High-Throughput Mapping of a Dynamic Signaling Network In Mammalian Cells

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ABSTRACT

Signaling pathways transmit information through protein interaction networks that are dynamically regulated by complex extracellular cues. We developed an automated high-throughput technology we call LUMIER to analyze dynamic protein-protein interaction networks in mammalian cells. LUMIER was used to systematically analyze the interaction of 518 proteins with components of the TGFβ pathway and identified 901 interactions from 11,914 tests. Analysis of the Smad network module in the presence and absence of TGFβ signaling revealed a dynamic network in which numerous interactions were lost, while others were gained. The TGFβ LUMIER network was analyzed using the BTSVQ algorithm, which incorporates self-organizing maps and *k*-means clustering. This identified a group of proteins that showed similar interactions with the TGFβ pathway and included components of both the p21 activated kinase (PAK) and polarity pathways. Moreover, TGFβ receptors made numerous connections with these two networks that otherwise display only sparse connectivity. High-throughput mapping of protein interactions in mammalian cells thus demonstrates a link between the TGFβ pathway and both the PAK and polarity subnetworks, that yields a large interconnected network involved in cell motility and polarity.

Dynamic protein-protein interactions (PPIs) are key for cell signaling and dictate timing and intensity of network outputs. However, systematic mapping of PPI networks have thus far focussed on static analyses in *S. cerevisiae*, *D. melanogaster* and *C. elegans* (*1-6*). Therefore, to begin building an understanding of how signaling networks convey information in vertebrates we developed a high-throughput (HTP) strategy to systematically map PPIs in mammalian cells. This strategy, which we call LUMIER, for LUminescence-based Mammalian IntERactome mapping (Fig. 1A), employs Renilla luciferase enzyme (RL) fused to proteins of interest. RL-tagged proteins are then co-expressed with individual Flag-tagged partners in mammalian cells and interaction determined by performing an RL enzymatic assay on anti-Flag immunoprecipitates.

Validation of LUMIER. As a model for a systematic study of mammalian cell signaling, we focussed on the TGFβ superfamily of extracellular morphogens, which regulate a plethora of biological processes in metazoans (*7-11*). The superfamily includes the TGFβs, bone morphogenetic proteins (BMPs) and activins, which signal through heteromeric complexes of type II and type I transmembrane ser/thr kinase receptors. The receptor complex is activated when the type II receptor kinase transphosphorylates the type I receptor (Fig. 1B), which stimulates binding and phosphorylation of receptor-regulated Smads (R-Smads) by the type I receptor. R-Smad2 and R-Smad3 function in TGFβ signaling, whereas the BMPs through different type I receptors (ALK2, ALK3 and ALK6) activate R-Smad1, R-Smad5 and R-Smad8. Phosphorylated R-Smads dissociate from the receptor, form a complex with the common mediator Smad, Smad4, and this

complex then accumulates in the nucleus where it regulates transcription by interacting with DNA binding proteins (*12*).

The Smad pathway provides an example of how post-translational modifications (PTMs) regulate the dynamics of PPI networks to control signal transduction (*13, 14*). Therefore, we used this pathway to determine whether LUMIER could map PTM-dependent interactions (Fig. 1). For this, we fused RL to Smad4 (Smad4-RL) and co-expressed it with Flag-Smad2 or the TGFβ receptor phosphorylation site mutant, Flag-Smad2(2SA), which does not bind Smad4. In the absence of signaling, little if any Smad4-RL was found associated with Smad2 (Fig. 1C), whereas TGFβ signaling induced strong association with WT Smad2 that was revealed by high levels of RL activity in the immune complexes (*15*). In contrast, no Smad4-RL was detected in Smad2(2SA) immunoprecipitates. We also examined signal-specific interactions using the BMP pathway and observed increased Smad4-RL bound to Flag-Smad1 but not Smad2, upon activation of BMP signaling (Fig. 1D). LUMIER also recapitulated constitutive interactions such as that between Smad4 and the co-repressor SnoN (Fig. 1E). Furthermore, it detected the transient interaction between Smad2 and constitutively active RL-tagged TβRI (Fig. 1F) that is difficult to detect by traditional means. Thus, LUMIER recapitulates pathway-specific PTM-dependent PPIs, constitutive protein interactions and interactions involving transmembrane receptors. The latter is noteworthy as transmembrane receptors are critical focal points in signaling networks, are important drug targets and have been difficult to study using HTP approaches (*16*).

High-throughput LUMIER. LUMIER demonstrated very high sensitivity and faithfully recapitulated dynamic interactions in the TGFβ pathway, suggesting that it might be amenable for mapping PPI networks in mammalian cells. For proof of principle, we optimized LUMIER in a 96-well format and performed a pilot-screen of Smad4-RL against 30 different Flag-tagged cDNAs in the presence or absence of TGFβ signaling (Fig. 2A). This revealed low background and strong, signal-dependent interactions between Smad4-RL and either Flag-Smad2 or Flag-Smad3, as well as the interaction of Smad4-RL with Flag-Ski, as previously reported (*17*). Therefore, LUMIER is amenable to HTP systematic mapping of PPIs in mammalian cells. To map a TGFβ PPI network, we RL-tagged core members of the pathway that included type I receptors, Smads, and the Smad regulatory ubiquitin ligases, Smurf1 and Smurf2 (Table S1). To systematically evaluate PPIs we used the FANTOM1 library of mouse cDNAs (*18*) and 3Flag-tagged 518 cDNAs (Fig. S1) that contained at least one of the domains summarized in Fig. 2B (*15*). This panel contained both well-characterized proteins and proteins of unknown function. Each tagged protein was then transiently expressed in mammalian cells and expression confirmed by automated immunofluorescence microscopy using a Cellomics Arrayscan system, which also allowed characterization of their subcellular localization (Fig. S2).

To analyze the interaction of each RL-tagged TGFβ pathway component in different signaling contexts with every Flag-tagged protein required approximately 12,000 experiments. Therefore, we used a robotics platform and performed automated LUMIER (*15*). To visualize the entire dataset, we generated a diagram in which each screen with RL-tagged protein is represented on the vertical axis and Flag-tagged proteins are on the

horizontal axis (Fig. 2B). The results of each PPI test are represented by a bar at the intersection, with tone of yellow reflecting the intensity, calculated as fold change over the negative control. We refer to this as the LUMIER interaction intensity ratio (LIR) (see Table S2 for all LIR values). This overview of LUMIER results revealed some global features of protein partners of TGFβ pathway components. For example, we observed that ras GTPase or kinase domain-containing proteins displayed numerous interactions. In contrast, others, such as phospho-tyrosine-binding SH2 domains, displayed a paucity of interactions, consistent with our present understanding of TGFβ signaling, which is dominated by ser/thr phosphorylation events. This suggests that the TGFβ pathway preferentially interacts with certain classes of signaling molecules.

Analysis of the TGFβ interactome. LUMIER not only provides qualitative information regarding PPIs, but also conveys quantitative data. The LIR can thus provide important information regarding the confidence in an interaction and its dynamic regulation by cell signaling pathways. Therefore, at low LIRs, background noise predominates, resulting in high false positive rates and a noisy network, whereas, at higher LIRs, interactions will be of high confidence, but many important interactions that may be transient, occur in specific compartments or are of lower affinity, will be undetected. Therefore, to build the interaction network graph, we examined false negative rates and, although difficult to accurately measure, false positive rates, as well as the statistical significance of interactions at different LIR cutoffs (*15*). Based on these analyses, we chose a conservative LIR cutoff of 3, which yielded false negative rates of about 30% and approximate false positive rates of 16%. Of note, important interactions may exist below this cutoff, and in the future the LUMIER 1.5 fold cutoff graph may be explored for

biologically relevant networks by computationally integrating diverse datasets such as gene expression and protein localization (Fig. S2) (*19-21*).

Analysis of the TGFβ interaction network at a LIR cutoff of 3 revealed 901 interactions amongst 276 proteins. These interactions formed an interconnected network with nodes displaying degrees that ranged from 1 to 130. Analysis of the degree distribution and clustering of the network revealed features of a scale-free network with possible hierarchical modularity (*15*) (Fig. S3). These topological features have also been noted in other PPI networks as well as other biological and real world networks (*5, 22-26*).

The TGFβ signaling network is dynamic. Analyses of network dynamics is important in understanding biological systems (*27*), particularly in the case of signaling networks such as the TGFβ system, which must be remodeled both in time and space in order to convey information (Fig. 1B). To determine how signaling regulates PPIs in our network, we focused on the dynamics of the Smad2 and Smad4 interactome in the absence and presence of TGFβ signaling (Fig. 3B) and Smad1 with BMP signaling (Table S2). To capture the dynamics we also generated a movie of the network changes (Movie S1). Analysis of these graphs and in particular the movie revealed considerable partner switching. Thus, numerous interactions were lost upon signaling, whereas others, such as the assembly of Smad complexes, were stimulated. This was particularly evident for Smad4, possibly reflecting modulation of its protein interaction surfaces upon assembly into complexes with phosphorylated R-Smads. We next surveyed the network, which included the known interactions amongst the R-Smads and Smad4, and the interaction of Smad4 with CAMK, which phosphorylates Smad4 (*28*). We also verified,

by immunoprecipitation and immunoblotting, a number of previously undescribed interactions (data not shown). In particular, Smad2 association with the homeodomain transcription factor goosecoid, the C2-WW-HECT ubiquitin ligase, WWP2, and the protein phosphatase 2 regulatory subunit, PPP2R2D, as well as interactions between Smad4 and either Map kinase kinase 3 (MAP2K3) or TC21 (RRAS2). The identification of WWP2, extends the range of C2-WW-HECT ubiquitin ligases that function in Smad signaling beyond the Smurf subfamily and the presence of PPP2R2D suggests one potential mechanism for turning off Smad signaling by dephosphorylation. Indeed, overexpressed PPP2R2D was found to inhibit TGFβ-dependent Smad signaling (data not shown). The interaction of MAP2K3 with Smads is also intriguing, since Smad7 has previously been found to bind MAP2K3 and this kinase is required for TGFβ-dependent activation of p38 (*29*). These studies thus identify considerable dynamics in the Smad network that are more complex than simple signal-dependent association with effector molecules. It will be interesting to understand what aspects of TGFβ biology are controlled by these fluxes.

The TGFβ receptor links the PAK1 and Polarity clusters. To identify novel TGFβ signaling networks of particular biological importance, we explored the TGFβ LUMIER dataset using a Binary Tree-Structured Vector Quantization (BTSVQ) algorithm, which combines tree-structured vector quantization and partitive *k*-means clustering (*30*). BTSVQ is useful for clustering high-dimensional datasets since it performs unsupervised clustering of both dimensions, and supports intuitive visualization of clusters, both as a binary tree dendrogram, and component planes of Kohonen's Self-Organizing Maps (SOMs). SOMs employ a neural network algorithm that clusters high dimensional data

within a two-dimensional component plane, placing similar data in the same area of the map. SOMs thus provide a powerful method to compress information content, visualize complex datasets and effectively exploit the quantitative information inherent in LUMIER. Therefore we clustered prey space (all the 3Flag-tagged cDNAs) using BTSVQ and identified homogeneous clusters. One of these included p21 activated kinase-1 (PAK1). PAKs are a family of kinases involved in regulating cytoskeletal dynamics, cell motility, survival, proliferation and gene expression through a variety of effectors (*31*). PAK activity is regulated by the low molecular weight GTPases Cdc42 and Rac1, which are activated by PAK interacting exchange factors, α-PIX and β-PIX.

PAKs were noteworthy because they have previously been implicated in TGFβ signaling (*32, 33*), although physical association with TGFβ pathway components have not been reported. Therefore, we anchored our unsupervised clustering on PAK1 and sorted the component planes to identify similar profiles. This yielded a cluster with a SOM profile that was clearly distinct from others, such as that containing IRF3 (Fig. 4A). This cluster contained known components, such as PAK1, as well as poorly characterized proteins such as ser/thr kinase STK22D and a pseudo-kinase (FLJ23356) we call TRIK (for TGFβ receptor interacting pseudo kinase). Remarkably, other component planes in this cluster included the PAK-interacting proteins, ARHGEF6 (α-PIX) and Oxidative Stress Response kinase-1 (OSR1) (*31, 34*). Therefore, we focussed on this cluster and examined binding to affinity-labeled receptor complexes. This showed a range of interactions from weak (Fbx034) to strong (PAK1) (Fig. 4B). Of note, both OSR1 and α-PIX bound to receptors (Fig. 4B), as did the related β-PIX, which interacted with both TβRII and receptor complexes (Fig. S4A). Cdc42 is a key player in PAK signaling and is

activated by TGFβ (*35*). Therefore, we extended our analysis to Cdc42, which we showed interacted with cell surface receptor complexes (Fig. S4B). Further, we observed that endogenous receptors bound specifically to a GST-CRIB affinity resin, which binds active Cdc42 and Rac1 (Fig. S4C), suggesting the possibility that active Cdc42 and Rac may bind to TGFβ receptors. Finally, we examined endogenous interactions using a mouse mammary gland epithelial cell line, and observed endogenous PAK1 bound to endogenous TβRI (Fig. 4C). Thus, we define a previously unknown link between TGFβ receptors and the PAK network that might suggest a model in which TGFβ receptors regulate PAK signaling by nucleating assembly of a Cdc42, PIX and PAK complex.

This cluster also contained one other notable member, Occludin, which we confirmed interacted with endogenous TβRI (Fig. 4D) and receptor complexes (Fig. 4E). Occludin is a tight junction (TJ) accessory phosphoprotein that has four transmembrane domains, three cytoplasmic domains and two extracellular loops. Occludin interacts with a number of proteins (Reviewed in (*36*)) including those that link it to the polarity network, which controls cell polarity and in epithelial cells regulates tight junction homeostasis and epithelial cell plasticity. The striking similarity in the SOMs of PAK1 components and Occludin thus prompted us to examine in the literature the physical relationship between these two networks. This revealed that they were only sparsely connected to each other (Fig. 4Fi). However, inclusion of the novel interactions with TGFβ pathway components identified in this study generated significant interconnectivity between the networks. In particular, the TGFβ receptor linked extensively to the PAK1 network, as well as the polarity complex through Par6 (Fig. 4Fii). Furthermore, we show in a separate study that the link to Par6 is critical for TGFβ-dependent epithelial-to-mesenchymal transition (*37*).

These results highlight the power of merging supervised and unsupervised clustering using BTSVQ analysis to extract and identify important PPI networks from LUMIER data. Furthermore, they reveal previously unappreciated complexity in signaling pathways regulated by TGFβ receptors and suggest that Ser/Thr kinase receptors form a hub that interconnects the PAK, polarity and Smad networks.

Defining how cell signaling PPI networks control mammalian cell function is one key goal of systems biology. Here we report the first systematic analysis in mammalian cells of protein interactions involved in cell signaling. Our approach allows for recapitulation of PTMs that are essential for controlling network flux during signaling. Although our strategy employs overexpressed proteins, analysis of assay performance suggests it is robust, a conclusion supported by our identification of many known, as well as readily validated novel interactions. Recently, a systematic analysis of the TGFβ-family dauer pathway in *C. elegans* employed Y2H coupled to genetic analysis (*38*). This identified a number of genes involved in the pathway, including daf-5, a *C. elegans* homolog of the mammalian Smad-interacting Ski oncoprotein (*38, 39*). Our present studies highlight how systematic analyses can uncover new connectivities in mammalian signaling pathways, such as that between TGFβ receptors and the PAK and polarity networks. Thus, HTP analysis of cell signaling in mammalian cells can begin to unravel how dynamic and highly interconnected signaling networks interpret complex spatio-temporal cues in multicellular organisms.

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SUPPORTING ONLINE MATERIAL

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Materials and Methods

Figs. S1, S2, S3, S4

Tables S1, S2

Movie S1

FIGURE LEGENDS

Figure 1. The luminescence-based strategy for the detection of mammalian protein-protein interactions. (**A**) LUMIER. RL-tagged protein A co-expressed with a Flag-tagged partner B in mammalian cells is detected in immunoprecipitates enzymatically as light emission. (**B**) Schematic of the TGFβ and BMP Smad signaling pathways. See text for details. (**C**) LUMIER detects phosphorylation-dependent interactions. HEK-293T cells were transfected with wild type or RL-tagged Smad4 together with either wild type (+) or the phosphorylation site mutant (SA) of Flag-Smad2. TGFβ signaling (+) was induced by expression of constitutively active TβRI(T/D)-HA. Smad4 interaction with Smad2 was determined by measuring RL activity in anti-Flag immunoprecipitates (histogram; RLU, relative luciferase units) or by immunoblotting (IB) with anti-Smad4 antibody. pRL-TK is RL driven by the thymidine kinase promoter and is a negative control. (**D**) LUMIER distinguishes signal-specific interactions. HEK293T cells were transfected with Smad4-RL and Flag-Smad1 or Flag-Smad2 in the presence (black) or absence (white) of BMP signaling. Protein interactions in anti-Flag immunoprecipitates were determined by measuring RL activity. (**E**) Detection of signal-independent interactions by LUMIER. HEK293T cells were transfected with Flag-SnoN and Smad4-RL or Smad4-HA and their association detected as in (**D**). (**F**) Detection of TβRI-Smad2 interaction by LUMIER. HEK-293T cells were transfected with constitutively active TβRI(TD)-HA-RL or TβRI(TD)-HA along with Flag-Smad2 and their association detected as in (**C**) (top panel). Levels of phosphorylated Smad2, total Smad2, and receptors were confirmed by immunoblotting with anti-phosphoSmad2 antibody (α-P-S2), anti-Flag and anti-HA, respectively (lower panels).

Figure 2. High-throughput LUMIER. (**A**) Pilot screen in 96-well plates. HEK293T cells were transfected with 30 different Flag-tagged cDNAs (indicated), or empty vector (V) and HA-tagged TβRI (TβRI-HA) as negative controls, together with Smad4-RL and interactions assessed by LUMIER in the presence or absence of TGFβ signaling. Results are plotted as the mean relative luciferase activity (RLU) $\pm$ SD of triplicates from a representative experiment. (**B**) Summary of results from the TGFβ pathway LUMIER screen. TGFβ pathway components (listed on the left), fused to Renilla Luciferase were screened against 518 3Flag-tagged cDNAs in the presence (*) or absence of TGFβ signal. Individual cDNAs, identified by numbers at the top of each panel, were grouped by domain composition. Each row corresponds to one pathway component and the LIR score for each test is represented colourimetrically, with the tone of yellow representing the LIR value as defined by the scale on the right. W, wild type, K, kinase-deficient, Q and T constitutively-active, C, catalytically inactive.

Figure 3. The TGFβ interactome by LUMIER. (**A**) Network graph of the TGFβ interactome. Proteins are vertices and are color-coded according to their Gene Ontology annotation (inset). Interactions with a LIR of 3 or greater are shown as edges (blue). For clarity, Smads under different signaling conditions and various wild type, activated and catalytically inactive versions of Smurfs and receptors have been condensed into single vertices. (**B**) Dynamics of the Smad subnetwork. The Smad (MADH2 and 4) network in the absence (left) and presence (right) of TGFβ signaling are shown, with the edge colour reflecting the LIR (inset). Note the dynamics of the network (see also Movie S1).

Figure 4. The TGFβ receptor connects subnetworks involved in cell motility and polarity. (**A**) Combined unsupervised and supervised BTSVQ clustering identifies a group of proteins with similar SOMs. IRF3 (lower right), which is part of a different cluster, is shown for comparison. (**B**) Association of Flag-tagged proteins with TGFβ receptors. HEK293T cells transiently transfected as indicated, were affinity-labeled and lysates subjected to immunoprecipitation with anti-Flag antibody. Coprecipitating receptors were visualized by autoradiography and the expression of Flag-tagged proteins confirmed by immunoblotting (IB). CHEK and DUSP3 did not interact with TβRI in the LUMIER screen. (**C, D**) Endogenous PAK1 and Occludin associate with the TGFβ receptor. NMuMG cell lysates were subjected to non-immune (NI) or anti-TβRI immunoprecipitation (αTβRI) followed by immunoblotting with anti-PAK1 (**C**) or anti-Occludin (**D**) antibodies. The antibody heavy chain is indicated (IgH) **(E)** Occludin associates with cell surface TGFβ receptors. Occludin interaction with TGFβ receptors was determined as in (**B**). (**F**) The TGFβ pathway links the otherwise sparsely connected PAK1 and polarity networks. The connectivity between the PAK1 (blue) and polarity (green) networks is shown before (i) and after (ii) the LUMIER screen with TGFβ pathway components (red nodes). Purple nodes are proteins from either network that were present in the LUMIER screen. Nodes connected by black edges represent interactions previously reported in the literature, whereas red edges indicate novel associations unveiled by LUMIER or our directed experiments (see text for details).

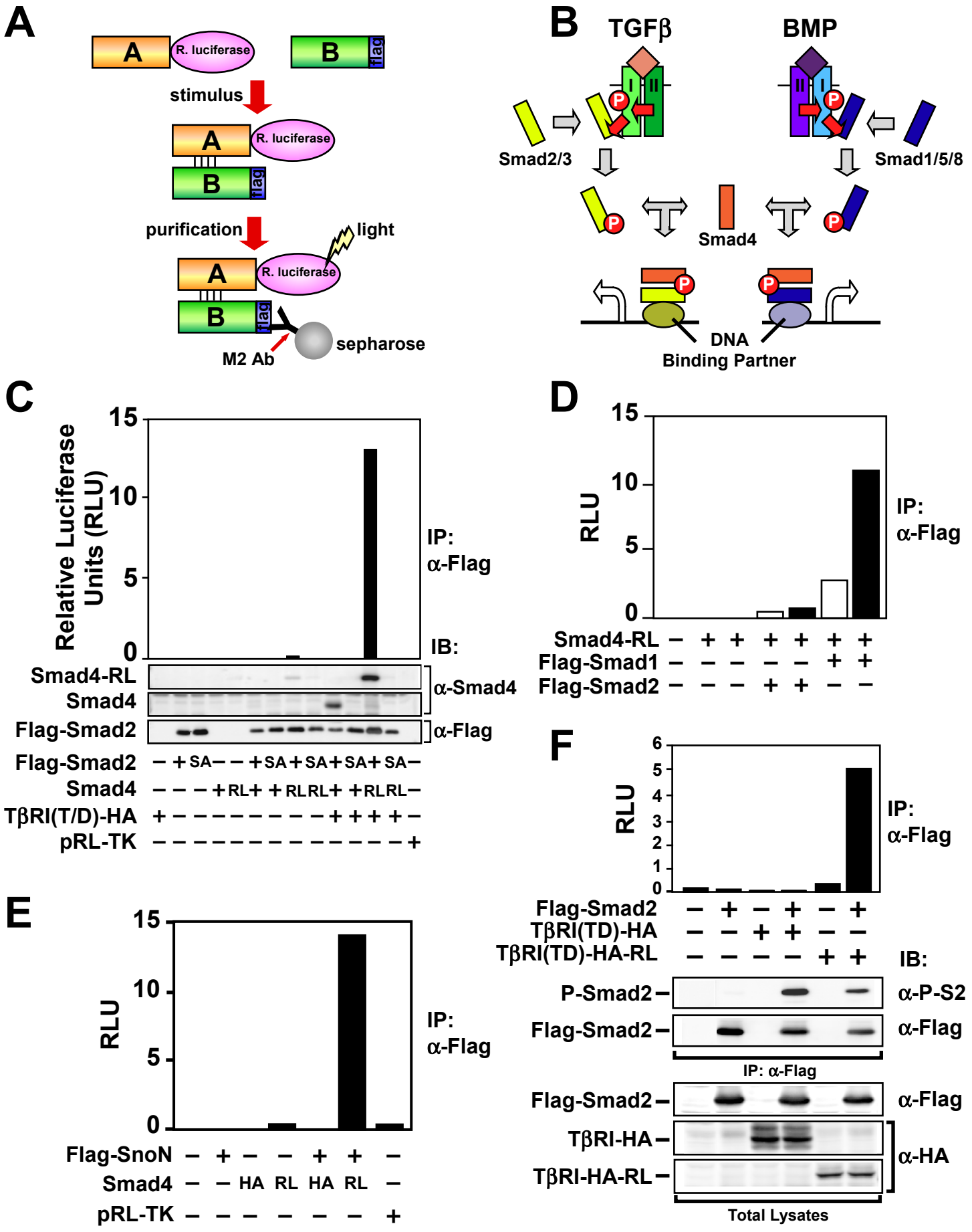


Fig. 1 Barrios-Rodiles *et al.*, 2004

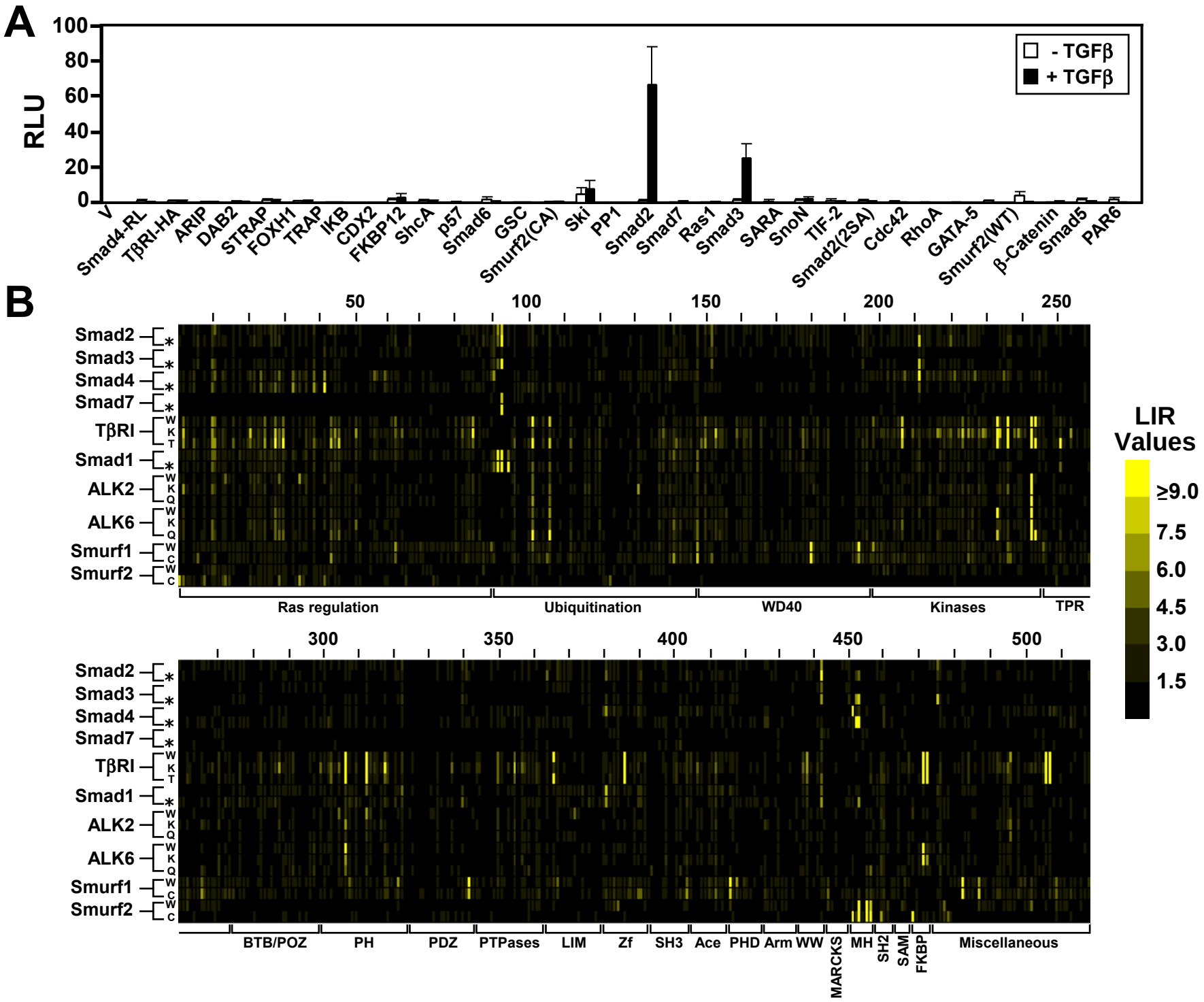
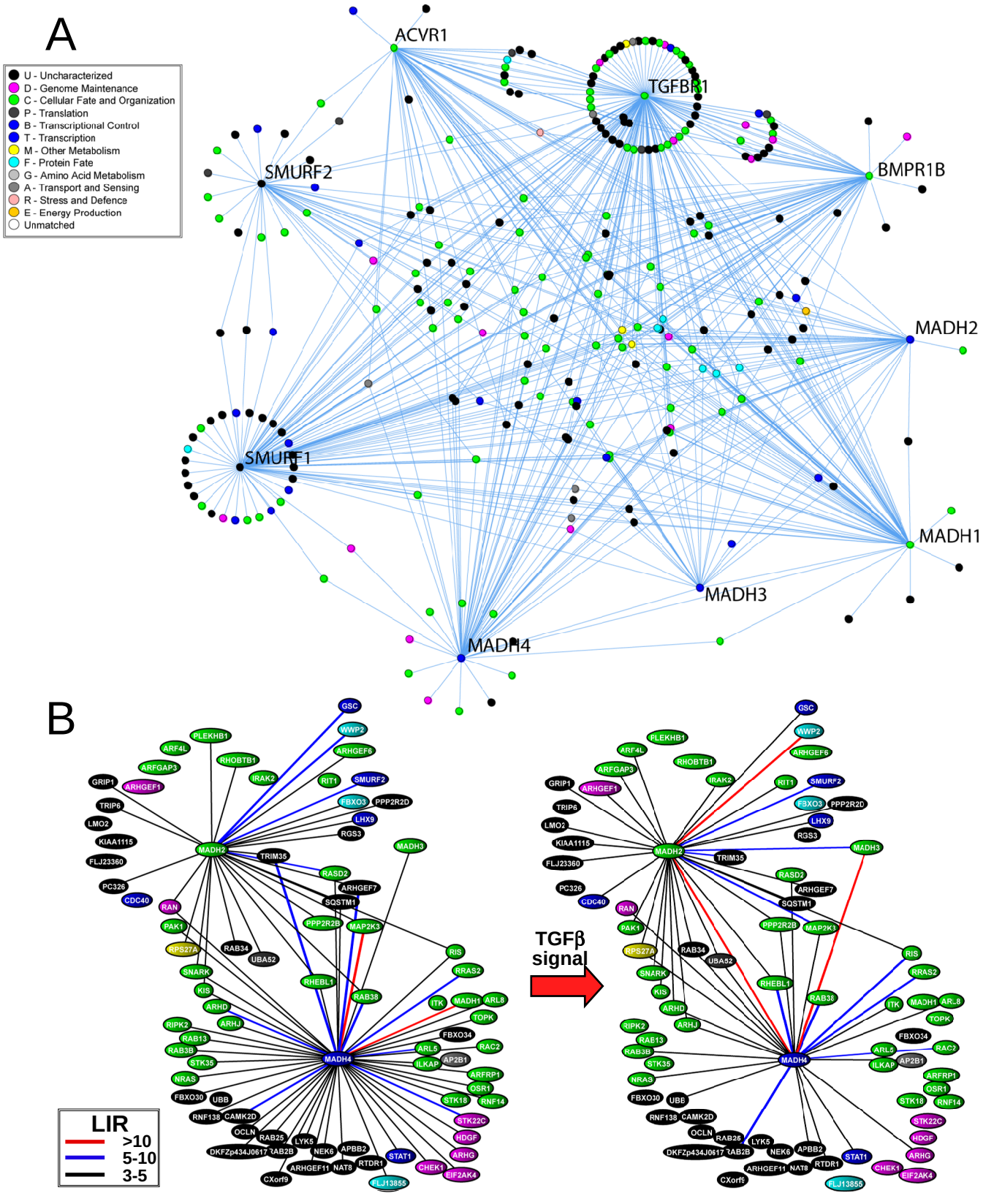


