

Human protein factory for converting the transcriptome into an *in vitro*-expressed proteome

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Appropriate resources and expression technology necessary for human proteomics on a whole-proteome scale are being developed. We prepared a foundation for simple and efficient production of human proteins using the versatile Gateway vector system. We generated 33,275 human Gateway entry clones for protein synthesis, developed mRNA expression protocols for them and improved the wheat germ cell-free protein synthesis system. We applied this protein expression system to the *in vitro* expression of 13,364 human proteins and assessed their biological activity in two functional categories. Of the 75 tested phosphatases, 58 (77%) showed biological activity. Several cytokines containing disulfide bonds were produced in an active form in a nonreducing wheat germ cell-free expression system. We also manufactured protein microarrays by direct printing of unpurified *in vitro*-synthesized proteins and demonstrated their utility. Our 'human protein factory' infrastructure includes the resources and expression technology for *in vitro* proteome research.

Proteomics on a whole-proteome scale by *in vitro* expression, defined here as *in vitro* proteome research (Fig. 1), is now becoming more plausible because of the accumulation of both genome sequencing data¹ and cDNA clones^{2–8}. By producing many active proteins easily and simultaneously, we can effectively analyze

many biological reactions such as enzyme-substrate reactions, protein-protein interactions, protein modifications and processing by peptidases. *In vitro* research has the advantage of being able to handle proteins that exist in a restricted fashion *in vivo*, such as proteins with tissue-specific, stage-specific or intrinsically rare expression. To pursue *in vitro* study effectively, both resources and expression technologies for proteins with very variable characteristics are required. We describe here the production of the 'human protein factory', an infrastructure with the necessary resources and expression technology for *in vitro* proteome research.

RESULTS

Production of Gateway entry clones and destination vectors

To construct the versatile expression system required for a 'human protein factory', we adopted the Gateway technology⁹. We made the Gateway entry clones⁹ by recombining the PCR-amplified open reading frame (ORF) of cDNAs with the *attP* sites of the pDONR201 vector (Supplementary Methods and Supplementary Fig. 1 online). To produce the maximum number of Gateway entry clones, we used 21,485 cDNA clones from multiple sources, including 'full-length long Japan' (FLJ) cDNA clones^{2–4} (full-length human cDNA sequencing project) and Mammalian Gene Collection (MGC) clones⁵ (Mammalian Gene Collection Program) (Table 1). We grouped these cDNAs into 14,862 clusters, which

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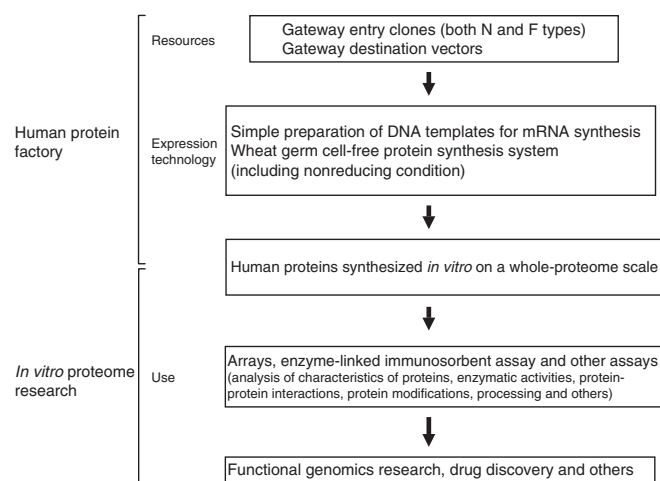


Figure 1 | Schematic representation of the human protein factory and *in vitro* proteome research.

correspond to approximately 70% of the 22,000 human genes¹. With these resources, we produced 33,275 entry clones, including N-type clones that have an intrinsic stop codon at the end of the ORF for the production of native or N-terminal fusion proteins, and F-type clones with the stop codon deleted for generating C-terminal tagged proteins (**Supplementary Tables 1 and 2** online). We also produced 35 kinds of Gateway destination vectors for the addition of small tags (Flag, hexahistidine (6His), Strep-Tactin (an engineered streptavidin) binding tag (Strep-II) and the epitope of the V gene of the SV5 virus (V5)), large tags (glutathione-S-transferase (GST) and maltose-binding protein) and a fluorescent protein tag, at either N or C termini (**Supplementary Fig. 2** online).

Whole-proteome-scale synthesis of human proteins *in vitro*

After comparing protein synthesis systems, including a wheat germ cell-free system^{10–12}, *Escherichia coli* *in vitro* and *in vivo*, and DM2 and CHO cell expression systems, we selected the wheat germ cell-free system because of its high level of protein expression (**Supplementary Fig. 3** online) and ease of handling. In this system, we modified a procedure to obtain templates for transcription to make the steps easier and more efficient (**Fig. 2**). Following the Gateway LR reaction, using a linearized destination vector DNA and an entry clone DNA, we PCR-amplified a template fragment for transcription using the LR reaction mixture as a substrate. This method bypasses the steps of *E. coli* transformation and DNA isolation from cells, thereby shortening the processing time and increasing the success rate by rescuing those expression clones whose proteins or clones are toxic to (and/or cannot be maintained in) *E. coli* cells. The salient feature of this modified method is its simplicity. As only the serial addition of an aliquot of a previous reaction mixture to the subsequent one is required, many samples can be handled simultaneously.

Using this modified procedure for preparing templates for transcription, we expressed 13,364 human proteins from entry clones that were randomly chosen and grouped into 9,351 clusters. We fused C-terminal V5 or 6His tags to ORFs of the clones (destination vectors pEW-3VH or pEW-3H) and separated the expressed proteins into soluble and insoluble fractions by

centrifugation at 19,000g for 20 min. We separated the samples by SDS-PAGE and detected the human proteins by either western blotting with antibodies to V5 or to 6His tags, or by radioisotopic labeling. We found that 12,996 clones (97.2%) produced proteins. In 12,682 clones (97.6%) among those expressed, proteins were detected in the soluble fraction (for SDS-PAGE images and other relevant data, see <http://www.hgpd.jp/>). We used the program SOSUI¹³ for secondary structure prediction, and it predicted that 3,040 proteins (24.0%) out of 12,682 soluble proteins would contain at least a single transmembrane domain.

We next randomly picked 57 out of the 365 clones that did not produce any detectable protein in the analysis described above and expressed them in pEW-5SG3Ven which encodes the cloned protein with a fluorescent tag. In all cases we detected fluorescence signals (**Supplementary Fig. 4** online). We then randomly picked 29 clones out of the 314 clones that expressed but did not produce any detectable soluble proteins in the first round of expression analysis, and expressed them in pEW-5SG3Ven. Again, we detected fluorescence signals in both the total and the soluble fraction in all cases (**Supplementary Fig. 5** online). Therefore, we assumed that the wheat germ extract system could be used to produce essentially all the proteins encoded in the Gateway entry clones.

To evaluate the average amounts of total and soluble proteins per reaction (150 µl of bilayer reaction¹², which contains wheat germ extract and mRNA in the lower layer and amino acids, ATP, GTP and buffer in the upper layer), we randomly expressed 96 proteins and analyzed them using coomassie brilliant blue staining. The average quantities of total and soluble human proteins per reaction were 4.2 µg and 2.6 µg respectively. This represented 1.6% and 1.0% of the total protein (254 µg) in each bilayer reaction (**Supplementary Fig. 6a** and **Supplementary Table 3** online). After purification using a GST tag, average protein recovery was ~23.8% and purity was ~50%, yielding a purification rate of about 29-fold (**Supplementary Fig. 6b**). The expression system was easily scaled: we obtained about 160 µg of TDP1 in 6 ml of bilayer reaction (**Supplementary Fig. 6c**).

We observed many proteins that migrated differently from what we expected. Discrepancies of apparent molecular weight determined by SDS-PAGE and the calculated molecular weight have been reported in a variety of proteins^{14,15}. Some proteins that migrated slower than expected had a higher content of acidic amino acids, suggesting that acidic amino acids could inhibit

Table 1 | Summary of Gateway entry clones with their cDNA clone sources

Source	Number of cDNA clones from each source	Total of clones	Number of Gateway entry clones		
			N type ^a	F type ^b	Both N and F types
FLJ ^c	18,235	29,560	12,283	17,277	11,323
MGC ^d	3,114	3,482	365	3,117	354
Others ^e	136	233	106	127	97
Total	21,485	33,275	12,754	20,521	11,774

^aClone harboring a translational termination codon. ^bClone deleting a translational termination codon.

^cFull-length human cDNA sequencing project^{2–4}. ^dUS Mammalian Gene Collection program⁵. ^eRT-PCR, 13 clones; chemical synthesis, 2 clones; and other resources, 121 clones.

For construction of Gateway entry clones, ORF regions of source cDNAs were PCR-amplified and recombined with the *attP* sites of the pDONR201 vector (**Supplementary Methods**).

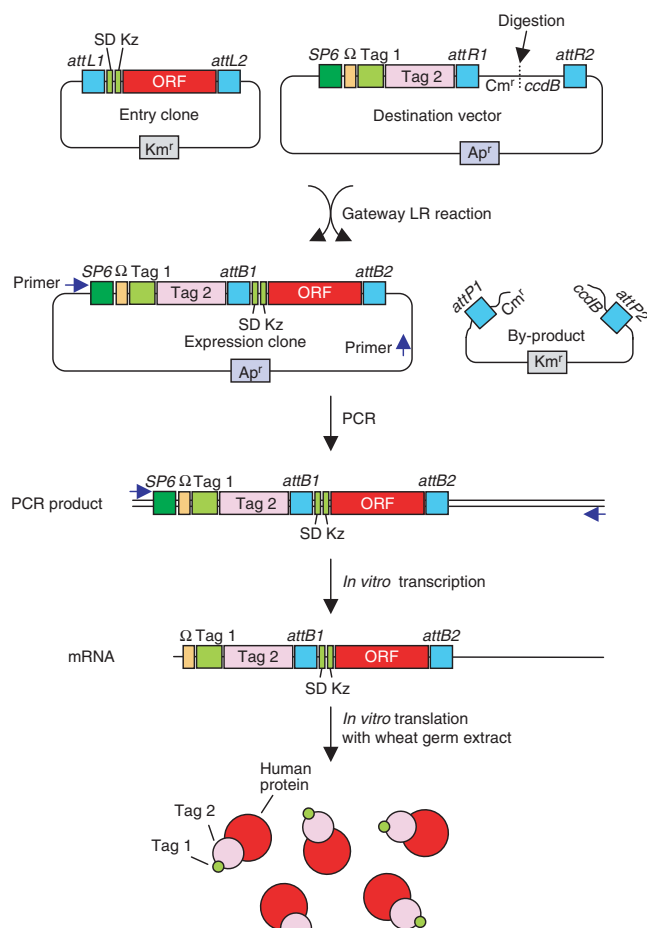


Figure 2 | Protein synthesis in the wheat germ cell-free system. Flow diagram of the stages in protein synthesis (LR reaction, PCR, transcription and translation). The destination vector DNA was digested by restriction endonucleases to increase the efficiency of the LR reaction two- to tenfold in most cases (unpublished data). The abbreviations used are as follows: *attL1*, *attL2*, *attR1*, *attR2*, *attB1*, *attB2*, *attP1* and *attP2* are Gateway recombination sites; SD, Shine-Dalgarno sequence; Kz, Kozak sequence; Km^r, kanamycin-resistance gene; Ap^r, ampicillin-resistance gene; Cm^r, chloramphenicol-resistance gene; *ccdB*, conditional lethal gene used as counter-selection; *SP6*, *SP6* promoter; Ω, Tobacco mosaic virus translational enhancer. Primers used for PCR amplification are indicated.

(addition of divalent cations and/or salt and pH variations), 58 phosphatases (77%) had enzymatic activity, of which 10 had weak activity in at least one buffer (**Supplementary Table 5** online). Although serine/threonine phosphatases specifically required Mn²⁺ or Mg²⁺ for enzymatic activity, protein tyrosine phosphatases and dual-specificity protein phosphatases showed no buffer specificity; 14 phosphatases, including those with inositol-lipid specificity¹⁸ or inactive phosphatase domains¹⁹, showed no or very faint enzymatic activity (**Supplementary Table 5**). To evaluate the specific activity of phosphatases produced in the wheat germ system, we chose CDC25B as an example and compared the specific activity of CDC25B produced in the wheat germ extract with that produced in *E. coli*²⁰. Both values were similar (**Supplementary Note** online), which means that proteins produced in wheat germ system, at least in some cases, display typical specific activities.

To test the substrate specificity of the phosphatases expressed *in vitro*, we incubated phosphatases PTPN5 and PTPN6 with their target proteins FYN and LYN, whose auto-phosphorylated tyrosine (p-Tyr420 in FYN²¹, p-Tyr397 in LYN²²) at the kinase catalytic domains is dephosphorylated by PTPN5 and PTPN6, respectively. We confirmed the specific dephosphorylation of FYN and LYN by these phosphatases (**Supplementary Fig. 9** online). These observations suggest that the wheat germ cell-free expression system not only produces proteins effectively, but produces proteins in the proper conformation.

Evaluation of cytokine activity by DNA microarrays

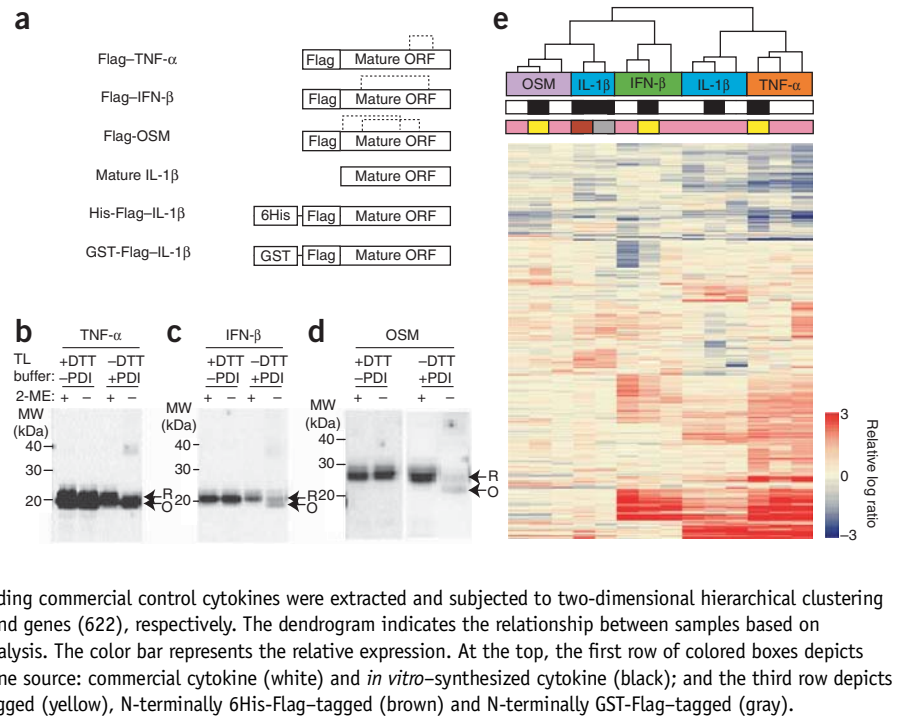
Many human proteins, including most secretory proteins, have one or more disulfide bonds that may be important in structural formation and/or function. Although the wheat germ cell-free expression system effectively produces active proteins, the formation of disulfide bonds may be impaired due to the presence of a reducing agent, dithiothreitol (DTT). Others have reported the successful production of single-chain antibodies with dual disulfide bonds in a DTT-deficient reaction mixture supplemented with PDI²³. We optimized *in vitro* translation methods using some cytokines as models, along with adjusting the concentration of DTT and adding protein disulfide isomerase (PDI). The model cytokines included tumor necrosis factor-α (TNF-α), interferon-β (IFN-β) and oncostatin M (OSM), all of which form disulfide bonds intramolecularly. The formation of internal disulfide bonds in IFN-β and OSM is required for their biological activity. We translated the cytokines in our wheat germ cell-free expression system under optimized nonreducing conditions to produce proteins tagged with the Flag tag at the N terminus (Flag-TNF-α, Flag-IFN-β and Flag-OSM). We confirmed their solubility (**Supplementary Fig. 10a,c-e** online) and analyzed them for disulfide bond formation by western blotting after nonreducing SDS-PAGE

binding to SDS in some cases¹⁴. Proteins containing hydrophobic regions have been shown to move faster, suggesting the binding of more SDS to proteins¹⁵. To examine this phenomenon using data from a large number of samples, we analyzed the sizes of 2,537 randomly chosen proteins (**Supplementary Table 4** online), of which 264 proteins (10.2%) migrated >20% slower than calculated. The fraction of slower-migrating proteins was greater among proteins that have a lower or higher isoelectric point compared to proteins that have a neutral isoelectric point (**Supplementary Fig. 7** online). In addition, 98 proteins (3.85%) migrated >20% faster than calculated and most of them had multiple transmembrane domains (**Supplementary Fig. 8** online). Although all irregular mobility cannot be explained, our data suggest that some of the discrepancies of apparent and calculated molecular weight can be attributed to the amount of SDS bound to the protein^{14,15}.

Expression and evaluation of protein phosphatases

After establishing an effective method of expressing various kinds of human proteins by the wheat germ cell-free expression system, we tested the enzymatic activities of these *in vitro*-expressed proteins. We selected 75 protein phosphatases to test based on previous reviews^{16,17} and public databases. We used an artificial substrate *p*-nitrophenyl phosphate, which displays activity with a broad spectrum of phosphatases. We expressed and purified these proteins using an N-terminal GST-tag (destination vector pEW-5SG). All 75 clones yielded proteins (data not shown). In biological activity assays using five different buffers of varying conditions

Figure 3 | Biological activity assays of *in vitro* synthesized cytokines. **(a)** Schematic representation of the construct of each model cytokine (IL-1 β , TNF- α , IFN- β and OSM) for synthesis of a mature ORF (processed ORF that is functional *in vivo*) and a tagged form (for TNF- α , the coding sequence of the extra-cellular soluble form was used). Disulfide bonds are indicated by dotted lines. **(b–d)** Western blotting analysis using anti-Flag. TNF- α **(b)**, IFN- β **(c)** and OSM **(d)** were synthesized under optimized nonreducing conditions in the wheat germ cell-free extraction system. The translation (TL) buffer conditions are designated, as well as the presence or absence of 2-mercaptoethanol (2-ME) in the SDS sample buffer. R, bands of the reduced form of the proteins; O, bands of oxidized form of the proteins (intramolecularly disulfide-bonded). **(e)** Overview of the gene expression assay in the HCAECs after *in vitro*-synthesized cytokine stimulation. The gene expressed after stimulation with Flag-TNF- α , Flag-IFN- β , Flag-OSM, 6His-Flag-IL-1 β , GST-Flag-IL-1 β , mature IL-1 β and the corresponding commercial control cytokines were extracted and subjected to two-dimensional hierarchical clustering analysis. The columns and rows indicate samples (14) and genes (622), respectively. The dendrogram indicates the relationship between samples based on dissimilarity coefficients calculated in the clustering analysis. The color bar represents the relative expression. At the top, the first row of colored boxes depicts the cytokine species; the second row depicts the cytokine source: commercial cytokine (white) and *in vitro*-synthesized cytokine (black); and the third row depicts the cytokine forms: mature (pink), N-terminally Flag-tagged (yellow), N-terminally 6His-Flag-tagged (brown) and N-terminally GST-Flag-tagged (gray).



with reducing or nonreducing buffer. A portion of all three proteins showed a mobility shift (Fig. 3a–d), indicating that the non-reducing condition of the wheat germ cell-free system yielded proteins with intramolecular disulfide bonds.

To assay the biological activity of these three cytokines, we treated human coronary artery endothelial cells (HCAECs) for 24 h with the three *in vitro*-synthesized cytokines and with the same three cytokines from a commercial source as controls, and obtained comprehensive gene expression profiles using DNA microarrays^{24–26}. We subjected the generated data matrix for the genes, in which at least one relative log ratio (Supplementary Methods) from among all the sample ratios was greater than 1.58 or less than –1.58 (622 genes), to two-dimensional hierarchical clustering analysis (Fig. 3e and Supplementary Table 6 online). Each pair of *in vitro*-synthesized and commercial control cytokines formed the same cluster with a high similarity in gene expression pattern, indicating that the *in vitro*-synthesized cytokines have biological activity, and our optimized nonreducing expression system effectively produces a large amount of biologically active, disulfide-bonded proteins.

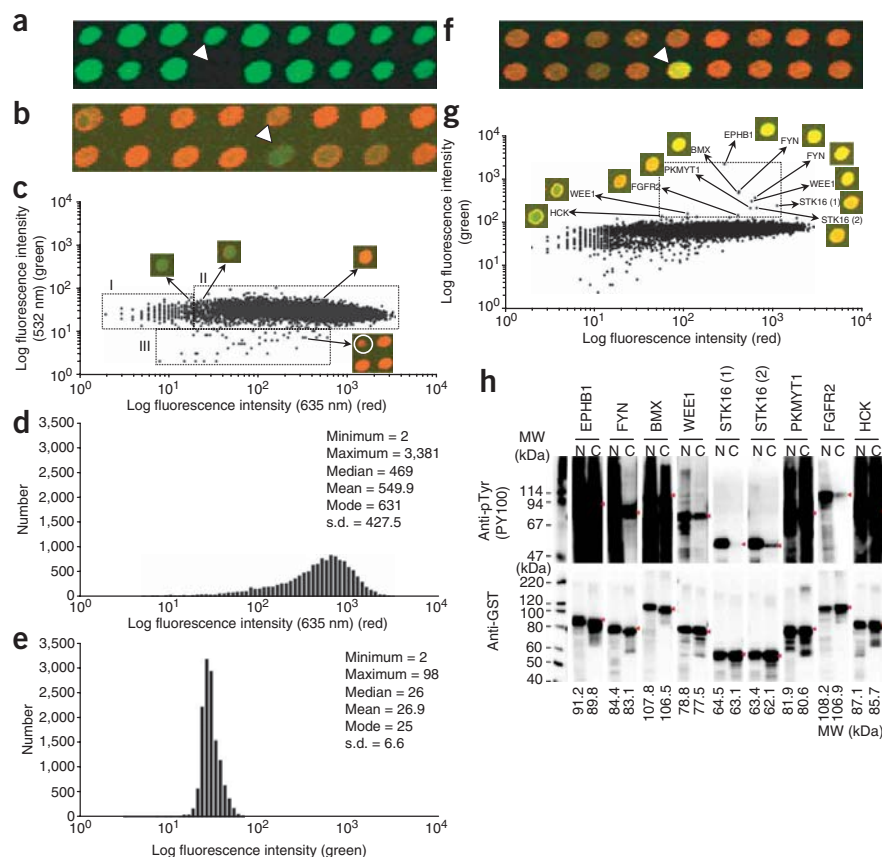
Many proteins, including cytokines, are post-translationally processed. To determine whether biologically active proteins can be obtained by digestion with protease in the wheat germ cell-free system, we used IL-1 β as the model. We synthesized mature IL-1 β N-terminally tagged with 6His and Flag tags (His-Flag-IL-1 β), mature IL-1 β N-terminally tagged with GST and Flag tags (GST-Flag-IL-1 β) (Fig. 3a, Supplementary Fig. 10b,g,h and Supplementary Table 7 online) and untagged mature IL-1 β generated via enterokinase cleavage of 6His-Flag-IL-1 β at the Flag tag site (Supplementary Fig. 10f). The results of the assessments according to the gene expression profiles from HCAECs treated with the above three forms of IL-1 β proved that mature IL-1 β and commercial IL-1 β formed a cluster, indicating that mature IL-1 β has the same activity as the commercial IL-1 β as a result of successful

processing by the protease. Notably, 6His-Flag-IL-1 β and GST-Flag-IL-1 β that formed the same cluster but belonged to other clusters than mature IL-1 β , suggesting negative influence of N-terminal tags on the biological activity of IL-1 β . Consistent with this result, a drastic decrease in IL-1 β activity had been reported when additional sequences are fused on the N-terminal of the mature protein²⁷.

Protein microarrays

Next we determined whether the wheat germ extract system can be used to make protein microarrays. We expressed 13,277 human proteins (Supplementary Table 8 online) labeled with GST tags at the N terminus using our wheat germ cell-free protein synthesis system. We printed the expressed GST-fusion proteins on glass slides as a protein microarray directly from the reaction mixture of the wheat germ system without purification using an arraying system for DNA microarrays identical to that described above. As we noticed that the reaction mixture contains a constituent(s) with intrinsic green fluorescence (Supplementary Fig. 11a online), we scanned the printed protein microarray using the scanning apparatus for DNA microarrays described above and evaluated the presence or absence of spots representing the printed reaction mixture (Fig. 4a). We found that 99.86% of the positions that we assumed to be printed contained green fluorescence signals, thus confirming that the system we established for fabricating DNA microarrays is directly applicable to the manufacture of protein microarrays. Subsequently, to assess the amount of the synthesized proteins on the spots, we stained the printed protein microarray with an antibody to the GST tag (anti-GST) and an Alexa Fluor 647-labeled antibody to mouse immunoglobulin gamma 2a (anti-mouse IgG2a), and then scanned them using the scanning conditions established for a DNA microarray hybridized with the dual fluorescence described above for gene expression analysis (Fig. 4b and Supplementary Fig. 11b). We performed a scatter plot

Figure 4 | Protein microarrays. (a) A representative image of a protein microarray obtained using a standard scanning apparatus for DNA microarrays, operated under default conditions installed for dual-color fluorescence analysis. Spots printed with a reaction mixture of *in vitro*-synthesized protein are weakly recognized (dark green stain) as the reaction mixture contains a constituent(s) with intrinsic green fluorescence detected under the same conditions. The white arrowhead indicates a position harboring no reaction mixture, reflecting a failure during the printing process. (b) A representative image of the protein microarray after the first scanning and subsequent staining with an anti-GST and an Alexa 647-labeled anti-mouse IgG2a that provides red fluorescence signals. The white arrowhead indicates a spot with no binding to the anti-GST, reflecting a failure of the *in vitro* protein synthesis. (c) Scatter plots representing the results of staining with anti-GST. The horizontal axis represents red fluorescence intensities, reflecting the amount of synthesized proteins on the spots, and the vertical axis represents green fluorescence intensities corresponding to the amount of the reaction mixture printed onto the spots. Groups I and II represent the subpopulations of plots with normal, nonreacted, round-shaped spots and those reacted with anti-GST, respectively. Group III contains plots with small irregular spots, indicating reaction with anti-GST. (d,e) Histogram representing the results shown in c for red (d) and green (e) fluorescence intensities. (f) A representative image of the protein microarray after the second scanning and subsequent staining with an anti-phosphotyrosine and an Alexa 555-labeled anti-mouse IgG1, which yields robust green fluorescence signals. The white arrowhead indicates a spot with binding to the antibody to phosphotyrosine, reflecting the presence of tyrosine residues generated by autophosphorylation during the *in vitro* protein synthesis with wheat germ extract. (g) Scatter plots representing the results of staining with anti-phosphotyrosine. Above the major horizontally distributed population, 11 plots are depicted with individual images of the spots and the gene symbols. These spots display robust signals highly stained with green fluorescence, reflecting the presence of the autophosphorylated proteins that differ markedly from the major population of spots. Two different clones for STK16 are indicated by (1) and (2). In case of FYN and WEE1, two spots are originated from the same clones. (h) Western blotting. Anti-phosphotyrosine (pTyr), PY100 (top), anti-GST (bottom). The molecular weights (MW) including the GST tags are indicated at the bottom. N, N-terminally tagged form; C, C-terminally tagged form.



analysis of the results of the scanning (Fig. 4c) and divided the scatter plots into three groups (I, II and III). Group I contained 238 spots that did not react with anti-GST, indicating that the success rate of the fusion protein synthesis was 98.2%. Groups II and III included spots that reacted with anti-GST, reflecting the detectable amount of the synthesized proteins. Group III contained irregular-shaped spots for which weak green fluorescence signals were detected, indicating that the amount of the reaction mixture printed on these spots was, for reasons unknown, less than that for the majority of the spots (Fig. 4c and unpublished data).

To evaluate the distribution of the fluorescence intensities depicted in the scatter plots mathematically, we generated histograms for red fluorescence (Fig. 4d) and for green fluorescence (Fig. 4e). The histograms and the calculated statistical values revealed that the green fluorescence was distributed with a single sharp peak, whereas the red fluorescence was distributed over a wide range of intensities. This indicated that the amount of printed reaction mixture was similarly maintained among the spots, whereas the amount of the synthesized proteins was heterogeneously differentiated among the spots. Thus, although our

protein-synthesis system exhibits nearly perfect efficiency for *in vitro* synthesis of individual proteins, the yields of the proteins were extremely variable, suggesting that yield should be monitored to be able to use the protein microarray efficiently in experiments.

To demonstrate the utility of protein microarrays in conjunction with a specific antibody, we reacted the microarrays with an antibody to phosphotyrosine (anti-phosphotyrosine) and an Alexa Fluor 555-labeled antibody to mouse immunoglobulin gamma 1 (anti-mouse IgG1) as a model system designed to leave the majority of spots unstained with the antibody but staining several spots as positive for the presence of phosphorylation during *in vitro* protein synthesis (Fig. 4f). We chose this system because (i) the wheat germ extract is assumed to contain no intrinsic tyrosine-phosphorylation activity²⁸, (ii) tyrosine kinases have autophosphorylation activities²⁹ and (iii) the protein microarrays that we manufactured include 29 previously identified protein tyrosine kinases (Supplementary Table 8). As expected, 11 spots corresponding to 8 genes were robustly stained (Fig. 4f,g), and we confirmed those signals by western blotting (Fig. 4h and Supplementary Table 9 online), whereas the majority of the spots exhibited a horizontal distribution similar to that shown in

Figure 4c. Among 8 positive genes, 7 were known protein tyrosine kinases (EPHB1, FYN, BMX, WEE1, PKMYT1, FGFR2 and HCK) and there was one protein serine/threonine kinase (STK16; see **Supplementary Note** for discussion). Twenty-one protein tyrosine kinases were not detected by our microarray. This could be due to a lack (or low level) of intrinsic protein tyrosine kinase activities, a lack of sensitivity in our microarray or a low level of protein expression.

Here we used protein microarrays manufactured by direct printing with an unpurified reaction mixture of high-throughput *in vitro*-synthesized proteins, indicating that we can successfully apply a system for DNA microarray printing and scanning to protein microarrays. Although the efficiency of the *in vitro* synthesis was almost 100% for 13,277 individual proteins, the yields of these proteins exhibited wide variability. Thus, we should monitor the amounts of individual proteins on spots to identify proteins of interest that are detectable with a probe such as a specific antibody. For successful monitoring and detection, we emphasize the importance of staining with dual-color indicators and subsequent analysis of the distribution of signals obtained from individual data elements on scatter plots and histograms, analogous to the well-established fluorescence-activated cell sorting analysis.

DISCUSSION

So far, we constructed 33,275 entry clones originating from 21,485 human high-quality cDNAs. Others have reported the construction of 12,212 entry clones³⁰ with which the ORFeome Collaboration was formed⁸ (<http://www.orfeomecollaboration.org/html/>). A sizeable proportion of the ORFeome clones are F-type ones; therefore proteins that possess a functional domain at the C terminus might not have full biological activity when proteins are expressed based on these clones (for example, see **Fig. 4h**).

