and **S2**). Such discrepancy between Affymetrix microarray data and other independent techniques has been noted before by others (Chen *et al.*, 2001; Rajasekhar *et al.*, 2003). We also corroborated the differential expression of 16 genes at the protein level by immunoblot analysis with appropriate antibodies (see **Figs. 2c, S3, S4 and S6,** data not shown), indicating that the altered transcript levels had also an impact in the proteome of these cells. Finally, we detected transcripts in our microarray-derived data that had been previously described as targets for RhoA (i.e., *cyr61*, *plaur*, *tnc*, *ctgf*, *ptgs2*) (Benitah *et al.*, 2003; Chowdhury & Chaqour, 2004; Han *et al.*, 2003; Muller *et al.*, 2000; Ott *et al.*, 2003; Sarasa-Renedo *et al.*, 2006), a result that further demonstrates that the microarray experiments yielded a bona-fide picture of the downstream signaling of these GTPases. However, our experiments indicated that RhoA^{Q63L} promoted the upregulation of the *thrombospondin 1* gene, a result that is in contrast to other report indicating that the downregulation of this gene in Ras-transformed kidney epithelial cells is both RhoA- and Rock-dependent (Watnick *et al.*, 2003). Unfortunately, we could not compare our transcriptional profile to that previously obtained using cDNA-bases arrays since that database was not present in the original publication (Teramoto *et al.*, 2003).

Section IV. Functional annotation of Rho-regulated genes

The global analysis of the microarray data indicated that the fold changes of the regulated genes follow a Poisson curve (**Fig. S2**). For example, the majority of RhoA^{Q63L}-regulated genes change between 1.5- and 3.4-fold while a small minority show variation levels outside that interval (**Fig. S2**). Up-regulated and down-regulated genes follow a similar trend, although we observed a significant enrichment of induced and repressed loci in the subset of genes displaying the lowest or highest fold change variations, respectively (**Fig. S2**). This small variation in transcript levels suggests that Rho-mediated transformation relies mainly in modulating the levels of activity of active genes rather than being based on turning on previously silent loci. In general, the fold changes detected were similar in RhoA^{Q63L}-, RhoB^{Q63L}- and RhoC^{Q63L}-transformed cells although, in a minority of cases, we found genes with marked expression differences among those cells. For instance, the *mrpplf3* mRNA increases 8-, 26.8, and 19-fold in RhoA^{Q63L}-, RhoB^{Q63L}- and RhoC^{Q63L}-transformed cells, respectively (**Table S1**). When classified in terms of total fold change variations, we observed that the most up-regulated genes encoded secreted proteins (Mrpplf3, Ccl7, CTGF, serpin1) (**Table S1**). The most down-regulated genes coded also for secreted proteins (Smoc2, osteoglycin) (**Table S1**). Interestingly, we observed that the percentages of up-regulated versus down-regulated genes were different depending on the subcellular localization of their encoded proteins. The nucleus was the subcellular site with predominant up-regulated loci whereas the extracellular compartment had a larger proportion of inhibited genes. As it will be discussed below, this is mainly due to the large number of nuclear genes involved in DNA-related functions and to the severe reduction in the expression of extracellular matrix proteins in Rho-transformed cells.

The functional annotation of the identified genes revealed that the cell transformation mediated by the chronic stimulation of Rho subfamily GTPase pathways targeted specific biological processes. Thus, we observed that Rho proteins promote a general shut-off of extracellular matrix components (8 collagen precursors, procollagen proteinases, fibronectin, laminin, decorin, lumican, matrilin, extracellular proteases, Timp3 and lysyl oxidase, among others), although there was a small fraction of those genes that were up-regulated by Rho proteins (**Table S1**). Most of the down-regulated genes in this functional class corresponded to a cluster of genes that are induced by TGFβ in mouse fibroblasts (Verrecchia *et al.*, 2001). Interestingly, we have found that other proteins up-regulated by TGFβ that belong to other functional classes were also down-regulated by Rho proteins (i.e., metallothionine 1 and 2) (Verrecchia *et al.*, 2001) (**Table S1**). Consistent with a possible antagonism between Rho- and TGFβ-dependent routes, we also observed the repression in these cells of other elements of the TGFβ pathway such as Ltbp4 (Sterner-Kock *et al.*, 2002), osteoglycin (Bentz *et al.*, 1989), and Smads (Hata *et al.*, 1998; Kretzschmar *et al.*, 1997; Kretzschmar & Massague, 1998; Lagna *et al.*, 1996; Liu *et al.*, 1996; Liu *et al.*, 1997). Conversely, we detected an increase in TGFβ antagonists such as Grem2 (Sudo *et al.*, 2004) (**Table S1**). These results suggest that Rho proteins orchestrate the inhibition of a specific subset of genes regulated by the TGFβ pathway in order to accomplish their tumorigenic program in mouse fibroblasts.

Another important subset of Rho-targeted genes include loci encoding extracellular ligands exerting autocrine/paracrine functions and of specific transmembrane receptors (**Table S1**). Thus, we observed changes in the induction (Ccl2, Ccl7, Cxcl1, Cxcl5) and inhibition (Cxcl1, Cxcl12) of two subsets of chemokines, the up-regulation of neurotrophins (BNDF, GDNF, NGF), and the induction (VEGF-A, EphrinB2, semaphorins, Plf1, Plf2, Mrpplf3) or repression (VEGF-B, VEGF-D) of proangiogenic factors. We also recorded the up-regulation of insulin-related molecules (IGF2, IGFbp6), CTGF-like proteins (CTGF, Cyr61), and EGF-receptor ligands (epiregulin, heparin-binding EGF-like factor). This spectrum of deregulated genes may contribute to the malignant properties of Rho transformed cells, since some of their human counterparts (*cxcl1* and *epiregulin*) have essential roles in the ability of cells to metastasize to specific tissues (Minn *et al.*, 2005). While the EGF-R- and insulin-related signaling appears to be promoted in these cells via the up-regulation of ligands, we have also observed that Rho-mediated transformation correlates with a strong repression of FGF and PDGF signaling routes. This is done via the down-modulation of the expression of genes encoding some of their receptors (FGF-R1, FGF-R2, PDGF-Rα, PDGF-Rβ) and, in addition, by repressing genes encoding regulatory molecules of these routes such as Twist1 (a transcriptional factor that modulates FGF-R expression) and Fibp (an intracellular FGF binding protein). The down-modulation of PDGF-R, a common event in some transformed cells (Bowen-Pope *et al.*, 1984; Stice *et al.*, 1999; Vaziri & Faller, 1996; Wang *et al.*, 1996), was confirmed by both real time quantitative RT-PCR and immunobloting (**Table S2** and **Fig. S3**).

Rho GTPases also impact on signal transduction pathways located downstream of tyrosine kinase receptors (**Table S1**). In the case of the Ras pathway, Rho proteins inhibit the expression of Ras subfamily proteins (R-Ras) and of RalGDS, a key downstream element of Ras oncoproteins (Hofer *et al.*, 1994; Kikuchi *et al.*, 1994; Rodriguez-Viciana & McCormick, 2005; Spaargaren & Bischoff, 1994). In addition, we observed the up-regulation of three phosphatases involved MAPK inactivation (Dusp1, Dusp6, Dusp9), and a RasGAP (Rasa4). The overexpression of Dusp1 was demonstrated by immunoblot experiments (**Fig. S3**). Finally, the microarray data indicated that Rho GTPases target phosphatidylinositol 3-kinase (PI3-K) signal transduction elements, including the repression of the PI3-K p85α regulatory subunit and PTEN, a lipid phosphatase that controls negatively the signaling output of the PI3-K route (Cully *et al.*, 2006; Li *et al.*, 1997; Maehama & Dixon, 1998; Myers *et al.*, 1997). In the case of Rho/Rac routes, we observed a consistent repression of a subset of genes encoding Rac/Cdc42 exchange factors (GEFT, Trio) and downstream targets (Stat3). Conversely, Rho proteins promoted the induction of the gene encoding for RacGAP1, a Rac subfamily negative regulator. By contrast, we noticed that the cell transformation mediated by Rho proteins involved the promotion of their own pathways, since we detected increased levels of mRNAs encoding for either Rho exchange factors (Net1, NGEF) or effectors (mDia1 and 3).

Given the important role of Rho proteins in the regulation of cytoskeletal dynamics and microtubule stability (Jaffe & Hall, 2005), it is not surprising the detection of a large collection of cytoskeletal- and microfilament-related genes in the transcriptome of Rho-transformed cells (**Table S1**). In the former group, Rho proteins up-regulate the expression of specific actin molecules (actin α1, γ2, actin-like 6A protein) while decreasing other isoforms (actin β). Rho proteins also stimulate transcription of genes encoding proteins involved in different regulatory steps of the cytoskeleton, including G-actin sequestration factors (thymosin β4), F-actin stabilization molecules (Ivns1abp), actin bundling and severing factors (actinins, Pdlim1, Capg), F-actin depolymerization molecules (cofilin2, transgelins 1 and 2), actin-binding proteins (i.e., coronin, Fez2, anillin), and nuclear proteins with recent cytoskeletal-related functions (Ezh2). Proteins belonging to those categories were also found targeted negatively by Rho proteins (i.e., Gas2, Fscn1, Aim1, Ablim, gelsolin) (**Table S1**). RhoA transformed cells also up-regulate genes encoding for integrin-related pathways, including some species of integrin subunits (α6), integrin-associated proteins (osteopontin, Alcam, CD151, CD44, ERM proteins, and plakophilin 4). At the same time, they down-regulate negative regulators of integrin signaling (thrombospondin 2) and proteins that anchor them to the spectrin scaffold system (ankyrin 3, α2 and β2 spectrin). These results indicate that Rho proteins may mediate integrin signaling not only by the induction of focal adhesions but also through the modification of the proteome of these structures.

A similar picture is observed in the case of proteins related with the microfilament network (**Table S1**). Thus, the analysis of the microarray data indicates that Rho proteins stimulate the expression of tubulin isoforms (β5, γ1) and a large collection of proteins involved in different aspects of microtubule (MT) biology such as MT stabilizers (Ckap2), tubulin sequestering proteins (stathmin), mitotic-associated MT proteins (NdeI, pericentrin), and 7 kinesin family members. In addition, they down-modulate other subsets of MT-associated proteins (MAPs), spindle assembly regulators (myosin X) and tubulin deacetylases (sirtuin 2). The simultaneous regulation by Rho GTPases of proteins with diverse, and sometimes antagonistic functions in the F-actin and tubulin cytoskeleton suggest that Rho proteins promote fluid cytoskeletal structures rather than fixing them in a polymerized, rigid status. The specific targeting of some of these loci may also contribute to the transforming program of Rho-transformed cells, since some of these cytoskeletal proteins have been linked to either growth promotion (i.e., the synergistic interaction of stathmin with osteopontin) or tumor suppression (Gas2, Aim1, sirtuin 2) (Brancolini *et al*., 1997; Ray *et al*., 1997; Yuan *et al*., 2006).

RhoA and RhoB proteins have been involved in the regulation of vesicle trafficking by post-translational events mediated by specific effectors such as mDia and PRK1 (Ellis &

Mellor, 2000; Gampel *et al.*, 1999; Jaffe & Hall, 2005; Lamaze *et al.*, 1996; Leung *et al.*, 1999; Mellor *et al.*, 1998; Ridley, 2001; Sandilands *et al.*, 2004). This function appears to be also extended at the level of transcription, since we have observed a consistent reduction of the transcript levels for 5 Rab proteins (Rab3d, 5b, 9, 11a, and 24), a Rab exchange factor (Rin2), Rab acceptors (Rabac1), and regulators of the excision, fusion or targeting of endocytic vesicles (dynamin 1, clathrin, caveolin, SNAPs, syntaxins). We have also noted the general down-modulation of at least 6 transcripts encoding lysosomal proteins (**Table S1**). These results indicate that, at least in the case of constitutive signaling, Rho GTPases may influence the dynamics of vesicle trafficking by modulating the mRNA levels of key regulators of this biological process.

One of the main functional classes affected by Rho-mediated transformation is the group of molecules related to the regulation of gene transcription. Among the usual targets of Rho proteins, we could identify the regulation of AP1, NFκB, Myc, E2F, and SRF family proteins (**Table S1**). In the former case, we observed the up-regulation of c-Jun and Fra1, a Fos-like protein involved in invasiveness and cell motility. Instead, JunD1, an AP1 protein with anti-angiogenic potential, became down-regulated under the same experimental conditions (Belguise *et al.*, 2005; Gerald *et al.*, 2004; Kustikova *et al.*, 1998; Tkach *et al.*, 2003). We could not detect any variations in the levels of NFκB proteins. However, Rho-transformed cells displayed increased levels of two NFκB inhibitors (NFκBia and NFκbIz) and of Hivep2/Shnurri 2, a transcriptional regulator that binds κB sites (Jin *et al.*, 2006; Karin, 2006; Kimura *et al.*, 2005). In the Myc family, we observed that Rho GTPases promoted c-Myc, Myb12 and N-Myc expression while inhibiting the c-Myc transcriptional repressor Mnt. In the case of the E2F complex, we detected the up-regulation of E2F1, E2F8, the E2F1 dimerization partner Dp1, and Lin9, an Rb-binding protein with growth suppressing properties (Gagrica *et al.*, 2004). A decrease in Cri1, a p300/CBP repressor was also observed (Miyake *et al.*, 2000). In addition to increased levels of E2F, the functional output of this route is probably further increased by the elevation of cyclin D1 and cyclin F detected at the mRNA and protein levels in Rho-transformed cells (**Table S1** and **Fig. S4a**, respectively). The up-regulation of the E2F pathway is also supported by the detection of a significant number of E2F-target genes in our microarray data (see below and **Fig. S4c**). We saw no major changes in *srf* mRNA levels, although Rho-transformed cells elicited a surprising reduction in the mRNA levels of MAL/Mkl1, a potent co-activator of SRE elements (Miralles *et al.*, 2003; Settleman, 2003). Despite these data, we surmise that there is an activation of SRF activity at the post-translational level, since the transcriptome of Rho-transformed cells contains many SRF-regulated genes. Thus, when considering the previously published microarray data on the SRF-dependent, Mlk1/MAL-independent transcriptome (Selvaraj & Prywes, 2004), we could see that 45% of the reported genes were similarly-regulated by Rho GTPases. Furthermore, 9 out of 10 Mkl1/MAL-dependent genes were also altered in a similar manner by Rho proteins, further supporting the constitutive activation of the SRF pathway in the Rho-expressing cell clones. We also detected the induction of p53 by Rho proteins, an event that was associated to the concomitant co-regulation of other elements of its pathway such as the kinase Vrk1 and the Mdm2 inhibitor (Brooks & Gu, 2006; Vega *et al.*, 2004). The elevation of E2F, c-Myc, and c-Jun proteins was demonstrated by immunoblot experiments (see main text, **Fig. 2c**). Finally, we noticed the up-regulation of transcriptional factors not previously linked to Rho GTPase function, such as the Pbx3 oncoprotein, Np95 (a transcriptional factor implicated in topoisomerase expression), Rrn3 (involved in inducing the expression of RNA polymerase I), and basonuclein (concerned in transcription from rRNA genes). Interestingly, we also observed increased mRNA levels for at least 6 transcriptional repressors (Ifrd1, Hdac1, Sin3, Lrrfip1, Klf4 and Sap30) as well as for molecules involved in the epigenetic regulation of gene expression (i.e., nucleosome assembly factors, phospho/methylated histone-binding proteins, and histone methyltransferases), indicating that the transcriptome dynamics of Rho-transformed cells are modulated by both transcriptional and epigenetic events. Our microarray data also revealed a significant percentage of transcriptional factors whose expression is inhibited by Rho-mediated cell transformation (**Table S1**). Those include retinoic acid and vitamin D receptors, nuclear receptor binding proteins (Nrbp2), Ddif3, Ebf1, and Ebf3 proteins. The inhibition of these genes seems to be an active goal of Rho GTPases, since Rho-transformed cells also promote the expression of Tgif1, a retinoic acid receptor inhibitor (Bertolino *et al.*, 1995). Notably, we also observed a consistent down-modulation of the ID family (ID2, ID3 and ID4), a group of basic helix-loop-helix transcriptional factors involved in matrix remodeling, angiogenesis, and cell proliferation (Norton, 2000) (**Table S1**). Likewise, the mRNA levels of other transcriptional factors usually linked to cell proliferation or tumorigenesis are also reduced in Rho-transformed cells (Stat3, Slug, Mkl1), suggesting that the regulation of transcriptional factors by Rho proteins is more complex than the mere activation of proliferation-related transcriptional regulators. In good agreement to the down-modulation of FGF-Rs, Rho proteins were found to repress Twist1, a transcriptional factor that regulates FGF-R expression.

Consistent with the wide transcriptomal changes induced by Rho GTPases, we noticed that the transformed cells stimulated a large number of genes encoding proteins related to RNA transcription (RNA polymerases inducers, RNA polymerase II and III subunits, RNA polymerase elongation factors, Cdk8), RNA splicing (Sf365, Slbp, snoRNP complexes), RNA polyadenylation (Cstf2), and RNA export. They also expressed higher levels of molecules involved in the transport of proteins between the nucleus and the cytosol such as structural components of the nuclear pore (nucleoporins 50, 62, 93 and 107), two Ran exchange factors (Chc1, RanGRNF), a Ran GAP, Ran-binding proteins (Nxt1), karyopherins (α2, α2, β3, importins 7 and 11), karyopherin-binding proteins (Cse1l), and exportins (Xpo1). Concomitant with this process, it is observed an increase in the transcription of genes encoding proteins related to rRNA biogenesis, including transcriptional factors involved in the expression of rRNA polymerases (Rrn3) and rRNA genes (basonuclein), RNA polymerases implicated in rRNA transcription (RNApol I and E), nucleolar proteins and snoRNPs that participate in pre-rRNA processing, ribosomal factors (Zrf2), and a small fraction of cytosolic (L1, L32) and mitochondrial (L12, L16, L18, L34, S10, S22, and S25) ribosomal proteins (**Table S1**). Coupled with the above processes, we observed that the transcriptome of Rho-transformed cells contained a significant percentage of transcripts encoding factors involved in amino acid anabolism (phosphoserine aminotransferase, serine racemase, branched chain aminotransferase), protein biosynthesis (Eif2b2, Eifs1, Eifes9, Eif4a2, Etf1, Hys- and Arg-tRNA synthetases) and protein folding (10 chaperone-like molecules and heat shock proteins) (**Table S1**). Finally, we also detected a significant number of genes involved in the regulation of proteins at the post-translational level, including 2 prenylation enzymes, 7 ubiquitin-related proteins, 7 proteasomal proteins, 20 serine/theonine kinases, 7 protein tyrosine kinases, and

8 protein phosphatases. With the exception of 13 (26%) of these genes that were down-regulated (*usp22*, *cask*, *clk*, *pftk1*, *eif2ak3*, *srpk2*, *pdfg-rα* and β, *fgf-r1* and *2*, *ptprm*, *ppp3ca*, *ptpn13*), all these post-translational factors were elevated in Rho-transformed cells.

Another functional class highly represented in the transcriptome of Rho-transformed cells is that concerned with cell cycle regulation, DNA synthesis, and DNA repair (**Table S1**). This group was mainly composed of up-regulated genes (**Fig. 2a**, **Table S1**). In addition to the expected cell cycle regulators, we observed the expression of a large collection of genes involved in DNA replication such as histones, mediators of histone biosynthesis and/or modification (Slbp, Hat1), topoisomerases (Top2a, Topbp1), helicases, structural components of replication origins (Mcms, Orcs, Cdc45l), DNA primases (Prim1, Prim2), DNA polymerases (Pola1, Pola2, Pold1, Pole2) and their regulators (PCNA, Rfc3, Rfc4), DNA ligases (Lig1), and regulators of the coating of nascent DNAs by histones (Asf1b, Chaf1b). Finally, there is a large plethora of genes encoding proteins specialized in DNA repair (**Table S1**). The differential expression of many of these genes in Rho-transformed cells versus the parental counterparts was corroborated at the protein level using immunoblot experiments (**Fig. S4**). To accommodate these high levels of DNA synthesis, we observed the concomitant up-and down-regulation of genes encoding metabolic enzymes involved in the anabolism (phosphoribosyl pyrophosphatase synthetase 1, ribonucleotide reductase, deoxycytidine kinase, adenylate kinase, dihydrofolate reductase, thymidine kinase) and catabolism (xantine dehydrogenase) of nucleotides, respectively (**Table S1**). Other enzymes associated to cell division were also induced by Rho proteins, especially those implicated in the synthesis of polyamines (spermidine synthase, ornithine decarboxylase). The high increase in polyamine synthesis is also supported by the detection of polyamine-responsive factors such as Pmf1 (**Table S1**).

The analysis of the metabolic pathways specifically targeted in Rho-transformed cells indicates that, in addition to those described already for nucleotide and amino acid biosynthesis, there is an specific modulation of glycolytic enzymes, oxidative stress-counteracting molecules, and of proteins involved in drug resistance and xenobiotic responses (**Table S1**). In the case of glycolysis, we have observed the up-regulation of key regulatory enzymes of the route such as hexokinase 2, phosphoglycerate kinase 1, phosphofructokinase, triosephosphate isomerase, and GADPH. We also observed an elevation in the mRNA levels of lactate dehydrogenase 1, an enzyme involved in the regeneration of glucose from lactate, and of glycerol phosphate dehydrogenase 2, the enzyme involved in the re-oxidation of the NADPH formed in glycolysis. Conversely, we detected diminished levels of Kreb's cycle enzymes (pyruvate dehydrogenase and the subunit C of the succinate dehydrogenase complex), suggesting that the production of energy in Rho-transformed cells shifts from the aerobic to the anaerobic metabolism. It should be noted, however, that such shift is quite idiosyncratic in the case of Rho-transformed cells, since they do not alter the expression of molecules previously shown to be deregulated in cancer cells, such as phosphoglycerate mutase, glucose transporters (Glut1 and 3) or cytochrome c oxidase complex regulators (Sco2) (Chung *et al.*, 1999; Gatenby & Gillies, 2004; Glick *et al.*, 1993; Kondoh *et al.*, 2005; Marom *et al.*, 2001; Matoba *et al.*, 2006; Mochizuki *et al.*, 2001; Sanchez-Alvarez *et al.*, 2005; Tian *et al.*, 2004; Zhao *et al.*, 2005; Zhao *et al.*, 2002).

In addition to the promotion of glycolysis, Rho-transformed cells also up-regulate reducing enzymes whose activity allows the elimination of oxidative radicals (superoxide dismutase 2, paraoxonase 2, peroxyredoxin 6, thioredoxin reductase 1, thioredoxin 1, glucose-6-phosphate dehydrogenase 2, and transaldolase 1). Furthermore, these cells inhibit the expression of Txnip, a thioredoxin binding protein that decreases the reducing activity of this enzyme. Finally, Rho-transformed cells seem to down-regulate the expression of genes encoding enzymes that eliminate xenobiotics and drugs (i.e., all but one GST isoforms, cytochrome P450, cytochrome b5, UDP glucoronosyl transferase 1). Some of these metabolic routes may be interconnected functionally, because glycolysis has been proposed to act as a potent anti-oxidant factor in cancer cells (Brand, 1997; Brand & Hermfisse, 1997; Gatenby & Gillies, 2004).

The analysis of the Rho-dependent transcriptome has also revealed the deregulation of pathways enhancing the fitness of the cancer cell and, at the same time, pinpointed deficits that may hamper the oncogenic potential of these GTPases in normal cells. Regarding the former issue, we have observed that these GTPases promote the down-modulation of a subset of TGFβ targets and of anti-mitogenic genes (TGFβ-related elements, nuclear hormone receptors), the induction of ligands previously shown to collaborate in the metastasis of cancer cells to specific tissues (Cxcl1, epiregulin) (Minn *et al.*, 2005), the inhibition of pathways involved in xenobiotics responses and drug metabolization, the promotion of factors implicated in stromal and inflammatory cell infiltration (CTNF, Cox2/Ptgs2, chemokines) or the enhancement of cancer cell survival strategies (autocrine molecules, PTEN down-modulation, Birc5/Survivin). We have also observed the up-regulation of loci previously involved in the cancerous state (*stm1*, *ssp1*/*opn*, *msln*, *aqp1 pbx3*, *nol1*) and, at the same time, the down-regulation of genes that are lost during tumor progression (*gas*, *aim1*, *sirt2*). Interestingly, the chronic stimulation of the Rho pathway also leads to the up-regulation of other routes commonly found in cancer cells, such as the induction of enzymes involved in glycolysis and oxidative stress clearance (Gatenby & Gillies, 2004). All these results indicate that the constitutive activation of Rho signaling promotes specific tumorigenic properties *per se* even in the absence of accumulating mutations or intra-tissular selective forces. Despite these proactive changes favoring tumorigenesis, a careful analysis of the Rho-dependent transcriptome disclosed a number of Achilles' heels of the biological program elicited by Rho subfamily proteins. For instance, the examination of the Rho "glycolytic program" indicates that it does not include the Glut1 and Glut3 transporters that may be crucial for maintaining high glycolytic rates under suboptimal glucose concentrations (Gatenby & Gillies, 2004). We have also observed that Rho proteins trigger the up-regulation of p53 and p53-dependent genes (Lats2, Gadd45a, Mdm2). While this may not be an impediment for NIH3T3 cells due to the loss of the *p16* gene (Linardopoulos *et al.*, 1995; Quelle *et al.*, 1995), it may be an insurmountable problem for normal cells having a fully competent p53 route.

As expected from the results discussed in **Section II** (see above), the analysis of the RhoB^{Q63L} and RhoC^{Q63L}-associated transcriptome generated similar functional distributions.

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TRANSCRIPTOMAL PROFILING OF THE CELLULAR TRANSFORMATION INDUCED BY Rho SUBFAMILY GTPases

SUPPLEMENTARY INFORMATION-2

SUPPLEMENTARY MATERIALS AND METHODS

Plasmids

Mammalian expression vectors encoding human RhoA^{Q63L} (pCEFL-AU5-RhoA^{Q63L}), RhoB^{Q63L} (pXRB159) or RhoC^{Q63L} (pXRB160) proteins have been described before (Schuebel *et al*., 1998). pCEFL-Myc (encoding an AU5-tagged version of wild type human c-Myc) was provided by Dr. P. Crespo (University of Cantabria-CSIC, Santander, Spain). The expression plasmid pSG-V12-H-Ras (encoding the human *H-ras* oncogene) was provided by J. Downward. pCMV-E2F1 (encoding the wild type human E2F1 protein), pCMV-Rb (encoding wild type human Rb), pECE-ΔCDK-Rb (encoding an HA-epitope tagged version of the human RbΔCDK mutant), and the luciferase reporter plasmid carrying E2F-responsive elements (pGL2E2F-*luc*) were all provided by Dr. M. Malumbres (Centro Nacional de Investigaciones Oncológicas, Madrid, Spain). pCMV-MadMyc (encoding the chimeric Mad/Myc protein that acts as a dominant negative mutant for c-Myc), pP2*luc (*containing the *luciferase* gene under the regulation of the *c-myc* promoter region) and pM4*luc* (containing the *luciferase* gene under the regulation of a promoter with *c-myc* responsive elements) were kindly provided by Dr. J. León (University of Cantabria, Santander, Spain). Luciferase reporter plasmids carrying AP1 (pAP-1-*luc*) and p53 (p53-*luc*) responsive elements were obtained from Stratagene. pTKHyg (containing the *hygromycin* resistance gene) and pRLSV40 (expressing the *Renilla sp* luciferase constitutively) were purchased from Promega. The pCEFL derivative encoding a c-Jun dominant negative mutant was provided by Dr. J.S. Gutkind (National Institutes of Health, Bethesda, MD, USA). The expression vector pIMB15 (containing a Mad/Myc chimera) was generated by subcloning a pCMV-Mad/Myc-derived HindIII/XbaI cDNA fragment into the HindIII/XbaI linearized pCEFL-AU5 vector. pSUPER.GFP/*neo* was provided by

Dr. C. Guerrero (Centro de Investigación del Cáncer, Salamanca, Spain). The pIMB20 plasmid containing the *c-myc* shRNA was generated by ligating into BglII/HindIII-linearized pSUPER.GFP/*neo* two annealed oligonucleotides containing *c-myc* cDNA sense (5’-*GATCCCC*GCTCGCCCAAATCCTGTAC**TTCAAGAGA**GTACAGGATTTGGGCGAGC*TTTTTGGAAA*-3’) and antisense (5’-*AGCTTTTCCAAAAA*GCTCGCCCAAATCCTGTAC**TCTCTTGAA**GTACAGGATTTGGGCGAGC*GGG*-3’) sequences, a 9 nucleotide-long spacer to form the hairpin structure (in bold), and sequences for cloning (in italics).

Cell lines

Information about the denomination of all cell lines used in this study can be found in the **List 1** available in page 8 of this Supplemental material.

Real-time quantitative RT-PCR

Exponentially growing cells were lysed and total RNA extracted using the RNAeasy kit (Qiagen). RNAs were quantified by loading aliquots into 6000 Nano Chips. Quantitative polynucleotide chain reactions were performed using the QuantiTect SYBR Green RT-PCR kit (Qiagen). 18S rRNA primers were used as controls for both loading and quantitation of relative expression levels of the genes tested. Amplifications were performed using the iCycler machine (Bio-Rad). Raw data were analyzed using the iCycler iQ Optical System software (version 3.0a, Bio-Rad). The sequences of the oligonucleotides used in the PCR amplifications can be found in **List 2** (page 8-11) of this Supplemental material.

Immunobloting, immunoprecipitations, and immunoflourescence antibodies

Exponentially growing cells were washed with chilled PBS and lysed by adding SDS-PAGE sample buffer onto the plates. After boiling and centrifugation, cell extracts were resolved by electrophoresis and transferred onto nitrocellulose filters (Schleicher and Shuell). Membranes were blocked in either 5% non-fat dried milk (when immunobloted with standard antibodies) or 5% BSA (when using phosphospecific antibodies) in TBS-T (25 mM Tris-HCl [pH 8,0], 150 mM NaCl, 0.1% Tween-20) and then incubated overnight at 4 ºC with the appropriate primary antibodies diluted in blocking buffer. After three washes with TBS-T, the membrane was incubated with the appropriate horseradish peroxidase-conjugated secondary antibody (1:5,000 dilution; GE Healthcare Life Biosciences) for 1 h at room temperature. Immunoreacting bands were developed using a standard chemoluminescent method (ECL, GE Healthcare Life Biosciences).

For the immunoprecipitation of HA-RbΔCDK protein, cells from two subconcluent 10-cm diameter dishes were washed with chilled PBS solution and disrupted in 1 ml of lysis buffer containing 10 mM Tris-HCl [pH 8,0], 150 mM NaCl, 1% Triton X-100, and a protease inhibitor mixture (Cømplete, Roche Molecular Biochemicals). Lysates were incubated on ice for 10 min and precleared by centrifugation at 14,000 rpm for 10 min at 4 ºC. After supernatant collection and protein concentration determinations (see above), lysates containing equal amounts of proteins were immunoprecipitated for 2 h at 4 ºC using anti-HA antibodies (40 μg/ml). Gammabind G-Sepharose beads (GE Healthcare Life Biosciences) were then added to the lysates and incubated for 1 h at 4 ºC. After washes, the HA-RbΔCDK protein present in the beads was separated electrophoretically, transferred onto nitrocellulose membranes, and revealed by immunoblot analysis using anti-HA antibodies.

For immunofluorescence experiments, cells grown on poly-L-lysine-coated coverslips were fixed in 3.7% formaldehyde in PBS for 15 min. Cells were then permeabilized once in 0.5% Triton X-100 (Sigma) in PBS for 10 min and thrice in 0.1% Triton X-100 in PBS for 5 min each. After three washes with PBS, cell preparations were blocked in 5% BSA in TBS (25 mM Tris-HCl [pH 8,0], 150 mM NaCl) for 10 min and then stained for 20 min with rhodamine-phalloidin (0.5 U/ml, Molecular Probes) diluted in blocking solution to reveal the F-actin cytoskeleton. In addition, the cell preparations were stained with DAPI (0.2 μg/ml, Sigma) to visualize the nuclei. Immunofluorescence analysis was done using a Zeiss LSM510 confocal microscope and a 63x objective. Microscope images were finally processed for presentation using the Canvas 8 software (8.0.5 version, ACD Systems). Information about the antibodies used in our work can be found in **List 3** of this Supplemental material (pages 11-12).

Luciferase reporter assays

In the case of transcriptional activation assays in stable cell lines, exponentially growing IMB11-1P cells were transfected with pRLSV40 (10 ng) and the appropriate reporter plasmid (1 μg) using a liposome-based method (FuGENE 6, Roche Molecular Biochemicals). In the case of transcriptional activation assays in transient transfections, the pCEFL-AU5-RhoA^{Q63L} plasmid (100 ng) was co-transfected with the plasmid mixture indicated above in NIH3T3 cells. 24 h after transfection, cells were washed and maintained in DMEM supplemented with 0.5% calf serum for 24 h. The luciferase activity was assayed using the Dual Reporter Luciferase Assay kit (Promega), as specified by the manufacturer. The light generated in each reaction was quantified in a luminometer (MiniLumat LB 9506, EG&G Berthold). To avoid spurious inter-sample variability, the values obtained in the luciferase readings were normalized taking into account the levels of the *Renilla* luciferase activity present in each lysate. In addition, each experiment was performed in triplicate at least three independent times.