Fig. 2 Barrios-Rodiles *et al.*, 2004



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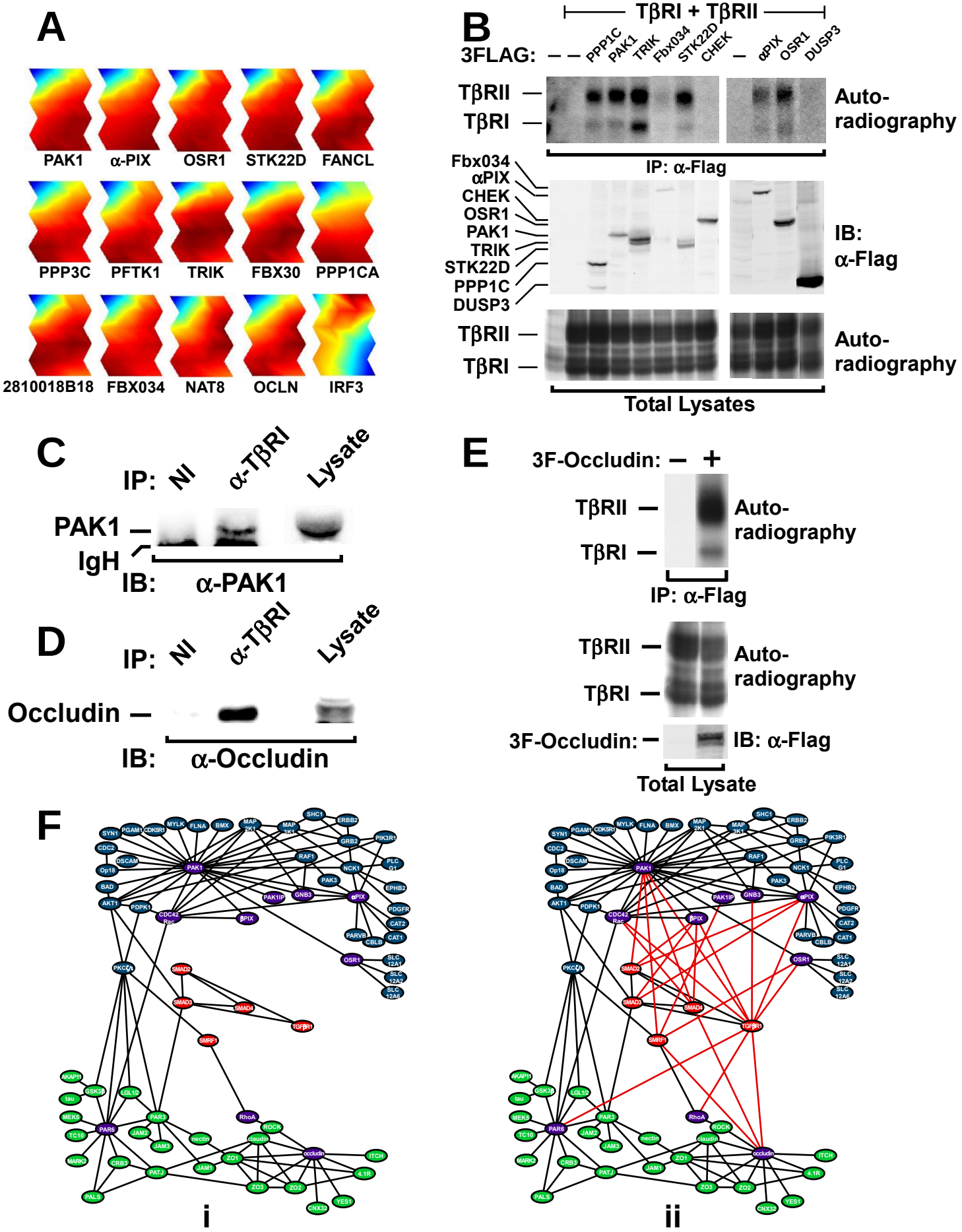

Fig. 4 Barrios-Rodiles et al., 2004

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High-throughput mapping of a
dynamic signaling network in mammalian cells

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MATERIALS AND METHODS

Development of LUMIER. HEK293T cells plated in 6-well dishes were manually transfected using the calcium-phosphate precipitation method. After 48 h, cells were lysed as in (*1*) and then immunoprecipitated using anti-Flag M2 monoclonal antibody (Sigma). Total protein expression was confirmed by immunoblotting with anti-Smad4 (rabbit) and anti-HA (rat, Roche) antibodies. Luciferase activity in immunoprecipitates and in aliquots of total cell lysates was determined using the Renilla Luciferase Assay System (Promega). For adaptation into the 96-well format, a Multiprobe II Ex 4 Tip (Packard) was used for liquid handling procedures.

Construction of the Renilla luciferase-tagged cDNAs. Renilla luciferase tagged baits were generated by PCR, subcloned into pCMV5 and verified by sequencing. Smad4 and TGFβ receptor type I (TβRI-HA) were tagged with Renilla luciferase (AF025846), and the others with a humanized version (AF362545). Smad1, 2 and 3, Smurf1 and Smurf2 were amino-terminally tagged while the receptors, Smad4 and Smad7 were tagged at the carboxy-terminus.

Construction of 3Flag-tagged cDNA collection. Approximately 600 cDNAs from the FANTOM1 mouse cDNA library (*2*) were manually curated to define the longest open reading frames containing identifiable domains involved in cell signaling (Fig. S1 and Table S2) and of these, 95% were successfully amplified using Platinum Pfx polymerase (Invitrogen). The blunt-ended PCR products were purified with the QIAquick gel extraction kit (QIAGEN) and then subcloned into a customized pCMV5-based directional

TOPO-vector (Invitrogen) that included an amino-terminal 3X Flag epitope tag. Eight colonies from each ligation reaction were then screened by PCR and insert orientation and the presence of a stop codon confirmed using a diagnostic EcoRI restriction site incorporated into the reverse primers. DNA from positive colonies was purified using the 96-well format QiaWell kit (QIAGEN). The overall cloning success rate for generating the 3Flag-tagged cDNA set was 77.5%. Twenty-eight in house Flag-tagged cDNAs were included in the set for the screens and can be identified by their Accession numbers in Table S2.

Automated imaging. To confirm expression and to obtain preliminary information on subcellular localization of the 3Flag-tagged proteins (Fig. S2), COS-7 cells plated in 96-well dishes were transiently-transfected with each clone using PolyFect (QIAGEN). After 48 h, cells were fixed, permeabilized and proteins visualized using an anti-Flag M2 antibody followed by AlexaFluor-488 conjugated goat anti-mouse antibody (Molecular Probes). Images were obtained using the high-throughput ArrayScan II System (Cellomics, Pittsburg, PA). Colonies from confirmed clones were pooled into one well of 96-well plate. Working aliquots (5 μl) of 3Flag-tagged cDNAs at 0.02 μg/μl were aliquoted into 96-well plates and stored at -80 ^{o}C for the LUMIER screens. Detailed information on each 3Flag-tagged cDNA will be made available via the Web upon publication.

LUMIER automation. The screens (Table S1) were carried out on a ThermoCRS (Burlington, ON) Robotic platform. This platform comprises a Robotics Articulated Arm which runs along a 3 m UMI-33 TRACK system (ThermoCRS), and has access to 14 pieces of equipment mounted on a custom designed table. HEK293T cells were plated at

a density of 22,000 per well in poly-D-lysine coated 96-well plates (COSTAR, Corning) in complete DMEM with antibiotics 24 h before transfection. Cells were transiently-transfected with 100 ng of each 3Flag-tagged cDNA and 125 ng of the Renilla luciferase tagged bait diluted in DMEM without serum or antibiotics using PolyFect (QIAGEN). Transfected cells were maintained at 37 ^{o}C and 48 h later were lysed as previously described (*1*). A Multimek 96 (Beckman) liquid handler was used to transfer seventy percent of the cell lysates to a white round-bottom NBS plate (COSTAR, Corning) containing 5 μl of paramagnetic beads (Dynal) coupled to protein G and the monoclonal M2 anti-Flag-antibody (Sigma). Immunoprecipitations were carried out for 1 h at 4 ^{o}C in a shaker-incubator (ThermoCRS) and the beads washed 8 times using a Biotek ELx405 MAGNA washer with a modified magnetic nest (ThermoCRS). Renilla luciferase activity in the immunoprecipitates was measured in a Berthold Luminometer with the Renilla Luciferase Assay System (Promega). Total expression of the Renilla luciferase-tagged protein was confirmed using ten percent of the cell lysates with the Dual-Glo Luciferase Assay System (Promega) in a CCD camera equipped chemiluminescence imaging plate reader (CLIPR, Molecular Devices, CA).

Biochemical analysis for validation of interactions. For affinity-labeling, HEK293T cells expressing the TGFβ type I and type II receptors along with the 3Flag-tagged cDNAs were incubated with 250 pM [^{125}I]-TGFβ in media for 1h at 37^{o}C and receptors then cross-linked to ligand and immunoprecipitated with anti-Flag M2 antibody as described (*9*). For GST-CRIB pull-down assays, affinity-labeled receptors were collected using GST-CRIB as previously reported (*10*). Endogenous interactions in mouse

mammary epithelial cells (NMuMG) were detected using anti-TβRI (V22, Santa Cruz), anti-PAK1 (Santa Cruz) and anti-Occludin (Zymed) antibodies.

Data Analysis and Visualization of LUMIER Results

LIR Calculations. To calculate each LUMIER interaction intensity ratio (LIR), the 8 negative control wells on each 96-well plate were averaged. Next, a ratio of the luciferase intensity of each bait (RL-fusions) and prey (3Flag-tagged cDNAs) combination against its corresponding mean negative control was obtained. A linear scaling factor was applied to the LIR dataset for each bait to normalize for experiment-to-experiment variability in luciferase intensity, that is due to variability in total expression levels of RL-tagged proteins. Finally, the LIR's from replicate experiments were averaged to provide the final LIR for each bait-prey combination. To generate a table of all LIR values (Table S2) each 3Flag-tagged FANTOM1 clone was grouped according to its domain as defined by *SMART*. We next performed BLAST analysis using the FANTOM1 sequences and the top scoring E value was used to label each clone. The corresponding mouse and human Unigene IDs for each clone are also provided in Table S2.

LUMIER Assay Performance. LUMIER provides quantitative information regarding protein interactions, which can be used to assess confidence that an interaction is real. To evaluate LUMIER performance we first determined reproducibility of the assay by calculating the Pearson's correlation coefficient for multiple repeated screens of TβRI, Smad2, Smad4 and ALK2. This revealed an average Pearson's correlation of 0.8. As perfect correlation (i.e. identical data in both screens), would be reflected by a score of 1,

this suggests that the screen yields good assay-to-assay reproducibility. Next, we evaluated false negative rates at different LIR cutoffs. For this we comprehensively searched the literature and generated a list of about 500 protein interactions in the TGFβ signaling pathway, of which 64 were tested in our LUMIER screen. At a LIR cutoff of 1 (i.e. all positive data points in the screen), the false negative rate was low at 9%. However, at LIR cutoffs of 2 and 3 this rose to 24% and 31%, respectively. False positive rates are difficult to accurately measure as it is hard to prove that two proteins do not interact *in vivo*, however we estimated these rates by examining 31 novel interactions of LIRs over 3, using secondary assays, and observed 5 that were not reproducible. This yielded an approximate false positive rate of 16% for LIRs over 3. Furthermore, when we examined the number of statistically significant hits as a function of the LIR cutoff we observed that the ratio of statistically significant to insignificant interactions at a p value $< .05$ was 18%, whereas at a LIR of 2 it climbed markedly to 48%. Therefore, for building the network graph we used a conservative LIR cutoff of 3, which yields a high quality PPI dataset. LUMIER thus delivers high confidence interaction data that compares very favourably to HTP Y2H screens, which are known to produce high rates of false negative (>70%) and false positive interactions (*3, 4*). Interactions with LIR cut-offs of 3 were integrated into a network, and visualized using a custom Java-based application (Fig. 3A). Network dynamics (Fig. 3B) were represented using a modification of the *Spring-Embedder* algorithm, whereby edge lengths were made inversely proportional to the LIR score and the final network adjusted manually to aid visualization of nodes. Edges in the dynamic network were then colour coded to reflect LIRs.

Network Analysis. The network generated at LIR cutoff of 3 has 901 protein interactions amongst 276 proteins. The degree distribution of the network followed a power-law distribution and appears scale-free (Fig. S3A). Furthermore, the C(k) clustering coefficient of degree k proteins scales as k^{-1} (Fig. S3B), indicating the network's hierarchical modularity. The diameter of the network, that is, the average of shortest path lengths over all pairs of nodes, is 2.8, which is close to log(n), indicating the small-world nature of the network. These features of the TGFβ network are similar to those displayed by other PPI networks (*5*), as well as other biological (*6*) and real-world networks (*7*).

Unsupervised clustering using BTSVQ. To identify biologically meaningful information from our PPI dataset, we employed Binary Tree-Structured Vector Quantization (BTSVQ), which combines tree-structured vector quantization and partitive *k*-means clustering (*8*). BTSVQ provides robust unsupervised clustering that is resilient to data preprocessing and normalization, and can extract biologically meaningful clusters from complex datasets. BTSVQ combines self-organizing maps (SOM) and partitive *k*-means clustering in a complementary fashion. The algorithm can be used for high-dimensional data clustering and visualization, both of preys and baits. To cluster preys, the algorithm partitions data using the standard *k*-means algorithm in prey space, where *k* is kept constant at 2. Iteratively applying the algorithm and using evaluation of variance as a stopping criterion, it generates a binary tree. The SOM algorithm is then used to cluster the bait space. This yields SOMs in which each component plane represents one of the 3Flag-tagged proteins used in the screen and the map unit colour reflects the relative LIR values for that protein (that is, the interaction profile of a particular protein

with TGFβ pathway components) (see Fig. 4A). For each level of the binary tree, the preys are then ranked both with respect to quantization error, which is the likelihood of the prey having differential interaction affinity across all baits in the same cluster, and *t*-statistics. This provides an accurate method of excluding baits with variable interaction affinity across preys, as well as baits with low significance, and thus enables selection of the most differentiating baits between clusters. The cluster structure in prey space is visualized using component planes of the already computed SOM and preys displaying similar patterns sorted for validation.

References for Supplementary Material

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Figure Legends for Supplemental Material

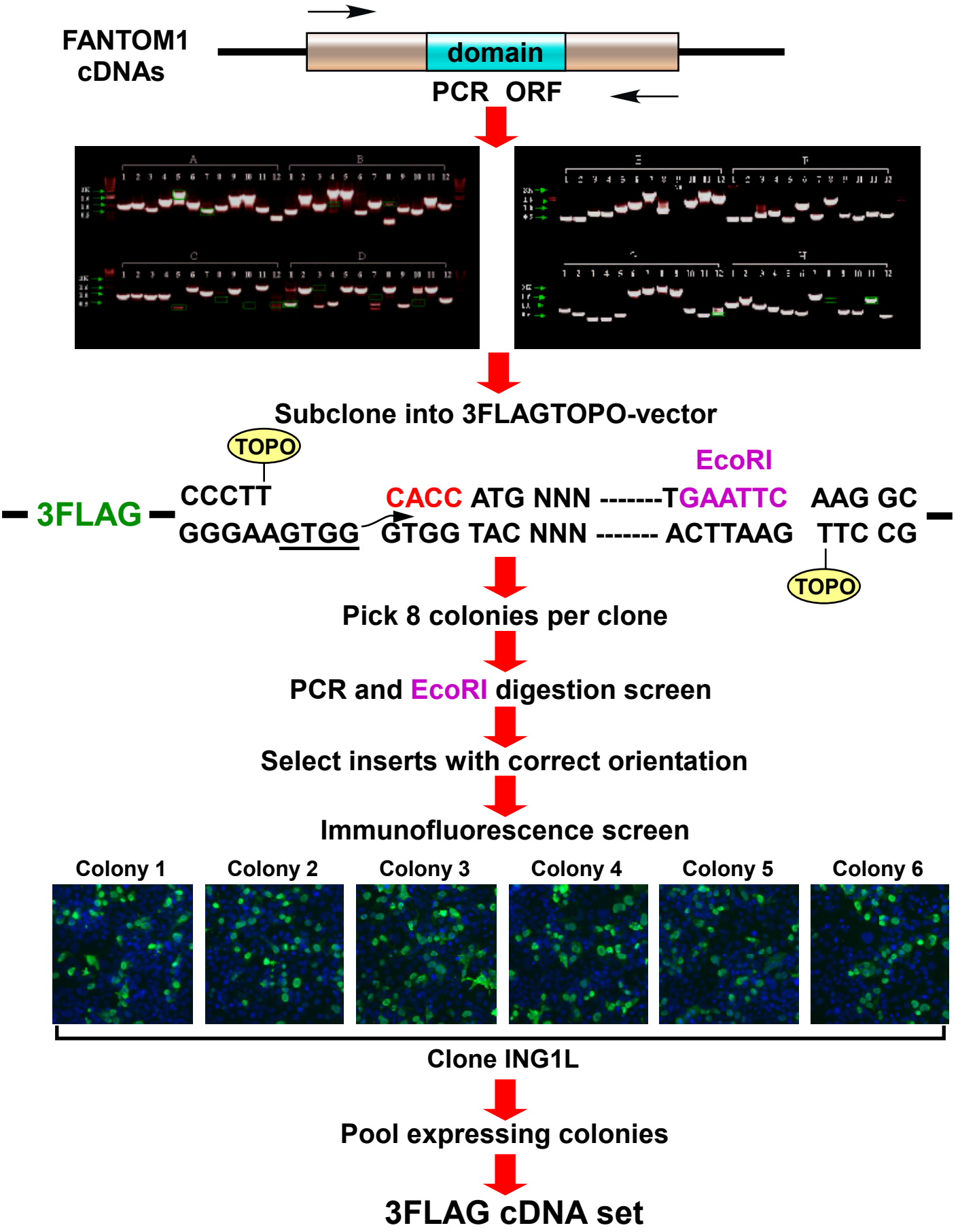
Figure S1. Construction of the 3Flag-tagged cDNA collection. Manually curated FANTOM1 cDNA clones were amplified by PCR. An example of 96 PCR reactions is shown. The purified bands were subcloned into the customized 3Flag-pCMV5 TOPO vector. Directionality in the vector is provided by the underlined GTGG overhang which hybridizes with the CACC (in red) from the PCR product. The EcoRI site (in magenta) was included in the reverse primer to confirm the presence of the stop codon. Eight colonies per clone were screened by PCR followed by EcoRI digestion. Only cDNAs containing inserts with the stop codon and in the correct direction were subjected to the expression screen by immunofluorescence in COS-7 cells. Six colonies from the same clone, displaying similar subcellular localization are shown. Expressing colonies from the same clone were pooled to perform the LUMIER screens.

Figure S2. Subcellular localization of the 3Flag-tagged set of cDNAS in mammalian cells. COS-7 cells expressing 3Flag-tagged cDNAs were immunostained with anti-Flag M2 antibody followed by AlexaFluor 488-conjugated goat anti-mouse. (**A**) Hypothetical protein, MGC 2941, with a PHD domain localized to the nucleus. (**B**) Myoneurin, containing BTB and zfC2H2 domains, localized to specific nuclear regions as reported (*11*). (**C**) Rac1 expressing cells showed an increased number of filopodia (*12*). (**D**) FBOXO30 containing a F-box domain is localized to the cytosol. (**E**) A BTB and Kelch domain containing hypothetical protein, SBB126, displayed a punctate cytosolic pattern. (**F**) ADP-ribosylation factor 6 localized to the plasma membrane as previously shown (*13*).

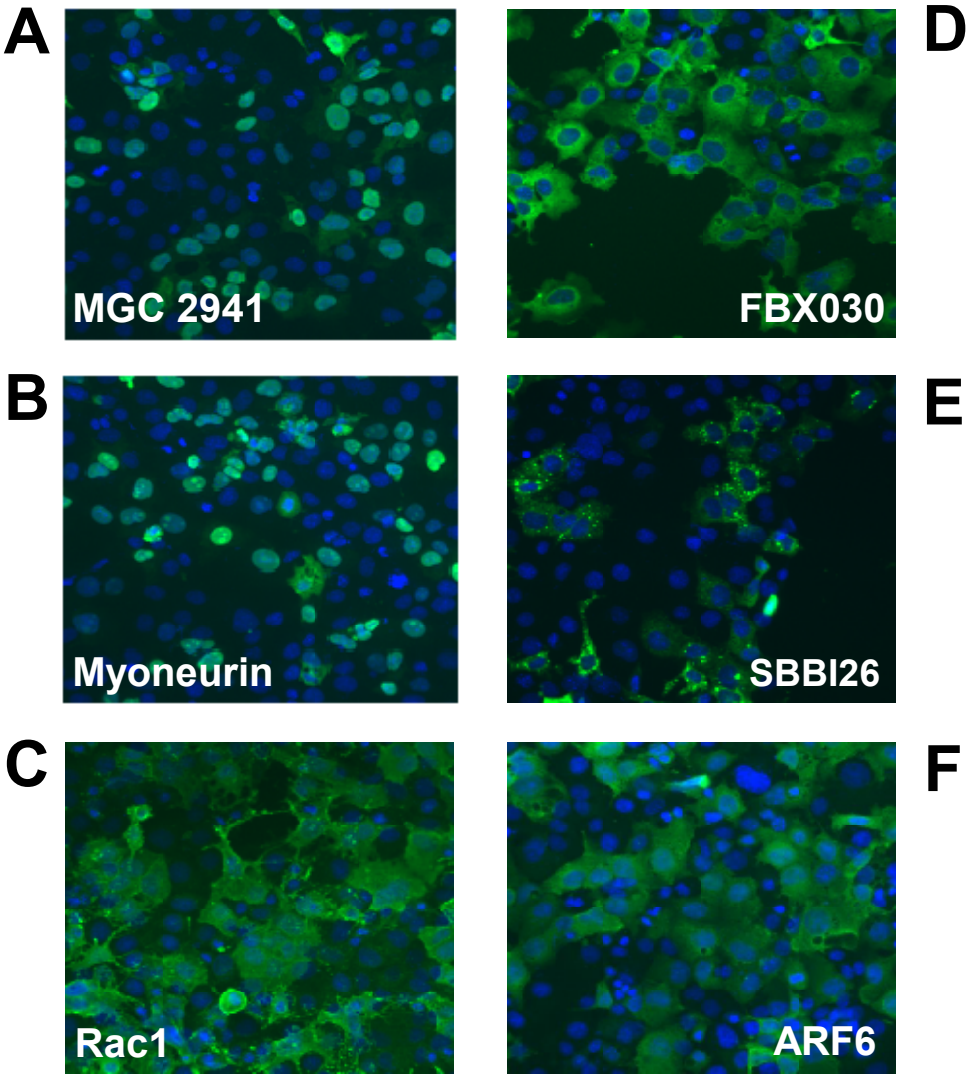
Figure S3. Network Graph Parameters. (**A**) Degree distribution of the TGFβ network. The Probability of proteins with degree k (P(k)) is plotted against their degree (k) in a log-log graph. The connectivity of the nodes in the network roughly follows a power-law (scale-free) with an exponent of 1.7. (**B**) Clustering coefficient of the network. The average clustering coefficient is shown as a function of all nodes of degree k in the network. C(k) approximately follows $C(k) \sim k^{-1}$ as shown by the fitted line in the graph.

Figure S4. Association of TGFβ receptor complexes with members of the PAK1 subnetwork. HEK293T cells were transiently-transfected with wild type or kinase-deficient (KR) TGFβ type I and type II receptors and the indicated Flag-tagged constructs. Cells were affinity-labelled with [^{125}I]-TGFβ and cell lysates subjected to anti-Flag immunoprecipitation (**A** and **B**) or to GST-CRIB affinity purification (**C**). (**A**) β-PIX associates with the TGFβ type II receptor and the TGFβ receptor complex. (**B**) Cdc42 associates with the TGFβ receptor complex. (**C**) TGFβ receptors may bind active Cdc42. Cell lysates were subjected to GST-CRIB pulldown to allow isolation of proteins associated with GTP-bound versions of Cdc42.

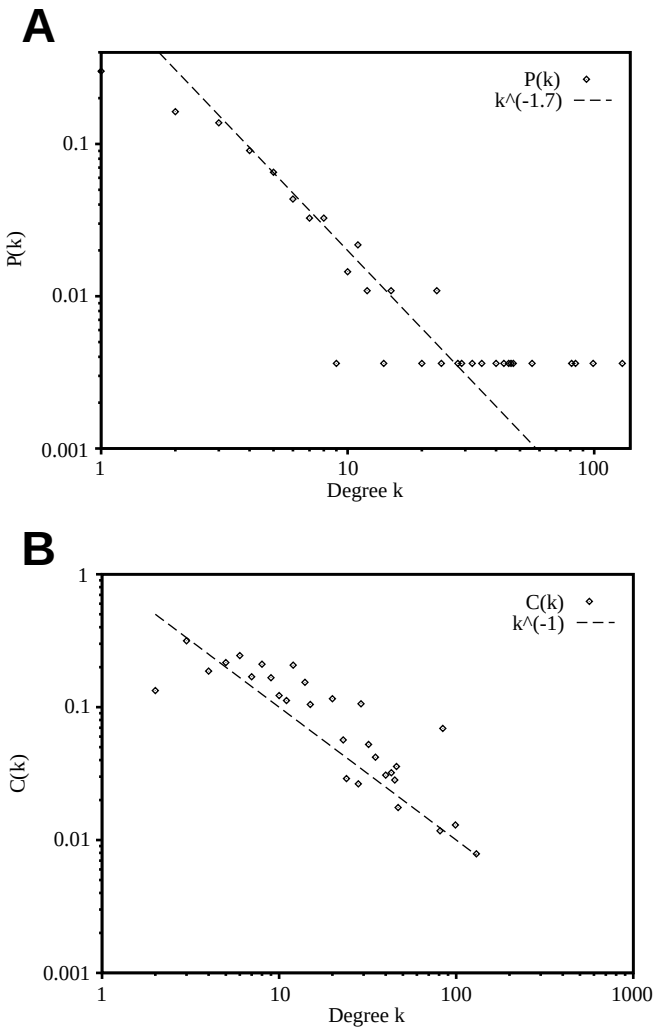
Movie S1 Dynamics of the Smad subnetwork in the absence and presence of TGFβ signalling. The movie shows the Smad2-Smad4 network in the absence and presence (+TGFβ) of TGFβ signalling. The distance between nodes is inversely proportional to the LIR value that is also shown by the colour of the edge.