Until now, comprehensive protein analysis has been mainly based on *in vivo* proteome research. We efficiently expressed active human proteins in the wheat germ cell-free system and produced protein microarrays by direct spotting of crude human proteins on glass slides. Others have described proteome chips featuring 6,566 GST tag-labeled yeast proteins³¹. The major advantage of our proteome chip compared to their chip is the simplicity, albeit chips made with purified proteins give better results (data not shown). The use of this protein supply method would make it possible to easily and effectively reconstitute and analyze not only *in vitro* reactions of the enzyme-substrate recognition, but also protein-protein interactions, post-translational modifications, processing and others. In conclusion, the 'human protein factory' has a wide range of capabilities and excellent functionality, and should greatly contribute to advancing post-genomic research.

METHODS

Evaluation of protein phosphatase activity. Protein phosphatases were synthesized by the standard bilayer method¹². The expressed crude proteins were purified using glutathione-Sepharose 4B (GE Healthcare) and subjected to an activity assay. The reaction mixture (5 μ l) contained 20 mM *p*-nitrophenyl phosphate and GST-purified phosphatase (3.6–480 ng) in each buffer. After incubating the reaction mixture at 30 °C for 15 h, the reaction was stopped by adding 2 μ l of 2 N NaOH. Phosphatase activities (optical density at 405 nm (OD₄₀₅) value) were measured by means of NanoDrop 1,000 (Thermo Scientific). The activity was

normalized per 100 ng of protein. The following five buffers were used: λ -PPase reaction buffer (New England Biolabs) containing 50 mM Tris-HCl (pH 7.5), 2 mM MnCl₂, 5 mM DTT and 0.01% Brij35; NEBuffer 3 (New England Biolabs) containing 50 mM Tris-HCl (pH 7.9), 10 mM MgCl₂, 100 mM NaCl and 1 mM DTT; YOP reaction buffer (New England Biolabs) containing 50 mM Tris-HCl (pH 7.0), 100 mM NaCl, 5 mM DTT, 2 mM EDTA and 0.01% Brij35; acidic buffer¹⁸ containing 50 mM MES (pH 6.0), 5 mM DTT and 1 mM EDTA; and imidazole-based buffer³² containing 25 mM imidazole (pH 7.2) and 10 mM DTT.

Evaluation of cytokine activity. Processed-type Gateway entry clones were constructed by inserting the coding sequence of the mature form of each cytokine (TNF- α , IFN- β and OSM; **Supplementary Table 7**) and the Flag tag. Cytokines were synthesized under optimized nonreducing conditions of the wheat germ cell-free expression system. DNA microarrays were prepared and gene expression profiles were acquired according to published methods^{24,26}.

Protein microarrays. Human proteins (13,277) were *in vitro*-synthesized with a GST tag using a wheat germ cell-free protein synthesis system with the total reaction volume of 30 μ l and printed on an aminosilan-coated glass slide (Matsunami) using a printing apparatus originally custom made for DNA microarrays^{25,26}. All the proteins printed are listed in **Supplementary Table 8**. After the printing, the protein microarray was scanned with a GenePix 4000A scanner (Axon instruments) and an initial image was obtained under unstained conditions. The protein microarray was subsequently subjected to blocking with a Blocking One-P reagent (Nacalai Tesque) at room temperature (24–26 °C) for 1 h, followed by staining with an anti-GST (500 ng ml⁻¹; Nacalai Tesque) at room temperature for 1 h and an Alexa Fluor 647-labeled anti-mouse IgG2a (400 ng ml⁻¹; Molecular Probes) at room temperature for 1 h. After washing with 0.5% BSA-MBST buffer (0.5% BSA, 25 mM MOPS, 150 mM NaCl, 0.2% Tween20), the stained microarray was scanned similarly, and a second image was obtained. The protein microarray was then subjected to staining with a mouse anti-phosphotyrosine (P-Tyr-100, 100 ng ml⁻¹; Cell Signaling Technology) at room temperature for 1 h and an Alexa Fluor 555-labeled anti-mouse IgG1 (400 ng ml⁻¹; Molecular Probes) at room temperature for 1 h. After the final staining, the protein microarray was washed with the solution described above and scanned.

Additional methods. Detailed methods for construction of Gateway entry clones, N- and C-terminal cloning methods, protein expression in the wheat germ cell-free system, preparation of mature IL-1 β , analysis of disulfide bond formation, effects of the cytokines on endothelial cells and the DNA microarrays are available in **Supplementary Methods**.

Resource availability. Gateway entry clones will be made available to all qualified potential users in both academia and industry who have agreed to the conditions of the materials transfer agreement. They will be distributed by the National Institute for Technology and Evaluation (Japan) Biological Resource Center (<http://www.nbrc.nite.go.jp/e/hgentry-e.html>), Department of Biotechnology (see <http://www.hgpd.jp/>).

Accession codes. DNA Data Bank of Japan (via Center for Information Biology gene Expression database (CIBEX)): CBX39.

Note: Supplementary information is available on the Nature Methods website.

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AUTHOR CONTRIBUTIONS

N.G., Yo.K., Ya.K., S.T., Ka.M., A.W., T.I., S.W. and N.N. designed and supervised the project. Ay.M., Yo.K., J.-i.I., N.G. and N.N. wrote the manuscript. T.I., A.W., J.-i.Y., Ko.K., T.N., T.A. and R.K. determined ORF regions and selected templates. T.A., N.K., R.K., K.I., At.M., T.O., Ki.K., Yuk.S., Ts.S., S.S., Ya.K., K.Y., N.S. and S.T. produced Gateway entry clones. Y.I., K.-i.K., Y.T. and Ki.M. sequenced Gateway entry clones. K.Y., R.S., Y.M., C.K. and N.S. re-examined identity and stability of Gateway entry clones at the final step. B.K., A.S., T.K., Mar.M., H.T. and N.K. produced Gateway destination vectors. R.M., Ay.M., A.F., Yut.S., To.S., Mas.M., To.T., H.K. and H.T. performed preliminary analysis for determining best conditions for protein production and other experimental protocols. A.F., Yut.S., H.Y., B.K., A.S., T.K., S.N. and M.K. expressed proteins and performed SDS-PAGE. A.F., To.S., To.T., Mas.M. and Yo.K. analyzed the SDS-PAGE data. A.F., Ay.M. and Yo.K. analyzed phosphatase activity. Ay.M., Ta.T., R.H., Y.Y., E.I., A.N. and J.-i.I. analyzed cytokine activity by DNA microarrays. A.F., H.Y., C.K., Yut.S., Yo.K. and J.-i.I. produced protein microarrays. A.F., Yo.K. and J.-i.I. analyzed data of protein microarrays. F.I. and Y.E. made comments and encouraged the idea.

COMPETING INTERESTS STATEMENT

The authors declare competing financial interests: details accompany the full-text HTML version of the paper at <http://www.nature.com/naturemethods/>.

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1. International Human Genome Sequencing Consortium. Finishing the euchromatic sequence of the human genome. *Nature* **431**, 931–945 (2004).
2. Ota, T. *et al.* Complete sequencing and characterization of 21,243 full-length human cDNAs. *Nat. Genet.* **36**, 40–45 (2004).
3. Kimura, K. *et al.* Diversification of transcriptional modulation: large-scale identification and characterization of putative alternative promoters of human genes. *Genome Res.* **16**, 55–65 (2006).
4. Otsuki, T. *et al.* Signal sequence and keyword trap *in silico* for selection of full-length human cDNAs encoding secretion or membrane proteins from oligo-capped cDNA libraries. *DNA Res.* **12**, 117–126 (2005).
5. Strausberg, R.L. *et al.* Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences. *Proc. Natl. Acad. Sci. USA* **99**, 16899–16903 (2002).
6. Wiemann, S. *et al.* Toward a catalog of human genes and proteins: sequencing and analysis of 500 novel complete protein coding human cDNAs. *Genome Res.* **11**, 422–435 (2001).
7. Nomura, N. *et al.* Prediction of the coding sequences of unidentified human genes. I. The coding sequences of 40 new genes (KIAA0001–KIAA0040) deduced by analysis of cDNA clones from human cell line KG-1. *DNA Res.* **1**, 251–262 (1994).
8. Temple, G. *et al.* From genome to proteome: developing expression clone resources for the human genome. *Hum. Mol. Genet.* **15**, R31–43 (2006).
9. Hartley, J.L., Temple, G.F. & Brasch, M.A. DNA cloning using *in vitro* site-specific recombination. *Genome Res.* **10**, 1788–1795 (2000).
10. Sawasaki, T., Ogasawara, T., Morishita, R. & Endo, Y. A cell-free protein synthesis system for high-throughput proteomics. *Proc. Natl. Acad. Sci. USA* **99**, 14652–14657 (2002).
11. Endo, Y. & Sawasaki, T. Cell-free expression systems for eukaryotic protein production. *Curr. Opin. Biotechnol.* **17**, 373–380 (2006).
12. Sawasaki, T. *et al.* A bilayer cell-free protein synthesis system for high-throughput screening of gene products. *FEBS Lett.* **514**, 102–105 (2002).
13. Hirokawa, T., Boon-Chieng, S. & Mitaku, S. SOSUI: classification and secondary structure prediction system for membrane proteins. *Bioinformatics* **14**, 378–379 (1998).
14. Takano, E. *et al.* Pig heart calpastatin: identification of repetitive domain structures and anomalous behavior in polyacrylamide gel electrophoresis. *Biochemistry* **27**, 1964–1972 (1988).
15. Robinson, N.C. & Tanford, C. The binding of deoxycholate, Triton X-100, sodium dodecyl sulfate, and phosphatidylcholine vesicles to cytochrome b5. *Biochemistry* **14**, 369–378 (1975).
16. Alonso, A. *et al.* Protein tyrosine phosphatases in the human genome. *Cell* **117**, 699–711 (2004).
17. Moorhead, G.B., Trinkle-Mulcahy, L. & Ulke-Lemee, A. Emerging roles of nuclear protein phosphatases. *Nat. Rev. Mol. Cell Biol.* **8**, 234–244 (2007).
18. Taylor, G.S., Maehama, T. & Dixon, J.E. Inaugural article: myotubularin, a protein tyrosine phosphatase mutated in myotubular myopathy, dephosphorylates the lipid second messenger, phosphatidylinositol 3-phosphate. *Proc. Natl. Acad. Sci. USA* **97**, 8910–8915 (2000).
19. Wishart, M.J. & Dixon, J.E. PTEN and myotubularin phosphatases: from 3-phosphoinositide dephosphorylation to disease. *Trends Cell Biol.* **12**, 579–585 (2002).
20. Honda, R., Ohba, Y., Nagata, A., Okayama, H. & Yasuda, H. Dephosphorylation of human p34^{cdc2} kinase on both Thr-14 and Tyr-15 by human cdc25B phosphatase. *FEBS Lett.* **318**, 331–334 (1993).
21. Nguyen, T.H., Liu, J. & Lombroso, P.J. Striatal enriched phosphatase 61 dephosphorylates Fyn at phosphotyrosine 420. *J. Biol. Chem.* **277**, 24274–24279 (2002).
22. Somani, A.K. *et al.* The SH2 domain containing tyrosine phosphatase-1 down-regulates activation of Lyn and Lyn-induced tyrosine phosphorylation of the CD19 receptor in B cells. *J. Biol. Chem.* **276**, 1938–1944 (2001).
23. Kawasaki, T., Gouda, M.D., Sawasaki, T., Takai, K. & Endo, Y. Efficient synthesis of a disulfide-containing protein through a batch cell-free system from wheat germ. *Eur. J. Biochem.* **270**, 4780–4786 (2003).
24. Miura, A. *et al.* Differential responses of normal human coronary artery endothelial cells against multiple cytokines comparatively assessed by gene expression profiles. *FEBS Lett.* **580**, 6871–6879 (2006).
25. Ito, E. *et al.* A tetraspanin-family protein, T-cell acute lymphoblastic leukemia-associated antigen 1, is induced by the Ewing's sarcoma-Wilms' tumor 1 fusion protein of desmoplastic small round-cell tumor. *Am. J. Pathol.* **163**, 2165–2172 (2003).
26. Sakamoto, A. *et al.* Influence of inhalation anesthesia assessed by comprehensive gene expression profiling. *Gene* **356**, 39–48 (2005).
27. Jobling, S.A. *et al.* Biological activity and receptor binding of human prointerleukin-1 beta and subpeptides. *J. Biol. Chem.* **263**, 16372–16378 (1988).
28. Miranda-Saavedra, D. & Barton, G.J. Classification and functional annotation of eukaryotic protein kinases. *Proteins* **68**, 893–914 (2007).
29. Lowell, C.A. Src-family kinases: rheostats of immune cell signaling. *Mol. Immunol.* **41**, 631–643 (2004).
30. Lamesch, P. *et al.* hORFeome v3.1: a resource of human open reading frames representing over 10,000 human genes. *Genomics* **89**, 307–315 (2007).
31. Zhu, H. *et al.* Global analysis of protein activities using proteome chips. *Science* **293**, 2101–2105 (2001).
32. Plutzky, J., Neel, B.G. & Rosenberg, R.D. Isolation of a src homology 2-containing tyrosine phosphatase. *Proc. Natl. Acad. Sci. USA* **89**, 1123–1127 (1992).

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Human protein factory for converting the transcriptome into an *in vitro*–expressed proteome

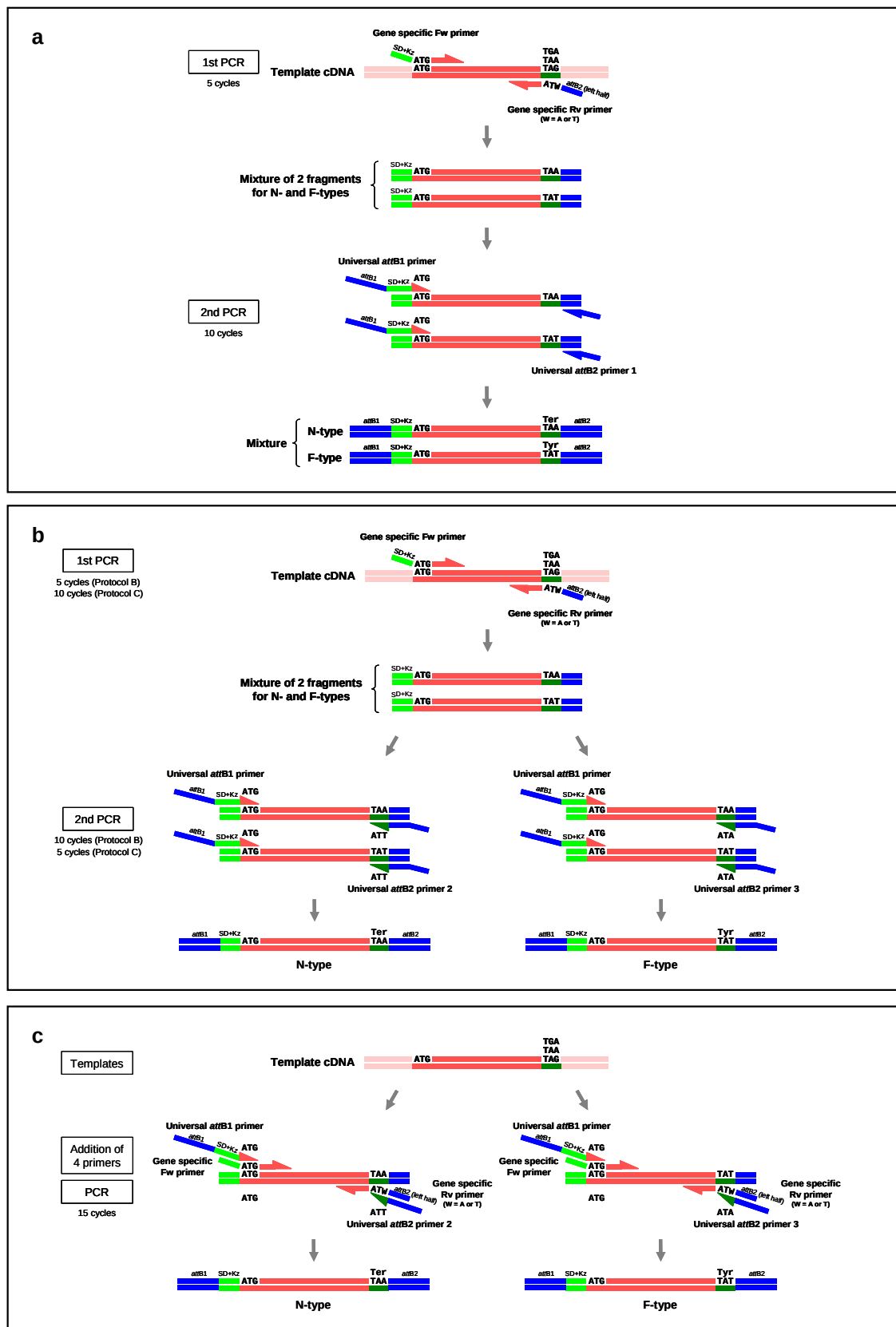
Naoki Goshima, Yoshifumi Kawamura, Akiko Fukumoto, Aya Miura, Reiko Honma, Ryohei Satoh, Ai Wakamatsu, Jun-ichi Yamamoto, Kouichi Kimura, Tetsuo Nishikawa, Taichi Andoh, Yuki Iida, Kumiko Ishikawa, Emi Ito, Naoko Kagawa, Chie Kaminaga, Kei-ichi Kanehori, Bunsei Kawakami, Kiyokazu Kenmochi, Rie Kimura, Miki Kobayashi, Toshihiro Kuroita, Hisashi Kuwayama, Yukio Maruyama, Kiyoshi Matsuo, Kazuyoshi Minami, Mariko Mitsubori, Masatoshi Mori, Riyo Morishita, Atsushi Murase, Akira Nishikawa, Shigemichi Nishikawa, Toshihiko Okamoto, Noriko Sakagami, Yutaka Sakamoto, Yukari Sasaki, Tomoe Seki, Saki Sono, Akio Sugiyama, Tsuyoshi Sumiya, Tomoko Takayama, Yukiko Takayama, Hiroyuki Takeda, Takushi Togashi, Kazuhide Yahata, Hiroko Yamada, Yuka Yanagisawa, Yaeta Endo, Fumio Imamoto, Yasutomo Kisu, Shigeo Tanaka, Takao Isogai, Jun-ichi Imai, Shinya Watanabe & Nobuo Nomura

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Supplementary Figure 2	List of Gateway destination vectors.
Supplementary Figure 3	Comparison of activities of various protein expression systems.
Supplementary Figure 4	A reanalysis of clones which did not produce any protein in the first round of expression analysis.
Supplementary Figure 5	A reanalysis of clones which produced only insoluble proteins in the first round of expression analysis.
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Supplementary Note	Comparison of phosphatase activity of human CDC25B expressed in wheat germ cell-free and <i>E. coli</i> systems. Possible protein tyrosine kinase activity detected in STK16.

Note: Supplementary Tables 2 and 8 are available on the Nature Methods website.

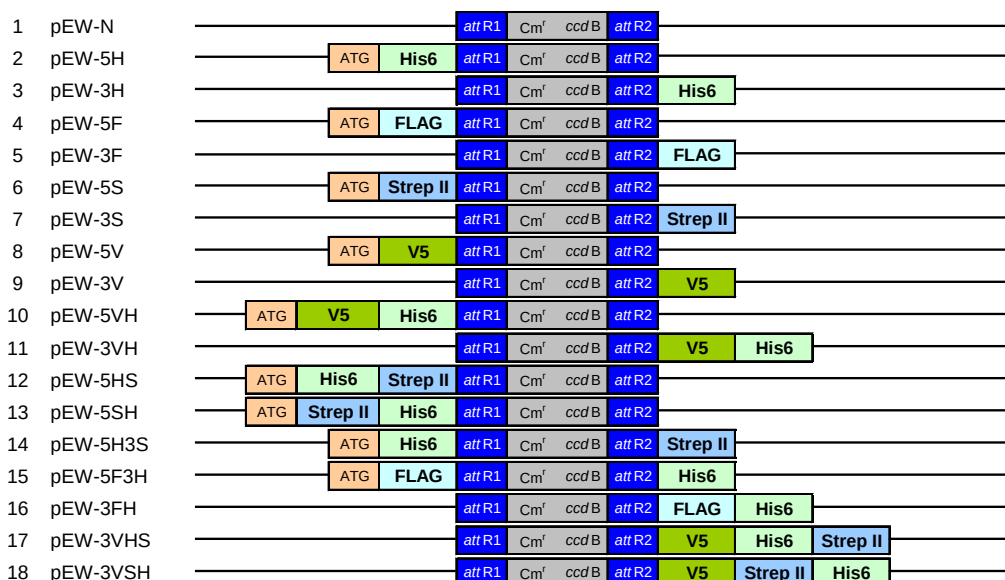
Supplementary Figure 1. Construction of Gateway entry clones.



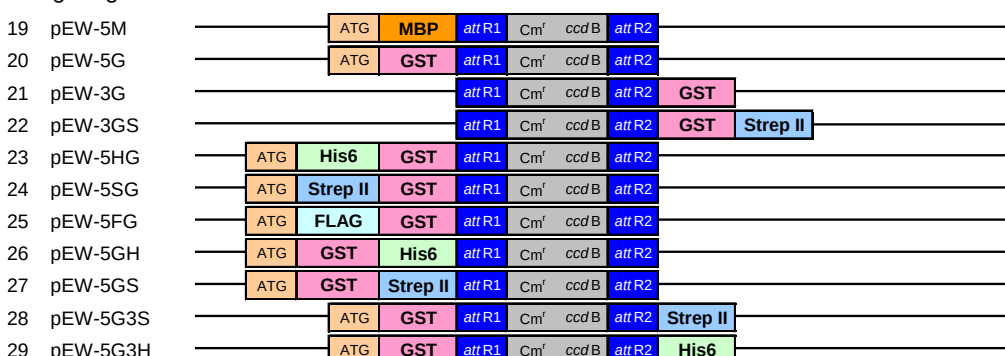
a, The two-step non-selective method (Protocol A). **b**, The two-step selective method (Protocols B and C). **c**, The one-step selective method (Protocols D, E and F). **a–c**, The PCR amplification of the ORF regions is illustrated. Each specific region is colored as follows: the vector region of the template, pink; SD (Shine-Dalgarno sequence) + Kz (Kozak sequence), light green; ATG (initiation codon), red; ORF (open reading frame), red; ter (termination codon), green; *attB1*, *attB2* (Gateway recombination site), blue. Those PCR-amplified and *attB*-attached fragments made by one of the methods described above were recombined with pDONR201 to produce entry clones.

Supplementary Figure 2. List of Gateway destination vectors.

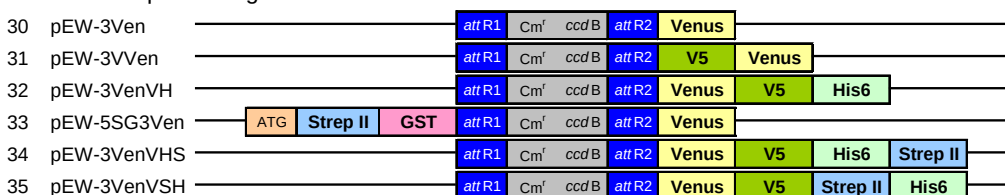
a Small tag



b Large tag



c Fluorescent protein tag



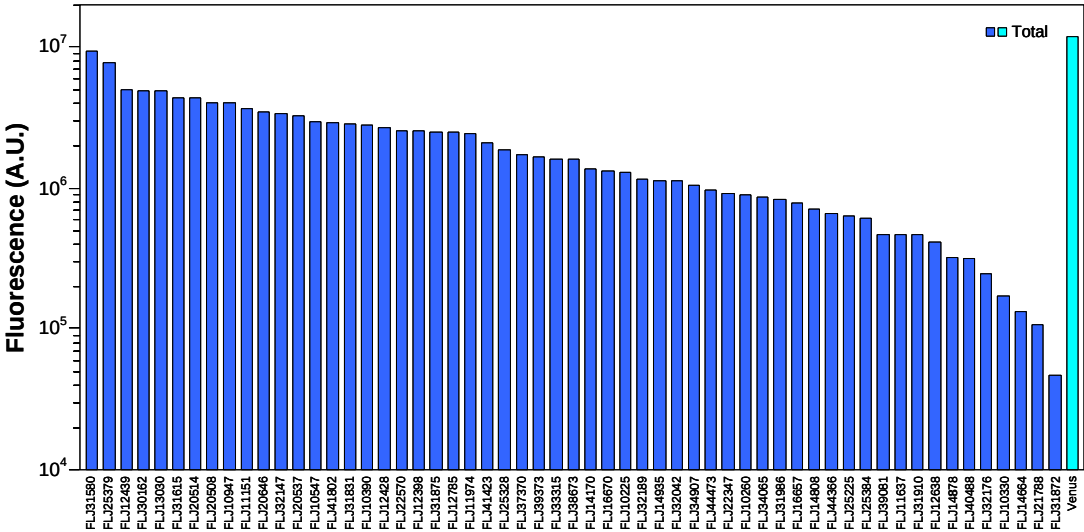
a, For addition of either single or multiple small tags. **b**, For addition of a GST or MBP-tag. In some cases, small tags can also be attached. **c**, For addition of a fluorescent protein tag. **a–c**, pEW-N was constructed by inserting a Gateway conversion cassette (Invitrogen) at the multicloning site of pEU3b¹. Destination vectors were produced by inserting tag-fragments to pEW-N. Only the tag regions of the vector sequences are illustrated. The abbreviations used are as follows: attR1, attR2, Gateway recombination sites; Cm^r, chloramphenicol resistance gene; ccdB, conditional lethal gene used as counter-selection; His6, hexahistidine tag; Strep II, Strep tag II; V5, V5 epitope tag; MBP, maltose-binding protein; GST, glutathione S-transferase; Venus, modified eYFP². An ATG initiation codon was placed at the N-terminal tag.

Supplementary Figure 3. Comparison of activities of various protein expression systems.

Number	Resource of ORF (FLJ ID)	Mw (kDa)	TM	Wheat germ (in vitro)		<i>E. coli</i> (in vitro)		<i>E. coli</i> (in vivo)	Cultured cell (DM2)	Cultured cell (CHO)
				5'GST	3'His	5'GST	3'His	3'His	3'His	3'TAP
1	FLJ20659	10.4	0	○	○	○	×	○	○	○
2	FLJ21903	14.7	0	○	○	×	×	×	○	×
3	FLJ20616	15.2	0	○	○	×	○	○	○	○
4	FLJ20852	17.1	0	○	○	×	N.D.	○	×	×
5	FLJ22873	17.8	0	○	○	×	×	○	○	○
6	FLJ21700	18.9	0	○	○	×	×	○	○	○
7	FLJ22881	20.0	0	○	○	○	×	○	○	○
8	FLJ20819	23.5	0	○	○	×	×	△	○	○
9	FLJ22273	25.3	0	○	○	○	×	○	○	○
10	FLJ22538	29.6	0	○	○	○	×	×	×	×
11	FLJ22880	33.3	0	○	○	○	×	○	○	○
12	FLJ20621	33.3	0	○	○	○	×	△	○	○
13	FLJ20855	33.5	0	○	○	○	×	○	○	○
14	FLJ21182	33.7	0	○	○	○	×	○	○	○
15	FLJ21486	34.9	0	○	○	○	×	○	○	○
16	FLJ22325	35.7	0	○	○	○	×	○	○	○
17	FLJ20586	37.0	0	○	○	○	○	×	○	○
18	FLJ22320	38.2	0	○	○	○	×	×	○	○
19	FLJ22491	39.0	0	○	○	○	×	○	○	N.D.
20	FLJ21861	50.1	0	○	○	○	○	△	○	×
21	FLJ21235	50.1	0	○	○	○	○	△	×	○
22	FLJ22470	52.7	0	○	○	○	×	△	△	N.D.
23	FLJ22779	57.3	0	○	○	○	○	×	○	N.D.
24	FLJ20768	66.9	0	○	○	○	×	△	○	○
25	FLJ22818	91.3	0	○	○	×	○	○	×	×
26	FLJ21907	101.3	0	○	○	△	×	△	×	×
27	FLJ21076	7.0	1	○	△	×	×	△	○	N.D.
28	FLJ21791	10.1	1	○	○	○	×	○	○	×
29	FLJ21558	15.3	2	○	○	×	×	○	○	×
30	FLJ20556	17.4	1	○	×	×	×	○	×	×
31	FLJ20489	25.7	1	○	△	×	×	×	×	○
32	FLJ20507	25.8	4	○	○	○	N.D.	N.D.	○	○
33	FLJ12627	26.0	1	○	×	○	×	△	×	×
34	FLJ10199	27.8	2	○	×	○	×	○	△	△
35	FLJ10191	28.6	4	○	○	×	×	×	×	N.D.
36	FLJ12791	32.3	4	○	○	○	×	×	×	○
37	FLJ10099	35.1	1	○	○	○	×	△	△	N.D.
38	FLJ12133	36.2	3	○	○	×	×	×	○	○
39	FLJ21879	37.7	7	△	△	○	×	×	×	○
40	FLJ11856	45.8	10	○	△	○	×	×	×	N.D.
41	FLJ10583	46.3	3	○	○	○	×	×	×	×
42	FLJ12397	48.5	1	○	○	×	×	×	△	△
43	FLJ12769	51.2	1	○	○	×	×	×	○	×
44	FLJ10494	53.9	9	○	○	△	×	△	×	N.D.
45	FLJ12646	63.1	1	○	○	×	×	×	△	N.D.
46	FLJ22958	64.7	8	○	○	○	×	×	×	N.D.
47	FLJ10375	68.3	9	○	○	×	×	△	×	N.D.
48	FLJ12756	76.1	14	○	○	×	×	×	×	×
49	FLJ10407	76.3	7	△	△	×	×	×	×	×
50	FLJ10572	80.1	1	○	×	×	×	△	○	○

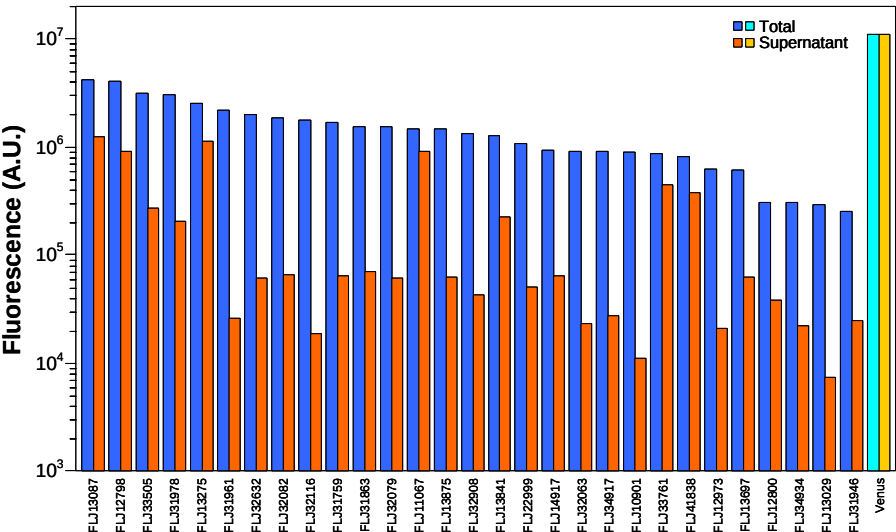
Twenty six clones for soluble protein category (Transmembrane (TM),0; Molecular weight (Mw), 10.4–101.3 kDa) and 24 clones for membrane protein category (TM, 1–14; Mw, 7.0–80.1 kDa) were chosen from our Gateway entry clone library. These entry clones were converted to expression clones harboring N-terminal GST (5'GST), C-terminal His (3'His) or C-terminal TAP (3'TAP) by the Gateway system, and were expressed in various expression systems, such as wheat germ cell-free system, *E. coli* in vitro expression system, *E. coli* in vivo expression system, and MD2 and CHO cultured cell expression system. Expressed proteins were separated with SDS-PAGE and detected by CBB staining or autoradiography of isotope-labeled Met or Leu (the specific activity of radioisotopes was adjusted to give equal signals to CBB-staining). The evaluation of protein expression done by visual inspection, is as follows: circle, high protein-expression; triangle, low protein-expression; cross, no protein-expression; N.D., no data.