Determination of proliferation rates

We used the 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide (MTT) assay (Sigma) to determine the growth properties of our cell lines. To this end, the indicated cell lines were plated in 24-well dishes (10,000 cells/well) and cultured in DMEM supplemented with 10% calf serum. At the indicated time post-plating, the culture medium was discarded and 250 μl of an MTT solution in DMEM (0.5 mg/ml) were added onto each well. After 1 hr in a 5% CO_2 atmosphere at 37 ºC, the formazan crystals formed were dissolved by adding 500 μl of dimethyl sulfoxide (Sigma) onto each well. The absorbance at 570 nm of each sample was measured 15 min later using a microplate reader (Ultraevolution, Tecan).

Focus formation assays

For primary focus formation assays, NIH3T3 cells (1.5 x 10^5) were transfected using the calcium phosphate technique with 0.6 μg of pCEFL-AU5-RhoA^{Q63L} either alone or in combination of 1 μg of the indicated expression vectors. After 15 d, the foci of transformed cells were scored *de visu* by staining the plates with Giemsa (Sigma). For secondary focus formation assays, 1,000 cells of the indicated cell clones were mixed with 30,000 parental

NIH3T3 cells and plated onto 35 mm diameter culture dishes. Cell cultures were maintained for 9 d in DMEM supplemented with 10% calf serum and then stained with Giemsa to visualize the foci of transformed cells. In all cases, the data reported are derived from an experiment performed in duplicate that repeated at least three other independent times.

List 1. Cell lines used in this study

NAME	ORIGINATED FROM	GENES INTRODUCED	TYPE OF SELECTION
IMB11-1P	NIH3T3	RhoA^{Q63L}	G418
IMB11-2P	NIH3T3	RhoB^{Q63L}	G418
IMB11-3P	NIH3T3	RhoC^{Q63L}	G418
12-3-17	IMB11-1P	RhoA^{Q63L} + MadMyc	G418 + Hygromicin
15-2-7	NIH3T3	c-Myc	G418
16-2-P3	IMB11-1P	RhoA^{Q63L} + c-Myc	G418 + Hygromicin
16-2-1	IMB11-1P	RhoA^{Q63L} + c-Myc	G418 + Hygromicin
16-2-48	IMB11-1P	RhoA^{Q63L} + c-Myc	G418 + Hygromicin
15-6-35	IMB11-1P	RhoA^{Q63L} + *c-myc* RNAsi	G418 + Hygromicin
15-6-69	IMB11-1P	RhoA^{Q63L} + *c-myc* RNAsi	G418 + Hygromicin
15-7-11	IMB11-1P	RhoA^{Q63L} + pSUPER	G418 + Hygromicin
21-2-20	IMB11-1P	RhoA^{Q63L} + RbΔCDK	G418 + Hygromicin
21-3-4	IMB11-1P	RhoA^{Q63L} + RbΔCDK	G418 + Hygromicin
21-3-6	IMB11-1P	RhoA^{Q63L} + RbΔCDK	G418 + Hygromicin

List 2. Oligonucleotides used in RT-PCR experiments

GENE	DIRECTION	OLIGONUCLEOTIDE
alcam	Forward	5’-ATTGACAAAAGGAACATGGCG-3’
	Reverse	5’-ACACCACAGTCGCGTTCCTAC-3’
atf5	Forward	5’-CCATGGCATCCCTACTCAAGA-3’
	Reverse	5’-AGGTCAAAGGTGGGCAAGG-3’
birc5	Forward	5’-GGAGGCTGGCTTCATCCAC-3’
	Reverse	5’-GACAGTGAGGAAGGCGCAG-3’
bnc	Forward	5’-CTGGGAAGGTGCTGGATCAC-3’
	Reverse	5’-GTGGGCGGTACGATGACAG-3’
ccl2	Forward	5’-AAAAACCTGGATCGGAACCAA-3’
	Reverse	5’-TGCTTGAGGTGGTTGTGGAA-3’
ccl7	Forward	5’-CTGCTCATAGCCGCTGCTTT-3’
	Reverse	5’-CTTCCCAGGGACACCGACTA-3’
cd44	Forward	5’-ATCCCAACGCTATCTGTGCAG-3’
	Reverse	5’-CCATCGAAGGAATTGGGTAGG-3’
ctgf	Forward	5’-AGTTTGAGCTTTCTGGCTGCA-3’
	Reverse	5’-AGTTGTAATGGCAGGCACAGG-3’
cxcl1	Forward	5’-AGCCACACTCAAGAATGGTCG-3’
	Reverse	5’-AGTGTTGTCAGAAGCCAGCGT-3’
cxcl5	Forward	5’-GCGTTGTGTTTGCTTAACCGT-3’
	Reverse	5’-TCACAGGAGCTTCTGGATCCA-3’

GENE	DIRECTION	OLIGONUCLEOTIDE
cxcl12	Forward	5'-AACTGTTGAGCAGGTTGCGAT-3'
	Reverse	5'-CAAGCAACACCCTTCAAAGCT-3'
cyr61	Forward	5'-TGTGAAGTGCGTCCTTGTGG-3'
	Reverse	5'-AGGAGCCGCAGTATTTGGG-3'
dap	Forward	5'-GACAAAGCAACATGGGCCTC-3'
	Reverse	5'-CTTGCCGAGTTCTGCTAA-3'
dtr	Forward	5'-CTCCACCATCTCGGCTCAAT-3'
	Reverse	5'-CAAACCGATCCCTGCACTCT-3'
ephrA2	Forward	5'-AGGCCGAGCGCATCTTTAT-3'
	Reverse	5'-GTCAATCTTGGTGAACTGGCG-3'
ephrB3	Forward	5'-AGAGTAAAGGCATCGCCTCCA-3'
	Reverse	5'-TTGTGGTCTCAAACTCAGCCG-3'
ephrinA1	Forward	5'-TGACCGCCACATCGTCTTC-3'
	Reverse	5'-TGTGTATCGCTCCATGGCTG-3'
ephrinB2	Forward	5'-CGAAGTGGCCTTATTCGCAG-3'
	Reverse	5'-GGCCAGTGTGCTGAGAGACA-3'
epireg	Forward	5'-CCCACCAAATGCTCAACCTTA-3'
	Reverse	5'-TGATTGGTCCCTTGGCACTT-3'
fhl1	Forward	5'-AGCATAGGCGATAAAGCTCCC-3'
	Reverse	5'-ACCATGCATTCTGGCAAGTTC-3'
figf	Forward	5'-TCTTCAAGCCCCCCTGTGTA-3'
	Reverse	5'-ACAGGCACTAACTCGGGCAC-3'
gas1	Forward	5'-ATCTGCGAATCGGTCAAAGAGA-3'
	Reverse	5'-CGTCATATTCTTCGTCGTAGTAGTCGT-3'
gas2	Forward	5'-CTGCAAGTGCCCAACCAAGT-3'
	Reverse	5'-GAGCAGATAGCCAGCGAAGGT-3'
gas6	Forward	5'-CAGGAGCGACTGGACACACTT-3'
	Reverse	5'-GGTCCAGGATTTTCCCGTTT-3'
idb2	Forward	5'-GAAAGCCTTCAGTCCGGTGA-3'
	Reverse	5'-GGGCACCAGTTCCTTGAGC-3'
idb4	Forward	5'-CTGCAGTGCGATATGAACGAC-3'
	Reverse	5'-AGCAGGGTGAGTCTCCAGC-3'
ier3	Forward	TCGGATTATGCGCTGGATCT-3'
	Reverse	GCGTTGCCTTAGAAATCCCA-3'
igf2	Forward	5'-AGATACCCCGTGGGCAAGTT-3'
	Reverse	5'-GACGATGACGTTTGGCCTCT-3'
c-jun	Forward	5'-CCAAGTGCCGGAAAAGGAA-3'
	Reverse	5'-ACGTTTGCAACTGCTGCGTTA-3'
kif20A	Forward	5'-ATGCAGCCAAATTCTCAGCC-3'
	Reverse	5'-ACGTCAGCTTCGTCTTCAGGA-3'

GENE	DIRECTION	OLIGONUCLEOTIDE
lats2	Forward	5'-CCCCGAAGTTTGGACCTTATC-3'
	Reverse	5'-GCCATCTCCTGGTCACATCC-3'
mad4	Forward	5'-ACAGCTTCAGCGGGAACATC-3'
	Reverse	5'-ACAGCTTCAGCGGGAACATC-3'
msln	Forward	5'-AAGCTGACCGTCATACACCCA-3'
	Reverse	5'-CACAAGGTCCATTTGTCTGGC-3'
mt2	Forward	5'-TCCTGTGCCTCCGATGGAT-3'
	Reverse	5'-TGTCGGAAGCCTCTTTGCA-3'
mybl2	Forward	5'-GACAAAGCAACATGGGCCTC-3'
	Reverse	5'-CTTGCCGAGTTCTGCTAA-3'
c-myc	Forward	5'-CTCCACCATCTCGGCTCAAT-3'
	Reverse	5'-CAAACCGATCCCTGCACTCT-3'
nr4a1	Forward	5'-GGCAAACAAGGATTGCCCT-3'
	Reverse	5'-CTTGGGTTTTGAAGGTAGCCG-3'
ogn	Forward	5'-AATGCCCACATGCCTGTTGT-3'
	Reverse	5'-TGCAAAATCCTTGGCAGTCAG-3'
osf2	Forward	5'-TTCACGCTCTTTGCTCCCAC-3'
	Reverse	5'-CTCCTCCAGTGATGGCCTCA-3'
pdcd4	Forward	5'-GGACTCTGGCCGAGGAGACT-3'
	Reverse	5'-GCCTGCACCACCTTTCTTTG-3'
pdfgr α	Forward	5'-ATCACAGAGCTCCCTCGCC-3'
	Reverse	5'-ATCGCAGAGTGGGAGCCAC-3'
pdfgr β	Forward	5'-ATCGCGCCACCTTAATCAAC-3'
	Reverse	5'-CCCTCGCAGATGAGCACAT-3'
plaur	Forward	5'-TACACCCACTGCAATGGTGG-3'
	Reverse	5'-GGCACTGATTCATTGGTCCC-3'
plf1	Forward	5'-TCTTCAAGCCCCCCTGTGTA-3'
	Reverse	5'-ACAGGCACTAACTCGGGCAC-3'
plf2	Forward	5'-ATCTGCGAATCGGTCAAAGAGA-3'
	Reverse	5'-CGTCATATTCTTCGTCGTAGTAGTCGT-3'
plf3	Forward	5'-CCCTTCTTCGATTCAACCATG-3'
	Reverse	5'-TGAGACAAACTGCCGGCTAAT-3'
ptgs1	Forward	5'-CACAGTGCGGTCCAACCTTAT-3'
	Reverse	5'-CTGTTTCTTCCCTTTGGTCCC-3'
ptgs2	Forward	5'-TAGCCAGCAAAGCCTAGAGCA-3'
	Reverse	5'-TCGAAGTTCAGCCTGGCAA-3'
serp2	Forward	5'-ACATTGTGACCGTGGCCAA-3'
	Reverse	5'-GCCCCTGGTCTCATTTTTGAC-3'
six1	Forward	5'-AAAAAGCAGGTCATCGGAAGC-3'
	Reverse	5'-GATACATCATTTTGCCCCAGC-3'
snai2	Forward	5'-GATGCACATTCGAACCCACAC-3'
	Reverse	5'-CAGATGTGCCCTCAGGTTTGA-3'

GENE	DIRECTION	OLIGONUCLEOTIDE
sparc	Forward	5'-GCTGGATCAGCACCCTATTGA-3'
	Reverse	5'-TCCTGCTCCTTGATGCCAA-3'
sparcl1	Forward	5'-GACACCAACTGCAGCTGGAT-3'T
	Reverse	5'-CATTGAGATAGCCGCCATGTT-3'
tcf3	Forward	5'-TCGCCATCTCCAGCACACT-3'
	Reverse	5'-TCTTTGGGTCGATCTCTGGG-3'
thbd	Forward	5'-AGTGAGCCCCACCGACTACC-3'
	Reverse	5'-GCCTTCAGGGCATTCACAAA-3'
thbs2	Forward	5'-CAGCCTGGTCTTCATGCTCC-3'
	Reverse	5'-TCAATTGGGCACGGATCAC-3'
timp3	Forward	5'-GAGCTGTTGGAGCCTTGGG-3'
	Reverse	5'-GACCAGAGTGCCAAAGGGC-3'
tnc	Forward	5'-CGGAACTGAATATGGGATTGGT-3'
	Reverse	5'-TGTCGTCCAGAAAAACGTCAGA-3'
18S	Forward	5'-AACGAACGAGACTCTGGCATG-3'
	Reverse	5'-AATCTCGGGTGGCTGAACCG-3'

List 3. Antibodies used in this work

ANTIBODY	SOURCE	SPECIFICITY	DILUTION
Anti-AU5	Covance	Monoclonal	1:1000
Anti-CDK1	Santa Cruz	Monoclonal	1:500
Anti-Cox2	Abcam	Polyclonal	1:5000
Anti-cyclin A	Sigma	Monoclonal	1:1000
Anti- cyclin B	Sigma	Monoclonal	1:300
Anti- cyclin D1	Sigma	Monoclonal	1:1000
Anti-Dusp1	Santa Cruz	Polyclonal	1:200
Anti-HA	Covance	Polyclonal	1:1000
Anti-c-Jun	Santa Cruz	Polyclonal	1:200
Anti-kariofern α	Transduction Labs	Monoclonal	1:2500
Anti-Mcm2	Dr. J. Méndez (CNIO)	Polyclonal	1:1000
Anti-Mcm5	Dr. J. Méndez (CNIO)	Polyclonal	1:1000
Anti-Mcm7	Dr. J. Méndez (CNIO)	Polyclonal	1:1000
Anti-MLC	Cell Signaling	Monoclonal	1:500
Anti-MLC (phosphospecific)	Cell Signaling	Polyclonal	1:1000
Anti-Myc	Santa Cruz	Monoclonal	1:200
Anti-MYPT1	Transduction Labs	Monoclonal	1:500
Anti-MYPT1 (phosphospecific)	Upstate Biotechnology	Polyclonal	1:500
Anti-p53	Covance	Monoclonal	1:200
Anti-PDGFRα	Dr. E Santos (CIC)	Polyclonal	1:1000

ANTIBODY	SOURCE	SPECIFICITY	DILUTION
Anti-PLAUR	Santa Cruz	Polyclonal	1:500
Anti-Rad51	Dr. P. Sansegundo (CIC)	Monoclonal	1:1000
Anti-Rb (phosphospecific)	Cell Signaling	Polyclonal	1:1000
Anti-tubulin α	Oncogene	Monoclonal	1:1000

REFERENCES OF THIS ONLINE SECTION

Schuebel, KE, Movilla, N, Rosa, JL, Bustelo, XR (1998). Phosphorylation-dependent and constitutive activation of Rho proteins by wild-type and oncogenic Vav-2. *Embo J* **17**: 6608-6621.

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SUPPLEMENTARY INFORMATION-3

LEGENDS TO SUPPLEMENTARY FIGURES

LEGENDS TO SUPPLEMENTARY FIGURES

FIGURE S1. Biological properties of the Rho subfamily-transformed cells used in this study. **(a)** Transforming activity of RhoA^{Q63L}, RhoB^{Q63L} and Rho^{CQ63L} proteins in focus formation assays. **(b)** Phase-contrast microscopy images of NIH3T3 and transformed cell lines expressing the indicated GTPase. **(c)** Status of the F-actin cytoskeleton in the parental NIH3T3 cells and the transformed cell lines expressing the indicated GTPase. **(d)** Total cellular extracts from NIH3T3 and the indicated Rho-transformed cells were immunobloted with anti-phospho-MLC (upper panel), anti-MLC (middle panel) and anti-tubulin (lower panel) antibodies. p, phospho.

FIGURE S2. Histogram showing the number of up- (red) and down-regulated (blue) genes with a given expression fold change value in the Rho-dependent transcriptome compared to that of the parental cell line.

FIGURE S3. Immunoblot analysis showing the expression of the indicated proteins (left) in total cellular lysates derived from the indicated cell lines (top).

FIGURE S4. Activation of the E2F pathway in Rho-transformed cells. **(a)** Expression of the indicated proteins (left) in NIH3T3, RhoA^{Q63L}-, RhoB^{Q63L}-, and RhoC^{Q63L}-transformed cells. When indicated, lysates were obtained from two independent, exponentially growing cultures (that have been labeled as “1” and “2”). **(b)** Transactivation of E2F promoter activity in stable (left panel) and transiently transfected (right panel) cells, as described in Materials and Methods. In the left panel, the E2F reporter plasmid was transfected in

NIH3T3 or in the indicated transformed cells. In the right panel, NIH3T3 cells were transfected with the E2F reporter plasmid in the absence (Mock) or presence of vectors expressing the indicated oncoproteins. Values are expressed as fold change variations of luciferase activity respect to those found in the appropriate control sample (that was given an arbitrary value of 1) and represent the mean ± SD of four independent experiments each of them performed in triplicate. **(c)** Expression of the indicated E2F targets (left) in NIH3T3, RhoA^{Q63L}-, RhoB^{Q63L}-, and RhoC^{Q63L}-transformed cells.

FIGURE S5. Corroboration of Affymetrix data by quantitative RT-PCR. The expression levels of the indicated mRNAs were determined by either microarray (A) or quantitative RT-PCR (Q) experiments in RhoA^{Q63L}-transformed cells that were either left untreated (-) or treated (+) with Y27632 for 24 h. Values are expressed as fold change of the appropriate gene respect to the transcript levels found in untreated NIH3T3 cells.

FIGURE S6. **(a)** Determination of c-Myc (upper panel) and Cox2/ Ptgs2 (middle panel) protein levels by immunoblot analysis of total cellular lysates obtained from the indicated cell types (top) that were either untreated (-) or treated (+) with 10 μM Y27632 for 24 h (top panel). As a loading control, the same lysates were probed with anti-tubulin antibodies (lower panel). **(b)** Example of Y27632-regulated genes that are c-Myc-dependent (left panel) and independent (right panel). The expression levels of selected transcripts (bottom) were determined by quantitative RT-PCR in the indicated cell lines. As a control, transcript levels were also determined in RhoA^{Q63L}-transformed cells treated with the Y27632 inhibitor for 24 hr. **(c)** Immunoblot analysis showing the levels of c-Myc (upper panel) and tubulin (lower panel) proteins in total cellular lysates obtained from the indicated, exponentially growing cell lines (top).

FIGURE S7. Characterization of the c-Myc overexpressing cell lines used in this study. **(a)** Transactivation reporter assays showing the hyperactivation of the c-Myc route in c-Myc-expressing cells. The indicated cell lines (bottom) were transfected with a luciferase reporter plasmid containing a c-Myc-responsive promoter (pM4*luc*) and, after 48 h, levels of promoter activity were determined as indicated in Materials and Methods. Values are expressed as fold change variations of luciferase activity respect to that found in the parental NIH3T3 cell line (that was given an arbitrary value of 1) and represent the mean ± SD of three independent experiments each of them performed in triplicate. **(b)** Proliferation curve of c-Myc-expressing cells. The indicated cell lines were subjected to MTT assays as indicated in Materials and Methods. Values represent the mean of a representative experiment performed in triplicate. The arrow indicates the time point in which cells reached 100% confluency.

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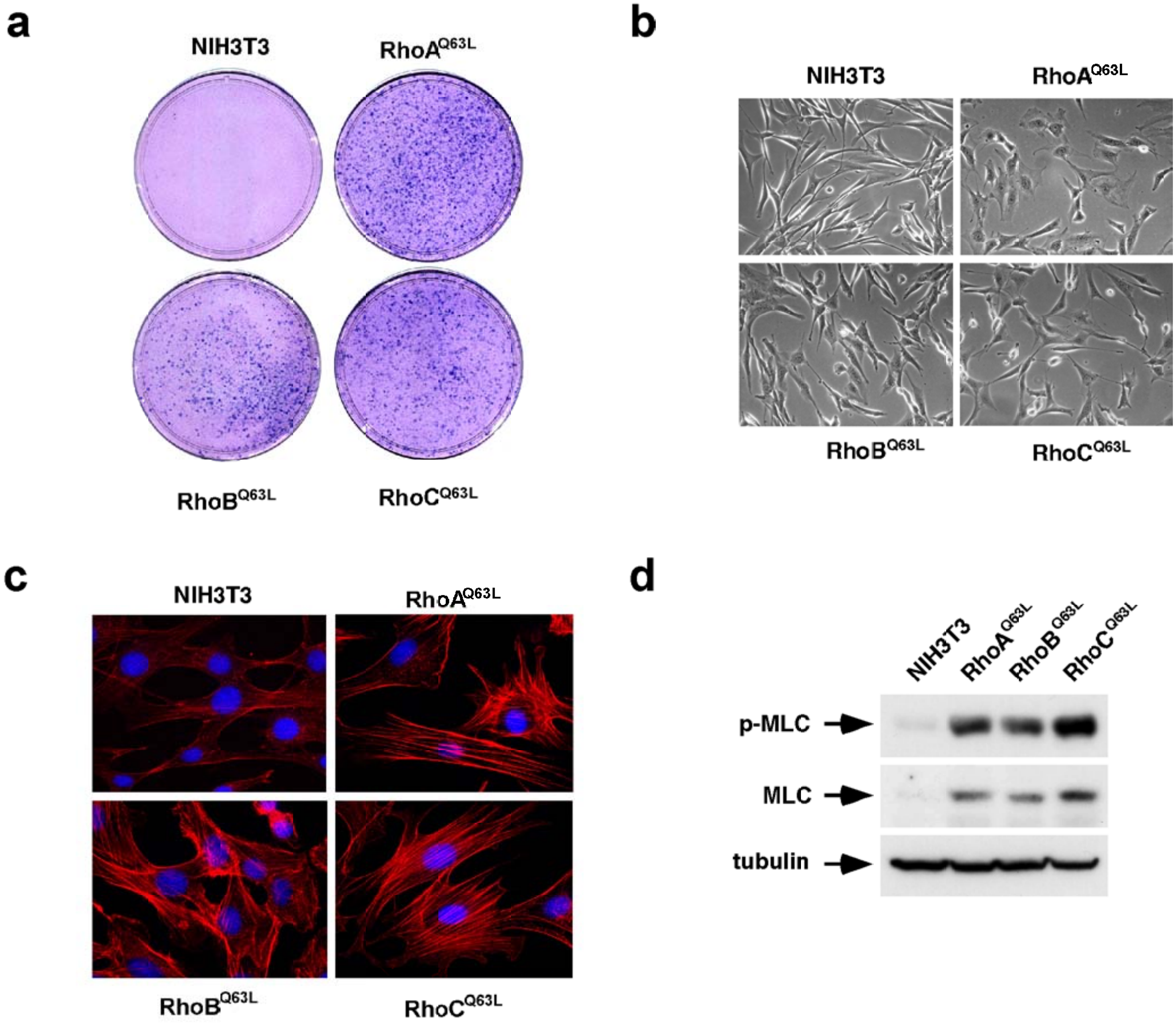
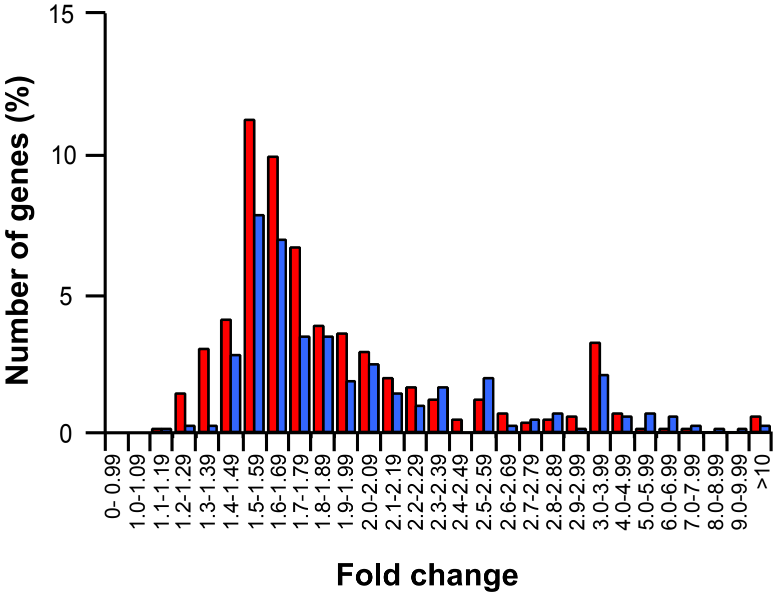
SUPPLEMENTARY INFORMATION-4