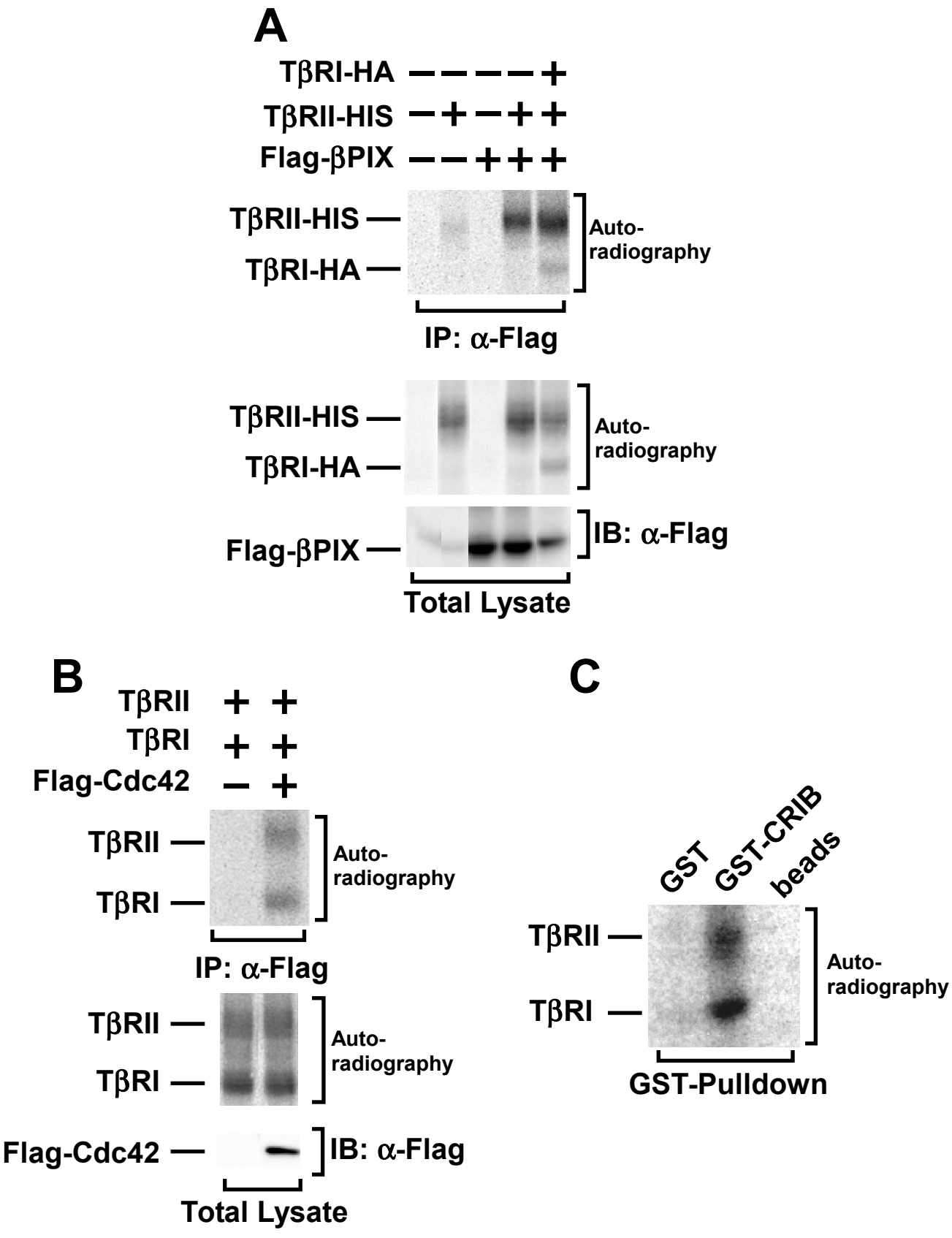
Supplemental Fig. S1 Barrios-Rodiles *et al.*, 2004



Supplemental Fig. S2 Barrios-Rodiles *et al.* 2004



Supplemental Fig. S3 Barrios-Rodilles et al., 2004



Supplemental Fig. S4 Barrios-Rodiles *et al.* 2004

Table S1: LUMIER screens performed.

Screen	UniGene ID	Interaction partners for positive control
Smad1	Hs. 388294	Smad1+ Flag-Smurf2 (C/A)
Smad1+ BMP	Hs. 388294	Smad1+ Flag-Smurf2 (C/A)
Smad2	Hs. 110741	Smad2+ Flag-Ski
Smad2+TGF-β	Hs. 110741	Smad2+ Flag-Ski
Smad3	Hs. 288261	Smad3+ Flag-Ski
Smad3+TGF-β	Hs. 288261	Smad3+ Flag-Ski
Smurf1 WT	Hs. 436249	Smurf2 (C/A)+ Flag-Smad1
Smurf1 C699A (catalytically inactive)	Hs. 436249	Smurf1(C/A)+ Flag-Smad1
Smurf2 WT	Hs. 438968	Smurf2 (C/A)+ Flag-Smad7
Smurf2 C716A (catalytically inactive)	Hs. 438968	Smurf2 (C/A)+ Flag-Smad7
Smad4	Hs. 75862	Smad4+ 3FlagSmad2+ TβRI(T/D)
Smad4+TGF-β	Hs. 75862	Smad4+ 3F-Smad2+ TβRI(T/D)
Smad7	Hs. 370849	Smad7+ Flag-Smurf2 (C/A)
Smad7+TGF-β	Hs. 370849	Smad7+ Flag-Smurf2 (C/A)
TβRI WT	Hs. 28005	TβRI (WT)+ Flag-FKBP12
TβRI (K232R)	Hs. 28005	TβRI (K/R) + Flag-FKBP12
TβRI (T204D)	Hs. 28005	TβRI (T/D) + Flag-FKBP12
ALK2 WT	Hs. 150402	ALK2 (WT)+ TβRI-Flag
ALK2 (K235R)	Hs. 150402	ALK2 (K/R)+ TβRI-Flag
ALK2 (Q207D)	Hs. 150402	ALK2 (Q/D)+ TβRI-Flag
ALK6 WT	Hs. 87223	ALK6 (WT)+ Flag-FKBP12
ALK6 (K231R)	Hs. 87223	ALK6 (K/R)+ Flag-FKBP12
ALK6 (Q203D)	Hs. 87223	ALK6 (Q/D)+ BMPRII-Flag

The TGF-β and BMP pathways were activated by overexpressing the TβRI (TD) and ALK2 (QD) receptors respectively.

Table S2 LIR Values for TGFβ LUMIER.

LIR values for each interaction test are shown. Values between 3-5 are in grey, 5-8 in orange and >8 in yellow.

CloneID	Domain	Label	Mm Unigene	Hs Unigene	hRLUC−SMAD2	hRLUC−SMAD2+TGFB signal	hRLUC−SMAD3	hRLUC−SMAD3+TGFB signal	SMAD4−RLUC	SMAD4−RLUC+TGFB signal	mSMAD7−hRL	mSMAD7−hRLUC+TGFB signal	TBRI−RLUC(WT)	TBRI−RLUC(KR)	TBRI−RLUC(TD)	hRL−hSMAD1	hRL−hSMAD1+BMP signal	ALK2−hRL(wt)	ALK2−hRL(KR)	ALK2−hRL(QD)	ALK6−hRL(WT)	ALK6−hRLUC(KR)	ALK6−hRLUC(QD)	hRLUC−SMURF1(WT)	hRLUC−SMURF1(CA)	hRLUC−SMURF2(WT)	hRLUC−SMURF2(CA)
2310047G11	Ras regulation	RAN	Mm.7521	Hs.10842	0.974	1.5891	0.507	0.9651	2.1261	2.0069	0.628	0.6518	1.0244	1.6754	2.1377	1.711	1.1913	2.051	1.0232	1.35	1.461	1.9342	1.526	1.414	1.0432	0.5191	7.634
2400004O09	Ras regulation	KBRAS1	Mm.264044	Hs.173202	1.61	1.0871	0.747	1.4529	2.022	1.6855	0.721	0.6917	4.6674	**8.0973**	7.2884	2.974	2.3668	2.889	6.106	1.616	3.037	3.9972	3.842	1.772	1.6422	0.9636	5.268
2600013G09	Ras regulation	RABL4	Mm.30191	Hs.415172	1.3403	0.8402	0.919	1.1483	0.9024	0.9662	0.721	0.5611	1.9106	2.398	2.9903	1.769	1.5132	1.351	2.2749	0.973	1.402	1.4464	1.428	1.304	1.4752	1.3004	2.435
2700023P08	Ras regulation	RAB28	Mm.41555	Hs.306899	1.3142	0.9092	1.215	1.1223	1.9722	1.6763	0.5	0.4801	0.9496	1.2817	0.7555	2.202	1.4713	0.803	1.0651	0.762	0.987	0.9612	0.806	1.058	1.1225	0.4918	1.633
2810426G09	Ras regulation	ARHG	Mm.259795	Hs.75082	1.8651	1.7053	1.441	2.2179	3.8557	4.1016	0.849	1.063	2.1111	2.8493	4.6472	3.29	2.1069	1.75	1.7122	1.777	2.209	2.0333	1.934	1.563	1.5004	0.8335	1.632
3110035H11	Ras regulation	RIT1	Mm.4009	Hs.446472	2.6089	4.0792	1.528	3.2481	1.2989	0.9132	0.174	0.2394	1.6109	0.8582	2.0437	2.627	2.4587	1.181	1.6628	1.359	1.416	1.0467	1.438	2.139	4.806	1.2356	0.461
3110082B04	Ras regulation	RAB11A	Mm.1387	Hs.75618	1.3357	0.6839	0.669	0.8756	0.7869	0.7642	0.555	0.722	0.5496	0.5797	0.5673	1.364	1.0979	0.774	0.7334	0.828	0.741	0.6953	1.502	1.565	1.4688	1.1111	1.607
3732413A17	Ras regulation	RAB22A	Mm.275304	Hs.281117	0.9736	1.7518	0.915	1.1776	1.9294	1.3987	0.449	0.5285	1.9937	2.4289	2.2878	2.2	1.5169	2.574	1.8726	1.615	1.51	1.5049	1.931	1.54	1.2973	2.7906	5.122
4021402C18	Ras regulation	RAP2B	Mm.273288	Hs.98643	1.1338	1.3079	0.609	1.0385	0.8153	1.0049	0.202	0.4487	0.9304	0.784	2.8768	1.876	1.3698	1.337	1.0788	0.994	1.394	1.3338	1.31	1.786	1.1541	2.2776	0.879
4631404I11	Ras regulation	RIS	Mm.35827	Hs.27018	4.3668	3.1252	2.252	5.0501	4.4902	5.4173	1.126	0.6772	6.1957	6.6299	6.7844	5.564	4.8547	2.749	4.7467	1.893	2.779	5.0625	4.838	2.209	2.7318	4.0754	2.345
4930526B11	Ras regulation	RASD2	Mm.179267	Hs.248222	5.2365	2.0753	1.472	3.3188	4.5052	2.9955	0.704	0.6724	4.7773	4.0474	6.1376	4.885	3.9734	1.704	3.4688	1.653	2.611	2.6998	3.178	2.927	3.4527	3.3078	2.289
4930527H08	Ras regulation	KBRAS2	Mm.274734	Hs.502910	1.79	1.7219	0.849	0.955	1.1753	1.1937	0.299	0.41	1.4414	1.689	1.768	1.726	1.8485	0.715	1.0004	0.847	1.061	0.8968	0.994	1.561	1.3346	1.6527	1.563
0610007N03	Ras regulation	RAB13	Mm.29355	Hs.151536	0.9028	1.7569	0.609	1.3168	3.6989	2.5323	0.744	0.5623	1.8475	4.2	3.4216	1.948	1.8164	2.992	1.7787	1.739	1.819	2.3831	1.869	2.129	1.198	2.0977	3.844
0610027H24	Ras regulation	RAB17	Mm.279780	Hs.44278	1.1166	2.4013	0.714	1.688	2.285	2.4101	0.264	0.3495	2.1382	2.7818	2.2657	2.12	2.1659	5.446	1.957	1.93	1.965	2.4965	2.79	1.554	1.1651	2.1538	5.411
0610030G24	Ras regulation	RAB14	Mm.29302	Hs.5807	1.006	1.019	1.394	1.1419	1.1405	0.9195	0.638	0.6688	1.1026	0.8888	1.278	1.643	1.4385	1.541	1.0833	1.03	1.01	1.0027	1.48	2.017	1.5274	1.7803	3.263
4930544G11	Ras regulation	ARHA	Mm.73114	Hs.77273	1.8218	1.9504	1.725	2.4876	1.8019	2.4746	0.729	1.0509	3.4821	2.6192	5.6431	2.743	1.9688	1.961	1.6662	1.768	1.891	2.4432	2.348	2.623	2.4746	1.5973	1.368
4931430N23	Ras regulation	RAB23	Mm.86744	Hs.94769	1.1424	0.6558	1.263	0.9719	0.5867	0.8973	0.367	0.4233	0.7182	0.8213	0.7855	1.395	0.9597	0.898	1.0044	0.971	0.886	0.8003	0.856	1.737	1.7969	0.9611	1.209
5033421K01	Ras regulation	RAB30	Mm.26935	Hs.445862	2.6028	2.1743	1.129	2.6117	2.4244	1.7744	0.385	0.497	1.9032	1.9264	2.4305	3.632	2.564	1.494	2.3062	1.568	1.416	1.2559	1.28	2.053	2.4359	1.3452	1.15
5730472O18	Ras regulation	RALB	Mm.27832	Hs.348024	1.1786	1.1099	1.236	1.0336	0.7804	1.0745	0.235	0.4753	1.0493	0.9083	2.0349	2.007	1.378	0.849	0.7208	1.1	1.197	0.9984	0.729	1.912	1.7022	1.1877	1.057
5830400A04	Ras regulation	ARHH	Mm.20323	Hs.109918	1.6994	1.3613	1.207	1.4969	1.5225	1.4399	0.351	0.4342	2.7845	2.0372	3.7555	2.446	1.9404	1.159	1.3966	1.177	2.698	1.6023	2.145	2	1.9536	1.4124	0.844
1110001O11	Ras regulation	RAB25	Mm.26994	Hs.150826	1.1399	2.3811	1.325	1.386	4.1097	1.8119	0.302	0.2975	3.4274	**8.7735**	5.3744	2.172	2.4624	4.142	2.322	2.12	1.762	3.7169	2.713	0.723	1.245	2.3965	4.214
1110005O19	Ras regulation	ARHJ	Mm.27467	Hs.243010	1.7903	4.13	1.065	1.7072	3.9484	3.274	0.435	0.4196	2.9917	2.9339	4.3651	2.789	2.5013	3.329	3.9322	1.51	2.227	3.0301	3.105	1.733	1.9194	1.4634	1.986
1300012N20	Ras regulation	RAB33B	Mm.1664	Hs.191070	2.1386	1.9063	0.78	2.1502	0.9687	1.0059	0.383	0.4366	2.4463	4.1874	3.3313	2.347	1.85	3.115	2.5375	1.653	1.955	2.0215	2.784	1.758	1.4778	2.1009	1.583
1500012D09	Ras regulation	RAB2B	Mm.32870	Hs.22399	2.675	2.3974	0.912	2.6399	4.5839	5.5888	0.473	0.7304	2.2161	1.9849	2.6825	3.39	2.4789	2.099	2.2842	2.159	1.825	2.1061	2.161	1.895	1.7608	2.4557	2.539
5830461H18	Ras regulation	RAP2A	Mm.261448	Hs.48554	1.5646	1.2811	1.161	1.8934	1.9304	2.0987	1.072	1.0606	4.5204	4.8915	6.2497	3.445	3.1159	1.85	4.3087	1.774	2.638	3.1164	4.096	2.145	2.5797	1.9739	2.352
6330580M05	Ras regulation	RAB39B	Mm.45148	Hs.24970	1.5559	1.2255	0.377	1.4544	1.0698	1.7392	0.184	0.5793	1.0625	1.1499	0.9727	2.063	1.67	0.849	0.8706	0.961	1.1	0.863	0.825	1.625	1.8182	1.9963	2.299
6430710G15	Ras regulation	RAB34	Mm.275864	Hs.301853	3.4773	3.3222	1.907	2.3985	2.1873	3.2052	0.605	0.8913	1.5288	1.8821	3.2868	3.152	2.8657	1.738	1.2571	1.799	1.858	2.3306	1.474	1.603	2.0858	1.5319	2.769
1810036J22	Ras regulation	RHEBL1	Mm.259708	Hs.159013	3.1987	3.0392	1.291	2.9837	3.779	5.089	0.78	1.3678	4.7078	**8.0699**	**9.1403**	3.309	3.5185	2.266	2.3268	3.542	5.045	5.5529	5.064	1.639	1.922	2.6312	1.485
2210410A21	Ras regulation	ARHD	Mm.27701	Hs.15114	1.8178	4.4947	1.257	2.5211	5.167	4.0903	0.889	0.8272	2.6889	5.0312	4.5637	2.013	2.0345	5.063	1.6913	2.242	3.528	4.247	5.022	1.854	2.1516	2.0741	4.936
C330006L04	Ras regulation	RAB6B	Mm.193647	Hs.352530	2.3264	1.4558	0.848	2.333	1.883	1.7067	0.639	0.6772	5.2664	7.3032	**11.475**	4.458	3.3042	2.794	3.7673	1.956	3.016	3.2613	5.342	1.895	1.9497	2.0554	2.137
2410015H04	Ras regulation	RAB5A	Mm.286286	Hs.73957	1.1702	0.5579	2.058	0.9038	1.3093	1.0939	0.604	0.7147	0.7376	0.9101	0.8743	1.569	1.4773	1.197	1.1441	1.173	0.644	1.0781	1.189	1.821	1.1515	1.596	1.635
2410064E05	Ras regulation	RAB9A	Mm.25306	Hs.444327	1.1807	0.8434	0.964	0.8703	0.9592	1.0812	0.391	0.4293	1.0017	0.9977	1.0999	0.916	1.3668	0.964	0.9785	1.064	1.097	0.9061	1.251	1.298	1.1399	1.029	1.313
2510038J24	Ras regulation	RAC2	Mm.1972	Hs.301175	2.7139	2.7768	2.266	2.1506	4.5281	6.3634	0.407	0.5648	2.5791	2.5173	2.9889	3.03	2.511	1.339	1.8111	1.617	1.988	2.0054	1.662	1.685	1.7886	1.5188	1.452
2610017M01	Ras regulation	ARHE	Mm.46497	Hs.6838	0.8519	0.9161	0.72	0.6875	2.1435	2.2165	0.159	1.4851	0.8659	1.023	1.201	1.504	1.4601	1.027	0.8498	1.377	0.935	1.0069	1.963	1.445	1.4004	1.1254	2.839
2610037B10	Ras regulation	NRAS	Mm.256975	Hs.260523	1.6414	1.9943	1.402	1.0907	3.7432	3.3749	0.765	0.5914	1.7525	2.1708	1.4633	1.303	1.384	6.657	1.6223	2.995	1.668	2.3323	2.244	1.822	1.3166	1.6079	6.085
2610100O16	Ras regulation	RAC1	Mm.292510	Hs.413812	1.1977	1.1491	0.856	1.3653	1.7456	1.075	0.266	0.5164	1.4298	1.1729	1.2214	1.841	1.4766	2.546	1.2916	1.703	1.283	1.1534	0.673	2.581	1.3875	1.5512	3.721
2610528C18	Ras regulation	RAB3B	Mm.41580	Hs.123072	2.295	2.5854	1.286	2.2037	3.3248	4.0442	0.658	0.6603	2.6231	4.2177	4.3304	3.252	2.6835	3.799	3.2102	2.431	2.388	2.5203	2.171	1.61	1.2708	2.9499	1.419
2700008D04	Ras regulation	MEL	Mm.162811	Hs.5947	0.6983	0.852	0.324	0.6439	0.508	0.7898	0.35	0.3568	1.8744	1.7979	2.1084	1.47	1.1965	1.14	1.0771	1.179	1.143	1.178	1.198	1.354	1.0342	1.2132	1.101
2310011F14	Ras regulation	RAB38	Mm.276669	Hs.108923	3.6892	2.8722	2.233	3.2714	5.3981	7.2658	0.918	1.4246	3.7557	4.4829	5.392	3.31	3.2399	2.372	2.8495	2.444	3.758	4.3749	2.567	1.761	1.8459	2.4806	1.935
3110037E15	Ras regulation	RAB3C	Mm.151600	Hs.184691	1.0375	0.8489	0.696	0.6213	0.9423	2.5921	0.404	0.5756	1.1964	1.2271	1.6822	1.304	1.1823	1.094	0.9246	1.457	1.217	1.0467	0.833	1.434	1.1058	1.5425	1.568
0610007B10	Ras regulation	CDC42	Mm.1022	Hs.355832	1.156	0.8043	0.914	0.6484	1.3482	1.2819	0.93	1.0799	0.9722	0.8159	2.362	1.492	1.133	1.199	0.8622	1.585	1.35	0.7342	0.93	1.342	1.3778	2.5621	1.657
2610016H24	Ras regulation	RRAS2	Mm.276572	Hs.206097	0.9824	1.8063	3.251	1.632	6.7787	**9.3527**	0.643	0.8211	1.0767	2.0654	1.9965	2.397	1.9471	4.138	1.2421	2.126	2.059	3.1308	1.388	1.684	1.3043	1.85	4.714
1300014J11	Ras regulation	RAB7	Mm.298257	Hs.356386	1.5398	0.9001	0.42	0.1252	0.8118	0.8717	1.065	1.0412	0.8672	0.6777	0.6886	1.551	1.3772	1.103	0.7524	1.026	1.086	0.8426	0.38	1.415	0.9046	1.6608	2.025
1700008H16	Ras regulation	RHOBTB1	Mm.31108	Hs.15099	3.9078	1.4176	1.804	0.501	1.5583	1.1804	0.762	0.7389	4.922	5.548	**8.6167**	2.618	3.4752	2.094	3.1571	2.16	3.278	3.4188	5.549	3.893	6.984	2.4245	1.023
1700009N14	Ras regulation	RAN	Mm.23522	Hs.10842	3.4008	1.9847	2.774	2.497	2.9673	2.8222	0.467	0.6337	3.298	6.143	4.9571	3.199	3.0151	1.929	2.7788	1.968	2.267	3.0301	3.043	1.839	1.6719	2.8236	1.894
1700025K02	Ras regulation	RAN	Mm.103632	Hs.10842	2.8016	1.1764	0.899	1.8377	1.7595	2.9832	0.564	0.6966	4.4639	5.2576	7.9407	3.984	3.8389	1.813	2.7234	2.229	2.73	3.0097	4.607	1.761	1.6654	1.4796	1.601
1810035F16	Ras regulation	ARFGAP3-v	Mm.286911	Hs.13014	1.0239	0.9678	1.525	0.2855	1.1166	0.9324	0.619	1.005	0.5531	1.0033	0.6255	1.759	0.7954	0.883	0.8853	1.127	0.887	0.9095	0.907	1.213	1.3353	0.77	0.952
2310032E02	Ras regulation	ZNF289	Mm.43636	Hs.436204	1.6387	1.3784	2.715	0.551	1.2844	1.5039	0.825	1.4113	1.3905	2.0179	1.5829	1.782	0.8701	1.917	1.5112	1.77	1.674	1.0247	1.657	2.598	2.3882	1.2039	1.249
2310075M19	Ras regulation	GNAI2	Mm.196464	Hs.77269	1.233	1.256	1.38	0.3577	1.4587	1.0692	0.655	0.7824	1.9135	2.0799	1.8319	1.994	0.9187	1.72	1.9799	1.588	2.078	1.6725	2.424	1.444	1.2515	0.5266	0.609
2310075M17	Ras regulation	SARA2	Mm.196592	Hs.279582	0.5196	0.6044	0.389	0.1301	0.4139	0.7912	1.181	1.3678	0.8859	1.4781	0.8493	1.163	0.4496	1.619	1.4859	1.375	0.893	0.9011	1.378	1.178	0.5023	0.5434	0.479
A930014M17	Ras regulation	DKFZp761H	Mm.96833	Hs.369885	1.9021	1.4447	1.7	0.5314	1.1684	1.8224	0.662	0.8248	3.7604	6.5884	3.907	3.876	1.6028	1.883	3.6383	2.139	2.96	4.6933	2.922	2.868	1.5616	0.7432	2.622
9130014L17	Ras regulation	FLJ22595	Mm.98122	Hs.287702	1.6553	1.9685	0.582	0.4051	0.8979	1.1867	0.296	0.4535	2.742	2.6667	1.7555	1.751	0.944	0.8	1.7361	0.987	1.506	1.2305	0.986	3.133	2.982	0.8397	1.54
2610009M23	Ras regulation	SNX15	Mm.21071	Hs.80132	0.8349	0.6675	0.662	0.1501	0.9159	1.0997	0.279	0.4789	0.755	0.7397	0.7408	0.968	0.4519	0.708	0.634	0.791	0.734	0.6013	0.619	1.42	0.7505	0.9026	1.347
1700025P09	Ras regulation	ARF6	Mm.318195	Hs.89474	0.7415	0.6117	0.291	0.1346	0.6275	0.8731	0.442	0.5829	0.4995	0.7649	0.2954	1.018	0.4197	0.742	0.5788	0.817	0.601	0.597	0.569	0.913	0.7473	1.4634	0.69
1110018H24	Ras regulation	MINA53	Mm.255635	Hs.23294	1.4222	1.1758	1.246	0.3942	2.3985	1.9731	0.689	0.7159	1.6778	2.3271	1.2484	2.037	0.8873	1.5	1.3185	1.241	1.445	1.6692	1.474	1.734	1.8073	1.568	0.978
2410015N24	Ras regulation	ARL5	Mm.280257	Hs.342849	1.2597	1.3787	1.14	0.589	5.0321	2.7863	0.497	0.7933	1.9862	3.8207	1.5153	3.359	1.0389	1.628	1.3768	1.189	1.301	1.8902	1.538	1.652	1.4423	1.479	0.941
1500006I01	Ras regulation	ARFRP1	Mm.87720	Hs.389277	1.1766	0.9831	1.181	0.3705	3.8876	1.4162	0.811	0.9614	1.7183	2.1283	2.2499	2.317	0.9567	1.258	0.9492	1.566	1.557	1.4295	2.085	1.76	1.5926	1.0557	0.873
1700023N04	Ras regulation	ARL4	Mm.12723	Hs.245540	1.1954	1.0696	1.513	0.3426	2.3089	1.3285	0.963	1.1779	1.2495	1.7388	1.4724	1.883	0.7543	1.393	1.086	1.316	1.01	1.3203	0.727	1.6	1.5062	1.3713	0.884
4930587A11	Ras regulation	ARL8	Mm.174068	Hs.25362	0.8717	1.4439	0.846	0.4935	4.5296	3.2167	0.53	0.6301	1.269	1.9601	0.9833	2.587	0.9455	1.352	1.3751	1.304	1.364	2.2044	0.845	1.544	0.9426	0.8671	2.385
4632412M04	Ras regulation	RGS12	Mm.196208	Hs.434933	1.0693	1.5857	2.013	0.7906	2.1226	2.3274	0.834	1.1223	1.3325	2.1828	1.9837	1.664	0.9523	1.804	2.1177	1.933	1.601	2.2865	1.056	1.971	2.3115	0.0679	2.439