Supplementary Figure 4. A reanalysis of clones which did not produce any protein in the first round of expression analysis.



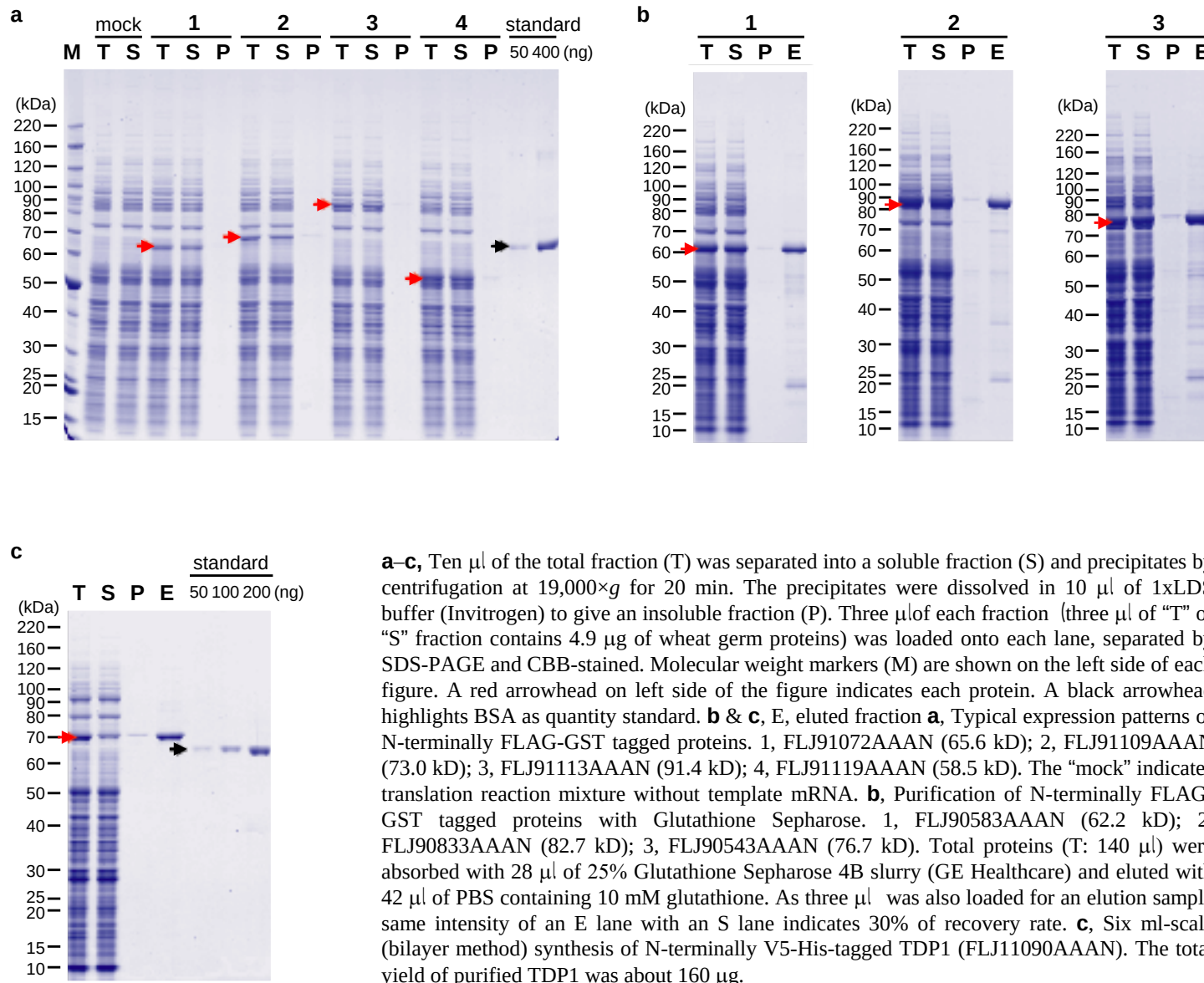
Fifty-seven clones were picked out of 365 clones which did not produce any detectable proteins. pEW-5SG3Ven was used as the destination vector. Protein synthesis was conducted by the standard bilayer method. The total fractions of the synthesized proteins were analyzed. The fluorescence was detected using a Typhoon 9200 (GE Healthcare) with SYAG laser (532 nm) excitation and a 526 SP filter for emission. A fluorescence value (Y-axis) is presented in arbitrary units (A.U.). The background level was 1,191 A.U. Values which were subtracted from the background are shown. A Venus protein fused only with an ATG codon, which was expressed well and was used as a control, is designated as “Venus.”

Supplementary Figure 5. A reanalysis of clones which produced only insoluble proteins in the first round of expression analysis.

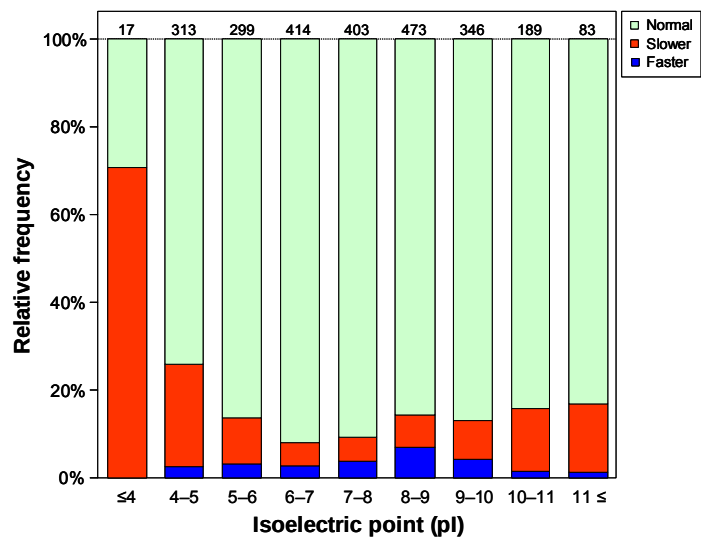


Twenty-nine clones were picked out of 314 clones which expressed but did not produce soluble proteins. pEW-5SG3Ven was used as the destination vector. Protein synthesis was conducted by the standard bilayer method. The soluble fractions of the synthesized proteins were obtained by centrifugation at $19,000\times g$ for 20 min. The fluorescence was detected using a Typhoon 9200 (GE Healthcare) with SYAG laser (532 nm) excitation and a 526 SP filter for emission. Fluorescence values (Y-axis) are presented in arbitrary units (A.U.). Those of both total and supernatant fractions are presented. The background level was 1,191 A.U. Values which were subtracted from the background are shown. A Venus protein fused only with an ATG codon, which was expressed well and was used as a control, is designated as “Venus.”

Supplementary Figure 6. SDS-PAGE patterns of human proteins expressed in the wheat germ cell-free system.

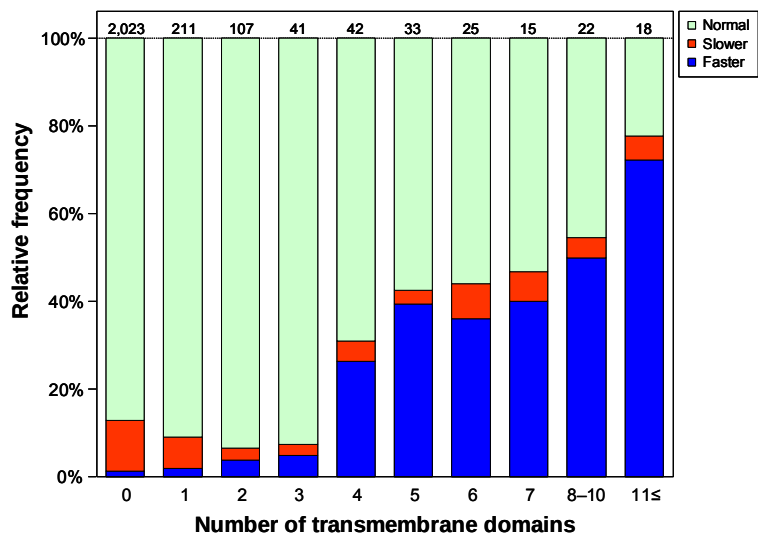


Supplementary Figure 7. Relationship between the isoelectric point and the mobility of proteins in SDS-PAGE.



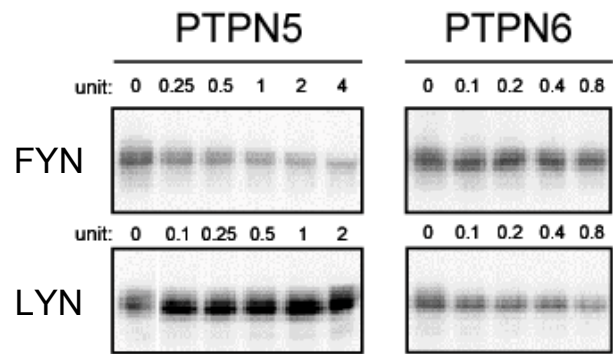
Two thousand five hundred and thirty-seven proteins are divided into 9 groups according to their isoelectric points. The number of clones in each group is represented at the top of each bar. Proteins were divided into 3 categories: faster-migrating (■), slower-migrating (■) and normal (■) proteins. Relative abundance of the proteins is shown for each category.

Supplementary Figure 8. Relationship between the number of transmembrane domains and mobility of proteins in SDS-PAGE.



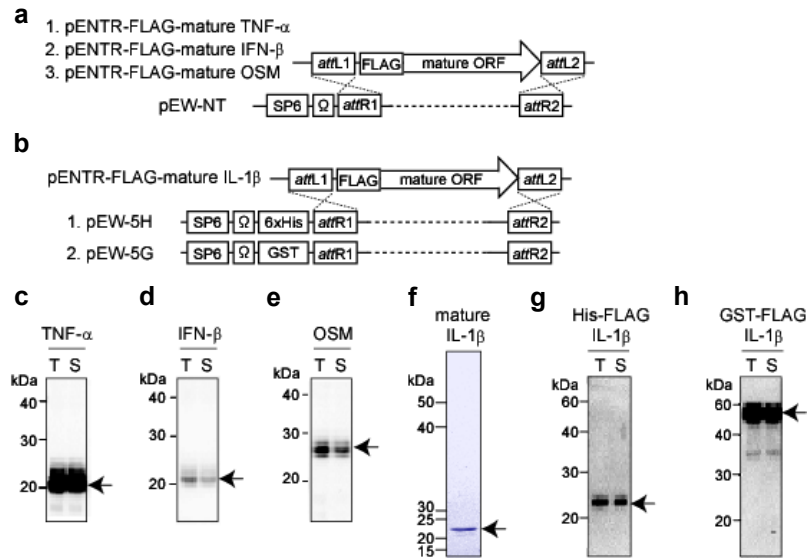
Two thousand five hundred and thirty-seven proteins are divided into 10 groups according to the number of transmembrane domains they possess. The number of clones in each group is represented at the top of each bar. Proteins were divided into 3 categories: faster-migrating (■), slower-migrating (■) and normal (■) proteins. Relative abundance of proteins is shown for each category.

Supplementary Figure 9. *In vitro* synthesized protein phosphatases harbor the substrate specificity.



PTPN5 and PTPN6 expressed *in vitro* were incubated with FYN and LYN whose auto-phosphorylated tyrosine (p-Tyr420 in FYN, p-Tyr397 in LYN) at the kinase catalytic domains were known to be dephosphorylated by PTPN5 and PTPN6, respectively. Dephosphorylation was assessed by Western blotting using anti-Src-pTyr416 antibody (Supplementary Table 9). One unit is defined as the amount of enzyme that hydrolyzes 0.7 nmol of pNPP in 15 h at 30°C in a total reaction volume of 5 μ l.

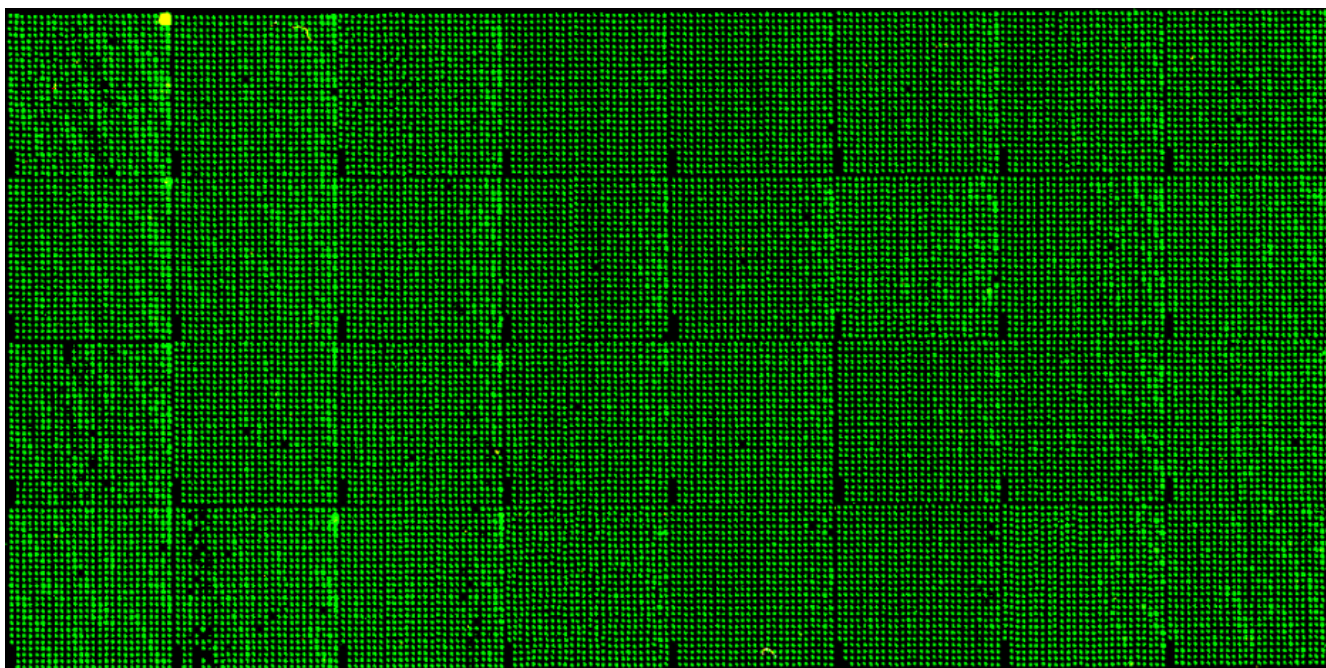
Supplementary Figure 10. *In vitro* synthesized cytokines.



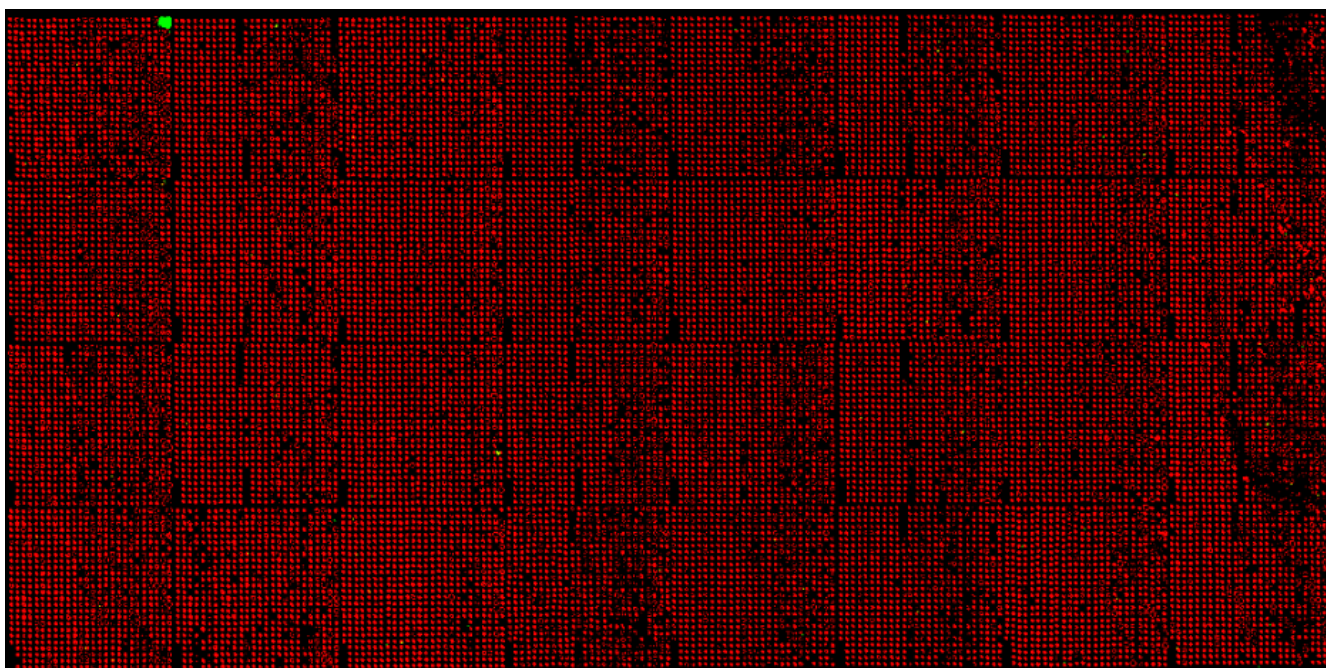
a, b, Schematic representation of the entry clone and the destination vector which was used for the *in vitro* cytokine synthesis. The abbreviations in the figures are as follows: attL1, attL2, attR1, attR2, Gateway recombination site; ORF, open reading frame; SP6, SP6 promoter; GST, glutathione S-transferase; Ω , translational enhancers. T, total fraction; S, soluble fraction. **c-e**, Proteins synthesized under optimized non-reduced conditions by Western blotting using anti-FLAG antibody. **f**, Purified mature IL-1 β . The samples were separated by SDS-PAGE and the gels were stained with CBB. **g, h**, Western-blotting analysis of His-FLAG-IL-1 β and GST-FLAG-IL-1 β using anti-IL-1 β antibody. Each protein is indicated by a black arrowhead. Molecular weight markers are shown on the left side of each figure.

Supplementary Figure 11. Representative pictures of an entire protein microarray.

a



b



a, An overview of a protein microarray obtained using a standard scanning apparatus for DNA microarrays, operated under default conditions installed for dual fluorescence analysis (red and green). Spots printed with a reaction mixture of an *in vitro* protein synthesis system with wheat germ extract are weakly recognized since the reaction mixture contains a constituent(s) with intrinsic green fluorescence detected under the same conditions. **b**, A picture of a protein microarray after the first scanning and subsequent staining with an anti-GST antibody and an Alexa 647-labeled anti-mouse IgG2a antibody that provides red fluorescence signals.

Supplementary Table 1. Summary of construction of Gateway entry clones.

Protocol*			A	B	C	D	E	F	G	Total
Number of Gateway entry clones			1,320	18,703	3,357	689	2,677	6,445	88	33,279
Enzyme†			Pfx	Taq High-Fidelity	KOD-Plus-	Taq High-Fidelity	Pfx	KOD-Plus-	Others	-
Selective or non-selective‡			Non-selective	Selective	Selective	Selective	Selective	Selective		
Amplification step			2-step	2-step	2-step	1-step	1-step	1-step		
1st PCR	Primer	Forward	Gene specific Fw primer	Gene specific Fw primer	Gene specific Fw primer	Gene specific Fw primer + Common att B1 primer				
		Reverse	Gene specific Rv primer §	Gene specific Rv primer	Gene specific Rv primer	Gene specific Rv primer + (Common att B2 primer 2 or 3)				
	Pre Denaturation		95°C, 2 min	95°C, 2 min	95°C, 2 min	95°C, 2 min	95°C, 2 min	95°C, 2 min		
	Amplification	Denaturation	94°C, 15 sec	94°C, 15 sec	94°C, 1 min	94°C, 15 sec	94°C, 1 min	94°C, 1 min		
		Annealing	55°C, 30 sec	55°C, 30 sec	55°C, 2 min	55°C, 30 sec	55°C, 2 min	55°C, 2 min		
		Extension	68°C, 3 min	68°C, 3 min	68°C, 3 min	68°C, 3 min	68°C, 3 min	68°C, 3 min		
		Cycles	5	5	10	15	15	15		
	Additional Extension		68°C, 5 min	68°C, 5 min	68°C, 5 min	68°C, 5 min	68°C, 5 min	68°C, 5 min		
2nd PCR	Primer	Forward	Common att B1 primer	Common att B1 primer	Common att B1 primer	-	-	-		
		Reverse	Common att B2 primer 1	Common att B2 primer 2 or 3	Common att B2 primer 2 or 3	-	-	-		
	Pre Denaturation		95°C, 2 min	95°C, 2 min	95°C, 2 min	-	-	-		
	Amplification	Denaturation	94°C, 15 sec	94°C, 15 sec	94°C, 1 min	-	-	-		
		Annealing	45°C, 30 sec (first 3 cycles)	45°C, 30 sec (first 3 cycles)	55°C, 2 min	-	-	-		
			55°C, 30 sec (last 7 cycles)	55°C, 30 sec (last 7 cycles)						
		Extension	68°C, 3 min	68°C, 3 min	68°C, 3 min	-	-	-		
		Cycles	10 (3 + 7)	10 (3 + 7)	5	-	-	-		
	Additional Extension		68°C, 5 min	68°C, 5 min	68°C, 5 min	-	-	-		

*See Supplementary Methods 1 and/or Supplementary Fig. 1.

†PCR enzyme.

‡Selective; a reaction is carried out in separate tubes, non-selective; a reaction is done in the same tube (in mixture).

§Two hundred and eighty two clones were constructed with a slightly different gene specific Rv primer, having a cystein residue displaced at the termination codon.

||Those clones were constructed by RT-PCR, total chemical synthesis or other methods.

Supplementary Table 3. Features and expression levels of proteins of 96 randomly chosen cDNA clones.

Gateway entry clone ID*	Gene symbol	Gene annotation	Expressed protein (total)†	Expressed protein (supernatant)‡	ORF size (Number of amino acid residues of human ORF)	Molecular weight (kDa)§	Isoelectric point (pI)	Number of trans-membrane domains (TM)
FLJ91072AAAN	SEMA4C	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4C	108.8	47.8	333	65.6	8.26	3
FLJ91109AAAN	ADCY3	adenylate cyclase 3	120.0	50.5	378	73.0	7.86	1
FLJ91113AAAN	PIGS	phosphatidylinositol glycan anchor biosynthesis, class S	62.0	80.7	555	91.4	6.58	2
FLJ91119AAAN	B3GNT3	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 3	83.5	9.0	256	58.5	9.25	1
FLJ90583AAAN	RELL2	RELT-like 2	127.1	118.1	303	62.2	6.91	1
FLJ90833AAAN	SCG3	secretogranin III	78.6	79.0	468	82.7	4.70	1
FLJ90543AAAN	TXNDC4	thioredoxin domain containing 4 (endoplasmic reticulum)	125.5	112.2	406	76.7	4.90	0
FLJ11090AAAN	TDP1	tyrosyl-DNA phosphodiesterase 1	112.3	63.2	608	98.2	7.72	0
FLJ30821AAAN	SEZ6	seizure related 6 homolog (mouse)	116.5	78.4	475	81.9	5.84	1
FLJ30826AAAN	TRIM9	tripartite motif-containing 9	66.9	3.5	802	119.6	7.17	0
FLJ30976AAAN	C6orf199	chromosome 6 open reading frame 199	88.9	77.9	421	78.2	4.60	0
FLJ80032AAAN	PHKG2	phosphorylase kinase, gamma 2 (testis)	88.0	67.3	406	76.2	6.35	0
FLJ30442AAAN	FLJ20433	hypothetical protein FLJ20433	125.9	35.0	599	95.2	8.16	0
FLJ30784AAAN	ARPM1	actin related protein M1	90.9	61.7	372	70.8	5.87	0
FLJ30973AAAN	Gcom1	GRINL1A combined protein	130.0	1.4	466	84.0	6.04	0
FLJ30982AAAN	C20orf12	chromosome 20 open reading frame 12	108.2	44.6	401	73.3	8.27	0
FLJ31006AAAN	GIMAP5	GTPase, IMAP family member 5	88.3	68.1	347	69.3	7.30	1
FLJ31173AAAN	C2orf54	chromosome 2 open reading frame 54	71.4	40.2	347	77.3	6.67	1
FLJ31009AAAN	SLC46A2	solute carrier family 46, member 2	N.I.¶	N.I.	475	80.8	9.29	12
FLJ31200AAAN	LEO1	Leo1, Paf1/RNA polymerase II complex component, homolog (S. cerevisiae)	51.3	43.0	425	76.8	3.81	0
FLJ31349AAAN	CNKSR3	CNKSR family member 3	83.5	17.4	555	91.6	9.00	0
FLJ31359AAAN	PWWP2A	PWWP domain containing 2A	N.I.	N.I.	455	80.3	10.65	0
FLJ31369AAAN	SHCBP1	SHC SH2-domain binding protein 1	81.1	79.2	672	105.4	4.41	0
FLJ32610AAAN	HIAT1	hippocampus abundant transcript 1	N.I.	N.I.	490	82.8	8.56	12
FLJ30760AAAN	PNMA6A	paraneoplastic antigen like 6A	118.8	94.5	399	73.6	4.98	0
FLJ30772AAAN	FAM49A	family with sequence similarity 49, member A	112.4	107.1	323	67.1	5.89	0
FLJ30775AAAN	ZNF213	zinc finger protein 213	69.1	18.6	204	52.5	9.74	0
FLJ30782AAAN	FBXO44	F-box protein 44	120.7	24.4	224	55.5	7.98	0
FLJ30804AAAN	EIF3C	eukaryotic translation initiation factor 3, subunit C	76.4	64.1	699	110.7	5.64	2
FLJ30817AAAN	MCM7	minichromosome maintenance complex component 7	105.3	97.7	543	90.4	6.15	0
FLJ30818AAAN	DLK2	delta-like 2 homolog (Drosophila)	83.6	75.1	383	70.3	6.52	2
FLJ30839AAAN	DOCK7	dedicator of cytokinesis 7	88.8	71.7	632	102.0	6.10	0
FLJ30840AAAN	CHDH	choline dehydrogenase	84.5	33.2	207	52.4	8.34	0
FLJ30841AAAN	OPTN	optineurin	129.4	111.2	577	95.7	4.85	0
FLJ30794AAAN	SLC16A14	solute carrier family 16, member 14 (monocarboxylic acid transporter 14)	N.I.	N.I.	336	67.1	6.60	7
FLJ30831AAAN	CENTG3	centaurin, gamma 3	99.6	19.4	580	92.6	8.72	0
FLJ30845AAAN	C6orf206	chromosome 6 open reading frame 206	133.8	123.5	306	64.2	5.00	0
FLJ30851AAAN	LOC653140	hypothetical protein LOC653140	76.4	26.6	224	55.7	6.15	0
FLJ30870AAAN	N.A.	N.A.	27.6	9.6	295	61.9	10.14	0
FLJ30880AAAN	BCAR3	breast cancer anti-estrogen resistance 3	72.1	19.5	825	122.3	7.89	0
FLJ30852AAAN	LASS4	LAG1 homolog, ceramide synthase 4	73.1	6.9	233	57.0	11.22	0
FLJ30864AAAN	TRIM17	tripartite motif-containing 17	122.5	92.3	262	60.5	6.40	0
FLJ30866AAAN	PLB1	phospholipase B1	128.6	84.9	270	60.6	7.03	0
FLJ30878AAAN	SYNE1	spectrin repeat containing, nuclear envelope 1	73.3	43.4	561	95.5	6.15	0
FLJ30879AAAN	OSGEPL1	O-sialoglycoprotein endopeptidase-like 1	37.7	31.0	364	69.3	8.88	0
FLJ30889AAAN	RUSC1	RUN and SH3 domain containing 1	116.4	56.2	433	76.3	8.94	0
FLJ30891AAAN	CACNG3	calcium channel, voltage-dependent, gamma subunit 3	15.3	7.4	315	65.3	9.84	4
FLJ30909AAAN	NLGN4X	neuroligin 4, X-linked	32.9	20.8	816	121.7	6.10	1
FLJ30910AAAN	NANP	N-acetylneuraminic acid phosphatase	86.0	80.1	248	57.6	6.35	0
FLJ30919AAAN	SAE1	SUMO1 activating enzyme subunit 1	110.9	98.9	318	65.1	5.16	0
FLJ30894AAAN	NSUN2	NOL1/NOP2/Sun domain family, member 2	66.6	56.5	531	89.1	6.52	0
FLJ30905AAAN	SULF1	sulfatase 1	99.0	86.0	285	62.3	5.36	0
FLJ30907AAAN	DIXDC1	DIX domain containing 1	112.0	79.8	211	53.7	7.09	0
FLJ30922AAAN	STXBP5	syntaxin binding protein 5 (tomosyn)	115.9	99.3	398	73.6	7.66	0
FLJ30927AAAN	ZNF582	zinc finger protein 582	59.7	33.5	517	90.3	8.56	0
FLJ30928AAAN	PSPN	persephin	79.2	67.3	213	51.9	10.89	0
FLJ30929AAAN	DYNC1I2	dynein, cytoplasmic 1, intermediate chain 2	36.8	27.9	638	101.2	4.85	0
FLJ30931AAAN	DOCK7	dedicator of cytokinesis 7	98.9	29.5	626	101.9	6.71	0
FLJ30934AAAN	FLJ30934	hypothetical protein FLJ30934	61.0	54.0	277	61.1	6.43	0
FLJ30937AAAN	GRSF1	G-rich RNA sequence binding factor 1	90.3	43.4	412	76.4	5.26	0
FLJ30940AAAN	RAPGEF3	Rap guanine nucleotide exchange factor (GEF) 3	100.5	65.7	216	54.9	10.84	0
FLJ30932AAAN	ZNF558	zinc finger protein 558	141.1	88.8	402	75.5	9.18	0
FLJ30946AAAN	RINT1	RAD50 interactor 1	45.6	36.8	792	120.4	5.12	0
FLJ30970AAAN	LHPP	phospholysine phosphohistidine inorganic pyrophosphate phosphatase	112.4	100.5	270	59.0	6.36	0
FLJ30983AAAN	FRMD6	FERM domain containing 6	124.3	12.0	622	101.8	7.48	0
FLJ80056AAAN	STK25	serine/threonine kinase 25 (STE20 homolog, yeast)	94.5	32.5	426	77.9	6.73	0
FLJ16003AAAN	CLEC4C	C-type lectin domain family 4, member C	89.2	51.0	213	54.7	7.05	1
FLJ31012AAAN	GNAI2	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 2	142.0	128.3	274	61.2	5.21	0
FLJ31014AAAN	PRSS27	protease, serine 27	40.1	27.1	254	57.4	7.75	0
FLJ31188AAAN	SYTL3	synaptotagmin-like 3	95.2	45.0	278	61.1	9.42	0
FLJ30977AAAN	LAYN	layilin	93.7	84.8	374	72.1	4.60	2
FLJ31185AAAN	FLJ13236	hypothetical protein FLJ13236	14.6	7.2	341	67.8	9.62	7
FLJ31202AAAN	SLC22A6	solute carrier family 22 (organic anion transporter), member 6	35.8	18.0	529	87.8	8.68	5
FLJ31204AAAN	FAAH2	fatty acid amide hydrolase 2	54.2	5.4	532	88.1	9.51	2
FLJ31210AAAN	N.A.	N.A.	38.3	22.5	201	51.6	10.45	0
FLJ31211AAAN	GALNT9	UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetyl-galacto-saminyltransferase 9 (GalNAc-T9)	94.8	33.3	460	82.2	7.87	0
FLJ31212AAAN	PAQR3	progesterin and adipoQ receptor family member III	23.2	23.5	221	55.4	8.46	5
FLJ31217AAAN	AKT2	v-akt murine thymoma viral oncogene homolog 2	98.6	79.5	382	73.7	6.08	0
FLJ31218AAAN	TTC19	tetratricopeptide repeat domain 19	113.7	98.8	273	61.0	5.14	0
FLJ31225AAAN	VPS16	vacuolar protein sorting 16 homolog (S. cerevisiae)	111.2	23.9	695	108.0	8.05	0
FLJ31213AAAN	ZNF396	zinc finger protein 396	101.1	78.9	333	68.0	7.37	0
FLJ31224AAAN	XRCC6	X-ray repair complementing defective repair in Chinese hamster cells 6 (Ku autoantigen, 70kDa)	110.7	76.8	568	94.9	6.47	0
FLJ31208AAAN	SPATA13	spermatogenesis associated 13	90.8	23.4	652	104.6	7.36	0
FLJ30001AAAN	UBAC2	UBA domain containing 2	90.7	50.6	309	64.6	9.08	4
FLJ30004AAAN	STARD4	StAR-related lipid transfer (START) domain containing 4	73.5	53.2	205	53.3	4.91	0
FLJ30019AAAN	CYYR1	cysteine/tyrosine-rich 1	97.3	23.4	262	57.9	8.94	2
FLJ30031AAAN	DTNBP1	dystrobrevin binding protein 1	111.6	100.6	270	60.1	4.08	0
FLJ30033AAAN	HEATR2	HEAT repeat containing 2	140.9	110.0	280	60.6	6.87	0
FLJ30051AAAN	ZNF501	zinc finger protein 501	52.0	17.1	215	54.6	9.73	0
FLJ30014AAAN	YIPF5	Yip1 domain family, member 5	N.I.	N.I.	257	57.7	3.96	5
FLJ30046AAAN	SLAIN1	SLAIN motif family, member 1	36.2	2.6	305	63.3	9.90	0
FLJ30053AAAN	STARD7	StAR-related lipid transfer (START) domain containing 7	98.6	86.7	269	61.4	6.61	0
FLJ30094AAAN	DPP9	dipeptidyl-peptidase 9	96.4	83.6	312	65.3	6.99	0
FLJ31052AAAN	FCRLB	Fc receptor-like B	51.8	9.2	312	62.3	12.18	0
FLJ31070AAAN	IGFBP3	insulin-like growth factor binding protein 3	120.1	20.7	317	64.1	9.08	0
FLJ31073AAAN	C13orf33	chromosome 13 open reading frame 33	110.1	81.0	303	63.8	5.54	0

*N-types were used.