SUPPLEMENTARY FIGURES

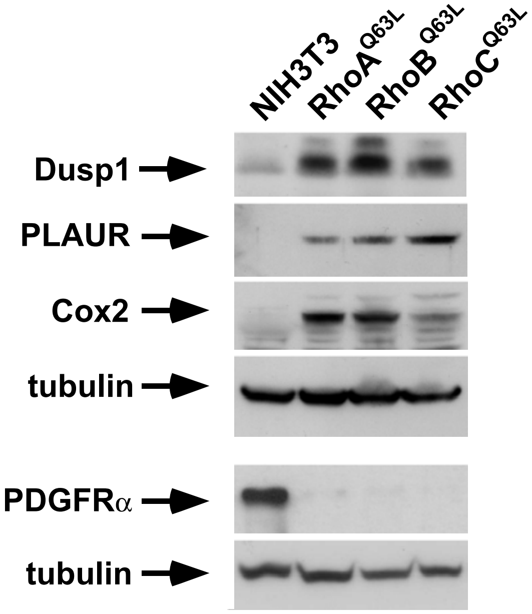
Berenjeno et al.
Figure S1



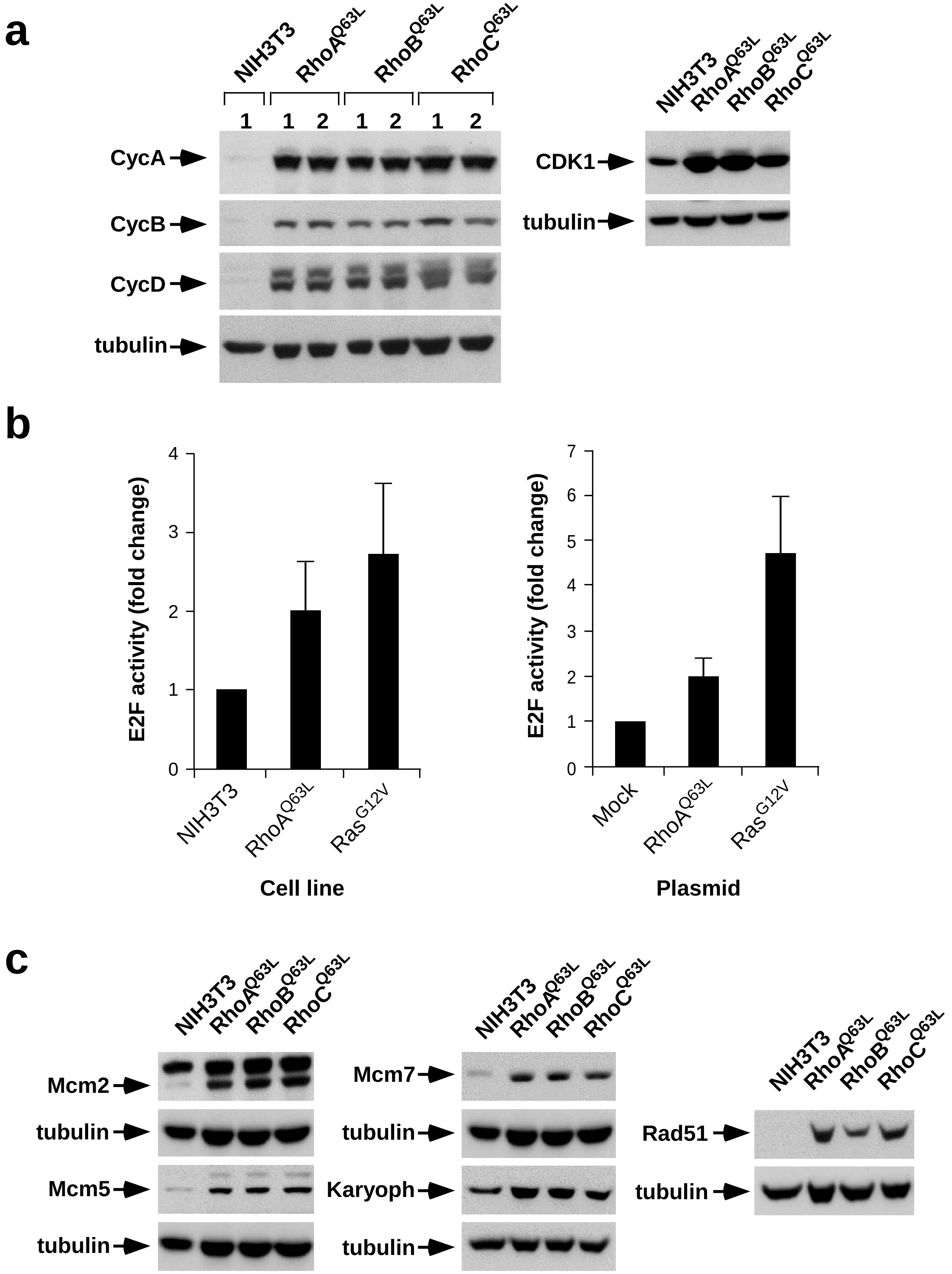
Berenjeno et al.
Figure S2



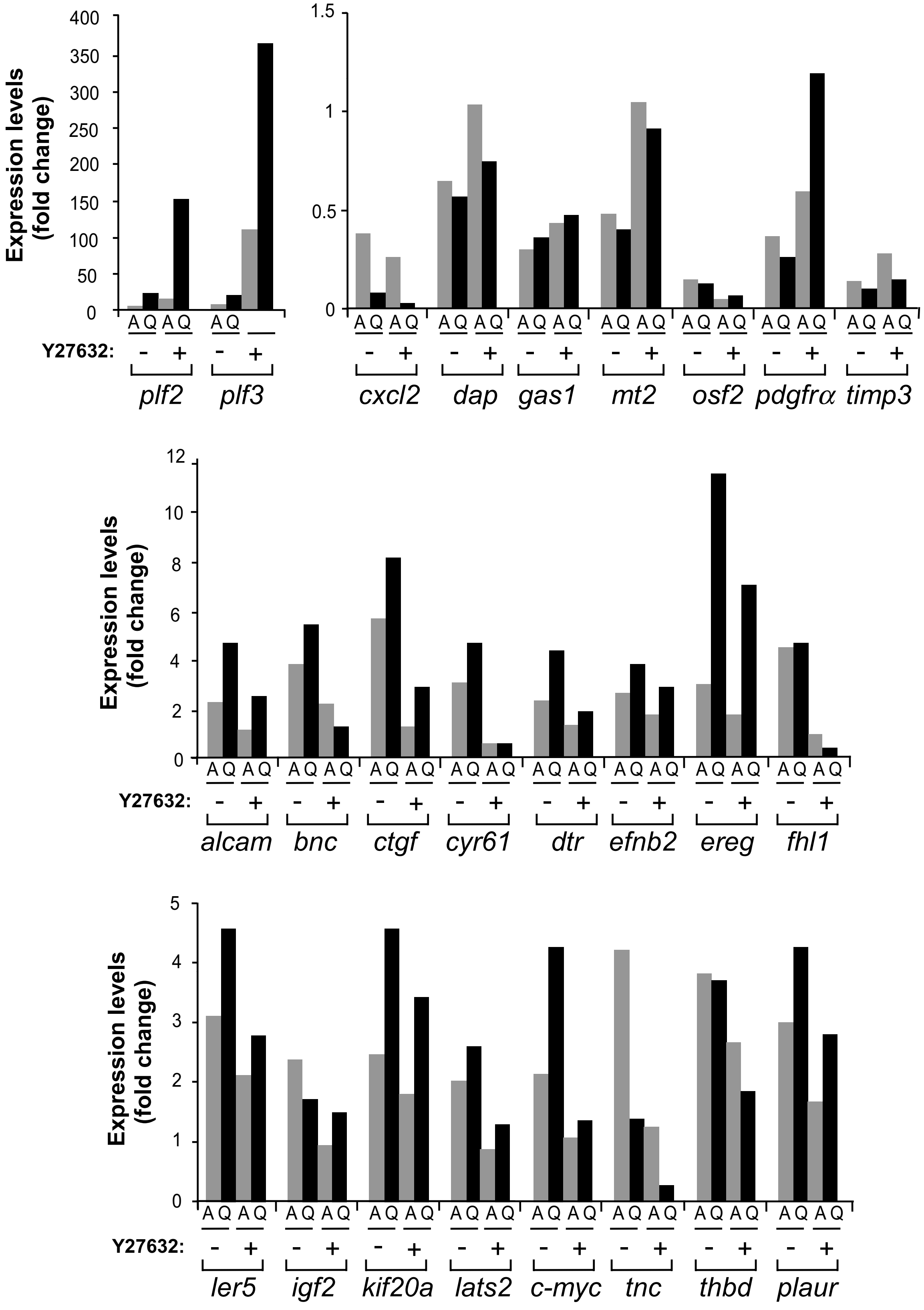
Berenjeno et al.
Figure S3



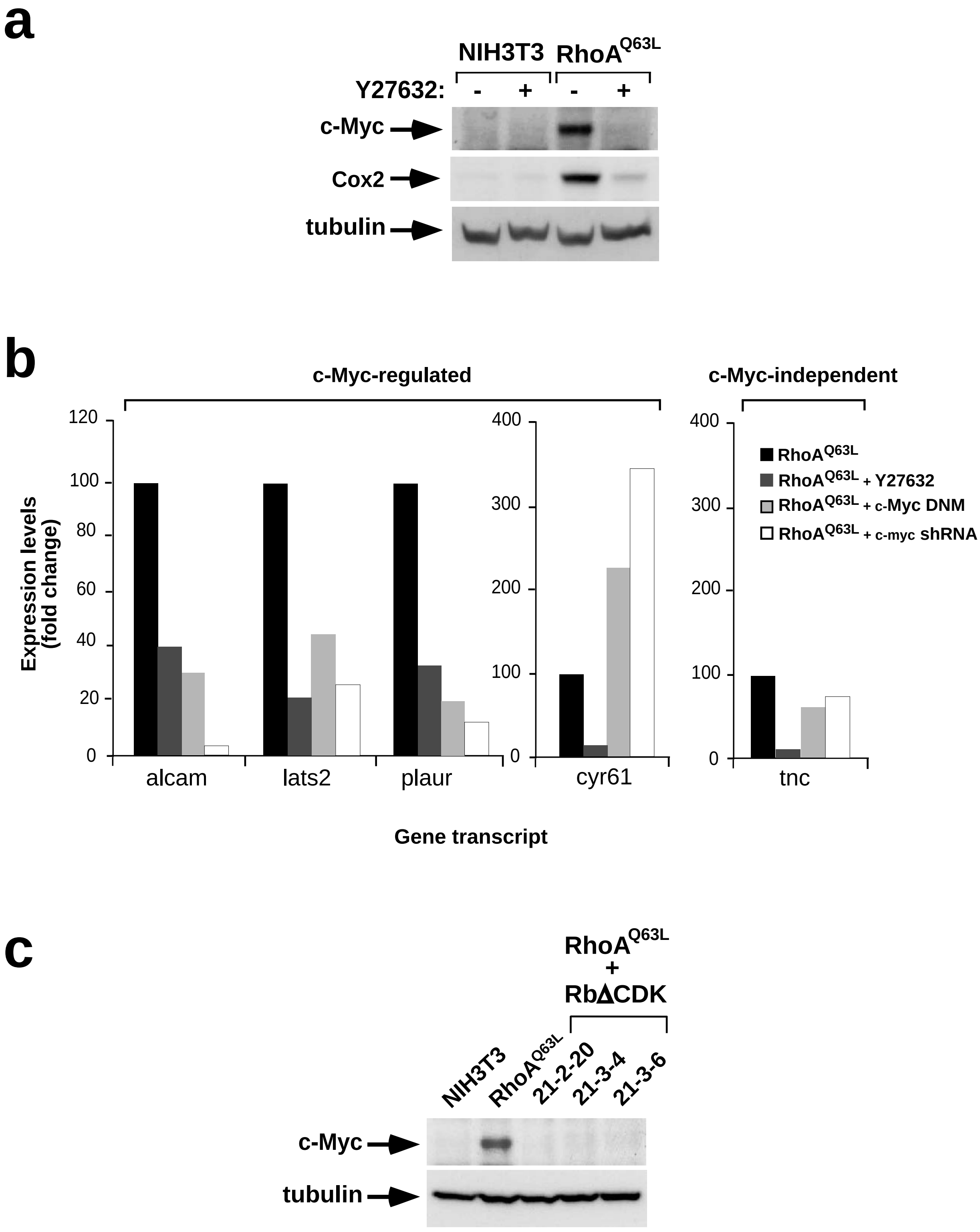
Berenjeno et al.
Figure S4



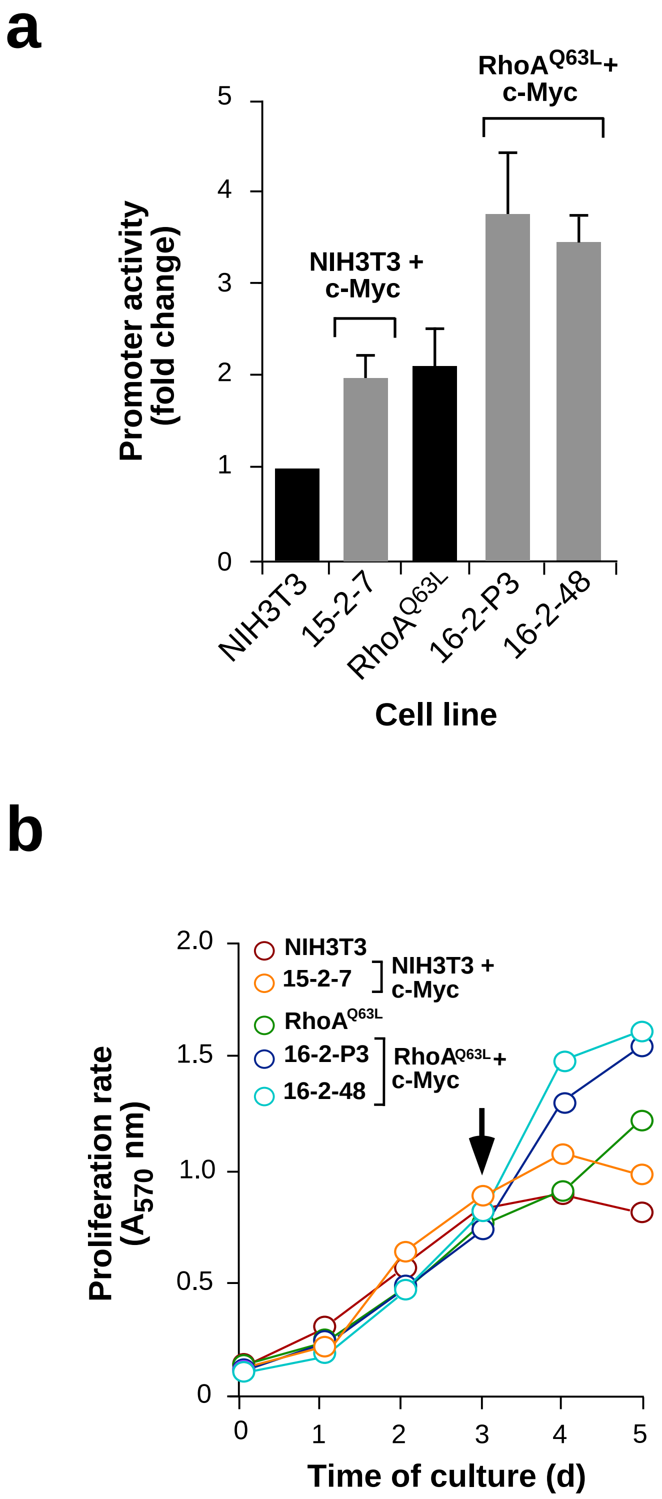
Berenjeno et al.
Figure S5



Berenjeno et al.
Figure S6



Berenjeno et al.
Figure S7



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SUPPLEMENTARY INFORMATION-5

SUPPLEMENTARY TABLES

Table S1. Rho-regulated genes determined by Affymetrix[a]

Function	Affy ID	Locus ID	Gene symbol	Description	Fold change[b]	p-value[c]
Extracellular	95158_at	12815	**Col11a2**	procollagen, type XI, alpha 2	1.66;1.61;1.62	8.6535e-06;3.1976e-05;3.1613e-05
Cell adhesion	103709_at	12842	**Col1a1**	procollagen, type I, alpha 1	0.63;0.49;0.6	4.8150e-06;7.3389e-09;1.7161e-06
	101130_at	12843	**Col1a2**	procollagen, type I, alpha 2	0.62;0.53;0.56	5.2383e-07;9.5689e-09;4.8811e-08
	161984_f_at	12825	**Col3a1**	procollagen, type III, alpha 1	0.49;0.41;0.32	3.9521e-07;1.6707e-08;1.3863e-10
	93220_at	12830	**Col4a5**	procollagen, type IV, alpha 5	0.5;0.49;0.51	9.1625e-12;1.1413e-11;5.1770e-11
	101080_at	12831	**Col5a1**	procollagen, type V, alpha 1	0.54;0.42;0.47	1.2244e-09;3.6022e-12;7.0395e-11
	162459_f_at	12833	**Col6a1**	procollagen, type VI, alpha 1	0.37;0.37;0.32	2.7044e-11;5.6861e-11;2.6320e-12
	93517_at	12834	**Col6a2**	procollagen, type VI, alpha 2	0.29;0.34;0.29	1.9136e-15;1.2602e-13;5.2094e-15
	101110_at	12835	**Col6a3**	procollagen, type VI, alpha 3	0.5;0.4;0.43	6.7455e-10;8.7644e-12;4.0416e-11
	100308_at	12837	**Col8a1**	procollagen, type VIII, alpha 1	1.67;1.71;1.76	1.2354e-06;1.3515e-06;5.8649e-07
	92777_at	16007	**Cyr61**	cysteine rich protein 61	2.95;1.75;2.68	1.6587e-07;0.0013042;1.3989e-06
	92852_at	14268	**Fn1**	fibronectin 1	0.73;0.64;0.82	1.296e-07;5.864e-10;0.00011902
	99010_at	26968	**Islr**	immunoglobulin superfamily containing leucine-rich repeat	0.65;0.64;0.64	1.8581e-09;2.0357e-09;2.4319e-09
	92366_at	16773	**Lama2**	laminin, alpha 2	0.5;0.45;0.47	2.0419e-06;4.3863e-07;1.0124e-06
	104587_at	16775	**Lama4**	laminin, alpha 4	0.32;0.33;0.32	4.3098e-09;1.3260e-08;9.9677e-09
	101359_at	16779	**Lamb2**	laminin, beta 2	0.4;0.36;0.42	5.7657e-09;1.5353e-09;2.3808e-08
	100428_at	16782	**Lamc2**	laminin, gamma 2	1.58;1.67;1.75	3.9991e-11;1.0370e-11;1.7617e-12
	93353_at	17022	**Lum**	lumican	0.42;0.49;0.47	5.6833e-10;4.3899e-08;1.4255e-08
	98475_at	17181	**Matn2**	matrilin 2	0.19;0.23;0.2	8.4601e-14;2.5681e-12;4.3941e-13
	93866_s_at	17313	**Mglap**	matrix gamma-carboxyglutamate (gla) protein	0.35;0.2;0.46	1.1442e-14;< 2.22e-16;1.2257e-11
	160118_at	17387	**Mmp14**	matrix metalloproteinase 14 (membrane-inserted)	0.55;0.68;0.75	1.0944e-07;8.8945e-05;0.0016156
	102953_at	56047	**Msln**	mesothelin	12.99;12.5;12.71	< 2.22e-16;< 2.22e-16;< 2.22e-16
	100120_at	18073	**Nid1**	nidogen 1	1.38;1.45;1.55	3.0231e-05;7.7861e-06;6.5347e-07
	103721_at	114249	**Npnt**	nephronectin	1.84;0.77;1	1.3170e-05;0.031481;0.995676

[a] Genes are classified into 19 different functional groups. The Affymetrix identification number (Affy ID), the locus identification number (Locus ID), the symbol and the description for each gene are shown.

Upregulated genes are shown in red and downregulated genes in blue

[b] Fold change in the expression levels compared to NIH3T3 cells. The first, second and third value corresponds to the expression levels obtained in RhoA^{Q63L}, RhoB^{Q63L} or RhoC^{Q63L} expressing cells, respectivelly.

Values not statistically significant are shown in black

[c] *P* -values determined with the F-statistic.The first, second and third value corresponds to the expression levels obtained in RhoA^{Q63L}, RhoB^{Q63L} or RhoC^{Q63L} expressing cells, respectivelly. The same colour code as in a and b is used

Function	Affy ID	Locus ID	Gene symbol	Description	Fold change	p-value
Extracellular	92593_at	50706	**Osf2**	osteoblast specific factor 2 (fasciclin I-like)	0.15;0.17;0.2	3.3611e-09;2.2447e-08;1.3050e-07
Cell adhesion	93981_at	18791	**Plat**	plasminogen activator, tissue	0.55;0.6;0.57	2.8644e-12;1.0508e-10;1.5721e-11
	94147_at	18787	**Serpine1**	serine (or cysteine) proteinase inhibitor, clade E, member 1	4.9;2.19;3.68	3.8098e-11;1.2708e-05;3.7970e-09
	97487_at	20720	**Serpine2**	serine (or cysteine) proteinase inhibitor, clade E, member 2	0.15;0.15;0.15	3.6452e-16;8.2546e-16;1.4285e-15
	160319_at	13602	**Sparcl1**	SPARC-like 1 (mast9, hevin)	0.35;0.37;0.33	1.4998e-11;1.4221e-10;1.4278e-11
	94930_at	21826	**Thbs2**	thrombospondin 2	0.18;0.39;0.4	1.0812e-08;0.00016432;0.00024442
	101464_at	21857	**Timp1**	tissue inhibitor of metalloproteinase 1	1.69;1.32;1.55	2.3659e-08;0.00037387;9.8859e-07
	160519_at	21859	**Timp3**	tissue inhibitor of metalloproteinase 3	0.14;0.22;0.17	1.9365e-15;1.3689e-12;4.3599e-14
	101993_at	21923	**Tnc**	tenascin C	4.24;1.35;2.43	< 2.22e-16;0.00025732;4.8885e-12
Immune response	95415_f_at	50909	**C1r**	complement component 1, r subcomponent	0.33;0.48;0.42	1.2624e-08;1.4808e-05;1.4772e-06
	103335_at	16859	**Lgals9**	lectin, galactose binding, soluble 9	0.57;0.56;0.68	1.4301e-09;2.0131e-09;1.8954e-06
	92731_at	19288	**Ptx3**	pentaxin related gene	0.17;0.13;0.17	< 2.22e-16;< 2.22e-16;< 2.22e-16
	102712_at	20210	**Saa3**	serum amyloid A 3	1.86;3.93;4.7	0.0002554;4.3627e-09;4.4500e-10
Ligand	102736_at	20296	**Ccl2**	chemokine (C-C motif) ligand 2	19.72;39.82;45.39	3.2765e-16;< 2.22e-16;< 2.22e-16
	94761_at	20306	**Ccl7**	chemokine (C-C motif) ligand 7	6.06;15.92;15.23	5.3387e-12;1.5477e-15;2.2014e-15
	98008_at	20312	**Cx3cl1**	chemokine (C-X3-C motif) ligand 1	0.62;0.49;0.5	1.0929e-06;1.9587e-09;4.4194e-09
	95348_at	14825	**Cxcl1**	chemokine (C-X-C motif) ligand 1	15.85;23.32;26.99	< 2.22e-16;< 2.22e-16;< 2.22e-16
	100112_at	20315	**Cxcl12**	chemokine (C-X-C motif) ligand 12	0.38;0.45;0.42	7.4791e-08;2.8338e-06;8.5527e-07
	98772_at	20311	**Cxcl5**	chemokine (C-X-C motif) ligand 5	18.84;42.48;37.19	< 2.22e-16;< 2.22e-16;< 2.22e-16
	93534_at	13179	**Dcn**	decorin	0.19;0.69;0.43	1.2224e-07;0.1243027;0.0012326
	99067_at	14456	**Gas6**	growth arrest specific 6	0.24;0.25;0.27	1.0374e-09;2.8577e-09;1.0553e-08
	103975_at	23893	**Grem2**	gremlin 2 homolog, cysteine knot superfamily (Xenopus laevis)	2.29;1.92;2.24	3.8945e-07;2.3012e-05;1.1242e-06
	103904_at	16012	**Igfbp6**	insulin-like growth factor binding protein 6	1.64;2;1.79	1.6195e-07;9.9714e-10;2.4210e-08
	97347_at	108075	**Ltbp4**	latent transforming growth factor beta binding protein 4	0.64;0.66;0.68	4.9118e-10;3.3674e-09;1.6565e-08
	93929_s_at	26421	**Mrpplf3**	mitogen regulated protein, proliferin 3	7.99;26.72;19.14	7.1335e-08;3.2896e-11;2.6731e-10
	104184_at	18158	**Nppb**	natriuretic peptide precursor type B	1.5;1.44;1.43	3.6441e-05;0.00019601;0.00024827
	94838_r_at	18811	**Plf**	proliferin	3.6;5.28;4.24	3.2443e-06;1.0639e-07;1.0158e-06
	93883_at	18812	**Plf2**	proliferin 2	4.68;12.51;9.72	1.0543e-07;2.6305e-11;2.0787e-10
	97519_at	20750	**Spp1**	secreted phosphoprotein 1	1.42;1.72;1.39	0.00928004;0.00031514;0.01784465

Function	Affy ID	Locus ID	Gene symbol	Description	Fold change	p-value
Extracellular	160469_at	21825	**Thbs1**	thrombospondin 1	1.52;0.58;1	0.00084988;7.4627e-05;0.98251916
	92782_at	21917	**Tmpo**	thymopoietin	1.64;1.65;1.5	2.2406e-05;3.1272e-05;0.00035676
	93188_at	50781	**Dkk3**	dickkopf homolog 3 (Xenopus laevis)	0.3;0.31;0.31	1.7288e-13;7.2931e-13;8.7559e-13
	102798_at	11535	**Adm**	adrenomedullin	1.89;1.64;1.81	4.0912e-09;5.9558e-07;2.8267e-08
	160971_at	107250	**Kazald1**	Kazal-type serine peptidase inhibitor domain 1	0.39;0.43;0.45	2.3912e-14;5.6005e-13;1.4655e-12
Other	96712_at	64075	**Smoc1**	SPARC related modular calcium binding 1	1.13;0.86;1.16	0.0030364;0.0010609;0.0007709
	96926_at	64074	**Smoc2**	SPARC related modular calcium binding 2	0.09;0.09;0.11	< 2.22e-16;5.0635e-16;2.5480e-15
Growth factor	102727_at	12064	**Bdnf**	brain derived neurotrophic factor	2.03;1.77;1.7	1.1240e-08;7.9944e-07;2.4193e-06
	93294_at	14219	**Ctgf**	connective tissue growth factor	5.57;1.95;2.99	2.2008e-08;0.0051919;3.7274e-05
	98802_at	13874	**Ereg**	epiregulin	2.93;2.21;1.93	2.9250e-12;2.5015e-09;6.5973e-08
	92365_at	14205	**Figf**	c-fos induced growth factor	0.18;0.27;0.24	1.2160e-09;2.8195e-07;8.2244e-08
	92738_at	14573	**Gdnf**	glial cell line derived neurotrophic factor	1.59;1.83;2.12	4.9002e-08;9.7175e-10;1.3973e-11
	93066_at	14824	**Grn**	granulin	0.48;0.76;0.86	9.4165e-08;0.012078;0.148130
	92730_at	15200	**Hbegf**	heparin-binding EGF-like growth factor	2.27;1.7;1.56	2.6118e-08;3.4829e-05;0.00026161
	98623_g_at	16002	**Igf2**	insulin-like growth factor 2	2.39;1.31;2	1.417e-05;0.11849290;0.00036781
	100277_at	16323	**Inhba**	inhibin beta-A	1.96;1.42;1.47	9.9861e-08;0.00091070;0.00034676
	102298_at	18049	**Ngfb**	nerve growth factor, beta	1.72;1.76;1.52	1.4433e-05;1.4601e-05;0.00051859
	160877_at	18295	**Ogn**	osteoglycin	0.09;0.1;0.08	2.1240e-15;1.9140e-14;2.4706e-15
	103520_at	22339	**Vegfa**	vascular endothelial growth factor A	1.67;1.48;1.82	3.8054e-07;3.3920e-05;6.1776e-08
	103001_at	22340	**Vegfb**	vascular endothelial growth factor B	0.6;0.91;0.84	1.0113e-06;0.249306;0.045929
Membranes	92414_at	11489	**Adam12**	a disintegrin and metalloproteinase domain 12 (meltrin alpha)	1.93;1.15;1.24	3.0819e-05;0.28868;0.11846
Plasma membrane	92357_at	23792	**Adam23**	a disintegrin and metalloprotease domain 23	0.61;0.57;0.62	6.1020e-10;9.0336e-11;2.7461e-09
Cell adhesion	11658	104407_a	**Alcam**	activated leukocyte cell adhesion molecule	2.21;1.63;1.06	4.8308e-05;0.007017;0.718930
	160271_at	71668	**Apr-03**	apoptosis related protein ARP3	0.43;0.55;0.55	1.5963e-10;1.7711e-07;1.8199e-07
	102327_at	11754	**Aoc3**	amine oxidase, copper containing 3	0.39;0.34;0.38	4.0091e-08;7.5461e-09;5.1364e-08
	102248_f_at	12361	**Cask**	calcium/calmodulin-dependent serine protein kinase	0.69;0.73;0.62	3.4591e-07;6.2644e-06;8.5441e-09
	97930_f_at	12476	**Cd151**	CD151 antigen	1.67;1.56;1.55	2.3730e-09;6.3082e-08;7.0755e-08
	103005_s_a	12505	**Cd44**	CD44 antigen	3.07;2.69;2.89	6.2525e-14;2.0850e-12;5.0465e-13
	103611_at	16423	**Cd47**	CD47 antigen	0.47;0.74;0.64	6.2859e-07;0.0162053;0.0010580

Function	Affy ID	Locus ID	Gene symbol	Description	Fold change	p-value
Membranes	101560_at	13723	**Emb**	embigin	0.24;0.26;0.25	1.1895e-14;1.0423e-13;5.4760e-14
Plasma membrane	104614_at	14733	**Gpc1**	glypican 1	1.79;1.54;1.53	5.7515e-09;1.8012e-06;2.2419e-06
Cell adhesion	102886_at	14735	**Gpc4**	glypican 4	0.5;0.52;0.48	1.8038e-11;1.2639e-10;1.7233e-11
	100759_at	17534	**Mrc2**	mannose receptor, C type 2	0.66;0.68;0.73	9.4921e-08;6.2691e-07;9.5466e-06
	102663_at	18793	**Plaur**	urokinase plasminogen activator receptor	3.02;2;2.41	8.8317e-13;1.6303e-08;1.9827e-10
	104256_at	227929	**Pscdbp**	pleckstrin homology, Sec7 and coiled-coil domains, binding protein	1.27;1.57;1.3	0.00040125;1.7834e-07;0.00030620
	103804_at	53614	**Reck**	reversion-inducing-cysteine-rich protein with kazal motifs	0.46;0.52;0.51	2.2025e-10;1.2880e-08;8.4339e-09
	102623_at	20350	**Sema3f**	semaphorin 3 F	0.58;0.59;0.58	1.4815e-08;8.2706e-08;3.7262e-08
	96766_s_at	22174	**Tyro3**	TYRO3 protein tyrosine kinase 3	1.33;1.53;1.47	3.6895e-06;9.8207e-09;4.7676e-08
	101993_at	21923	**Tnc**	tenascin C	4.24;1.35;2.43	< 2.22e-16;0.00025732;4.8885e-12
Channel-Transporter	92428_at	56495	**Asna1**	arsA (bacterial) arsenite transporter, ATP-binding, homolog 1	1.41;1.48;1.52	1.4205e-08;2.4203e-09;6.4750e-10
	99579_at	11933	**Atp1b3**	ATPase, Na+/K+ transporting, beta 3 polypeptide	1.59;1.56;1.65	8.6489e-13;4.3771e-12;3.7823e-13
	93330_at	11826	**Aqp1**	aquaporin 1	2.31;3.75;4.03	2.0867e-06;2.0822e-09;7.6773e-10
	92445_at	12286	**Cacna1a**	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit	0.63;0.64;0.7	1.8843e-07;6.5224e-07;1.4835e-05
	101441_i_at	16442	**Itpr2**	inositol 1,4,5-triphosphate receptor 2	0.42;0.62;0.47	1.0278e-07;0.00065248;1.6525e-06
	104460_at	12291	**Cacna1g**	calcium channel, voltage-dependent, T type, alpha 1G subunit	0.66;0.55;0.62	8.6320e-09;1.6907e-11;1.9831e-09
	93705_at	11443	**Chrnb1**	cholinergic receptor, nicotinic, beta polypeptide 1 (muscle)	1.69;1.59;1.81	1.1501e-12;3.6083e-11;2.0945e-13
	102786_at	12725	**Clcn3**	chloride channel 3	1.76;1.71;1.51	4.1010e-12;2.8277e-11;4.7588e-09
	104652_at	16526	**Kcnk2**	potassium channel, subfamily K, member 2	1.49;1.56;1.61	8.2934e-08;3.0311e-08;8.9802e-09
	95586_at	18438	**P2rx4**	purinergic receptor P2X, ligand-gated ion channel 4	0.47;0.75;0.74	3.2470e-07;0.014600;0.013369
	100951_at	18764	**Pkd2**	polycystic kidney disease 2	0.44;0.47;0.42	2.0114e-11;2.7565e-10;1.5615e-11
	104451_at	18174	**Slc11a2**	solute carrier family 11, member 2	1.43;1.72;1.82	1.8326e-06;3.7213e-09;6.5271e-10
	99500_at	20496	**Slc12a2**	solute carrier family 11, member 2	0.52;0.57;0.54	1.2888e-08;4.0296e-07;6.8034e-08
	92582_at	20514	**Slc1a7**	solute carrier family 1, member 7	0.65;0.57;0.63	0.00017185;1.0428e-05;9.5481e-05
	95571_at	22785	**Slc30a4**	solute carrier family 30 (zinc transporter), member 4	1.7;1.86;1.58	2.1570e-08;2.6108e-09;4.9954e-07
	103527_at	103710	**Slc35e4**	solute carrier family 35, member E4	1.83;1.7;1.73	1.5707e-15;5.5595e-14;3.3477e-14
	94433_at	67760	**Slc38a2**	solute carrier family 38, member 2	0.64;0.6;0.6	1.6604e-05;4.3306e-06;3.2893e-06
	99445_at	68682	**Slc44a2**	solute carrier family 44, member 2	0.61;0.68;0.65	4.9437e-06;0.00019027;5.3829e-05
	54403	98457_at	**Slc4a4**	solute carrier family 4 (anion exchanger), member 4	1.54;1.41;1.19	1.0420e-06;3.8273e-05;0.01983

Function	Affy ID	Locus ID	Gene symbol	Description	Fold change	p-value
Membranes	93454_at	17064	**C1qr1**	complement component 1, q subcomponent, receptor 1	1.71;1.46;1.77	9.3130e-11;1.2365e-07;7.0702e-11
Plasma membrane	100600_at	12484	**Cd24a**	CD24a antigen	0.34;0.08;0.28	3.7674e-14;< 2.22e-16;1.9236e-15
Immune response	93174_at	102657	**Cd276**	CD276 antigen	0.62;0.69;0.74	2.2891e-06;0.00014260;0.00122836
	160253_at	66141	**Fgls**	fragilis	0.56;0.71;0.63	4.2852e-06;0.00295734;0.00013444
	101886_f_at	14964	**H2-D1**	histocompatibility 2, D region locus 1	1.24;1.46;1.68	0.00048772;5.0923e-07;2.4914e-09
	98472_at	15040	**H2-T23**	histocompatibility 2, T region locus 23	0.48;0.95;0.82	8.3716e-07;0.64705;0.10109
	93874_s_at	16158	**Il11ra2**	interleukin 11 receptor, alpha chain 2	0.23;0.31;0.29	2.0847e-13;6.4075e-11;1.9380e-11
	99991_at	16172	**Il17r**	interleukin 17 receptor	0.64;0.68;0.7	3.8190e-07;5.5271e-06;1.9021e-05
	98500_at	17082	**Il1rl1**	interleukin 1 receptor-like 1	3.17;3.51;3.38	5.3829e-10;2.3544e-10;4.3548e-10
	94776_f_at	16635	**Klra4**	killer cell lectin-like receptor, subfamily A, member 4	2.51;2.12;1.95	1.0563e-10;1.0090e-08;7.7322e-08
	93078_at	110454	**Ly6a**	lymphocyte antigen 6 complex, locus A	0.53;0.85;1.04	1.2384e-05;0.20218;0.71851
	103258_at	17076	**Ly75**	lymphocyte antigen 75	1.77;1.47;1.46	1.3867e-06;0.00036797;0.00046235
	102649_s_a	19370	**Raet1c**	retinoic acid early transcript gamma	1.42;1.53;1.66	4.1338e-06;3.8887e-07;2.2230e-08
	100154_at	21356	**Tapbp**	Tap binding protein	0.5;0.88;0.8	1.1807e-06;0.256327;0.050242
Ligand	160857_at	13642	**Efnb2**	ephrin B2	2.54;2.32;1.7	2.9731e-08;3.2824e-07;0.00018397
Receptor activity	97733_at	11541	**Adora2b**	adenosine A2b receptor	1.68;1.76;1.93	6.1353e-12;2.5327e-12;1.1185e-13
	94934_at	11609	**Agtr2**	angiotensin II receptor, type 2	0.16;0.2;0.14	4.5468e-12;1.3460e-10;1.6789e-12
	95020_at	71587	**Cd47**	CD47 antigen (Rh-related antigen, integrin-associated signal transducer)	0.45;0.68;0.64	2.0462e-07;0.00279598;0.00084421
	93430_at	12778	**Cmkor1**	chemokine orphan receptor 1	3.56;2.62;2.2	1.1838e-10;4.1954e-08;1.0792e-06
	100435_at	14745	**Edg2**	endothelial differentiation, lysophosphatidic acid G-protein-coupled receptor, 2	0.51;0.63;0.53	3.7466e-09;3.5529e-06;2.4619e-08
	103980_at	13836	**Epha2**	Eph receptor A2	1.9;1.65;1.71	9.0675e-12;2.4336e-09;7.8530e-10
	95313_at	14062	**F2r**	coagulation factor II (thrombin) receptor	0.71;0.65;0.78	0.00023326;2.6224e-05;0.00548098
	97509_f_at	14182	**Fgfr1**	Fibroblast growth factor receptor 1	0.58;0.97;1.02	3.8189e-06;0.71358;0.79883
	93090_at	14183	**Fgfr2**	fibroblast growth factor receptor 2	0.6;0.58;0.62	1.1514e-08;1.1332e-08;1.0514e-07
	161040_at	14362	**Fzd1**	frizzled homolog 1 (Drosophila)	0.53;0.58;0.57	5.2194e-08;1.2288e-06;7.8724e-07
	99108_s_at	14600	**Ghr**	growth hormone receptor	0.71;0.64;0.79	0.00292282;0.00050885;0.03802902
	99160_s_at	66168	**Grina**	glutamate receptor, ionotropic, N-methyl D-asparate-associated protein 1	0.42;0.62;0.76	7.4826e-07;0.0016845;0.0467210
	104435_at	242050	**Igsf10**	immunoglobulin superfamily, member 10	0.42;0.45;0.49	9.1413e-13;9.5842e-12;7.1809e-11
	94345_at	71317	**Il6st**	interleukin 6 signal transducer	0.54;0.73;0.65	5.0875e-07;0.00322937;0.00015192
	95511_at	16403	**Itga6**	integrin alpha 6	1.76;1.79;1.23	3.1527e-06;4.1831e-06;0.047507

Function	Affy ID	Locus ID	Gene symbol	Description	Fold change	p-value
Membranes	160095_at	16948	**Lox**	lysyl oxidase	0.42;0.35;0.45	3.8515e-13;1.5613e-14;4.6066e-12
Plasma membrane	103271_at	16974	**Lrp6**	low density lipoprotein receptor-related protein 6	0.51;0.51;0.48	2.9423e-08;4.0671e-08;8.6306e-09
Receptor activity	97711_at	319900	**Npr3**	natriuretic peptide receptor 3	0.42;0.36;0.34	1.6366e-05;3.2853e-06;1.9669e-06
	102255_at	18414	**Osmr**	oncostatin receptor	0.68;0.58;0.72	0.00096093;3.3678e-05;0.00540438
	95079_at	18595	**Pdgfra**	platelet derived growth factor receptor, alpha polypeptide	0.37;0.53;0.4	3.5602e-10;1.9803e-06;3.8701e-09
	160867_at	18596	**Pdgfrb**	platelet derived growth factor receptor, beta polypeptide	0.3;0.34;0.44	8.0039e-12;1.7108e-10;1.7713e-08
	96662_at	68448	**Ppap2b**	phosphatidic acid phosphatase type 2B	0.49;0.45;0.46	2.2888e-07;6.1227e-08;7.8434e-08
	98018_at	19124	**Procr**	protein C receptor, endothelial	1.65;1.63;1.75	6.0113e-07;1.5948e-06;1.7443e-07
	103362_at	19219	**Ptger4**	phosphotriesterase related	1.79;1.38;1.37	4.8594e-08;0.00032118;0.00042746
	101932_at	19267	**Ptpre**	protein tyrosine phosphatase, receptor type, E	1.38;1.48;1.63	1.1871e-06;9.7964e-08;2.0210e-09
	99933_at	19294	**Pvrl2**	poliovirus receptor-related 2	1.39;1.4;1.63	3.2487e-06;4.6883e-06;1.1675e-08
	104423_at	76843	**Ramp**	retinoic acid-regulated nuclear matrix-associated protein	1.99;1.94;1.75	9.6417e-06;2.9775e-05;0.00022334
	93503_at	20319	**Sfrp2**	secreted frizzled-related sequence protein 2	0.15;0.15;0.15	4.0426e-13;1.1375e-12;1.1715e-12
	99610_at	268996	**Ss18**	synovial sarcoma translocation, Chromosome 18	1.51;1.29;1.35	3.0934e-06;0.00146876;0.00024708
	94643_at	21332	**Taa1**	tumor-associated antigen 1	1.56;1.51;1.91	4.1432e-07;2.3913e-06;1.3307e-09
	104601_at	21824	**Thbd**	thrombomodulin	3.84;2.86;3.65	2.3096e-12;7.2315e-10;1.2037e-11
	98304_at	21899	**Tlr6**	toll-like receptor 6	0.65;0.62;0.67	7.1843e-09;2.2128e-09;4.6808e-08
	102887_at	18383	**Tnfrsf11b**	tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin)	0.62;0.57;0.61	4.2540e-08;8.5958e-09;7.6442e-08
	103957_at	22042	**Trfr**	transferrin receptor	3.49;2.52;2.69	1.1594e-11;8.3820e-09;2.3970e-09
Receptor binding	160320_at	20411	**Sorbs1**	sorbin and SH3 domain containing 1	1.82;1.15;1.38	0.00016606;0.30982869;0.02911455
Signal transducer activity	93498_s_at	11804	**Aplp2**	amyloid beta (A4) precursor-like protein 2	0.47;0.53;0.57	2.1236e-07;4.1639e-06;2.5069e-05
	99598_g_at	14678	**Gnai2**	guanine nucleotide binding protein, alpha inhibiting 2	0.65;0.8;0.78	1.1448e-06;0.0035726;0.0015992
	96865_at	17118	**Marcks**	myristoylated alanine rich protein kinase C substrate	0.25;0.24;0.21	7.5409e-12;1.1258e-11;1.4668e-12
	102395_at	18858	**Pmp22**	peripheral myelin protein	0.15;0.22;0.2	2.5425e-16;5.0655e-14;1.5998e-14
	100607_at	18807	**Pld3**	phospholipase D3	0.49;0.6;0.62	1.3060e-08;3.8685e-06;1.1478e-05
	92309_i_at	19274	**Ptprm**	protein tyrosine phosphatase, receptor type, M	0.46;0.47;0.5	3.1944e-09;9.9684e-09;3.4540e-08
	92871_at	20338	**Sel1h**	Sel1 (suppressor of lin-12) 1 homolog (C. elegans)	0.62;0.66;0.63	3.4418e-06;4.1084e-05;1.1992e-05
	99057_at	21838	**Thy1**	thymus cell antigen 1, theta	1.54;1.08;1.37	1.1915e-07;0.19915;2.4894e-05