2610313E07	Ras regulation	FLJ10702	Mm.271178	Hs.277255	2.4059	2.0669	1.497	0.7774	2.4807	2.1792	0.571	0.8103	3.1315	2.0986	2.6795	2.756	1.381	0.949	1.4783	1.627	1.548	1.4939	1.548	1.977	1.9652	0.9511	0.864
1110036H21	Ras regulation	ARF4L	Mm.266840	Hs.183153	2.5999	3.1742	2.175	0.9877	1.9	1.3265	0.487	0.5382	5.2463	5.7592	3.9621	3.31	1.5707	1.056	2.6307	1.747	2.282	2.4694	2.29	7.11	5.7435	1.2549	0.724
2310008D22	Ras regulation	ARL1	Mm.291247	Hs.372616	1.3934	0.9287	2.12	0.4367	2.15	2.3597	0.583	0.4946	1.4817	2.0071	2.1578	2.345	0.8589	1.385	1.189	1.495	1.563	1.3355	1.234	1.994	1.3662	1.2188	0.558
5830420E16	Ras regulation	GIT2	Mm.195632	Hs.418057	0.9221	0.7104	1.141	0.252	1.013	0.7752	0.995	0.8332	2.7998	4.6594	2.7096	1.828	0.8208	1.469	1.948	1.698	1.335	1.2948	1.526	2.069	1.2721	1.8867	0.545
4921525H11	Ras regulation	SMAP1	Mm.196452	Hs.410882	1.2703	1.2298	1.783	0.2418	1.0384	1.7833	0.784	1.1658	0.42	0.724	0.9517	1.317	0.6909	0.931	0.7152	1.25	1.262	1.3084	1.466	1.833	0.9072	1.8239	3.175
1810004P07	Ras regulation	ARFGAP3-v	Mm.286911	Hs.13014	1.9136	3.3156	1.588	0.7154	1.9274	2.2164	0.305	0.5115	1.6325	1.6321	1.1687	1.811	0.9889	1.343	2.0251	1.718	1.458	1.2821	0.904	2.108	1.8666	0.0766	1.398
1200003G10	Ras regulation	GNAI3	Mm.271703	Hs.73799	1.3284	1.1426	1.409	0.3505	0.7515	0.9947	0.343	0.5321	1.3596	1.7273	1.462	1.793	0.8552	0.79	1.2749	1.002	1.29	1.2169	1.212	2.075	2.2289	0.793	0.946
2610200H14	Ras regulation	GNA13	Mm.193925	Hs.9691	1.142	0.8973	1.272	0.3757	0.9214	0.9629	0.214	0.8695	1.344	3.1227	1.2756	1.807	1.0016	0.959	1.5076	1.23	1.025	1.073	1.097	2.836	2.2766	1.3452	0.817
0610037B21	Ras regulation	GNG11	Mm.25547	Hs.83381	1.0422	0.9689	0.9	0.4088	1.3432	1.1655	0.935	1.1779	1.8001	1.5667	2.7634	1.705	0.9523	1.626	1.417	1.54	1.143	1.2779	0.941	3.438	2.7196	1.4803	1.003
A930015K11	Ras regulation	GNGT1	Mm.95398	Hs.73112	1.0225	0.9546	1.332	0.2922	1.9597	1.5051	0.199	0.7353	0.9772	1.1278	0.7482	1.359	0.8313	1.252	0.9031	1.215	0.819	0.8206	0.83	2.215	1.9136	1.5649	0.873
1500031D04	Ras regulation	GNG13	Mm.218764	Hs.247888	0.8532	0.7853	0.922	0.2065	1.3322	1.3876	0.859	1.0195	0.6495	1.5492	0.631	1.377	0.605	1.001	1.0749	1.528	1.042	1.0196	1.322	2.473	1.4636	1.6216	0.768
2410018N20	Ras regulation	GNGT2	Mm.46299	Hs.181781	1.0997	0.8256	0.755	0.2768	1.7884	2.0047	1.071	1.5165	0.7695	0.7252	0.8503	1.667	0.9358	1.535	0.7117	1.491	0.865	0.7537	0.785	2.028	1.2573	2.4382	1.411
1110008L10	Ras regulation	GNG2	Mm.41737	Hs.112928	0.9315	1.2227	1.389	0.3039	0.9134	1.9097	0.89	1.2359	1.3928	1.9539	1.3414	1.217	0.6543	1.255	1.1553	1.528	1.149	1.2618	1.11	2.015	0.8865	1.2132	3.545
1190002P14	Ras regulation	GNG3	Mm.27307	Hs.179915	1.0072	1.2465	1.145	0.2554	1.2605	1.8086	0.472	0.861	1.4714	2.2996	1.3917	0.94	0.6431	1.161	1.2779	1.388	1.031	1.0577	0.685	1.939	1.4307	0.826	2.376
1600029K01	Ras regulation	GNG12	Mm.13080	Hs.8107	0.9431	1.4501	0.887	0.3543	0.7201	1.1158	0.398	0.3991	1.1936	1.0702	1.0038	1.114	0.7865	0.693	0.7877	1.116	0.879	0.6114	0.835	2.775	1.9962	0.8186	0.797
0710005M12	Ras regulation	0710005M1	Mm.254898	Hs.443810	1.4538	1.0469	1.461	0.2907	0.7814	1.658	0.674	0.6857	0.787	0.8416	0.6155	1.581	0.8761	1.049	0.7202	1.111	0.554	0.7969	0.325	2.035	1.4404	0.7532	1.123
5830418G11	Ras regulation	RALGPS1A	Mm.274249	Hs.432842	1.4451	0.9795	0.905	0.3242	1.3462	2.407	0.677	0.6482	1.5461	2.0949	1.0301	1.65	1.1166	1.088	1.4372	1.334	0.686	1.2	1.18	2.841	1.6499	1.0507	1.369
1300003D20	Ras regulation	RGL3	Mm.110594	Hs.375142	0.4382	0.4515	0.584	0.1181	0.2201	0.3863	0.297	0.2661	0.3945	0.518	0.3924	0.857	0.3951	0.772	0.4682	0.923	0.589	0.5589	0.409	1.559	0.7924	0.5596	0.458
5830477L08	Ras regulation	CDGAP	Mm.268397	Hs.300670	1.1031	1.0363	1.005	0.3411	0.9652	1.0346	0.513	0.6252	3.1526	3.5135	2.6372	2.125	1.1076	1.866	1.9068	1.667	1.905	1.9054	2.159	3.351	1.7035	0.8827	1.222
3110043J09	Ras regulation	3110043J09	Mm.128411		1.2889	2.1107	0.353	0.4077	0.999	0.9469	0.395	0.4608	0.7754	0.9704	0.9069	1.331	0.7461	0.964	0.6975	1.055	0.66	0.8223	0.724	1.949	1.4462	0.9779	2.382
1700026N20	Ras regulation	CHN2	Mm.253127	Hs.407520	1.9979	1.0366	1.577	0.5435	2.0559	1.3153	0.516	0.9747	3.1207	5.1969	3.0727	1.754	1.0658	1.061	2.9268	1.937	1.206	1.8868	1.702	2.088	2.2734	1.0551	1.341
1200004L23	Ras regulation	INPP5B	Mm.296202	Hs.449942	2.2707	1.1925	1.695	0.4807	2.0026	2.0238	0.608	0.8103	1.5976	1.7344	1.6203	1.635	1.0673	2.235	1.7514	2.128	1.389	1.5269	1.625	2.819	3.2128	1.3763	1.32
5133400C09	Ras regulation	BCR	Mm.182202	Hs.446394	2.1742	1.8135	1.43	0.5138	2.2536	0.9357	0.476	0.6204	3.9524	3.8913	3.2017	2.743	1.7551	2.154	2.5465	2.417	2.966	1.9139	3.663	2.736	2.2766	0.8242	0.521
0710001E19	Ras regulation	CHN1	Mm.257073	Hs.380138	1.5837	1.2306	1.721	0.3829	2.8746	2.0934	1.199	1.0557	6.0254	12.129	5.4446	1.571	0.9179	3.145	4.2481	2.384	2.054	2.5101	3.724	2.198	1.6048	1.1821	0.991
4933411B03	Ras regulation	ARHGAP19	Mm.21646	Hs.80305	1.6195	1.5796	1.319	0.5476	1.2172	1.571	0.58	0.5998	0.9645	0.7124	0.9022	1.344	0.8522	1.182	1.3192	1.388	1.092	1.2186	1.067	2.583	2.503	0.7532	1.933
1700006A11	Ras regulation	1700006A11	Mm.158761		1.2492	0.8318	1.512	0.3667	1.3945	1.7347	0.87	1.1864	2.2972	2.5257	1.5098	1.468	0.8544	1.917	1.5005	2.502	1.47	1.5921	4.362	1.93	1.6016	0.7924	0.875
2610528A06	Ras regulation	ARHGEF1	Mm.3181	Hs.278186	2.4346	3.1764	0.969	2.6279	2.7446	2.2623	0.679	0.8066	1.0766	1.524	1.4212	1.751	1.9792	1.032	1.1686	0.703	0.651	0.8511	0.725	3.68	3.0168	3.4342	0.462
4833419J07	Ras regulation	ARHGAP18	Mm.276368	Hs.413282	1.7823	2.2177	0.803	1.1682	2.7158	1.3412	1.238	1.092	1.3883	2.5859	0.9658	1.206	1.6648	1.121	1.1821	1.322	1.15	1.316	1.204	2.144	2.8105	1.2082	0.528
KIAA0380	Ras regulation	ARHGEF11	Mm.179723	Hs.371602	1.2216	1.9894	1.988	1.758	3.0952	1.3676	1.665	1.3097	1.8207	1.2628	1.018	1.596	1.5527	1.169	1.0459	1.469	0.885	0.9925	1.283	4.606	1.9033	1.2661	1.091
NM_145735	Ras regulation	ARHGEF7	Mm.244068	Hs.172813	3.1999	3.3825	3.481	3.8657	6.2677	2.6003	0.728	0.901	1.1694	1.3178	1.0776	4.226	5.3483	1.239	1.0032	1.404	1.132	1.2788	0.839	2.689	3.6255	0.7812	0.163
AY014180	ubiquitination	SMURF2-W	Mm.200086	Hs.438968	6.3645	5.8177	1.497	5.9885	0.6733	0.7359	0.642	0.751	0.6355	0.6401	1.3388	27.601	26.97	0.91	0.6845	0.824	1.25	0.7122	0.463	1.34	0.9697	1.3601	0.893
AY014180	ubiquitination	SMURF2(C/	Mm.200086	Hs.438968	8.7328	9.8934	2.277	13.017	0.8686	1.1253	8.813	9.0652	0.9129	0.7583	0.7244	32.463	67.005	1.05	0.9045	1.146	1.52	1.0196	0.313	1.101	1.3237	0.9978	1.514
XM_166483	ubiquitination	SMURF1-W	Mm.27735	Hs.436249	0.6379	0.8581	0.476	0.492	0.2082	0.2883	0.132	0.1862	0.5368	0.346	0.8391	1.182	0.9538	0.986	0.4719	0.75	0.678	0.6436	0.456	1.685	1.343	1.0439	0.79
XM_166483	ubiquitination	SMURF1-C/	Mm.27735	Hs.436249	1.5167	2.7873	0.637	1.4574	0.503	0.5212	0.665	0.5321	0.5697	0.4261	0.6494	5.601	14.48	0.834	0.8631	0.823	0.671	0.8367	0.928	1.729	1.1509	0.887	1.309
4930511O11	ubiquitination	4930511O1	Mm.79212	Hs.498027	1.3596	1.41	1.496	0.4859	0.8825	1.2457	0.835	0.9421	1.4015	2.0814	1.8211	2.096	0.9134	1.61	1.0988	1.515	1.181	1.4761	1.622	2.816	1.5887	0.658	2.024
4930455J02	ubiquitination	LOC51035	Mm.27839	Hs.351296	2.257	1.771	1.696	1.2141	2.1565	2.6591	1.832	1.3121	4.34	2.0097	4.7194	1.539	3.7747	3.458	3.2719	2.295	3.387	2.9293	3.056	2.853	3.6139	2.4868	1.129
2700092A01	ubiquitination	UBAP1	Mm.289795	Hs.436169	0.8737	0.7394	1.028	0.5488	1.6116	2.6965	2.118	0.9965	0.621	1.001	0.8403	1.224	1.1308	1.156	1.506	1.109	1.332	0.8994	1.323	1.475	1.7176	1.3943	0.698
8030447B05	ubiquitination	HIP2	Mm.263318	Hs.246603	0.9096	0.6207	0.613	0.2757	1.2316	2.0324	1.553	0.6881	0.6459	0.4702	0.5744	1.134	1.1405	0.86	1.2953	0.7	0.887	0.7198	1.143	1.403	1.2489	1.2923	0.63
2510040N03	ubiquitination	UBL1	Mm.259278	Hs.81424	1.4457	0.7717	0.676	0.4171	1.0444	1.6633	1.166	0.7063	0.7812	0.9515	1.5434	1.123	1.204	0.923	0.8289	0.839	0.827	0.918	1.081	1.143	0.7898	1.4342	1.197
3000008M07	ubiquitination	UBB	Mm.282093	Hs.356190	2.0682	2.1752	1.224	1.4022	1.654	3.0943	0.862	0.5236	3.9425	1.1154	3.8168	1.63	2.2563	1.266	1.4891	1.797	2.584	1.4947	2.602	4.37	2.5681	2.2602	1.298
0610006J14	ubiquitination	RPS27A	Mm.180003	Hs.311640	3.721	3.5702	2.231	2.6618	2.8368	3.3814	1.777	1.3448	9.0509	4.8179	11.66	2.768	5.1437	5.358	4.9978	6.351	5.615	5.6519	11.132	5.837	4.0265	2.7931	2.188
0610008O06	ubiquitination	FAU	Mm.298117	Hs.387208	1.305	1.5667	1.232	0.5202	2.2775	1.6563	0.556	1.3835	1.71	0.6126	0.7717	1.201	1.3078	0.966	0.7929	1.351	1.553	1.0374	1.511	1.569	1.6358	1.2331	1.936
1200014H24	ubiquitination	SF3A1	Mm.190766	Hs.406277	0.8184	1.0179	1.113	0.5792	1.1041	0.7278	0.488	0.9397	0.6437	0.5892	0.5724	1.311	1.5737	1.145	1.2064	1.156	1.144	0.8841	0.747	2.432	3.0362	1.3414	1.124
2010309G22	ubiquitination	UBD	Mm.140210	Hs.44532	1.7605	1.0847	1.156	0.6747	1.2326	2.571	1.518	1.0775	3.7618	2.6673	4.4127	1.309	2.4303	1.094	2.218	1.205	1.566	1.3719	2.841	1.853	2.5919	1.1852	0.853
2310065A10	ubiquitination	Oasl2	Mm.228363	Hs.525059	0.5696	0.4814	0.239	0.3001	0.2983	0.5565	0.889	0.4849	0.4896	0.503	0.4443	1.286	1.0075	0.781	0.712	0.665	0.788	0.7105	0.418	2.706	5.9195	1.4379	0.426
0610008D13	ubiquitination	UBA52	Mm.43005	Hs.5308	3.9411	3.6025	1.87	2.2326	2.392	3.9903	0.813	1.0485	8.1613	3.9901	8.214	2.039	4.7972	3.536	4.7521	4.94	7.141	5.4165	9.54	3.735	3.4346	1.7635	1.473
4930522D07	ubiquitination	4930522D07	Mm.55982	Hs.374027	1.1813	0.8548	0.607	0.3441	1.1166	1.0971	1.462	0.7619	1.4777	1.5579	1.0907	1.177	1.3362	1.086	1.3905	1.031	1.197	0.9036	1.401	1.18	1.4501	0.2776	0.925
4931431F19	ubiquitination	4931431F19	Mm.158518		1.6368	0.9132	0.971	0.6063	0.9184	2.0309	1.286	0.7643	1.0326	0.9569	1.5385	1.235	1.5318	1.121	1.307	1.143	1.048	1.1128	1.132	1.484	1.6441	1.3576	1.06
3110003A22	ubiquitination	LOC137886	Mm.41643	Hs.155572	0.6127	1.8787	0.401	0.6108	0.7685	1.7816	1.666	1.6338	1.8859	2.1742	1.3161	1.106	1.4698	1.678	1.2328	1.339	1.179	1.996	1.305	1.967	1.5049	1.1149	1.992
2810407C17	ubiquitination	NSFL1C	Mm.272186	Hs.12865	0.6983	1.5101	1.068	0.4957	0.8999	1.7268	1.127	1.0062	1.1598	0.6742	0.7925	1.144	1.4071	1.311	0.949	1.307	1.243	0.9451	0.477	1.238	1.4804	0.9686	1.493
2610020P14	ubiquitination	D8S2298E	Mm.29301	Hs.153678	0.5878	0.91	0.499	0.2779	0.3302	0.7438	0.548	0.4644	1.2393	0.8075	1.1899	1.03	1.0815	0.82	0.8547	0.883	1.05	0.6546	1.219	1.19	1.5184	0.8939	0.379
4930550B20	ubiquitination	USP45	Mm.154306	Hs.512802	2.3437	2.4085	1.134	0.9177	1	2.7549	1.634	1.1888	3.0741	2.6657	5.1166	1.757	3.1996	1.298	2.5337	1.442	2.334	2.4136	3.928	3.499	3.5436	1.8705	0.836
2610005K12	ubiquitination	USP14	Mm.182319	Hs.75981	0.645	1.0099	0.824	0.3799	1.0165	1.4829	1.476	0.7897	1.1011	1.5794	1.0135	1.368	1.2346	0.931	1.9578	1.01	1.117	1.0653	1.478	1.619	2.0142	1.1074	1.377
4921514G19	ubiquitination	USP15	Mm.244209	Hs.339425	0.8773	0.8489	0.914	0.3359	1.0977	2.1282	1.993	1.115	1.028	0.8487	1.3746	1.115	1.0591	0.883	1.3289	1.001	1.127	1.4397	1.522	1.39	1.5055	1.6122	1.001
1200004E02	ubiquitination	USP16	Mm.152941	Hs.99819	0.805	0.9837	0.778	0.4867	0.3755	1.3873	0.403	0.7099	0.7892	0.8283	0.8811	1.169	0.9978	0.935	0.7457	1.055	0.965	1.1145	0.247	1.884	1.6009	1.9602	1.169
9130006G10	ubiquitination	USP39	Mm.281900	Hs.12820	0.7476	0.8245	0.412	0.815	0.5289	1.1634	1.08	0.907	1.3026	2.729	2.5457	2.134	1.6028	1.857	3.3926	2.299	2.674	2.5753	2.185	1.642	1.2702	0.5615	0.355
2600002H24	ubiquitination	USP21	Mm.287370	Hs.8015	1.315	1.6976	1.11	1.6831	2.1326	1.1563	1.233	0.9542	1.6934	2.6424	4.1913	2.731	2.4617	1.767	3.2608	1.672	2.315	1.9004	1.499	1.539	2.7293	0.7544	0.501
1700124H18	ubiquitination	Ube2l3	Mm.3074	Hs.446584	0.7604	0.7051	0.441	0.7789	0.7366	0.4815	0.975	1.1972	0.4103	1.0934	0.7441	1.204	0.8821	0.919	0.7375	0.949	1.211	1.0255	0.408	1.241	1.2302	0.6673	0.552
0710008M05	ubiquitination	UBE2J1	Mm.32920	Hs.184325	0.8159	1.2687	1.666	1.5691	2.3233	0.9923	1.614	1.6435	1.3612	1.7709	1.5554	1.852	1.5378	1.53	2.7766	1.774	1.497	1.3677	0.837	1.715	2.5674	1.0707	0.729
1600023F01	ubiquitination	FLJ13855	Mm.38802	Hs.369120	1.6539	1.3688	0.626	1.4616	3.8089	1.0914	1.877	1.3907	3.5588	3.6281	3.4779	4.108	3.2638	2.803	2.5414	2.05	2.033	3.1927	2.301	2.223	2.3405	1.6931	1.399
2510040H03	ubiquitination	UBE2M	Mm.295670	Hs.406068	1.6784	1.5527	2.731	0.8534	1.7341	0.5695	0.936	1.502	1.6129	0.9166	0.8719	0.977	0.8216	1.201	0.7712	1.119	1.017	0.968	1.61	0.926	1.6661	1.7541	1.908
2610009I04	ubiquitination	UBE2B	Mm.280233	Hs.385986	0.7681	0.9324	1.902	0.6759	0.6514	1.1486	1.25	1.6459	1.381	0.8158	1.7361	1.222	1.1741	1.326	0.6171	1.142	1.151	0.7893	1.289	1.344	1.3463	0.5011	1.836
2700059C12	ubiquitination	UBE2G1	Mm.18485	Hs.78563	0.762	0.8325	0.282	0.6905	0.4109	1.1333	2.496	2.0438	1.5057	0.9208	1.391	1.348	0.9851	1.476	0.6579	1.361	0.926	1.3888	0.935	1.188	0.5293	0.9511	5.056
2700084L22	ubiquitination	HSPC150	Mm.284587	Hs.5199	0.5029	1.0675	0.737	0.5736	0.504	0.9241	0.411	1.2226	0.3959	0.7191	0.4671	1.047	1.0897	1.406	0.6142	1.301	1.548	0.8977	1.313	1.284	0.7879	2.2602	0.428
2810489I21	ubiquitination	UBE2L6	Mm.38261	Hs.425777	0.6846	1.072	1.214	0.645	0.7236	0.7382	0.791	0.9469	0.4138	1.1982	0.5807	1.259	1.0635	1.014	0.7424	1.108	1.152	1.0137	0.686	1.286	1.6138	1.1783	0.224
1700013N18	ubiquitination	UBE2D2	Mm.45616	Hs.108332	0.9689	0.8519	1.18	0.7782	1.5693	1.0549	1.265	1.4585	0.7492	1.1399	2.5739	1.47	1.1577	1.11	0.587	1.186	1.476	1.0891	0.795	1.786	2.5004	1.3097	0.159
2510010F15	ubiquitination	NCE2	Mm.183368	Hs.157804	0.669	1.0984	1.386	0.8779	2.1002	0.9447	1.309	0.9904	1.2572	1.2941	0.6573	1.31	1.1816	1.229	0.7977	1.119	1.323	0.9451	1.207	1.398	2.0536	1.6527	0.401
6130401J04	ubiquitination	6130401J04	Mm.122430		1.2735	1.3328	2.202	0.9629	1.6042	1.1602	1.319	0.283	0.7532	2.3229	0.5413	1.42	1.378	1.573	0.6686	1.261	1.363	1.51	1.167	1.712	2.4598	1.3315	0.81
6720465F12	ubiquitination	RPL28	Mm.3111	Hs.356371	1.1512	1.6077	0.508	1.421	2.1181	1.7805	1.201	1.4669	1.0632	1.2191	1.0616	1.872	1.9068	1.302	0.775	1.333	1.65	1.1162	1.237	1.864	2.1387	1.0408	1.651
1200007B18	ubiquitination	UBE2J2	Mm.295719	Hs.441183	0.596	1.062	1.178	0.5081	0.4462	0.5886	1.397	1.5286	1.1991	0.9423	0.9108	1.235	1.0561	1.424	0.9452	1.345	1.15	1.2212	1.522	1.247	1.031	1.69	2.439
1810012G14	ubiquitination	UBE2E3	Mm.1485	Hs.449501	1.0485	1.1734	1.456	1.0734	1.5837	1.0387	1.743	1.3557	1.7867	2.9211	3.023	2.343	1.6513	1.743	6.8384	1.884	2.289	2.5541	1.884	2.631	2.7808	0.8615	0.271
1110015A16	ubiquitination	UBE2C	Mm.89830	Hs.93002	1.1314	1.6705	1.608	1.6421	2.0335	1.7173	0.917	1.0074	0.5155	0.6227	1.0338	1.842	1.322	1.808	1.2986	1.341	1.484	1.1653	0.586	1.499	1.5745	1.1765	0.358
0910001J09	ubiquitination	E2-EPF	Mm.22491	Hs.462306	1.3073	0.996	0.551	1.2927	1.636	1.9457	0.507	0.6228	0.6667	0.6605	1.0461	1.833	1.2667	0.802	0.8904	1.016	1.196	1.0797	0.233	1.933	2.4114	1.1721	0.235
1500026J17	ubiquitination	UBE2N	Mm.30233	Hs.458359	0.979	1.0866	1.077	0.9975	1.6445	1.5247	0.773	1.3569	0.5901	0.9169	0.6038	1.027	1.1315	0.99	0.7207	1.153	1.564	0.8274	0.887	1.33	1.7563	1.0346	0.218
1300019E17	ubiquitination	UBE2I	Mm.240044	Hs.302903	1.1403	1.299	1.416	1.0377	2.6251	0.9674	1.821	1.4415	1.3702	1.9366	1.6244	1.353	1.136	1.276	0.6773	1.375	1.327	1.0967	1.112	1.693	1.9497	1.545	0.575
1200003M11	ubiquitination	UBE2R2	Mm.258805	Hs.11184	1.4085	1.3364	1.421	1.1577	2.2088	1.2127	0.794	0.9771	1.3214	1.3252	1.5037	1.259	1.3362	0.84	0.7675	1.106	1.201	0.8875	0.415	2.103	2.1354	1.5917	0.513