† Total amounts of expressed proteins (ng) in 3 µl out of 150 µl.

‡ Amounts of expressed proteins (ng) detected in the supernatant fraction per 3 µl out of 150 µl.

§ kDa of the whole protein including human ORF, the tag and attB1 region.

|| Not available.

¶ Not-informative possibly due to either low level of expression or high level of concomitant wheat germ proteins. We regarded the amount of proteins in these columns as zero for calculation of average values.

Supplementary Table 4. List of 2,537 proteins whose mobility was analyzed.

FLJ ID	TM*	pI†	Mobility‡	FLJ ID	TM*	pI†	Mobility‡	FLJ ID	TM*	pI†	Mobility‡	FLJ ID	TM*	pI†	Mobility‡
FLJ10027	0	6.41	-	FLJ10056	1	6.52	-	FLJ10058	0	8.06	L	FLJ10061	0	4.17	L
FLJ10063	2	6.67	-	FLJ10076	0	7.95	-	FLJ10085	0	6.96	L	FLJ10088	0	10.46	-
FLJ10122	0	4.82	L	FLJ10167	0	4.23	-	FLJ10181	0	7.11	-	FLJ10215	0	9.2	-
FLJ10232	0	4.13	L	FLJ10246	0	8.13	-	FLJ10280	0	5.35	L	FLJ10287	0	8.37	-
FLJ10304	0	8.88	L	FLJ10314	0	7.16	-	FLJ10315	5	9.71	-	FLJ10316	4	5.86	S
FLJ10355	0	7.96	-	FLJ10362	0	4.44	L	FLJ10397	0	6.06	-	FLJ10403	0	10.08	-
FLJ10413	0	5.11	L	FLJ10415	0	7.89	-	FLJ10424	0	10.65	L	FLJ10432	0	6.13	-
FLJ10435	0	5.36	-	FLJ10511	0	5.46	-	FLJ10538	0	5.32	-	FLJ10540	0	6.42	-
FLJ10601	0	6.39	-	FLJ10628	0	5.79	L	FLJ10697	0	8.63	-	FLJ10702	0	8.62	-
FLJ10704	0	8.21	-	FLJ10757	0	5.01	-	FLJ10762	0	5.17	-	FLJ10770	0	10.79	L
FLJ10775	0	3.8	-	FLJ10776	4	7.99	-	FLJ10781	0	10.83	L	FLJ10790	0	10.35	-
FLJ10827	2	5.62	-	FLJ10831	0	7.8	-	FLJ10864	0	4.82	-	FLJ10901	0	9.39	L
FLJ10915	0	7.56	-	FLJ10929	0	6.15	-	FLJ10986	0	6.72	-	FLJ10987	0	6.85	-
FLJ10996	0	9.88	L	FLJ10997	0	4.6	L	FLJ11000	4	7.83	-	FLJ11004	0	8.97	-
FLJ11006	5	6.42	-	FLJ11007	0	6.41	-	FLJ11012	0	9.62	-	FLJ11014	1	5.74	L
FLJ11016	0	9.26	-	FLJ11017	0	4.13	-	FLJ11026	0	6.58	-	FLJ11029	0	10.91	-
FLJ11030	0	5.7	-	FLJ11033	0	6.91	-	FLJ11039	0	5	L	FLJ11040	0	7.09	-
FLJ11043	0	9.39	-	FLJ11045	0	4.81	-	FLJ11050	0	4.57	-	FLJ11051	0	6.14	-
FLJ11054	0	7.58	-	FLJ11055	0	4.97	-	FLJ11064	0	5.78	-	FLJ11067	0	10.41	L
FLJ11068	0	5.9	-	FLJ11073	0	6.72	-	FLJ11082	2	5.83	-	FLJ11084	0	4.75	-
FLJ11085	0	4.48	-	FLJ11094	0	9.36	-	FLJ11112	0	9.28	L	FLJ11116	0	9.29	-
FLJ11121	0	9.86	L	FLJ11140	0	9.07	-	FLJ11145	0	4.56	-	FLJ11149	0	8.22	L
FLJ11176	3	5.11	-	FLJ11230	0	4.62	L	FLJ11234	0	4.63	L	FLJ11314	0	10.45	-
FLJ11315	0	9.98	-	FLJ11316	0	9.56	-	FLJ11318	0	9.47	-	FLJ11326	0	9.6	-
FLJ11328	0	5.43	-	FLJ11329	0	11.23	-	FLJ11332	0	4.52	-	FLJ11336	0	5.3	-
FLJ11343	1	7.08	-	FLJ11345	0	7.86	-	FLJ11347	0	9.59	-	FLJ11349	2	5.64	-
FLJ11350	1	5.67	-	FLJ11356	0	10.32	-	FLJ11362	0	4.29	L	FLJ11372	0	8.73	-
FLJ11378	0	4.16	L	FLJ11421	1	8.61	-	FLJ11426	0	7	-	FLJ11458	2	5.55	-
FLJ11515	0	6.64	-	FLJ11561	0	8.9	-	FLJ11593	5	5.56	-	FLJ11699	0	8.48	L
FLJ11725	0	7.97	L	FLJ11764	0	10.56	L	FLJ11800	0	6.21	L	FLJ11811	0	10.19	L
FLJ11815	0	10.51	-	FLJ11834	0	4.36	-	FLJ11861	0	6.4	-	FLJ11894	0	5.01	-
FLJ11895	0	7.54	-	FLJ11912	0	4.96	-	FLJ11940	1	4.61	L	FLJ12046	2	9.04	-
FLJ12057	0	5.93	-	FLJ12060	1	4.08	L	FLJ12121	0	10.26	-	FLJ12123	3	8.44	-
FLJ12130	0	12.18	L	FLJ12193	0	8.31	-	FLJ12241	0	9.16	-	FLJ12272	0	10.42	-
FLJ12294	0	7.1	-	FLJ12335	0	6.42	-	FLJ12354	0	10.24	L	FLJ12408	0	8.02	-
FLJ12457	0	8.16	-	FLJ12462	0	9.74	L	FLJ12482	0	8.38	-	FLJ12488	0	9.65	-
FLJ12504	0	8.87	-	FLJ12516	0	7.23	-	FLJ12523	0	10.88	-	FLJ12526	1	7.95	-
FLJ12582	0	3.96	L	FLJ12611	0	4.9	L	FLJ12616	0	10.37	L	FLJ12622	0	9.09	-
FLJ12626	0	9.32	-	FLJ12635	0	9.74	L	FLJ12642	0	8.16	-	FLJ12680	1	7.11	-
FLJ12700	0	10.34	L	FLJ12737	0	5.6	L	FLJ12738	0	5.88	L	FLJ12747	0	8.67	-
FLJ12775	0	10.87	-	FLJ12782	0	4.75	L	FLJ12798	0	4.81	S	FLJ12800	0	12.32	S
FLJ12845	0	7.17	-	FLJ12867	0	8.51	-	FLJ12903	0	6.51	L	FLJ12940	0	8.4	L
FLJ12941	0	5.7	-	FLJ12967	0	9.93	L	FLJ12973	0	9.69	-	FLJ12983	0	4.79	L
FLJ12986	0	7.74	L	FLJ13028	0	9.08	-	FLJ13029	0	8.83	-	FLJ13087	0	10.35	L
FLJ13093	0	5.17	-	FLJ13109	0	5.58	-	FLJ13115	0	4.63	-	FLJ13118	0	4.57	-
FLJ13123	0	8.51	-	FLJ13177	0	3.73	L	FLJ13190	0	10.47	L	FLJ13194	0	9.08	-
FLJ13195	0	6.66	-	FLJ13257	0	3.88	L	FLJ13275	0	12.07	L	FLJ13283	0	4.48	-
FLJ13293	0	5.25	-	FLJ13398	1	10.09	-	FLJ13408	0	6.77	-	FLJ13426	0	8.65	-
FLJ13431	0	9.58	L	FLJ13437	0	5.52	-	FLJ13438	1	4.64	L	FLJ13448	0	10.03	-
FLJ13449	0	4.78	L	FLJ13450	0	6.35	L	FLJ13462	0	6.13	-	FLJ13467	0	5.99	L
FLJ13478	0	6.35	-	FLJ13479	0	9.02	L	FLJ13484	0	7.34	-	FLJ13490	0	6.06	-
FLJ13498	0	5.25	-	FLJ13508	7	5.9	-	FLJ13519	0	4.77	L	FLJ13521	0	4.69	-
FLJ13532	0	4.91	-	FLJ13544	0	11.53	-	FLJ13588	0	5.1	S	FLJ13606	0	8	-
FLJ13607	0	9.58	-	FLJ13609	0	6.16	-	FLJ13611	0	5.92	-	FLJ13617	5	6.31	S
FLJ13626	0	9.45	-	FLJ13631	1	8.47	-	FLJ13633	0	10.31	-	FLJ13636	0	4.38	-
FLJ13639	0	7.03	-	FLJ13641	0	4.92	-	FLJ13642	0	6.33	-	FLJ13645	0	4.92	-
FLJ13653	0	9.12	-	FLJ13657	0	4.34	-	FLJ13659	0	8.7	-	FLJ13661	0	10.14	-
FLJ13662	0	6.03	-	FLJ13664	0	6.85	-	FLJ13670	0	9.77	-	FLJ13673	0	6.53	-
FLJ13676	0	6.48	-	FLJ13678	0	8	-	FLJ13682	0	4.88	-	FLJ13684	0	8.24	-
FLJ13685	0	7.42	-	FLJ13688	0	4.77	-	FLJ13693	1	9.95	-	FLJ13697	0	8.89	-
FLJ13700	0	8.65	-	FLJ13710	0	5.42	-	FLJ13716	0	6.18	-	FLJ13718	0	6.53	-
FLJ13720	0	7.45	-	FLJ13726	0	4.82	-	FLJ13732	0	8.88	-	FLJ13734	0	9.81	-
FLJ13737	0	6.5	-	FLJ13742	4	9.61	-	FLJ13743	1	7.04	-	FLJ13761	0	10.38	-
FLJ13770	0	6.58	S	FLJ13772	1	7.72	-	FLJ13778	0	6.67	-	FLJ13780	0	5.93	-
FLJ13782	0	5.92	-	FLJ13787	0	6.78	-	FLJ13788	0	8.22	-	FLJ13797	0	6.2	-
FLJ13798	0	5.76	-	FLJ13801	0	8.52	S	FLJ13804	0	6.19	-	FLJ13812	0	5.09	-
FLJ13813	0	6.67	-	FLJ13814	0	8.13	S	FLJ13817	2	10.46	-	FLJ13822	0	4.38	-
FLJ13823	0	8.42	-	FLJ13828	0	9.12	-	FLJ13832	0	7.54	-	FLJ13834	0	6.24	-
FLJ13838	1	10.05	-	FLJ13839	0	3.87	L	FLJ13841	0	8.28	-	FLJ13842	0	9.82	-
FLJ13852	0	7.78	-	FLJ13854	0	8.63	-	FLJ13855	0	6.03	-	FLJ13861	0	4.61	-
FLJ13862	0	8.55	-	FLJ13865	0	4.74	-	FLJ13869	0	4.96	-	FLJ13870	0	7.06	-
FLJ13875	0	7.68	-	FLJ13888	0	3.77	L	FLJ13891	0	6.39	-	FLJ13894	0	7.96	-
FLJ13906	0	6.4	-	FLJ13907	0	7.56	-	FLJ13908	0	5.85	-	FLJ13909	0	8.71	-
FLJ13913	0	9.52	-	FLJ13914	0	7.79	-	FLJ13918	0	7.66	-	FLJ13923	0	9.34	-
FLJ13924	0	5.57	-	FLJ13925	0	7.88	-	FLJ13927	0	9.42	-	FLJ13928	0	6.84	-
FLJ13929	1	10.32	-	FLJ13931	0	8.28	-	FLJ13933	0	6.76	-	FLJ13935	1	4.5	-
FLJ13941	0	7.13	-	FLJ13944	0	6.41	-	FLJ13946	2	6.06	-	FLJ13948	4	5.43	-
FLJ13949	0	7.32	-	FLJ13953	0	9.39	-	FLJ13957	0	8.9	-	FLJ13960	0	10.02	-
FLJ13961	0	5.96	-	FLJ13963	0	5.35	-	FLJ13964	0	5.92	-	FLJ13968	0	6.03	-
FLJ13969	0	9.97	L	FLJ13970	0	9.28	-	FLJ13977	1	9.45	-	FLJ13979	0	6.1	-
FLJ13981	0	6.8	-	FLJ13982	0	9.7	-	FLJ13983	0	6.83	-	FLJ13985	0	6.09	-
FLJ13986	0	6.83	-	FLJ13987	0	10.41	-	FLJ13989	0	11.64	-	FLJ13990	0	8.77	-
FLJ13992	1	7.43	-	FLJ13998	0	8.55	-	FLJ13999	0	7.48	-	FLJ14000	0	9.1	-
FLJ14002	0	5.65	-	FLJ14003	0	5.05	-	FLJ14005	0	5.93	-	FLJ14007	0	7.42	-
FLJ14008	2	6.9	-	FLJ14015	0	8.27	L	FLJ14031	0	8.62	L	FLJ14033	0	7.87	-
FLJ14034	0	5.04	-	FLJ14048	0	9.03	L	FLJ14103	1	9.15	-	FLJ14126	0	4.78	-
FLJ14171	0	8.52	-	FLJ14184	0	7.83	-	FLJ14204	0	5.14	L	FLJ14250	0	9.99	-
FLJ14264	0	7.6	-	FLJ14276	0	9.54	-	FLJ14314	0	6.05	-	FLJ14330	0	7.91	-
FLJ14335	0	9.23	-	FLJ14342	0	11.03	-	FLJ14347	1	8.47	S	FLJ14352	0	5.35	-
FLJ14356	0	8.82	-	FLJ14358	0	6.68	-	FLJ14360	0	6.14	-	FLJ14362	0	4.85	-
FLJ14363	2	6.91	-	FLJ14373	0	6.65	-	FLJ14376	0	4.28	-	FLJ14389	1	8.33	-
FLJ14391	2	7.49	-	FLJ14393	0	6.68	-	FLJ							

FLJ ID	TM*	pI†	Mobility‡	FLJ ID	TM*	pI†	Mobility‡	FLJ ID	TM*	pI†	Mobility‡	FLJ ID	TM*	pI†	Mobility‡
FLJ14689	0	7.84	-	FLJ14690	2	5.02	-	FLJ14691	0	8.57	-	FLJ14692	6	7.14	-
FLJ14694	0	5.57	-	FLJ14696	0	5.47	-	FLJ14697	9	9.41	-	FLJ14698	4	9.27	S
FLJ14699	2	9.78	-	FLJ14702	0	5.34	-	FLJ14707	0	8.26	-	FLJ14714	0	5.26	-
FLJ14716	0	10.59	-	FLJ14721	0	9.32	-	FLJ14722	0	8.23	-	FLJ14726	4	9.36	-
FLJ14728	0	9.12	-	FLJ14729	0	6.28	-	FLJ14730	0	5.6	-	FLJ14735	2	6.43	-
FLJ14736	0	9.9	-	FLJ14739	0	8.67	-	FLJ14742	1	5.56	-	FLJ14743	3	6.64	-
FLJ14745	0	9.05	-	FLJ14746	3	6.18	-	FLJ14748	1	9.19	-	FLJ14752	1	4.86	L
FLJ14757	0	7.32	-	FLJ14767	0	5.03	-	FLJ14773	0	10.47	-	FLJ14784	11	8.53	S
FLJ14796	0	4.52	-	FLJ14809	5	4.61	-	FLJ14841	7	8.55	L	FLJ14857	0	5.23	-
FLJ14859	0	5.69	-	FLJ14861	0	10.03	-	FLJ14873	0	8.67	-	FLJ14874	6	10.32	-
FLJ14877	0	5.55	-	FLJ14879	0	7.77	-	FLJ14880	1	4.36	S	FLJ14890	0	8.79	-
FLJ14892	1	9.07	-	FLJ14895	0	7.73	-	FLJ14905	0	7.14	-	FLJ14912	0	10.01	-
FLJ14913	0	8.7	-	FLJ14914	0	7.91	-	FLJ14917	0	7.73	-	FLJ14927	0	5.48	-
FLJ14938	1	4.49	-	FLJ14939	0	9.43	-	FLJ14943	0	9.92	-	FLJ14949	9	8.12	S
FLJ14950	0	7.88	-	FLJ14954	0	8.49	-	FLJ14963	0	6.3	-	FLJ14965	0	4.39	-
FLJ14966	0	9.99	-	FLJ14967	0	10.19	-	FLJ14980	0	6.67	-	FLJ14984	0	9	-
FLJ14989	0	10.86	-	FLJ14993	2	8.33	-	FLJ14995	0	7.5	-	FLJ14996	0	5.16	-
FLJ14997	6	8.03	L	FLJ14998	0	4.85	-	FLJ16009	0	11.52	-	FLJ16011	0	6.88	-
FLJ16012	1	10.04	-	FLJ16013	1	5.77	-	FLJ16016	6	7.33	-	FLJ16017	2	4.16	-
FLJ16019	0	6.13	-	FLJ16022	2	9.29	-	FLJ16028	0	7.01	-	FLJ16029	1	6.12	-
FLJ16031	1	6.82	-	FLJ16040	0	6.01	-	FLJ16049	12	8.46	-	FLJ16050	0	7.06	-
FLJ16052	1	4.53	-	FLJ16057	5	9	-	FLJ16058	6	10.38	-	FLJ16063	0	11.58	-
FLJ16067	0	9.24	-	FLJ16069	0	9.57	-	FLJ16070	5	8.45	-	FLJ16071	7	9.59	-
FLJ16072	0	6.76	-	FLJ16073	0	6.17	-	FLJ16074	4	7.97	-	FLJ16078	0	6.34	-
FLJ16082	0	7.46	-	FLJ16084	8	9.14	-	FLJ16085	0	9.81	-	FLJ16086	0	9.87	-
FLJ16087	0	6.63	-	FLJ16088	0	7.92	-	FLJ16089	14	4.89	S	FLJ16090	7	8.31	S
FLJ16093	0	6.76	-	FLJ16097	1	8.16	-	FLJ16109	6	8.48	S	FLJ16111	6	8.61	S
FLJ16117	7	8.26	-	FLJ16118	0	7.6	-	FLJ16120	0	8.27	-	FLJ16122	0	4.49	-
FLJ16123	0	6.04	-	FLJ16125	0	9	-	FLJ16128	0	4.53	-	FLJ16129	3	8.27	L
FLJ16131	1	6.29	-	FLJ16136	0	8.49	-	FLJ16150	0	4.81	-	FLJ16154	0	7.31	-
FLJ16186	0	9.9	-	FLJ16195	0	8.76	-	FLJ16208	0	6.13	-	FLJ16216	0	5.18	-
FLJ16217	0	5.29	-	FLJ16228	1	7.28	-	FLJ16229	0	8.21	-	FLJ16234	5	4.79	-
FLJ16235	2	8.79	-	FLJ16236	0	7.24	-	FLJ16237	4	8.04	S	FLJ16239	3	4.97	-
FLJ16243	0	8.17	-	FLJ16244	0	6.83	-	FLJ16245	0	4.2	-	FLJ16247	0	7.15	-
FLJ16249	0	6.81	-	FLJ16250	1	9.44	-	FLJ16251	0	6.67	-	FLJ16252	0	4.64	-
FLJ16253	0	10.31	-	FLJ16254	3	5.06	-	FLJ16255	0	7.37	-	FLJ16257	0	10.46	-
FLJ16258	0	8.2	-	FLJ16260	0	10.2	L	FLJ16261	0	4.4	-	FLJ16262	0	5.28	-
FLJ16264	0	8.76	-	FLJ16265	2	7.7	-	FLJ16268	0	6.66	-	FLJ16269	0	8.95	-
FLJ16270	0	7.1	-	FLJ16271	0	4.94	-	FLJ16272	0	6.77	-	FLJ16273	0	6.82	-
FLJ16274	0	8.63	-	FLJ16275	6	8.05	S	FLJ16282	0	8.26	-	FLJ16284	0	10.57	-
FLJ16285	0	6.84	-	FLJ16288	0	10.27	-	FLJ16289	0	4.6	-	FLJ16290	0	8.54	-
FLJ16292	1	7.96	-	FLJ16293	0	9.96	-	FLJ16295	2	6.61	-	FLJ16298	0	5.94	-
FLJ16301	0	10.37	-	FLJ16306	1	7.66	-	FLJ16307	0	9.09	-	FLJ16308	0	9.34	-
FLJ16309	0	7.5	-	FLJ16312	1	7.47	-	FLJ16316	0	8.52	-	FLJ16325	0	8.73	-
FLJ16333	0	9.51	-	FLJ16335	0	6.73	-	FLJ16337	0	10.38	-	FLJ16344	3	7.83	-
FLJ16375	0	7.95	-	FLJ16382	5	9.78	S	FLJ16383	0	4.28	S	FLJ16384	0	7.65	-
FLJ16390	0	6.42	-	FLJ16397	0	6.25	-	FLJ16399	0	8.63	-	FLJ16403	1	8.94	-
FLJ16407	0	6.17	-	FLJ16416	0	6.17	-	FLJ16419	0	6.3	-	FLJ16428	0	5.42	L
FLJ16432	0	7.78	-	FLJ16437	5	9.06	-	FLJ16441	0	9.59	-	FLJ16444	0	7.86	L
FLJ16445	6	9	-	FLJ16446	0	7.91	-	FLJ16447	0	6.59	-	FLJ16448	0	4.66	-
FLJ16453	0	4.42	-	FLJ16455	0	10.62	-	FLJ16458	4	8.23	S	FLJ16469	0	6.99	-
FLJ16482	1	7.17	-	FLJ16483	0	3.77	-	FLJ16484	0	4.06	L	FLJ16485	0	7.5	-
FLJ16501	1	8.71	-	FLJ16506	0	10.03	-	FLJ16511	7	8.21	-	FLJ16524	0	7.92	-
FLJ16525	0	7.96	-	FLJ16527	0	9.7	-	FLJ16528	0	6.18	-	FLJ16529	0	8.15	-
FLJ16534	1	8.19	-	FLJ16537	0	9.87	-	FLJ16539	0	6.41	-	FLJ16540	0	7.91	-
FLJ16543	0	7.09	-	FLJ16545	0	8.73	-	FLJ16548	0	9.13	-	FLJ16549	0	5.96	-
FLJ16551	0	4.68	-	FLJ16554	0	10.19	-	FLJ16555	0	9.44	-	FLJ16567	1	9.81	-
FLJ16568	0	6.89	-	FLJ16571	0	8.15	-	FLJ16574	0	6.56	-	FLJ16577	0	9.58	-
FLJ16588	0	6.4	-	FLJ16589	0	5.45	-	FLJ16591	0	8.37	-	FLJ16593	4	9.35	L
FLJ16595	0	5.88	-	FLJ16597	0	6.2	-	FLJ16602	0	7.74	-	FLJ16603	0	9.04	-
FLJ16605	0	10.82	-	FLJ16606	0	9.56	-	FLJ16616	0	8.53	-	FLJ16617	0	8.36	-
FLJ16618	4	8.05	-	FLJ16620	1	8.38	-	FLJ16621	0	8.67	-	FLJ16623	0	9.37	-
FLJ16628	0	8.22	-	FLJ16630	2	9.12	-	FLJ16632	0	6.54	-	FLJ16638	0	5.2	-
FLJ16640	0	9.89	S	FLJ16641	0	6.66	-	FLJ16646	2	10.29	-	FLJ16647	0	4.24	L
FLJ16654	11	8.57	L	FLJ16662	0	6.95	-	FLJ16672	0	4.73	-	FLJ16673	0	8.24	-
FLJ16677	0	6.77	-	FLJ16679	4	8.23	S	FLJ16681	0	4.68	-	FLJ16685	0	6.24	-
FLJ16691	0	6.41	-	FLJ16695	0	11.13	-	FLJ16708	0	7.36	-	FLJ16712	2	10.19	-
FLJ16713	0	4.61	-	FLJ16731	0	8.61	-	FLJ16736	6	9.07	-	FLJ16737	1	8.54	-
FLJ16738	0	6.16	-	FLJ16748	0	5.94	-	FLJ22999	0	6.46	-	FLJ30009	0	8.2	-
FLJ30028	0	5.24	L	FLJ30030	0	7.74	-	FLJ30067	0	5.57	-	FLJ30120	0	8.68	-
FLJ30150	2	4.94	-	FLJ30182	1	11.66	-	FLJ30197	2	7.79	-	FLJ30231	2	10.26	L
FLJ30242	0	9.27	-	FLJ30254	0	5.29	-	FLJ30284	0	7.07	L	FLJ30314	0	8.31	L
FLJ30317	0	7.44	L	FLJ30321	2	6.65	-	FLJ30325	0	9.32	L	FLJ30346	0	8.38	L
FLJ30365	0	7.24	-	FLJ30375	0	11.6	-	FLJ30412	0	6.77	L	FLJ30430	1	9.52	L
FLJ30431	0	8.65	-	FLJ30439	0	8.5	-	FLJ30441	1	4.82	L	FLJ30453	0	9.8	-
FLJ30470	0	4.97	-	FLJ30475	0	6.52	-	FLJ30548	0	8.23	-	FLJ30553	0	5.74	-
FLJ30562	0	9.76	L	FLJ30573	0	6.83	-	FLJ30594	0	10.1	L	FLJ30643	1	8.42	-
FLJ30657	0	9.86	L	FLJ30659	0	8.92	-	FLJ30662	0	8.52	-	FLJ30675	0	11.77	L
FLJ30701	0	10.14	-	FLJ30720	0	9.57	-	FLJ30748	0	8.36	-	FLJ30758	2	10.47	-
FLJ30764	3	4.57	-	FLJ30803	2	7.51	-	FLJ30805	1	7.98	L	FLJ30812	0	6.94	S
FLJ30837	0	10.28	L	FLJ30859	0	10.58	L	FLJ30874	0	5.2	-	FLJ30886	0	9.34	-
FLJ30888	0	6.97	-	FLJ30899	0	6.17	-	FLJ30938	0	7.91	L	FLJ30950	2	5.27	-
FLJ30968	0	6.33	-	FLJ30979	0	8.59	-	FLJ30998	0	6.5	-	FLJ31007	0	8.05	L
FLJ31044	0	7.91	-	FLJ31106	0	5.68	-	FLJ31149	0	10.3	-	FLJ31151	0	10.59	-
FLJ31166	1	5.51	-	FLJ31170	0	7.41	-	FLJ31193	0	5.32	-	FLJ31230	0	10.55	L
FLJ31233	0	8.79	L	FLJ31255	0	8.65	L	FLJ31264	0	8.45	-	FLJ31273	0	5.11	-
FLJ31295	0	6.22	-	FLJ31304	0	11.37	-	FLJ31308	0	4.76	L	FLJ31313	0	8.46	-
FLJ31334	0	9.17	L	FLJ31338	2	7.49	-	FLJ31342	0	7.86	-	FLJ31346	7	9.11	-
FLJ31367	0	7.69	L	FLJ31377	0	11.01	-	FLJ31382	0	6.43	-	FLJ31383	2	10.05	-
FLJ31393	0	4.78	S	FLJ31402	0	8.63	-	FLJ31410	1	5.85	-	FLJ31413	0	10.04	-
FLJ31425	1	5.9	-	FLJ31428	0	8.11	-	FLJ31434	0	8.21	-	FLJ31440	0	9.08	-
FLJ31448	0	8.43	-	FLJ31450	0	10.3	-	FLJ31451	0	12.51	-	FLJ31455	0	7.47	