Function	Affy ID	Locus ID	Gene symbol	Description	Fold change	p-value
Membranes	95531_at	319434	**Amot**	angiomotin	0.53;0.45;0.52	7.1799e-08;2.1845e-09;8.9984e-08
Plasma membrane	96037_at	55950	**Bri3**	brain protein I3	0.63;0.91;0.91	1.9904e-06;0.21753;0.23279
Other	101047_at	66478	**Cd99**	CD99 antigen	0.61;0.71;0.78	3.1590e-08;2.3602e-05;0.00085775
	100064_f_at	14609	**Gja1**	gap junction membrane channel protein alpha 1	4.68;3.61;3.12	2.4259e-09;1.3027e-07;8.9438e-07
	101123_at	16432	**Itm2b**	integral membrane protein 2B	0.43;0.6;0.54	4.8606e-10;3.6263e-06;2.9641e-07
	96283_at	64294	**Itm2c**	integral membrane protein 2C	0.6;0.74;0.78	8.9904e-11;2.5230e-06;2.8265e-05
	97885_at	65963	**Lr8**	LR8 protein	1.31;1.92;1.93	0.0016063;2.4227e-08;1.9217e-08
	104523_at	100604	**Lrrc8c**	leucine rich repeat containing 8 family, member C	2.1;1.63;1.66	4.4635e-10;1.3039e-06;6.7045e-07
	100633_at	67247	**Mosc2**	MOCO sulphurase C-terminal domain containing 2	0.46;0.64;0.61	2.3729e-09;2.2456e-05;6.7897e-06
	94047_at	56700	**NCU-G1**	Kidney predominant protein NCU-G1	0.62;0.9;1	7.4868e-06;0.22294;0.96271
	102839_at	22038	**Plscr1**	phospholipid scramblase 1	1.37;2;1.98	3.6234e-06;5.1811e-12;7.6045e-12
	160373_i_at	20324	**Sdpr**	serum deprivation response	3.58;3.05;3.37	2.4476e-16;1.1490e-14;1.7535e-15
	95387_f_at	20352	**Sema4b**	semaphorin 4B	1.51;1.74;1.49	2.3748e-06;3.9538e-08;6.4274e-06
	103078_at	232086	**TM6P1**	fasting-inducible integral membrane protein TM6P1	0.42;0.55;0.65	5.6158e-09;4.7544e-06;0.00023151
	103402_at	67623	**Tm7sf3**	transmembrane 7 superfamily member 3	0.48;0.58;0.54	5.5420e-10;1.7156e-07;3.1307e-08
	100039_at	56530	**Tmem4**	transmembrane protein 4	0.65;0.76;0.75	2.8418e-07;0.00030185;0.00012958
	100477_at	56277	**Tmem45a**	transmembrane protein 45a	0.48;0.62;0.51	2.9436e-10;9.6571e-07;4.2276e-09
	95477_at	76287	**Tmem59**	transmembrane protein 59	0.64;0.73;0.72	1.5247e-05;0.00100594;0.00060083
	95137_at	69071	**Tmem97**	transmembrane protein 97	1.93;1.42;1.53	4.5659e-10;2.8875e-05;1.7368e-06
Mitochondrial membrane	97472_at	20524	**Slc25a17**	solute carrier family 25, member 17	0.59;0.57;0.52	8.8216e-12;5.3968e-12;2.4820e-13
	96849_at	30058	**Timm8a**	chloride intracellular channel 4 (mitochondrial)	3.29;2.96;2.44	2.6034e-09;3.0126e-08;7.6950e-07
	95441_at	53600	**Timm23**	translocase of inner mitochondrial membrane 23 homolog (yeast)	1.52;1.42;1.36	7.0124e-08;2.4525e-06;1.2624e-05
	160653_at	53333	**Tomm40**	translocase of outer mitochondrial membrane 40 homolog (yeast)	1.6;1.47;1.42	4.7284e-09;3.2255e-07;1.3076e-06
	95432_f_at	28185	**Tomm70a**	translocase of outer mitochondrial membrane 70 homolog A (yeast)	1.54;1.3;1.16	1.4928e-06;0.0011160;0.0465923
Nuclear membrane	101083_s_a	114584	**Clic1**	chloride intracellular channel 1	1.63;1.72;1.69	2.5406e-07;8.1238e-08;1.4025e-07
	160890_at	98386	**Lbr**	lamin B receptor	1.56;1.35;1.23	4.5351e-05;0.0033662;0.0390313
	93046_at	69508	**Nup50**	nucleoporin 50	1.5;1.32;1.22	8.606e-06;0.0011536;0.0117265
	160167_at	18226	**Nup62**	nucleoporin 62	1.54;1.49;1.38	5.8644e-09;5.5332e-08;1.5223e-06
	102412_at	103468	**Nup107**	nucleoporin 107	1.58;1.43;1.32	1.6684e-07;1.2493e-05;0.00026259

Function	Affy ID	Locus ID	Gene symbol	Description	Fold change	p-value
Nuclear membrane	98975_at	71805	**Nup93**	nucleoporin 93	1.91;1.88;1.62	5.6049e-06;1.4348e-05;0.00032123
Cytoskeleton	103574_at	226251	**Ablim1**	actin-binding LIM protein 1	0.35;0.47;0.42	1.6755e-09;9.5934e-07;1.3626e-07
	100381_at	11459	**Acta1**	actin, alpha 1, skeletal muscle	1.9;1.26;1.67	4.1831e-06;0.05085172;0.00014500
	95705_s_at	11461	**Actb**	actin, beta, cytoplasmic	0.39;0.66;0.56	4.7122e-05;0.046135;0.007920
	93102_f_at	11468	**Actg2**	actin, gamma 2, smooth muscle, enteric	1.68;1.02;1.26	3.731e-05;0.884285;0.040829
	95659_at	56456	**Actl6a**	actin-like 6A	1.99;1.86;1.67	1.5282e-06;1.1439e-05;0.00013121
	104578_f_at	109711	**Actn1**	actinin, alpha 1	1.52;1.32;1.41	3.3192e-07;0.00016254;1.3289e-05
	96343_at	60595	**Actn4**	actinin alpha 4	1.76;1.4;1.34	6.3861e-08;0.00017703;0.00072491
	98476_at	11735	**Ank3**	ankyrin 3, epithelial	0.61;0.59;0.48	7.8937e-10;5.2048e-10;9.7272e-13
	96784_at	68743	**Anln**	anillin, actin binding protein	3.12;3.01;2.57	5.8447e-07;1.7841e-06;1.6002e-05
	102632_at	12316	**Calmbp1**	calmodulin binding protein 1	1.55;1.63;1.55	0.0018509;0.0010772;0.0025617
	160106_at	12332	**Capg**	capping protein (actin filament), gelsolin-like	1.22;1.79;1.64	0.00092273;1.7753e-10;3.7437e-09
	97549_at	12632	**Cfl2**	cofilin 2, muscle	2.08;1.95;1.93	4.5844e-11;5.9359e-10;8.1621e-10
	104322_at	80986	**Ckap2**	cytoskeleton associated protein 2	2.16;2.11;2.06	4.2995e-06;1.1430e-05;1.8293e-05
	160150_f_at	71994	**Cnn3**	calponin 3, acidic	0.69;0.65;0.64	1.7754e-05;4.0155e-06;2.5305e-06
	98107_at	23790	**Coro1c**	coronin, actin binding protein 1C	1.44;1.52;1.42	6.0801e-11;8.4057e-12;3.2078e-10
	92608_at	13007	**Csrp1**	cysteine and glycine-rich protein 1	0.71;0.63;0.9	5.7313e-05;1.6046e-06;0.14028
	94299_at	69654	**Dctn2**	dynactin 2	0.65;0.79;0.81	3.6275e-06;0.0031723;0.0076335
	100472_at	17987	**Enah**	enabled homolog (Drosophila)	0.59;0.71;0.61	5.8579e-08;7.9910e-05;3.2683e-07
	95637_at	286940	**Flnb**	filamin, beta	1.83;1.47;1.87	1.9902e-08;3.1897e-05;2.3262e-08
	92838_at	14086	**Fscn1**	fascin homolog 1, actin bundling protein (Strongylocentrotus) purpuratus	0.6;0.64;0.62	7.1422e-09;1.4386e-07;7.2841e-08
	96869_at	56486	**Gabarap**	gamma-aminobutyric acid receptor associated protein	0.42;0.63;0.65	2.8889e-09;7.6758e-05;0.00022146
	94813_at	14451	**Gas1**	growth arrest specific 1	0.3;0.36;0.27	5.7029e-15;7.0592e-13;3.8083e-15
	94338_g_at	14453	**Gas2**	growth arrest specific 2	0.61;0.52;0.46	0.00025001;1.5063e-05;9.6512e-07
	93750_at	227753	**Gsn**	gelsolin	0.6;0.68;0.73	7.5197e-10;3.1229e-07;4.4329e-06
	94826_at	16418	**Itgb4bp**	integrin beta 4 binding protein	1.66;1.67;1.5	2.9058e-08;4.4184e-08;2.0898e-06
	97302_at	117198	**Ivns1abp**	influenza virus NS1A binding protein	1.73;1.54;1.25	0.00071315;0.00760964;0.14007705
	99541_at	16551	**Kif11**	kinesin family member 11	2.07;1.88;1.72	4.406e-05;0.0003503;0.0015575
	160501_at	19348	**Kif20a**	kinesin family member 20A	2.5;2.07;2.04	1.1720e-05;0.00032122;0.00040856
	95118_r_at	110032	**Kif22-ps**	kinesin family member 22, pseudogene	1.56;1.47;1.31	2.3732e-06;2.7665e-05;0.0013980

Function	Affy ID	Locus ID	Gene symbol	Description	Fold change	p-value
	96168_at	71819	**Kif23**	kinesin family member 23	1.92;1.73;1.77	2.3170e-06;4.4804e-05;2.4339e-05
Cytoskeleton	160755_at	73804	**Kif2c**	kinesin family member 2C	2.64;2.4;2.26	3.0840e-06;2.3922e-05;5.8891e-05
	104644_at	16571	**Kif4**	kinesin family member 4	2.36;2.09;1.98	1.8023e-06;2.7884e-05;7.1763e-05
	98471_f_at	16580	**Kifc1**	kinesin family member C1	1.66;1.49;1.4	6.0875e-07;3.3972e-05;0.00023083
	94561_at	65970	**Lima1**	LIM domain and actin binding 1	0.57;0.57;0.61	5.5225e-07;9.4731e-07;8.8061e-06
	160288_at	67443	**Map1lc3**	microtubule-associated protein 1 light chain 3 beta	0.53;0.76;0.78	6.3114e-08;0.0035385;0.0081012
	97447_at	66734	**Map1lc3a**	microtubule-associated protein 1 light chain 3 alpha	0.54;0.56;0.72	1.0525e-07;6.4994e-07;0.00090845
	104368_at	100732	**Mapre3**	microtubule-associated protein, RP/EB family, member 3	0.66;0.81;0.78	1.1628e-07;0.00110624;0.00015939
	160308_at	17698	**Msn**	moesin	1.83;1.6;1.7	1.0558e-09;1.6709e-07;2.5335e-08
	94537_at	67938	**Mylc2b**	myosin light chain, regulatory B	0.55;0.71;0.73	1.6077e-11;6.3741e-07;2.2681e-06
	100923_at	17909	**Myo10**	myosin X	0.69;0.57;0.72	2.6070e-05;1.0163e-07;0.00017803
	93427_at	338367	**Myo1d**	myosin ID	0.62;0.6;0.77	4.4414e-08;3.1502e-08;0.00025147
	94910_at	67203	**Nde1**	nuclear distribution gene E homolog 1 (A nidulans)	1.82;1.72;1.53	2.9573e-05;0.00017192;0.00191956
	161000_i_at	108907	**Nusap1**	nucleolar protein ANKT	1.99;2.21;1.87	0.00067667;0.00024193;0.00223473
	100554_at	54132	**Pdlim1**	PDZ and LIM domain 1 (elfin)	2.58;2.21;2.4	3.6716e-12;3.1920e-10;4.5132e-11
	99662_at	18541	**Pcnt2**	pericentrin 2	1.58;1.62;1.54	7.0412e-05;6.1368e-05;0.00021778
	96187_at	67756	**Pkp4**	plakophilin 4	2.2;2.09;1.76	8.5194e-09;5.2868e-08;3.5648e-06
	95502_at	64383	**Sirt2**	sirtuin 2 (silent mating type information regulation 2, homolog) 2 (S. cerevisiae)	0.55;0.71;0.77	2.6263e-07;0.00068828;0.00551248
	93898_at	24051	**Sgcb**	sarcoglycan, beta (dystrophin-associated glycoprotein)	0.66;0.8;0.8	2.9346e-06;0.0046526;0.0058987
	103345_at	20740	**Spna2**	spectrin alpha 2	0.53;0.48;0.56	1.6702e-06;3.1733e-07;1.0114e-05
	93571_at	20742	**Spnb2**	spectrin beta 2	0.53;0.51;0.56	2.4659e-07;1.4755e-07;1.4556e-06
	102378_at	16651	**Sspn**	sarcospan	0.64;0.66;0.67	2.1241e-10;1.6944e-09;3.0101e-09
	94991_at	104027	**Synpo**	synaptopodin	0.19;0.23;0.2	8.6459e-14;2.4190e-12;3.6325e-13
	93541_at	21345	**Tagln**	transgelin	2.13;1.12;1.85	0.00022055;0.52685997;0.00247711
	160162_at	21346	**Tagln2**	transgelin 2	2.07;2.41;2.43	8.7421e-10;5.5177e-11;4.4937e-11
	96426_at	19241	**Tmsb4x**	thymosin, beta 4, X chromosome	1.57;1.51;1.45	0.00018301;0.00069227;0.00171838
	100593_at	21956	**Tnnt2**	troponin T2, cardiac	1.52;1.13;1.5	4.3451e-06;0.11413;1.3394e-05
	160461_f_at	67951	**Tubb6**	tubulin, beta 6	2.54;2.2;1.96	1.6113e-08;5.5314e-07;5.5863e-06
	99924_at	103733	**Tubg1**	tubulin, gamma 1	1.59;1.56;1.55	1.1344e-08;4.1225e-08;6.3937e-08
	100084_at	22350	**Vil2**	villin 2	1.71;1.99;1.7	1.1791e-07;3.5778e-09;3.0041e-07

Function	Affy ID	Locus ID	Gene symbol	Description	Fold change	p-value
Intracellular	160227_s_a	53414	**Bysl**	bystin-like	1.77;1.44;1.38	9.9810e-14;1.5377e-09;1.4764e-08
Cell adhesion	98151_s_at	12388	**Catns**	catenin src	0.65;0.71;0.65	0.00049149;0.00601105;0.00085516
Signal transducer activity	95022_at	83397	**Akap12**	A kinase (PRKA) anchor protein (gravin) 12	0.48;0.45;0.5	4.8127e-07;2.4486e-07;2.0113e-06
	92968_at	11844	**Arf5**	ADP-ribosylation factor 5	0.65;0.77;0.76	5.1535e-07;0.00049680;0.00027604
	97811_at	66251	**Arfgap3**	ADP-ribosylation factor GTPase activating protein 3	0.56;0.63;0.64	9.6581e-10;1.2729e-07;2.5883e-07
	92185_at	320982	**Arl4c**	ADP-ribosylation factor-like 4C	1.72;2.27;1.87	1.9873e-10;1.1953e-13;2.8216e-11
	96203_at	75600	**Calml4**	calmodulin-like 4	0.38;0.42;0.37	2.3441e-11;4.3086e-10;3.9493e-11
	93274_at	12747	**Clk**	CDC-like kinase	0.63;0.67;0.66	0.0009400;0.0036045;0.0026288
	98928_at	23789	**Coro1b**	coronin, actin binding protein 1B	0.6;0.81;0.83	9.8488e-08;0.0074887;0.0150791
	94483_at	13000	**Csnk2a2**	casein kinase II, alpha 2, polypeptide	1.56;1.39;1.3	2.2986e-07;3.7198e-05;0.00051794
	95701_at	67393	**Cxxc5**	CXXC finger 5	0.64;0.63;0.65	3.6971e-14;5.6949e-14;3.4340e-13
	160976_at	225390	**Diap1**	diaphanous homolog 1 (Drosophila)	1.55;1.5;1.45	2.4236e-06;1.4314e-05;4.0313e-05
	95628_at	56419	**Diap3**	diaphanous homolog 3 (Drosophila)	2.05;1.9;1.69	6.6842e-08;8.4604e-07;1.6407e-05
	104598_at	19252	**Dusp1**	dual specificity phosphatase 1	2.74;2.85;3.47	1.5286e-13;1.5917e-13;4.0837e-15
	93285_at	67603	**Dusp6**	dual specificity phosphatase 6	2.62;2.22;1.98	1.9749e-07;6.5004e-06;5.0713e-05
	102925_at	75590	**Dusp9**	dual specificity phosphatase 9	2.54;2.68;2.18	1.2696e-09;1.0152e-09;6.7136e-08
	97411_at	13605	**Ect2**	ect2 oncogene	3.66;3.5;2.88	2.1412e-07;7.4156e-07;8.5875e-06
	93974_at	74155	**Errfi1**	ERBB receptor feedback inhibitor 1	2.07;1.82;1.51	4.6405e-07;1.4698e-05;0.00095967
	101934_at	225020	**Fez2**	fasciculation and elongation protein zeta 2 (zygin II)	2.05;1.27;1.52	1.3822e-07;0.02416479;0.00034975
	99176_at	58249	**Fibp**	fibroblast growth factor (acidic) intracellular binding protein	0.66;0.77;0.76	1.0935e-07;0.00016428;8.4859e-05
	103699_i_at	212398	**Frat2**	frequently rearranged in advanced T-cell lymphomas 2	1.43;1.79;1.7	4.5382e-06;3.0561e-09;1.4408e-08
	104358_at	52666	**GEFT**	RAC/CDC42 exchange factor	0.63;0.69;0.72	5.8980e-12;6.4705e-10;1.0048e-08
	102040_at	26385	**Gprk6**	G protein-coupled receptor kinase 6	1.53;1.4;1.27	7.1280e-09;7.3881e-07;7.0692e-05
	93690_at	14783	**Grb10**	growth factor receptor bound protein 10	0.55;0.57;0.67	0.00031828;0.00096883;0.01326198
	100113_s_a	16579	**Kifap3**	kinesin-associated protein 3	0.57;0.62;0.58	1.5067e-09;6.3998e-08;6.2399e-09

Function	Affy ID	Locus ID	Gene symbol	Description	Fold change	p-value
Intracellular	160261_i_at	50523	**Lats2**	large tumor suppressor 2	2.07;1.58;1.62	1.3447e-08;3.1665e-05;1.6287e-05
Signal transducer activity	99164_at	83409	**Mapbpip**	mitogen activated protein binding protein interacting protein	0.66;0.79;0.79	2.2309e-08;0.00016253;0.00018699
	103416_at	50772	**Mapk6**	mitogen-activated protein kinase 6	1.94;1.96;1.87	2.6038e-13;4.8584e-13;2.0295e-12
	93573_at	17748	**Mt1**	metallothionein 1	0.41;0.69;0.77	1.0600e-08;0.0022949;0.0200567
	101561_at	17750	**Mt2**	metallothionein 2	0.48;0.73;0.83	1.5322e-07;0.005129;0.086463
	94223_at	56349	**Net1**	neuroepithelial cell transforming gene 1	1.7;1.28;1.37	3.0156e-06;0.0128797;0.0019038
	93178_at	53972	**Ngef**	neuronal guanine nucleotide exchange factor	1.54;2.16;1.61	1.1161e-08;2.6652e-13;4.0195e-09
	102207_at	223649	**Nrbp2**	nuclear receptor binding protein 2	0.62;0.62;0.59	9.1054e-08;2.2124e-07;4.5411e-08
	93421_at	18647	**Pftk1**	PFTAIRE protein kinase 1	0.56;0.54;0.47	5.4574e-08;4.3424e-08;1.7408e-09
	96592_at	18708	**Pik3r1**	PI3-kinase, regulatory subunit, polypeptide 1 (p85 alpha)	0.58;0.68;0.69	8.2975e-07;0.00014111;0.00023742
	98005_at	18767	**Pkia**	protein kinase inhibitor, alpha	1.9;2.17;1.65	9.3107e-10;5.3395e-11;1.6580e-07
	104580_at	18799	**Plcd**	phospholipase C, delta	0.59;0.63;0.69	5.5519e-13;3.0727e-11;2.0774e-09
	160078_at	18938	**Ppp1r14b**	protein phosphatase 1, regulatory (inhibitor) subunit	1.83;1.9;1.79	4.9379e-09;3.7861e-09;1.9430e-08
	95092_at	19055	**Ppp3ca**	protein phosphatase 3, catalytic subunit, alpha isoform	0.66;0.86;0.69	1.1377e-05;0.058362;9.3250e-05
	94989_at	70161	**Pten**	phosphatase and tensin homolog	0.77;0.67;0.62	0.00062152;1.0254e-05;6.4266e-07
	98424_at	19249	**Ptpn13**	protein tyrosine phosphatase, non-receptor type 13	0.53;0.53;0.52	3.1351e-09;6.3181e-09;5.8406e-09
	94953_at	26934	**Racgap1**	Rac GTPase-activating protein 1	1.67;1.65;1.54	4.8526e-05;0.00010028;0.00048874
	100530_at	19730	**Ralgds**	ral guanine nucleotide dissociation stimulator	0.61;0.84;0.8	2.0352e-09;0.00313068;0.00043433
	98573_r_at	19385	**Ranbp1**	RAN binding protein 1	1.71;1.51;1.52	7.0359e-07;4.6407e-05;3.7760e-05
	100562_at	57785	**Rangnrf**	RAN guanine nucleotide release factor	1.53;1.38;1.28	4.9663e-07;4.5224e-05;0.00076261
	160965_at	54153	**Rasa4**	RAS p21 protein activator 4	0.7;0.65;0.72	2.3106e-05;3.0787e-06;0.00011231
	102821_s_a	19428	**Rasl2-9**	RAS-like, family 2, locus 9	1.57;1.49;1.5	3.0550e-07;3.5645e-06;3.1013e-06

Function	Affy ID	Locus ID	Gene symbol	Description	Fold change	p-value
Intracellular	161609_at	19734	**Rgs16**	regulator of G-protein signaling 16	1.73;1.49;1.74	1.1459e-09;5.8703e-07;1.9425e-09
Signal transducer activity	98950_at	54170	**Rragc**	Ras-related GTP binding C	0.64;0.84;0.89	3.8046e-06;0.029782;0.150484
	94394_at	20130	**Rras**	Harvey rat sarcoma oncogene, subgroup R	0.56;0.79;0.72	2.9907e-07;0.01207990;0.00078678
	93713_at	20416	**Shc1**	src homology 2 domain-containing transforming protein C1	0.64;0.71;0.79	1.7882e-05;0.00065112;0.01272289
	104063_at	71943	**Srcasm**	Src activating and signaling molecule	2.13;2.03;1.83	1.5559e-10;1.1996e-09;2.2295e-08
	92310_at	20620	**Snk**	serum-inducible kinase	1.54;1.58;1.68	7.2620e-08;5.4060e-08;5.5493e-09
	101995_at	18412	**Sqstm1**	sequestosome 1	0.64;0.83;0.96	1.5008e-05;0.041524;0.593926
	97909_at	16765	**Stmn1**	stathmin 1	1.49;1.84;1.68	0.00390271;9.3291e-05;0.00055743
	96531_at	213773	**Tbl3**	transducin (beta)-like 3	1.64;1.55;1.59	8.6258e-08;1.0474e-06;4.3281e-07
	102850_at	51789	**Tnk2**	tyrosine kinase, non-receptor, 2	2.3;1.74;1.87	5.1765e-15;5.9443e-11;5.2883e-12
	95010_at	22031	**Traf3**	Tnf receptor-associated factor 3	1.68;1.84;1.78	5.7201e-11;4.3638e-12;1.3826e-11
	104053_at	223435	**Trio**	triple functional domain (PTPRF interacting)	0.6;0.61;0.56	1.0927e-06;4.0530e-06;4.1355e-07
	93538_at	56196	**Ttrap**	Traf and Tnf receptor associated protein	1.62;1.57;1.43	5.0469e-06;2.3180e-05;0.00032115
	97393_at	22367	**Vrk1**	vaccinia related kinase 1	1.47;1.51;1.31	2.3179e-06;1.8990e-06;0.00034914
Protein biosynthesis	97318_at	66044	**Hars2**	histidyl-tRNA synthetase	0.63;0.77;0.73	3.3930e-08;0.00016896;1.6132e-05
	103537_at	13666	**Eif2ak3**	eukaryotic translation initiation factor 2 alpha kinase 3	0.69;0.7;0.62	1.5690e-07;8.0157e-07;4.2129e-09
	94530_at	217715	**Eif2b2**	eukaryotic translation initiation factor 2B, subunit 2 beta	1.49;1.59;1.62	9.3266e-09;1.2806e-09;4.8878e-10
	94253_at	13665	**Eif2s1**	eukaryotic translation initiation factor 2, subunit 1 alpha	1.77;1.71;1.53	1.0573e-08;5.7924e-08;2.2186e-06
	97205_at	78655	**Eif3s1**	eukaryotic translation initiation factor 3, subunit 1 alpha	1.52;1.29;1.15	4.6294e-05;0.0072067;0.1198724
	93973_at	27979	**Eif3s9**	eukaryotic translation initiation factor 3, subunit 9	1.68;1.48;1.48	7.8131e-13;3.9472e-10;4.5841e-10
	160974_at	13682	**Eif4a2**	eukaryotic translation initiation factor 4A2	1.61;1.4;1.39	2.8954e-11;3.3510e-08;6.1076e-08
	96628_at	107508	**Eprs**	glutamyl-prolyl-tRNA synthetase	0.68;0.62;0.58	0.00032076;4.237e-05;6.968e-06
	160451_at	225363	**Etf1**	eukaryotic translation termination factor 1	1.67;1.51;1.6	2.7885e-10;3.4844e-08;3.6719e-09
	92580_at	15115	**Hars**	histidyl-tRNA synthetase	1.54;1.42;1.23	5.8242e-05;0.00076542;0.03501292
	160431_at	56282	**Mrpl12**	mitochondrial ribosomal protein L12	1.73;1.59;1.52	4.4483e-11;2.3862e-09;1.6121e-08
	99140_at	94063	**Mrpl16**	mitochondrial ribosomal protein L16	1.53;1.52;1.47	2.0533e-06;3.9749e-06;1.3013e-05

Function	Affy ID	Locus ID	Gene symbol	Description	Fold change	p-value
Protein biosynthesis	93786_i_at	67681	**Mrpl18**	mitochondrial ribosomal protein L18	1.52;1.62;1.46	0.00087637;0.00033434;0.00290320
	160345_at	94065	**Mrpl34**	mitochondrial ribosomal protein L34	1.35;1.5;1.41	7.7382e-06;1.9964e-07;2.3316e-06
	97251_at	64657	**Mrps10**	mitochondrial ribosomal protein S10	1.52;1.55;1.47	2.1570e-06;2.0637e-06;1.4797e-05
	160621_at	64655	**Mrps22**	mitochondrial ribosomal protein S22	1.36;1.55;1.31	0.00550669;0.00039047;0.01799110
	102128_f_at	64658	**Mrps25**	mitochondrial ribosomal protein S25	1.66;1.79;1.51	9.3150e-07;2.1218e-07;2.8591e-05
	96693_at	104458	**Rars**	arginyl-tRNA synthetase	1.57;1.61;1.65	7.8076e-11;6.6199e-11;2.4007e-11
	92857_at	67183	**Rpl22**	ribosomal protein L22	0.44;0.51;0.47	9.3540e-12;8.7251e-10;1.2865e-10
	99198_at	19951	**Rpl32**	ribosomal protein L32	1.57;1.57;1.41	7.0254e-07;1.4449e-06;6.2902e-05
	160071_at	54364	**Rpp30**	RNaseP protein p30	2.13;2.01;1.74	1.1096e-06;6.5593e-06;0.0001189
	96778_at	59014	**Rrs1**	RRS1 ribosome biogenesis regulator homolog (S. cerevisiae)	2.11;1.94;1.68	1.1638e-09;2.1234e-08;1.2416e-06
	160283_at	66409	**Rsl1d1**	ribosomal L1 domain containing 1	1.57;1.44;1.33	2.0440e-07;9.3271e-06;0.00020352
Protein folding and modificatio	98153_at	12462	**Cct3**	chaperonin subunit 3 (gamma)	1.6;1.55;1.39	1.4246e-06;6.6649e-06;0.00023406
	160562_at	12468	**Cct7**	chaperonin subunit 7 (eta)	1.62;1.56;1.46	1.4709e-11;1.8153e-10;3.7601e-09
	94531_at	67914	**Coq9**	coenzyme Q9 homolog (yeast)	0.61;0.7;0.71	1.0337e-11;1.8735e-08;2.5054e-08
	160230_at	12856	**Cox17**	cytochrome c oxidase, subunit XVII assembly protein homolog (yeast)	1.39;1.54;1.45	0.00018921;1.015e-05;7.810e-05
	99082_at	14230	**Fkbp10**	FK506 binding protein 10	0.72;0.64;0.7	4.7200e-07;4.9698e-09;2.1393e-07
	102689_at	14976	**H2-Ke2**	H2-K region expressed gene 2	0.59;0.81;0.87	1.7477e-05;0.052969;0.194556
	100279_at	20444	**Siat5**	sialyltransferase 5	0.66;0.83;0.85	0.00024228;0.07394097;0.12468240
	97310_at	70356	**St13**	suppression of tumorigenicity 13	0.63;0.8;0.81	2.9535e-06;0.011013;0.015929
	162279_f_at	12466	**Cct6a**	chaperonin subunit 6a (zeta)	1.62;1.45;1.22	1.9411e-06;0.00011699;0.01947969
	99546_at	14227	**Fkbp2**	FK506 binding protein 2	1.5;1.43;1.53	8.6915e-08;1.2482e-06;7.1973e-08
	92808_f_at	14228	**Fkbp4**	FK506 binding protein 4	1.67;1.58;1.4	2.2210e-09;3.4795e-08;5.1099e-06
	104746_at	14231	**Fkbp7**	FK506 binding protein 7	0.63;0.61;0.63	5.8694e-05;4.1201e-05;8.1186e-05
	93731_at	27055	**Fkbp9**	FK506 binding protein 9	0.65;0.62;0.63	3.8688e-08;1.6557e-08;2.4316e-08
	102761_at	17714	**Grpel2**	GrpE-like 2, mitochondrial	1.43;1.47;1.52	4.1018e-09;2.8614e-09;4.8443e-10
	102047_at	18107	**Nmt1**	N-myristoyltransferase 1	1.51;1.49;1.42	5.1442e-08;1.8417e-07;1.3203e-06