Table S2

3010034A12	ubiquitination	FBX30	Mm.220327	Hs.321687	1.7849	1.7632	1.857	1.5022	2.6391	1.6712	1.759	1.4294	2.9522	3.9448	4.0896	2.436	3.0286	2.236	4.2842	2.527	2.85	3.9303	2.583	3.153	2.5571	1.5406	0.751
2810025M06	ubiquitination	FBXL12	Mm.24608	Hs.12439	2.5437	2.624	1.696	1.8159	0.8118	0.5432	1.064	0.7897	4.4033	4.5087	3.596	3.672	3.2743	1.362	1.5572	1.807	2.224	2.4855	2.124	2.47	2.3011	1.5251	0.799
2610511F20	ubiquitination	MGC15482	Mm.218350	Hs.194498	0.7633	1.0726	1.773	0.9158	1.5235	2.1621	1.38	1.8793	0.8851	2.048	1.7011	1.181	1.0531	1.694	2.8187	1.284	1.671	1.3186	0.314	1.104	1.3611	1.3346	0.153
1700026A16	ubiquitination	FBXO30	Mm.276229	Hs.421095	1.4291	1.4474	1.806	1.9039	4.7841	2.8121	1.259	1.3569	1.1696	2.5504	2.1902	3.14	2.2533	1.703	3.7661	1.542	1.93	2.5279	2.475	2.054	3.1812	0.9804	1.654
1200002G09	ubiquitination	FBXO3	Mm.143768	Hs.406787	3.3361	1.8829	1.761	3.3798	2.1116	1.2482	1.257	1.5709	1.9456	3.1853	3.4772	4.591	3.2175	1.453	2.6638	1.42	3.991	5.1201	3.303	4.428	7.1117	0.7675	0.143
5830426G16	ubiquitination	FBXO34	Mm.11935	Hs.15467	1.332	1.54	1.272	1.6116	3.021	1.2855	1.008	1.1864	2.4821	2.9252	4.9083	2.373	2.1017	2.162	2.1295	2.138	2.212	2.2196	2.657	2.663	2.6538	0.8572	0.08
4933422D21	ubiquitination	FBXO24	Mm.158603	Hs.283764	2.5785	1.8198	1.77	2.1141	1.7202	1.0297	1.396	0.9989	2.7443	2.8896	4.2732	4.088	2.9479	2.015	2.1068	2.237	2.878	3.4391	2.183	4.113	4.0459	1.0458	0.114
6430603C09	ubiquitination	Skp1a	Mm.42944	Hs.488433	1.1843	1.6713	1.793	1.8351	2.2083	0.7884	1.473	0.9977	0.9072	1.2526	1.5276	2.483	1.6528	1.235	1.0057	0.953	1.667	1.1416	1.202	2.035	1.5951	0.8933	0.309
4932411N15	ubiquitination	CUL2	Mm.291707	Hs.82919	1.0817	1.1898	0.644	1.518	1.6066	0.8716	0.943	0.439	1.7439	1.784	2.1095	2.485	1.5752	1.96	2.6279	1.573	2.275	1.8089	1.334	2.24	2.9885	0.8105	0.232
8430423K24	ubiquitination	CUL5	Mm.218910	Hs.440320	1.2404	0.9864	0.354	1.1874	2.3626	1.4376	0.895	0.8659	1.5776	2.1533	3.4946	2.271	1.5856	1.407	2.1034	1.503	1.564	1.7047	0.773	1.616	3.4817	1.3744	0.158
2700050M05	ubiquitination	CUL4B	Mm.26885	Hs.155976	0.8748	1.4151	1.302	1.1242	2.8547	1.7677	1.64	1.3472	0.5969	0.9733	1.0466	1.209	0.956	1.879	1.7664	1.331	1.848	1.9114	1.512	1.444	1.2521	0.5808	0.093
NM_003900	ubiquitination	SQSTM1	Mm.40828	Hs.182248	3.2329	4.1547	2.828	3.528	3.3144	2.2444	2.209	2.051	3.5472	2.0972	2.5023	5.621	5.2139	3.519	4.2638	3.782	4.461	5.016	4.714	6.517	7.8087	1.3975	0.868
1110001N06	WD40	FLJ11294-v	Mm.277705	Hs.107000	0.8815	0.726	0.36	0.5672	0.9199	1.243	0.677	1.1477	2.0781	2.7419	4.6086	1.305	1.1106	1.257	1.226	1.573	1.017	1.3948	1.44	1.23	1.0722	1.0358	2.157
1200006M05	WD40	PC326	Mm.219421	Hs.280168	3.7573	1.7933	2.455	1.4341	1.4562	2.2556	0.921	1.0969	4.5221	5.6529	6.4171	2.576	2.5117	2.509	3.4548	2.269	3.955	4.0539	4.144	2.974	2.708	0.9437	0.681
1300004C11	WD40	GTF3C2	Mm.271923	Hs.75782	2.0094	1.2278	1.77	0.6947	1.0683	1.9923	0.993	1.1174	1.6719	1.728	1.8538	1.462	1.5707	1.5	1.243	1.991	1.241	1.8749	1.271	1.656	2.1619	0.7096	0.849
1300017E19	WD40	PPP2R2D	Mm.258739	Hs.380372	4.6581	4.6697	4.19	5.9445	1.637	1.7979	0.78	1.1731	2.4913	1.734	2.1244	2.342	2.3504	1.562	1.4747	2.074	1.544	1.6895	2.493	2.921	4.5107	1.1093	0.761
1500001L20	WD40	KIAA1892	Mm.28891	Hs.102669	1.9108	1.3121	1.54	0.6838	0.887	2.5486	1.063	0.3761	4.1266	**8.9632**	5.3814	1.54	1.4728	1.679	2.6271	2.841	2.672	3.8236	3.398	1.092	1.4997	0.5023	0.846
1500009K01	WD40	APG16L	Mm.272972	Hs.419213	1.0309	0.8393	0.527	0.2084	0.8183	1.6373	1.092	0.9638	2.4825	3.7738	3.0655	1.074	1.0501	1.341	1.7676	2.15	1.52	1.9766	3.083	0.976	0.8788	0.3735	1.004
1600015H11	WD40	PRPF4	Mm.22833	Hs.374973	1.4367	1.4828	0.793	0.63	0.9044	1.1666	1.5	1.1501	2.3415	3.2143	3.5253	1.419	1.49	1.546	1.2921	1.998	1.554	2.3297	2.456	1.839	1.5822	0.5677	0.825
1700012F10	WD40	HAN11	Mm.9671	Hs.410596	2.5618	2.0555	1.917	1.046	1.1848	1.0607	1.395	1.271	1.4419	2.4041	2.0915	1.045	2.2272	1.666	1.2498	1.301	3.194	2.6761	1.882	2.678	2.1232	1.118	0.756
1700057K18	WD40	CSTF1	Mm.26944	Hs.172865	1.2492	1.4363	1.039	0.8639	0.6778	1.35	0.607	0.8103	0.8662	0.7243	0.84	0.836	0.9373	1.114	0.517	0.817	0.951	0.6267	0.358	1.208	1.1341	0.6318	0.85
1700120F24	WD40	WDFY1	Mm.293273	Hs.44743	1.8373	2.7309	1.086	0.378	1.3815	1.3543	0.821	0.7038	1.1442	1.1424	0.9269	1.848	1.7365	1.268	1.0183	1.218	1.121	1.2415	0.926	1.294	1.7415	1.1609	0.97
2310011G05	WD40	FLJ11294-v	Mm.277705	Hs.107000	1.219	1.0163	0.696	0.6025	0.642	0.9825	0.661	0.6772	3.2971	5.5926	3.7499	1.039	1.3055	1.655	1.931	2.021	1.461	2.1358	1.596	1.369	1.6854	0.732	0.966
2310012I10	WD40	WDR18	Mm.35828	Hs.325321	1.0674	1.2452	1.541	0.5536	1.0493	1.2495	0.684	0.4728	1.6483	2.1871	1.4427	1.235	1.2293	1.711	1.8795	1.922	1.474	1.8563	1.658	1.91	1.08	0.4034	0.745
2310042N09	WD40	CDC20	Mm.289747	Hs.82906	1.6187	1.9874	1.443	0.7812	0.8227	1.4476	0.638	0.7546	2.5955	3.3616	3.6638	1.591	1.8627	1.229	1.3425	1.766	1.839	1.9139	2.122	1.608	1.6532	0.4507	0.772
2410003J24	WD40	KATNB1	Mm.28382	Hs.275675	1.5295	1.4889	1.492	0.5882	0.7216	1.2951	0.439	0.884	2.0388	3.6439	2.9528	1.868	2.1652	1.798	2.4274	2.09	1.57	1.7826	2.255	1.786	1.6209	0.6001	0.599
2410003L22	WD40	Nup37	Mm.222184	Hs.5152	1.5364	1.0708	1.515	0.5585	1.0025	1.2024	0.948	1.0969	2.3084	3.2138	3.9958	1.864	1.7671	1.816	1.8304	1.645	1.985	1.9808	1.679	1.441	1.1496	0.4911	0.83
2410022P04	WD40	CKN1	Mm.212208	Hs.32967	1.111	0.9487	0.83	0.451	0.8043	1.1593	0.759	0.5611	1.0422	1.0682	1.2248	0.914	1.1659	1.023	0.73	1.007	1.168	0.929	0.89	0.941	1.1509	0.4027	0.812
0610007C05	WD40	ARPC1B	Mm.30010	Hs.433506	2.288	2.129	1.35	1.0148	0.9542	1.5922	0.495	0.6047	1.0497	1.2336	1.1016	1.364	1.3645	1.048	0.7431	0.901	1.12	0.9282	1.046	2.362	2.5571	0.521	0.675
4833431H09	WD40	GNB3	Mm.130145	Hs.71642	2.1907	1.8032	1.415	0.7229	1.1305	1.5729	0.781	0.4886	3.2932	3.1449	3.6533	2.163	1.6259	1.566	1.9829	1.737	2.449	1.9994	2.14	1.754	1.5603	0.7401	0.667
2510003I12	WD40	TBL2	Mm.36746	Hs.52515	0.5568	0.9878	0.747	0.4972	0.4522	0.4177	0.299	0.2201	1.5039	1.2801	1.3345	1.107	1.0927	1.123	1.1671	1.234	1.401	1.3821	1.611	3.685	2.915	0.371	0.201
4930447M07	WD40	CIAO1	Mm.45179	Hs.12109	1.2076	1.1832	0.833	0.5999	0.7779	0.735	0.931	0.7546	0.9964	1.339	0.5552	1.285	1.3705	1.118	0.7262	1.343	0.908	0.7571	0.566	1.612	1.8176	0.6984	0.73
2700045C12	WD40	EIF3S2	Mm.250874	Hs.192023	1.5766	1.241	0.947	0.4171	0.8706	1.1097	0.46	0.9155	1.1523	2.0349	1.2082	1.587	1.3093	1.136	1.2051	1.376	1.336	1.46	2.168	1.144	0.7415	0.3828	0.657
1110003H02	WD40	SEC13L1	Mm.29296	Hs.227949	0.9907	0.9866	1.681	0.3381	1.1863	1.3992	1.363	0.2564	1.085	1.2043	0.98	1.001	1.1151	1.105	0.8415	1.257	0.964	0.8867	1.045	1.378	1.4572	0.6735	0.899
4933427G20	WD40	Gnb1l	Mm.236139		1.061	1.1007	0.479	0.3735	0.514	0.7884	0.772	0.8562	1.7962	2.3853	2.7696	0.939	1.0538	1.168	0.9264	0.872	1.404	1.3126	0.913	1.54	1.1509	0.6212	0.726
4921538B03	WD40	WDR20	Mm.219475	Hs.55209	1.8799	1.6562	0.875	0.8241	0.9846	1.9605	0.357	0.5756	1.6053	2.524	2.2967	1.963	2.6633	1.18	1.1442	0.937	1.802	1.6539	1.71	1.778	1.6886	0.7769	0.665
2600017H24	WD40	CHAF1B	Mm.274222	Hs.75238	2.2725	1.6633	1.33	0.8549	0.6544	0.9866	0.422	0.647	1.0335	1.0788	1.3542	1.866	1.661	0.995	1.0537	0.858	1.348	1.0781	1.508	1.998	1.9091	0.7993	0.456
2700038M07	WD40	WSB1	Mm.287354	Hs.315379	2.2744	1.2979	1.89	1.1148	1.2431	1.7121	1.046	1.0594	3.782	4.4404	4.2667	3.082	2.7926	1.911	2.3964	2.161	1.442	2.444	1.997	2.215	2.3186	1.2219	0.92
0610009C03	WD40	HPRP8BP	Mm.29606	Hs.379357	0.8327	0.9987	0.964	0.4611	0.4756	0.766	0.571	0.5708	0.7762	1.1956	0.7711	0.895	0.6543	0.964	0.6215	0.97	1.035	1.2305	0.992	1.624	1.0677	0.1201	0.916
2610044M17	WD40	WDR8	Mm.46508	Hs.31714	2.1777	2.9211	1.048	0.8387	0.6952	1.6938	0.373	0.3991	1.2006	1.1887	1.026	1.529	1.62	0.905	0.7206	1.207	0.901	0.8909	0.963	2.202	2.0387	0.6461	0.557
3230401I12	WD40	RAE1	Mm.4113	Hs.371698	2.3916	1.6612	1.345	0.6435	0.8417	1.4722	0.275	0.8913	1.251	2.0649	1.3183	1.361	1.5176	1.179	0.859	1.47	0.942	1.2644	1.259	1.529	1.3392	0.6872	1.451
2810452E04	WD40	PREB	Mm.15928	Hs.279784	1.7917	2.3607	1.794	0.9158	1.0115	1.4417	0.986	0.676	3.8517	5.9387	4.6116	3.148	3.1047	2.173	2.3052	2.276	2.441	2.4805	2.845	2.247	2.2257	0.5453	0.843
5730411P10	WD40	WDR13	Mm.284162	Hs.12142	1.6363	1.9913	1.497	0.6725	0.5608	0.5835	0.591	0.5055	2.8205	3.2838	3.4529	1.459	1.7619	1.775	1.9802	1.491	2.048	1.8885	2.014	1.796	1.5113	0.6088	0.556
1200003H23	WD40	CDC40	Mm.46063	Hs.116674	2.8492	3.6438	2.273	2.6072	1.3845	1.7355	1.46	1.9531	1.0443	1.3089	1.1956	1.39	1.7492	1.67	1.2739	1.002	1.788	1.4346	2.076	**16.399**	**15.949**	0.6897	0.876
2700038L12	WD40	REC14	Mm.245683	Hs.125457	2.2584	1.3722	1.418	1.1682	2.0813	2.3736	0.982	1.4391	2.3308	3.2244	2.924	2.373	2.1995	1.864	3.2768	1.469	2.143	2.4821	2.535	3.33	3.2322	0.8055	0.653
0610012H09	WD40	GNB2	Mm.30141	Hs.185172	1.9705	1.9131	1.428	0.9692	0.9004	1.257	0.929	0.6784	3.4079	3.0714	3.5715	2.208	1.9583	1.3	1.8455	1.527	1.641	1.6404	2.37	2.23	2.0026	0.6175	0.596
2610203K23	WD40	SMU-1	Mm.289929	Hs.327749	1.1556	0.8966	0.947	0.3825	0.9029	1.4207	0.612	0.9179	0.7771	1.0286	0.7017	0.912	0.9187	1.111	0.702	1.196	1.142	1.2152	1.18	2.032	1.365	0.7955	0.564
4930535L09	WD40	PLRG1	Mm.286349	Hs.249996	1.7397	1.6274	1.368	0.6665	0.8755	1.2477	0.673	0.9711	1.3852	1.8078	1.8878	1.445	1.3526	1.173	0.9851	1.65	1.289	1.7428	2.152	2.423	2.1857	0.7825	0.677
6330404L05	WD40	PPP2R2B-v	Mm.259912	Hs.380764	2.3239	1.9415	2.007	0.794	1.6963	1.5048	1.061	0.9796	2.8901	3.7674	3.3616	2.185	2.3736	2.291	1.8635	2.187	1.942	2.3585	2.368	2.809	2.4565	0.6517	0.908
2510005J23	WD40	PEX7	Mm.2440	Hs.79993	1.1803	1.2162	0.701	0.6409	0.895	1.0327	0.57	1.1053	0.7695	0.8169	0.6639	1.174	1.0187	1.005	0.5544	0.922	1.381	0.8731	0.996	1.267	1.0884	0.686	0.676
2410080P20	WD40	FLJ20195	Mm.271719	Hs.286261	0.3273	0.4609	0.406	0.2659	0.1693	0.1923	0.189	0.2153	0.3288	0.3784	0.2936	0.678	0.6311	0.859	0.3775	0.649	0.741	0.5259	0.517	0.499	0.559	0.1762	0.271
2610024M05	WD40	RBBP4	Mm.12145	Hs.16003	1.4153	0.9022	0.941	0.5679	0.8083	0.9751	0.627	0.2902	0.8984	1.3237	0.8474	1.274	1.1845	1.152	0.9428	1.203	1.051	1.1035	1.071	2.332	1.8247	1.1535	0.831
2410026A21	WD40	NEDD1	Mm.2998	Hs.14456	1.374	1.1643	1.326	0.6943	1.4209	2.8587	0.676	1.0533	1.4565	1.223	1.489	1.148	1.1166	1.473	0.9902	1.764	1.176	1.1848	0.623	1.657	1.3637	0.6598	0.76
2510040D07	WD40	DKFZP434C	Mm.23054	Hs.59461	0.8661	1.3219	0.961	0.6225	0.8521	1.2536	0.947	0.8514	1.6991	1.8269	1.7758	1.328	1.08	1.268	0.8199	1.397	1.049	1.0958	0.696	1.652	1.3888	0.5422	0.561
5730515M10	WD40	GNB2L1	Mm.5305	Hs.5662	0.9953	1.2933	1.24	0.4607	0.8566	1.1956	0.67	0.6434	1.1513	1.267	1.2983	1.332	1.3765	1.214	0.9662	1.16	0.857	0.9188	1.327	1.541	0.9568	0.4544	0.615
5930415H02	WD40	PAK1IP1	Mm.24789	Hs.310231	0.8839	1.3027	2.012	0.6845	1.4811	1.3496	0.902	0.9445	0.7356	1.3575	0.6717	1.076	1.363	1.477	0.7978	1.037	1.172	1.145	1.447	3.182	3.1026	1.2201	0.951
2610205J09	WD40	PWP1	Mm.18834	Hs.172589	1.7282	1.4556	0.814	0.7763	1.2376	1.5219	1.41	0.8743	1.5224	1.915	1.5718	1.769	1.8029	1.957	1.6376	1.69	2.167	2.9708	2.54	3.823	3.3295	0.6405	0.578
2810410J09	WD40	RNU3IP2	Mm.239997	Hs.153768	1.4377	1.5148	1.21	0.6037	0.7779	0.9099	0.536	0.6385	0.7898	2.1185	1.0599	0.994	1.1233	1.302	0.7256	1.547	1.267	1.797	1.382	**11.354**	7.3309	0.9013	0.488
2900026H06	WD40	PPP2R2B-v	Mm.259912	Hs.380764	4.1752	3.2845	2.227	3.8055	2.2924	2.9712	0.934	0.8695	2.3566	1.9031	3.0465	1.782	1.9695	1.746	1.6035	2.155	1.314	1.7784	1.833	2.514	3.3508	0.3405	0.945
4930533L09	WD40	FBXW5	Mm.273981	Hs.82023	2.8159	2.2885	2.465	0.9298	1.6878	2.458	1.252	1.0352	2.5539	3.9187	3.1105	2.556	3.2818	1.943	1.7235	2.113	2.455	2.3627	4.243	1.592	1.7718	0.6455	0.663
NM_011499	WD40	UNRIP	Mm.22584	Hs.3727	1.9401	0.9801	1.528	1.0324	1.9657	0.9888	0.837	1.0654	0.5019	1.1137	0.8215	1.513	1.254	0.96	0.9324	1.029	1.208	1.0662	1.056	2.229	3.1851	0.5322	0.079
0610043C19	kinase	CSNK2A2	Mm.51136	Hs.82201	1.3905	1.7182	0.777	0.8271	2.1998	1.1096	0.85	0.8707	5.5088	3.3464	4.4386	1.093	1.4474	1.114	1.3596	1.803	1.439	2.1307	1.632	6.162	3.9994	1.8239	0.515
4932415A06	kinase	DKFZp434E	Mm.159174	Hs.255960	1.1798	1.134	0.698	1.0102	1.524	1.1371	1.123	1.0424	1.7444	2.7524	1.3492	1.513	1.8037	1.027	1.3459	1.564	1.896	1.9588	2.002	3.674	3.3695	1.8326	0.447
4933411O17	kinase	CDKL1	Mm.132325	Hs.380788	1.9963	2.2963	1.475	1.5383	2.1365	0.7032	1.444	1.8031	1.456	3.341	1.4935	1.463	1.3937	1.916	1.2833	1.988	1.606	1.886	1.156	3.197	3.0252	0.8584	0.435
4933424F08	kinase	C14orf20	Mm.171300	Hs.314432	0.8412	1.1202	0.546	1.0637	0.6539	0.3942	0.387	0.4221	2.1384	4.492	2.4566	1.646	1.3854	0.887	1.5113	0.835	1.385	1.5235	2.098	2.054	2.4881	3.6054	0.53
1300007C09	kinase	NEK6	Mm.143818	Hs.387222	1.4223	2.7083	0.895	1.7561	3.1789	1.6564	0.615	0.7232	2.0263	3.8858	2.9363	2.283	1.9949	1.222	2.2121	1.039	1.313	1.659	0.823	2.171	2.6409	3.5929	0.506
1300013P10	kinase	PCTK3	Mm.28130	Hs.445402	1.744	2.7334	0.936	1.4785	1.4692	0.7959	0.378	0.3821	1.2376	2.7159	1.6776	1.201	1.3384	0.907	1.4231	1.027	1.204	1.2838	0.833	1.683	2.3437	1.0962	0.338
1700054C12	kinase	STK35	Mm.260334	Hs.100057	1.7579	2.4211	0.794	1.7237	3.2088	1.5217	1.522	1.7511	2.6176	4.1569	1.5606	1.411	2.2682	1.615	2.6218	1.982	2.487	3.185	2.484	2.852	3.5907	1.8506	0.542
1700091F14	kinase	1700091F14	Mm.159026		2.675	2.6678	1.088	1.4097	1.9129	0.8976	0.611	0.5805	3.3833	4.1142	2.9932	1.521	2.936	1.27	2.0465	1.746	1.79	1.9308	1.779	2.396	3.1103	1.1896	0.382
2010016G11	kinase	MKNK2	Mm.42126	Hs.512094	1.3431	1.1582	1.03	0.6815	2.2929	0.8069	1.274	1.1005	**8.0123**	**9.7764**	7.7528	1.175	1.2981	2.069	2.1251	2.155	4.386	4.5155	3.229	1.462	1.8608	1.1528	0.578
2210420D18	kinase	RIPK2	Mm.112765	Hs.103755	1.6325	2.2572	0.624	0.6386	4.6815	1.9013	1.29	1.3436	1.489	1.553	1.4648	1.091	1.0583	2.049	0.7415	2.407	1.273	1.0924	1.17	2.431	3.7016	1.3663	0.837
2410015K02	kinase	MELK	Mm.268668	Hs.184339	1.8103	1.922	0.463	0.9215	1.8009	1.1568	0.992	1.3109	0.8601	1.3189	1.0342	1.228	1.1868	1.537	1.1101	1.816	1.343	1.4126	0.95	2.675	2.0587	1.5325	0.806
2410042H09	kinase	AURKB	Mm.3488	Hs.442658	1.6988	2.6093	0.611	1.4078	1.5319	0.7586	0.761	0.7909	2.5173	5.6387	2.8794	2.676	2.1637	1.865	2.0545	1.539	2.423	2.4008	2.507	1.978	1.6744	1.911	0.321
2410048M24	kinase	MKNK1	Mm.209327	Hs.79516	1.219	1.412	0.951	1.0783	1.7302	1.0508	0.369	0.6131	0.8658	2.0311	1.1121	1.689	1.5453	1.083	0.8371	0.819	0.704	0.9307	0.84	2.378	1.8221	2.0212	0.392
2510027C03	kinase	MAP2K3	Mm.18494	Hs.180533	3.4536	**8.4717**	2.783	7.6912	**19.239**	4.6746	1.727	1.2432	2.1157	3.7442	3.0656	3.748	3.5342	1.823	2.7791	1.909	3.423	2.6202	0.971	2.679	3.2857	1.6402	0.502
2600014H12	kinase	WEE1	Mm.287173	Hs.249441	2.1904	2.4697	1.656	3.4482	1.4034	1.4852	0.836	0.5055	0.6954	1.7068	0.4434	1.392	1.85	1.259	1.2816	1.596	1.337	1.9427	1.863	2.162	3.1458	2.9387	0.514
2610001I03	kinase	CHEK1	Mm.16753	Hs.24529	1.8681	1.9245	0.828	1.1678	3.2222	1.5233	0.701	0.9215	1.1632	2.3063	0.7227	1.108	1.496	1.469	0.9666	1.504	1.025	1.3888	1.417	2.829	2.6274	1.8046	0.547
2610009E10	kinase	IKBKB	Mm.277886	Hs.413513	1.8538	1.5608	0.764	0.9177	2.155	1.3653	1.197	1.3944	2.0982	3.8779	2.3501	1.448	1.974	2.333	3.0104	3.035	2.792	2.5135	2.186	2.406	2.6048	1.2985	0.393
2610019A05	kinase	LYK5	Mm.37985	Hs.279731	1.1544	1.1396	0.821	0.7526	3.146	1.3753	1.16	0.8465	1.0969	1.5071	1.365	1.306	1.2174	1.318	0.8379	1.502	0.837	1.1119	0.404	1.429	1.8704	1.0657	0.531
2610203O19	kinase	CDK4	Mm.6839	Hs.95577	1.7335	1.8619	0.837	0.8952	1.8103	1.0844	1.218	1.2371	1.7373	6.4287	1.4225	1.326	1.3929	1.996	1.9217	1.882	2.052	2.3009	3.039	1.664	1.6873	1.3751	0.635