FLJ ID	TM*	pI†	Mobility‡	FLJ ID	TM*	pI†	Mobility‡	FLJ ID	TM*	pI†	Mobility‡	FLJ ID	TM*	pI†	Mobility‡
FLJ31883	0	10.21	-	FLJ31884	0	4.82	-	FLJ31886	0	8.45	-	FLJ31890	0	9.37	-
FLJ31891	0	7.94	-	FLJ31892	0	6.43	-	FLJ31893	0	6.64	L	FLJ31894	0	6.27	-
FLJ31895	0	6.86	-	FLJ31896	0	6.44	-	FLJ31897	0	4.5	L	FLJ31898	2	4.75	-
FLJ31901	0	8.58	-	FLJ31903	0	6.04	-	FLJ31905	0	7.79	-	FLJ31907	0	8.51	-
FLJ31909	0	5.28	L	FLJ31915	0	7.98	-	FLJ31917	1	6.77	-	FLJ31930	0	6.67	-
FLJ31932	0	5.06	-	FLJ31933	0	7.44	-	FLJ31935	3	8.49	-	FLJ31942	0	10.35	-
FLJ31945	0	11.26	L	FLJ31946	0	10.39	-	FLJ31957	3	7.72	-	FLJ31961	0	6.56	-
FLJ31963	0	5.15	-	FLJ31964	2	5.72	-	FLJ31968	2	7.23	-	FLJ31969	0	7.52	-
FLJ31970	2	4.72	-	FLJ31972	0	11.29	L	FLJ31975	0	8.58	-	FLJ31978	0	6.43	-
FLJ31980	0	9.92	-	FLJ31983	0	5.28	-	FLJ31991	0	7.03	-	FLJ31992	3	7.85	-
FLJ31994	0	12.32	L	FLJ32001	1	4.14	L	FLJ32014	0	4.63	S	FLJ32015	0	5.77	-
FLJ32030	0	5.35	-	FLJ32033	4	6.65	-	FLJ32039	1	6.46	-	FLJ32043	0	9.64	-
FLJ32045	0	8.63	-	FLJ32054	3	6.68	-	FLJ32055	0	6.19	-	FLJ32058	0	5.34	-
FLJ32063	0	9.4	L	FLJ32066	0	8.68	-	FLJ32069	0	5.77	-	FLJ32071	0	5.95	-
FLJ32075	0	6.07	-	FLJ32076	0	6.98	-	FLJ32079	0	7.38	-	FLJ32082	2	7.35	-
FLJ32083	0	6.88	-	FLJ32085	0	5.3	-	FLJ32086	0	6.92	-	FLJ32087	3	7.71	-
FLJ32091	0	6.07	-	FLJ32094	0	6.37	-	FLJ32097	0	9.78	-	FLJ32101	0	6.17	-
FLJ32103	2	9.13	-	FLJ32107	0	4.21	-	FLJ32112	0	10.78	-	FLJ32115	0	4.28	-
FLJ32116	0	8.54	-	FLJ32120	0	8.58	-	FLJ32125	0	8.51	-	FLJ32130	0	9.27	-
FLJ32131	0	4.76	-	FLJ32132	0	9.45	-	FLJ32133	0	9.11	-	FLJ32135	0	8.31	-
FLJ32136	0	4.8	L	FLJ32138	1	8.54	-	FLJ32139	0	7.99	-	FLJ32142	0	6.04	-
FLJ32149	0	4.78	-	FLJ32150	0	8.64	-	FLJ32151	11	8.46	-	FLJ32165	0	11.58	-
FLJ32169	0	10.79	L	FLJ32178	0	8.94	-	FLJ32188	0	4.44	-	FLJ32198	0	7.23	-
FLJ32203	0	8.86	-	FLJ32204	0	4.72	-	FLJ32206	0	7.9	-	FLJ32210	1	9.41	-
FLJ32214	1	8.92	-	FLJ32227	0	8.18	-	FLJ32228	0	4.66	L	FLJ32232	0	6.61	-
FLJ32288	0	8.6	-	FLJ32332	0	5.21	-	FLJ32350	0	6.41	-	FLJ32363	0	7.99	-
FLJ32370	1	7.43	-	FLJ32415	0	5.45	-	FLJ32421	0	7.74	-	FLJ32422	0	4.19	L
FLJ32442	0	6.71	-	FLJ32446	0	8.28	-	FLJ32449	0	10.21	-	FLJ32460	0	8.98	-
FLJ32463	0	9.96	-	FLJ32464	8	8.62	-	FLJ32468	0	8.5	-	FLJ32469	7	5.94	-
FLJ32474	0	8.96	-	FLJ32480	0	8.62	-	FLJ32486	0	5.79	-	FLJ32489	0	5.2	-
FLJ32530	0	7.83	-	FLJ32535	3	7.67	-	FLJ32543	0	8.16	-	FLJ32549	0	9.36	-
FLJ32552	0	8.1	-	FLJ32553	0	3.98	L	FLJ32562	0	8.16	L	FLJ32567	0	10.03	-
FLJ32585	0	9.85	-	FLJ32603	1	6.5	-	FLJ32606	0	7.55	-	FLJ32613	0	8.95	-
FLJ32616	0	8.93	-	FLJ32618	0	5.97	-	FLJ32620	0	4.73	-	FLJ32624	0	4.63	-
FLJ32630	0	8.02	-	FLJ32631	0	9.77	-	FLJ32632	2	9.36	-	FLJ32635	0	10.51	-
FLJ32637	0	5.54	-	FLJ32644	0	7.39	-	FLJ32663	0	9.24	-	FLJ32666	1	8.12	-
FLJ32674	0	7.08	-	FLJ32679	0	7.06	L	FLJ32682	0	4.48	-	FLJ32685	0	5.37	-
FLJ32686	0	5.36	-	FLJ32690	0	7.13	L	FLJ32692	0	7.96	-	FLJ32693	0	7.94	-
FLJ32696	0	5.21	-	FLJ32701	0	9.1	-	FLJ32702	0	8.65	-	FLJ32704	0	6.07	-
FLJ32705	1	9.44	-	FLJ32714	0	4.98	-	FLJ32716	0	6.74	-	FLJ32718	0	7.84	-
FLJ32720	0	5.78	-	FLJ32724	0	8.35	-	FLJ32725	7	8.87	S	FLJ32728	0	8.26	-
FLJ32730	0	5.53	-	FLJ32731	5	8.93	-	FLJ32732	0	6.03	L	FLJ32734	0	9.76	-
FLJ32737	0	7.94	-	FLJ32740	0	7.43	-	FLJ32741	0	9.36	-	FLJ32743	0	8.73	-
FLJ32745	0	8.75	-	FLJ32746	0	4.13	L	FLJ32748	0	5.62	-	FLJ32754	1	8.59	L
FLJ32761	0	8.18	-	FLJ32762	0	6.25	-	FLJ32763	0	6.29	-	FLJ32767	0	6.52	-
FLJ32768	0	7.84	-	FLJ32771	0	8.88	-	FLJ32773	0	5.47	-	FLJ32777	0	6.06	-
FLJ32778	8	7.45	-	FLJ32779	0	4.57	-	FLJ32780	0	9.36	-	FLJ32781	0	4.77	L
FLJ32784	0	9.7	-	FLJ32785	3	9.27	-	FLJ32787	0	10.47	-	FLJ32791	0	7.77	-
FLJ32793	0	10.62	-	FLJ32796	0	10.18	-	FLJ32799	0	7.32	-	FLJ32800	0	9.3	-
FLJ32802	2	7.27	-	FLJ32804	0	9	-	FLJ32806	2	10.43	-	FLJ32808	0	8.11	-
FLJ32809	0	6.61	-	FLJ32816	0	4.4	-	FLJ32818	0	6.58	-	FLJ32820	0	9.66	-
FLJ32821	0	8.92	-	FLJ32822	1	6.19	-	FLJ32825	0	5.26	-	FLJ32828	0	7.37	-
FLJ32829	0	4.86	-	FLJ32830	0	9.77	S	FLJ32839	0	8.88	-	FLJ32842	0	9.9	L
FLJ32844	0	7.22	-	FLJ32845	0	9.41	-	FLJ32850	0	8.61	-	FLJ32854	0	6.52	-
FLJ32855	0	6.72	-	FLJ32856	0	5.59	-	FLJ32858	0	6.7	-	FLJ32859	0	5.6	-
FLJ32861	0	4.75	-	FLJ32862	0	5.83	-	FLJ32864	0	4.39	-	FLJ32867	0	4.94	-
FLJ32871	0	7.14	-	FLJ32875	0	5.64	-	FLJ32879	0	10.72	-	FLJ32880	0	10.71	-
FLJ32882	0	8.95	-	FLJ32883	0	7.08	-	FLJ32884	0	10.64	-	FLJ32888	0	4.86	-
FLJ32891	0	10.51	-	FLJ32897	0	3.82	L	FLJ32898	0	8.44	S	FLJ32899	0	4.73	-
FLJ32901	0	9.27	-	FLJ32904	0	11.06	-	FLJ32907	1	4.89	-	FLJ32908	6	7.93	L
FLJ32912	0	7.95	-	FLJ32990	0	4.59	-	FLJ32991	0	9.52	-	FLJ32998	1	6.38	-
FLJ33008	1	4.37	-	FLJ33026	1	4.13	L	FLJ33042	0	5.58	L	FLJ33048	0	7.42	-
FLJ33058	0	7.69	-	FLJ33084	0	9.31	-	FLJ33087	0	6.38	-	FLJ33093	0	4.62	-
FLJ33094	0	5.8	-	FLJ33101	0	6.51	-	FLJ33103	0	9.68	-	FLJ33105	0	8.67	-
FLJ33129	0	4.46	L	FLJ33130	0	10.22	-	FLJ33140	0	6.96	-	FLJ33154	0	9.37	-
FLJ33157	0	8.75	-	FLJ33173	2	5.62	-	FLJ33279	1	8.48	-	FLJ33296	11	8.39	S
FLJ33352	0	4.87	-	FLJ33376	0	6.53	-	FLJ33401	0	11.11	-	FLJ33415	0	10.33	L
FLJ33453	0	4.75	L	FLJ33456	1	4.64	-	FLJ33461	3	10.02	-	FLJ33465	0	6.73	-
FLJ33487	2	6.57	-	FLJ33495	0	9.61	-	FLJ33499	0	6.68	-	FLJ33501	0	8.84	-
FLJ33505	0	7.13	-	FLJ33516	0	4.82	-	FLJ33522	0	6.46	-	FLJ33548	0	10.46	-
FLJ33549	0	6.41	-	FLJ33552	0	8.98	-	FLJ33557	0	5.04	L	FLJ33559	1	5.83	-
FLJ33562	0	7.5	-	FLJ33563	0	6.04	-	FLJ33567	0	5.9	-	FLJ33570	0	6.13	-
FLJ33574	0	8.7	-	FLJ33589	0	5.98	L	FLJ33590	1	6.44	-	FLJ33600	5	8.74	-
FLJ33603	0	11.3	-	FLJ33608	0	9.14	-	FLJ33611	0	6.59	S	FLJ33612	0	4.43	L
FLJ33620	0	7.51	-	FLJ33627	1	8.92	-	FLJ33640	0	6.8	-	FLJ33645	0	6.41	-
FLJ33648	0	5.06	-	FLJ33655	0	5.72	-	FLJ33682	1	7.78	-	FLJ33720	0	8.16	-
FLJ33726	6	7.68	S	FLJ33738	5	8.11	S	FLJ33752	0	9.43	-	FLJ33758	0	7.91	-
FLJ33760	9	7.9	-	FLJ33761	2	7.7	-	FLJ33764	1	6.04	-	FLJ33770	0	8.46	-
FLJ33812	2	8.76	-	FLJ33814	0	4.72	-	FLJ33832	0	12.59	-	FLJ33838	3	8.23	-
FLJ33857	1	5.2	-	FLJ33882	0	5.03	-	FLJ33934	1	9.51	-	FLJ33947	0	6.44	-
FLJ33994	1	7.77	-	FLJ33999	0	7.64	-	FLJ34004	0	8.67	-	FLJ34020	0	4.73	-
FLJ34056	0	12	L	FLJ34057	0	9.05	-	FLJ34064	0	7.65	-	FLJ34071	1	8.71	-
FLJ34073	0	6.37	-	FLJ34181	0	7.96	-	FLJ34186	0	8.62	-	FLJ34241	0	5.13	-
FLJ34245	0	9.84	-	FLJ34255	0	5.38	-	FLJ34262	0	9.34	-	FLJ34277	0	8.26	-
FLJ34304	0	10.2	-	FLJ34306	1	8.96	-	FLJ34325	0	5.88	-	FLJ34337	0	9.33	-
FLJ34340	0	7.15	-	FLJ34352	10	7.16	S	FLJ34368	0	9.68	-	FLJ34373	0	10.41	-
FLJ34375	0	11.74	-	FLJ34384	0	6.23	-	FLJ34388	0	8.62	-	FLJ34389	0	9.15	-
FLJ34392	0	6.78	L	FLJ34393	0	4.73	-	FLJ34406	0	8.57	-	FLJ34415	0	7.89	-
FLJ34452	0	10.01	-	FLJ34459	0	4.2	L	FLJ34463	0	7.07	-	FLJ34465	0	8.85	-
FLJ34483	0	9.85	-	FLJ34552	0	4.86	L	FLJ34604	0	9.98	-	FLJ34607	11	7.5	S
FLJ34613	1	6.37	-	FLJ34615	1	4.92	L	FLJ34617	0	6	-	FLJ34620	0	10.01	-
FLJ34622	0	6.07	-	FLJ34626	0	5.28	-	FLJ34633	0	6.35	L	FLJ34640	0	6.37	

FLJ ID	TM*	pI†	Mobility‡	FLJ ID	TM*	pI†	Mobility‡	FLJ ID	TM*	pI†	Mobility‡	FLJ ID	TM*	pI†	Mobility‡
FLJ35207	0	6.69	-	FLJ35211	0	8.77	L	FLJ35234	0	7.88	-	FLJ35266	0	6.86	-
FLJ35272	0	8.54	L	FLJ35279	1	8.38	-	FLJ35283	1	7.2	-	FLJ35308	0	8.11	-
FLJ35312	6	8.49	-	FLJ35322	0	7.67	-	FLJ35327	0	5	-	FLJ35343	0	10.18	-
FLJ35350	0	4.55	L	FLJ35353	0	3.49	-	FLJ35412	0	6.66	-	FLJ35435	1	8.86	-
FLJ35441	0	8.77	-	FLJ35446	0	6.35	-	FLJ35451	0	9.65	-	FLJ35478	0	5.15	-
FLJ35499	0	7.88	-	FLJ35533	0	7.61	-	FLJ35539	0	5.34	-	FLJ35546	0	7.62	-
FLJ35553	0	6.26	-	FLJ35564	0	5.29	-	FLJ35566	0	7.57	-	FLJ35567	0	7.64	-
FLJ35573	0	8.03	-	FLJ35584	0	8.57	-	FLJ35594	0	4.46	L	FLJ35661	1	8.57	-
FLJ35671	0	4.99	-	FLJ35693	0	9.83	-	FLJ35712	0	7.05	-	FLJ35785	0	10.24	-
FLJ35801	0	10.76	-	FLJ35880	0	5.23	-	FLJ35906	0	5.1	-	FLJ35914	0	4.98	L
FLJ35918	0	7.74	-	FLJ35931	0	10.63	-	FLJ35976	0	7.69	L	FLJ35991	0	4.74	-
FLJ35995	0	6.68	L	FLJ36014	0	10.73	-	FLJ36038	1	11.01	-	FLJ36045	0	6.16	-
FLJ36053	0	7.72	-	FLJ36059	0	5.37	L	FLJ36134	0	7.08	-	FLJ36176	1	7.81	-
FLJ36207	0	6.66	-	FLJ36231	0	11.52	-	FLJ36242	3	8.16	-	FLJ36251	4	7.66	-
FLJ36256	0	6.09	L	FLJ36274	0	11.57	L	FLJ36294	0	7.07	-	FLJ36303	1	8.41	-
FLJ36306	0	9.51	L	FLJ36307	0	10.4	L	FLJ36310	4	8.38	-	FLJ36326	0	5.16	L
FLJ36338	0	8.21	-	FLJ36339	0	6	-	FLJ36364	0	10.71	-	FLJ36391	0	4.94	L
FLJ36398	0	7.3	-	FLJ36437	0	7.05	-	FLJ36517	0	9.05	-	FLJ36522	0	11	L
FLJ36523	0	3.7	L	FLJ36535	0	6.51	-	FLJ36666	0	8.51	-	FLJ36673	0	9	-
FLJ36674	0	10.56	-	FLJ36688	0	5.07	-	FLJ36689	2	6.24	-	FLJ36691	0	4.73	L
FLJ36696	0	8.33	S	FLJ36767	0	10.19	L	FLJ36771	0	8.75	L	FLJ37164	0	6.53	-
FLJ37209	2	7.83	-	FLJ37231	3	4.64	-	FLJ37245	0	5.01	L	FLJ37251	0	7.59	-
FLJ37254	1	5.4	-	FLJ37287	0	11.41	-	FLJ37292	0	10.15	-	FLJ37301	0	4.47	-
FLJ37322	0	7.43	-	FLJ37323	0	7.61	L	FLJ37339	0	11.71	-	FLJ37342	0	5.3	-
FLJ37349	0	5.09	-	FLJ37357	0	4.66	-	FLJ37362	0	10.92	-	FLJ37379	0	6.77	-
FLJ37388	0	9.49	-	FLJ37401	5	6.87	-	FLJ37409	0	4.3	-	FLJ37415	0	6.52	-
FLJ37421	0	8.92	-	FLJ37428	0	10.7	-	FLJ37432	0	10.41	-	FLJ37451	0	8.67	-
FLJ37528	0	7.98	-	FLJ37538	0	9.71	L	FLJ37550	5	9.8	-	FLJ37561	4	10.19	-
FLJ37562	0	10.44	-	FLJ37568	0	10.2	-	FLJ37578	0	4.45	-	FLJ37635	0	8.29	-
FLJ37642	0	4.87	-	FLJ37670	0	9.46	-	FLJ37679	0	5.3	-	FLJ37689	0	5.67	-
FLJ37698	0	6.68	-	FLJ37790	0	8.76	-	FLJ37987	2	4.45	-	FLJ37999	2	7.92	-
FLJ38006	3	9.71	-	FLJ38008	0	7.8	-	FLJ38024	0	8.38	-	FLJ38041	0	4.96	-
FLJ38117	0	7.22	-	FLJ38124	0	6.13	-	FLJ38127	0	4.59	-	FLJ38129	0	5.38	-
FLJ38131	0	10.8	-	FLJ38135	0	5.54	-	FLJ38138	2	7.87	-	FLJ38139	0	6.87	-
FLJ38140	0	4.26	L	FLJ38141	1	7.1	-	FLJ38143	0	8	-	FLJ38145	0	11.76	-
FLJ38148	0	6.65	-	FLJ38152	0	8.86	-	FLJ38154	11	7.84	-	FLJ38175	0	10.04	-
FLJ38176	0	7.33	-	FLJ38183	1	10.57	-	FLJ38190	0	4.48	-	FLJ38194	0	4.78	L
FLJ38198	0	6.44	-	FLJ38204	0	8.21	L	FLJ38205	0	9.65	-	FLJ38208	0	6.14	-
FLJ38210	1	7.06	-	FLJ38238	0	8.08	-	FLJ38241	0	8.17	L	FLJ38243	0	9.59	-
FLJ38287	0	6.57	-	FLJ38292	0	9.31	-	FLJ38313	0	5.76	-	FLJ38348	0	4.7	-
FLJ38349	0	7.47	-	FLJ38437	4	5.44	-	FLJ38448	0	7.5	-	FLJ38452	0	12.03	-
FLJ38453	0	9.99	-	FLJ38455	0	8.57	-	FLJ38457	0	8.38	-	FLJ38466	0	7.96	-
FLJ38467	0	10.54	L	FLJ38471	0	8.08	-	FLJ38477	0	12.83	-	FLJ38483	0	10.87	L
FLJ38487	0	7.93	S	FLJ38492	0	6.13	-	FLJ38496	0	9.53	-	FLJ38497	2	5.68	-
FLJ38500	0	9.52	-	FLJ38501	0	4.38	-	FLJ38504	0	9.55	-	FLJ38517	0	8.6	-
FLJ38519	1	4.96	-	FLJ38529	0	9.9	-	FLJ38531	0	6.88	-	FLJ38532	0	8.35	-
FLJ38533	0	6.6	-	FLJ38537	0	7.26	-	FLJ38538	0	7.63	-	FLJ38539	0	8.54	-
FLJ38540	0	5.8	-	FLJ38541	0	5.84	L	FLJ38543	0	7.77	-	FLJ38548	0	8.64	-
FLJ38553	0	8.22	-	FLJ38558	0	4.85	-	FLJ38560	0	4.53	-	FLJ38562	1	8.55	-
FLJ38563	0	9.77	L	FLJ38566	0	3.95	L	FLJ38580	0	5.29	-	FLJ38584	0	8.2	-
FLJ38592	0	6.51	L	FLJ38617	2	9.64	-	FLJ38627	0	5.02	L	FLJ38629	0	8.58	-
FLJ38670	0	8.16	-	FLJ38700	4	8.39	-	FLJ38716	0	8.65	-	FLJ38718	0	4.42	-
FLJ38719	0	6.53	L	FLJ38720	2	8.05	-	FLJ38725	0	7.07	-	FLJ38727	3	8.68	-
FLJ38732	0	8.24	-	FLJ38742	0	10.68	-	FLJ38754	0	6.67	-	FLJ38762	0	10.07	L
FLJ38767	0	12.12	L	FLJ38795	0	7.04	L	FLJ38797	1	9.49	-	FLJ38803	0	4.82	L
FLJ38811	0	5.22	L	FLJ38822	1	5.84	-	FLJ38897	0	3.87	-	FLJ38898	0	8.62	-
FLJ38899	1	7.87	-	FLJ38906	0	10.65	-	FLJ38913	0	4.7	-	FLJ38923	0	5.52	-
FLJ38924	4	5.98	-	FLJ38925	0	4.88	-	FLJ38927	0	5.03	-	FLJ38928	1	5.9	-
FLJ38936	0	10.72	-	FLJ38939	0	7.94	-	FLJ38944	0	4.37	L	FLJ38962	0	8.05	-
FLJ38967	0	5.44	L	FLJ38971	2	7.86	-	FLJ38975	0	8.58	-	FLJ38977	0	6.42	-
FLJ38978	0	10.07	L	FLJ38985	0	7.12	-	FLJ38993	3	6.63	-	FLJ38994	0	6.31	-
FLJ38997	0	7.05	-	FLJ39007	0	10.94	-	FLJ39009	0	4.93	-	FLJ39018	1	9.9	-
FLJ39024	0	8.15	-	FLJ39031	0	4.22	L	FLJ39036	0	5.83	-	FLJ39094	0	5.4	L
FLJ39099	0	6.11	L	FLJ39101	1	4.47	L	FLJ39105	1	8.46	-	FLJ39121	0	7.19	-
FLJ39122	1	6.82	-	FLJ39147	0	5.95	L	FLJ39174	5	5.91	-	FLJ39187	0	9.07	-
FLJ39196	0	5	-	FLJ39203	0	6.59	-	FLJ39220	0	6.09	-	FLJ39236	0	7.34	L
FLJ39247	0	6.91	L	FLJ39270	0	8.6	L	FLJ39287	0	8.14	-	FLJ39290	0	8.87	L
FLJ39295	0	6.88	-	FLJ39307	0	6.64	-	FLJ39308	2	7.51	-	FLJ39311	4	8.5	-
FLJ39338	0	10.88	-	FLJ39341	0	11.3	L	FLJ39365	0	9.92	L	FLJ39417	0	8.6	-
FLJ39428	0	5.27	L	FLJ39520	0	7.44	-	FLJ39614	0	8.45	-	FLJ39650	0	4.5	L
FLJ39689	0	10.78	-	FLJ39714	0	8.56	-	FLJ39727	0	6.88	-	FLJ39729	0	4.44	-
FLJ39741	0	9.91	L	FLJ39763	0	4.58	-	FLJ39787	0	8.24	-	FLJ39804	0	8.97	-
FLJ39885	0	8.74	-	FLJ39887	1	7.82	-	FLJ39929	0	7.45	-	FLJ39965	0	8.09	-
FLJ39980	2	11.57	-	FLJ39981	0	9.98	-	FLJ39989	2	9.7	-	FLJ40034	0	8.11	-
FLJ40036	0	8.17	-	FLJ40039	0	11.2	-	FLJ40040	0	8.51	-	FLJ40042	0	8.18	-
FLJ40043	0	6.98	-	FLJ40059	0	10.36	-	FLJ40070	0	5.96	-	FLJ40072	3	6.79	-
FLJ40076	0	8.24	-	FLJ40081	0	10.4	-	FLJ40084	0	5.49	-	FLJ40088	0	6.63	-
FLJ40089	0	9.17	-	FLJ40094	2	6.41	-	FLJ40103	0	9.1	-	FLJ40108	0	9.06	-
FLJ40110	1	7.27	-	FLJ40111	0	8.45	-	FLJ40112	0	4.45	L	FLJ40113	0	4.43	-
FLJ40117	0	9.63	-	FLJ40120	0	7.21	-	FLJ40121	0	9.62	-	FLJ40125	0	10.58	-
FLJ40126	1	7.81	-	FLJ40132	0	8.15	-	FLJ40137	0	6.94	-	FLJ40141	0	8.19	-
FLJ40144	0	8.89	-	FLJ40146	0	5.93	-	FLJ40154	8	7.07	S	FLJ40157	1	6.59	-
FLJ40158	0	4.47	-	FLJ40161	0	8.5	-	FLJ40166	0	4.95	-	FLJ40170	0	7.34	-
FLJ40172	0	9.74	-	FLJ40178	0	10.59	-	FLJ40179	0	4.77	-	FLJ40182	0	4.51	-
FLJ40184	0	8.42	-	FLJ40185	0	8.7	-	FLJ40190	0	9.81	-	FLJ40195	0	7.81	-
FLJ40237	0	6.56	-	FLJ40279	8	8.72	-	FLJ40297	0	5.56	-	FLJ40298	0	9.6	-
FLJ40300	4	8.95	S	FLJ40302	5	6.51	-	FLJ40304	0	4.63	-	FLJ40308	0	4.44	-
FLJ40311	0	4.7	-	FLJ40314	0	7.34	-	FLJ40316	1	7.85	-	FLJ40317	0	4.91	-
FLJ40318	0	11.72	-	FLJ40322	0	7.12	-	FLJ40323	0	7.1	-	FLJ40324	0	7.33	-
FLJ40325	0	9.34	-	FLJ40326	0	6.84	-	FLJ40327	0	6.85	-	FLJ40329	0	9.45	-
FLJ40332	0	8.91	-	FLJ40340	0	8.6	-	FLJ40346	0	4.42	-	FLJ40347	0	7.37	-
FLJ40348	2	7.12	-	FLJ40350	0	7.67	-	FLJ40351	0	5.3	-	FLJ40358	0	7.25	-
FL															