Function	Affy ID	Locus ID	Gene symbol	Description	Fold change	p-value
Protein folding and modificatio	97445_at	67738	**Ppid**	peptidylprolyl isomerase D (cyclophilin D)	2.05;1.71;1.41	3.4595e-06;0.00022633;0.00996325
	95077_at	19352	**Rabggtb**	RAB geranylgeranyl transferase, b subunit	1.62;1.63;1.57	5.4808e-07;8.1669e-07;2.9187e-06
	98596_s_at	20454	**Siat9**	sialyltransferase 9 (CMP-NeuAc:lactosylceramide alpha-2,3-sialyltransferase)	0.59;0.67;0.75	7.2939e-08;7.3880e-06;0.00045895
	104738_at	22792	**Zrf2**	zuotin related factor 2	1.77;1.66;1.51	9.6346e-09;1.6047e-07;4.1648e-06
Proteolysis and peptidolysis	101997_at	67526	**Apg12l**	autophagy 12-like (S. cerevisiae)	0.49;0.55;0.64	1.1477e-08;4.5358e-07;2.5836e-05
	97941_at	12338	**Capn6**	calpain 6	0.31;0.47;0.35	3.5621e-12;3.2188e-08;6.1261e-11
	98405_at	20723	**Serpinb9**	serine (or cysteine) peptidase inhibitor, clade B, member 9	0.59;0.85;0.73	1.5793e-08;0.018959;5.1909e-05
	94916_at	13121	**Cyp51**	cytochrome P450, 51	0.87;0.64;0.78	0.008686;1.1041e-08;5.1839e-05
	93595_at	12751	**Cln2**	ceroid-lipofuscinosis, neuronal 2	0.59;0.86;0.94	2.6621e-05;0.15617;0.54953
	104036_at	83768	**Dpp7**	dipeptidylpeptidase 7	0.57;0.82;0.98	4.7098e-05;0.09774;0.85408
	101055_at	19025	**Ppgb**	protective protein for beta-galactosidase	0.53;0.8;0.92	1.1815e-05;0.065344;0.471702
	96065_at	17035	**Lxn**	latexin	0.27;0.35;0.38	1.0253e-10;1.4388e-08;5.9299e-08
	101070_at	54484	**Mkrn1**	makorin, ring finger protein, 1	0.62;0.7;0.72	7.5979e-10;3.0656e-07;1.1244e-06
	161079_at	72560	**Naalad2**	N-acetylated alpha-linked acidic dipeptidase 2	0.53;0.64;0.55	1.2718e-06;0.00025985;6.5608e-06
	103637_at	17939	**Naga**	N-acetylated alpha-linked acidic dipeptidase 2	0.66;0.74;0.75	4.5727e-06;0.00040880;0.00062016
	103906_f_at	83814	**Nedd4l**	neural precursor cell expressed, developmentally down-regulated gene 4-like	1.75;1.5;1.48	5.9291e-11;5.1712e-08;7.8272e-08
	94923_f_at	73945	**Otud4**	OTU domain containing 4	1.66;1.4;1.37	8.6652e-12;4.4560e-08;1.2873e-07
	100125_at	18813	**Pa2g4**	proliferation-associated 2G4	2.33;2.12;2.14	3.0845e-07;3.6412e-06;3.1549e-06
	93349_at	18542	**Pcolce**	procollagen C-proteinase enhancer protein	0.47;0.58;0.6	8.6118e-13;1.2981e-09;6.3612e-09
	12301	92596_at	**Cacybp**	calcyclin binding protein	1.49;1.55;1.31	0.0018599;0.0011960;0.0300726
	230484	160234_a	**Usp1**	ubiquitin specific protease 1	2.15;1.8;1.5	9.441e-05;0.0020791;0.0255462
	93039_at	54381	**Pgcp**	plasma glutamate carboxypeptidase	0.63;0.78;0.74	2.1863e-07;0.00096906;0.00012506
	96920_at	56213	**Prss11**	protease, serine, 11 (Igf binding)	1.62;1.72;1.38	2.9815e-09;7.4300e-10;4.3764e-06
	96892_at	26440	**Psma1**	proteasome (prosome, macropain) subunit, alpha type 1	1.47;1.53;1.36	5.9533e-05;2.5761e-05;0.0010621
	93988_at	26444	**Psma7**	proteasome (prosome, macropain) subunit, alpha type 7	1.55;1.59;1.48	0.00019325;0.00016172;0.00090251
	94025_at	26446	**Psmb3**	proteasome (prosome, macropain) subunit, beta type 3	1.58;1.64;1.62	3.8466e-09;2.3198e-09;3.5984e-09
	101558_s_a	19173	**Psmb5**	proteasome (prosome, macropain) subunit, beta type 5	1.35;1.51;1.44	0.00098468;5.3772e-05;0.00019119
	95448_at	19181	**Psmc2**	proteasome (prosome, macropain) 26S subunit, ATPase 2	1.53;1.53;1.53	9.029e-05;0.00016124;0.00016378
	160305_at	69077	**Psmd11**	proteasome (prosome, macropain) 26S subunit, non-ATPase, 11	1.52;1.57;1.48	6.2139e-05;4.2754e-05;0.00019676

Function	Affy ID	Locus ID	Gene symbol	Description	Fold change	p-value
Proteolysis and peptidolysis	95742_at	23997	**Psmd13**	proteasome (prosome, macropain) 26S subunit, non-ATPase, 13	1.51;1.48;1.45	1.8906e-07;9.7100e-07;1.9552e-06
	98555_at	22129	**Ttc3**	tetratricopeptide repeat domain	0.65;0.69;0.63	6.9849e-08;1.2886e-06;4.0077e-08
	100528_at	22214	**Ube2h**	ubiquitin-conjugating enzyme E2H	0.59;0.69;0.63	1.3642e-06;0.00022428;1.8160e-05
	96701_at	50995	**Uble1b**	ubiquitin-like 1 (sentrin) activating enzyme E1B	1.53;1.44;1.34	1.6683e-06;2.5817e-05;0.00034916
	100512_at	56207	**Uchl5**	ubiquitin carboxyl-terminal esterase L5	2.04;2.05;1.8	6.2618e-07;1.0185e-06;1.7679e-05
	100955_at	67196	**Ube2**	ubiquitin-conjugating enzyme E2T	2.54;2.58;2.21	1.6933e-06;2.4241e-06;2.7764e-05
	99639_at	22224	**Uchrp**	ubiquintin c-terminal hydrolase related polypeptide	1.64;1.49;1.41	1.3107e-10;1.4765e-08;1.5579e-07
	96061_at	59025	**Usp14**	ubiquitin specific protease 14	1.64;1.4;1.4	5.9261e-06;0.0008616;0.0008283
	97960_at	216825	**Usp22**	ubiquitin specific protease 22	0.64;0.7;0.65	1.0609e-05;0.00023153;2.7545e-05
	95703_at	56459	**Uble1a**	ubiquitin-like 1 (sentrin) activating enzyme E1A	1.62;1.51;1.4	7.1075e-07;1.1637e-05;0.00013997
Heat Shock	98451_at	56812	**Dnajb10**	DnaJ (Hsp40) homolog, subfamily B, member 10	0.66;0.79;0.83	5.5251e-05;0.015012;0.045862
	101890_f_at	22791	**Dnajc2**	DnaJ (Hsp40) homolog, subfamily C, member 2	2.07;1.88;1.74	4.9585e-09;1.2869e-07;1.0194e-06
	160203_at	108671	**Dnajc9**	DnaJ (Hsp40) homolog, subfamily C, member 9	2.03;2.21;1.99	4.1108e-06;1.4726e-06;1.0858e-05
	98111_at	15505	**Hsp105**	heat shock protein	2.14;1.9;1.98	7.6058e-12;5.0240e-10;1.4443e-10
	101562_at	50497	**Hsp70-4**	heat shock protein 4	1.74;1.79;1.69	6.2610e-07;5.9578e-07;2.5587e-06
	97894_at	15482	**Hspa1l**	heat shock protein 1-like	1.61;1.47;1.4	1.5017e-09;1.4283e-07;1.2895e-06
	99816_at	15512	**Hspa2**	heat shock protein 2	0.5;0.58;0.56	3.3669e-09;4.4923e-07;1.6882e-07
	100353_g_a	15525	**Hspa4**	heat shock protein 4	1.5;1.4;1.51	1.2638e-07;3.8053e-06;1.9239e-07
	95282_at	15519	**Hspca**	heat shock protein 1, alpha	1.81;1.63;1.59	6.7740e-11;6.5251e-09;1.7588e-08
	93277_at	15510	**Hspd1**	heat shock protein 1 (chaperonin)	1.61;1.49;1.4	8.7909e-11;5.7988e-09;9.1821e-08
	99489_at	18415	**Osp94**	osmotic stress protein	1.67;2.25;1.83	1.0822e-07;5.1486e-11;1.2512e-08
	100081_at	20867	**Stip1**	stress-induced phosphoprotein 1	1.88;1.79;1.66	3.8126e-09;3.7990e-08;3.7922e-07
Apoptosis	101521_at	11799	**Birc5**	baculoviral IAP repeat-containing 5	2.99;2.74;2.54	4.8188e-06;2.6595e-05;7.1946e-05
Antiapoptotic	94384_at	15937	**Ier3**	immediate early response 3	3.13;3.59;4.04	1.2233e-10;3.0586e-11;5.0082e-12
	99392_at	21929	**Tnfaip3**	tumor necrosis factor, alpha-induced protein 3	1.45;1.36;1.65	5.2586e-05;0.00064913;1.4408e-06
	160829_at	21664	**Phlda1**	pleckstrin homology-like domain, family A, member 1	3.02;2.88;2.71	4.2150e-06;1.4329e-05;3.1231e-05
Proapoptotic	93536_at	12028	**Bax**	Bcl2-associated X protein	1.2;1.47;1.53	0.0068103;2.5993e-06;6.9523e-07
	98436_s_at	12367	**Casp3**	caspase 3, apoptosis related cysteine protease	1.75;1.89;1.37	1.2193e-06;3.0221e-07;0.0018225
	104290_at	26885	**Casp8ap2**	caspase 8 associated protein 2	1.85;1.61;1.39	1.1740e-07;1.0350e-05;0.00075622

Function	Affy ID	Locus ID	Gene symbol	Description	Fold change	p-value
Apoptosis	103711_at	12371	**Casp9**	caspase 9	0.65;0.72;0.73	5.5506e-07;5.1249e-05;7.2493e-05
Proapoptotic	93842_at	223453	**Dap**	death-associated protein	0.65;0.87;0.84	1.6423e-07;0.0349726;0.0087313
	99629_at	13663	**Ei24**	etoposide induced 2.4 mRNA	1.57;1.55;1.5	5.1940e-07;1.5471e-06;5.2763e-06
Cell cycle	92639_at	20878	**Aurka**	serine/threonine kinase 6	3.56;3.22;2.82	1.0000e-06;6.3192e-06;3.1912e-05
	98469_at	20877	**Aurkb**	serine/threonine kinase 12	1.63;1.6;1.5	2.4207e-06;8.0373e-06;5.5586e-05
	161172_f_at	215387	**Brrn1**	barren homolog (Drosophila)	1.67;1.68;1.52	1.8280e-05;2.7464e-05;0.00030846
	96146_at	12228	**Btg3**	B-cell translocation gene 3	1.63;1.65;1.52	3.7738e-08;5.1220e-08;9.8559e-07
	104097_at	12235	**Bub1**	budding uninhibited by benzimidazoles 1 homolog (S. cerevisiae)	2.81;2.65;2.26	2.4054e-06;1.0409e-05;9.9151e-05
	101961_at	12237	**Bub3**	budding uninhibited by benzimidazoles 3 homolog (S. cerevisiae)	1.56;1.44;1.35	4.9687e-06;0.00010128;0.00094001
	99186_at	12428	**Ccna2**	cyclin A2	1.67;1.55;1.48	6.2357e-05;0.00054819;0.00173187
	160159_at	268697	**Ccnb1**	cyclin B1	2.75;2.48;1.94	1.7401e-05;0.00011531;0.00249326
	94231_at	12443	**Ccnd1**	cyclin D1	1.67;1.93;1.68	1.8242e-07;5.2854e-09;3.1915e-07
	99073_at	12449	**Ccnf**	cyclin F	2.08;1.93;1.85	1.1282e-07;1.1943e-06;3.1300e-06
	160127_at	12450	**Ccng1**	cyclin G1	2.02;2.01;1.8	2.9245e-10;6.9909e-10;1.7437e-08
	98478_at	12452	**Ccng2**	cyclin G2	0.52;0.75;0.8	1.4131e-06;0.013060;0.042835
	96319_at	107995	**Cdc20**	cell division cycle 20 homolog (S. cerevisiae)	2.41;2.3;2.17	6.5130e-06;2.4179e-05;6.2914e-05
	102934_s_a	12532	**Cdc25c**	cell division cycle 25 homolog C (S. cerevisiae)	1.7;1.58;1.47	8.9866e-05;0.00066517;0.00297706
	100128_at	12534	**Cdc2a**	cell division cycle 2 homolog A (S. pombe)	2.56;2.49;2.37	1.1923e-06;3.4415e-06;7.8485e-06
	94048_at	216150	**Cdc34**	cell division cycle 34 homolog (S. cerevisiae)	1.6;1.84;1.78	1.1013e-06;3.1893e-08;8.3793e-08
	103797_at	12545	**Cdc7**	cell division cycle 7 (S. cerevisiae)	2.03;1.96;1.73	5.8688e-07;2.5024e-06;4.0563e-05
	160699_at	67849	**Cdca5**	cell division cycle associated 5	1.65;1.57;1.53	7.2780e-06;4.7880e-05;9.5107e-05
	95063_at	66953	**Cdca7**	cell division cycle associated 7	2.16;2.03;1.67	4.5739e-07;3.2126e-06;0.00019638
	96726_at	264064	**Cdk8**	cyclin-dependent kinase 8	1.52;1.39;1.27	4.2180e-07;3.0397e-05;0.0009333
	94881_at	12575	**Cdkn1a**	cyclin-dependent kinase inhibitor 1A (P21)	2.01;2.4;2.55	1.5494e-09;4.5280e-11;1.1855e-11
	103064_at	12649	**Chek1**	checkpoint kinase 1 homolog (S. pombe)	2.01;1.89;1.62	4.0751e-08;3.6225e-07;2.0673e-05

Function	Affy ID	Locus ID	Gene symbol	Description	Fold change	p-value
Cell cycle	97468_at	54124	**Cks1**	CDC28 protein kinase 1	1.78;1.78;1.73	2.1523e-05;3.4600e-05;7.1384e-05
	97527_at	66197	**Cks2**	CDC28 protein kinase regulatory subunit 2	2.86;2.63;2.25	5.5983e-06;2.9669e-05;0.00023352
	102292_at	13197	**Gadd45a**	growth arrest and DNA-damage-inducible 45 alpha	1.28;1.71;1.6	3.6691e-05;1.9549e-10;2.1930e-09
	99522_at	14841	**Gsg2**	germ cell-specific gene 2	1.94;1.69;1.46	1.0942e-06;4.6252e-05;0.0015415
	103270_at	29870	**Gtse1**	G two S phase expressed protein 1	1.61;1.59;1.59	1.5392e-09;5.2858e-09;5.9447e-09
	93758_at	16319	**Incenp**	inner centromere protein	1.77;1.67;1.63	6.628e-05;0.00033392;0.00057127
	99632_at	56150	**Mad2l1**	MAD2 (mitotic arrest deficient, homolog)-like 1 (yeast)	2.81;2.63;2.27	3.7981e-06;1.6686e-05;0.00012573
	99457_at	17345	**Mki67**	antigen identified by monoclonal antibody Ki 67	2.61;2.1;1.97	4.0313e-05;0.0010466;0.0022946
	100885_at	18005	**Nek2**	NIMA (never in mitosis gene a)-related expressed kinase 2	1.74;1.81;1.8	2.3065e-05;1.6349e-05;1.7411e-05
	98996_at	20873	**Plk4**	polo like kinase 4	2.73;2.47;2.13	3.5926e-06;2.6381e-05;0.0002205
	95032_at	233406	**Prc1**	protein regulator of cytokinesis 1	3.05;2.75;2.54	4.4394e-07;3.7377e-06;1.1598e-05
	101027_s_a	30939	**Pttg1**	translocase of inner mitochondrial membrane 8 homolog a (yeast)	1.5;1.72;1.58	0.00014796;6.8561e-06;6.3203e-05
	104476_at	19650	**Rbl1**	retinoblastoma-like 1 (p107)	1.93;2.07;1.7	7.4518e-07;2.9196e-07;2.9164e-05
	161787_f_at	67177	**Ris2**	retroviral integration site 2	1.64;1.82;1.6	7.1523e-07;6.0441e-08;2.9390e-06
	97421_at	14211	**Smc2l1**	SMC2 structural maintenance of chromosomes 2-like 1 (yeast)	3.12;2.68;2.35	2.0564e-06;2.6398e-05;0.00014816
	103201_at	22137	**Ttk**	Ttk protein kinase	1.93;1.76;1.54	4.548e-07;7.699e-06;0.00023115
DNA replication, repair and recombination	97364_at	66929	**Asf1b**	ASF1 anti-silencing function 1 homolog B (S. cerevisiae)	1.91;1.89;1.74	1.4999e-08;4.0443e-08;3.9969e-07
	101105_at	23825	**Banf1**	barrier to autointegration factor 1	1.44;1.55;1.37	3.0338e-05;4.2632e-06;0.00026263
	102976_at	12189	**Brca1**	breast cancer 1	1.9;1.71;1.71	2.4823e-06;5.2757e-05;4.7462e-05
	104259_at	12419	**Cbx5**	chromobox homolog 5 (Drosophila HP1a)	1.69;1.48;1.51	1.0588e-06;8.9743e-05;5.8100e-05
	102403_at	12544	**Cdc45l**	cell division cycle 45 homolog (S. cerevisiae)-like	1.76;1.85;1.72	6.0438e-09;2.9426e-09;2.7726e-08
	103821_at	23834	**Cdc6**	cell division cycle 6 homolog (S. cerevisiae)	3.7;3.3;2.92	2.2555e-10;2.7962e-09;2.0108e-08
	100616_at	12615	**Cenpa**	centromere autoantigen A	1.69;1.7;1.57	4.2187e-05;6.0210e-05;0.00038000
	100890_at	110749	**Chaf1b**	chromatin assembly factor 1, subunit B (p60)	1.65;1.76;1.61	3.5364e-08;8.1618e-09;1.4521e-07
	101459_at	12648	**Chd1**	chromodomain helicase DNA binding protein 1	1.93;1.64;1.51	6.0016e-10;1.8520e-07;3.2370e-06
	92840_at	101437	**Dhx32**	helicase DDX32	1.58;1.51;1.36	1.4680e-09;2.1890e-08;2.3798e-06
	103444_at	327762	**Dna2l and**	DNA2 DNA replication helicase 2-like (yeast)	2.02;1.89;1.77	4.7430e-10;6.9135e-09;4.1851e-08
	101445_at	13433	**Dnmt1**	DNA methyltransferase (cytosine-5) 1	1.66;1.51;1.47	1.5574e-07;7.7864e-06;2.0368e-05

Function	Affy ID	Locus ID	Gene symbol	Description	Fold change	p-value
DNA replication, repair and recombination	96297_at	69072	**Ebna1bp2**	EBNA1 binding protein 2	1.9;1.83;1.67	3.0254e-06;1.1750e-05;9.4478e-05
	92317_at	15569	**Elavl2**	ELAV (embryonic lethal, abnormal vision, Drosophila)-like 2 (Hu antigen B)	0.59;0.54;0.54	1.8383e-06;2.6076e-07;2.5950e-07
	97327_at	14156	**Fen1**	flap structure specific endonuclease 1	3.28;3.4;2.96	5.5807e-07;6.9836e-07;4.1440e-06
	160069_at	57441	**Gmnn**	geminin	2.36;2.41;2.04	7.4473e-07;1.0269e-06;2.0810e-05
	101954_at	51788	**H2afz**	H2A histone family, member Z	1.69;1.67;1.52	0.00015527;0.00029460;0.00207575
	100380_at	15078	**H3f3a**	H3 histone, family 3A	0.58;0.75;0.7	3.1648e-07;0.00131133;0.00016662
	97895_f_at	107435	**Hat1**	histidine aminotransferase 1	1.73;1.7;1.62	2.9486e-08;1.0331e-07;5.4316e-07
	99058_at	15364	**Hmga2**	high mobility group AT-hook 2	2.4;2.3;2.42	5.7052e-13;3.7027e-12;1.1251e-12
	93250_r_at	97165	**Hmgb2**	high mobility group box 2	1.94;1.89;1.69	0.0010280;0.0021329;0.0089560
	98038_at	15354	**Hmgb3**	high mobility group box 3	1.92;1.92;1.78	4.1125e-05;7.0726e-05;0.00028134
	94805_f_at	319172	**Hist1h2ab**	histone 1	2.56;2.46;2.17	2.6576e-05;7.8836e-05;0.00041054
	92551_at	16881	**Lig1**	ligase I, DNA, ATP-dependent	1.63;1.55;1.5	1.5208e-06;1.1940e-05;3.6679e-05
	103553_at	70024	**Mcm10**	minichromosome maintenance protein 10	1.8;1.75;1.67	4.6481e-09;2.5978e-08;1.1018e-07
	93112_at	17216	**Mcm2**	minichromosome maintenance protein 2	2.05;2.03;1.89	1.6958e-08;4.9843e-08;2.9039e-07
	92384_at	22590	**Xpa**	xeroderma pigmentosum, complementation group A	0.56;0.79;0.66	6.9247e-06;0.03047158;0.00067399
	100062_at	17215	**Mcm3**	minichromosome maintenance protein 3	3.35;3.34;3.01	3.4630e-07;7.0634e-07;2.8006e-06
	93041_at	17217	**Mcm4**	minichromosome maintenance protein 4	2.37;2.3;2.2	8.8596e-07;2.8857e-06;6.2493e-06
	100156_at	17218	**Mcm5**	minichromosome maintenance protein 5	3.08;3;2.73	2.4254e-06;6.1447e-06;2.0685e-05
	93356_at	17220	**Mcm7**	minichromosome maintenance protein 7	2.64;2.63;2.36	4.3067e-08;9.3542e-08;6.5700e-07
	100033_at	17685	**Msh2**	mutS homolog 2 (E. coli)	1.34;1.54;1.43	7.8584e-07;2.0719e-09;7.1028e-08
	103654_at	50887	**Nsbp1**	nucleosome binding protein 1	1.62;1.7;1.53	1.9387e-07;8.5939e-08;2.4526e-06
	101906_at	70099	**Smc4l1**	SMC4 structural maintenance of chromosomes 4-like 1 (yeast)	1.87;1.71;1.43	3.4865e-05;0.00033553;0.01084495
	92458_at	18392	**Orc1l**	origin recognition complex, subunit 1-like (S.cereviaiae)	2.3;2.32;2.17	5.9603e-11;1.1455e-10;5.6682e-10
	95712_at	56452	**Orc6l**	origin recognition complex, subunit 6-like (S. cerevisiae)	1.7;1.62;1.51	6.1002e-07;4.6450e-06;3.6176e-05
	92867_at	54383	**Phc2**	polyhomeotic-like 2 (Drosophila)	1.76;1.54;1.48	2.0467e-10;5.6576e-08;3.2844e-07
	101065_at	18538	**Pcna**	proliferating cell nuclear antigen	2.23;2.24;1.99	2.2647e-06;4.0678e-06;3.2512e-05
	103207_at	18968	**Pola1**	polymerase (DNA directed), alpha 1	1.99;1.96;1.68	4.3933e-06;1.1069e-05;0.00027739
	98006_at	18969	**Pola2**	polymerase (DNA directed), alpha 2	1.73;1.97;1.77	1.8217e-06;1.2772e-07;1.9044e-06
	103057_at	18971	**Pold1**	polymerase (DNA directed), delta 1, catalytic subunit	1.68;1.59;1.5	2.5956e-07;2.8094e-06;2.1333e-05
	101920_at	18974	**Pole2**	polymerase (DNA directed), epsilon 2 (p59 subunit)	1.71;1.95;1.59	1.7984e-05;1.4616e-06;0.00017835
	96772_at	19075	**Prim1**	DNA primase, p49 subunit	1.8;2.17;1.75	6.9493e-05;2.9846e-06;0.00020348

Function	Affy ID	Locus ID	Gene symbol	Description	Fold change	p-value
DNA replication, repair and recombination	95549_at	19076	**Prim2**	DNA primase, p58 subunit	1.81;1.87;1.62	1.1073e-05;9.3360e-06;0.00023378
	104527_at	19361	**Rad51**	RAD51 homolog (S. cerevisiae)	2.27;2.36;2.29	3.7409e-06;3.5609e-06;6.1848e-06
	93676_at	19362	**Rad51ap1**	RAD51 associated protein 1	1.55;1.58;1.57	3.5410e-05;3.9472e-05;4.5675e-05
	160072_at	69263	**Rfc3**	replication factor C (activator 1) 3	1.51;1.47;1.39	1.1305e-06;6.0543e-06;4.1789e-05
	103418_at	106344	**Rfc4**	replication factor C (activator 1) 4	1.41;1.67;1.42	0.00475506;0.00015993;0.00534600
	95612_at	72151	**Rfc5**	replication factor C (activator 1) 5	2.11;2.16;1.92	5.1814e-06;5.7787e-06;5.3413e-05
	96106_at	69724	**Rnaseh2a**	ribonuclease H2, large subunit	1.36;1.51;1.39	0.00014913;5.2993e-06;0.00010105
	95427_at	68275	**Rpa1**	replication protein A1	1.98;2.13;1.93	4.0456e-09;1.2647e-09;1.6693e-08
	160422_at	20174	**Ruvbl2**	RuvB-like protein 2	1.85;1.8;1.56	2.9044e-09;1.5158e-08;1.2864e-06
	160068_at	60406	**Sap30**	sin3 associated polypeptide	1.62;1.7;1.58	1.2474e-06;5.2911e-07;4.3589e-06
	103504_at	66970	**Ssbp2**	single-stranded DNA binding protein 2	0.62;0.67;0.58	8.2255e-09;2.2360e-07;1.2668e-09
	100974_at	76900	**Ssbp4**	single stranded DNA binding protein 4	0.64;0.69;0.72	8.9366e-10;6.4419e-08;4.0887e-07
	101437_at	20874	**Stk2**	serine/threonine kinase 2	1.63;1.8;1.87	1.9442e-07;1.7537e-08;5.0263e-09
	99578_at	21973	**Top2a**	topoisomerase (DNA) II alpha	3.03;2.63;2.34	2.1461e-06;2.5431e-05;0.00012068
	104045_at	72480	**Tspyl4**	TSPY-like 4	0.35;0.32;0.32	1.0795e-12;5.1536e-13;5.0777e-13
	103071_at	235559	**Topbp1**	topoisomerase (DNA) II beta binding protein	2.55;2.42;1.99	3.4468e-07;1.6483e-06;4.9751e-05
	103406_at	74254	**Xab1**	XPA binding protein 1	1.76;1.61;1.42	1.2269e-09;6.1696e-08;6.6995e-06
Regulation of transcription	100412_g_a	11568	**Aebp1**	AE binding protein 1	0.59;0.76;0.89	0.0005148;0.0540452;0.3948459
	160215_at	14797	**Aes**	amino-terminal enhancer of split	0.55;0.67;0.64	1.4931e-08;2.0372e-05;4.8669e-06
	92375_at	69090	**Ascc1**	activating signal cointegrator 1 complex subunit 1	0.55;0.69;0.59	9.6078e-10;5.4753e-06;2.2008e-08
	103006_at	107503	**Atf5**	activating transcription factor 5	0.39;0.42;0.44	8.1772e-11;7.4903e-10;2.9411e-09
	97998_at	12034	**Bcap37**	dentatorubral pallidoluysian atrophy	0.52;0.73;0.77	6.3207e-05;0.032535;0.077699
	160531_at	12034	**Bcap37**	B-cell receptor-associated protein 37	1.58;1.59;1.35	0.00013037;0.00018525;0.00886135
	104701_at	20893	**Bhlhb2**	basic helix-loop-helix domain containing, class B2	0.5;0.6;0.59	1.5420e-05;0.00085395;0.00050298
	93371_at	12173	**Bnc**	basonuclin	3.7;3.79;3.26	< 2.22e-16;< 2.22e-16;< 2.22e-16
	104573_at	66162	**Bola2**	bolA-like 2	1.38;1.54;1.4	0.00550056;0.00058872;0.00483558
	93527_at	16601	**Bteb1**	basic transcription element binding protein 1	0.61;0.78;0.79	3.9806e-06;0.0076346;0.0104499

Function	Affy ID	Locus ID	Gene symbol	Description	Fold change	p-value
Regulation of transcription	103212_at	217946	**Cdca7l**	cell division cycle associated 7 like	1.47;1.57;1.47	3.0197e-06;4.8079e-07;5.0050e-06
	102048_at	107765	**Crap**	carnitine palmitoyltransferase 1, liver	2.29;2.24;2.12	5.0697e-10;1.9390e-09;6.8843e-09
	99191_at	58521	**Cri1**	CREBBP/EP300 inhibitory protein 1	0.57;0.58;0.57	2.4030e-08;7.1816e-08;4.4432e-08
	95755_at	56449	**Csda**	cold shock domain protein A	1.6;1.47;1.43	3.4089e-09;1.9419e-07;6.9162e-07
	101429_at	13198	**Ddit3**	DNA-damage inducible transcript 3	0.5;0.55;0.58	7.5252e-14;2.6184e-12;2.5846e-11
	102963_at	13555	**E2f1**	E2F transcription factor 1	1.36;1.53;1.45	2.0748e-07;1.7688e-09;1.9111e-08
	103203_f_at	101449	**E2f8**	E2F transcription factor 8	2.2;2.04;1.77	2.3944e-07;2.4111e-06;4.7852e-05
	92535_at	13591	**Ebf1**	early B-cell factor 1	0.59;0.64;0.64	1.4508e-09;6.9988e-08;6.9343e-08
	104492_at	13593	**Ebf3**	early B-cell factor 3	0.63;0.68;0.65	2.2969e-07;4.4122e-06;1.1503e-06
	98525_f_at	170942	**edr**	erythroid differentiation regulator	1.62;1.47;1.43	6.6354e-06;0.00019752;0.00039431
	103342_at	13626	**Eed**	embryonic ectoderm development	1.75;1.57;1.4	5.7577e-07;2.2096e-05;0.00064866
	103891_i_at	192657	**Ell2**	elongation factor RNA polymerase II 2	4.09;4.23;4.63	< 2.22e-16;< 2.22e-16;< 2.22e-16
	96523_at	13798	**En1**	engrailed 1	0.55;0.71;0.74	1.5563e-07;0.00050272;0.00145818
	99917_at	14056	**Ezh2**	enhancer of zeste homolog 2 (Drosophila)	2.43;2.36;2.02	8.0385e-07;2.6075e-06;3.7984e-05
	99835_at	14283	**Fosl1**	fos-like antigen 1	3.76;4.05;3.68	3.1947e-09;2.4987e-09;9.0928e-09
	102800_at	14234	**Foxc2**	forkhead box C2	1.74;1.78;1.76	2.9419e-09;2.7992e-09;4.4200e-09
	93704_at	15227	**Foxf1a**	forkhead box M1	0.68;0.66;0.73	2.1982e-06;1.3869e-06;5.1447e-05
	98305_at	14235	**Foxm1**	forkhead box M1	1.5;1.46;1.55	0.00051116;0.00142669;0.00034236
	97334_at	55927	**Hes6**	hairy and enhancer of split 6 (Drosophila)	0.64;0.82;0.81	1.1483e-06;0.0088633;0.0063437
	92484_at	15273	**Hivep2**	human immunodeficiency virus type I enhancer binding protein 2	1.99;2.72;2.6	1.7633e-07;5.1865e-10;1.2406e-09
	93013_at	15902	**Idb2**	inhibitor of DNA binding 2	0.6;0.49;0.52	4.0006e-06;4.5689e-08;2.2932e-07
	92614_at	15903	**Idb3**	inhibitor of DNA binding 3	0.74;0.66;0.79	0.00524779;0.00044558;0.03081184
	96144_at	15904	**Idb4**	inhibitor of DNA binding 4	0.53;0.43;0.41	8.5875e-08;1.0497e-09;4.5221e-10
	94774_at	26388	**Ifi202b**	interferon activated gene 202B	0.51;0.61;0.48	1.2854e-06;0.00016999;7.0124e-07
	160092_at	15982	**Ifrd1**	interferon-related developmental regulator 1	2.26;1.8;1.82	3.9913e-08;1.1238e-05;8.8047e-06

Function	Affy ID	Locus ID	Gene symbol	Description	Fold change	p-value
Regulation of transcription	100130_at	16476	**Jun**	Jun oncogene	1.57;1.61;1.65	1.1648e-10;8.3976e-11;3.2086e-11
	102364_at	16478	**Jund1**	Jun proto-oncogene related gene d1	0.63;0.8;0.74	1.2216e-06;0.00614997;0.00056188
	99622_at	16600	**Klf4**	Kruppel-like factor 4 (gut)	1.91;2.66;2.35	3.7798e-05;1.6141e-07;1.3291e-06
	92564_at	16978	**Lrrfip1**	leucine rich repeat (in FLII) interacting protein 1	2.64;2.36;1.96	3.7651e-10;7.9552e-09;5.1678e-07
	95379_at	23937	**Mab21l2**	mab-21-like 2 (C. elegans)	0.56;0.49;0.58	2.4577e-10;1.1704e-11;1.4265e-09
	99024_at	17122	**Mad4**	Max dimerization protein 4	0.46;0.51;0.48	9.9977e-12;4.5660e-10;1.0017e-10
	104220_at	17130	**Madh6**	MAD homolog 6 (Drosophila)	0.58;0.62;0.63	3.3233e-12;9.3438e-11;1.7821e-10
	96703_at	94275	**Maged1**	melanoma antigen, family D, 1	0.6;0.6;0.61	1.0185e-10;1.7649e-10;2.7891e-10
	98110_at	17246	**Mdm2**	transformed mouse 3T3 cell double minute 2	1.58;1.87;1.87	1.0225e-07;9.5069e-10;8.3754e-10
	98790_s_at	17268	**Meis1**	myeloid ecotropic viral integration site 1	0.58;0.57;0.56	1.0121e-09;1.8164e-09;9.6661e-10
	103779_at	223701	**Mkl1**	megakaryoblastic leukemia (translocation) 1 homolog (human)	0.64;0.58;0.6	8.0553e-11;3.1268e-12;9.4145e-12
	98979_at	17420	**Mnat1**	menage a trois 1	0.58;0.64;0.59	5.6839e-08;2.2131e-06;2.3442e-07
	92300_at	17428	**Mnt**	max binding protein	0.53;0.65;0.7	4.9768e-09;6.2203e-06;5.1241e-05
	92753_at	17537	**Mrg2**	myeloid ecotropic viral integration site-related gene 2	0.64;0.78;0.8	1.4315e-07;0.00051288;0.00143221
	100023_at	17865	**Mybl2**	myeloblastosis oncogene-like 2	1.58;1.52;1.43	1.7916e-10;1.8112e-09;3.9551e-08
	104712_at	17869	**Myc**	myelocytomatosis oncogene	2.16;1.89;1.86	7.1266e-06;0.00014138;0.00018854
	100962_at	17937	**Nab2**	Ngfi-A binding protein 2	0.71;0.59;0.61	0.00023112;1.7485e-06;4.6083e-06
	103791_at	74838	**Narg1**	NMDA receptor-regulated gene 1	1.74;1.57;1.43	3.2759e-07;1.3459e-05;0.00020755
	160859_s_a	18028	**Nfib**	nuclear factor I/B	0.45;0.63;0.56	2.1146e-06;0.00198121;0.00020248
	100307_at	18032	**Nfix**	nuclear factor I/X	0.51;0.7;0.64	5.338e-06;0.0077796;0.0010470
	101554_at	18035	**Nfkbia**	nuclear factor of kappa light chain gene enhancer in B-cells inhibitor, alpha	1.41;2.02;2.19	6.5687e-10;6.3942e-16;< 2.22e-16
	98988_at	80859	**Nfkbiz**	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta	1.69;2.83;2.59	1.4671e-05;4.0981e-10;2.1647e-09
	103048_at	18109	**Nmyc1**	neuroblastoma myc-related oncogene 1	1.54;1.61;1.31	1.5905e-05;7.7360e-06;0.0033130
	99564_at	18140	**Np95**	nuclear protein 95	1.87;1.81;1.64	2.3631e-06;9.2573e-06;9.2588e-05
	99076_at	353187	**Nr1d2**	nuclear receptor subfamily 1, group D, member 2	1.26;1.83;1.73	0.0012535;3.8891e-09;2.0815e-08
	102371_at	15370	**Nr4a1**	nuclear receptor subfamily 4, group A, member 1	3.23;2;2.58	5.5814e-13;3.1347e-08;9.4145e-11