4933428O03	kinase	EIF2AK4	Mm.26931	Hs.412102	2.2756	2.4273	1.486	1.8317	3.3582	1.5348	1.354	0.9336	2.5127	5.8244	2.6644	4.192	4.2258	1.319	2.447	1.252	2.01	2.5262	2.947	2.967	2.9543	2.0367	0.472
1110062I02	kinase	DAPK2	Mm.41755	Hs.129208	1.4193	2.8666	0.889	1.7136	2.0205	1.1595	0.859	0.5515	3.6278	3.6882	3.3594	1.882	2.4751	1.297	1.6409	1.192	1.606	1.7733	1.029	1.913	1.9594	2.6455	0.395
1200006A05	kinase	CSNK1D	Mm.216227	Hs.378918	1.8171	1.7865	0.774	1.3386	2.4737	0.9721	0.573	0.5611	2.7296	3.2147	1.5042	1.328	1.4467	0.96	1.6166	1.172	1.628	2.1248	0.97	2.786	2.3443	1.451	0.305
1200013B22	kinase	SNARK	Mm.100666	Hs.172012	3.8309	4.619	1.436	2.5598	3.6804	1.7443	1.036	0.8635	2.5533	5.8749	3.2417	1.543	2.4243	2.501	3.0161	2.466	1.79	2.533	1.214	2.71	2.5919	1.6489	0.395
1700014N07	kinase	STK22C	Mm.143802	Hs.512763	2.458	2.3292	1.317	1.6553	5.2373	1.5202	1.24	0.8937	2.0561	2.8363	2.6453	1.513	1.9717	1.632	1.5224	2.491	1.78	2.0011	1.372	2.041	2.9459	1.6409	1.65
1700029P02	kinase	STK22D	Mm.18470	Hs.333138	2.0432	2.3352	1.239	1.5455	2.2302	1.5135	0.571	0.5103	2.8724	5.5517	2.5546	1.521	2.2795	1.34	2.1028	1.755	2.453	2.4711	2.521	2	2.9266	0.9474	0.316
2810003O05	kinase	FANCL	Mm.18875	Hs.411433	1.2753	2.0261	0.88	1.1389	2.2212	0.7292	0.757	0.9433	5.9173	8.7878	5.3951	1.444	1.6812	1.697	3.6563	1.814	3.812	2.8539	2.803	2.65	2.521	1.6209	0.443
2810434B10	kinase	TOPK	Mm.24337	Hs.104741	0.9979	1.3909	0.988	0.8173	3.0066	1.242	2.221	0.3701	0.8459	1.5801	1.0171	1.584	1.3825	1.075	0.8381	0.981	0.988	1.3101	1.169	1.548	1.3482	1.8575	0.703
2810454O04	kinase	KIS	Mm.209150	Hs.127310	3.8864	4.0706	0.954	2.2375	3.8891	2.221	1.484	1.5516	3.2984	7.2189	2.3126	2.526	3.8419	1.498	3.4908	1.742	2.48	2.3898	3.418	4.081	4.9111	0.902	0.426
2210022N24	kinase	OSR1	Mm.293565	Hs.95220	2.2283	1.7593	1.407	1.7388	2.9887	1.4874	0.841	0.8743	2.5688	5.1179	2.7623	1.812	2.7074	1.304	2.9655	2.448	3.475	3.3993	2.419	3.459	3.4553	1.6141	0.379
2810011D23	kinase	CAMK2D	Mm.255822	Hs.111460	1.5669	1.8271	0.811	0.7436	5.1461	1.3554	1.329	1.5359	0.8201	1.8214	1.4466	1.026	1.1599	1.277	2.0795	1.547	0.917	1.1543	1.277	2.085	1.8447	1.7815	0.635
4632401F23	kinase	NEK8	Mm.23788	Hs.448468	2.2038	1.8322	1.098	1.2596	2.3801	0.9319	0.405	0.7377	3.0975	5.0944	3.2187	1.909	2.5984	2.306	4.24	2.546	2.707	2.2552	2.452	2.38	2.6777	0.6001	0.435
4632404G05	kinase	CSNK1A1	Mm.26908	Hs.318381	1.8393	1.4434	0.777	0.8842	2.7486	1.1369	1.65	1.4766	2.9433	7.335	1.9101	1.226	1.5266	1.558	1.7139	2.204	1.269	1.2779	1.528	1.447	2.1541	0.9119	0.593
4833426L05	kinase	HRI	Mm.220921	Hs.434986	1.2392	1.2191	0.621	0.809	1.6355	1.5598	0.951	1.1561	2.6892	4.6564	2.6339	1.279	1.2943	1.384	2.1024	1.957	1.362	1.4744	1.221	1.882	1.786	1.8201	0.826
4921505G21	kinase	STK33	Mm.79075	Hs.148135	0.6238	1.3999	1.15	0.8478	1.8437	1.2032	1.162	1.3484	0.4382	1.7832	0.5776	1.58	1.2308	1.176	0.9217	0.936	0.875	1.1297	1.013	1.886	1.4887	1.9266	0.696
4921506N09	kinase	TLK2	Mm.126976	Hs.445078	0.8743	1.3057	1.373	1.0106	2.529	1.9101	1.022	1.0642	1.7671	2.8774	2.0892	1.674	1.49	1.261	0.8301	1.103	1.479	1.4625	0.763	1.673	1.9336	1.1124	0.453
4930444A02	kinase	FLJ23356	Mm.17631	Hs.277431	0.8264	1.0823	0.722	0.6849	1.5867	0.8451	0.525	0.4402	12.598	11.573	10.709	1.197	1.3698	1.356	1.6841	1.413	10.457	3.5983	8.571	1.634	1.3959	0.8074	0.09
4930588P12	kinase	PFTK1	Mm.6456	Hs.57856	2.1061	2.1618	1.145	1.5229	2.3094	1.2409	1.31	1.2432	3.7863	8.3266	3.7179	1.318	1.6767	2.366	3.5831	2.311	2.479	3.1181	1.821	2.623	3.1806	1.7386	0.511
4930594I21	kinase	STK22C	Mm.143802	Hs.512763	1.9673	2.4672	1.535	1.4258	4.925	2.3338	1.074	1.2746	2.3739	2.8879	2.8112	1.411	1.9127	1.908	1.5853	2.086	1.421	1.8284	1.736	1.41	2.559	1.3906	0.545
5730422C08	kinase	PAK1	Mm.260227	Hs.64056	2.3372	3.3032	1.243	1.7136	3.3069	2.4976	0.98	1.4173	10.836	12.065	9.4093	1.67	3.3437	1.627	5.078	2.986	2.933	3.2206	4.234	5.722	5.8177	1.0831	0.304
6330415L08	kinase	IRAK2	Mm.152142	Hs.424542	2.2778	3.7253	1.019	1.5989	1.647	1.4253	0.286	0.3749	1.4184	1.3806	1.0913	1.26	1.7544	0.982	1.0747	1.159	0.868	0.791	0.588	4.491	5.5372	0.7737	0.197
6430598J10	kinase	PCTK2	Mm.45746	Hs.258536	1.0064	1.4401	0.802	1.1156	1.1898	0.7643	1.243	0.4293	1.6824	4.8157	1.6395	1.177	1.183	1.286	1.6455	1.647	1.137	1.6607	0.719	1.923	2.2341	1.4977	0.584
9030416P08	kinase	MYO3A	Mm.221230	Hs.148228	0.7312	2.317	0.984	0.8602	1.6231	1.4518	1.432	1.4512	2.2164	7.4585	2.795	1.985	1.3444	1.875	2.4045	1.571	1.931	2.7599	1.248	1.73	1.3353	1.6682	0.801
9130411F08	kinase	CHUK	Mm.3996	Hs.198998	0.6944	2.1322	1.09	1.1874	2.5574	1.7161	0.925	1.1114	1.5395	3.7057	1.6614	1.75	1.4116	1.788	2.3296	1.679	1.904	2.1663	2.246	1.949	2.5133	2.2179	0.678
9130423C03	kinase	CDK6	Mm.88747	Hs.38481	1.0613	1.0528	0.694	0.6401	1.4044	0.7684	0.467	0.5454	1.8215	4.2041	1.1446	1.248	1.3205	0.887	1.3731	1.064	1.475	1.5641	1.829	0.903	1.4062	0.7744	0.292
4432415E19	kinase	MAP4K5	Mm.291936	Hs.246970	0.7043	0.5332	0.278	0.2825	0.1449	0.1938	0.348	0.2467	0.4259	0.4142	0.4906	1.044	0.8985	0.603	0.6115	0.689	0.615	0.509	0.309	1.191	1.1851	1.1808	0.245
L11695	kinase	TGFBR1	Mm.197552	Hs.28005	1.7641	1.6884	1.31	1.4315	2.518	0.4916	1.035	0.8647	231.13	61.051	102.24	1.473	1.3727	14.18	11.597	11.6	45.91	58.173	41.194	2.881	2.3559	0.7731	0.089
NM_001204	kinase	BMPR2	Mm.7106	Hs.53250	1.2287	0.9473	0.808	1.1754	1.8422	0.8833	1.494	0.5744	19.085	3.7122	13.399	1.237	1.3018	1.538	1.0032	1.427	1.11	1.5879	16.436	2.288	2.6603	0.6928	0.338
L29479	kinase	STK18	Mm.3794	Hs.172052	1.3512	1.5709	2.311	1.4003	3.4628	1.7533	1.31	0.8731	3.2171	1.8454	1.6498	1.635	1.67	1.446	1.439	1.779	1.645	2.1637	1.68	2.576	2.1761	0.7208	0.186
D76446	kinase	MAP3K7	Mm.258589	Hs.290346	2.3213	1.7527	1.18	1.3047	0.7162	0.6143	0.472	0.2673	2.2849	1.5398	1.8455	1.817	1.3481	1.194	0.9761	1.276	1.244	1.0891	1.541	5.075	4.2593	0.7227	0.334
1200014P03	TPR	KNSL8	Mm.279599	Hs.53447	2.2289	2.2929	1.212	1.1618	1.5294	1.9153	0.687	0.5031	1.3984	0.7673	1.6418	1.311	1.6745	0.817	0.9302	1.082	1.827	0.8951	2.121	1.757	2.4243	1.6981	0.818
4933404O19	TPR	DKFZP434H	Mm.31590	Hs.201134	1.0581	0.6475	0.403	0.3897	0.4906	0.9898	0.788	0.8635	0.6404	0.6717	0.8441	1.194	0.965	1.018	0.6101	0.747	0.876	0.7656	0.653	1.726	1.236	0.8914	0.737
4930506L13	TPR	FLJ13946	Mm.282339	Hs.128384	1.4719	1.1885	0.332	0.5236	1.0573	1.5502	1.013	1.7318	1.7209	1.573	1.5622	0.998	1.1636	2.457	2.1952	2.253	1.911	1.5362	1.038	1.369	1.149	1.6191	0.645
4930564J03	TPR	PPID	Mm.295252	Hs.143482	1.6664	1.4694	0.664	0.7752	0.891	1.1343	1.387	1.011	1.6523	1.3557	1.6486	1.068	1.4123	1.469	0.8278	1.325	0.962	0.9299	1.437	1.775	1.6906	1.8151	3.253
0610033N24	TPR	STUB1	Mm.45165	Hs.414390	2.5432	2.092	0.571	0.8508	0.9089	1.7858	0.417	0.3023	3.8111	3.1803	9.0378	1.618	4.7247	1.137	2.3274	1.191	2.124	2.6337	3.269	1.973	3.1677	1.2661	0.736
0610011H21	TPR	EIF3S6IP	Mm.206404	Hs.119503	1.2714	0.7213	0.4	0.4863	0.4203	0.6615	0.519	0.4849	1.6892	1.3682	1.7609	1.119	1.1435	0.602	1.6452	0.924	1.022	0.7224	1.1	1.768	2.296	1.5624	0.413
2810460C24	TPR	FLJ20343	Mm.69739	Hs.171044	1.4173	0.6434	0.539	0.3848	0.7859	0.8544	1.178	1.017	1.0437	1.1156	1.2442	1.314	0.9926	0.638	1.172	0.948	0.892	0.9188	1.086	1.316	1.3463	1.982	0.869
4833412C19	TPR	TTC1	Mm.271974	Hs.7733	1.5398	0.6948	0.679	0.352	1.015	1.2098	1.143	0.6168	2.8208	7.1136	3.41	1.227	1.1442	0.955	2.3941	1.078	1.064	1.1246	1.546	1.415	1.5236	1.4124	1.48
4921531G14	TPR	KIAA0103	Mm.244512	Hs.130456	0.9966	0.6025	0.524	0.2306	0.7092	1.4866	1.08	0.5454	0.7169	0.9868	0.779	1.097	0.7827	0.737	0.8364	0.833	0.933	0.8121	0.848	1.609	1.5274	1.4983	1.039
1700016J08	TPR	PEX5R	Mm.151332	Hs.46780	1.1274	0.926	0.728	0.5104	1.2889	0.8173	1.171	0.3568	1.127	1.5378	1.555	1.325	0.6729	1.12	1.3081	1.167	1.244	1.7022	1.27	1.251	1.1857	1.8475	0.617
1300003O07	TPR	APPBP2	Mm.271997	Hs.84084	0.6139	0.8807	0.525	0.3675	0.3252	0.7505	0.578	0.7135	1.4341	1.0955	0.9248	0.913	1.006	1.396	1.3876	1.148	1.028	1.0586	1.354	1.755	2.0226	1.4709	0.809
2210019E14	TPR	MGC29649	Mm.259531	Hs.31704	2.1493	1.6082	0.979	0.7067	1.3805	1.7043	1.51	1.1634	1.1104	2.0952	1.6295	0.998	1.4183	1.081	1.2867	1.574	1.272	0.9713	2.016	1.671	2.4075	1.3458	2.101
2010003F24	TPR	DNAJC7	Mm.258140	Hs.446481	1.1155	1.0125	0.498	0.4799	0.3128	1.0057	0.387	0.2394	1.4707	2.0213	2.1001	1.087	1.667	0.871	1.3298	0.832	1.207	0.9087	1.235	1.006	3.4669	0.6947	0.339
2900001O04	TPR	OSRF	Mm.254979	Hs.280811	1.7743	1.1023	1.019	1.0125	1.1096	1.2929	1.15	0.6119	0.9954	1.1559	0.7605	1.454	1.6125	0.844	1.574	0.863	0.971	0.8037	1.008	2.212	2.8318	2.31	0.599
2410024H11	TPR	CDC23	Mm.196638	Hs.153546	1.4653	2.1343	0.564	0.5826	0.504	0.9729	0.44	0.3084	1.4874	1.0433	1.324	1.146	1.5931	0.686	1.0182	0.763	1.212	0.6733	1.259	2.366	2.8363	1.5164	0.34
2510006G12	TPR	ANAPC5	Mm.45312	Hs.7101	1.2393	0.7519	0.573	0.4995	0.514	1.6331	0.875	0.4136	2.1481	2.2547	3.0281	1.425	1.3922	0.883	1.7973	0.852	1.258	1.0416	1.219	3.824	3.6229	3.395	0.706
2510042P03	TPR	FLJ13946	Mm.275109	Hs.128384	0.8819	0.5888	0.645	0.3148	0.7615	1.2232	1.31	1.0388	1.2793	1.7471	1.9768	1.118	0.8962	1.103	1.2	1.044	0.973	0.8062	0.905	1.288	1.728	1.3526	0.65
2610009O10	TPR	STIP1	Mm.258633	Hs.257827	2.2756	1.7285	1.084	0.9143	1.2107	1.4222	0.871	1.8297	2.5618	1.2264	1.3424	0.951	1.4377	1.948	0.998	1.486	1.267	1.2771	0.596	1.605	1.9046	1.3228	1.703
2610029G12	TPR	AIP	Mm.10433	Hs.412433	1.4826	1.3326	0.911	0.5476	1.1549	1.8174	1.043	0.5793	0.9516	0.973	0.9165	1.009	1.3899	0.909	0.9151	1.24	1.157	0.9366	1.291	1.545	2.4817	1.3863	1.143
9130020K17	TPR	FLJ10890	Mm.248504	Hs.17283	2.3973	1.243	1.297	1.0369	0.9761	1.563	1.124	0.7897	2.4695	1.5499	2.4671	1.458	2.7321	1.222	3.3667	1.447	1.647	1.471	3.697	4.541	6.8776	1.8438	1.017
1300019C06	TPR	FLJ22054	Mm.24425	Hs.13277	2.0776	0.9584	0.822	0.812	0.9846	1.8364	1.093	0.7486	1.467	1.1791	1.7027	1.195	1.4624	1.016	1.6473	0.967	1.219	1.1848	2.58	2.252	3.5217	1.8039	1.16
2310015L07	TPR	2310015L07	Mm.158287	Hs.207472	1.5133	1.1343	0.778	0.8252	0.5085	1.2535	0.545	0.2564	1.4814	1.7894	0.9456	1.412	1.6685	0.69	1.6782	0.713	1.138	0.9891	0.689	2.468	2.8672	1.7448	0.609
2310042P20	TPR	FLJ21908	Mm.12255	Hs.323473	1.2099	0.6905	0.461	0.3483	1.011	1.5817	0.66	0.3785	0.5828	3.6859	1.1066	1.145	1.0568	0.717	1.4475	0.73	0.762	0.6343	0.484	1.632	2.3095	1.8525	0.601
3110002K08	TPR	ST13	Mm.180337	Hs.377199	1.5449	0.8907	0.657	0.5111	1.6271	0.8643	2.327	0.8973	0.887	0.8881	0.738	1.254	1.2555	0.994	1.2859	0.818	0.888	0.7546	0.306	1.822	2.5887	1.8581	1.559
2610511O17	TPR	FLJ20272	Mm.209503	Hs.26090	1.5106	1.0255	1.01	0.9219	2.4364	1.4996	1.727	1.0763	3.6655	3.5307	3.8565	1.895	2.8725	1.65	3.0428	1.489	2.218	3.0351	3.021	2.583	2.688	2.4974	1.225
4831420N21	TPR	OGT	Mm.259191	Hs.405410	1.435	1.3208	0.507	0.4171	1.3272	1.8242	1.555	2.1405	1.1141	0.5868	0.9877	0.989	1.2025	1.53	1.0086	1.487	1.484	1.0933	1.317	1.353	1.8949	0.9069	0.416
2310038F17	TPR	RAPSN	Mm.1272	Hs.81218	2.1753	2.0859	0.763	0.8086	0.8008	1.3541	0.438	0.2818	2.8587	1.1823	1.9492	1.424	3.3497	1.004	1.2793	1.172	1.667	1.3414	2.85	2.835	3.8363	0.8559	0.366
4932412G04	TPR	RNF127	Mm.259741	Hs.144266	2.5335	1.2356	1.342	0.9414	1.0962	1.605	1.463	0.9179	1.9311	2.2174	2.8105	1.199	2.5409	1.477	2.0789	1.901	1.22	1.6192	1.814	1.903	3.2289	1.24	1.073
2410081M15	BTB/POZ	ZBTB8	Mm.32997	Hs.129837	2.9009	1.5675	0.954	1.843	0.7052	1.8865	1.003	1.086	1.3442	1.2447	1.9493	1.976	2.0427	1.548	0.7964	1.198	1.078	0.9231	1.382	2.891	3.9524	0.6125	1.313
1200009E17	BTB/POZ	SPOP	Mm.285454	Hs.129951	1.3667	0.8245	1.049	0.6428	0.5996	1.2654	0.606	0.4414	0.764	1.1603	0.5713	1.151	1.2764	0.641	0.4423	0.844	0.854	0.5318	0.385	1.748	1.4462	0.8901	0.962
1700017G21	BTB/POZ	1700017G2	Mm.312625		2.7242	1.826	2.097	1.7046	1.0419	1.7145	1.085	0.7292	2.8621	3.3081	3.0987	2.21	3.2825	1.342	1.5111	1.704	2.236	1.5972	2.415	2.325	2.5507	0.5677	0.798
2810049M13	BTB/POZ	BTBD14B	Mm.289698	Hs.185254	1.7941	1.7277	0.462	1.8181	1.0215	1.6201	0.515	0.6409	1.0777	0.888	0.8257	1.629	2.5013	0.81	0.8713	1.055	1.218	0.6817	1.054	2.119	2.8589	0.503	0.655
2810011C24	BTB/POZ	MYNN	Mm.200378	Hs.507025	1.1684	0.9857	0.947	0.6947	0.9746	2.2	0.577	0.3205	1.4172	2.0959	0.8825	1.095	1.5811	1.43	0.7485	1.335	1.312	0.7402	1.127	2.846	0.3269	0.7781	1.476
2700038B03	BTB/POZ	SBBI26	Mm.273768	Hs.376793	0.8409	0.9444	0.684	0.4167	0.8676	1.2286	0.697	0.7425	0.7957	1.2226	0.8869	1.034	1.4049	0.779	0.5353	1.013	1.327	0.8418	0.962	1.048	1.4887	0.3822	1.138
2610109I01	BTB/POZ	ZNF131	Mm.139115	Hs.97845	1.1291	0.8614	1.07	0.8034	0.887	1.4987	1.134	0.8429	1.1695	2.0467	1.3873	1.073	1.7664	1.392	1.1004	1.247	1.456	1.1263	1.408	1.305	1.3443	0.7656	1.651
2610019F01	BTB/POZ	BTBD4	Mm.56581	Hs.437574	1.2368	0.7974	1.298	0.7962	0.5966	1.2475	0.828	0.6361	1.7628	2.2388	1.2788	2.023	1.2674	2.096	1.0291	1.225	1.352	1.5675	1.497	1.695	0.9981	0.0373	0.628
2210011M23	BTB/POZ	ENC1	Mm.241073	Hs.104925	2.4112	1.3319	1.658	2.0438	0.5319	1.326	0.618	0.8562	4.0193	3.2561	3.5686	2.95	2.7589	1.733	2.1042	1.608	2.06	1.5582	2.352	1.79	1.53	0.0548	0.637
1700126I16	BTB/POZ	IVNS1ABP	Mm.33764	Hs.197298	0.8178	0.9146	1.376	0.7748	0.9956	2.3097	1.001	0.959	1.1593	2.749	1.4832	1.611	1.7305	1.526	1.442	1.384	1.481	1.2347	0.998	1.482	1.5326	0.8111	1.154
1700010E06	BTB/POZ	ZNF297B	Mm.44186	Hs.376585	1.1322	0.9547	0.711	0.8463	0.4901	0.7178	0.931	1.0086	0.6071	0.6948	0.3982	1.313	2.0195	1.039	0.5648	0.815	1.055	0.6241	0.841	1.153	1.7105	0.1002	0.813
2510026C23	BTB/POZ	KBTBD4	Mm.279804	Hs.440695	2.1095	1.6534	0.771	1.3213	1.9164	2.0048	0.809	0.965	1.8293	2.8243	2.6257	1.981	2.8523	1.055	0.9807	1.325	1.459	1.2102	1.86	1.616	2.0432	0.0436	1.198
2610037C03	BTB/POZ	BTBD2	Mm.60720	Hs.369288	1.6382	1.3922	0.799	0.759	0.4507	0.9792	0.528	0.5805	1.8184	3.236	1.3843	2.017	3.6529	0.933	1.004	1.055	2.056	1.1873	1.263	1.492	1.5938	0.2148	0.494
2810406K13	BTB/POZ	FLJ33790	Mm.153585	Hs.292451	1.1723	1.1662	1.278	0.7643	2.5663	2.9299	1.364	1.5201	3.0475	6.7564	2.8766	2.435	2.7724	2.99	3.0992	2.34	1.779	1.471	1.464	1.247	1.1515	0.1581	1.21
1200011O19	BTB/POZ	FLJ13057	Mm.74594	Hs.243122	0.9928	1.5512	1.973	0.431	0.6708	1.5135	1.068	1.369	1.1825	1.6906	1.3162	2.047	0.7148	1.377	0.8248	1.648	1.426	1.7191	2.023	1.847	0.7402	1.0918	2.506
4931401E10	BTB/POZ	BTBD5	Mm.248678	Hs.99398	1.2212	1.733	0.695	0.4547	1.5663	1.8742	0.843	1.0424	1.7058	1.7835	1.9076	1.95	0.8955	1.234	1.3929	1.244	1.763	1.5235	1.373	2.004	1.7886	0.9916	2.705
1190005H08	BTB/POZ	BTBD1	Mm.296945	Hs.321501	1.6932	1.2274	1.879	0.5299	1.013	1.4426	0.593	0.9263	2.6001	2.2885	2.3517	1.94	1.2069	1.367	1.9554	1.452	2.257	1.8758	1.978	2.208	1.697	0.5453	0.75
1300013C10	BTB/POZ	KLHL1	Mm.125006	Hs.106808	1.7791	1.2242	1.068	0.4927	1.1465	1.2362	1.163	1.2831	3.5494	3.5404	2.4893	1.968	1.1106	2.358	1.8593	2.205	2.618	2.6456	3.903	2.782	1.4262	0.7669	0.772
1200013C18	BTB/POZ	KEAP1	Mm.248266	Hs.57729	1.405	1.7122	1.593	0.5047	0.9408	1.1848	0.76	1.4125	0.941	1.02	0.7475	1.888	0.7603	1.317	0.9168	1.442	0.929	1.0713	1.291	1.7	1.6171	0.8273	0.939
2310024D23	BTB/POZ	KBTBD5	Mm.45734	Hs.350288	0.7974	1.5225	0.887	0.5168	0.8984	1.3282	0.77	0.855	0.4522	0.7373	0.5002	1.765	0.7215	0.894	0.7224	0.959	0.977	1.2195	1.669	1.671	0.9375	1.2904	2.348
1200009K10	BTB/POZ	Bklhd2	Mm.224306	Hs.348262	0.7859	0.9937	0.737	0.226	0.4462	1.0956	0.181	0.2939	1.1491	1.4008	1.2434	1.489	0.711	0.724	0.7163	0.866	0.972	0.9595	0.752	0.864	0.913	0.2079	0.431
2900016J09	BTB/POZ	RB1	Mm.273862	Hs.408528	0.7762	0.609	1.526	0.2249	0.6798	2.1698	0.614	1.0896	0.5982	1.4289	0.705	1.005	0.5303	0.698	0.7582	0.979	1.226	1.1729	0.908	1.667	1.0439	0.7084	1.512

4930429H24	BTB/POZ	DRE1	Mm.274579	Hs.246875	1.2687	0.97	0.731	0.3882	0.6798	1.1961	0.577	0.7014	1.9317	1.9703	1.3626	1.853	0.7633	1.098	1.4198	1.536	1.733	1.7733	1.944	2.25	1.757	1.1391	0.551
1200003E21	BTB/POZ	LZTR1	Mm.161726	Hs.78788	1.9808	1.6346	1.971	0.4762	1.5608	2.7064	0.849	0.8453	2.0604	1.3835	2.4025	1.513	0.9717	1.589	1.035	1.592	3.229	2.7074	3.04	2.178	1.4604	0.8379	0.745
1300017A20	BTB/POZ	ZNF288	Mm.211212	Hs.436987	0.7607	1.0755	0.687	0.1888	0.4243	0.7335	0.43	0.5478	0.706	0.6333	0.5125	1.297	0.6147	1.059	0.6339	0.779	0.798	0.7334	0.682	1.1	0.9517	0.3592	0.243
2610021A10	PH	SCAP2	Mm.156651	Hs.410745	1.8456	0.9339	1.765	0.6443	1.0608	1.8766	1.43	1.161	1.9809	5.6707	2.515	1.509	1.1001	1.707	2.6553	1.796	1.643	2.1527	1.26	1.423	1.539	0.7451	1.071
6430512N22	PH	PLEKHA2	Mm.261122	Hs.470847	2.3587	2.0895	0.893	1.7343	1.77	1.5091	0.591	0.6966	1.5128	2.4596	1.3517	1.788	2.4109	0.907	0.9365	1.018	1.632	1.1441	1.716	2.653	2.501	0.7775	1.038
A430106A18	PH	ITK	Mm.274218	Hs.211576	1.2876	1.0095	0.9	0.7684	1.0832	3.0508	0.316	0.2975	2.7219	3.8575	2.5745	1.183	2.322	1.281	1.1682	1.671	1.674	1.0687	1.775	1.419	1.3327	0.6717	0.978
4933426D16	PH	SNTG1	Mm.129083	Hs.388360	1.9986	0.9861	0.896	0.7161	1.7496	2.7147	1.317	1.1706	4.1048	5.5779	4.9218	1.863	2.8396	1.946	1.9667	2.399	2.613	2.1671	1.413	1.445	1.9768	0.5665	1.09
5730427K19	PH	APS	Mm.277333	Hs.371366	1.0663	0.9801	1.086	0.586	1.4592	1.322	1.331	1.5806	1.266	2.6388	1.2942	1.222	1.6371	1.183	0.8691	1.18	1.321	1.0357	1.206	0.836	0.9639	0.6916	1.2
1810074L23	PH	PLEK	Mm.98232	Hs.77436	1.632	1.1046	0.395	0.8466	1.3282	1.124	0.808	1.4319	2.1677	4.8873	1.5378	1.9	0.3899	4.839	1.6255	2.005	1.556	2.2628	2.331	1.653	1.1644	0.7961	1.366
2010320F03	PH	PLEK2	Mm.103380	Hs.170473	1.2745	0.9767	0.311	0.6879	0.3685	0.5558	0.655	0.4499	0.6707	0.8728	1.2597	1.38	1.1173	1.3	0.7321	0.922	0.799	0.6707	0.813	1.705	1.149	0.5409	0.605
1500001N23	PH	PLEKHB1	Mm.26633	Hs.445489	2.992	2.0725	1.442	2.0622	2.139	2.276	1.005	0.4692	14.249	11.135	9.5328	3.467	3.8001	3.156	6.6784	3.765	11.272	7.2872	5.948	2.794	2.873	0.9511	1.218
1200014M06	PH	OSBPL3	Mm.44153	Hs.197955	2.6369	2.1386	0.877	2.2149	1.6201	2.4574	0.611	0.7498	2.1054	2.5798	1.357	2.323	3.0502	1.616	1.5437	1.168	2.725	2.0164	2.78	4.503	3.7963	1.1883	1.426
1200004I24	PH	ARHGEF3	Mm.207446	Hs.25951	1.5991	1.4124	0.818	1.1156	0.9438	1.0137	1.377	0.3821	1.3382	1.3534	0.8035	1.858	2.7978	1.174	0.9597	1.05	1.404	0.8206	1.293	2.831	2.9324	0.1432	2.124
3110056A02	PH	POLR2J2	Mm.127418	Hs.406505	2.2235	1.4971	0.824	1.6997	1.6126	2.2556	1.091	1.3073	2.33	3.1546	2.0474	2.207	4.2265	2.27	2.4474	2.394	2.77	2.3373	2.12	2.489	2.5971	0.1656	1.916
4933433D06	PH	OSBPL10	Mm.259777	Hs.368238	1.447	1.361	0.612	0.8662	0.6136	0.6931	0.558	0.6651	1.3501	1.49	1.0989	1.012	2.2839	0.868	0.4835	1.004	1.379	0.5344	1.063	1.579	1.5236	0.2154	0.682
2410043H07	PH	PSCD2	Mm.272130	Hs.8517	0.884	1.1554	0.452	0.6669	0.4452	0.6499	0.414	0.2975	0.7734	0.8897	0.8483	0.946	0.9261	0.947	0.7895	0.916	0.809	0.5098	1.148	1.047	1.1058	0.3393	1.357
2810471M23	PH	FLJ12604	Mm.235383	Hs.126485	2.6924	2.2585	1.624	2.315	1.0329	2.0744	0.849	0.7498	14.969	12.47	10.012	4.559	0.171	6.022	3.7771	3.512	2.163	2.9742	3.465	2.038	2.5223	0.8428	1.189
9530063M10	PH	GNRPX	Mm.41479	Hs.512626	1.7741	1.4398	0.783	1.4285	1.0259	1.3271	0.617	0.7607	3.724	3.575	2.8957	2.225	1.9785	3.458	2.511	1.82	1.933	1.7056	1.388	1.642	1.4746	0.0616	0.94
6230420N16	PH	FLJ12987	Mm.255342	Hs.296730	1.7079	1.0222	1.058	0.9512	0.766	1.7549	0.625	0.7933	1.852	3.6644	1.8731	1.496	1.7708	1.397	1.5776	1.316	1.296	1.3592	1.269	1.422	1.3198	1.0265	1.016
5031433E13	PH	SWAP70	Mm.282528	Hs.153026	1.021	0.969	0.502	0.7936	1.0244	1.0392	1.273	0.624	1.6925	2.8425	1.5795	1.345	1.3048	1.366	1.2836	1.141	0.936	0.5699	0.728	1.549	1.9949	0.7146	1.341
4933427A08	PH	FGD6	Mm.269596	Hs.170623	1.6154	1.143	0.394	0.8903	0.7914	1.3503	1.028	0.9397	1.3435	2.0552	1.0807	1.52	1.9598	1.508	3.109	2.236	1.185	0.8054	0.856	1.488	2.4024	0.7812	1.312
9130014M22	PH	FLJ10244	Mm.28376	Hs.220745	2.5345	2.1411	0.527	1.6229	1.1161	1.7071	0.728	0.6107	5.6313	10.26	5.0977	2.281	3.6238	1.48	2.9901	2.771	3.99	2.9979	4.006	4.269	4.3624	0.8634	1.066
5830480G12	PH	ARHGAP15	Mm.239239	Hs.433597	0.758	1.0508	0.796	0.7048	0.7231	0.9973	0.935	1.0243	2.743	4.3762	3.1181	1.405	1.7507	1.14	1.2628	1.305	1.603	1.0857	0.929	3.843	3.2341	1.4043	2.07
2810487K11	PH	PSCD3	Mm.281003	Hs.7984	0.8342	1.013	0.21	0.8463	0.4104	0.5722	0.149	0.1657	0.6748	0.5387	0.642	0.829	1.0516	0.687	0.6656	0.664	0.567	0.3133	0.424	1.568	1.3121	0.7619	0.46
2410008H17	PH	GEFT	Mm.22583	Hs.61581	2.231	2.0019	1.055	1.3014	0.8023	1.296	0.493	0.5563	2.5345	2.9282	2.3555	2.123	3.5693	1.275	1.224	1.215	2.485	1.5718	1.31	1.457	1.8769	0.4139	1.07
2810052M02	PH	CKIP-1	Mm.29475	Hs.173380	1.4572	1.6615	0.976	1.7903	0.4721	0.6007	0.213	0.335	0.7387	0.5338	0.3805	1.79	1.1965	1.959	0.6203	1.222	0.731	0.708	0.53	6.305	3.6674	1.7672	0.476
1700038J06	PH	ARHGEF6	Mm.261443	Hs.372800	3.0382	1.7584	1.866	3.0194	1.9209	2.6425	0.971	0.8731	3.6542	3.0595	2.5032	4.944	3.8785	1.748	2.0952	1.56	2.252	1.7598	3.261	2.313	2.5036	0.9424	0.481
1300015B16	PH	DNM2	Mm.39292	Hs.432832	0.8051	0.6946	0.664	0.4464	0.4672	0.5821	0.276	0.289	0.5698	0.4477	0.4739	0.9	0.826	0.703	0.4666	0.69	0.689	0.3862	0.777	1.361	1.2173	0.4108	0.545
0610010K16	PDZ	RGS19IP1	Mm.20945	Hs.6454	0.7166	0.5897	0.966	0.4716	0.3885	0.5176	0.853	0.7183	0.8791	0.8757	0.3725	1.46	0.13	1.949	0.6874	1.165	0.909	1.1382	1.14	1.227	1.0858	0.6586	1.124
2610024J09	PDZ	AUP1	Mm.275961	Hs.411480	1.0753	0.7666	0.662	0.7737	0.3695	0.5213	0.538	0.5684	1.8483	2.5923	0.9839	2.09	1.2898	1.348	1.0251	1.168	2.312	1.2093	1.554	1.2	0.8034	0.1699	0.448
2700099C19	PDZ	LOC51248	Mm.291607	Hs.11042	1.2674	0.5596	1.276	0.4574	0.4452	1.4783	0.863	0.988	0.6398	0.7965	0.6741	1.195	1.1935	1.225	0.6943	0.868	1.111	0.8384	1.006	1.202	1.3218	1.0856	1.478
4833411E15	PDZ	SDCBP	Mm.247473	Hs.164067	0.9446	0.8615	0.754	0.5826	0.6614	1.101	0.528	0.8211	0.6063	0.9984	0.6537	1.156	1.189	0.921	0.6309	0.851	0.847	0.5843	0.544	0.931	1.6377	0.4718	0.883
4921513F16	PDZ	PDZK1	Mm.28015	Hs.15456	1.1161	0.7012	0.748	0.4555	0.4642	1.2705	0.718	0.7583	0.6784	1.1911	0.4569	0.961	1.3436	0.842	0.5871	0.89	1.104	0.6377	0.899	1.149	1.5784	0.8316	1.126
1300011C24	PDZ	TIP-1	Mm.186	Hs.12956	0.6593	0.5572	0.567	0.3227	0.3058	0.831	0.723	0.7764	0.7551	0.801	0.5403	0.961	1.0867	0.96	0.4338	0.805	0.851	0.5098	0.451	0.737	0.8537	0.3131	1.045
2900002D01	PDZ	FLJ10490	Mm.2535	Hs.221737	1.1237	0.958	0.325	0.6811	0.38	0.3683	0.316	0.8248	0.651	0.5912	0.3607	2.072	0.7065	2.054	0.6929	1.217	0.671	0.8392	0.501	1.016	0.6551	0.422	0.527
1110001A05	PDZ	LIM	Mm.117709	Hs.154103	0.5273	0.6571	0.952	0.5574	0.8217	1.3016	0.838	1.2202	1.0453	0.8733	0.9069	1.254	0.9642	1.731	0.8441	1.164	0.99	0.614	1.113	1.045	1.3882	0.1787	1.938
2900002K10	PDZ	SYNJ2BP	Mm.279603	Hs.443661	1.6556	1.5505	1.384	0.8782	1.1863	1.1695	0.366	0.6059	2.3647	1.7538	1.9306	1.531	2.0845	2.238	2.6309	2.038	2.001	1.3745	1.917	1.577	1.5268	0.2222	0.828
0610011L07	PDZ	SLC9A3R2	Mm.21587	Hs.440896	1.3674	1.3244	0.895	1.1942	1.008	1.5057	0.643	0.8103	0.7383	0.8606	0.4582	1.169	2.21	1.148	0.8411	0.833	0.807	0.647	1.158	1.235	2.1155	0.7569	1.583
1110032B18	PDZ	LDB3	Mm.29733	Hs.49998	1.101	0.7321	0.738	0.4743	0.9477	1.1154	0.7	0.6349	0.8818	1.2375	0.6448	0.882	1.3414	0.924	0.8767	0.957	1.258	0.3794	1.267	1.003	1.49	0.8609	1.565
2610202L11	PDZ	PSMD9	Mm.30237	Hs.131151	1.9619	2.0955	0.586	1.0136	1.1166	1.7309	0.825	0.9155	0.7099	1.4253	0.6089	1.332	2.0606	1.146	0.7268	1.012	1.035	0.6301	0.251	1.131	1.5932	1.113	2.374
0710008C04	PDZ	PARD6A	Mm.250566	Hs.112933	1.8066	2.0722	1.216	1.2731	0.7331	1.0779	0.73	0.965	2.3882	5.0041	2.1912	1.418	2.9561	1.47	2.5564	1.723	1.998	1.3372	2.026	1.144	1.7254	0.6237	0.847
9130022D09	PDZ	LIN7C	Mm.235300	Hs.91393	0.8746	0.966	0.827	0.6055	1.3681	1.3069	0.875	1.3702	1.1034	1.428	1.2179	1.303	1.4586	1.309	1.0729	1.245	1.094	0.7901	0.809	1.013	1.0032	0.6144	2.109
2200002N01	PDZ	GIPC2	Mm.97	Hs.147975	1.4476	0.7691	0.171	0.7274	0.8287	1.2206	0.914	0.7329	0.7283	0.4368	0.5552	1.165	1.1853	0.731	0.7637	0.872	1.345	0.8003	1.554	1.521	1.2805	0.7345	1.093
4930506N09	PDZ	RGS3	Mm.286753	Hs.82294	3.2646	2.822	1.599	3.1789	1.9996	1.9672	1.256	1.2746	1.4371	1.8037	1.0599	3.931	4.9137	1.338	1.0729	1.077	1.619	0.962	0.557	2.029	2.0349	0.8154	1.501
4931400F03	PDZ	GRIP1	Mm.196692	Hs.372377	3.5474	3.4986	1.167	2.318	1.3332	2.3019	0.787	0.8115	1.1981	2.1127	0.8722	1.499	1.9725	1.364	1.0242	1.417	1.296	0.9637	1.081	1.806	3.6661	1.2499	1.223
2010002N16	PDZ	ALS2CR19-I	Mm.35593	Hs.26981	1.4707	2.1462	1.242	0.6623	1.3541	1.5975	0.548	0.7196	0.8363	1.5529	1.3342	1.417	0.7245	0.886	0.8716	1.11	0.867	0.9849	1.286	15.768	8.9995	1.1142	1.757
AB029485	PDZ	Acvrinp1	Mm.319105	Hs.22599	1.6425	1.4567	1.359	1.1321	2.5041	1.3365	0.995	1.1767	0.7074	0.8104	0.5795	1.379	1.26	1.554	0.8923	1.21	1.27	1.0128	1.178	1.926	1.5403	0.7451	0.111
1700011C14	phosphatase	MK-STYX	Mm.247666	Hs.11615	0.7353	0.9532	1.153	0.322	1.0737	1.6503	0.423	0.5769	2.0327	3.2754	1.6019	1.304	0.72	0.964	2.1127	1.455	1.406	1.2508	0.729	2.449	2.2263	0.5851	1.053
2610306G15	phosphatase	DUSP10	Mm.266191	Hs.177534	1.3765	0.8472	1.037	0.287	0.9238	0.6908	0.26	0.653	1.5301	3.0257	1.3827	2.529	0.8992	1.464	1.4957	1.401	1.258	1.3338	1.185	1.104	1.7918	1.1111	0.765
1700022L10	phosphatase	DUSP13	Mm.52571	Hs.178170	1.0453	1.3305	0.888	0.2896	1.0334	0.8586	0.529	0.751	1.2373	1.4298	1.0532	1.313	0.5138	1.206	0.6574	1.162	0.756	0.7579	0.557	1.872	1.227	0.9742	0.704
4930527G07	phosphatase	DUSP18	Mm.32588	Hs.128782	0.8388	0.9897	0.787	0.2125	0.5762	0.8137	0.482	0.6385	0.5796	0.963	0.4543	1.268	0.4436	0.87	0.6869	0.963	0.589	0.6326	0.443	0.613	0.5384	0.5739	1.071
2210015O03	phosphatase	DUSP3	Mm.196295	Hs.181046	1.659	2.0289	1.337	0.4051	2.2093	1.9796	0.565	0.6409	0.6345	0.961	0.9425	1.498	0.8499	0.904	0.9728	1.051	1.178	0.9095	0.744	1.525	1.4204	1.3968	1.519
2310042C07	phosphatase	DUSP14	Mm.240885	Hs.91448	1.0076	0.9346	0.754	0.2573	0.6444	0.9846	0.344	0.4765	0.8619	1.1371	1.0645	1.205	0.5333	0.695	0.6343	0.972	0.697	0.7469	0.469	1.22	1.5513	0.8254	0.259
2310043K02	phosphatase	DUSP13-like	Mm.52571	Hs.178170	2.203	1.4991	1.08	0.6638	1.9483	2.2717	1.053	0.5841	5.7725	5.8433	4.6749	2.135	1.2503	3.158	3.6804	4.21	2.788	2.7574	2.385	3.362	2.9414	0.8366	0.747
1700094E07	phosphatase	1700094E07	Mm.159027		1.3958	1.093	1.039	0.4288	2.1734	1.9446	0.638	0.751	1.6898	2.4079	1.6981	1.24	0.6692	1.321	1.2427	1.46	1.743	1.443	1.613	1.77	1.904	1.0451	0.625
0610039A20	phosphatase	STYX	Mm.202561	Hs.364980	0.9855	0.9601	0.419	0.3031	1.4781	2.4046	0.72	0.9904	1.2588	0.9627	1.2222	1.187	0.6401	0.857	0.9116	1.095	1.073	1.2085	1.104	1.564	1.3701	0.7961	0.842
1300019I03	phosphatase	DUSP6	Mm.1791	Hs.298654	1.2614	1.0895	1.368	0.472	2.2112	1.1174	0.584	0.9348	1.4794	3.6112	1.1527	2.299	1.071	2.322	1.9859	2.311	1.267	1.3694	0.76	0.492	0.9974	0.7856	0.283
1190004O14	phosphatase	DUSP12	Mm.34365	Hs.416216	1.2857	1.2125	1.234	0.2968	1.0399	1.0544	0.621	0.8175	0.84	0.9429	0.6733	1.981	0.7177	1.37	0.8025	1.257	0.937	1.0298	0.778	1.469	1.0045	0.7538	0.487
1600009O09	phosphatase	ILKAP	Mm.234179	Hs.92033	1.3244	2.0836	0.564	0.9298	3.0464	1.8129	1.272	1.473	5.8437	8.5031	5.7645	1.627	1.9486	1.637	3.9531	3.238	2.158	3.274	2.805	1.862	2.4539	1.456	0.675
2410007M08	phosphatase	PPM1A	Mm.261045	Hs.130036	0.9321	1.0056	0.664	0.5115	2.4254	0.8593	1.056	1.1307	0.5009	2.0067	0.4738	1.092	1.1987	1.193	0.8535	1.393	0.859	0.7012	0.974	1.288	1.1245	0.9655	0.858
4921535M01	phosphatase	PPP3CC	Mm.1567	Hs.75206	1.6897	1.6176	1.334	1.2517	1.9413	1.653	1.68	1.7136	3.077	5.4995	2.6994	1.667	1.7469	2.653	2.5545	2.511	2.283	3.0131	1.375	2.186	1.9891	1.1547	0.186
1810062E21	phosphatase	PPP1CA	Mm.277629	Hs.183994	1.2024	1.3694	0.849	0.475	0.7221	0.6214	0.488	0.6736	2.778	3.1248	1.6661	1.03	2.0068	1.582	1.1253	1.536	1.627	1.4083	2.29	1.931	1.9001	1.1429	0.023
2810407I23	phosphatase	PPP2CA	Mm.260288	Hs.91773	1.8591	1.737	1.482	0.718	0.9657	2.1979	1.223	1.2456	2.6206	1.9088	2.0545	1.276	2.5431	1.477	1.6871	1.528	1.702	1.3101	3.053	1.069	2.3456	2.1569	1.768
2610028M06	phosphatase	PPP1CC	Mm.280784	Hs.79081	0.8365	1.2677	0.697	0.3893	0.4935	0.9105	0.461	0.3253	1.5212	1.7071	1.7781	1.103	1.6162	0.717	0.7224	0.999	1.13	0.7656	0.926	1.18	1.6738	1.5388	0.373
2310003C10	phosphatase	PPP6C	Mm.25345	Hs.356739	1.7989	1.2409	0.647	0.7985	1.4015	2.5494	1.802	1.6798	1.9205	3.1948	4.3638	1.404	2.3093	1.503	1.5404	1.585	2.152	2.3873	2.967	1.623	2.3392	2.2334	1.321
1200010B19	phosphatase	PPP1CB	Mm.241931	Hs.21537	1.3867	1.0524	0.963	0.689	0.7724	1.578	1.469	0.4511	1.4407	2.2261	1.8756	1.735	2.6043	1.126	2.3152	1.108	1.943	2.0714	2.36	2.262	3.1129	2.3287	0.768
1200007O21	LIM	NEBL	Mm.120298	Hs.5025	1.3931	1.032	0.436	0.5676	0.7112	1.8018	0.837	1.317	0.5198	1.0733	0.6147	0.84	1.0344	1.112	0.7143	0.87	0.788	0.7368	0.365	1.048	0.7034	0.704	1.283
2810478G04	LIM	LMO2	Mm.29266	Hs.283063	2.0087	4.6698	2.432	1.2652	2.0339	1.8609	0.485	2.0172	1.7769	2.9891	2.1444	2.919	2.3482	1.745	1.2049	1.381	1.769	1.4159	2.679	2.417	1.6048	0.8827	0.693
2210410P18	LIM	LMCD1	Mm.234441	Hs.279943	1.6764	1.2621	1.274	0.6571	0.5329	0.2387	0.805	0.9941	0.9322	1.1106	1.4743	1.433	1.4415	1.054	0.77	0.904	0.956	0.8198	1.201	1.666	0.942	0.6698	0.585
4921524A02	LIM	LIMS1-v1	Mm.57734	Hs.112378	1.0601	1.4684	2.945	0.8237	0.8506	1.5417	1.151	1.0691	9.7911	4.4665	9.059	1.782	1.4833	1.416	1.4747	1.32	1.751	1.7225	2.938	4.309	2.8099	2.1339	0.643
2810049E20	LIM	LHX9	Mm.250732	Hs.442578	3.3253	3.3155	2.969	1.4717	1.3895	1.8979	1.102	0.8211	2.7429	2.6496	2.7879	2.323	1.9807	1.571	1.6282	1.825	1.453	1.4549	2.377	5.125	3.2599	0.8727	0.807
E130113K05	LIM	CSRP1	Mm.196484	Hs.108080	1.7399	1.9878	1.994	0.7387	1.0205	1.1071	1.384	1.0231	0.7084	0.7403	0.5398	1.698	1.6805	1.357	0.764	1.284	0.877	0.9984	1.012	1.258	1.4849	0.7252	0.584
0610010I23	LIM	CRIP2	Mm.294801	Hs.70327	1.8982	1.6169	2.681	0.7037	0.9448	1.6839	1.011	1.1851	0.7232	1.6861	0.7127	1.549	1.5326	1.275	0.5399	1.528	1.057	0.9891	0.987	1.508	1.1657	1.0258	0.783
2810002M14	LIM	CSRP2	Mm.2020	Hs.10526	1.8271	2.0718	1.644	0.838	1.0155	1.7482	1.475	0.9917	1.3329	1.3616	1.2088	1.574	1.5864	1.409	0.7239	1.695	1.03	0.9138	0.395	1.595	1.2218	0.5963	0.796
2310016J22	LIM	LIMS1-v2	Mm.57734	Hs.112378	1.7222	1.7471	0.979	0.8812	1.1485	1.6455	1.6	1.4742	1.0248	1.3926	1.4538	2.047	1.4863	2.445	0.8335	1.665	0.795	1.233	1.001	1.891	1.2044	0.8565	0.661
2610509F17	LIM	JUB	Mm.100253	Hs.434997	0.889	0.675	0.308	0.5288	0.6639	0.2603	1.287	0.9771	2.5471	0.814	0.6397	1.637	0.2592	4.586	0.6364	1.723	1.492	2.2577	1.744	1.38	0.6938	0.3181	1.033
2610507L09	LIM	CRIP1	Mm.272368	Hs.423190	0.855	0.9029	1.165	0.815	0.7187	0.9454	1.008	0.8864	1.3209	1.1498	0.7161	1.849	1.1046	1.617	0.5113	1.08	1.023	0.7901	1.43	1.076	0.8317	1.3657	1.541
1700027G07	LIM	FHL5	Mm.87325	Hs.283689	2.1762	1.9393	1.801	2.391	0.9179	1.2684	1.002	0.8864	2.2352	1.5691	1.4992	3.163	2.5461	1.227	0.7483	1.122	1.511	1.2855	0.518	1.738	2.1335	0.7358	1.061
1700010N06	LIM	FHL1	Mm.46163	Hs.421383	0.9874	0.5034	0.674	0.5961	0.8008	1.4267	0.741	0.6712	0.5421	0.5848	0.3254	1.298	1.0904	0.632	0.4667	0.746	0.916	0.7325	0.495	0.94	0.8711	0.8074	0.915
2410007B04	LIM	TRIP6	Mm.27063	Hs.380230	2.99	2.3714	1.714	2.7441	2.1251	2.3657	1.063	0.965	1.4985	1.3439	1.4101	2.501	4.0182	1.169	1.0098	1.443	1.539	0.6927	1.205	1.403	2.3908	0.9225	1.19
2610029O20	LIM	CSRP3	Mm.17235	Hs.83577	1.2506	1.3235	0.438	1.0576	0.2216	0.3546	0.558	0.5236	0.5765	0.5622	0.4788	1.75	1.7335	0.763	0.533	0.786	0.926	0.4615	0.521	0.873	1.4185	0.7065	0.901
6720456D19	LIM	ALP	Mm.282900	Hs.71719	0.5196	0.8541	0.862	0.5563	0.7545	1.0397	0.813	1.1235	0.6334	0.9808	0.7996	1.279	1.2167	0.83	0.3949	0.969	0.969	0.5538	0.587	0.903	0.7847	0.6187	1.875