FLJ ID	TM*	pI†	Mobility‡	FLJ ID	TM*	pI†	Mobility‡	FLJ ID	TM*	pI†	Mobility‡	FLJ ID	TM*	pI†	Mobility‡
FLJ40675	0	8.41	-	FLJ40678	0	8.9	-	FLJ40680	1	6.79	-	FLJ40686	0	5.33	-
FLJ40688	2	6.36	-	FLJ40692	0	8.2	-	FLJ40693	0	11.25	-	FLJ40696	0	12.46	-
FLJ40698	0	12.34	-	FLJ40699	0	9.08	-	FLJ40704	0	9.63	-	FLJ40707	0	5.69	-
FLJ40708	0	5.41	-	FLJ40709	0	4.58	-	FLJ40710	0	8.65	-	FLJ40722	0	7.63	-
FLJ40725	0	4.72	-	FLJ40731	0	10.13	-	FLJ40744	0	8.5	-	FLJ40745	3	5.84	-
FLJ40746	1	8.62	-	FLJ40749	0	6.28	-	FLJ40751	0	5.89	-	FLJ40754	1	9.22	-
FLJ40757	0	6.68	-	FLJ40758	0	5.16	-	FLJ40760	0	7.83	-	FLJ40765	0	8.38	-
FLJ40766	6	4.99	-	FLJ40770	0	6.62	-	FLJ40773	0	9.68	-	FLJ40779	0	7.14	-
FLJ40780	0	8.91	-	FLJ40789	0	7.45	-	FLJ40791	0	4.73	-	FLJ40796	0	6.95	-
FLJ40802	0	8.14	-	FLJ40803	1	7.78	-	FLJ40851	0	8.04	-	FLJ40856	0	8.96	-
FLJ40868	0	5.24	-	FLJ40870	0	7.62	-	FLJ40872	0	11.02	-	FLJ40873	0	9.29	-
FLJ40876	0	6.24	-	FLJ40884	0	4.74	-	FLJ40886	0	9.2	-	FLJ40890	0	12.44	-
FLJ40893	2	5.97	-	FLJ40895	0	4.55	-	FLJ40896	0	8.63	-	FLJ40897	0	9.36	-
FLJ40898	5	8.23	S	FLJ40900	0	8.97	-	FLJ40905	0	7.06	-	FLJ40906	0	8.92	-
FLJ40909	0	8.45	-	FLJ40916	0	10.19	-	FLJ40917	2	8.82	-	FLJ40918	0	7.77	-
FLJ40920	0	8.95	S	FLJ40925	0	10.86	-	FLJ40927	0	6.79	-	FLJ40933	0	8.82	-
FLJ40935	0	7.45	-	FLJ40936	1	7.44	-	FLJ40941	0	5.91	-	FLJ40943	0	8.38	-
FLJ40946	1	9.94	-	FLJ40948	0	7.98	-	FLJ40950	0	4.64	L	FLJ40958	0	9.58	-
FLJ40964	0	5.65	L	FLJ40973	0	4.73	-	FLJ40988	0	8.99	L	FLJ40997	0	8.4	-
FLJ41000	0	4.43	L	FLJ41008	0	4.54	-	FLJ41010	0	11.79	-	FLJ41023	0	8.59	-
FLJ41025	0	7.97	-	FLJ41032	0	8.53	-	FLJ41034	7	7.47	-	FLJ41036	5	6.29	L
FLJ41037	0	7.91	-	FLJ41038	0	5.87	-	FLJ41042	0	6.45	-	FLJ41046	1	11.5	-
FLJ41059	0	8.65	-	FLJ41060	0	5.51	-	FLJ41075	0	8.23	-	FLJ41081	0	4.93	-
FLJ41111	0	7.4	-	FLJ41117	0	4.18	L	FLJ41122	0	9.82	L	FLJ41124	0	11.63	-
FLJ41140	0	4.93	-	FLJ41160	0	9.52	-	FLJ41164	0	9.36	-	FLJ41167	0	4.28	-
FLJ41169	0	6.76	-	FLJ41175	0	7.11	-	FLJ41296	2	8.87	-	FLJ41313	1	7.57	-
FLJ41327	0	11.51	-	FLJ41328	1	7.38	-	FLJ41341	0	5.5	-	FLJ41415	1	7.67	-
FLJ41442	1	7.09	-	FLJ41471	0	10.82	-	FLJ41541	0	8.31	-	FLJ41561	0	8.26	-
FLJ41597	0	5.74	-	FLJ41598	0	5.68	-	FLJ41602	0	9.25	-	FLJ41607	0	5.16	-
FLJ41610	0	7.71	-	FLJ41641	0	6.09	-	FLJ41643	0	7.77	-	FLJ41645	0	9.35	-
FLJ41648	0	4.63	-	FLJ41649	0	9.55	-	FLJ41656	0	4.82	-	FLJ41664	0	10.48	-
FLJ41668	0	7.92	-	FLJ41669	0	12.16	-	FLJ41676	0	12.2	-	FLJ41678	0	7.05	-
FLJ41684	0	7.24	-	FLJ41687	9	7.87	S	FLJ41693	0	4.36	-	FLJ41695	1	6.77	-
FLJ41697	0	5.26	-	FLJ41698	0	5.45	-	FLJ41699	0	4.9	-	FLJ41700	0	5.36	-
FLJ41701	0	7.04	-	FLJ41707	4	7.86	S	FLJ41710	0	9.89	-	FLJ41712	0	7.95	-
FLJ41713	0	8.35	-	FLJ41716	1	4.98	-	FLJ41717	0	9.75	-	FLJ41724	0	5.6	-
FLJ41725	0	4.77	-	FLJ41741	0	9.83	-	FLJ41744	2	7.18	-	FLJ41746	0	7.78	-
FLJ41750	0	5.23	-	FLJ41753	6	9.87	S	FLJ41754	0	8.82	-	FLJ41755	9	9.17	S
FLJ41758	1	6.13	-	FLJ41765	1	10.69	-	FLJ41767	0	4.58	-	FLJ41768	0	11.66	-
FLJ41769	0	8.23	-	FLJ41774	0	10.26	-	FLJ41781	0	9.21	L	FLJ41783	0	4.41	-
FLJ41785	5	6.24	S	FLJ41786	0	9.89	-	FLJ41789	0	6.42	-	FLJ41793	0	4.87	-
FLJ41795	0	11.76	-	FLJ41801	1	5.54	-	FLJ41803	0	7.61	-	FLJ41806	0	7.45	-
FLJ41812	0	6.31	-	FLJ41814	0	11.54	L	FLJ41816	0	10.72	-	FLJ41819	0	10.27	-
FLJ41823	0	4.61	-	FLJ41834	0	4.38	-	FLJ41835	0	7.19	-	FLJ41838	0	4.7	-
FLJ41841	0	9.6	-	FLJ41846	0	7.77	-	FLJ41849	1	5.95	-	FLJ41850	0	10.15	-
FLJ41854	0	8.91	-	FLJ41856	0	5.08	-	FLJ41857	0	8.34	-	FLJ41859	0	8.53	-
FLJ41860	0	8.36	-	FLJ41861	0	6.74	-	FLJ41866	0	7.46	-	FLJ41868	1	4.47	-
FLJ41876	0	8.48	-	FLJ41879	0	11.83	-	FLJ41880	0	4.22	L	FLJ41882	0	7.82	-
FLJ41891	0	9.23	-	FLJ41892	0	6.95	-	FLJ41893	0	4.13	L	FLJ41895	2	4.75	-
FLJ41902	0	6.72	-	FLJ41904	0	4.39	-	FLJ41907	0	6.93	-	FLJ41914	0	8.49	-
FLJ41923	0	9.64	-	FLJ41936	0	8.9	-	FLJ41942	0	9.19	-	FLJ41943	0	10.01	-
FLJ41945	0	4.65	-	FLJ41959	4	5.5	S	FLJ41961	0	9.75	-	FLJ41975	0	10.46	-
FLJ41981	0	5.78	-	FLJ41994	0	10.56	-	FLJ41997	0	6.25	-	FLJ42007	2	6.24	-
FLJ42011	0	6.22	-	FLJ42019	0	9.13	-	FLJ42024	0	11.15	-	FLJ42034	0	9.9	-
FLJ42035	1	9.89	-	FLJ42053	0	8.04	-	FLJ42065	0	8.6	-	FLJ42073	0	6.94	-
FLJ42075	0	10.03	-	FLJ42080	0	8.44	-	FLJ42082	4	8.39	S	FLJ42089	0	6.84	-
FLJ42093	0	8.79	-	FLJ42097	0	10.34	-	FLJ42098	1	9.25	-	FLJ42114	1	12.18	-
FLJ42124	0	9.06	L	FLJ42125	0	12.07	L	FLJ42128	3	7.17	-	FLJ42138	0	7.86	-
FLJ42145	0	9.41	-	FLJ42146	0	6.17	-	FLJ42147	0	7.75	-	FLJ42160	2	8	-
FLJ42162	1	11.61	-	FLJ42229	1	7.43	-	FLJ42243	0	9.56	-	FLJ42247	0	7.53	-
FLJ42282	0	9.09	S	FLJ42289	0	11.72	-	FLJ42297	0	7.55	-	FLJ42298	0	8.55	-
FLJ42318	0	6.59	-	FLJ42347	0	5.16	-	FLJ42348	4	7.37	-	FLJ42349	1	7.28	-
FLJ42352	0	8.95	-	FLJ42354	0	3.7	L	FLJ42366	0	5.84	L	FLJ42367	0	10.42	-
FLJ42371	1	9.43	-	FLJ42379	0	5.66	-	FLJ42461	0	9.25	-	FLJ42510	0	6.15	-
FLJ42526	0	6.67	-	FLJ42527	0	4.3	L	FLJ42544	0	8.28	-	FLJ42551	0	12.13	-
FLJ42562	0	7.19	-	FLJ42566	0	5.31	-	FLJ42579	6	9.75	-	FLJ42591	0	4.95	-
FLJ42659	0	8.84	L	FLJ42661	1	6.21	-	FLJ42668	0	4.66	L	FLJ42669	0	4.77	-
FLJ42697	2	7.93	-	FLJ42702	0	7.7	-	FLJ42706	0	9.32	-	FLJ42707	0	8.94	-
FLJ42714	0	6.41	-	FLJ42719	0	8.03	L	FLJ42721	0	8.16	-	FLJ42730	0	6.3	L
FLJ42736	1	4.74	L	FLJ42754	0	4.77	-	FLJ42761	0	5.73	-	FLJ42763	0	12.66	-
FLJ42769	2	6.24	-	FLJ42771	0	10.62	-	FLJ42772	0	8.87	-	FLJ42774	1	9.8	-
FLJ42780	0	11.57	-	FLJ42787	0	12.62	-	FLJ42789	2	9.22	-	FLJ42791	2	8.5	-
FLJ42794	0	7.98	L	FLJ42795	0	10.84	-	FLJ42797	0	8.59	-	FLJ42798	0	3.99	L
FLJ42800	0	4.59	L	FLJ42841	0	5.04	-	FLJ42845	0	6.44	-	FLJ42848	0	7.23	-
FLJ42868	0	8.7	-	FLJ42873	0	12.33	-	FLJ42874	2	8.77	-	FLJ42879	0	8.33	-
FLJ42886	0	5.16	-	FLJ42889	0	5.26	-	FLJ42890	0	5.09	-	FLJ42897	0	6.81	-
FLJ42925	0	7.91	-	FLJ42929	1	6.57	-	FLJ42935	0	9.09	S	FLJ42941	0	4.49	-
FLJ42946	0	9.49	-	FLJ42972	0	6.96	-	FLJ43036	12	7.57	S	FLJ43037	0	5.94	-
FLJ43038	0	4.66	-	FLJ43042	0	9.49	L	FLJ43043	0	6.33	-	FLJ43049	0	8.12	-
FLJ43108	6	9.72	-	FLJ43110	0	5.78	-	FLJ43154	0	5	-	FLJ43157	0	5.36	-
FLJ43158	0	11.45	-	FLJ43168	0	4.86	-	FLJ43173	0	8.91	-	FLJ43180	0	8.68	-
FLJ43188	1	8.77	-	FLJ43190	0	4.88	-	FLJ43193	0	4.33	-	FLJ43197	0	8.9	-
FLJ43200	0	12.15	-	FLJ43202	0	9.97	-	FLJ43207	0	8.37	L	FLJ43209	0	10.06	-
FLJ43211	2	9.31	-	FLJ43214	0	7.07	-	FLJ43237	4	6.47	-	FLJ43238	0	4.97	-
FLJ43251	0	8.35	-	FLJ43253	0	4.5	L	FLJ43254	0	8.1	-	FLJ43277	12	7.17	-
FLJ43284	3	7.05	-	FLJ43286	2	8.29	-	FLJ43287	0	8.67	-	FLJ43289	0	10.12	L
FLJ43295	0	6.9	-	FLJ43354	0	8.86	-	FLJ43357	0	8.87	-	FLJ43363	0	6.18	-
FLJ43370	0	5.66	-	FLJ43372	5	6.18	S	FLJ43373	0	4.71	-	FLJ43374	0	5.08	-
FLJ43385	5	9.87	-	FLJ43388	0	9.86	-	FLJ43395	0	5.58	S	FLJ43439	0	7.24	-
FLJ43447	0	7.67	L	FLJ43465	0	10.45	-	FLJ43468	0	6.17	-	FLJ43472	0	6.11	-
FLJ43481	0	5.69	-	FLJ43485	6	9.84	-	FLJ43488	1	6.52	-	FLJ43493	0	7.86	-
FLJ43531	1	7.27	-	FLJ43535	0	5.69	-	FLJ43547	0	6.72	-	FLJ43554			

FLJ ID	TM*	pI†	Mobility‡	FLJ ID	TM*	pI†	Mobility‡	FLJ ID	TM*	pI†	Mobility‡	FLJ ID	TM*	pI†	Mobility‡
FLJ44306	0	7.77	-	FLJ44309	1	5.78	-	FLJ44317	0	7.34	-	FLJ44352	0	9.09	-
FLJ44353	0	6.77	-	FLJ44359	0	6.52	-	FLJ44403	0	5.22	-	FLJ44410	0	8.38	-
FLJ44420	0	5.96	-	FLJ44436	0	6.92	-	FLJ44445	2	9.1	-	FLJ44452	0	9.76	-
FLJ44463	0	10.3	-	FLJ44464	1	6.75	-	FLJ44466	0	9.02	-	FLJ44470	3	6.26	-
FLJ44474	0	5.21	-	FLJ44483	0	8.48	-	FLJ44484	0	6.49	S	FLJ44490	0	9.36	-
FLJ90002	0	9.89	-	FLJ90003	5	7.49	S	FLJ90005	2	6.19	-	FLJ90012	0	9.16	-
FLJ90014	0	4.9	-	FLJ90016	0	8.22	-	FLJ90018	0	4.23	-	FLJ90023	4	9.09	-
FLJ90024	6	7.44	S	FLJ90033	4	5.92	-	FLJ90034	0	6.94	-	FLJ90035	0	8.21	-
FLJ90037	0	10.26	-	FLJ90039	0	6.77	-	FLJ90041	1	6.13	-	FLJ90043	0	7.18	-
FLJ90048	0	7.42	S	FLJ90049	2	4.48	-	FLJ90051	0	7.09	-	FLJ90052	0	9.94	-
FLJ90053	0	4.51	-	FLJ90056	0	6.39	-	FLJ90057	1	9.42	-	FLJ90059	0	5.29	-
FLJ90061	0	5.32	-	FLJ90062	1	5.13	-	FLJ90063	0	8.83	-	FLJ90067	0	6.84	-
FLJ90069	1	5.82	-	FLJ90071	0	5.33	-	FLJ90072	0	6.58	-	FLJ90074	0	4.26	-
FLJ90075	1	7.37	-	FLJ90079	0	10.56	-	FLJ90083	11	7.13	S	FLJ90085	0	4.61	-
FLJ90088	0	7.96	-	FLJ90089	0	8.06	-	FLJ90092	0	4.13	-	FLJ90093	1	5.97	-
FLJ90094	7	9.62	S	FLJ90095	1	6	S	FLJ90097	0	8.53	-	FLJ90098	0	9.75	-
FLJ90102	1	7.94	-	FLJ90110	0	10.34	-	FLJ90111	0	9.41	-	FLJ90115	0	8.54	-
FLJ90118	0	5.53	-	FLJ90119	7	8.77	S	FLJ90120	0	5.45	-	FLJ90121	0	9.45	-
FLJ90127	0	8.92	-	FLJ90130	5	5.93	S	FLJ90132	0	4.53	-	FLJ90135	0	7.05	-
FLJ90138	1	10.02	-	FLJ90142	1	7.58	-	FLJ90143	0	4.92	-	FLJ90144	0	8.55	-
FLJ90146	6	10.24	S	FLJ90147	0	4.87	-	FLJ90151	2	4.85	-	FLJ90156	2	6.51	-
FLJ90158	1	10.95	-	FLJ90160	0	9.35	-	FLJ90162	1	9.03	-	FLJ90164	2	10.06	-
FLJ90165	3	5.86	-	FLJ90166	2	8.94	-	FLJ90167	3	8.99	S	FLJ90168	1	7.88	-
FLJ90302	0	10.99	-	FLJ90304	1	9.74	-	FLJ90305	2	7.03	-	FLJ90306	0	9.86	-
FLJ90307	0	10.29	-	FLJ90309	2	6.83	-	FLJ90310	2	4.41	-	FLJ90312	2	7.23	-
FLJ90313	0	7.59	-	FLJ90314	0	9.12	-	FLJ90315	0	4.01	-	FLJ90316	11	8.38	S
FLJ90317	0	9.26	-	FLJ90318	0	6.87	-	FLJ90319	0	5.91	-	FLJ90321	0	8.22	-
FLJ90323	0	5.84	-	FLJ90324	0	4.38	-	FLJ90325	0	8.12	-	FLJ90326	0	7.78	-
FLJ90328	0	9.78	-	FLJ90329	0	9.67	-	FLJ90331	0	4.76	-	FLJ90333	1	8.61	-
FLJ90336	0	4.33	-	FLJ90338	4	9.78	-	FLJ90340	0	7.33	-	FLJ90341	0	8.45	-
FLJ90342	9	5.4	S	FLJ90344	1	4.74	-	FLJ90346	1	9.12	-	FLJ90347	2	6.94	-
FLJ90350	0	7.6	-	FLJ90352	0	8.91	-	FLJ90355	10	9.22	S	FLJ90356	0	5.46	-
FLJ90357	4	4.01	-	FLJ90358	0	8.44	-	FLJ90361	0	7.98	-	FLJ90363	2	7.64	S
FLJ90364	0	6.75	-	FLJ90365	0	9.13	-	FLJ90366	0	5.14	-	FLJ90367	3	8.96	-
FLJ90369	0	6.79	-	FLJ90370	4	5.8	S	FLJ90373	1	8.16	-	FLJ90374	1	8.04	-
FLJ90375	0	5.21	L	FLJ90377	0	7.5	-	FLJ90378	0	7.84	-	FLJ90382	0	6.34	-
FLJ90383	1	6.31	-	FLJ90384	13	6.31	S	FLJ90385	0	6.35	-	FLJ90386	0	9.34	-
FLJ90389	8	6.72	S	FLJ90392	0	9.58	-	FLJ90393	9	8.6	S	FLJ90395	3	4.86	-
FLJ90397	0	8.8	-	FLJ90399	0	6.79	-	FLJ90402	2	8	-	FLJ90403	0	7.08	-
FLJ90404	0	8.1	-	FLJ90408	6	9.74	S	FLJ90409	8	8.25	S	FLJ90410	0	6.82	-
FLJ90411	0	10.32	-	FLJ90412	0	6.72	-	FLJ90415	0	10.27	-	FLJ90416	4	6.07	-
FLJ90417	5	9.25	S	FLJ90418	0	5.3	-	FLJ90530	1	9.72	-	FLJ90531	2	5.9	-
FLJ90532	0	6.79	-	FLJ90533	13	6.11	S	FLJ90534	5	8.73	-	FLJ90536	1	8.59	-
FLJ90539	0	6.41	-	FLJ90540	0	6.51	-	FLJ90542	1	8.73	-	FLJ90543	0	4.9	-
FLJ90545	0	7.99	-	FLJ90548	0	8.35	-	FLJ90556	0	6.93	-	FLJ90558	4	9.51	-
FLJ90561	0	8.28	-	FLJ90562	0	11.08	-	FLJ90565	9	8.01	-	FLJ90567	0	7.82	-
FLJ90568	1	5	-	FLJ90573	0	9.01	-	FLJ90574	0	5	-	FLJ90575	0	4.61	L
FLJ90576	0	10.07	-	FLJ90581	0	8.72	-	FLJ90582	0	10.09	-	FLJ90583	1	6.91	-
FLJ90584	1	6.04	-	FLJ90585	0	9.67	-	FLJ90586	2	4.42	L	FLJ90587	10	8.79	S
FLJ90591	3	8.19	S	FLJ90595	1	10.05	-	FLJ90597	5	8.58	-	FLJ90598	0	9.1	-
FLJ90599	0	4.69	-	FLJ90600	5	7.8	S	FLJ90602	1	7.22	-	FLJ90603	0	9.34	-
FLJ90604	0	4.2	L	FLJ90614	0	5.18	-	FLJ90616	0	4.97	-	FLJ90619	0	5.14	-
FLJ90620	1	6.16	-	FLJ90621	0	5.22	-	FLJ90622	4	10.12	S	FLJ90623	0	7.16	-
FLJ90624	0	8.47	-	FLJ90625	4	6.66	-	FLJ90626	0	5.95	-	FLJ90627	0	9.11	-
FLJ90628	0	7.43	-	FLJ90629	0	7.15	-	FLJ90630	0	9.01	-	FLJ90631	0	6.39	-
FLJ90633	1	6.3	-	FLJ90634	0	6.58	-	FLJ90636	1	7.49	-	FLJ90637	0	11.37	-
FLJ90638	7	8.33	-	FLJ90642	0	5.41	-	FLJ90646	3	11.37	-	FLJ90647	4	6.54	-
FLJ90650	0	5.52	-												

*The number of transmembrane domains was predicted using SOSui system (<http://bp.nuap.nagoya-u.ac.jp/sosui/>).

†The isoelectric point.

‡S, faster-migrating; L, slower-migrating.

Supplementary Table 5. Protein phosphatase activity in five different buffers.

Family	Class	Gene	FLJ ID	Buffer*					Intrinsic inability against pNPP†			
				Lambda	NEBuffer 3	YOP	Acidic	Imidazole-based	Description‡	References		
Serine/Threonine Phosphatase												
PPP family	PP1	PPP1CA	FLJ94150	+++	++	–	–	n.t.				
		PPP1CB	FLJ92643	++	+	–	–	–				
		PPP1CC	FLJ82577	+++	+++	–	–	–				
	PP2A	PPP2CA	FLJ40280	–	–	–	–	–				
		PPP2CB	FLJ34556	–	–	–	n.t.	–				
	PP2B	PPP3CA	FLJ85501	+++	++	–	–	–				
		PPP3CB	FLJ83551	+++	++	–	–	–				
	PP4	PPP4C	FLJ80951	+/–	–	–	–	–				
		PP5	PPP5C	FLJ93076	+++	++	++	+	++			
	PPM family	PP6	PPP6C	FLJ92648	–	–	–	+/–	–			
			PPM1A	FLJ93859	++	++	–	–	–			
		PP2C	PPM1B	FLJ31447	++	++	–	–	–			
			PPM1D	FLJ93348	+++	+	–	–	–			
		PPM1F	FLJ75716	++	+/–	–	–	–				
PPM1G		FLJ92810	+++	++	–	–	–					
PPM1J		FLJ35951	+++	++	–	–	–					
PPM1K		FLJ30116	++	–	–	–	–					
PPM1M		FLJ32332	–	–	–	–	+					
ILKAP		FLJ10181	++	+/–	–	–	–					
PDP	PPM2C	FLJ44914	–	–	–	–	–					
	PDP2	FLJ75807	+/–	–	–	–	–					
Tyrosine Phosphatase												
Class I PTPs (classic)	Receptor PTP	PTPRE	FLJ80893	+++	+++	+++	+++	+++				
		PTPRF	FLJ43335	++	++	+++	+++	+++				
		PTPRN	FLJ16131	+/–	–	–	+/–	–	M	3		
		PTPRN2	FLJ80529	–	–	–	–	–	M	3		
		PTPRR	FLJ92701	+++	+++	+++	+++	+++				
	Non-receptor PTP	PTPN1	FLJ75657	+++	+++	+++	+++	+++				
		PTPN2	FLJ75808	+++	+++	+++	+++	+++				
		PTPN4	FLJ95723	++	+++	+++	++	+++				
		PTPN5	FLJ45381	++	n.t.	++	++	++				
		PTPN6	FLJ93911	+++	+++	+++	+++	+++				
		PTPN7	FLJ45281	+++	+++	+++	+++	+++				
		PTPN11	FLJ75588	++	+	++	++	++				
		Class I PTPs (DSPs)	MAPKP	DUSP4	FLJ95698	++	++	++	+	+++		
				DUSP5	FLJ82357	++	++	++	++	++		
DUSP6	FLJ34434			+	+/–	+/–	+/–	–				
Atypical DSP	DUSP9		FLJ94996	–	–	–	–	–				
	DUSP16		FLJ31411	+	+	+	+	+/–				
	STYXL1		FLJ82648	+	–	–	–	–	M	4		
	DUSP3		FLJ26312	+++	+++	+++	+++	+++				
	DUSP11		FLJ96281	–	++	+++	–	++				
	DUSP12		FLJ81785	–	–	+/–	–	–				
	DUSP13		FLJ32450	++	++	++	n.t.	n.t.				
	DUSP14	FLJ95796	+++	+++	+++	+++	+++					
	DUSP15	FLJ34641	–	–	–	+	–					
	DUSP18	FLJ31512	++	++	+++	+++	++					
	DUSP19	FLJ94749	+	+	+	+	+					
	DUSP22	FLJ35864	–	–	–	–	–					
	DUSP23	FLJ20442	–	–	+/–	+/–	+					
	DUSP26	FLJ31142	–	–	+/–	+/–	n.t.					
	RNGTT	FLJ92740	–	–	–	–	–					
	Class II PTPs	Sling-shots	STYX	FLJ40876	–	–	–	–	–			
			SSH1	FLJ38102	+/–	–	–	–	–			
SSH3			FLJ23852	++	++	++	+/–	++				
PRLs		PTP4A1	FLJ08177	–	–	+/–	+/–	–				
		PTP4A2	FLJ84787	–	–	+/–	+/–	n.t.				
CDC14		CDC14B	FLJ44424	++	++	+++	+++	+++				
		CDKN3	FLJ25787	n.t.	+/–	–	+	–				
PTEN		PTPDC1	FLJ75103	–	–	–	–	–				
		PTEN	FLJ94145	+/–	–	+/–	–	–	SS	5		
Myotubularins		TPTE	FLJ95041	–	–	+	–	+	SS	5		
		TENC1	FLJ16320	–	–	–	–	–	M	6		
		MTM1	FLJ84905	–	–	–	–	–	SS	5		
		MTMR4	FLJ82188	–	+/–	+/–	+	+/–	SS	7		
		MTMR6	FLJ95421	–	–	–	–	–	SS	7		
	MTMR8	FLJ84237	–	–	–	–	–	SS	7			
	MTMR9	FLJ20437	–	–	–	–	–	M	7			
	MTMR10	FLJ20313	–	–	–	–	–	M	7			
CDC25s	MTMR11	FLJ39681	–	–	–	–	–	M	7			
	MTMR14	FLJ90311	–	–	–	–	–	SS	8			
Class II PTPs	CDC25s	CDC25A	FLJ81806	–	++	++	–	++				
		CDC25C	FLJ40391	–	–	++	–	+/–				
Asp-based Others	Eya	EYA1	FLJ45899	++	++	–	+	+				
-	RCP/SCP	SSU72	FLJ10947	++	++	++	+/–	++				
	-	PHPT1	FLJ82653	++	++	++	++	++				

Phosphatase activities were shown as +++, ++, +, +/-, –, n.t., not tested.

* Ingredients of each buffer are as follows: 1) λ -PPase Reaction Buffer (New England Biolabs) containing 50 mM Tris-HCl (pH 7.5), 2 mM MnCl₂, 5 mM DTT and 0.01% Brij35; 2) NEBuffer 3 (New England Biolabs) containing 50 mM Tris-HCl (pH 7.9), 10 mM MgCl₂, 100 mM NaCl and 1 mM DTT; 3) YOP reaction buffer (New England Biolabs) containing 50 mM Tris-HCl (pH 7.0), 100 mM NaCl, 5 mM DTT, 2 mM EDTA and 0.01% Brij35; 4) acidic buffer containing 50 mM MES (pH 6.0), 5 mM DTT and 1 mM EDTA; 5) imidazole-based buffer containing 25 mM imidazole (pH 7.2) and 10 mM DTT.

† Feature of clones harboring intrinsic inability against pNPP.

‡ M, mutation in a phosphatase domain; SS, phosphatidylinositol-specific substrate specificity.

Supplementary Table 6. Relative log ratios of 622 genes of which expression levels were altered.