Function	Affy ID	Locus ID	Gene symbol	Description	Fold change	p-value
Regulation of transcription	93615_at	18516	**Pbx3**	pre B-cell leukemia transcription factor 3	1.59;1.52;1.24	0.00025182;0.00096051;0.06249960
	93619_at	18626	**Per1**	period homolog 1 (Drosophila)	0.55;0.59;0.57	9.2718e-13;3.4698e-11;6.2797e-12
	104491_at	68770	**Phtf2**	putative homeodomain transcription factor 2	1.66;1.29;1.28	2.0866e-09;0.00011705;0.00020023
	160615_at	229615	**Pias3**	protein inhibitor of activated STAT 3	0.62;0.77;0.72	7.955e-07;0.00203520;0.00024886
	93325_at	66420	**Polr2e**	polymerase (RNA) II (DNA directed) polypeptide E	1.31;1.51;1.26	0.0025186;6.2924e-05;0.0104956
	104304_r_a	67005	**Polr3k**	polymerase (RNA) III (DNA directed) polypeptide K	1.6;1.56;1.38	0.00065267;0.00171916;0.01639016
	160793_at	19009	**Pou6f1**	POU domain, class 6, transcription factor 1	0.66;0.77;0.73	1.9787e-09;8.0745e-06;3.7476e-07
	103327_at	20204	**Prrx2**	paired related homeobox 2	0.31;0.31;0.36	4.8897e-12;1.7017e-11;1.5138e-10
	92901_at	19401	**Rara**	retinoic acid receptor, alpha	0.46;0.52;0.53	3.0885e-07;9.0358e-06;1.1677e-05
	96781_at	106298	**Rrn3**	RRN3 RNA polymerase I transcription factor homolog (yeast)	1.57;1.41;1.28	2.1037e-05;0.00071227;0.01087688
	92399_at	12394	**Runx1**	runt related transcription factor 1	1.66;1.98;1.61	1.9398e-08;1.9053e-10;1.1237e-07
	92722_f_at	20471	**Six1**	sine oculis-related homeobox 1 homolog (Drosophila)	0.25;0.22;0.2	9.7255e-14;6.4005e-14;1.7322e-14
	92999_at	20474	**Six4**	sine oculis-related homeobox 4 homolog (Drosophila)	0.53;0.51;0.47	1.0728e-09;7.5546e-10;9.3930e-11
	102384_at	67155	**Smarca2**	subunit of the SWI/SNF chromatin remodeling complex	0.36;0.5;0.39	9.7934e-09;1.0086e-05;8.1614e-08
	99552_at	20583	**Snai2**	snail homolog 2 (Drosophila)	0.52;0.59;0.61	2.4290e-11;3.5561e-09;9.5730e-09
	96260_at	56463	**Snd1**	staphylococcal nuclease domain containing 1	0.61;0.59;0.6	6.3724e-09;6.7419e-09;1.0621e-08
	95069_at	20833	**Ssrp1**	structure specific recognition protein 1	1.65;1.64;1.47	3.0832e-09;7.7409e-09;5.2481e-07
	99099_at	20848	**Stat3**	signal transducer and activator of transcription 3	0.62;0.61;0.7	1.2572e-09;2.2872e-09;4.1497e-07
	103746_at	52615	**Suz12**	suppressor of zeste 12 homolog (Drosophila)	1.84;1.97;1.74	9.8792e-06;3.7107e-06;5.3532e-05
	103889_at	99912	**Tbl1xr1**	transducin (beta)-like 1X-linked receptor 1	0.67;0.78;0.65	9.9534e-05;0.010027;4.9521e-05
	100354_at	21383	**Tbx14**	T-box 14	0.51;0.54;0.52	1.2123e-07;1.0490e-06;4.3363e-07
	102256_at	21384	**Tbx15**	T-box 15	0.54;0.48;0.48	1.0597e-08;7.6736e-10;1.0163e-09
	102344_s_a	21401	**Tcea3**	transcription elongation factor A (SII), 3	0.64;0.69;0.67	5.6786e-08;2.8980e-06;9.3769e-07
	101008_at	56070	**Tcerg1**	transcription elongation regulator 1 (CA150)	1.53;1.36;1.2	0.00012409;0.00407763;0.06446105
	102354_at	106795	**Tcf19**	transcription factor 19	1.93;1.93;1.75	1.0233e-05;1.6775e-05;0.00013473
	160780_at	21415	**Tcf3**	transcription factor 3	0.65;0.66;0.59	3.3589e-06;8.1498e-06;3.0537e-07

Function	Affy ID	Locus ID	Gene symbol	Description	Fold change	p-value
Regulation of transcription	160483_at	21413	**Tcf4**	transcription factor 4	0.77;0.69;0.66	0.00080502;2.0528e-05;3.8171e-06
	101959_r_at	21781	**Tfdp1**	transcription factor Dp 1	1.56;1.31;1.29	4.3554e-06;0.0021808;0.0035364
	101502_at	21815	**Tgif**	TG interacting factor	1.71;1.69;1.67	1.3089e-08;4.6017e-08;6.6716e-08
	92348_at	21833	**Thra**	thyroid hormone receptor alpha	0.51;0.51;0.55	2.9785e-13;5.9202e-13;5.8677e-12
	101372_at	69716	**Trip13**	thyroid hormone receptor interactor 13	1.88;1.81;1.81	3.3254e-07;1.6888e-06;1.6818e-06
	104154_at	22059	**Trp53**	transformation related protein 53	1.35;1.59;1.51	3.6025e-05;1.0676e-07;7.8102e-07
	98028_at	22160	**Twist1**	twist gene homolog 1 (Drosophila)	0.62;0.67;0.65	1.3548e-07;5.0924e-06;1.1209e-06
	99964_at	22337	**Vdr**	vitamin D receptor	0.43;0.44;0.44	2.1270e-09;5.9743e-09;6.8457e-09
	92480_f_at	24132	**Zfp118**	Zinc finger protein 118	1.52;1.75;1.5	5.7494e-05;2.1072e-06;0.00013935
	92934_at	22751	**Zfp90**	zinc finger protein 90	0.67;0.66;0.65	2.1003e-05;1.4833e-05;9.5780e-06
	92355_at	22762	**Zfpm2**	zinc finger protein, multitype 2	1.35;1.64;1.46	1.3506e-06;3.9267e-10;5.2592e-08
	160848_at	22770	**Zhx1**	zinc fingers and homeoboxes protein 1	0.55;0.65;0.53	1.8892e-09;1.0493e-06;1.7529e-09
	96707_at	22697	**Zipro1**	zinc finger proliferation 1	0.56;0.65;0.63	1.0996e-12;8.8886e-10;2.8420e-10
RNA metabolism	104399_at	108062	**Cstf2**	cleavage stimulation factor, 3' pre-RNA subunit 2	1.57;1.5;1.3	1.8866e-06;1.5746e-05;0.0019072
mRNA synthesis and processing	104126_at	83410	**Cstf2t**	cleavage stimulation factor, 3' pre-RNA subunit 2, tau	0.69;0.71;0.62	5.3751e-05;0.00017837;2.3337e-06
	160141_r_at	110809	**Sfrs1**	splicing factor, arginine/serine-rich 1 (ASF/SF2)	1.5;1.34;1.08	9.7234e-05;0.0030466;0.3903750
	160377_at	97174	**Tardbp**	TAR DNA binding protein	1.51;1.4;1.33	0.00044762;0.00389451;0.01210598
	95732_at	66125	**Sf3b5**	splicing factor 3b, subunit 5	1.42;1.52;1.33	0.00067536;0.00016127;0.00531412
	101506_at	68981	**Snrpa1**	small nuclear ribonucleoprotein polypeptide A'	2.04;1.92;1.68	7.7768e-05;0.00035503;0.00284476
	96038_at	319714	**Rnase4**	ribonuclease, RNase A family 4	0.46;0.65;0.73	2.6111e-05;0.010888;0.053641
	104610_at	226169	**Pprc1**	Peroxisome proliferative activated receptor, gamma, coactivator-related 1	1.53;1.34;1.19	0.00083296;0.01738228;0.14634258
	94455_at	67678	**Lsm3**	U6 small nuclear RNA associated	1.88;1.75;1.53	7.7031e-07;9.0208e-06;0.00025695
	93008_at	50783	**Lsm4**	U6 snRNA-associated SM-like protein 4	1.74;1.74;1.65	3.4107e-06;7.0859e-06;2.6874e-05
	102409_at	76522	**Lsm8**	LSM8 homolog, U6 small nuclear RNA associated	1.71;1.91;1.59	1.7656e-05;2.5042e-06;0.00019258
	103029_at	18569	**Pdcd4**	programmed cell death 4	0.3;0.41;0.34	1.4179e-10;5.6751e-08;1.8472e-09
	95649_at	68479	**Phf5a**	PHD finger protein 5A	1.68;1.54;1.42	3.6145e-07;9.9182e-06;0.00012506

Function	Affy ID	Locus ID	Gene symbol	Description	Fold change	p-value
RNA metabolism	95677_at	66585	**Prp8bp**	U5 snRNP-specific protein (Prp8-binding)	1.67;1.54;1.46	1.5853e-07;4.2634e-06;2.6617e-05
mRNA synthesis and processing	96029_at	75062	**Sf3a3**	splicing factor 3a, subunit 3, 60kDa	1.5;1.42;1.34	3.7746e-06;4.2236e-05;0.00035744
	100577_at	20641	**Snrpd1**	small nuclear ribonucleoprotein D1	1.46;1.52;1.33	0.00064639;0.00037611;0.00999292
	95049_at	107686	**Snrpd2**	small nuclear ribonucleoprotein D2	1.79;1.68;1.48	1.3273e-05;0.00010506;0.00177064
	98077_at	67332	**Snrpd3**	small nuclear ribonucleoprotein D3	1.59;1.52;1.47	0.00024621;0.00095799;0.00217753
	103969_at	20817	**Srpk2**	serine/arginine-rich protein specific kinase 2	0.53;0.63;0.56	3.2539e-08;8.2681e-06;3.8198e-07
	160471_at	20492	**Slbp**	stem-loop binding protein	1.93;2.08;1.69	1.3608e-06;5.1512e-07;5.3502e-05
	93892_at	14007	**Cugbp2**	CUG triplet repeat,RNA binding protein 2	0.62;0.66;0.62	1.2101e-06;1.7451e-05;2.0722e-06
	93518_at	19826	**Rnps1**	ribonucleic acid binding protein S1	1.63;1.55;1.47	6.7795e-11;1.5409e-09;1.3992e-08
	160429_at	56488	**Nxt1**	NTF2-related export protein 1	2.15;2.06;2.16	3.0451e-09;1.7390e-08;6.1514e-09
	160192_at	19656	**Rbmxrt**	RNA binding motif protein, X chromosome retrogene	1.66;1.67;1.53	3.4800e-06;5.2555e-06;6.2984e-05
	160633_at	21681	**Refbp1**	RNA and export factor binding protein 1	1.85;1.65;1.57	7.3270e-07;2.5328e-05;9.9415e-05
	104303_i_at	67005	**Polr3k**	polymerase (RNA) III (DNA directed) polypeptide K	1.63;1.64;1.41	5.6081e-05;8.7355e-05;0.0031478
rRNA synthesis and processing	94361_at	56200	**Ddx21**	DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 21 (RNA helicase II/Gu)	1.71;1.53;1.48	2.6133e-09;3.5070e-07;1.1680e-06
	160878_at	12181	**Bop1**	block of proliferation 1	1.84;1.7;1.57	1.0630e-09;3.2483e-08;4.2768e-07
	160503_at	14113	**Fbl**	fibrillarin	1.61;1.53;1.45	1.8258e-08;2.5999e-07;2.0250e-06
	95756_at	56095	**Ftsj3**	FtsJ homolog 3	1.81;1.65;1.41	4.6595e-06;7.5201e-05;0.0030554
	98531_g_at	14455	**Gas5**	growth arrest specific 5	0.5;0.62;0.52	2.1744e-09;2.4630e-06;1.6163e-08
	96804_at	110109	**Nol1**	nucleolar protein 1	1.82;1.62;1.58	3.1540e-13;5.9001e-11;1.9161e-10
	92569_f_at	55989	**Nol5**	nucleolar protein 5	1.88;1.57;1.43	8.9182e-07;0.00013373;0.00143720
	104766_at	68147	**Nola1**	nucleolar protein family A, member 1 (H/ACA small nucleolar RNPs)	1.51;1.41;1.37	1.4252e-05;0.00020120;0.00057371
	97824_at	52530	**Nola2**	nucleolar protein family A, member 2	2.69;2.51;2.53	3.5986e-09;2.7336e-08;2.4154e-08
	99194_at	71701	**Pnpt1**	3'-5' RNA exonuclease polynucleotide phosphorylase	1.6;1.68;1.43	2.8430e-08;1.0204e-08;4.8263e-06
	98923_at	59028	**Rcl1**	RNA terminal phosphate cyclase-like 1	1.55;1.56;1.39	1.1630e-06;1.6899e-06;8.3987e-05
	98021_at	64424	**Polr1e**	polymerase (RNA) I polypeptide E	1.57;1.49;1.38	8.9531e-10;1.6161e-08;6.0282e-07
	100037_at	66942	**Ddx18**	DEAD (Asp-Glu-Ala-Asp) box polypeptide 18	1.46;1.57;1.4	4.7496e-06;6.2204e-07;3.8318e-05

Function	Affy ID	Locus ID	Gene symbol	Description	Fold change	p-value
rRNA synthesis and processing	98938_at	68209	**AYP1**	RNase H1 small subunit	1.47;1.72;1.58	8.8575e-06;8.5572e-08;1.2231e-06
	100138_f_at	56275	**Rbm14**	RNA binding motif protein 14	1.57;1.45;1.27	3.7331e-07;1.4537e-05;0.0015650
	92517_at	56516	**Rbms2**	RNA binding motif, single stranded interacting protein 2	0.6;0.67;0.67	7.2340e-08;5.0902e-06;7.0393e-06
	98624_at	56190	**Rnpc1**	RNA-binding region (RNP1, RRM) containing 1	1.81;1.96;2	1.4799e-10;3.0106e-11;1.5905e-11
Metabolism	96346_at	12583	**Cdo1**	cysteine dioxygenase 1, cytosolic	0.12;0.17;0.18	9.7282e-14;1.1341e-11;2.3285e-11
Amino acid metabolism	160350_at	14874	**Gstz1**	glutathione transferase zeta 1 (maleylacetoacetate isomerase)	0.6;0.7;0.64	5.1513e-10;8.3115e-07;2.2361e-08
	104547_at	13361	**Dhfr**	dihydrofolate reductase	1.64;1.57;1.58	2.3341e-08;2.5008e-07;1.9757e-07
	96295_at	107272	**Psat1**	phosphoserine aminotransferase 1	1.51;1.3;1.25	0.00044702;0.02062371;0.04355673
	102022_at	73724	**Mcee**	methylmalonyl CoA epimerase	0.61;0.84;0.74	4.4492e-06;0.0510682;0.0021588
	160844_at	19286	**Pts**	6-pyruvoyl-tetrahydropterin synthase	0.62;0.67;0.65	6.7857e-07;1.2801e-05;3.8814e-06
	96763_at	192166	**Sardh**	sarcosine dehydrogenase	0.65;0.65;0.68	2.9935e-09;5.6179e-09;3.9190e-08
	93488_at	27364	**Srr**	serine racemase	1.7;1.46;1.38	2.2441e-07;5.1250e-05;0.00032439
Carbohydrate metabolism	94815_at	12183	**Bpgm**	2,3-bisphosphoglycerate mutase	1.28;1.7;1.52	0.007638;4.3455e-06;9.9365e-05
	93582_at	12850	**Coq7**	demethyl-Q 7	1.49;1.72;1.75	1.7824e-05;3.9366e-07;2.4156e-07
	101294_g_a	14380	**G6pd2**	glucose-6-phosphate dehydrogenase 2	1.27;1.52;1.39	0.00295764;1.2198e-05;0.00024172
	160516_at	14387	**Gaa**	glucosidase, alpha, acid	0.64;0.73;0.83	2.5886e-07;6.7676e-05;0.0083571
	160121_at	69976	**Galk2**	galactokinase 2	0.59;0.72;0.72	7.5436e-09;2.6480e-05;2.2823e-05
	101214_f_at	14433	**Gapd**	glyceraldehyde-3-phosphate dehydrogenase	1.46;1.51;1.35	1.2181e-10;5.9815e-11;2.4440e-08
	100488_at	14466	**Gba**	glucosidase, beta, acid	0.66;0.83;0.95	8.0422e-05;0.050273;0.567398
	96803_at	74185	**Gbe1**	glucan (1,4-alpha-), branching enzyme 1	1.49;1.6;1.4	0.00231644;0.00076589;0.01157655
	100565_at	26384	**Gnpi**	glucosamine-6-phosphate deaminase 1	0.63;0.96;0.99	1.0399e-05;0.66002;0.94373
	98931_at	75612	**Gns**	glucosamine (N-acetyl)-6-sulfatase	0.58;0.72;0.82	1.256e-06;0.00093185;0.03104001
	98984_f_at	14571	**Gpd2**	glycerol phosphate dehydrogenase 2, mitochondrial	1.65;2.06;1.83	3.5478e-08;8.6347e-11;2.8030e-09
	97525_at	14933	**Gyk**	glycerol kinase	1.51;1.43;1.41	5.2393e-11;2.0508e-09;3.3832e-09
	160571_at	15926	**Idh1**	isocitrate dehydrogenase 1 (NADP+), soluble	0.37;0.46;0.44	3.8265e-11;7.3288e-09;3.0086e-09
	94375_at	15277	**Hk2**	hexokinase 2	2.09;1.81;1.94	9.2950e-09;7.5906e-07;1.2578e-07
	96072_at	16828	**Ldh1**	lactate dehydrogenase 1, A chain	1.92;1.85;1.58	5.0196e-11;3.6138e-10;6.9587e-08

Function	Affy ID	Locus ID	Gene symbol	Description	Fold change	p-value
Metabolism	104628_at	17158	**Man2a1**	mannosidase 2, alpha 1	0.65;0.56;0.57	2.5939e-08;2.5809e-10;4.2545e-10
Carbohydrate metabolism	97398_at	74551	**Pck2**	phosphoenolpyruvate carboxykinase 2	0.6;0.57;0.53	3.6790e-08;9.3454e-09;1.4622e-09
	92637_at	18641	**Pfkl**	phosphofructokinase, liver, B-type	1.25;1.51;1.01	0.00072995;3.5743e-07;0.85754318
	160091_at	18648	**Pgam1**	phosphoglycerate mutase 1	1.56;1.65;1.39	3.9984e-09;1.1512e-09;1.1904e-06
	93346_at	18655	**Pgk1**	phosphoglycerate kinase 1	1.55;1.62;1.33	1.3913e-08;5.2487e-09;1.9605e-05
	97489_at	110078	**Pygb**	brain glycogen phosphorylase	0.57;0.62;0.59	1.4502e-07;3.0076e-06;8.0261e-07
	93738_at	20525	**Slc2a1**	solute carrier family 2 (facilitated glucose transporter), member 1	1.58;1.49;1.43	7.8051e-09;1.6633e-07;9.0816e-07
	104413_at	242585	**Slc35d1**	solute carrier family 35, member D1	1.91;1.66;1.75	1.4359e-09;2.3113e-07;4.3811e-08
	94216_at	66052	**Sdhc**	succinate dehydrogenase complex, subunit C, integral membrane protein	0.66;0.85;0.78	1.4023e-08;0.0032225;4.7255e-05
	95066_at	21351	**Taldo1**	transaldolase 1	1.75;1.99;1.9	3.1184e-10;1.0728e-11;4.3229e-11
Glutathione metabolism	160335_at	14630	**Gclm**	glutamate-cysteine ligase , modifier subunit	1.37;1.5;1.43	6.3448e-05;3.9073e-06;2.3883e-05
	160646_at	14782	**Gsr**	glutathione reductase 1	1.69;1.67;1.64	2.9095e-08;9.8841e-08;1.6784e-07
	96085_at	14860	**Gsta4**	glutathione S-transferase, alpha 4	0.44;0.72;0.59	8.2664e-11;0.00030913;6.0465e-07
	96258_at	66447	**Mgst3**	microsomal glutathione S-transferase 3	0.49;0.88;0.83	2.4868e-07;0.242287;0.089993
	102094_f_at	14862	**Gstm1**	glutathione S-transferase, mu 1	0.26;0.41;0.32	1.9429e-14;1.4851e-10;1.3950e-12
	93009_at	14863	**Gstm2**	glutathione S-transferase, mu 2	0.44;0.55;0.5	4.2280e-09;1.9440e-06;1.6882e-07
	97681_f_at	14864	**Gstm3**	glutathione S-transferase, mu 3	0.53;0.62;0.56	3.6912e-13;2.5364e-10;5.5546e-12
	100629_at	14866	**Gstm5**	glutathione S-transferase, mu 5	0.42;0.59;0.52	2.2918e-12;6.4724e-08;9.7648e-10
	97819_at	14873	**Gsto1**	glutathione S-transferase omega 1	2.21;2.41;2.84	3.2888e-15;8.9653e-16;< 2.22e-16
Electron transporter	100568_at	24015	**Abce1**	ATP-binding cassette, sub-family E (OABP), member 1	1.74;1.41;1.41	2.7292e-08;5.4472e-05;5.8826e-05
	93845_at	27407	**Abcf2**	ATP-binding cassette, sub-family F (GCN20), member 2	1.56;1.46;1.46	3.5493e-14;2.9869e-12;2.1772e-12
	160286_at	218214	**Aof1**	amine oxidase, flavin containing 1	1.67;1.56;1.34	0.0004291;0.0023866;0.0356377
	103275_at	11975	**Atp6v0a1**	ATPase, H+ transporting, lysosomal V0 subunit a isoform 1	0.6;0.64;0.78	6.7410e-06;8.9152e-05;0.012910
	92603_at	11972	**Atp6v0d1**	ATPase, H+ transporting, V0 subunit D isoform 1	0.43;0.6;0.68	5.2081e-09;1.9884e-05;0.00070951
	95746_at	11964	**Atp6v1a1**	ATPase, H+ transporting, V1 subunit A, isoform 1	0.55;0.74;0.83	7.965e-06;0.012312;0.105990
	95656_i_at	66144	**Atp6v1f**	ATPase, H+ transporting, V1 subunit F	1.76;1.67;1.49	8.1112e-07;7.0821e-06;0.00016804
	98132_at	13063	**Cycs**	cytochrome c, somatic	2.18;2.06;1.8	6.6381e-07;4.0899e-06;6.4559e-05
	99979_at	13078	**Cyp1b1**	cytochrome P450, family 1, subfamily b, polypeptide 1	0.33;0.22;0.32	2.2348e-11;7.0039e-14;2.9078e-11
	160611_at	102294	**Cyp4v3**	cytochrome P450, family 4, subfamily v, polypeptide 3	0.57;0.7;0.71	1.1200e-06;0.00054137;0.00085302

Function	Affy ID	Locus ID	Gene symbol	Description	Fold change	p-value
Metabolism	93749_at	17161	**Maoa**	monoamine oxidase A	0.64;0.78;0.85	4.6328e-05;0.014504;0.091659
Electron transporter	160237_at	67130	**Ndufa6**	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 6 (B14)	0.62;0.89;0.75	1.0256e-05;0.1992589;0.0046108
	94515_at	59010	**Sqrdl**	sulfide quinone reductase-like (yeast)	1.4;2.23;1.8	0.00013943;4.3729e-10;1.0298e-07
	92807_at	22166	**Txn1**	thioredoxin 1	1.37;1.51;1.37	5.6268e-05;2.5627e-06;9.0346e-05
	99985_at	50493	**Txnrd1**	thioredoxin reductase 1	1.77;1.72;1.63	3.0160e-10;1.7187e-09;1.1363e-08
	97950_at	22436	**Xdh**	xanthine dehydrogenase	0.43;0.99;0.99	0.000625;0.954339;0.948791
Lipid metabolism	92581_at	11364	**Acadm**	acetyl-Coenzyme A dehydrogenase, medium chain	0.56;0.61;0.64	4.2167e-10;1.6484e-08;1.1441e-07
	94850_at	64833	**Acot10**	acyl-CoA thioesterase 10	1.59;1.8;1.76	3.0384e-07;1.2427e-08;2.1802e-08
	100539_at	70025	**Acot7**	acyl-CoA thioesterase 7	1.39;1.57;1.47	2.5680e-10;1.1588e-12;2.8692e-11
	160171_f_at	56360	**Acot9**	acyl-CoA thioesterase 9	1.66;1.7;1.59	1.0033e-09;8.6808e-10;1.0785e-08
	100931_at	11883	**Arsa**	arylsulfatase A	0.33;0.47;0.48	3.8613e-10;8.9930e-07;1.0945e-06
	100026_at	12035	**Bcat1**	branched chain aminotransferase 1, cytosolic	1.5;1.29;1.37	2.0137e-05;0.0040235;0.0006209
	93320_at	12894	**Cpt1a**	carnitine palmitoyltransferase 1a, liver	0.66;0.83;0.8	7.3191e-08;0.00319984;0.00060124
	98533_at	109672	**Cyb5**	cytochrome b-5	0.55;0.73;0.62	3.4944e-08;0.00037959;2.6703e-06
	160711_at	67460	**Decr1**	2,4-dienoyl CoA reductase 1, mitochondrial	0.56;0.71;0.64	2.7082e-09;2.0594e-05;6.5239e-07
	98989_at	13360	**Dhcr7**	7-dehydrocholesterol reductase	0.48;0.46;0.49	3.4188e-12;2.6366e-12;1.4363e-11
	102370_at	114664	**Dhrs8**	dehydrogenase/reductase (SDR family) member 8	0.35;0.51;0.53	3.2081e-09;9.1488e-06;2.3354e-05
	93754_at	51798	**Ech1**	enoyl coenzyme A hydratase 1, peroxisomal	0.44;0.59;0.55	4.8663e-14;7.2508e-10;6.3666e-11
	97456_at	71879	**Facl5**	fatty acid Coenzyme A ligase, long chain 5	1.42;1.54;1.32	0.00016576;2.2111e-05;0.00249462
	102123_at	16889	**Lip1**	lysosomal acid lipase 1	0.6;0.82;0.77	5.3631e-07;0.0142504;0.0022718
	98865_at	15117	**Has2**	hyaluronan synthase 2	1.87;1.14;1.23	6.567e-08;0.130943;0.019215
	94325_at	208715	**Hmgcs1**	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1	0.71;0.55;0.61	2.1285e-08;1.7018e-12;6.7925e-11
	98892_at	14245	**Lpin1**	lipin 1	0.39;0.45;0.48	8.1210e-09;2.5187e-07;1.1207e-06
	160737_at	16987	**Lss**	lanosterol synthase	0.69;0.63;0.68	6.7958e-08;3.4976e-09;9.1358e-08
	160770_at	192156	**Mvd**	mevalonate (diphospho) decarboxylase	0.64;0.64;0.74	6.0272e-08;1.0975e-07;3.8572e-05
	93316_at	64291	**Osbpl1a**	oxysterol binding protein-like 1A	0.62;0.85;0.7	0.00015759;0.13931461;0.00343534
	92845_at	67041	**Oxct**	3-oxoacid CoA transferase	0.55;0.62;0.61	7.8808e-07;2.6556e-05;1.9175e-05
	102049_at	27273	**Pdk4**	pyruvate dehydrogenase kinase, isoenzyme 4	0.32;0.31;0.34	8.6601e-14;8.7205e-14;4.2227e-13

Function	Affy ID	Locus ID	Gene symbol	Description	Fold change	p-value
Metabolism	96608_at	16922	**Phyh**	phytanoyl-CoA hydroxylase	0.46;0.52;0.49	6.3607e-10;3.5950e-08;6.1946e-09
Lipid metabolism	92304_at	18700	**Piga**	phosphatidylinositol glycan, class A	1.55;1.42;1.26	7.1103e-05;0.0011263;0.0211443
	99513_at	18783	**Pla2g4a**	phospholipase A2, group IVA (cytosolic, calcium-dependent)	2.05;1.82;1.84	5.7346e-12;4.8563e-10;3.7526e-10
	101923_at	27226	**Pla2g7**	phospholipase A2, group VII (platelet-activating factor acetylhydrolase, plasma)	0.67;0.76;0.57	4.4016e-06;0.00083822;5.7615e-08
	100927_at	18830	**Pltp**	phospholipid transfer protein	0.31;0.43;0.41	1.4999e-10;9.8542e-08;3.4556e-08
	100332_s_a	11758	**Prdx6**	peroxiredoxin 6	1.77;1.98;1.96	3.0580e-07;3.4726e-08;4.0742e-08
	97114_at	19156	**Psap**	prosaposin	0.61;0.87;0.98	8.8255e-06;0.12890;0.79436
	94056_at	20249	**Scd1**	stearoyl-Coenzyme A desaturase 2	0.56;0.5;0.52	1.5236e-08;1.5818e-09;4.6571e-09
	93278_at	20280	**Scp2**	sterol carrier protein 2, liver	0.54;0.63;0.57	1.4507e-09;5.0729e-07;2.2794e-08
	95787_s_at	20282	**Scp2-ps2**	sterol carrier protein 2, pseudogene 2	0.59;0.75;0.71	8.2499e-09;9.7510e-05;1.1115e-05
	99566_at	21991	**Tpi**	triosephosphate isomerase	1.38;1.5;1.2	4.1128e-07;1.9136e-08;0.0011107
Nucleobase, nucleoside and nucleotide metabolism	99521_at	11639	**Ak4**	adenylate kinase 4	1.57;1.54;1.3	4.0213e-13;2.4599e-12;3.2752e-08
	98071_f_at	13178	**Dck**	deoxycytidine kinase	2.21;2.15;1.97	5.2396e-08;1.9648e-07;1.3104e-06
	93290_at	18950	**Pnp**	purine-nucleoside phosphorylase	0.62;0.75;0.76	6.409e-05;0.010573;0.014318
	98618_at	21915	**Dtymk**	deoxythymidylate kinase	1.5;1.46;1.43	2.5526e-09;2.0678e-08;4.6303e-08
	92244_at	26909	**Exo1**	exonuclease 1	1.79;1.61;1.48	4.6102e-09;3.0530e-07;5.8018e-06
	103341_at	51797	**Ctps**	cytidine 5'-triphosphate synthase	1.78;1.59;1.62	3.7144e-12;6.3435e-10;3.3011e-10
	100066_at	14450	**Gart**	phosphoribosylglycinamide formyltransferase	1.56;1.43;1.28	2.3695e-09;2.3810e-07;4.4698e-05
	160107_at	15452	**Hprt**	hypoxanthine guanine phosphoribosyl transferase	1.71;1.66;1.58	1.0831e-07;5.1868e-07;2.3551e-06
	96876_at	17775	**Laptm4a**	lysosomal-associated protein transmembrane 4A	0.44;0.57;0.69	1.3286e-06;0.0003055;0.0098469
	92794_f_at	18102	**Nme1**	expressed in non-metastatic cells 1, protein	1.83;1.72;1.61	6.2381e-05;0.00031783;0.00119703
	94982_f_at	79059	**Nme3**	expressed in non-metastatic cells 3	0.61;0.86;0.73	2.878e-05;0.1324438;0.0040271
	100606_at	19122	**Prnp**	prion protein	0.7;0.6;0.74	5.5535e-11;1.6114e-13;3.3991e-09
	100612_at	20133	**Rrm1**	ribonucleotide reductase M1	2.36;1.94;1.86	7.8585e-08;8.3218e-06;1.9227e-05
	96081_at	21877	**Tk1**	thymidine kinase 1	2.2;2.1;2.1	1.2849e-07;6.7540e-07;6.6016e-07
	93236_s_at	22171	**Tyms**	thymidylate synthase	2.02;2.09;1.91	6.8530e-06;6.3986e-06;3.4332e-05
	94367_at	80914	**Uck2**	uridine-cytidine kinase 2	2.14;2.03;2.19	4.5326e-10;3.7856e-09;5.5312e-10
Other	96024_at	269378	**Ahcy**	S-adenosylhomocysteine hydrolase	1.68;1.64;1.45	9.1027e-08;3.7241e-07;2.4090e-05
	100068_at	11668	**Aldh1a1**	aldehyde dehydrogenase family 1, subfamily A1	0.14;0.17;0.19	3.8405e-09;6.4974e-08;1.4285e-07