2410002J21	LIM	ENIGMA	Mm.275648	Hs.436339	1.1329	1.4843	0.773	1.067	0.6509	1.3619	0.611	0.9046	0.7669	0.9688	0.5649	1.042	1.5923	0.879	0.7181	0.82	0.867	0.4861	0.565	1.329	1.3746	1.0638	1.408
4931439A04	zf-C3HC4	DKFZp434J	Mm.120835	Hs.104744	1.4679	1.3543	1.075	1.3732	3.044	1.1388	1.215	1.3738	1.7353	2.5797	2.1668	1.901	1.6551	1.267	2.281	1.384	1.614	1.8563	1.023	2.608	2.8569	1.2761	0.245
A430106H13	zf-C3HC4	TRIM35	Mm.288225	Hs.137732	3.4469	5.2823	1.49	3.9605	6.6547	1.7792	1.287	0.9735	1.877	2.1769	1.0484	**8.776**	6.3977	1.173	0.9083	1.268	1.377	1.7327	0.985	2.968	3.9246	1.7902	0.632
2610509H23	zf-C3HC4	RNF146	Mm.28930	Hs.267120	1.6831	2.1448	0.381	1.4601	2.8278	0.9813	1.532	1.3895	0.8092	1.5551	3.7221	1.857	1.5774	1.473	0.9284	0.849	1.17	1.2508	1.024	2.312	1.973	2.1034	0.409
2610005D23	zf-C3HC4	RNF14	Mm.22086	Hs.170926	2.4877	2.7656	1.998	2.7193	3.0534	1.4354	1.716	1.3496	2.2379	2.6876	2.3805	3.284	2.9128	1.582	1.0828	1.479	1.797	1.9029	0.691	4.186	4.4334	3.9695	1.062
2700043E10	zf-C3HC4	RNF2	Mm.31512	Hs.124186	1.9027	1.8015	1.445	1.7038	2.5873	2.4794	1.724	1.7269	2.2669	2.5759	1.9032	1.844	2.3497	1.108	1.9727	1.473	1.667	1.366	0.83	2.34	2.6022	4.6219	0.768
2310043C01	zf-C3HC4	TRIM34	Mm.26466	Hs.125300	0.9912	1.4933	1.347	0.7556	1.6933	0.9935	1.196	1.2238	0.9831	1.0883	1.196	1.018	0.9978	1.38	1.2992	1.054	1.627	1.0975	1.403	1.514	1.6138	1.0146	0.083
2510042A13	zf-C3HC4	Rnf130	Mm.166372	Hs.525059	0.6031	0.9228	0.317	0.7646	0.9806	1.1149	0.736	0.8151	**10.742**	**9.6882**	**15.269**	1.57	1.1472	1.2	2.3153	0.914	1.661	1.4016	0.966	1.759	2.1341	1.3333	2.583
2610110L04	zf-C3HC4	RNF141	Mm.268926	Hs.44685	1.7375	1.7233	2.479	1.8242	2.0265	1.0138	1.364	0.9445	1.0159	0.929	0.8657	2.117	2.1375	1.074	1.1596	1.116	1.207	1.0383	1.033	1.891	4.3979	1.1846	0.125
2810430O10	zf-C3HC4	RNF12	Mm.44069	Hs.122121	0.9976	1.1954	0.982	1.1227	1.2635	0.8856	0.577	0.5527	0.781	1.5419	0.8023	1.624	1.3332	1.011	0.9727	0.984	1.058	0.9976	0.54	3.447	4.4153	1.489	0.075
3110001L12	zf-C3HC4	RFP2	Mm.23959	Hs.436922	1.1497	1.3076	0.855	1.2036	2.2949	0.705	1.219	1.2879	1.7621	2.2639	2.6283	1.482	1.3563	1.81	1.5056	1.74	1.824	1.792	0.508	2.399	2.581	1.3309	0.088
2410015A17	zf-C3HC4	RNF138	Mm.253542	Hs.180403	2.2589	2.2679	2.083	2.8141	3.2272	1.6155	0.949	0.8961	2.5791	3.7901	1.3552	3.604	3.2832	1.349	1.5492	1.084	1.354	1.67	0.924	2.829	4.6687	1.357	0.362
1300004G08	zf-C3HC4	FLJ23360	Mm.267353	Hs.161279	2.6688	3.0791	1.757	2.7058	2.525	1.5863	1.351	0.884	2.0694	1.225	1.5796	3.567	3.4102	1.355	1.9847	1.395	1.65	1.2474	1.472	2.466	4.7087	1.2618	0.762
2410131O05	zf-C3HC4	RNF5	Mm.274542	Hs.512071	1.0806	1.2818	0.401	1.0407	2.1236	0.9376	1.343	0.9953	3.4979	2.8825	2.5707	2.179	1.6528	1.669	1.9837	1.655	1.717	1.8953	1.111	2.773	1.512	1.8151	0.72
4921523A11	SH3	NCK2	Mm.144978	Hs.101695	1.2538	1.2473	0.952	0.8666	0.503	0.854	0.694	1.3557	0.8101	1.0487	0.9691	1.355	1.13	0.734	0.7609	1.332	1.332	0.8917	0.581	1.58	1.9169	1.0551	1.298
1200007H22	SH3	SH3KBP1	Mm.167131	Hs.153260	0.8376	0.8339	0.413	0.4284	0.4726	0.3734	1.325	1.473	0.4748	0.6494	0.5143	0.99	0.897	1.257	0.4805	0.841	0.669	1.1263	3.001	1.391	0.8014	0.8403	1.131
1600023G18	SH3	OSTF1	Mm.172222	Hs.47011	2.0535	0.6592	1.92	0.2858	0.4681	1.8011	0.674	0.8707	0.9958	1.0912	0.5488	0.849	0.9179	1.112	0.8116	1.141	1.02	0.6064	1.298	1.232	0.7041	0.6331	1.172
2610511H05	SH3	SH3GL3	Mm.736	Hs.518629	0.8614	0.6265	0.765	0.2121	0.5528	1.5337	1.28	1.5213	0.9912	1.1521	0.4735	0.749	0.8141	1.102	0.7115	1.107	1.352	1.1263	1.42	1.072	0.9355	0.6107	1.189
4632407K17	SH3	Tnnt1-v2	Mm.258670	Hs.411875	2.2081	1.2513	1.981	0.8564	0.9373	1.5263	0.935	1.1731	1.5922	2.0829	1.4758	0.957	1.1016	1.127	1.2023	1.437	1.251	1.1153	1.025	1.547	1.5642	0.6312	1.226
4930572H05	SH3	SRGAP1	Mm.249576	Hs.408259	2.5703	1.6754	1.861	1.4522	1.4981	2.8511	1.69	1.8793	1.3187	2.8024	1.6075	1.839	1.9389	1.904	1.7823	2.311	1.912	3.4188	2.029	1.63	1.5139	0.7912	1.212
6330413E15	SH3	PACSIN3	Mm.288732	Hs.334639	0.5865	0.9153	1.05	0.5284	0.4149	0.5978	0.572	0.5829	0.4199	0.5583	0.4527	1.01	1.077	1.266	0.3478	1.236	0.889	0.8325	0.868	1.382	0.8775	0.8123	1.121
8430435N19	SH3	GRAP	Mm.202760	Hs.159517	0.9317	1.1746	0.632	0.3404	0.2889	0.7923	0.358	0.3314	1.6949	2.085	1.6485	0.844	0.9007	1.029	0.8152	1	1.056	0.8968	1.232	0.77	0.5274	0.3922	0.384
2310034C04	SH3	NOXO1	Mm.269293	Hs.191762	1.2631	0.9996	1.073	0.3573	1.2122	1.7361	1.021	1.5322	2.9954	4.0884	3.3248	1.663	0.8686	2.233	2.46	1.827	1.433	1.9622	1.537	1.881	1.6287	0.8758	0.575
1200013B08	SH3	CXorf9	Mm.276131	Hs.61469	2.3862	2.5054	1.392	1.9851	4.3015	1.3696	2.259	3.2809	1.4511	2.7808	0.953	1.548	1.7917	2.737	2.2327	2.213	1.455	0.9544	3.429	1.485	3.6777	1.4753	0.768
4930548L11	SH3	SAMSN1	Mm.131406	Hs.221851	0.4819	0.9274	0.536	0.6541	2.5106	1.4666	1.112	1.3387	0.9936	2.1918	1.124	1.11	0.8462	1.253	1.2823	1.277	1.159	1.5252	1.015	1.197	1.5145	1.629	0.426
4632411K03	SH3	Tnnt1-v1	Mm.258670	Hs.411875	2.7456	3.5469	1.339	2.242	2.9249	1.7813	1.128	1.2758	3.1846	4.3769	3.1907	2.557	4.355	1.52	1.9105	1.463	2.461	3.1994	2.28	5.986	6.7274	2.0996	0.36
2610016A03	Acetyltransferase	05/02/04	Mm.20155	Hs.10846	1.2973	1.5713	1.98	1.1475	1.9408	1.0572	1.045	1.0908	3.8301	4.0777	2.8452	1.873	1.8418	1.501	1.3432	1.304	1.199	2.3297	1.103	1.802	2.657	1.2493	0.11
0610011E04	Acetyltransferase	SAT	Mm.2734	Hs.28491	0.2285	0.3241	0.154	0.1978	0.1873	0.2376	0.222	0.2213	0.4557	0.471	0.379	0.769	0.4675	0.746	0.3349	0.669	0.698	0.4463	0.159	0.231	0.4455	0.3038	0.071
0610037O16	Acetyltransferase	NAT8	Mm.154782	Hs.14637	0.8439	1.1706	1.569	1.0358	3.2222	0.6979	0.322	1.2638	2.1275	5.0966	3.5619	1.692	1.425	2.427	2.6295	2.276	1.397	2.5414	1.169	1.249	1.4913	1.4298	0.417
2310039H09	Acetyltransferase	ARD1	Mm.5934	Hs.433291	1.1785	2.0609	0.582	1.4883	1.5812	0.8131	1.21	1.034	0.7075	1.5972	1.542	2.033	1.4527	1.669	1.5043	1.331	1.78	1.5083	0.41	1.643	2.0723	1.0738	0.137
2600005K24	Acetyltransferase	MAK3P	Mm.278726	Hs.288932	0.7525	0.9793	0.285	0.6943	1.3063	1.0403	0.759	0.774	0.4163	0.9332	0.5436	1.316	0.9426	1.208	0.9197	1.021	1.197	0.8443	0.632	1.795	1.9459	1.0171	0.109
2610507P14	Acetyltransferase	ELP3	Mm.29719	Hs.267905	1.9791	1.4587	1.097	1.3593	1.1016	0.8726	0.629	0.4765	1.2505	2.1087	2.7772	3.935	2.7395	0.86	1.3021	1.142	2.178	1.6183	1.214	3.352	4.1368	0.7096	0.075
1810018F03	Acetyltransferase	Cml5	Mm.46315	Hs.458287	1.345	1.5157	1.054	1.3213	2.3034	2.2037	0.941	1.2396	1.7391	2.5083	1.4755	1.928	1.6177	1.636	2.5319	1.653	1.207	1.9131	1.041	1.87	2.7331	1.1043	0.085
1500004D14	Acetyltransferase	NAT5	Mm.151168	Hs.109253	2.1497	1.7324	1.513	2.1559	1.895	1.1666	0.633	1.3133	3.2328	5.8407	3.3986	3.251	3.0674	2.863	3.8557	2.428	2.641	3.5983	2.094	3.676	4.6042	1.6296	0.082
1200013P24	Acetyltransferase	FLJ14154	Mm.133257	Hs.312841	1.1781	1.5352	1.443	1.3503	2.6879	1.0195	0.437	0.8344	2.0126	2.2128	0.9378	1.619	1.4736	1.39	1.2329	1.446	1.222	1.0653	0.812	2.386	2.2786	1.1678	0.138
1110028N05	Acetyltransferase	DKFZP564C	Mm.86823	Hs.144058	1.4204	2.1388	1.201	2.1281	2.1983	1.6617	1.458	1.2456	1.7384	2.2527	1.045	3.249	2.4945	1.358	1.0583	1.266	1.288	1.6327	0.863	1.511	2.2483	1.7218	0.372
1810043O14	Acetyltransferase	GNPNAT1	Mm.233534	Hs.478025	0.6839	1.2568	1.008	0.6322	1.4338	0.7563	1.764	1.1307	1.5923	1.3427	0.9007	1.489	1.2532	1.144	0.6485	1.221	0.78	0.9527	0.689	1.932	1.4997	0.8821	0.683
2810011M06	PHD	ING1L	Mm.272313	Hs.107153	1.2018	2.1743	1.036	1.9099	1.7625	1.2636	0.276	0.7909	2.1388	2.3847	1.0597	3.121	1.3518	2.353	0.9367	1.194	0.896	1.3558	1.57	**14.078**	7.9325	3.2624	1.431
1300013A07	PHD	ING3	Mm.39999	Hs.143198	1.2396	1.1479	1.648	1.5398	1.3905	1.8949	1.049	0.8477	2.3859	1.9987	1.4306	2.218	1.6693	2.49	1.5417	1.657	1.446	1.2677	0.867	2.298	1.7808	0.9113	1.652
3321402G02	PHD	DKFZP727G	Mm.286766	Hs.119960	2.2497	1.6157	1.732	1.5616	0.4726	0.9169	0.327	0.3265	1.8836	1.9639	1.5805	1.874	2.331	1.169	1.1796	1.146	1.554	0.9629	1.496	7.467	4.4804	0.9026	0.534
2810027J24	PHD	LOC57117	Mm.246726	Hs.432952	1.5052	1.3307	0.778	1.1513	0.9199	1.5038	0.686	0.7534	0.7273	0.7763	0.6515	1.458	1.8724	0.855	0.7449	1.078	0.936	0.409	0.65	1.447	2.1393	0.7569	0.95
2410002I16	PHD	CGBP	Mm.17537	Hs.180933	1.1968	1.2059	0.651	0.7947	0.5334	0.6866	0.2	0.2261	1.0179	0.8605	0.6513	0.79	1.0845	0.664	0.4316	0.804	0.862	0.4971	0.732	3.425	2.4688	0.5721	0.544
2410141M05	PHD	MGC2941	Mm.20805	Hs.380734	1.5318	1.2262	0.6	0.9877	0.5648	1.0181	0.171	0.9324	0.8052	1.1534	1.4063	1.169	1.8373	1.052	0.8349	1.12	1.035	0.636	0.477	1.856	2.5133	0.3922	0.854
2600014C22	PHD	PYGO1	Mm.273605	Hs.256587	1.1848	1.0417	0.472	0.873	1.1146	2.089	0.811	0.2528	0.9678	2.0003	0.5459	0.977	1.7731	1.357	0.955	1.003	1.146	0.603	1.124	1.138	1.6796	0.6548	0.954
2310010G05	PHD	ING4	Mm.262547	Hs.108183	1.1789	1.142	0.418	0.7695	1.3362	1.5557	0.163	0.6397	0.9869	1.1875	0.7177	1.574	2.1286	0.948	0.8544	1.009	1.167	0.6216	0.648	1.572	1.1657	0.5521	0.975
1200016G04	PHD	DPF2	Mm.259204	Hs.13495	1.1677	1.1945	0.89	0.9516	0.7894	1.0725	0.721	0.7619	1.426	1.9868	1.3841	1.488	1.7544	1.427	1.0652	1.3	0.983	0.7266	0.699	1.446	1.3798	0.7918	0.806
D230038D11	PHD	MLL5	Mm.205190	Hs.380021	0.3964	0.5193	1.051	0.3919	0.4173	1.1749	0.979	1.3339	0.558	1.1844	1.2018	1.36	1.0038	1.926	0.6278	1.242	1.076	1.0171	1.923	1.011	0.7215	0.9175	0.789
1300012O03	armadillo	AP2B1	Mm.39053	Hs.370123	2.0783	1.2544	0.829	1.008	2.1943	3.1248	1.376	0.9856	1.7688	1.5227	2.009	1.379	1.6177	1.424	3.1157	1.399	1.286	1.5887	1.506	2.285	3.3012	1.7317	0.806
4933431K05	armadillo	RTDR1	Mm.67658	Hs.445808	2.1122	1.2202	1.053	1.0102	1.7092	3.7854	0.921	0.8284	1.0854	1.1196	1.1421	1.368	1.7372	0.929	1.5613	0.933	0.88	0.8308	0.968	1.025	2.4108	1.5039	0.822
1300016C01	armadillo	PKP2	Mm.2252	Hs.25051	1.371	1.7847	1.201	0.938	0.4612	1.0733	0.452	0.2951	1.0583	0.6754	0.6913	1.129	1.443	0.74	1.1681	0.753	0.977	0.7147	0.814	2.685	2.9427	1.535	0.468
1500019G21	armadillo	1500019G2	Mm.305300	Hs.527950	1.9835	2.4952	0.665	1.4003	1.1709	1.0572	0.628	0.3991	1.0664	0.9261	1.1893	1.255	1.5288	0.68	1.0347	0.781	1.04	0.9942	0.728	1.568	1.285	1.5649	0.503
1200015K23	armadillo	HSPC056	Mm.234823	Hs.102708	0.8785	1.4798	1.205	0.6714	1.4498	0.6639	1.519	1.768	1.8589	1.4599	2.0924	1.064	1.4205	2.048	2.2188	2.199	1.994	2.3881	2.44	1.68	2.0297	1.0246	2.342
1700007K14	armadillo	SPAG6	Mm.31701	Hs.158213	0.9765	1.2122	0.695	0.5078	0.9368	1.5938	0.813	0.6821	1.1139	0.6244	1.2094	1.01	1.2174	0.993	0.9357	1.132	1.148	0.8359	0.432	1.677	2.9446	1.6689	1.293
2410044B12	armadillo	KPNA2	Mm.12508	Hs.252712	0.6051	0.6854	0.626	0.6661	0.5249	0.8369	0.909	0.6216	0.7166	0.8492	0.6564	1.008	0.8432	0.76	1.0393	0.843	0.953	0.8782	0.809	1.781	1.9801	2.1021	1.055
2310016N05	armadillo	FLJ10511	Mm.200383	Hs.106768	0.5531	1.4544	0.676	0.4607	0.7167	1.0006	0.344	0.6325	1.3142	1.8143	0.8687	1.013	1.2816	1.481	1.5438	1.383	1.042	0.885	0.818	1.341	1.4668	1.2941	0.914
X87838	armadillo	CTNNB1	Mm.291928	Hs.410086	0.9499	0.8815	1.624	0.9196	1.7162	1.4038	0.741	0.7631	0.7055	0.9259	0.7588	1.448	1.1203	1.065	0.9945	1.195	0.986	0.7037	0.919	1.615	1.973	0.3747	0.145
1300018I05	WW	KIAA0082	Mm.296974	Hs.202331	1.121	1.6465	0.827	0.5521	0.6375	1.0255	0.662	0.7256	1.0683	1.1108	1.304	1.386	1.5498	1.734	0.6695	1.724	1.384	1.3118	0.869	1.057	0.9407	0.6536	0.326
0610025L01	WW	PIN1	Mm.7906	Hs.161362	0.5743	1.1792	0.916	0.3171	0.8337	0.7383	0.214	0.8393	0.6324	0.6239	0.4063	0.89	0.9485	1.404	0.638	1.371	1.977	1.3287	2.354	0.91	0.5571	0.8329	0.701
5330426P09	WW	WWOX-v1	Mm.33369	Hs.519	1.3138	1.328	1.215	0.6984	0.6036	0.881	0.456	0.4426	3.5435	5.33	4.2632	1.589	2.1756	1.43	1.5762	1.186	1.478	1.0247	1.746	1.164	1.3585	0.3038	0.232
9030416C10	WW	WWOX-v2	Mm.33369	Hs.519	1.8679	2.0623	1.448	0.9534	0.9771	0.8377	0.824	0.4995	6.3192	6.4866	5.2836	3.773	3.5902	1.848	2.087	2.23	1.594	1.8174	2.274	2.338	2.2431	0.483	0.387
2310058J06	WW	TAZ	Mm.227202	Hs.24341	1.5088	1.8162	1.327	1.1498	1.2132	1.3378	0.794	0.7691	1.0618	1.8493	0.9743	1.209	1.3436	1.734	0.7919	1.882	0.997	1.2127	1.236	0.837	0.8111	0.8447	0.458
5430434O07	WW	GAS7	Mm.40338	Hs.226133	1.6166	1.2298	0.909	0.5213	0.6186	1.3996	0.235	0.4886	0.7451	0.8159	0.5902	0.918	1.2002	1.446	0.5934	1.114	0.885	0.8367	0.707	1.824	1.4198	1.0501	0.867
2310014F10	WW	HYPB	Mm.218959	Hs.6947	1.4555	1.123	1.815	0.4577	0.8362	2.0244	0.852	0.7849	1.6666	3.3898	1.7405	0.909	1.1225	1.877	1.3586	1.84	0.948	1.731	1.817	1.308	0.8743	0.9549	0.814
1300010O06	WW	WWP2	Mm.294777	Hs.315485	7.0001	**14.285**	5.375	6.9465	1.1639	1.9875	3.422	3.6074	3.7077	2.1589	4.579	4.724	6.6419	2.686	1.4067	2.318	1.645	1.2923	2.088	2.578	2.8537	0.9711	2.15
4833419B05	MARCKS	HCN1	Mm.131973	Hs.353176	1.1676	0.7277	1.079	0.6161	1.1654	0.9825	1.825	0.9263	1.0352	1.0282	0.9576	1.342	1.1972	1.045	1.5194	1.02	1.217	0.8121	0.456	2.168	1.9697	1.2089	0.981
C430047J18	MARCKS	NOLA1	Mm.24873	Hs.69851	0.7226	0.8257	1.085	0.5585	0.5249	1.3604	2.173	1.4911	0.9102	1.2251	0.8768	1.325	1.0845	1.009	1.0033	0.942	1.1	1.0501	0.85	4.474	5.0981	3.8183	1.16
4930523M17	MARCKS	EIF4G3	Mm.268903	Hs.402697	1.2113	0.7088	0.828	0.574	0.371	0.7777	1.224	1.0304	0.5612	0.6255	0.9575	1.153	0.944	0.964	0.7563	0.849	1.025	0.7063	1.03	1.084	1.2005	2.1164	0.756
4833436C19	MARCKS	KRT1	Mm.183137	Hs.80828	1.0615	1.2348	1.086	0.5589	1.1056	1.1004	0.34	0.4825	0.8594	1.7623	0.8579	0.963	1.1345	2.907	0.7848	1.857	1.78	1.0967	2.812	1.591	0.6822	0.9599	0.106
0610011M24	MARCKS	DP1L1	Mm.28147	Hs.76277	0.3408	0.933	0.375	0.185	0.2854	0.9843	0.549	0.52	0.6946	0.5758	0.7238	0.89	0.9986	0.976	0.459	1.169	0.908	0.6877	0.407	0.958	1.0381	1.0675	0.293
3300001N19	MARCKS	KRT10	Mm.22662	Hs.99936	1.5837	0.708	1.025	0.3332	0.2709	1.986	0.578	0.3531	0.8682	0.6811	0.6327	0.957	1.0523	0.819	0.8407	0.942	0.979	0.7478	1.376	1.417	1.9059	1.0912	1.001
2410014M22	MARCKS	MLP	Mm.2769	Hs.75061	1.6467	1.0532	2.454	0.7391	0.5538	1.4954	1.258	0.6385	0.6922	0.4836	0.462	1.291	1.6722	0.823	0.8198	0.871	0.705	0.8071	0.724	1.797	1.5655	2.2658	0.736
2310014E01	MARCKS	SFRS16	Mm.296949	Hs.43543	1.7374	2.0278	1.733	3.599	0.502	1.5237	1.194	0.884	0.7836	0.8989	0.8352	1.658	2.3803	0.976	1.3859	1.157	0.966	1.0205	0.839	0.844	2.5532	1.146	0.656
NM_005900	MH1/MH2	Madh1	Mm.223717	Hs.388294	0.5766	0.6868	0.394	0.4562	**12.301**	2.601	1.84	0.7994	1.0978	0.621	0.5324	0.873	1.7761	1.458	0.7289	1.181	0.749	1.5557	1.502	1.248	1.7505	2.1202	**9.896**
NM_005901	MH1/MH2	MADH2	Mm.152699	Hs.110741	0.9967	3.6677	0.804	7.4779	1.6888	**28.347**	1.28	1.0799	1.5351	1.1031	0.4822	1.582	1.0635	1.784	0.9125	1.448	0.888	1.3211	0.392	1.002	0.9201	1.4995	3.786
NM_005902	MH1/MH2	MADH3	Mm.7320	Hs.288261	1.2474	4.9599	0.417	**8.2012**	4.1321	**21.393**	0.517	0.5841	0.5517	0.7702	0.5757	2.559	6.9758	1.253	0.6258	0.937	1.255	1.1848	0.299	1.047	3.2496	**14.483**	**16.908**
U58993	MH1/MH2	MADH5	Mm.272920	Hs.167700	0.957	0.606	0.279	0.3882	0.642	0.9905	1.637	1.525	0.5742	0.9952	1.1445	1.117	0.8417	1.006	0.5037	1.237	1.096	1.0586	0.353	0.955	0.8956	1.2325	1.87
AF035528	MH1/MH2	MADH6	Mm.27935	Hs.153863	0.8447	0.9091	0.603	1.2126	1.5245	0.4845	2.128	1.2662	0.7457	1.0689	1.1854	1.034	1.3384	2.71	0.9024	1.768	1.594	1.4769	4.312	2.576	3.9711	**13.218**	**31.283**
NM_008543	MH1/MH2	MADH7	Mm.34407	Hs.370849	1.3366	1.1555	0.895	0.4118	1.0932	1.4751	1.195	0.5938	2.0424	1.629	3.3922	1.328	1.1845	2.177	1.4347	1.884	1.611	1.3872	5.244	2.188	3.0736	7.6839	**57.248**
2210402M20	SH2	FLJ20967	Mm.40974	Hs.17433	1.1748	0.7948	0.735	1.0464	0.8232	0.8315	0.479	0.4958	0.9355	1.1413	1.2847	1.863	1.3063	0.892	2.1635	0.88	1.08	0.9087	1.243	1.456	1.5984	1.1883	0.784
2900029A15	SH2	MATK	Mm.2918	Hs.437808	1.8375	1.8377	0.857	1.2374	0.7231	0.9564	0.168	0.2781	1.2948	1.2795	2.1654	1.983	1.5804	0.998	0.8649	1.246	1.889	1.2542	2.333	1.977	2.3211	1.192	1.221
5830401B18	SH2	SOCS4	Mm.91920	Hs.44439	1.0049	1.6286	1.212	1.7064	0.9507	1.1317	1.354	0.8562	2.1957	4.2836	4.4549	1.592	2.1054	3.512	2.4412	2.06	2.173	4.015	3.162	1.946	1.7628	2.8783	6.953