No	Description of gene function	GenBank accession number	commercial OSM_2	<i>in vitro</i> synthesized FLAG-OSM	commercial OSM_1	<i>in vitro</i> synthesized His-FLAG-IL-1β	<i>in vitro</i> synthesized GST-FLAG-IL-1β	commercial IFN-β_2	<i>in vitro</i> synthesized FLAG-IFN-β	commercial IFN-β_1	commercial IL-1β_1	<i>in vitro</i> synthesized mature IL-1β	commercial IL-1β_2	<i>in vitro</i> synthesized FLAG-TNF-α	commercial TNF-α_1	commercial TNF-α_2
1	poly(A) binding protein, cytoplasmic 4 (inducible form) (PABPC4), mRNA	NM_003819	-0.1339	-0.1809	0.0124	0.3315	0.0019	-1.6749	-0.9684	-1.0749	-0.4958	-0.3165	-0.3673	-0.3811	-0.8913	-1.2278
2	eukaryotic translation initiation factor 3, subunit 6 interacting protein (EIF3S6IP), mRNA	NM_016091	0.0104	-0.0487	0.0591	-0.21	-0.029	-1.5933	-0.966	-1.0602	-0.4696	-0.3832	-0.3074	-0.3324	-0.9565	-1.3403
3	eukaryotic translation initiation factor 3, subunit 5 (epsilon, 47kD) (EIF3S5), mRNA	NM_003754	-0.2323	-0.2323	-0.0284	-0.2434	-0.1339	-1.6723	-0.9319	-0.6086	-0.4122	-0.3703	-0.2732	-0.4406	-0.6045	-1.2285
4	HSP22-like protein interacting protein (LOC64165), mRNA	NM_022348	-0.1371	-0.1162	-0.2776	-0.4391	-0.2616	-1.6358	-1.303	-0.649	-0.2154	-0.1151	-0.363	-0.6611	-0.8765	-0.8442
5	ribosomal protein L17 (RPL17), mRNA	NM_000985	-0.3871	-0.3298	0.2823	0.1906	-0.0007	-1.0882	-0.7018	-0.7021	0.1291	-0.0375	-0.3789	-0.3084	-0.4828	-1.6005
6	glutathione S-transferase M3 (brain) (GSTM3), mRNA	NM_000849	-0.7771	-0.5858	-0.2128	-0.5834	-0.4792	-1.3359	-0.6543	-0.9808	-0.3899	-0.2947	-0.0441	-0.7938	-0.8854	-1.684
7	ribosomal protein L13a (RPL13A), mRNA	NM_012423	-0.6459	-0.5385	0.0556	-0.3564	-0.1204	-0.9731	-0.6451	-0.7563	-0.3958	-0.2469	-0.3937	-0.8232	-0.82	-1.8045
8	ribosomal protein L7 (RPL7), mRNA	NM_000971	-0.2159	-0.2561	0.0814	-0.5185	-0.0989	-1.4157	-0.6064	-1.0617	-0.5664	-0.25	-0.6199	-0.5712	-0.7401	-1.7477
9	cDNA FLJ31899 fis, clone NT2RP7004173.	AK056461	-0.4013	-0.6795	-0.2158	-0.3256	-0.2654	-0.7827	-0.6069	-0.4522	-0.7182	-0.4804	-0.1958	-1.1784	-0.9487	-1.5916
10	extracellular matrix protein 1 (ECM1), transcript variant 1, mRNA	NM_004425	-0.6185	-0.9021	-0.2605	-0.2527	0.278	-0.5427	-0.3521	-0.0454	-0.54	-0.2449	-0.565	-0.5946	-0.6094	-1.8446
11	discs, large (Drosophila) homolog 4 (DLG4), mRNA	NM_001365	-0.336	-0.3496	0.0232	0.0637	0.2988	-0.0997	0.3292	-0.286	-0.6276	-0.4633	-0.27	-0.4623	-0.8853	-1.5838
12	latexin protein (LXN), mRNA	NM_020169	0.1468	0.4809	-0.0597	-0.6163	-0.4604	-2.1121	-0.8644	-0.6375	-0.5023	0.1976	-0.3273	-1.466	-1.4083	-2.0078
13	T-cell leukemia/lymphoma 6 (TCL6), transcript variant TCL6a1, mRNA	NM_012468	-1.0552	0.0213	0.104	-0.3684	0.841	-1.3953	-0.0501	-0.4956	-1.5822	-0.4582	0.3217	-0.1677	-0.5889	-1.8269
14	Lutheran blood group (Auberger b antigen included) (LU), mRNA	NM_005581	-0.2384	-0.2989	0.4077	-0.3549	-0.1963	-0.297	-0.079	-0.0757	-0.8998	-0.991	-1.3528	-1.2182	-1.3593	-1.816
15	similar to phospholipase C, delta (LOC113026), mRNA	NM_133373	-0.7199	-0.3093	-0.2961	-0.6046	0.226	-0.6405	-0.178	-0.3476	-0.8706	-1.0108	-1.306	-1.3631	-1.1115	-2.1591
16	hypothetical protein MGC11134 (MGC11134), mRNA	NM_031472	-0.4541	-0.3632	-0.0224	-0.1984	-0.0385	-0.5743	-0.3798	-0.3433	-1.4522	-1.254	-0.8308	-0.8318	-0.9468	-1.6329
17	cDNA FLJ42307 fis, clone TRACH2005066.	AK124300	0.0949	0.097	-0.0905	-0.4946	-0.0586	-0.3413	-0.5602	-0.3083	-1.5142	-1.667	-1.03	-0.7323	-1.3011	-0.9442
18	gap junction protein, alpha 4, 37kD (connexin 37) (GJA4), mRNA	NM_002060	-0.2052	-0.6825	-0.1401	-0.4853	0.0018	-0.2515	-0.4335	-0.8136	-1.7244	-1.2423	-1.9263	-1.2792	-0.7194	-1.1586
19	L-3-hydroxyacyl-Coenzyme A dehydrogenase, short chain (HADHSC), mRNA	NM_005327	-0.1776	-0.2705	0.0589	-0.5231	0.0312	-0.8977	-0.5063	-0.1755	-1.509	-0.6096	-1.719	-1.1391	-0.5552	-1.2866
20	transgelin (TAGLN), mRNA	NM_003186	0.037	-0.1025	0.3776	-0.5027	0.0037	0.0742	0.1506	-0.8193	-0.8254	-0.7759	-1.0946	-0.4319	-1.6318	-1.3468
21	leukotriene B4 12-hydroxydehydrogenase	NM_012212	-0.2352	0.311	0.3721	-0.5816	-0.3473	-0.4541	-0.1199	0.2557	-1.0776	-0.7951	-0.4936	-1.1401	-0.828	-1.7262
22	platelet/endothelial cell adhesion molecule (CD31 antigen) (PECAM1), mRNA	NM_000442	0.1697	0.2226	0.0848	-0.1032	-0.472	-0.1167	-0.0723	0.5492	-0.6303	-0.4216	-0.3113	-1.2855	-0.3079	-1.7126
23	epithelial V-like antigen 1 (EVA1), mRNA	NM_005797	0.6536	0.6523	-0.0395	-0.6404	-0.7682	-0.259	-0.3528	-0.0155	-0.6047	-0.4382	-0.7451	-1.4253	-1.0805	-1.6533
24	hairy homolog (Drosophila) (HRY), mRNA	NM_005524	-0.2775	-0.0671	0.2665	-0.8339	-0.348	0.0533	0.0702	0.2704	-0.6591	-0.5962	-0.584	-1.7033	-1.3493	-1.9443
25	TRAM-like protein (KIAA0057), mRNA	NM_012288	-0.3579	-0.4135	-0.5583	-0.978	-0.5067	-0.2698	0.1714	0.0046	-0.3283	-0.6252	-0.6121	-1.1502	-1.3709	-1.8119
26	mRNA for FLJ00269 protein.	AK122582	-0.2721	-0.6414	-0.1056	-0.5673	-0.1131	-0.7094	-0.5159	0.0574	-0.6446	-0.513	-0.7996	-1.8917	-0.9136	-1.6313
27	caveolin 1, caveolae protein, 22kD (CAV1), mRNA	NM_001753	-0.7137	-0.2111	-0.4393	-0.1558	-0.5915	-0.6266	-0.9502	0.7284	-0.7203	-0.6531	-0.9276	-1.5846	-0.7567	-1.1809
28	cDNA FLJ13209 fis, clone NT2RP4000424.	AK023271	-0.3544	0.4676	-0.1513	-0.648	-0.713	-1.1055	-0.9094	0.4944	-0.5332	-0.6722	-0.2672	-1.484	-1.0152	-1.6043
29	LIM domain binding 2 (LDB2), mRNA	NM_001290	-0.1945	0.2595	-0.5959	-0.8549	-1.1064	-0.8889	-0.9148	0.1684	-1.2596	-1.0577	-0.317	-1.3349	-0.2531	-1.8266
30	similar to immediate early protein homo	XM_293537	-0.462	-0.392	-0.1736	-1.6022	-1.5217	-0.898	-0.6374	-0.4417	-0.7913	-0.5058	-0.7052	-1.2894	-0.6311	-1.4065
31	protein kinase C, eta, mRNA (cDNA clone	BC037268	-1.0602	-0.684	0.1028	-0.1996	-0.8313	-1.0799	-1.0634	0.2595	0.0991	-0.0554	-0.5969	-1.4987	-0.3777	-1.6913
32	kinase insert domain receptor (a type III receptor tyrosine kinase) (KDR), mRNA	NM_002253	-0.7789	-0.2021	0.032	-0.4634	-0.9822	-0.7009	-1.0002	0.6514	0.1576	0.5457	-0.3329	-0.8939	-0.1604	-2.0705
33	insulin-like growth factor binding protein 5 (IGFBP5), mRNA	NM_000599	-0.7472	-0.1248	0.5221	-0.143	-0.3496	-0.4793	-0.1291	0.7685	-0.5224	-0.3619	-0.5567	-1.7719	0.3219	-2.0961
34	discs, large (Drosophila) homolog 1 (DLG1), mRNA	NM_004087	-0.3545	0.3622	0.4515	-0.0292	-0.8663	-1.7899	-1.0455	0.9556	-0.9109	-0.1932	-0.6004	-1.0765	-0.2535	-1.3807
35	retinal short-chain dehydrogenase/reductase retSDR2 (LOC51170), mRNA	NM_016245	0.2021	0.5353	0.4632	-0.4672	-0.3745	-1.6285	-1.2057	0.215	-0.521	-0.2108	-0.4323	-0.7762	0.1607	-1.1999
36	fatty acid binding protein 5 (psoriasis-associated) (FABP5), mRNA	NM_001444	-0.7945	-0.3603	-0.3156	-0.3409	-0.0096	-2.1892	-1.1009	-0.1699	-0.8092	-0.4513	-0.1482	-1.3876	0.0518	-1.4571
37	regulator of G-protein signalling 5 (RGSS5), mRNA	NM_003617	0.6003	0.194	-0.8506	-0.4354	-1.2025	-1.102	-0.8063	-0.862	-1.6751	-0.6929	-0.2232	-0.7576	-1.0091	-0.8128
38	cytokine-like protein C17 (C17), mRNA	NM_018659	-0.1341	0.857	-0.4898	-0.9027	-0.9254	-1.0645	-0.9239	-1.1373	-2.0793	-0.3469	-1.0053	-0.8708	-1.4136	-1.1022
39	DnaJ (Hsp40) homolog, subfamily B, member 4 (DNAJB4), mRNA	NM_007034	0.732	1.25	-0.7057	-0.3822	-1.3538	-0.891	-0.0973	0.4459	-1.6511	-0.4323	-1.0999	-1.8353	-1.4231	-1.4548
40	cysteine and tyrosine-rich protein 1 (CYR1), mRNA	NM_052954	1.1718	1.6322	-0.0079	-0.3354	-0.858	-0.5462	-0.122	-0.0383	-1.0737	0.0732	-0.1934	-1.6576	-1.5686	-1.7888
41	immunity associated protein 1 (IMAP1), mRNA	NM_130759	0.4231	-0.0085	-0.2532	-0.7048	-0.8153	0.2533	0.3703	-0.4657	-1.611	-0.939	-0.2031	-1.6492	-0.9916	-1.7497
42	5-hydroxytryptamine (serotonin) receptor 1B (HTR1B), mRNA	NM_000863	0.0148	0.9117	-0.7009	0.2067	-0.3798	0.6277	0.0651	-0.1174	-1.581	-0.9678	-0.4283	-1.196	-0.9969	-1.053
43	AT2 receptor-interacting protein 1 (ATIP1), mRNA	NM_020749	0.5439	0.7932	0.1366	0.4131	-0.4305	0.0052	-0.0142	0.4496	-0.8866	-0.0288	-0.3257	-1.8874	-0.7758	-0.8785
44	cDNA FLJ39952 fis, clone SPLEN2024577.	AK097271	-0.1356	-0.3685	-0.1012	-0.3154	0.0106	-0.1575	0.1137	-0.2062	-1.765	-0.6159	0.2771	-0.5456	-0.5552	-0.6152
45	hypothetical protein FLJ12768 (FLJ12768), mRNA	NM_025163	-0.3404	-0.234	-0.1693	-0.1172	-0.5911	-0.3155	-0.2286	-0.4771	-1.6971	-1.3027	0.3894	-0.5013	-0.5303	-1.058
46	cDNA: FLJ21638 fis, clone COL08269.	AK025291	-0.4795	-0.3153	-0.8097	0.073	0.3521	-0.0664	0.1378	-0.3556	-1.8183	-0.7866	0.9266	-0.4578	-0.5116	-0.5226
47	hypothetical protein MGC12837 (MGC12837), mRNA	NM_032726	-0.8341	-0.5801	0.5202	-0.1218	0.0998	0.2654	-0.7568	0.0325	-1.5831	-0.5448	0.1513	-0.9108	-0.2906	-1.0997
48	KIAA0808 gene product (KIAA0808), mRNA	NM_014729	-1.1765	-0.8243	-0.7522	0.0382	-0.1841	0.1105	0.2635	0.1358	-1.6352	-1.2501	-1.134	0.3374	0.1176	0.076
49	T-box 1 (TBX1), transcript variant B, mRNA	NM_005992	-0.6874	-0.3964	-0.4993	-0.4253	-0.0021	0.3108	-0.0304	-0.2619	-0.9805	-0.7214	-0.9417	-1.6675	-1.8166	-2.0513
50	thioredoxin reductase 2 (TXNRD2), mRNA	NM_006440	-0.9019	-0.6241	-0.6065	-0.3133	0.1828	0.4273	0.0943	-0.4058	-0.8816	-0.8557	-0.9796	-1.6931	-2.2296	-2.3018
51	intercellular adhesion molecule 2 (ICAM2), mRNA	NM_000873	-0.4662	-1.1602	-1.0283	-0.4716	-0.3092	0.3376	0.4958	-1.1702	-0.9153	-0.7015	-0.8446	-1.2833	-1.7603	-2.7282
52	biglycan (BGN), mRNA	NM_001711	-0.6331	-0.8107	-1.0157	-1.0792	-0.8623	-0.0635	0.3564	-1.1861	-0.9041	-1.201	-0.2633	-1.5158	-1.7153	-2.0113
53	NOTCH4-like protein (ZNEU1) mRNA, comple	AF186111	0.1077	-0.3423	0.0156	-0.6703	-0.1163	0.8799	0.4013	-0.3554	-0.3778	-0.0633	-0.4084	-1.2737	-0.9903	-1.6708
54	cDNA: FLJ23163 fis, clone LNG09751.	AK026816	-0.5224	-0.4356	-1.0035	-0.4641	-0.1797	0.4384	0.1523	-0.6008	-0.6609	-0.0448	0.0923	-1.3436	-1.7179	-1.4218
55	cDNA DKFZp564C1516 (from clone DKFZp564C	AL049930	-1.0138	-1.4525	-0.3275	-0.4473	-0.6403	-0.5682	0.0006	-0.6616	-1.2265	-0.4792	-0.3892	-1.063	-0.6658	-1.582
56	phospholipase C, beta 2 (PLCB2), mRNA	NM_004573	-0.5281	-0.9534	-0.589	-0.7034	-0.0219	0.0749	0.5725	-0.5361	-1.6912	-0.7061	-0.788	-1.2058	-0.9321	-1.5624
57	hypothetical protein FLJ10044 (FLJ10044), mRNA	NM_017980	-0.3007	-0.8537	0.229	-0.6733	-0.4324	0.2251	0.4509	-0.2667	-1.5073	-0.7625	-1.6427	-1.0814	-0.7919	-2.2561
58	endothelial cell adhesion molecule (ESAM	NM_138961	-0.3579	-0.9455	-0.0759	-1.4349	-1.7195	0.2687	0.1494	-0.2932	-1.0548	-0.5199	-1.0537	-1.0232	-0.7416	-2.7247
59	mRNA for FLJ00133 protein.	AK074062	0.1284	0.0594	-0.5507	-1.6699	-0.9345	0.2223	-0.0445	-1.0268	-1.1362	-0.375	-1.1875	-1.5013	-1.7821	-1.3721
60	von Willebrand factor (VWF), mRNA	NM_000552	0.4839	0.0662	0.1825	-0.7333	-1.5383	0.6393	0.7009	-1.4114	-1.1146	-0.1486	-0.5747	-0.4598	-1.9368	-1.9529
61	ribonuclease, RNase A family, 1 (pancreatic) (RNASE1), mRNA	NM_002933	-0.6033	-0.3725	-1.2354	-1.2294	-1.244	0.229	1.379	-1.55						

No	Description of gene function	GenBank accession number	commercial OSM_2	<i>in vitro</i> synthesized FLAG-OSM	commercial OSM_1	<i>in vitro</i> synthesized His-FLAG-IL-1 β	<i>in vitro</i> synthesized GST-FLAG-IL-1 β	commercial IFN- β _2	<i>in vitro</i> synthesized FLAG-IFN- β	commercial IFN- β _1	commercial IL-1 β _1	<i>in vitro</i> synthesized mature IL-1 β	commercial IL-1 β _2	<i>in vitro</i> synthesized FLAG-TNF- α	commercial TNF- α _1	commercial TNF- α _2
79	aldehyde dehydrogenase 1, soluble (ALDH1), mRNA	NM_000689	0.684	1.2651	1.108	-0.1069	0.1535	-0.7829	-1.0148	0.7532	-1.1146	-1.1146	-1.0362	-2.4522	-1.7871	-1.7892
80	glycoprotein hormone beta 5 (GPHB5), mRN	NM_145171	0.0098	-0.2764	-0.0584	-1.643	-0.3411	0.2746	0.0741	-0.2432	-0.1317	0.3523	0.5286	0.2686	0.0247	-0.5765
81	TMTSP for transmembrane molecule with thrombospondin module (LOC55901), mRNA	NM_018676	-0.0603	-0.1101	-0.439	-1.9043	-0.1305	0.7909	0.2622	-0.1365	-0.1248	0.4135	0.1324	0.1767	-0.2285	0.0114
82	cDNA: FLJ22945 fis, clone KAT09065.	AK026598	-0.217	-0.4005	-0.2794	-1.6187	-0.829	-0.0478	0.2848	-0.2336	-0.127	-0.3739	-0.4851	-0.207	-0.7888	-0.5184
83	cDNA FLJ32276 fis, clone PROST2000105, moderately similar to CALPAIN 2, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17)	AK056838	-0.22	0.088	-0.2956	-1.6684	-1.3622	0.5782	1.0091	-0.3851	-0.7756	-0.5135	0.0604	0.3972	-0.2626	0.2403
84	KIAA1858 protein (KIAA1858), mRNA.	XM_040592	-0.3625	-0.0074	-0.1886	-1.8056	-1.5979	-0.0938	0.0712	-0.4286	-0.7459	0.0055	1.1816	-0.2026	-0.0836	-0.0095
85	cDNA FLJ34546 fis, clone HLUNG2008959.	AK091865	-0.7725	-0.3744	-0.9949	-1.2004	-1.9789	-0.5812	-0.3736	-0.6755	-0.981	-0.2207	0.9911	-0.3711	-0.5771	-0.7394
86	cDNA FLJ35340 fis, clone PROST2015710.	AK092659	-0.0079	0.2642	-0.1344	-0.8021	-1.4467	-0.2923	-0.2064	-0.416	-0.2808	0.3059	-0.4092	-0.4795	-0.3826	-1.964
87	MD-2 protein (MD-2), mRNA.	NM_015364	0.1568	-0.3642	0.1801	-1.0858	-1.1066	0.4024	0.6035	-0.319	-0.2025	0.9946	-0.987	-0.933	-0.4281	-1.7
88	Rap1 guanine-nucleotide-exchange factor directly activated by cAMP (EPAC), mRNA	NM_006105	-0.4135	-0.6488	-0.4014	-1.6747	-1.0565	0.0997	0.4626	-1.3947	-0.8305	0.434	-0.771	-0.3493	-0.7449	-1.5762
89	roundabout homolog 4, magic roundabout i	NM_019055	-0.9491	-1.3156	-0.4626	-1.0566	-1.1779	0.2809	-0.1077	-0.5088	0.5316	1.0781	-0.4819	1.608	-0.2004	-2.1058
90	ankyrin repeat and MYND domain containiir	NM_020319	-0.3799	-0.528	0.2867	-0.1709	-1.8603	-0.8793	-0.2247	0.186	-0.374	-0.3216	-0.4343	-0.3343	0.2407	-0.179
91	a disintegrin and metalloproteinase domain 23 (ADAM23), mRNA	NM_003812	0.7378	0.2625	0.6775	-1.11	-1.6324	-1.0395	-0.0201	-0.2136	-0.5372	0.0286	-0.6183	-0.2861	0.395	-1.5005
92	protein tyrosine phosphatase, receptor type, B (PTPRB), mRNA	NM_002837	-0.16	0.712	0.2113	-2.0807	-1.9417	0.0811	-0.3871	0.566	-0.1488	1.4663	-0.7611	0.494	0.4295	-0.5612
93	adenylate cyclase 4 (ADCY4), mRNA.	NM_139247	-0.3023	0.4383	0.9362	-1.8719	-1.3773	1.2007	-0.1424	0.4198	-0.5148	0.4019	-1.0812	0.7479	-0.0827	-0.7064
94	putative G protein-coupled receptor (GPCR150), mRNA	NM_014373	-0.8596	-0.925	0.7918	0.0921	0.2926	-0.4919	-0.5754	0.9904	0.3337	0.1174	-1.7907	-0.8771	0.4213	-1.0859
95	aryl hydrocarbon receptor interacting protein-like 1 (AIP1), mRNA	NM_014336	-0.4951	-1.0915	1.0467	0.4765	0.8457	0.0631	-0.4951	0.8182	0.1926	-0.9329	-1.64	-0.6011	0.6225	-0.8988
96	NGFI-A binding protein 2 (EGR1 binding protein 2) (NAB2), mRNA	NM_005967	-0.4144	-0.5346	0.4112	-0.1927	-0.0786	-0.7171	-0.9226	-0.0216	-0.2542	-0.4062	-1.7589	-0.8994	-0.4586	-0.9327
97	lymphoid enhancer-binding factor 1 (LEF1), mRNA	NM_016269	-0.8169	-0.792	-0.1926	0.5615	0.7359	-0.2545	-0.5497	-0.5546	1.6404	0.6873	-1.5595	-0.7756	-0.5267	-0.8253
98	CD48 antigen (B-cell membrane protein) (CD48), mRNA.	NM_001778	0.0766	-1.109	0.0721	0.0242	-0.0247	-0.4776	0.0641	-0.8704	1.3024	0.2925	-2.3014	-0.5916	0.368	-1.0535
99	chromosome 21 open reading frame 45 (C21orf45), mRNA.	NM_018944	-0.4729	-1.8824	0.1344	0.2147	0.2262	-0.1238	-0.6538	0.1193	0.8093	0.6201	-0.3782	-0.1944	0.1231	-0.4403
100	layilin (LOC143903), mRNA	NM_178834	0.9754	1	0.2529	0.0247	-0.1165	0.2353	0.3109	0.5438	0.7095	-0.3945	-1.6862	-0.2815	-0.372	0.1611
101	cDNA FLJ37812 fis, clone BRSSN2002160, weakly similar to RING CANAL PROTEIN	AK095131	0.0045	0.1432	-0.163	0.5104	0.0609	0.3413	-0.0313	-0.2385	0.0646	0.0794	-1.597	-0.5221	-0.7144	0.6428
102	ATPase, Class I, type 8B, member 1 (ATP8B1), mRNA.	NM_005603	0.2279	0.4095	-0.1142	0.0812	-0.7425	-0.5662	-0.3286	0.0753	-0.5802	0.6101	-1.5936	-0.0367	-0.6326	-0.6309
103	chromosome 5 open reading frame 4 (C5orf4), mRNA.	NM_032385	0.077	-0.0086	-0.2765	-0.235	-0.5078	-0.0243	-0.546	-0.2473	0.4819	0.1138	-0.8332	-1.8095	-1.1553	-0.8805
104	phosphatidylinositol glycan, class H (PIGH), mRNA	NM_004569	-0.4201	-0.7319	-0.5373	-0.6167	-0.9764	-0.3378	-1.689	-0.3204	0.5468	0.4306	-0.9692	-1.3629	-0.171	-0.6996
105	v-myc myelocytomatosis viral related oncogene, neuroblastoma derived (avian) (MYCN), mRNA	NM_005378	-0.9061	-1.3172	0.7723	-1.3666	-1.2532	-0.9701	-0.5189	-0.0923	0.2048	0.6172	-1.1169	-1.7217	-0.4983	-1.1315
106	keratin 8 (KRT8), mRNA.	NM_002273	-0.3575	-0.6571	-0.2701	-0.8231	-0.969	-1.5502	-0.6387	0	0.4209	-1.3073	-1.7513	-1.733	-0.8982	-0.1611
107	stabilin 1 (stab1), mRNA.	NM_015136	-0.3129	-0.7777	-1.3932	-1.8241	-1.3479	-0.3134	-0.2804	-0.8714	1.4503	0.5968	-0.3844	-0.9496	-1.5659	-1.0022
108	keratin 7 (KRT7), mRNA.	NM_005556	-0.7032	-0.8642	-0.7827	-0.2306	0.5742	-0.9361	-0.6855	-1.2529	-1.7059	-1.6604	-1.6051	-1.4482	-2.1954	-2.1365
109	hypothetical protein LOC144501 (LOC144501), mRNA.	NM_182507	-0.6515	-0.8258	-1.2835	-0.3175	0.1369	-1.4353	-0.8355	-0.9798	-1.54	-1.8505	-1.5233	-2.3914	-2.4146	-1.6258
110	cDNA FLJ11819 fis, clone HEMBA1006426	AK021881	-1.7282	-1.5652	-0.675	-0.842	-0.9601	0.2842	0.3552	0.3752	-1.6538	-1.2091	-1.2256	-2.1177	-1.0999	-2.6299
111	apelin; peptide ligand for APJ receptor (APELIN), mRNA	NM_017413	-1.828	-1.7541	-0.5179	-1.2819	-1.0492	0.19	-0.6449	-0.0147	-1.848	-0.4051	-1.4291	-2.1318	-1.0593	-2.2543
112	cDNA FLJ34773 fis, clone NT2NE2003280.	AK092092	-1.2728	-1.4287	-0.518	-0.8832	-0.1042	-0.5409	-0.3277	-0.583	-0.8471	-0.9273	-1.4496	-1.8246	-2.2523	-2.2412
113	collagen, type I, alpha 2 (COL1A2), mRNA.	NM_000089	-1.7364	-1.477	-1.1427	-0.3904	-0.4343	0.0321	-0.1422	-0.189	-1.2499	-1.2803	-0.6393	-1.7021	-1.6619	-2.1176
114	keratin 19 (KRT19) gene, complete cds.	AF202321	-1.9776	-1.7359	-1.1089	-0.6433	0.0123	-0.7741	-0.4371	-0.7125	-1.9663	-1.7214	-1.6709	-1.4305	-1.6736	-2.4226
115	CD34 antigen (CD34), mRNA.	NM_001773	-2.1987	-1.4474	-1.4565	-1.1755	0.354	-0.4584	-0.5884	0.348	-1.8551	-1.2176	-2.0007	-2.6949	-1.4706	-2.419
116	cytochrome c oxidase subunit VIIa polypeptide 1 (muscle) (COX7A1), nuclear gene encoding mitochondrial protein, mRNA/	NM_001864	-1.377	-1.1964	-0.5535	-1.621	-1.2253	-1.4942	-0.3591	-0.0943	-0.439	0.3782	-0.3637	-1.6345	-0.726	-3.4852
117	tyrosine kinase with immunoglobulin and epidermal growth factor homology domains (TIE), mRNA^	NM_005424	-0.954	-1.4665	-1.2081	-1.45	-1.1601	-1.1082	-0.3434	-1.5827	-0.8167	-0.6831	0.3934	-2.043	-0.9058	-2.4837
118	copine V (CPNE5), mRNA.	NM_020939	-1.8051	-2.246	-1.2081	-2.4168	-0.9465	-0.964	-0.261	-0.513	-1.3585	-0.9767	-0.2765	-2.7834	-0.6408	-3.1174
119	gap junction protein, alpha 5, 40kDa (cc	NM_181703	-1.0209	-0.4709	-1.3652	-2.1542	-1.0087	-1.5658	-1.0799	-1.6402	-1.5172	-1.3916	-1.0636	-2.9228	-2.6469	-2.6844
120	hypothetical protein FLJ14834 (FLJ14834), mRNA	NM_032849	-1.5812	-1.0265	-0.9625	-0.1038	-0.63	-2.3644	-1.5031	-0.7587	-0.5013	0.329	0.0272	-1.6234	-0.9956	-3.079
121	hypothetical protein BC009514 (LOC127253), mRNA	XM_005122	-1.488	-2.0068	-0.2709	0.1809	-0.3653	-2.1791	-1.7053	-0.6214	-0.1172	-0.1621	0.107	-1.8855	-0.2652	-1.6598
122	cDNA FLJ20750 fis, clone HEP05174.	AK000757	-1.0295	-0.6407	-0.5441	-0.1283	0.1178	-2.344	-0.9928	0.0927	-0.1415	-0.8345	-0.8342	-2.3256	-1.2352	-1.6986
123	N-myristoyltransferase 2 (NMT2), mRNA.	NM_004808	-1.5311	-0.7093	-0.849	-0.3379	-0.7489	-1.6872	-0.9237	0.0764	-1.0434	-0.1845	-1.831	-0.7539	-0.9015	-1.6602
124	RGC32 protein (RGC32), mRNA.	NM_014059	-1.4606	-0.8701	-0.2614	0.1272	0.3024	-0.6849	0.2267	0.4264	-0.2402	-0.0984	-0.153	-2.0685	-0.8911	-3.0189
125	inhibitor of DNA binding 1, dominant negative helix-loop-helix protein (ID1), mRNA^	NM_002165	1.4123	1.1553	0.926	0.2309	0.2158	-0.0093	0.4025	0.0046	0.0953	0.0702	0.3345	-1.212	-1.9712	-1.1576
126	multimerin (MMRN), mRNA.	NM_007351	0.1216	1.1658	0.2948	1.1177	0.9113	-1.4323	-0.7199	-0.3159	-0.5527	0.12	-0.5578	-1.7172	-1.9075	-1.7511
127	alpha-2-macroglobulin (A2M), mRNA.	NM_000014	0.9137	0.9608	1.4619	-1	0.026	0.431	-0.0795	0.9586	-0.3132	-0.3132	-0.916	-3.8074	-1.6404	-0.8532
128	cDNA FLJ43586 fis, clone SKNMC2007504	AK125574	-1.4047	-1.1531	0.7848	0.9601	1.2847	-1.2568	-1.3775	0.4009	0.1847	-0.2972	-0.4169	-1.0929	0.6932	-1.6006
129	granzyme K (serine protease, granzyme 3; tryptase II) (GZMK), mRNA.	NM_002104	-1.523	-1.0699	0.4112	1.1828	1.7447	-0.7257	-0.4816	0.7308	0.2599	-0.8442	-0.4093	-1.1871	0.8117	-1.5513
130	septin 1 (SEPT1), mRNA.	NM_052838	-1.1339	-1.6173	0.2705	0.4816	0.52	-1.1239	-1.5356	0.3309	0.429	-0.5877	0.065	-0.9462	0.3774	-1
131	S100 calcium binding protein A4 (calcium protein, calvasculin, metastasin, murine placental homolog) (S100A4), transcript variant 1, mRNA^	NM_002961	-1.4919	-1.4919	-0.3744	0.737	0.6521	-1.0996	-0.2065	0.1561	0	-0.0325	0.2411	-1.585	-0.8074	-0.737
132	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 (SERPINA1), mRNA^	NM_000295	-1.6089	-1.4072	0	0.7589	0.6214	-1.2303	-1.0239	0.5406	-0.415	-0.8744	0.1313	-2.1234	0	-1.6089
133	potassium voltage-gated channel, shaker-related subfamily, beta member 2 (KCNA2), mRNA	NM_003636	-0.6215	-0.7237	-0.2696	1.602	1.4021	-1.17	-0.4807	0.322	0.1959	-0.737	-0.4014	-2	-0.652	-1.152
134	chromosome 6 open reading frame 32 (C6orf32), mRNA.	NM_015864	-1.2525	-1.7081	-0.0991	1.52	1.7478	-0.3439	-0.5271	0.0558	0.7984	-0.9121	0.2622	-1.3219	-0.1348	-1.2473
135	pre-alpha (globulin) inhibitor, H3 polypeptide (ITI3), mRNA	NM_002217	-0.5636	-0.6177	0.3463	0.6256	1.1312	-1.7203	0.5037	0.1835	-0.0435	-0.9213	0.202	-1.276	0.3781	0.473
136	SPANX family, member B2 (SPANXB2), mRNA.	NM_145664	-0.4519	-1.1496	0.6189	0.5766	0.7641	-1.3301	0.9918	0.4573	1	-0.388	0.1881	-1.6693	0.6039	-0.0786
137	hydroxysteroid (17-beta) dehydrogenase 8 (HSD17B8), mRNA	NM_014234	-0.6356	-0.8731	0.0329	-0.1639	0.1295	-0.2335	0.5132	0.3191	0.393	-0.8525	0.1795	-1.6616	-0.6733	-0.6356
138	collagen, type XII, alpha 1 (COL12A1), transcript variant long, mRNA	NM_004370	-0.6719	-1.031	-0.3626	0.1927	0.1927	-0.8822	-0.0952	0.8218	1.585	-0.2423	0.2313	-0.9696	-0.0444	-0.5102
139	serine/threonine kinase 17b (apoptosis-inducing) (STK17B), mRNA	NM_004														