Function	Affy ID	Locus ID	Gene symbol	Description	Fold change	p-value
Metabolism	94778_at	26358	**Aldh1a7**	aldehyde dehydrogenase family 1, subfamily A7	0.52;0.55;0.58	2.0871e-07;1.8807e-06;6.6548e-06
Other	96231_at	68021	**Bphl**	biphenyl hydrolase-like	0.56;0.68;0.73	5.7247e-10;1.5237e-06;2.9538e-05
	95620_at	66375	**Dhrs7**	dehydrogenase/reductase (SDR family) member 7	0.5;0.85;0.76	3.3062e-10;0.03048014;0.00051235
	92553_at	13885	**Es10**	esterase 10	2.26;2.37;2.16	1.0652e-12;7.5547e-13;7.9855e-12
	101408_at	14431	**Gamt**	guanidinoacetate methyltransferase	0.59;0.67;0.66	1.6255e-12;8.5152e-10;3.5377e-10
	103085_at	15199	**Hebp1**	heme binding protein 1	0.59;0.72;0.78	9.3636e-09;3.4334e-05;0.00074836
	100046_at	17768	**Mthfd2**	methylenetetrahydrofolate dehydrogenase (NAD+ dependent)	1.99;1.48;1.45	6.0795e-06;0.0040112;0.0061833
	97385_at	56174	**Nagk**	N-acetylglucosamine kinase	0.47;0.57;0.59	6.6752e-13;5.9608e-10;1.1918e-09
	101473_at	18113	**Nnmt**	nicotinamide N-methyltransferase	0.63;0.65;0.66	1.1052e-10;1.4087e-09;2.2959e-09
	160084_at	18263	**Odc**	ornithine decarboxylase, structural	1.86;1.66;1.54	1.0871e-07;4.6532e-06;4.1837e-05
	161433_f_at	18700	**Piga**	phosphatidylinositol glycan, class A	1.51;1.4;1.21	8.2918e-09;6.2258e-07;0.00062098
	104378_at	18980	**Pon2**	paraoxonase 2	2.04;1.9;1.88	7.3819e-11;1.3172e-09;1.6579e-09
	161694_f_at	19224	**Ptgs1**	prostaglandin-endoperoxide synthase 1	1.49;1.51;1.39	8.2291e-08;1.1667e-07;3.6683e-06
	104647_at	19225	**Ptgs2**	prostaglandin-endoperoxide synthase 2	14.83;7.85;10.36	9.0410e-10;2.1966e-07;2.5941e-08
	94259_at	56351	**Ptges3**	prostaglandin E synthase 3 (cytosolic)	1.52;1.38;1.14	5.803e-06;0.00024395;0.08143506
	160314_at	67895	**Pyp**	pyrophosphatase	2.1;1.81;1.69	2.3833e-09;2.3486e-07;1.6218e-06
	98459_at	20425	**Shmt1**	serine hydroxymethyl transferase 1 (soluble)	1.62;1.74;1.55	7.6218e-11;1.1221e-11;1.0069e-09
	96042_at	20656	**Sod2**	superoxide dismutase 2, mitochondrial	1.4;1.67;1.54	1.9668e-06;3.1061e-09;7.5215e-08
	93557_at	20768	**Sps2**	selenophosphate synthetase 2	1.5;1.66;1.65	0.00010530;1.1268e-05;1.2370e-05
	92540_f_at	20810	**Srm**	spermidine synthase	1.69;1.57;1.44	2.4916e-07;4.9671e-06;7.9820e-05
	99580_s_at	94284	**Ugt1a6**	UDP glucuronosyltransferase 1 family, polypeptide A6A	0.51;0.81;0.73	7.3065e-07;0.0505476;0.0061588
	95709_at	27973	**Vkorc1**	vitamin K epoxide reductase complex, subunit 1	0.51;0.59;0.59	7.3512e-09;1.0255e-06;1.0174e-06
Transport	99138_at	100088	**Chc1**	chromosome condensation 1	1.72;1.68;1.71	3.8809e-06;1.4099e-05;8.2386e-06
Protein-nucleus import	104317_at	110750	**Cse1l**	chromosome segregation 1-like (S. cerevisiae)	1.86;1.68;1.43	3.8849e-07;1.1656e-05;0.00080526
	104297_at	76582	**Ipo11**	importin 11	1.5;1.34;1.28	1.0218e-08;4.3154e-06;3.4529e-05
	93970_at	233726	**Ipo7**	importin 7	1.94;1.68;1.53	8.5540e-07;4.6038e-05;0.00043933
	92790_at	16647	**Kpna2**	karyopherin (importin) alpha 2	2.84;2.48;2.22	8.5420e-06;8.9834e-05;0.000376
	93111_at	16211	**Kpnb1**	karyopherin (importin) beta 1	1.65;1.55;1.51	3.5047e-08;6.0160e-07;1.5648e-06

Function	Affy ID	Locus ID	Gene symbol	Description	Fold change	p-value
Transport	93070_at	70572	**Kpnb3**	karyopherin (importin) beta 3	1.76;1.55;1.42	1.7560e-06;9.8113e-05;0.0010786
Protein-nucleus import	98602_at	19387	**Rangap1**	RAN GTPase activating protein 1	1.86;1.58;1.87	3.3836e-07;4.5458e-05;6.1552e-07
	94228_at	103573	**Xpo1**	exportin 1, CRM1 homolog (yeast)	1.66;1.4;1.23	2.6836e-06;0.00071009;0.02209569
Vesicular transport	101393_at	11745	**Anxa3**	annexin A3	1.82;1.73;1.76	8.6111e-07;5.5960e-06;3.6151e-06
	94304_at	11749	**Anxa6**	annexin A6	0.51;0.48;0.5	1.8302e-11;4.8420e-12;1.8809e-11
	100584_at	11746	**Anxa4**	annexin A4	0.57;0.69;0.66	9.3793e-11;5.7582e-07;7.1154e-08
	160734_at	11777	**Ap3s1**	adaptor-related protein complex 3, sigma 1 subunit	0.39;0.52;0.53	1.2813e-11;2.8723e-08;3.1730e-08
	160280_at	12389	**Cav**	caveolin, caveolae protein	0.59;0.52;0.5	2.6903e-07;1.3423e-08;7.2626e-09
	100579_s_a	12757	**Clta**	clathrin, light polypeptide (Lca)	0.62;0.77;0.76	2.7534e-06;0.0042745;0.0026236
	104143_at	56358	**Copz2**	coatomer protein complex, subunit zeta 2	0.4;0.43;0.44	< 2.22e-16;< 2.22e-16;3.854e-16
	103030_at	13429	**Dnm**	dynamin 1	0.61;0.83;0.81	4.8988e-05;0.079789;0.049787
	99187_f_at	67023	**Ed2**	mouse embryonic development factor 2	0.57;0.69;0.66	8.7108e-08;8.2149e-05;1.2597e-05
	160812_at	74105	**Gga2**	golgi associated, gamma adaptin ear containing, ARF binding protein 2	0.66;0.71;0.77	8.8614e-08;3.1528e-06;0.00013274
	97409_at	15944	**Ifi1**	interferon inducible protein 1	1.58;1.42;1.59	1.0240e-06;7.3933e-05;1.4894e-06
	104464_s_a	105785	**Kdelr3**	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3	0.71;0.65;0.61	0.00021878;1.8299e-05;2.5934e-06
	101590_at	16784	**Lamp2**	lysosomal membrane glycoprotein 2	0.52;0.67;0.65	3.0926e-08;8.4442e-05;2.8554e-05
	161086_at	22343	**Lin7c**	lin 7 homolog c (C. elegans)	1.5;1.44;1.49	0.00057984;0.00229227;0.00103356
	104264_at	80877	**Lrba**	LPS-responsive beige-like anchor	0.71;0.66;0.78	1.5814e-07;1.5253e-08;3.5195e-05
	92854_at	53869	**Rab11a**	RAB11a, member RAS oncogene family	0.61;0.79;0.76	1.3452e-06;0.0077403;0.0017326
	93347_at	19336	**Rab24**	RAB24, member RAS oncogene family	0.66;0.85;0.89	6.6551e-05;0.070623;0.195845
	97415_at	19340	**Rab3d**	RAB3D, member RAS oncogene family	0.59;0.67;0.67	6.1466e-10;1.4280e-07;1.4909e-07
	98731_at	19344	**Rab5b**	RAB5B, member RAS oncogene family	0.61;0.75;0.84	0.00015922;0.01815095;0.13976382
	95516_at	56382	**Rab9**	RAB9, member RAS oncogene family	0.47;0.61;0.61	1.5935e-07;9.5515e-05;0.00010924
	94269_at	14470	**Rabac1**	Rab acceptor 1 (prenylated)	0.6;0.72;0.75	1.9571e-07;0.00017296;0.00062891
	160827_at	74030	**Rin2**	Ras and Rab interactor 2	0.48;0.57;0.65	1.1791e-08;2.0123e-06;5.5604e-05
	93440_at	75365	**Sec22l1**	SEC22 vesicle trafficking protein-like 1 (S. cerevisiae)	0.7;0.68;0.63	7.5880e-08;7.6684e-08;2.9367e-09
	104709_at	20334	**Sec23a**	SEC23A (S. cerevisiae)	0.58;0.54;0.49	5.2045e-10;1.2221e-10;1.0683e-11
	103381_at	69162	**Sec31l1**	SEC31-like 1 (S. cerevisiae)	0.63;0.66;0.63	2.4233e-11;4.1282e-10;8.9115e-11
	160792_at	20615	**Snap25bp**	SNAP-associated protein	0.66;0.84;0.85	2.0107e-07;0.0072867;0.0120099

Function	Affy ID	Locus ID	Gene symbol	Description	Fold change	p-value
Vesicular transport	103781_at	20909	**Stx4a**	syntaxin 4A (placental)	0.66;0.78;0.77	4.9793e-05;0.0094163;0.0056483
	96076_at	56389	**Stx5a**	syntaxin 5A	0.64;0.73;0.72	1.0024e-12;2.3167e-09;1.1292e-09
	96708_at	66111	**Tmed3**	transmembrane emp24 domain containing 3	0.56;0.62;0.62	5.4486e-10;4.6471e-08;4.0062e-08
	161006_at	68581	**Tmed10**	transmembrane emp24-like trafficking protein 10 (yeast)	1.54;1.38;1.59	4.0592e-10;1.5763e-07;2.5754e-10
	103578_at	21968	**Tom1**	target of myb1 homolog (chicken)	0.64;0.7;0.82	3.3790e-07;1.5047e-05;0.0054067
	96847_at	66914	**Vps28**	vacuolar protein sorting 28 (yeast)	0.64;0.81;0.76	1.1953e-08;0.00051976;3.0449e-05
	96667_at	218035	**Vps41**	vacuolar protein sorting 41 (yeast)	0.63;0.78;0.76	1.7444e-07;0.00089835;0.00028699
Other	103069_at	72568	**Lin9**	lin-9 homolog	1.79;1.71;1.49	5.2505e-08;4.0042e-07;3.0563e-05
	103443_at	11630	**Aim1**	absent in melanoma 1	0.63;0.59;0.61	3.4292e-09;5.2005e-10;1.7852e-09
	160713_at	100494	**Airap**	arsenite inducible RNA associated protein	1.23;1.43;1.59	0.0008981;2.2364e-06;3.3864e-08
	161359_s_a	246703	**Apoa1bp**	apolipoprotein A-I binding protein	0.58;0.74;0.68	3.2921e-10;1.0206e-05;2.7939e-07
	95058_f_at	70456	**Brp44**	brain protein 44	0.59;0.78;0.63	0.00018651;0.05033056;0.00107928
	92525_i_at	68136	**Btbd14a**	BTB (POZ) domain containing 14A	0.66;0.71;0.71	3.1524e-13;4.0166e-11;3.1143e-11
	160585_at	67239	**Bxdc1**	brix domain containing 1	1.62;1.59;1.2	8.5558e-05;0.00021759;0.09343778
	96775_at	12412	**Cbx1**	chromobox homolog 1 (Drosophila HP1 beta)	1.69;1.22;1.06	6.3586e-07;0.022970;0.463789
	96902_at	67282	**Ccdc53**	coiled-coil domain containing 53	0.65;0.78;0.73	8.6874e-07;0.00162150;0.00014691
	160298_at	67896	**Ccdc80**	coiled-coil domain containing 80	0.71;0.57;0.57	0.0024131;1.6880e-05;1.7109e-05
	96200_at	71963	**Cdca4**	cell division cycle associated 4	1.53;1.49;1.4	8.6838e-08;5.3126e-07;5.2361e-06
	97295_at	52276	**Cdca8**	cell division cycle associated 8	2.44;2.22;2.19	6.3002e-06;5.0125e-05;5.9483e-05
	93094_at	12585	**Cdr2**	cerebellar degeneration-related 2	1.72;1.63;1.45	2.8491e-07;2.7426e-06;9.8114e-05
	102215_at	12589	**Cdv1**	carnitine deficiency-associated gene expressed in ventricle 1	0.58;0.67;0.62	1.4087e-12;1.6438e-09;5.5064e-11
	97841_at	68953	**Chmp2a**	chromatin modifying protein 2A	0.63;0.75;0.71	2.6349e-08;6.5959e-05;6.1113e-06
	97928_at	52809	**Cln6**	ceroid-lipofuscinosis, neuronal 6	0.62;0.7;0.72	7.6415e-11;4.3117e-08;1.6143e-07
	93550_at	13008	**Csrp2**	cysteine and glycine-rich protein 2	0.62;0.79;0.59	2.7440e-05;0.021156;1.2186e-05
	95161_at	52468	**Ctdsp2**	nuclear LIM interactor-interacting factor 2	0.6;0.66;0.63	7.6816e-10;4.6378e-08;1.0400e-08
	96912_s_at	13024	**Ctla2a**	cytotoxic T lymphocyte-associated protein 2 alpha	0.11;0.2;0.24	2.0027e-08;5.6687e-06;3.3753e-05
	103518_at	13025	**Ctla2b**	cytotoxic T lymphocyte-associated protein 2 beta	0.55;0.78;0.83	7.6956e-05;0.071214;0.161957
	103467_g_a	54151	**Cyhr1**	cysteine and histidine rich 1	1.58;1.56;1.37	5.3907e-10;1.9906e-09;7.9378e-07
	103442_at	216820	**Dhrs7b**	dehydrogenase/reductase (SDR family) member 7B	1.54;1.51;1.49	1.2681e-06;4.8195e-06;8.6044e-06

Function	Affy ID	Locus ID	Gene symbol	Description	Fold change	p-value
Other	98489_at	218977	**Dlg7**	discs, large homolog 7 (Drosophila)	1.64;1.55;1.53	3.4242e-06;3.2581e-05;3.9933e-05
	101975_at	13386	**Dlk1**	delta-like 1 homolog (Drosophila)	0.28;0.28;0.28	< 2.22e-16;< 2.22e-16;< 2.22e-16
	101503_at	22240	**Dpysl3**	UDP-glucose ceramide glucosyltransferase	1.67;1.83;1.58	1.0614e-07;1.3134e-08;1.4247e-06
	97498_at	14199	**Fhl1**	four and a half LIM domains 1	4.35;1.73;2.65	7.6561e-10;0.0016759;1.6961e-06
	160648_at	60530	**Fignl1**	fidgetin-like 1	2.22;2.2;2.01	1.6546e-06;3.5979e-06;1.9078e-05
	97124_at	14210	**Fin15**	fibroblast growth factor inducible 15	1.64;1.54;1.26	0.00021061;0.00123549;0.06495189
	104333_at	110956	**G7e**	G7e protein	1.83;1.93;1.89	0.00012519;7.1102e-05;0.00010945
	101001_at	68151	**Gpr177**	G protein-coupled receptor 177	0.59;0.63;0.63	1.7722e-08;2.8712e-07;3.3400e-07
	103853_at	101612	**Grwd1**	glutamate rich WD repeat protein GRWD	1.89;1.53;1.44	9.0858e-09;1.1609e-05;7.3557e-05
	160172_at	17263	**Gtl2**	GTL2, imprinted maternally expressed untranslated mRNA	0.35;0.34;0.38	4.0400e-12;6.1611e-12;5.8476e-11
	160399_r_at	26914	**H2afy**	H2A histone family, member Y	1.53;1.35;1.16	0.00017813;0.00568215;0.14078386
	94266_at	353502	**Hcfc1r1**	host cell factor C1 regulator 1	0.52;0.65;0.66	4.0714e-10;1.1295e-06;2.1329e-06
	93228_at	15201	**Hells**	helicase, lymphoid specific	2.94;2.76;2.4	5.9207e-07;2.8693e-06;2.1832e-05
	101094_at	56295	**Higd1a**	HIG1 domain family, member 1A	1.41;1.5;1.34	4.4786e-05;8.4571e-06;0.00042613
	103639_at	15958	**Ifit2**	interferon-induced protein with tetratricopeptide repeats 2	1.2;1.66;1.44	0.0081353;6.9621e-08;9.6119e-06
	104760_at	15983	**Ifrd2**	interferon-related developmental regulator 2	2;1.87;1.74	4.8086e-09;6.0575e-08;4.8167e-07
	104640_f_at	75316	**Josd3**	osephin domain containing 3	1.54;1.34;1.27	1.0269e-05;0.0012067;0.0061611
	160341_at	231872	**Jtv1**	JTV1 gene	1.83;1.73;1.5	2.7727e-08;3.2698e-07;2.4050e-05
	100136_at	16784	**Lamp2**	lysosomal membrane glycoprotein 2	0.6;0.84;0.81	2.2139e-06;0.060032;0.022221
	93451_at	223152	**Lmo7**	LIM domain only 7	0.18;0.17;0.21	1.4515e-11;2.8900e-11;2.9129e-10
	94486_at	98238	**Lrrc59**	leucine rich repeat containing 59	1.74;1.37;1.39	3.2822e-11;1.6674e-06;8.8940e-07
	94289_r_at	80884	**Maged2**	melanoma antigen, family D, 2	0.51;0.53;0.58	2.0702e-11;1.5564e-10;3.5580e-09
	97252_at	69902	**Mg684**	muscle protein684	1.51;1.45;1.38	8.1290e-10;1.3243e-08;1.2013e-07
	94499_at	76055	**Mgea5**	meningioma expressed antigen 5 (hyaluronidase)	0.68;0.73;0.65	1.1582e-05;0.00023586;5.9886e-06
	101108_at	50927	**Nasp**	nuclear autoantigenic sperm protein (histone-binding)	2.12;2.04;1.76	1.7211e-06;6.8860e-06;0.00013196
	93025_at	65113	**Ndfip1**	Nedd4 family interacting protein 1	0.65;0.8;0.72	2.9385e-06;0.00548469;0.00017405
	98554_at	29812	**Ndr3**	N-myc downstream regulated 3	0.65;0.71;0.66	5.8499e-08;5.6164e-06;2.7425e-07
	160344_at	67963	**Npc2**	Niemann Pick type C2	0.52;0.7;0.76	9.3323e-08;0.00066816;0.00615136
	94450_at	28114	**Nsun2**	NOL1/NOP2/Sun domain family 2	1.69;1.53;1.62	6.8667e-07;2.5410e-05;5.1147e-06

Function	Affy ID	Locus ID	Gene symbol	Description	Fold change	p-value
Other	94528_at	26425	**Nubp1**	nucleotide binding protein 1	1.5;1.56;1.48	5.3617e-08;2.6568e-08;1.8922e-07
	102197_at	53322	**Nucb2**	nucleobindin 2	0.66;0.72;0.7	0.00059925;0.00571144;0.00372258
	160395_at	52653	**Nudcd2**	NudC domain containing 2	1.57;1.4;1.25	0.00050847;0.00860807;0.06556086
	102907_at	208177	**Phldb2**	pleckstrin homology-like domain, family B, member 2	1.67;1.45;1.68	3.8683e-06;0.00032602;6.1010e-06
	98552_at	67037	**Pmf1**	polyamine-modulated factor 1	1.29;1.5;1.36	0.00118806;1.2479e-05;0.00028937
	99366_at	217430	**Pqlc3**	PQ loop repeat containing	1.38;1.69;1.57	5.7074e-07;1.8621e-10;3.0783e-09
	160204_at	73139	**Prr6**	proline-rich polypeptide 6	1.34;1.99;1.48	3.8013e-05;4.4722e-11;9.2106e-07
	99599_s_at	84113	**Ptov1**	prostate tumor over expressed gene 1	0.5;0.58;0.62	7.3414e-12;1.9817e-09;1.7298e-08
	160896_at	19672	**Rcn**	reticulocalbin	0.71;0.67;0.61	6.7060e-05;1.3075e-05;7.5255e-07
	100959_at	20196	**S100a13**	S100 calcium binding protein A13	0.48;0.64;0.57	9.7918e-13;2.4815e-08;6.0393e-10
	160708_at	30953	**Schip1**	schwannomin interacting protein 1	2.13;1.72;1.82	6.7921e-14;1.3554e-10;1.9779e-11
	96345_at	66366	**Sdbcag84**	serologically defined breast cancer antigen 84	0.64;0.76;0.76	2.6224e-10;1.9548e-06;3.6514e-06
	95731_at	140742	**Sesn1**	sestrin 1	0.42;0.52;0.44	2.4738e-12;1.2952e-09;1.8490e-11
	102942_at	76364	**Specc1**	spectrin domain with coiled-coils 1	3.1;2.92;2.74	3.6079e-16;2.8168e-15;1.0990e-14
	97238_at	21335	**Tacc3**	transforming, acidic coiled-coil containing protein 3	2.35;2.24;1.96	0.00014899;0.00044494;0.00236115
	103385_at	56306	**Tera**	teratocarcinoma expressed, serine rich	2.24;2.16;1.95	1.2099e-12;7.5083e-12;1.1977e-10
	101551_s_a	21753	**Tes**	testis derived transcript	1.75;1.85;1.58	6.1093e-07;2.6206e-07;1.9977e-05
	102315_at	21771	**Tex292**	testis expressed gene 292	1.81;1.68;1.51	2.7070e-08;4.6730e-07;1.2809e-05
	100953_at	21853	**Timeless**	timeless homolog (Drosophila)	1.54;1.6;1.5	5.5730e-06;3.1396e-06;2.6296e-05
	95497_at	66131	**Tipin**	timeless interacting protein	1.62;1.77;1.58	7.9631e-05;1.5629e-05;0.00022477
	103254_at	231712	**Trafd1**	TRAF type zinc finger domain containing 1	0.57;0.66;0.65	5.0026e-13;5.3254e-10;3.5565e-10
	99149_at	66949	**Trim59**	tripartite motif-containing 59	1.58;1.47;1.34	7.7672e-05;0.00068692;0.00747874
	160376_at	68728	**Trp53inp2**	tumor protein p53 inducible nuclear protein 2	0.67;0.6;0.82	1.1094e-05;7.4391e-07;0.015729
	160394_at	217449	**Ttc15**	tetratricopeptide repeat domain 15	0.61;0.72;0.6	4.2740e-06;0.00093626;5.2405e-06
	160547_s_a	56338	**Txnip**	thioredoxin interacting protein	0.46;0.55;0.59	2.1280e-09;4.5075e-07;2.5468e-06
	96625_at	218973	**Wdhd1**	WD repeat and HMG-box DNA binding protein 1	1.55;1.47;1.42	9.0449e-07;9.8380e-06;3.5964e-05
	160776_at	98193	**Wdr42a**	WD repeat domain 42A	0.66;0.73;0.73	2.0071e-10;6.1063e-08;7.0562e-08
	102385_at	72515	**Wdr43**	WD repeat domain 43	1.54;1.32;1.29	4.9160e-09;1.3010e-05;3.5266e-05
	103056_at	217109	**Wdr50**	WD repeat domain 50	1.56;1.51;1.43	2.0993e-08;1.4752e-07;1.2780e-06

Function	Affy ID	Locus ID	Gene symbol	Description	Fold change	p-value
Other	95643_at	83669	**Wdr6**	WD repeat domain 6	0.62;0.7;0.7	8.8842e-08;1.1714e-05;1.2519e-05
	96615_at	66090	**Ypel3**	yippee-like 3	0.61;0.68;0.71	3.6167e-10;4.1866e-08;4.6006e-07
	104361_at	232337	**Zfp637**	zinc finger protein 637	0.66;0.78;0.73	3.8805e-10;8.1427e-06;1.4153e-07
Unknown	96605_at	66058	**0610011I04Rik**	RIKEN cDNA 0610011I04 gene	1.36;2.22;2.11	0.0067077;1.8300e-07;4.9775e-07
	160240_at	68552	**1110003E01Rik**	hypothetical protein LOC68552	0.42;0.62;0.68	8.8338e-10;2.2951e-05;0.00027477
	96756_at	68493	**1110007M04Rik**	RIKEN cDNA 1110007M04 gene	1.47;1.5;1.23	3.4838e-05;3.0842e-05;0.01369
	98594_at	68861	**1190002N15Rik**	hypothetical protein LOC68861	1.26;1.21;1.68	0.0013544;0.0077207;6.1908e-08
	160799_at	67527	**1300007C21Rik**	RIKEN cDNA 1300007C21 gene	1.5;1.62;0.88	0.0055227;0.0017607;0.3823104
	160723_at	68971	**1500001M20Rik**	hypothetical protein LOC68971 e	1.54;1.48;1.32	7.2226e-06;3.8683e-05;0.0015293
	96791_at	76566	**1500005K14Rik**	hypothetical protein LOC76566	1.54;1.18;1.5	6.0368e-10;0.00089908;4.4695e-09
	97874_at	78330	**1500032D16Rik**	RIKEN cDNA 1500032D16 gene	0.56;0.77;0.71	3.3406e-06;0.0148595;0.0019205
	97237_at	66249	**1810003N24Rik**	RIKEN cDNA 1810003N24 gene	1.65;1.51;1.42	4.2204e-07;1.2580e-05;9.4197e-05
	103565_at	66276	**1810009A15Rik**	RIKEN cDNA 1810009A15 gene	1.45;1.52;1.47	6.1514e-07;1.8476e-07;6.8286e-07
	95518_at	66270	**1810015C04Rik**	hypothetical protein LOC66270	1.49;1.71;1.93	0.00024063;9.4492e-06;4.9653e-07
	95406_at	67704	**1810037I17Rik**	hypothetical protein LOC67704	1.41;1.51;1.55	9.0957e-08;8.1322e-09;3.0217e-09
	94453_at	103742	**1810046J19Rik**	RIKEN cDNA 1810046J19 gene	0.64;0.87;0.89	2.3265e-06;0.067742;0.137601
	100877_at	67705	**1810058I24Rik**	RIKEN cDNA 1810058I24 gene	0.54;0.72;0.8	7.2525e-07;0.0023106;0.0272589
	94802_at	76527	**2010004A03Rik**	hypothetical protein LOC76527	0.47;0.5;0.49	5.8388e-13;6.1129e-12;3.5338e-12
	160955_at	66488	**2010309E21Rik**	RIKEN cDNA 2010309E21 gene	1.56;1.34;1.23	1.8416e-05;0.0025455;0.0270903
	98524_f_at	73644	**2210039B01Rik**	RIKEN cDNA 2210039B01 gene	3.34;2.57;2.15	1.4999e-09;2.3201e-07;5.8148e-06
	93877_at	73661	**2210419D22Rik**	RIKEN cDNA 2210419D22 gene	0.48;0.47;0.47	3.9813e-11;4.1922e-11;4.2994e-11
	103873_i_at	66365	**2310015N07Rik**	hypothetical protein LOC66365	0.57;0.74;0.61	1.4247e-06;0.0027982;1.4201e-05
	160218_at	70186	**2310056P07Rik**	RIKEN cDNA 2310056P07 gene	1.56;1.77;1.24	0.00458959;0.00073397;0.15276935
	96212_at	69662	**2310061I04Rik**	hypothetical protein LOC69662	1.35;1.49;1.51	6.1916e-05;2.0568e-06;1.2635e-06
	94366_at	66566	**2310079N02Rik**	hypothetical protein LOC66566	0.59;0.72;0.69	8.1101e-11;9.9229e-07;8.7400e-08
	93986_at	67872	**2410003A14Rik**	RIKEN cDNA 2410003A14 gene	1.47;1.56;1.45	0.00032134;9.3042e-05;0.00064513
	96293_at	66422	**2410015N17Rik**	hypothetical protein LOC66422	1.64;1.59;1.49	8.2838e-08;5.0587e-07;4.4836e-06
	160908_r_at	72421	**2510042P03Rik**	hypothetical protein LOC72421	0.48;0.6;0.59	2.4082e-10;4.8420e-07;2.8579e-07
	160845_at	70385	**2600001J17Rik**	hypothetical protein LOC70385	1.9;1.74;1.69	2.3496e-07;4.3484e-06;8.7750e-06

Function	Affy ID	Locus ID	Gene symbol	Description	Fold change	p-value
Unknown	95927_f_at	70434	**2610201A13Rik**	RIKEN cDNA 2610201A13 gene	1.62;1.23;1.25	0.00028243;0.09789569;0.07231341
	102368_at	108755	**2610208E05Rik**	hypothetical protein LOC108755	0.66;0.78;0.76	2.6321e-06;0.00187772;0.00069945
	92282_at	70470	**2610304G08Rik**	RIKEN cDNA 2610304G08 gene	1.64;1.52;1.28	7.9912e-06;0.00012167;0.01114157
	160223_at	74196	**2610511O17Rik**	hypothetical protein LOC74196	1.51;1.51;1.3	1.0408e-05;1.8926e-05;0.0025276
	92268_at	212772	**2700007P21Rik**	RIKEN cDNA 2700007P21	1.62;1.21;1.31	1.5853e-06;0.0267816;0.0025712
	94360_at	72612	**2700029M09Rik**	RIKEN cDNA 2700029M09 gene	1.52;1.49;1.22	0.0001640;0.0004852;0.0496948
	94038_at	68045	**2700060E02Rik**	hypothetical protein LOC68045	0.66;0.77;0.67	3.5889e-05;0.005271;8.9235e-05
	98613_at	67201	**2700085E05Rik**	hypothetical protein LOC67201	0.62;0.73;0.64	6.4848e-09;1.0495e-05;3.2524e-08
	93441_at	77022	**2700099C18Rik**	RIKEN cDNA 2700099C18 gene	2.03;1.89;1.76	0.00076872;0.00281390;0.00709702
	97374_at	69953	**2810025M15Rik**	hypothetical protein LOC69953	1.58;1.57;1.51	7.7811e-10;1.9847e-09;1.1442e-08
	100116_at	68026	**2810417H13Rik**	hypothetical protein LOC68026	2.35;2.46;2.05	0.00029256;0.00027671;0.00230106
	160400_at	69956	**2810422B04Rik**	hypothetical protein LOC69956	1.56;1.38;1.28	2.2696e-07;3.8803e-05;0.00083319
	103664_r_at	67236	**2810452K22Rik**	RIKEN cDNA 2810452K22 gene	1.69;1.46;1.29	9.1366e-06;0.00070256;0.01469318
	104085_at	72938	**2900042B11Rik**	hypothetical protein LOC72938	0.59;0.71;0.68	4.3150e-09;7.4983e-06;1.1824e-06
	98493_at	75430	**3200002M19Rik**	hypothetical protein LOC75430	1.62;1.41;1.35	1.0048e-05;0.00077928;0.00301920
	93437_f_at	74038	**4632419I22Rik**	RIKEN cDNA 4632419I22 gene	1.54;1.34;1.28	1.9360e-06;0.00040025;0.00193145
	93436_i_at	74038	**4632419I22Rik**	RIKEN cDNA 4632419I22 gene	1.59;1.38;1.27	0.00043843;0.01207115;0.05688651
	93478_at	78121	**4930461P20Rik**	RIKEN cDNA 4930461P20 gene	1.49;1.76;1.27	9.9826e-06;8.7616e-08;0.0040628
	103343_at	73847	**5430432M24Rik**	hypothetical protein LOC73847	1.34;1.51;1.49	5.6235e-06;6.8084e-08;9.9389e-08
	161005_at	70561	**5730420B22Rik**	hypothetical protein LOC70561	0.51;0.61;0.61	2.6392e-08;7.0553e-06;5.9657e-06
	96634_at	70564	**5730469M10Rik**	hypothetical protein LOC70564	0.55;0.72;0.74	6.9912e-08;0.00047438;0.00108797
	103364_f_at	66648	**5730494M16Rik**	hypothetical protein LOC66648	1.49;1.53;1.47	5.8744e-07;5.0850e-07;1.9320e-06
	100290_f_at	230376	**6230416J20Rik**	hypothetical protein LOC230376	3.25;2.96;2.38	6.6877e-08;5.1965e-07;1.3888e-05
	94211_at	109212	**6720460F02Rik**	hypothetical protein LOC109212	1.68;1.63;1.6	3.223e-05;0.00010236;0.00016119
	160963_at	269233	**9630050M13Rik**	RIKEN cDNA 9630050M13 gene	1.67;1.48;1.3	2.9641e-12;1.5237e-09;1.5089e-06
	94995_at	68252	**A030007L17Rik**	hypothetical protein LOC68252	1.68;1.59;1.66	4.5462e-10;8.3531e-09;1.6716e-09
	96545_s_at	234069	**A730042J05Rik**	RIKEN cDNA A730042J05 gene	1.61;1.42;1.24	7.8579e-05;0.0025129;0.0523338
	104034_at	99968	**AA408153**	expressed sequence AI464131	0.59;0.63;0.65	1.4031e-10;3.5817e-09;2.0656e-08
	103485_at	105415	**AA409373**	expressed sequence AA409373	0.53;0.59;0.59	4.9079e-09;3.5777e-07;3.6376e-07
	94359_at	101476	**AA960558**	expressed sequence AA960558	1.69;1.67;1.26	1.3716e-07;3.3839e-07;0.0047181