9030611B09	SH2	STAT1	Mm.277406	Hs.21486	2.7457	1.9036	1.403	1.9156	3.3846	3.4277	0.702	0.9082	1.9657	2.4531	4.1188	2.15	2.4572	2.46	3.9826	2.039	1.823	2.4534	1.794	1.981	3.1432	2.5441	2.486
A930009E21	SH2	SLA2	Mm.31910	Hs.334489	1.2008	0.9483	0.872	0.4416	0.5887	1.2472	0.611	0.8332	1.1764	1.7593	2.5367	1.395	1.3123	1.202	0.7548	1.197	1.572	1.0958	1.083	1.311	1.4481	3.1298	2.508
4933424C13	SH2	LOC284948	Mm.128597	Hs.209542	1.4768	0.847	1.401	0.2783	1.259	2.2549	0.574	0.5696	1.357	1.4714	0.9988	1.33	0.6244	0.972	1.034	1.23	0.946	0.8545	1.162	2.135	1.6499	0.5366	0.792
2610014F08	SAM	FLJ36175	Mm.288734	Hs.20848	1.0598	0.9558	0.977	0.2753	0.8945	1.2603	0.536	0.4813	0.8419	1.0664	0.8466	1.405	0.7685	1.064	0.6321	0.892	1.057	0.8723	0.547	1.866	1.7254	0.5845	0.578
1110008G13	SAM	PPFIA4	Mm.295105	Hs.153648	1.3261	1.0864	1.75	0.4024	0.9154	1.0998	0.453	0.5297	1.898	2.3084	2.1523	1.852	1.0516	1.658	1.8023	1.786	1.539	1.0306	2.055	2.579	1.7408	0.7308	0.682
2010107E08	SAM	EPHA1	Mm.250517	Hs.89839	0.7362	0.491	0.169	0.4886	0.4896	0.6277	1.581	1.4512	0.8707	1.6178	1.406	1.233	0.8455	1.029	0.6837	0.87	1.013	1.2754	1.787	1.127	0.6183	3.0165	0.49
8030473B06	SAM	ETV6	Mm.269995	Hs.171262	1.187	1.2172	0.521	1.0512	1.5524	0.9532	1.367	1.6157	1.1432	1.9007	0.9809	1.789	1.2846	1.176	0.7345	0.927	1.2	1.3829	1.565	3.397	1.5919	2.2671	0.418
1700021J16	SAM	SAMD8	Mm.236484	Hs.282105	0.6584	0.9256	0.419	0.6582	0.763	0.6811	0.392	0.3568	3.6981	3.9092	2.5632	1.099	0.9747	0.906	1.3958	2.009	2.742	1.5235	1.383	1.641	1.354	1.07	0.189
2610002F09	FKBP	FKBP4	Mm.12758	Hs.848	0.7793	1.6788	1.078	1.5063	1.4064	1.1394	0.829	0.5164	0.7408	1.8164	1.341	1.149	1.6932	3.822	1.33	1.782	1.158	1.8648	2.255	1.35	1.078	0.6337	**9.184**
2700038N19	FKBP	FKBP3	Mm.28480	Hs.379557	1.3414	0.8542	0.578	0.5743	0.5583	0.7097	0.49	0.722	0.4503	0.6498	0.5816	1.098	0.9948	0.809	0.6047	0.912	0.893	0.719	0.356	1.453	1.7357	1.8531	1.503
1110002O23	FKBP	FKBP11	Mm.30729	Hs.438695	0.8391	0.8744	0.528	0.7255	0.4532	0.3788	0.28	0.3229	1.3366	1.2497	1.6716	1.443	1.1502	1.281	0.7153	1.177	2.355	1.7217	1.616	1.426	1.0452	0.9206	1.277
1500011D07	FKBP	FKBP1B	Mm.20453	Hs.407482	1.0642	0.6711	0.278	0.5627	0.3192	0.5555	0.617	0.5744	**86.518**	**45.981**	**113.18**	1.508	1.2062	2.484	1.4554	1.081	**16.365**	**13.258**	4.293	1.155	1.0148	1.4647	1.887
0610037L19	FKBP	FKBP1A	Mm.278458	Hs.374638	1.139	0.8072	0.965	0.4622	0.4502	0.6223	0.551	0.7087	**46.276**	**19.842**	**77.171**	1.336	1.0307	1.837	1.2498	1.88	4.206	6.1736	1.954	1.427	0.9343	0.9138	1.636
NM_004799	Miscellaneous	MADHIP	Mm.150197	Hs.162051	2.3762	0.7408	0.972	1.2246	0.5568	1.2246	0.939	1.2238	0.4227	0.6367	0.7605	1.255	0.8798	1.066	1.1038	1.017	1.613	1.0433	1.66	1.075	0.8182	0.8721	0.615
AF069303	Miscellaneous	FOXH1	Mm.42011	Hs.159251	1.5626	0.8444	0.473	0.689	0.7102	1.4087	0.792	0.7268	0.4181	1.3599	0.6771	0.923	0.8977	1.136	0.8173	1.015	1.64	0.8096	0.283	1.241	1.2766	0.8161	2.782
Y13149	Miscellaneous	GSC	Mm.129	Hs.440438	4.9539	3.1626	2.639	**8.4761**	0.5369	0.6337	0.489	0.5793	1.0575	0.9865	1.8405	3.446	2.1054	1.336	1.5603	1.84	1.366	1.5218	1.238	1.089	1.6983	1.3284	1.463
0610039E12	miscellaneous	IRF7	Mm.3233	Hs.166120	2.8922	2.26	1.075	2.1627	1.7844	2.1747	0.344	0.8103	2.3472	3.0468	3.1604	2.53	2.4258	1.541	1.9559	2.124	3.477	2.4449	3.377	1.588	1.7221	1.817	1.64
3110001G18	miscellaneous	IRF3	Mm.3960	Hs.75254	0.3222	1.1534	0.908	0.9798	1.4587	1.6698	0.512	0.393	0.5794	0.7511	0.6619	1.171	1.5326	1.867	0.7965	1.195	1.151	1.8191	1.267	1.184	0.9729	4.5186	4.012
9030603A05	miscellaneous	ICSBP1	Mm.249937	Hs.14453	1.4554	2.3193	0.572	1.9351	1.1385	0.8011	0.831	0.6954	1.0319	1.317	1.1693	2.324	1.791	2.136	1.0762	1.395	1.528	1.7572	2.476	1.444	1.274	0.9393	4.762
2310004H24	Miscellaneous	MEF2C	Mm.24001	Hs.368950	1.0073	1.5196	0.792	0.5014	0.4258	1.2317	0.736	0.7728	0.6109	0.9083	0.7009	1.153	0.6102	0.928	0.6476	1	0.7	0.6995	0.572	2.567	1.0709	0.8572	2.22
2010013E14	Miscellaneous	FLJ38819	Mm.23165	Hs.115959	0.7993	0.7668	1.39	0.331	1.384	1.8586	0.754	0.8296	1.2952	2.1881	0.9677	1.398	0.6468	1.443	0.9023	1.248	1.117	1.2838	2.441	1.985	1.4894	0.7046	0.457
3110030A04	miscellaneous	CED-6	Mm.133132	Hs.107056	0.5955	0.7816	0.741	0.2076	1.4448	0.9606	0.8	0.7244	1.2434	1.893	1.2375	1.362	0.5908	1.132	0.8743	1.426	1.327	1.1323	1.237	2.29	1.0819	0.0448	0.707
0610007A18	Miscellaneous	SFRS5	Mm.43331	Hs.166975	2.0117	1.5993	2.141	0.5683	1.6943	1.0753	0.635	0.7171	1.9917	2.0894	2.7222	1.57	0.7939	1.001	0.9775	1.386	1.268	1.615	2.216	**16.806**	**12.196**	0.9816	1.084
0610011A23	Miscellaneous	ARHGDIB	Mm.2241	Hs.292738	1.7279	0.9489	2.037	0.3231	1.4378	1.9738	0.901	0.9421	1.1465	1.1353	1.4303	1.703	0.894	1.449	1.2614	1.554	1.071	1.2008	1.106	1.477	1.8575	1.2599	0.833
2310004J15	Miscellaneous	EFNA1	Mm.15675	Hs.399713	0.9293	0.638	0.97	0.2595	1.3133	1.5032	0.753	0.8514	4.026	4.4689	3.624	1.863	1.024	1.234	1.3644	1.786	1.815	1.7657	1.28	2.781	1.6241	0.6468	0.647
2410003E11	Miscellaneous	TXNL2	Mm.267692	Hs.42644	1.2616	0.9368	1.456	0.3404	1.6435	1.2565	0.958	1.1549	0.7687	1.3804	0.9977	1.789	0.9732	1.534	0.8896	1.469	1.133	1.2728	1.234	1.594	1.5158	0.658	0.822
2010007O02	Miscellaneous	LENG8	Mm.22831	Hs.380446	1.0573	0.9404	1.376	0.2659	1.3178	1.1449	1.407	1.8733	1.1516	1.7686	1.2595	1.72	0.7655	1.841	0.8875	1.425	1.147	1.6937	1.051	2.3	1.2579	0.3417	0.685
1810005H01	Miscellaneous	SFRS4	Mm.2478	Hs.76122	0.399	0.9139	0.324	0.6439	0.6001	0.9068	0.375	0.3882	0.4525	0.6896	0.4442	1.166	0.7588	0.827	0.4976	0.579	0.576	0.6987	0.358	7.031	**8.1111**	3.5512	0.726
0610041G12	miscellaneous	DIABLO	Mm.46716	Hs.169611	0.9254	0.6862	0.28	0.6473	0.8501	1.2819	0.965	0.9566	2.6646	2.9476	2.1601	1.313	0.9597	1.013	0.9347	0.729	1.07	1.2305	0.834	1.791	1.4268	2.9798	0.591
6330408J11	Miscellaneous	CGN	Mm.87634	Hs.18376	1.625	1.5825	0.93	1.0934	1.4358	0.9281	0.868	1.1718	0.829	1.3046	0.6079	0.967	0.9762	0.848	0.6242	1.152	1.056	1.2042	1.188	1.628	1.8769	1.8444	0.435
4921513I03	Miscellaneous	CRB1	Mm.158473	Hs.444511	1.4277	0.8819	1.024	0.7793	1.9737	1.6134	1.136	1.0025	1.7818	2.1638	1.4085	1.233	1.1816	1.282	1.4325	1.363	1.26	1.4617	0.984	1.106	1.4662	1.9726	0.447
4921514D13	miscellaneous	DAP3	Mm.29028	Hs.270920	1.0976	1.027	0.673	0.6763	1.4353	1.2523	0.682	1.1102	1.5669	2.4657	1.3894	1.249	1.0404	1.294	1.4001	1.481	1.343	1.1797	1.152	1.505	1.6409	1.5251	0.439
1300002E07	Miscellaneous	RHPN2	Mm.286600	Hs.335798	1.3681	2.3972	0.93	1.0633	0.9756	0.93	0.148	0.5502	3.1956	3.7583	2.7976	1.331	1.4803	1.237	1.6218	1.46	1.346	1.3389	1.87	2.261	3.5139	0.7557	0.263
3200001L20	Miscellaneous	RTKN	Mm.4139	Hs.58215	1.1283	1.781	0.607	1.1216	1.0518	0.1957	1.098	1.0316	1.6854	3.609	1.4657	1.306	1.1158	1.719	2.0046	1.772	1.758	1.8174	1.758	1.552	3.0407	0.8248	0.422
1500041M20	miscellaneous	CDC42EP4	Mm.293378	Hs.3903	0.9117	1.0434	0.618	1.4529	1.7227	0.5003	1.009	1.2553	1.3127	3.0087	1.6401	1.703	1.5191	1.638	1.7363	1.302	1.817	1.9512	1.566	1.969	1.5751	1.9757	0.704
2610011H01	miscellaneous	STX8	Mm.3973	Hs.380938	1.6244	1.1347	0.781	1.1742	2.8965	2.1583	1.483	1.3424	2.9456	5.2511	3.9073	2.302	1.8754	1.525	4.3464	1.31	1.559	2.411	0.846	1.768	2.1715	2.0996	0.556
2810018B18	miscellaneous	2810018B18	Mm.305491		1.075	1.3058	0.759	0.9929	1.4866	0.8184	0.755	0.849	6.1933	3.7983	4.0422	1.331	1.1442	3.357	4.8936	4.941	2.282	2.798	2.689	1.085	1.708	1.9353	0.33
2810455B10	miscellaneous	ALS2CR19-I	Mm.35593	Hs.26981	0.7581	0.8762	0.477	0.3569	1.7879	0.7309	1.011	0.965	0.8047	1.1289	1.0955	1.08	0.9493	1.277	0.8899	1.099	1.069	1.0162	0.817	1.477	1.8053	1.5195	0.748
3322402E17	Miscellaneous	KIAA0290	Mm.22025	Hs.96485	1.3051	1.5122	0.92	1.2385	2.0474	1.1925	1.302	1.1331	1.6691	2.9818	1.5486	1.304	2.1331	1.976	3.5881	1.874	2.03	1.8783	2.196	2.802	3.7486	0.9406	0.694
1300010N03	Miscellaneous	UBTF	Mm.2845	Hs.89781	0.9216	0.64	0.289	0.3581	0.5458	0.5264	0.784	0.7655	0.8834	1.3855	1.4011	1.1	0.841	1.214	0.6983	1.365	1.197	1.1831	1.489	3.918	2.2999	1.347	0.611
1700056A21	miscellaneous	AVEN	Mm.292041	Hs.63168	1.8732	2.2935	0.883	2.0133	1.6714	0.8994	1.2	0.6047	1.2757	2.9054	1.0404	2.355	2.1756	1.457	1.0926	1.142	1.404	1.3296	1.563	3.092	1.5513	1.9795	0.501
5430439E07	Miscellaneous	TP73	Mm.103715	Hs.192132	1.2104	1.2264	0.685	0.7763	1.5309	1.3606	0.906	1.1114	0.7458	1.9063	0.6537	1.6	1.6349	1.195	0.8709	0.828	0.927	0.9561	0.972	1.492	1.7357	2.3729	0.704
2310003I18	miscellaneous	ASH2L	Mm.27706	Hs.6856	1.3869	1.7894	1.157	1.509	2.4762	1.254	1.133	1.1065	1.1401	3.8331	1.4998	1.738	1.6319	1.021	1.5121	0.941	1.355	1.4981	1.203	4.179	3.512	5.4255	0.386
5830472M02	Miscellaneous	C20orf121	Mm.89828	Hs.283869	1.4135	1.1613	0.802	0.674	2.4478	1.04	1.835	1.4984	1.7102	3.9289	1.4159	1.182	1.3802	1.408	1.4038	1.51	1.409	1.9173	2.775	1.699	2.6796	1.3253	0.776
2610529M21	Miscellaneous	EFNA4	Mm.16332	Hs.449913	1.0056	0.9633	0.518	0.4231	0.9637	1.0059	0.854	1.0739	1.7422	2.3091	1.3438	1.151	1.0777	1.032	0.8463	1.16	1.173	0.8773	2.272	1.168	0.6222	1.2605	0.322
3010029E15	Miscellaneous	RGS19	Mm.274366	Hs.422336	1.3298	1.03	0.584	0.6981	1.6968	0.895	2.082	2.0268	1.2699	3.5602	2.0247	1.387	1.2331	1.149	1.5612	1.639	1.237	1.4278	1.825	1.447	2.1728	0.9561	0.867
E130111N18	Miscellaneous	RRH	Mm.3917	Hs.158338	0.6611	0.8443	0.4	0.5299	1.1659	0.8813	0.603	0.5889	**29.803**	**20.225**	**26.48**	1.507	1.0068	1.425	1.1703	1.408	1.792	1.5184	1.112	1.103	0.9865	1.6072	0.245
5031426K15	Miscellaneous	OCLN	Mm.4807	Hs.171952	1.4761	1.2623	0.858	1.1107	3.9399	1.1404	1.074	0.832	**10.916**	**12.002**	**12.842**	1.345	1.2704	1.708	2.6741	2.394	1.568	2.035	2.338	2.338	3.287	0.8553	0.388
5730571J11	miscellaneous	HDGF	Mm.292208	Hs.89525	1.8466	1.837	0.776	0.7462	3.3896	0.853	1.156	1.5794	0.6324	0.8389	0.5428	1.421	1.9986	0.885	0.7206	1.35	0.676	0.5606	0.602	2.433	2.2715	1.4	1.277
4632410H03	miscellaneous	HDGFRP3	Mm.28887	Hs.127842	1.1294	1.4299	1.071	0.8286	2.2845	0.9386	1.069	1.1295	1.052	1.1234	0.6089	1.157	1.2346	0.911	0.74	1.02	0.93	0.9663	1.034	5.943	5.2051	3.0925	1.689
1200002O22	miscellaneous	NUMB	Mm.4390	Hs.445301	2.3632	1.4001	1.337	1.2942	2.01	2.4921	1.147	0.5454	1.2374	0.9062	1.7736	1.396	1.741	0.881	1.0191	0.916	1.058	0.8604	1.395	2.235	2.7312	1.6234	1.121
1700003H06	miscellaneous	DAB1	Mm.289682	Hs.333942	0.8824	0.9449	0.557	0.5788	1.0404	2.3949	1.179	0.8913	0.7268	0.7752	0.5036	1.219	1.2682	0.804	0.8702	0.777	0.755	0.6707	0.793	2.704	2.5249	1.6682	1.068
2900010F03	Miscellaneous	GUK1	Mm.3624	Hs.376933	1.141	0.8222	0.508	0.4686	0.8925	1.4192	1.436	0.9663	0.6447	0.6527	0.7387	1.387	1.1539	0.793	1.0408	0.736	0.601	0.5716	0.627	1.426	1.7499	1.8475	1.309
1200015I07	miscellaneous	APBB2	Mm.5159	Hs.324125	2.4043	1.8618	1.578	1.3145	2.6938	3.5235	1.223	1.0908	1.1559	1.7365	1.4656	1.036	1.8829	1.611	1.3128	1.643	1.415	1.2119	1.498	2.311	3.423	1.3109	1.547
AF022795	miscellaneous	TGFBRAP1	Mm.246069	Hs.446350	1.4085	1.2349	0.224	0.7176	2.0718	2.0539	0.751	0.722	1.5625	1.0327	0.6806	1.412	1.0344	1.069	0.8714	1.448	1.197	1.0366	1.216	1.77	1.971	0.6125	0.091
NM_001343	Miscellaneous	DAB2	Mm.240830	Hs.81988	0.9856	0.7596	1.334	0.6601	0.633	0.8654	0.67	0.6035	0.592	0.5477	0.5183	1.017	1.1726	1.128	0.9772	1.131	1.205	0.8977	1.09	1.16	0.8227	0.7675	0.64
X97674	Miscellaneous	NCOA2	Mm.2537	Hs.446678	0.7797	1.2692	1.123	0.8169	0.9159	0.3612	1.73	0.4595	0.6989	1.4382	0.5803	1.244	1.2249	1.295	1.1509	1.166	1.451	0.9426	1.061	2.281	1.7673	1.8936	0.857
AF175574	Miscellaneous	PSMD4	Mm.2261	Hs.505059	1.0246	1.0431	0.342	0.7319	1.5618	0.867	1.214	0.6796	2.9949	1.8694	2.1963	1.275	1.1711	1.577	1.3745	1.309	1.746	1.3313	1.305	1.418	2.4075	0.5272	0.077
NM_012029	miscellaneous	SITPEC	Mm.271672	Hs.22199	0.7326	1.6284	0.982	0.4863	0.8193	0.2915	0.79	0.4511	2.6924	1.5004	1.5031	1.099	1.2032	1.35	0.9631	1.463	1.408	1.4939	1.345	3.547	2.4552	0.7638	0.317