Function	Affy ID	Locus ID	Gene symbol	Description	Fold change	p-value
Unknown	93180_at	100694	**AI506816**	expressed sequence AI506816	2.16;1.83;1.81	6.4314e-10;1.0960e-07;1.3255e-07
	94784_at	99678	**AI593484**	expressed sequence AI593484	1.74;1.83;1.83	3.4141e-05;1.9449e-05;2.0250e-05
	102400_at	100261	**AU014645**	expressed sequence AU014645	1.57;1.42;1.35	4.9055e-10;8.8925e-08;1.1494e-06
	104252_at	101757	**AU020206**	expressed sequence AU020206	2.11;1.9;1.95	1.8460e-11;8.5841e-10;3.9756e-10
	93235_at	233315	**BB128963**	hypothetical protein LOC233315	1.79;1.44;1.34	9.2268e-08;0.00011666;0.00107842
	93980_at	234138	**BC019943**	hypothetical protein LOC234138	1.78;1.67;1.49	2.0978e-08;2.8716e-07;1.3933e-05
	103497_at	234728	**BC025546**	cDNA sequence BC025546	1.72;1.62;1.37	2.9582e-06;2.7209e-05;0.0025797
	160973_at	224171	**C330027C09Rik**	hypothetical protein LOC224171	3.06;2.6;2.33	2.5505e-06;3.8820e-05;0.00016839
	97179_at	98052	**C76683**	expressed sequence C76683	1.32;1.53;1.45	2.1200e-06;2.8186e-09;3.7575e-08
	97897_at	97863	**C78339**	expressed sequence C78339	0.66;0.74;0.7	5.3187e-07;8.9990e-05;1.1662e-05
	103308_at	217653	**C79407**	expressed sequence C79407	1.52;1.45;1.3	1.1231e-06;1.2786e-05;0.00062441
	95984_at	97294	**C79468**	expressed sequence C79468	1.45;1.57;1.39	6.2703e-06;7.4977e-07;6.4278e-05
	103312_f_at	96988	**C79684**	expressed sequence C79684	1.77;1.58;1.35	2.0940e-06;7.3269e-05;0.0043596
	160768_at	225995	**D030056L22**	hypothetical protein LOC225995	1.58;1.64;1.54	5.2367e-07;3.5462e-07;2.4063e-06
	94526_at	52637	**D10Ertd214e**	hypothetical protein LOC52637	1.45;1.64;1.61	1.9386e-06;3.7166e-08;7.2127e-08
	93775_at	52668	**D12Ertd647e**	hypothetical protein LOC52668	0.56;0.7;0.72	1.1653e-11;2.0401e-07;6.6623e-07
	160310_at	52874	**D19Bwg1357e**	DNA segment, Chr 19, Brigham & Women's Genetics 1357 expressed	1.52;1.35;1.33	1.0861e-12;1.8278e-09;4.5096e-09
	104122_at	223658	**D330001F17Rik**	RIKEN cDNA D330001F17 gene	0.6;0.78;0.83	2.3597e-05;0.018206;0.075381
	92542_at	27981	**D4Wsu53e**	hypothetical protein LOC27981	0.62;0.72;0.75	7.151e-06;0.0009588;0.0028379
	98880_at	28006	**D6Wsu116e**	DNA segment, Chr 6, Wayne State University 116, expressed	0.64;0.84;0.87	1.3982e-06;0.025355;0.081033
	95442_at	235043	**MGC18837**	hypothetical protein LOC235043	0.62;0.67;0.7	2.5193e-09;2.0132e-07;9.2620e-07
	161076_at	231123	**MGC36997**	hypothetical protein LOC231123	1.96;1.73;1.69	1.2156e-06;4.1022e-05;6.6385e-05
	100717_at	57425	**U90926**	hypothetical protein LOC57425	2.9;2.54;2.89	4.8603e-12;1.6068e-10;1.2310e-11

Table S2. Corroboration of Affymetrix data by RT-quantitative PCR

	Affymetrix[a]			**Q-PCR**[b]		
	RhoA^{Q63L}	**RhoB^{Q63L}**	**RhoC^{Q63L}**	**RhoA^{Q63L}**	**RhoB^{Q63L}**	**RhoC^{Q63L}**
Upregulated						
birc5	2.99	2.74	2.54	8	5.65	4
bnc	3.7	3.79	3.26	5.27	2.63	3.73
ccl2	19.72	39.82	45.39	55.71	34.29	84.44
ccl7	6.06	15.92	15.23	25.99	12.12	36.75
cd44	3.07	2.69	2.89	3.2	1.7	5.6
ctgf	5.57	1.95	2.99	8	3	8.57
cxcl1	15.85	23.32	26.99	59.71	22.62	97
cxcl5	18.84	42.48	37.19	90.5	48.5	128
epha2	1.9	1.65	1.71	4	2.46	4.59
efnb2	2.54	2.32	1.7	3.73	3.24	3.48
ereg	2.93	2.21	1.93	11.31	3.73	10.55
ier3	3.13	3.59	4.04	4.6	2.3	4
igf2	2.39	N.D.	2	1.74	N.D.	5.28
jun	1.57	1.61	1.65	2.63	1.41	3.24
kif20a	2.5	2.07	2.04	4.59	2.63	8.57
msln	12.99	12.5	12.71	73.5	55.7	27.8
mybl2	1.58	1.52	1.43	12.99	6.49	13.92
myc	2.16	1.89	1.86	4.28	2.63	5.27
nr4a1	3.23	2	2.58	45.25	9.8	34.3
plf	3.6	5.28	4.24	12.99	19.69	13.9
plf2	4.68	12.51	9.72	24.25	21.11	42.22
mrpplf3	7.99	26.72	19.14	21.11	18.37	25.99
ptgs1	1.49	1.51	1.39	2.82	1.41	2
ptgs2	14.83	7.85	10.36	42.22	13.9	48.5
tnc	4.24	1.35	2.43	1.41	0.57	2.29
thbd	3.84	2.86	3.65	3.73	1.86	6.96
plaur	3.02	2	2.41	4.28	4.92	13.92
Downregulated						
atf5	0.39	0.42	0.44	0.53	0.125	0.2
cxcl12	0.38	0.45	0.42	0.08	0.21	0.108
figf	0.18	0.27	0.24	0.095	0.125	0.101
gas1	0.3	0.36	0.27	0.13	0.1	0.05
gas2	0.61	0.52	0.46	0.93	0.32	0.37
gas6	0.24	0.25	0.27	0.05	0.03	0.02
Idb2	0.6	0.49	0.52	0.23	0.14	0.43
Idb4	0.53	0.43	0.41	0.047	0.01	0.02
mad4	0.46	0.51	0.48	0.16	0.1	0.08
ogn	0.09	0.1	0.08	0.027	0.027	0.038
osf2	0.15	0.17	0.2	0.13	0.18	0.26
pdcd4	0.3	0.41	0.34	0.21	0.2	0.17
pdgfr α	0.37	0.53	0.4	0.26	0.28	0.53
pdgfr β	0.3	0.34	0.44	0.15	0.14	0.46
serpine2	0.15	0.15	0.15	0.02	0.01	0.033
six1	0.25	0.22	0.2	0.13	0.13	0.08
snai2	0.52	0.59	0.61	0.28	0.17	0.3
sparcl1	0.35	0.37	0.33	0.03	0.016	0.047
tcf3	0.65	0.66	0.59	0.26	0.18	0.25
thbs2	0.18	0.39	0.4	0.1	0.14	0.26

[a] Affymetrix based determination of gene expression levels in the indicated cell lines compared tc NIH3T3 cells

[b] RT-quantitative PCR based determination of gene expression levels in the indicated cell lines compared to NIH3T3 cells. N.D., not determined

Red labeled: Not corroborated gene by RT-quantitative PCR in the indicated cell line

Table S3. Rho-regulated genes with reverted expresion levels after ROCK inhibition[a]

Function	Affy ID	Locus ID	Gene symbol	Description	RhoAi[b]	RhoA[c]	RhoB[c]	RhoC[c]	p-value RhoAi[d]
Extracellular	92777_at	16007	**Cyr61**	cysteine rich protein 61	0.19	2.95	1.75	2.68	<1.00E-04
Cell adhesion	94147_at	18787	**Serpine1**	serine (or cysteine) proteinase inhibitor, clade E, mem1	0.31	4.86	2.28	3.71	< 1.00E-04
	101993_at	21923	**Tnc**	tenascin C	0.31	4.24	1.35	2.43	< 1.00E-04
Ligand	102798_at	11535	**Adm**	adrenomedullin	0.4	1.84	1.64	1.81	< 1.00E-04
	160469_at	21825	**Thbs1**	thrombospondin 1	0.25	1.52	0.58	1	< 1.00E-04
Growth factor	93294_at	14219	**Ctgf**	connective tissue growth factor	0.22	5.57	1.95	2.99	1.00E-04
	98623_g_at	16002	**Igf2**	insulin-like growth factor 2	0.41	2.39	1.31	2	6.00E-04
	100277_at	16323	**Inhba**	inhibin beta-A	0.58	1.96	1.42	1.47	0.0018
Membrane	104407_at	11658	**Alcam**	activated leukocyte cell adhesion molecule	0.5	2.21	1.63	1.01	0.0081
	93078_at	110454	**Ly6a**	lymphocyte antigen 6 complex, locus A	2.5	0.53	0.85	1.04	< 1.00E-04
	103258_at	17076	**Ly75**	lymphocyte antigen 75	0.64	1.77	1.47	1.46	0.002
	103362_at	19219	**Ptger4**	prostaglandin E receptor 4 (subtype EP4)	0.54	1.79	1.38	1.37	< 1.00E-04
	160320_at	20411	**Sorbs1**	sorbin and SH3 domain containing 1	0.52	1.82	1.15	1.34	0.0045
	94928_at	21938	**Tnfrsf11b**	tumor necrosis factor receptor superfamily, mem1b	1.57	0.62	0.57	0.61	3.00E-04
	99057_at	21838	**Thy1**	thymus cell antigen 1, theta	0.53	1.54	1.08	1.37	< 1.00E-04
Cytoskeleton	100381_at	11459	**Acta1**	actin, alpha 1, skeletal muscle	0.56	1.9	1.26	1.67	0.0049
	93102_f_at	11468	**Actg2**	actin, gamma 2, smooth muscle, enteric	0.57	1.68	1.02	1.26	0.0066
	96343_at	60595	**Actn4**	calpain 12	0.6	1.76	1.4	1.34	< 1.00E-04
	93541_at	21345	**Tagln**	transgelin	0.17	2.13	1.12	1.85	< 1.00E-04
	96426_at	19241	**Tmsb4x**	thymosin, beta 4, X chromosome	0.66	1.57	1.51	1.45	0.009
Intracellular	93285_at	67603	**Dusp6**	dual specificity phosphatase 6	0.4	2.62	2.22	1.98	< 1.00E-04
signal transducer	93974_at	74155	**Errfi1**	ERBB receptor feedback inhibitor 1	0.5	2.07	1.82	1.51	< 1.00E-04
	101934_at	225020	**Fez2**	fasciculation and elongation protein zeta 2 (zygin II)	0.52	2.05	1.27	1.52	6.00E-04
	160261_i_at	50523	**Lats2**	large tumor suppressor 2	0.43	2.07	1.58	1.62	< 1.00E-04
	101561_at	17750	**Mt2**	metallothionein 2	2.18	0.48	0.73	0.83	< 1.00E-04
	96592_at	18708	**Pik3r1**	PI3-kinase, regulatory subunit, polypep1 (p85α)	1.79	0.58	0.68	0.69	1.00E-04
	101995_at	18412	**Sqstm1**	sequestosome 1	1.54	0.64	0.83	0.96	0.0083
Proapoptotic	93842_at	223453	**Dap**	death-associated protein	1.59	0.65	0.87	0.84	< 1.00E-04

[a] Genes are classified into functional groups as in table S1. The Affymetrix identification number (Affy ID), the locus identification number (Locus ID), the symbol and the description for each gene are shown. Upregulated genes after the Y27632 treatment are shown in red and downregulated genes in blue

[b] Fold change in the expression levels in RhoA^{Q63L}-transformed cells after the Y27632 treatment

[c] Fold change in the expression levels in Rho-transformed cells compare to NIH3T3 (see Table S1).Values not statistically significant are shown in black

[d] *P* -values of genes affected in RhoA^{Q63L}-transformed cells after the Y27632 treatment determined with the F-statistic.P-values lower than 1.00E-04 are shown as < 1.00E-04. The same colour code as in a is used

Function	Affy ID	Locus ID	Gene symbol	Description	RhoAi[c]	RhoA[d]	RhoB[d]	RhoC[d]	p-value RhoAi[d]
Regulation of transcription	104712_at	17869	**Myc**	myelocytomatosis oncogene	0.5	2.16	1.89	1.86	1.00E-04
	93615_at	18516	**Pbx3**	pre B-cell leukemia transcription factor 3	0.6	1.59	1.52	1.24	0.0015
Metabolism	96085_at	14860	**Gsta4**	glutathione S-transferase, alpha 4	2.13	0.44	0.72	0.59	< 1.00E-04
Glutathion Metabolism	96258_at	66447	**Mgst3**	microsomal glutathione S-transferase 3	2.23	0.49	0.88	0.83	< 1.00E-04
Nucleob., Nucleos., Nucleot. and Nucleic acid Metabolism	99959_at	11639	**Ak4**	adenylate kinase 4	0.63	1.57	1.54	1.3	0.0043
Other	99580_s_at	94284	**Ugt1a6**	UDP glycosyltransferase 1 family, polypeptide A6	1.89	0.51	0.81	0.73	0.0021
Transport	103031_g_at	13429	**Dnm**	dynamin	1.57	0.61	0.83	0.81	0.0031
Vesicular transport	97409_at	15944	**Ifi1**	interferon inducible protein 1	0.6	1.58	1.42	1.59	5.00E-04
Other	96775_at	12412	**Cbx1**	chromobox homolog 1 (Drosophila HP1 beta)	0.55	1.69	1.22	1.06	< 1.00E-04
	97498_at	14199	**Fhl1**	four and a half LIM domains 1	0.21	4.35	1.73	2.65	< 1.00E-04
	102907_at	208177	**Phldb2**	pleckstrin homology-like domain, family B, member 2	0.6	1.67	1.45	1.68	< 1.00E-04
Unknown	103664_r_at	67236	**2810452K22Rik**	RIKEN cDNA 2810452K22 gene	0.64	1.69	1.46	1.29	0.0052
	93436_i_at	74038	**4632419I22Rik**	RIKEN cDNA 4632419I22 gene	0.66	1.54	1.34	1.28	0.0045

Table S4. Rho-regulated genes not reverted after the Y27632 treatment[a]

Function	Affy ID	Locus ID	Gene symbol[b]	Description	RhoAi[c]	RhoA[d]	RhoB[d]	RhoC[d]	p-value RhoAi[e]
Extracellular	161984_f_at	12825	**Col3a1***	procollagen, type III, alpha 1	0.53	0.49	0.41	0.32	1.00E-04
Cell adhesion	93866_s_at	17313	**Mglap***	matrix gamma-carboxyglutamate (gla) protein	0.45	0.35	0.2	0.46	<1.00E-04
	103721_at	114249	**Npnt**	nephronectin	0.31	1.84	0.77	1	<1.00E-04
	92593_at	50706	**Osf2***	osteoblast specific factor 2 (fasciclin I-like)	0.31	0.15	0.18	0.21	2.00E-04
	160519_at	21859	**Timp3**	tissue inhibitor of metalloproteinase 3	2	0.14	0.22	0.17	<1.00E-04
Ligand	95348_at	14825	**Cxcl1**	chemokine (C-X-C motif) ligand 1	0.52	15.85	23.32	26.99	0.002
	93534_at	13179	**Dcn**	decorin	2.09	0.19	0.69	0.43	0.0086
	93929_s_at	26421	**Mrpplf3***	proliferin 3	4	7.99	26.72	19.14	<1.00E-04
	93883_at	18812	**Plf2***	proliferin 2	3.45	4.68	12.51	9.72	1.00E-04
Growth factor	98802_at	13874	**Ereg**	epiregulin	0.59	2.93	2.21	1.93	6.00E-04
	92730_at	15200	**Hbegf**	heparin-binding EGF-like growth factor	0.56	2.27	1.71	1.56	3.00E-04
Membrane/ Cell adhesion	102663_at	18793	**Plaur**	urokinase plasminogen activator receptor	0.57	3.02	2	2.41	4.00E-04
Channel-Transporter	93330_at	11826	**Aqp1***	aquaporin 1	5.27	2.31	3.75	4.03	<1.00E-04
Immune response	93874_s_at	16158	**Il11ra2**	interleukin 11 receptor, alpha chain 2	1.54	0.23	0.31	0.29	4.00E-04
Receptor activity	103980_at	13836	**Epha2**	Eph receptor A2	0.63	1.9	1.65	1.71	<1.00E-04
	95474_at	14062	**F2r***	coagulation factor II (thrombin) receptor	0.65	0.71	0.65	0.77	<1.00E-04
	95079_at	18595	**Pdgfra**	platelet derived growth factor receptor, α polypeptide	1.62	0.37	0.53	0.4	0.0033
Signal transducer	102395_at	18858	**Pmp22**	peripheral myelin protein	1.73	0.15	0.22	0.2	<1.00E-04
Other	95531_at	319434	**Amot***	angiomotin	0.57	0.53	0.45	0.52	2.00E-04
	100065_r_at	14609	**Gja1**	gap junction membrane channel protein a 1	0.58	4.68	3.61	3.12	8.00E-04
	97885_at	65963	**LR8***	LR8 protein	2.44	1.31	1.92	1.93	<1.00E-04
	160373_i_at	20324	**Sdpr**	serum deprivation response	0.48	3.58	3.05	3.37	<1.00E-04
Cytoskeleton	95637_at	286940	**Flnb**	filamin, beta	0.63	1.83	1.47	1.87	1.00E-04
Intracellular	97411_at	13605	**Ect2**	ect2 oncogene	0.66	3.66	3.5	2.88	6.00E-04
Signal transducer activity	93573_at	17748	**Mt1**	metallothionein 1	1.93	0.41	0.69	0.77	1.00E-04
	93178_at	53972	**Ngef***	neuronal guanine nucleotide exchange factor	1.52	1.54	2.16	1.61	<1.00E-04
	104063_at	71943	**Srcasm**	Src activating and signaling molecule	0.62	2.13	2.03	1.83	1.00E-04
	102850_at	51789	**Tnk2**	tyrosine kinase, non-receptor, 2	0.63	2.3	1.74	1.87	<1.00E-04

[a] Genes are classified into functional groups as in table S1. The Affymetrix identification number (Affy ID), the locus identification number (Locus ID), the symbol and the description for each gene are shown.Upregulated genes after the Y27632 treatment are shown in red and downregulated genes in blue

[b] Genes with the same pattern of change as in Rho-trasnformed cells are indicated with *

[c] Fold change in the expression levels in RhoA^{Q63L}-transformed cells after the Y27632 treatment

[d] Fold change in the expression levels in Rho-transformed cells compare to NIH3T3 (see Table S1).Values not statistically significant are shown in black

[e] *P* -values of genes affected in RhoA^{Q63L}-transformed determined with the F-statistic. *P* -values lower than 1.00E-04 are shown as <1.00E-04

Function	Affy ID	Locus ID	Gene symbol[b]	Description	RhoAi[c]	RhoA[d]	RhoB[d]	RhoC[d]	p-value RhoAi[e]
Signal transducer activity	95022_at	83397	**Akap12***	A kinase (PRKA) anchor protein (gravin) 12	0.6	0.48	0.45	0.5	3.00E-04
Proteolysis and peptidolysis	96065_at	17035	**Lxn**	latexin	1.76	0.27	0.35	0.38	1.00E-04
Heat Shock	98111_at	15505	**Hsp105**	heat shock protein 105	0.66	2.14	1.9	1.98	7.00E-04
Apoptosis	160829_at	21664	**Phlda1**	pleckstrin homology-like domain, family A, member 1	0.51	3.02	2.88	2.71	<1.00E-04
	94384_at	15937	**Ier3**	immediate early response 3	0.65	3.13	3.59	4.04	5.00E-04
Cell cycle	102292_at	13197	**Gadd45a***	growth arrest and DNA-damage-inducible 45 alpha	1.82	1.28	1.71	1.6	<1.00E-04
	99522_at	14841	**Gsg2**	germ cell-specific gene 2	0.67	1.94	1.69	1.46	0.0026
DNA replic., rep. and rec.	101459_at	12648	**Chd1**	chromodomain helicase DNA binding protein 1	0.67	1.93	1.64	1.51	4.00E-04
Regulation of transcription	93371_at	12173	**Bnc**	basonuclin	0.57	3.7	3.79	3.26	<1.00E-04
	102048_at	107765	**Crap**	cardiac responsive adriamycin protein	0.35	2.29	2.24	2.12	<1.00E-04
	101429_at	13198	**Ddit3**	DNA-damage inducible transcript 3	1.7	0.5	0.55	0.58	<1.00E-04
	92564_at	16978	**Lrrfip1**	leucine rich repeat (in FLII) interacting protein 1	0.53	2.64	2.36	1.96	0.0012
	99076_at	353187	**Nr1d2***	nuclear receptor subfamily 1, group D, member 2	1.76	1.26	1.83	1.72	<1.00E-04
	103327_at	20204	**Prrx2**	paired related homeobox 2	2	0.31	0.31	0.36	<1.00E-04
Metabolism/Amino acid metabolism	96346_at	12583	**Cdo1**	cysteine dioxygenase 1, cytosolic	1.79	0.12	0.17	0.18	5.00E-04
Carbohidrate Metabolism	96803_at	74185	**Gbe1***	glucan (1,4-alpha-), branching enzyme 1	1.52	1.49	1.6	1.4	0.0017
Lipid metabolism	102370_at	114664	**Dhrs8**	dehydrogenase/reductase (SDR family) member 8	1.54	0.35	0.51	0.53	0.0095
	95620_at	66375	**Dhrs7**	dehydrogenase/ reductase	1.82	0.5	0.85	0.76	<1.00E-04
Other	104647_at	19225	**Ptgs2**	prostaglandin-endoperoxide synthase 2	0.21	14.83	7.85	10.36	<1.00E-04
RNA metabolsim	92569_f_at	55989	**Nol5**	nucleolar protein 5	0.63	1.88	1.57	1.43	4.00E-04
Vesicular transport	101393_at	11745	**Anxa3**	annexin A3	0.62	1.82	1.73	1.76	9.00E-04
Other	100068_at	11668	**Aldh1a1**	aldehyde dehydrogenase family 1, subfamily A1	1.89	0.14	0.17	0.19	2.00E-04
	160298_at	67896	**Ccdc80***	coiled-coil domain containing 80	0.66	0.71	0.57	0.57	5.00E-04
	96912_s_at	13024	**Ctla2a**	cytotoxic T lymphocyte-associated protein 2 alpha	2.13	0.11	0.2	0.24	<1.00E-04
Unknown	93235_at	233315	**BB128963**	expressed sequence BB128963	0.66	1.79	1.44	1.34	<1.00E-04
	96605_at	66058	**0610011I04Rik***	RIKEN cDNA 0610011I04 gene	2.86	1.36	2.22	2.11	<1.00E-04
	160799_at	67527	**1300007C21Rik**	RIKEN cDNA 1300007C21 gene	0.43	1.5	1.62	0.88	<1.00E-04
	98524_f_at	73644	**2210039B01Rik**	RIKEN cDNA 2210039B01 gene	0.63	3.34	2.57	2.15	8.00E-04

Table S5.Not Rho-regulated genes affected after the Y27632 treatment[a]

Function	Affy ID	Locus ID	Gene symbol	Description	RhoAi[b]	p-value RhoAi[c]
Extracelluar	101093_at	12826	**Col4a1**	procollagen, type IV, alpha 1	0.54	4.00E-04
Cell adhesion	101039_at	12827	**Col4a2**	procollagen, type IV, alpha 2	0.67	<1.00E-04
	92567_at	12832	**Col5a2**	procollagen, type V, alpha 2	0.38	<1.00E-04
	161346_f_at	259277	**Klk8**	kallikrein 8	1.67	6.00E-04
	97160_at	20692	**Sparc**	secreted acidic cysteine rich glycoprotein	0.62	2.00E-04
Ion transport	92851_at	12870	**Cp**	ceruloplasmin	1.93	0.0073
Ligand	96055_at	12424	**Cck**	cholecystokinin	2.86	<1.00E-04
	161639_f_at	14459	**Gast**	gastrin	1.67	3.00E-04
Growth factor	101450_at	12977	**Csf1**	colony stimulating factor 1 (macrophage)	0.48	<1.00E-04
Membrane	104363_at	106647	**Cdsn**	corneodesmosin	1.76	<1.00E-04
Cell adhesion	100906_at	16421	**Itgb7**	integrin beta 7	1.59	0.0064
	92558_at	22329	**Vcam1**	vascular cell adhesion molecule 1	0.57	<1.00E-04
Channel-transporter	100379_f_at	11832	**Aqp7**	aquaporin 7	0.64	<1.00E-04
Immune reponse	98472_at	15040	**H2-T23**	histocompatibility 2, T region locus 23	1.76	1.00E-04
	160358_at	12490	**Cd34**	CD34 antigen	1.57	<1.00E-04
Receptor activity	103923_at	83924	**Gpr137b**	G protein-coupled receptor 137B	1.54	0.0016
	93042_at	12257	**Bzrp**	benzodiazepine receptor, peripheral	1.59	<1.00E-04
	97689_at	14066	**F3**	coagulation factor III	0.53	<1.00E-04
	102224_at	16001	**Igf1r**	insulin-like growth factor I receptor	0.66	1.00E-04
	95016_at	18186	**Nrp**	neuropilin	0.43	2.00E-04
	97769_at	19220	**Ptgfr**	prostaglandin F receptor	1.86	1.00E-04
Cytoskeleton	93100_at	11475	**Acat2**	actin, alpha 2, smooth muscle, aorta	0.15	<1.00E-04
	101029_f_at	11464	**Actc1**	actin, alpha, cardiac	0.57	2.00E-04
	94536_s_at	67268	**MLC-B**	myosin light chain, regulatory B like	0.65	<1.00E-04
	102108_f_at	17886	**Myh9**	myosin heavy chain IX	0.58	<1.00E-04
	160367_at	67399	**Pdlim7**	PDZ and LIM domain 7	0.62	8.00E-04
	96774_at	218952	**Plekhc1**	pleckstrin homology domain containing, family C memb.1	0.49	<1.00E-04
	160532_at	22003	**Tpm1**	tropomyosin 1, alpha	0.59	<1.00E-04
	94963_at	22330	**Vcl**	vinculin	0.52	<1.00E-04

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[a] Genes are classified into functional groups as in table S1. The Affymetrix identification number (Affy ID), the locus identification number (Locus ID), the symbol and the description for each gene are shown. Upregulated genes after the Y27632 treatment are shown in red and downregulated genes in blue

[b] Fold change in the expression levels in RhoA^{Q63L}-transformed cells after the Y27632 treatment

[c] *P* -values of genes affected in RhoA^{Q63L}-transformed determined with the F-statistic. *P* -values lower than 1.00E-04 are shown as <1.00E-04

Function	Affy ID	Locus ID	Gene symbol	Description	RhoAi[b]	p-value RhoAi[c]
Intracellular	97529_at	11752	**Anxa8**	annexin A8	2	<1.00E-04
Signal Transducer	104432_at	11858	**Arhn**	ras homolog N (RhoN)	1.52	
	96736_at	106140	**Lpp**	LIM domain containing preferred translocation partner in lipoma	0.66	7.00E-04
	160746_at	19877	**Rock1**	Rho-associated coiled-coil forming kinase 1	0.65	0.0013
	98946_at	78889	**Wsb1**	WD-40-repeat-containing protein with a SOCS box 1	0.67	1.00E-04
	160296_at	59043	**Wsb2**	WD-40-repeat-containing protein with a SOCS box 2	0.63	1.00E-04
Proteolysis and peptidolysis	101587_at	13849	**Ephx1**	epoxide hydrolase 1, microsomal	1.52	<1.00E-04
	94238_at	76453	**Prss23**	protease, serine, 23	0.47	0.0027
Heat shock	101955_at	14828	**Hspa5**	heat shock 70kD protein 5 (glucose-regulated protein)	0.65	<1.00E-04
Apoptosis	98945_at	54673	**Bif-1**	SH3-domain GRB2-like B1 (endophilin)	0.66	1.00E-04
	93439_f_at	114774	**Pawr**	PRKC, apoptosis, WT1, regulator	0.59	<1.00E-04
Regulation of transcription	104155_f_at	11910	**Atf3**	activating transcription factor 3	1.52	<1.00E-04
	102916_s_at	12915	**Crebl1**	cAMP responsive element binding protein-like 1	1.54	5.00E-04
	98579_at	13653	**Egr1**	early growth response 1	0.25	<1.00E-04
	104561_at	70239	**Gtf3c5**	general transcription factor IIIC, polypeptide 5	1.5	<1.00E-04
	97937_at	12224	**Klf5**	Kruppel-like factor 5	0.63	0.0069
	98083_at	81841	**Klf6**	Kruppel-like factor 6	0.63	<1.00E-04
	103052_r_at	11819	**Nr2f2**	nuclear receptor subfamily 2, group F, member 2	0.59	<1.00E-04
	104070_at	18519	**Pcaf**	p300/CBP-associated factor	0.66	2.00E-04
	99021_at	18933	**Prrx1**	paired related homeobox 1	1.67	0.0037
	161067_at	228775	**Trib3**	tribbles homolog 3 (Drosophila)	1.52	<1.00E-04
	160939_at	13345	**Twist2**	twist homolog 2 (Drosophila)	1.73	<1.00E-04
	94821_at	22433	**Xbp1**	X-box binding protein 1	0.53	2.00E-04
RNA metabolism	160791_at	67684	**Luc7a**	RIKEN cDNA 3300001P08 gene	0.66	5.00E-04
	96777_at	81898	**Sf3b1**	splicing factor 3b, subunit 1	0.57	1.00E-04
	92579_at	20823	**Ssb**	Sjogren syndrome antigen B	0.61	0.0083
Metabolism						
Carboidrate Met	100088_at	19046	**Ppp1cb**	protein phosphatase 1, catalytic subunit, beta isoform	0.6	1.00E-04
Lipid metabolism	95064_at	52538	**Acaa2**	acetyl-Coenzyme A acyltransferase 2	1.5	<1.00E-04
	98575_at	14104	**Fasn**	fatty acid synthase	0.62	1.00E-04
	102768_i_at	235293	**Sc5d**	sterol-C5-desaturase homolog	0.54	0.0062

Function	Affy ID	Locus ID	Gene symbol	Description	RhoAi[b]	p-value RhoAi[c]
Metabolism/Other	96058_s_at	11669	**Aldh2**	aldehyde dehydrogenase 2, mitochondrial	1.52	0.0046
	160647_at	12353	**Car6**	carbonic anhydrase 6	1.54	<1.00E-04
	98440_at	67103	**Ltb4dh**	leukotriene B4 12-hydroxydehydrogenase	1.97	<1.00E-04
	104406_at	64292	**Ptges**	prostaglandin E synthase	1.7	7.00E-04
	104716_at	19659	**Rbp1**	retinol binding protein 1, cellular	1.64	<1.00E-04
	96623_at	22234	**Ugcg**	UDP-glucose ceramide glucosyltransferase	0.62	1.00E-04
ER protein transport	160291_at	53421	**Slc6a9**	solute carrier family 6 , memb. 9	1.52	0.0041
Other	160131_at	56332	**Amotl2**	angiomotin like 2	0.46	<1.00E-04
	162399_f_at	20239	**Atxn2**	ataxin 2	0.59	5.00E-04
	102811_at	14042	**Ext1**	exostoses (multiple) 1	0.65	2.00E-04
	99109_at	15936	**Ier2**	immediate early response 2	0.45	<1.00E-04
	92773_at	15939	**Ier5**	immediate early response 5	0.32	<1.00E-04
	160464_s_at	17988	**Ndr1**	N-myc downstream regulated 1	1.52	<1.00E-04
	94351_r_at	18104	**Nqo1**	NAD(P)H dehydrogenase, quinone 1	1.7	2.00E-04
	95883_at	269424	**Phf17**	PHD finger protein 17	0.59	8.00E-04
	96278_at	66151	**Prr13**	proline rich 13	1.7	<1.00E-04
	160726_at	19317	**Qk**	quaking	0.57	0.0011
	100878_at	94186	**Strn3**	striatin, calmodulin binding protein 3	0.65	3.00E-04
	93821_at	52357	**Wwc2**	WW, C2 and coiled-coil domain containing 2	0.57	1.00E-04
Unknown	103260_at	68813	**1110060D06Rik**	RIKEN cDNA 1110060D06 gene	0.64	1.00E-04
	96135_at	73112	**3110003A17Rik**	RIKEN cDNA 3110003A17 gene	0.65	0.0082
	92211_at	100563	**AF013969**	expressed sequence AF013969	0.67	0.0039