No	Description of gene function	GenBank accession number	commercial OSM_2	<i>in vitro</i> synthesized FLAG-OSM	commercial OSM_1	<i>in vitro</i> synthesized His-FLAG-IL-1 β	<i>in vitro</i> synthesized GST-FLAG-IL-1 β	commercial IFN- β _2	<i>in vitro</i> synthesized FLAG-IFN- β	commercial IFN- β _1	commercial IL-1 β _1	<i>in vitro</i> synthesized mature IL-1 β	commercial IL-1 β _2	<i>in vitro</i> synthesized FLAG-TNF- α	commercial TNF- α _1	commercial TNF- α _2
160	adenylate kinase 3 alpha like (AKL3L), mRNA	NM_016282	0.1175	0.5812	0.2005	0.1231	-0.6657	-1.6253	-0.8477	0.7763	0.1828	-0.2222	0.252	0.0299	0.2102	-0.1865
161	Glutamate dehydrogenase-2 (GLUD2), mRNA	NM_012084	0.0948	0.4104	0.5487	0.5122	-0.1869	-1.6997	-0.8684	0.5446	0.0621	-0.0551	-0.4634	-0.1147	0.628	-0.118
162	isopentenyl-diphosphate delta isomerase (IDI1), mRNA	NM_004508	-0.0351	0.4543	0.1624	0.3819	-0.1471	-1.613	-0.959	0.4364	-0.1809	-0.1809	0.1812	0.2303	0.587	0.5235
163	eukaryotic translation elongation factor 1 alpha 1 (EEF1A1), mRNA	NM_001402	0.1156	0.4927	0.415	-0.0659	-0.3182	-2.1883	-1.2617	0.0487	-0.1638	0.0057	-0.2167	-0.1313	0.2408	-0.3674
164	reticulocalbin 2, EF-hand calcium binding domain (RCN2), mRNA	NM_002902	0.2722	0.6407	0.2825	0.1433	-0.4442	-1.7152	-1.3551	0.6188	0.002	-0.0242	-0.2628	-0.4326	0.1686	-0.2975
165	clone 669 unknown mRNA, complete sequenc	AF091090	-0.5416	0.2692	-0.1544	0.1948	-0.2354	-1.7196	-0.8116	0.3394	-0.4877	0.0232	0.5315	-0.1162	0.2366	-0.1272
166	acyl-Coenzyme A dehydrogenase, C-4 to C-12 straight chain (ACADM), nuclear gene encoding mitochondrial protein, mRNA/	NM_000016	-0.0496	0.438	0.1096	0.9232	-0.0087	-1.7832	-1.0496	0.3066	-0.0184	-0.5526	0.7631	-0.1273	-0.243	-0.1062
167	thioredoxin reductase 1 (TXNRD1), mRNA	NM_003330	-0.5856	0.7652	-0.2526	0.1963	-0.3566	-1.7739	-0.9516	1.0248	0.2767	-0.5752	-0.0055	-0.4123	-0.0263	-0.3778
168	cyclin G1 (CCNG1), mRNA	NM_004060	-0.008	1.0512	0.2915	0.2492	-0.2843	-2.2759	-0.8552	1.0265	-0.2913	-0.3507	-0.3817	0.0199	0.267	-0.7414
169	ribosomal protein S6 (RPS6), mRNA	NM_001010	-0.0048	0.1717	0.0922	0.2192	0.15	-1.8521	-1.0909	-0.4186	-0.138	0.0227	-0.3383	-0.113	-0.325	-0.9259
170	poly(A) binding protein, cytoplasmic 1 (PABPC1), mRNA	NM_002568	0.3034	0.2281	0.4799	0.1687	0.2399	-1.7074	-0.9587	-0.2416	-0.3185	-0.2171	-0.4356	-0.2746	-0.2568	-0.6315
171	similar to Polyadenylate-binding protein	XM_114265	-0.1397	0.3223	-0.2079	0.3836	-0.4627	-2.1936	-0.8373	-0.4135	0.0153	-0.1928	-0.206	-0.57	-0.4209	-0.8195
172	hypothetical protein FLJ20375 (FLJ20375), mRNA	NM_017794	-0.2794	-0.1412	-0.2626	-0.3475	0.2226	-1.769	-0.5978	-0.7819	-0.2643	0.1904	-0.6216	0.0069	-0.1731	-0.2682
173	cofactor required for Sp1 transcriptional activation, subunit 6 (77kD) (CRSP6), mRNA	NM_004268	0.5663	0.3137	0.329	0.7661	0.1467	-2.5351	-0.1341	0.2558	-0.332	-0.26	0.3673	-0.5456	0.1738	0.2276
174	ubiquitin specific protease 7 (herpes virus-associated) (USP7), mRNA	NM_003470	-0.0115	0.7811	0.2728	0.1735	-0.7638	-1.8694	-0.97	0.6967	0.4122	0.3377	0.2372	0.2049	0.6801	0.5334
175	clathrin, heavy polypeptide (Hc) (CLTC), mRNA	NM_004859	0.0413	0.6235	0.1672	0.1072	-0.4833	-1.5903	-1.0699	0.7411	0.3253	0.3147	-0.2457	0.5187	0.73	0.3145
176	cDNA FLJ46274 fis, clone TEST14029297.	AK128151	0.0153	0.5018	0.1194	0.2808	0.0358	-1.6343	-1.2966	0.3386	0.5011	0.6044	0.2828	0.0649	0.632	0.5268
177	pleckstrin homology domain containing, .	NM_006832	0.7183	1.0677	0.275	0.5637	-0.2582	-1.7671	-0.6757	0.7228	0.3883	0.6939	0.0924	0.6842	0.6057	0.7143
178	splicing factor 3b, subunit 1, 155kD (SF3B1), mRNA	NM_012433	0.3331	0.7618	0.1504	0.6961	-0.377	-1.6465	-0.7514	0.9398	0.4421	0.609	-0.1512	0.3636	0.6078	0.3125
179	CDC23 (cell division cycle 23, yeast, homolog) (CDC23), mRNA	NM_004661	0.5813	1.1087	0.2787	0.4341	-0.3181	-1.8239	-1.1265	1.1109	0.3111	0.2492	-0.4921	0.1712	0.6839	0.8944
180	plastin 3 (T isoform) (PLS3), mRNA	NM_005032	0.4216	1.1253	0.1256	0.0312	-0.4815	-1.5926	-0.7885	0.9784	-0.0761	0.141	-0.0479	0.3189	0.2334	0.195
181	hypothetical protein DKFZp586G0123 (DKFZp586G0123), mRNA	NM_013386	-0.154	0.9264	0.2176	-0.0745	-0.8107	-1.5929	-1.3299	1.3331	0.3119	0.3718	0.3586	-0.008	1.2626	0.4485
182	cellular repressor of E1A-stimulated genes (CREG), mRNA	NM_003851	-0.0856	0.1848	0.6363	0.458	-0.6872	-1.2121	-1.6927	0.4764	0.8344	0.5389	-0.0614	0.3404	0.5208	0.2989
183	activating transcription factor 2 (ATF2), mRNA	NM_001880	0.1094	0.7028	0.4579	0.7865	-0.2924	-1.8779	0.2229	1.3202	0.1637	0.522	-0.0621	0.2081	1.2312	0.3499
184	amyloid beta precursor protein binding protein 1, 59kD (APPBP1), mRNA	NM_003905	-0.3773	0.096	0.29	0.4275	-0.0041	-1.9069	-0.9482	0.8654	0.5516	0.3281	-0.2808	-0.3652	0.9158	-0.1993
185	sterol-C4-methyl oxidase-like (SC4MOL), mRNA	NM_006745	-0.637	0.0419	0.4618	0.6067	-0.0371	-2.3177	-1.2554	0.9826	-0.0968	0.1894	0.2878	0.2813	1.092	0.2169
186	hexosaminidase B (beta polypeptide) (HEXB), mRNA	NM_000521	-0.162	0.1042	0.0073	-0.0596	-0.3038	-1.2449	-0.4191	0.5947	-0.2302	0.1227	0.2405	-0.1354	1.6017	-0.0873
187	tumor necrosis factor receptor superfamily, member 21 (TNFRSF21), mRNA	NM_014452	0.0561	0.2004	-0.3376	0.4102	0.3146	-1.7232	-0.4645	0.1946	0.1567	0.7222	0.2701	0.7954	0.6178	0.8722
188	CGI-111 protein (LOC51015), mRNA	NM_016048	0.1285	0.0441	-0.0045	1.1759	0.6896	-1.6371	-0.6929	0.3938	0.0287	0.158	0.1344	0.5428	0.194	0.6114
189	TRAF family member-associated NFKB activator (TANK), transcript variant 1, mRNA	NM_004180	-0.2616	0.2135	-0.0316	0.3466	-0.3014	-1.8043	-0.8441	0.2643	0.7263	0.424	0.7821	0.5975	1.4386	0.8956
190	cDNA FLJ20816 fis, clone ADSE00693.	AK000823	0.4099	0.3029	-0.1381	0.195	0.0582	-1.7228	0.4375	-0.0697	0.5307	0.5856	0.3817	0.5531	-0.0446	0.3931
191	ELL-related RNA polymerase II, elongation factor (ELL2), mRNA	NM_012081	-0.2167	1.0694	0.1199	0.2452	-0.1246	-2.1885	-0.0074	0.1786	0.6235	0.2736	0.5385	0.455	0.4912	0.0788
192	associated molecule with the SH3 domain of STAM (AMSH), mRNA	NM_006463	0.1871	0.4073	0.4438	0.6277	-0.217	-1.8365	-0.4374	0.5414	1.17	0.17	-0.375	0.0044	0.2588	0.1675
193	hypothetical protein FLJ22060 (FLJ22060), mRNA	NM_024612	0.742	0.9769	-0.2441	0.6827	-0.1762	-2.2918	0.2382	0.5873	0.2262	0.1145	-0.4234	0.1356	0.173	0.358
194	armadillo repeat protein ALEX2 (ALEX2), mRNA	NM_014782	-0.9867	-0.4201	0.0751	-0.0792	-0.4356	-1.7661	-0.8812	0.0914	0.1325	0.9206	-0.2799	-0.2721	0.3422	-0.7495
195	protein kinase (cAMP-dependent, catalytic) inhibitor alpha (PKIA), mRNA	NM_006823	-0.5411	-0.2553	-0.2808	-0.1785	-0.7375	-1.7954	-1.305	-0.1256	-0.0383	0.5542	0.5195	0.7665	0.3282	0.0846
196	hypothetical protein MGC3195 (MGC3195), mRNA	NM_031905	-0.8577	-0.5982	-0.8373	0.3394	0.016	-2.6256	-0.5573	-0.4457	0.4718	0.2319	0.228	0.0271	0.0178	-0.5604
197	hypothetical protein FLJ13910 (FLJ13910), mRNA	NM_022780	0.264	0.7392	0.6853	-0.009	-0.5495	-1.0462	-0.5964	0.7549	-0.0065	-0.0162	0.3265	1.8615	0.5574	-0.1558
198	stromal antigen 2 (STAG2), mRNA	NM_006603	0.5513	1.6086	0.2236	0.1399	-0.8947	0	0.1998	0.9337	0.0501	-0.0732	0.3392	0.4398	0.3168	1.1166
199	sex comb on midleg-like 1 (Drosophila) (SCML1), mRNA	NM_006746	0.415	1.6693	0.1836	0.3785	-0.4799	0.2619	0.3219	0.7287	0.2451	-0.3883	-0.1536	0.4835	0.1722	1.1369
200	hypothetical protein MGC14797 (MGC14797), mRNA	NM_023335	0.5793	1.6439	-0.3986	0.79	-0.2369	-0.1069	0.2224	0.5514	-0.0727	-0.0419	-0.1232	0.17	-0.0288	0.9161
201	cDNA FLJ33272 fis, clone ASTRO2007948.	AK090591	0.4774	1.7393	0.1789	0.2154	-0.6904	-0.2947	-0.2165	0.9494	0.5235	0.7881	-0.7472	0.4086	0.5209	0.6996
202	hypothetical protein FLJ20396 (FLJ20396), mRNA	NM_017801	1.2623	1.5937	-0.0101	0.3661	-0.8809	-0.1853	0.1172	0.4075	0.3266	0.5405	0.0722	0.5689	0.2467	0.7967
203	pleckstrin homology-like domain, family	NM_145753	0.6715	1.6043	-0.8323	0.2806	-1.0341	-0.9251	-0.4683	0.7702	-0.0221	-0.1136	-0.0534	0.9306	0.3074	1.1335
204	phosphoinositide-3-kinase, regulatory su	NM_181523	1.1956	1.6938	0.0688	-0.0753	-0.6587	-0.5164	-0.1963	0.1919	-0.3061	0.1925	-0.2373	-0.096	0.1511	0.0278
205	fatty-acid-Coenzyme A ligase, very long-chain 1 (FACVL1), mRNA	NM_003645	0.9711	1.3689	0.4378	0.2702	-0.2131	-0.3436	-0.6685	0.8491	0.3165	0.3433	0.1021	0.9662	0.6086	1.632
206	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 10 (MLLT10), mRNA#	NM_004641	0.2393	1.4635	0.573	-0.3313	-0.2582	-0.1863	-0.8055	0.9659	0.5013	0.0782	0.248	0.4253	0.8538	1.7288
207	retinoblastoma 1 (including osteosarcoma) (RB1), mRNA	NM_000321	0.489	1.7905	0.4863	0.0125	-0.595	0.147	-0.7246	1.1196	-0.8875	-0.6533	0.3528	0.4577	0.9186	1.1217
208	phospholipid scramblase 4 (PLSCR4), mRNA	NM_020353	0.5446	1.2423	-0.1277	-0.1623	-1.6536	-1.0872	-0.797	0.4101	-0.6352	1.0868	0.0734	0.6024	0.6258	0.846
209	cDNA: FLJ22425 fis, clone HRC08686.	AK026078	0.8816	1.197	-0.5367	-0.3779	-1.5813	-1.1699	-0.5002	0.1264	-1.2255	-0.5205	-0.6265	0.2668	-0.3852	0.1015
210	hematopoietically expressed homeobox (HHEX), mRNA	NM_002729	0.043	0.6968	-0.2429	0.0646	-0.3787	-0.3479	-0.3368	0.7541	-0.5703	-0.4624	1.7076	0.3657	0.252	0.3779
211	protein phosphatase 1, regulatory (inhibitor) subunit 3B (PPP1R3B), mRNA	NM_024607	-0.0877	0.2685	0.3717	-0.0983	-1.0845	-0.0063	0.0151	0.3577	-0.7174	-0.0571	1.8832	0.0851	0.6136	-0.2482
212	baculoviral IAP repeat-containing 4 (BIRC4), mRNA	NM_001167	0.229	0.7905	-0.0356	0.5385	-0.3628	-0.0616	-0.3651	0.9036	-0.1156	0.8505	1.7589	0.8369	0.7593	0.3395
213	NIF3 NGG1 interacting factor 3-like 1 (S. pombe) (NIF3L1), mRNA	NM_021824	0.119	0.4333	-0.0207	0.4162	0.6332	-1.6652	0.1233	-0.3066	1.2215	0.8616	0.3798	-0.5397	-0.7272	0.4966
214	TTK protein kinase (TTK), mRNA	NM_003318	0.152	1.2161	-0.2773	0.6456	0.5217	-1.344	1.078	-0.1214	1.5172	-0.0678	-0.6666	0.4999	-0.1643	1.8218
215	retinol binding protein 1, cellular (RBP1), mRNA	NM_002899	-0.4456	0.0676	-0.5195	-0.2763	0.0647	0.1418	-1.071	-0.2804	1.7137	-0.044	0.2175	-0.6985	-0.649	0.7025
216	v-ets erythroblastosis virus E26 oncogene homolog 2 (avian) (ETS2), mRNA	NM_005239	1.7851	1.6034	1.2203	0.3137	-0.4032	0.0892	-0.1869	0.4959	0.9174	1.0098	0.6049	0.402	0.7302	0.6131
217	transmembrane protein 2 (TMEM2), mRNA	NM_013390	1.6244	1.4703	0.6074	0.49	-0.5089	-0.0188	-0.1051	0.6632	0.7794	1.1556	0.5317	0.1637	0.3041	0.4184
218	B-cell CLL/lymphoma 6 (zinc finger protein 51) (BCL6), mRNA	NM_001706	1.6819	1.3237	1.0375	0.4212	-0.3822	-0.1104	0	0.4212	0.6609	0.9934	0.9838	-0.2299	0.2825	-0.5531
219	hypothetical protein FLJ22833 (FLJ22833), mRNA	NM_022837	1.5109	1.8419	1.1911	0.254	-0.2306	-0.3475	-0.3816	0.5558	0.1794	-0.0135	0.475	0.5283	0.7623	0.4932

No	Description of gene function	GenBank accession number	commercial OSM_2	<i>in vitro</i> synthesized FLAG-OSM	commercial OSM_1	<i>in vitro</i> synthesized His-FLAG-IL-1 β	<i>in vitro</i> synthesized GST-FLAG-IL-1 β	commercial IFN- β _2	<i>in vitro</i> synthesized FLAG-IFN- β	commercial IFN- β _1	commercial IL-1 β _1	<i>in vitro</i> synthesized mature IL-1 β	commercial IL-1 β _2	<i>in vitro</i> synthesized FLAG-TNF- α	commercial TNF- α _1	commercial TNF- α _2
241	ribosomal protein S6 kinase, 90kD, polypeptide 2 (RPS6KA2), mRNA	NM_021135	0.4061	0.5541	0.311	-0.8117	-0.7504	0.2094	1.3847	-0.4847	-0.0153	1.6466	1.0045	1.6066	-0.5525	0.2868
242	protocadherin 12 (PCDH12), mRNA	NM_016580	0.5878	0.1998	-0.9162	-0.7371	-0.6036	0.4898	0.4765	-0.8925	1.016	1.0447	1.8187	0.0037	-1.1162	-0.1173
243	likely ortholog of mouse myocytic induc	NM_020778	-0.4176	-0.5345	-1.1969	-0.6986	-0.7918	0.344	0.3889	-0.9714	0.6746	1.2355	2.2814	0.5465	-0.5413	0.0079
244	cDNA: FLJ21176 fis, clone CAS11106	AK024829	-0.1476	-0.8752	-0.4715	0.1479	0.186	-0.2698	0.5294	-0.4685	0.176	0.6926	1.7007	-0.1682	0.0757	-0.9533
245	similar to selenophosphate synthetase 2	XM_302161	-0.1289	-0.0837	-0.343	-0.3265	0.2775	-0.1141	0.0406	-0.6044	0.3698	0.2996	1.7231	-0.4834	-0.7479	-0.1373
246	growth factor receptor-bound protein 14 (GRB14), mRNA	NM_004490	0.7082	0.5752	0.1064	-0.9346	-0.7515	-0.1229	0.1685	-0.0053	-0.1211	0.6854	1.6321	-0.3534	-0.8255	-0.9365
247	apolipoprotein D (APOD), mRNA	NM_001647	0.2816	0.1237	-0.4934	-0.9209	-0.9718	1.626	0.9458	0.0006	-0.0514	0.698	1.3045	-0.4383	-0.3838	-0.8293
248	solute carrier family 12 (sodium/potassium/chloride transporters), member 2 (SLC12A2), mRNA	NM_001046	-0.5812	0.2449	-0.2074	0.4221	-0.3819	-1.0434	-0.4516	0.9066	3.095	3.1379	2.6864	0.2743	1.5971	0.8135
249	phospholipase A2, group IVA (cytosolic	NM_024420	-0.1982	0.2668	0.4729	0.5053	-0.6877	-1.4712	-1.0383	0.5937	1.3814	1.7566	1.9263	0.5253	2.3656	0.2554
250	interleukin 1, beta (IL1B), mRNA	NM_000576	0.1312	-0.2487	-0.303	0.3038	0.5792	0.0931	0.0187	-0.0651	2.7215	3.0029	3.2811	-0.0035	-0.2624	0.176
251	hypothetical protein FLJ22757 (FLJ22757), mRNA	NM_024898	0.6796	0.6869	0.0661	0.1952	1.0694	0.3884	0.2572	0.0017	-0.4034	-0.0993	-0.0593	-0.733	0.0301	1.8761
252	syntrophin associated serine/threonine kinase (SAST), mRNA	XM_032034	0.548	0.3848	-0.1958	0.3264	0.9054	0.3477	0.5173	-0.2256	-0.4755	-0.1059	-0.1316	-0.4037	-0.0208	1.5986
253	Alport syndrome, mental retardation, midface hypoplasia and elliptocytosis chromosomal region, gene 1 (AMMECR1), mRNA	NM_015365	0.9377	0.9128	-0.2481	0.4084	0.613	-0.0908	0.3042	0.4944	-0.1846	-0.1348	0.2357	-0.5748	0.2981	1.9289
254	natural killer cell receptor 2B4 (CD244), mRNA	NM_016382	0.4601	1.2282	-0.2992	0.3071	0.9908	0.6747	-0.0693	0.3889	-0.0434	0.1336	0.1252	-0.6794	0.1092	1.9778
255	dihydropyrimidinase-like 2 (DPYSL2), mRNA	NM_001386	1.125	0.7823	0.0286	0.7279	0.3655	-0.3742	-0.4234	0.4158	0.0937	0.5507	0.8837	0.3612	0.1349	1.7401
256	carboxypeptidase E (CPE), mRNA	NM_001873	1.0082	0.676	-0.4865	1	1.1245	-0.6616	0.0648	0.3391	0.3955	-0.1644	0.36	-0.0679	-0.1391	1.7269
257	Kruppel-like factor 5 (intestinal) (KLF5), mRNA	NM_001730	-0.1877	1.5372	-0.1344	0.1343	0.7085	0.6868	0.3567	0.1231	0.0432	-0.5371	0.4372	0.6536	-0.1139	1.8148
258	cystathionase (cystathionine gamma-lyase) (CTH), mRNA	NM_001902	0.0682	1.0626	0.2156	-0.0789	0.6451	0.9883	-0.0962	0.4544	-0.2394	-0.0494	0.2366	0.3219	-0.1119	1.6933
259	ets variant gene 4 (E1A enhancer binding	NM_001986	0.5083	1.0962	-0.3745	0.1672	1.1149	0.8699	0.3464	-0.1628	0.3145	-0.3672	0.0178	0.7419	-0.295	1.9267
260	PCTAIRE protein kinase 3 (PCTK3), mRNA	XM_053746	-0.6582	1.5167	-0.6557	-0.2643	0.6854	1.4052	-0.0071	0	-0.0785	-0.3986	0.3661	1.0178	0.0831	2.0612
261	centaurin, gamma 1 (CENTG1), mRNA	NM_014770	-0.3095	1.1465	-0.1506	0.3658	1.0937	0.985	-0.1912	0.4572	0.6743	-0.126	0.5547	-0.3095	0.5127	2.31
262	Bloom syndrome (BLM), mRNA	NM_000057	0.0861	0.8231	0.1593	-0.0793	0.7292	0.6987	0.7921	-0.1843	0.5421	0.1344	0.8845	0.4165	2.6711	
263	polymerase (DNA directed), delta 3 (POLD	XM_166243	0.3688	0.8318	-0.344	-0.1072	0.5211	0.1464	-0.4197	0.1959	0.0325	-0.0519	-0.1502	0.2715	-0.1332	1.5834
264	hypothetical protein FLJ10468 (FLJ10468), mRNA	NM_018101	1.2003	0.7308	-0.3539	-0.1611	-0.1611	0.4678	-0.2327	-0.2718	-0.1812	-0.2471	-0.3615	0.5007	0.1712	1.6053
265	NALP2 protein (NALP2), mRNA	NM_017852	1.1769	1.0644	-0.1377	0.0209	0.074	0.6859	0.2735	0.0873	0.5966	0.4634	-0.1992	0.6504	0.036	1.7414
266	retinoblastoma-like 1 (p107) (RBL1), mRNA	NM_002895	0.497	1.0892	-0.7962	-0.5936	-0.3381	1.2441	-0.1971	0.0483	0.4779	-0.5333	-0.0368	0.3603	-0.2374	1.7153
267	CD79B antigen (immunoglobulin-associated beta) (CD79B), transcript variant 1, mRNA	NM_000626	0.7978	0.1674	-0.4197	-0.0577	0.4221	-0.241	1.6884	-0.1371	-0.4276	0.0225	0.304	-0.0916	-0.1016	0.7055
268	fucosyltransferase 7 (alpha (1.3) fucosyltransferase) (FUT7), mRNA	NM_004479	1.1441	0.4784	-0.077	0.2294	0.3804	-0.2102	1.6456	0.0653	-0.3276	-0.4113	-0.0508	0.319	0.0432	1.0314
269	clone MGC:17422 IMAGE:4214343, mRNA, com	BC011057	0.775	0.152	0.084	0.1725	0.8571	0.1846	1.6838	-0.0065	0.3874	-0.6182	0.3207	-0.2439	0.1458	1.0802
270	prostaglandin E synthase, clone MGC:1031	BC008280	0.4789	-0.2205	0.7064	1.0655	1.8222	0.746	0.5349	1.0793	-0.1307	-0.6136	-0.3766	0.3151	0.517	0.6334
271	natural killer cell group 7 sequence (NKG7), mRNA	NM_005601	0.2955	0.1845	0.7957	0.5966	1.6977	0.7304	0.5179	1.673	-0.3048	-0.6918	-0.2411	0.1256	0.5009	0.5179
272	adenylate cyclase 7 (ADCY7), mRNA	NM_001114	0.5057	0.3859	0.6209	0.698	1.698	1.2636	1.0102	0.9183	0.3459	-1.0441	-0.0076	0.8646	0.7607	1.0827
273	apolipoprotein A-II (APOA2), mRNA	NM_001643	0.4151	1.152	1.0418	0.6629	1.5025	1.3537	0.8301	1.7705	0.348	-0.4594	-1.3219	0.5306	0.8194	1.5306
274	somatostatin receptor 2 (SSTR2), mRNA	NM_001050	-0.0425	0.7595	0.6949	0.7954	1.5849	0.4923	0.427	1.2743	0.5885	-0.6529	-0.3807	0.7876	1.4297	1.657
275	apolipoprotein C-II (APOC2), mRNA	NM_000483	1.0696	0.9075	0.0261	0.878	1.3669	1.6258	1.2251	0.1624	-0.2262	-0.4378	-0.3193	0.7443	-0.1256	1.9873
276	cadherin 1, type 1, E-cadherin (epithelial) (CDH1), mRNA	NM_004360	1.0686	0.7276	0.2612	0.4168	1.1715	1.5787	0.923	0.4069	-0.6236	-0.667	-0.5288	0.2251	-0.1123	1.9548
277	breast cancer 2, early onset (BRCA2), mRNA	NM_000059	1.1364	0.7641	0.121	0.7441	0.7318	1.0904	0.4996	0.4731	0.3253	0.0845	-0.2359	0.5808	0.1512	1.8969
278	hypothetical protein FLJ36445 (FLJ36445	NM_155233	0.8166	0.186	0.0513	0.7313	1.3883	1.1696	0.7258	-0.0773	-0.1948	0.028	-0.2467	0.6742	0.3402	1.6625
279	v-myb myeloblastosis viral oncogene homolog (avian) (MYB), mRNA	NM_005375	1.106	0.4482	-0.216	1.4748	1.4594	0.9439	0.8789	0.5722	0.1471	-0.4913	0.5275	0.0831	-0.2105	1.9628
280	neuronatin (NNAT), mRNA	NM_005386	0.9329	0.5224	-0.0453	1.0566	0.9855	1.0641	0.9191	0.4662	-0.6498	-0.8931	0.2491	0.3479	-0.2248	1.9601
281	ras homolog gene family, member H (ARHH), mRNA	NM_004310	1.3544	1.0875	0.2882	1.6379	1.4032	0.8805	0.9069	0.5317	0.3846	-0.8108	0.1201	0.6699	-0.0568	1.8982
282	ATP-binding cassette, sub-family C (CFTR/MRP), member 2 (ABCC2), mRNA	NM_000392	1.0059	1.0631	0.6229	0.8499	1.017	1.0233	0.5005	0.9222	0.2685	-0.7091	-0.2746	0.145	0.1505	1.8091
283	thrombospondin repeat containing 1 (TSRC	NM_019032	1.0087	1.197	0.657	0.166	0.8123	1.2349	0.404	0.3492	0.4354	-0.5866	-0.4458	0.0175	-0.1692	2.2217
284	neogenin homolog 1 (chicken) (NEO1), mRNA	NM_002499	0.3046	0.3518	0.5687	1.0395	0.6374	0.9701	0.4923	0.8968	0.3073	-0.3403	-0.4833	0.0786	0.4341	1.7605
285	KIAA1712 (KIAA1712), mRNA	NM_030633	1.1055	0.6719	0.4568	0.4615	0.5459	0.5982	0.32	0.9113	-0.5086	-0.6711	-0.1058	0.3039	0.4236	1.621
286	granzyme A (granzyme 1, cytotoxic T-lymphocyte-associated serine esterase 3) (GZMA), mRNA	NM_006144	0.8007	0.5694	0.585	1.17	1.6089	1.2356	0.5694	0.6067	0.3309	-1.1173	-1.2659	0.1333	0.0642	2.1438
287	contactin associated protein-like 2 (CNTNAP2), mRNA	NM_014141	1.449	1.0423	0.4845	0.5817	1.0639	2.215	1.3469	-0.2913	0.3495	-0.262	-0.8155	0.5964	-0.3268	2.3345
288	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4 (SLC1A4), mRNA	NM_003038	0.4517	0.599	0.1367	0.8342	0.9282	0.8254	1.0924	0.806	-0.1953	-0.4294	-0.3089	1.3304	0.9952	1.7004
289	hypothetical protein FLJ20302 (FLJ20302), mRNA	NM_017754	0.6018	0.8185	-0.0228	1.0763	0.459	1.0763	1.3081	0.0688	0.0323	-0.8307	-0.5604	1.6199	0.7294	1.7761
290	sema domain, immunoglobulin domain (Ig), and GPI membrane anchor, (semaphorin) 7A (SEMA7A), mRNA	NM_003612	0.2525	0.0912	1	0.8941	0.7581	1.1824	0.4674	1.1428	-1.0789	-0.4249	-0.4461	1.0704	1.0764	1.7376
291	apolipoprotein B (including Ag(x) antigen) (APOB), mRNA	NM_000384	1.1313	1.034	0.6666	1.5502	1.7162	1.1927	0.6952	1.5773	0.594	0.0795	0.0809	0.3626	0.449	2.0996
292	glutathione peroxidase 2 (gastrointestinal) (GPX2), mRNA	NM_002083	0.3786	1.8177	0.2942	1.4883	2.152	2	1.5608	1.3693	0.3759	-0.5888	-0.4346	0.2017	0.2224	1.8876
293	dehydrogenase/reductase (SDR family) member 2 (DHRS2), mRNA	NM_005794	0.922	0.9616	0.5646	0.9125	1.5849	1.4526	1.7521	0.9061	0.4197	0.1255	0.4777	0.922	0.0939	0.922
294	hemoglobin, gamma G (HBG2), mRNA	NM_000184	0.6629	0.7369	-0.5306	0.9386	1.7004	0.2224	0.5849	0.2995	-0.3847	-1.0952	0.8541	-0.2631	0.2537	2.1699
295	gap junction protein, beta 3, 31kD (connexin 31) (GJB3), mRNA	NM_024009	0.9286	0.3879	0.1442	1.164	1.854	-0.4075	0.5033	0.1744	0.3992	-0.9756	0.8115	-0.519	-0.0445	1.7611
296	cDNA FLJ41566 fis, clone CTONG2001513	AK123560	0.3219	0.9386	-0.415	1	2.0642	0.5025	0.1155	0.2895	0.2115	-1.2479	0.6881	0.6629	-0.1255	1.7726
297	guanine nucleotide binding protein 4 (GNG4), mRNA	NM_004485	0.3923	0.1699	0.4267	0.7697	1.3266	-0.8707	1.1396	0.7276	0.4192	-0.6698	0.3978	-0.3276	0.378	1.9308
298	lumican (LUM), mRNA	NM_002345	1.1103	-0.0833	-0.516	1.7925	1.4594	-1.2496	0.5804	0.0496	0.0614	-1.1312	0.5395	0.201	-0.1712	1.7584
299	hypothetical protein DKFZp566J091 (DKFZP566J091), mRNA	NM_030915	0.8787	0.2552	0.1727	1.6952	1.9476	0.1473	0.1047	0.5097	0.2391	-0.3014	0.0267	0.3797	0.0203	1.3797
300	hypothetical protein MOT8 (MOT8), mRNA	NM_018836	1.1326	0.1396	0.0326	1.3809	1.895	0.7339	1.3449	0.2258	0.1339	-0.6189	-0.5226	0.3296	-0.1656	0.8752
301	endogenous retrovirus mRNA, clone HERV-H	AJ431196	1.3251	-0.0654	-0											

No	Description of gene function	GenBank accession number	commercial OSM_2	<i>in vitro</i> synthesized FLAG-OSM	commercial OSM_1	<i>in vitro</i> synthesized His-FLAG-IL-1 β	<i>in vitro</i> synthesized GST-FLAG-IL-1 β	commercial IFN- β _2	<i>in vitro</i> synthesized FLAG-IFN- β	commercial IFN- β _1	commercial IL-1 β _1	<i>in vitro</i> synthesized mature IL-1 β	commercial IL-1 β _2	<i>in vitro</i> synthesized FLAG-TNF- α	commercial TNF- α _1	commercial TNF- α _2
322	mRNA for FLJ00304 protein.	AK131091	-0.4889	-0.3041	-0.0126	0.0086	0.658	-0.1554	-0.5034	0.0671	0.415	-0.5128	-1.7534	1.08	0.8171	1.165
323	FXYP domain-containing ion transport regulator 6 (FXYP6), mRNA	NM_022003	-0.4179	0.3374	0.5318	0.3219	0.8835	0.9695	-0.1169	0.3487	0.2031	-0.939	-0.9478	1.6163	1.8789	1.6303
324	mRNA for FLJ00172 protein.	AK074101	-0.1343	-0.5849	0.5146	1.5986	1.5001	-0.4474	-0.0881	0.8664	-0.4353	-0.7038	-0.034	-0.81	0.276	0.2178
325	cDNA FLJ36947 fis, clone BRACE2005681	AK094266	0.2122	-0.3636	0.469	1.2076	1.6684	-0.207	0.0423	0.8813	-0.5608	-0.9054	-0.3006	-0.2319	0.3668	0.0353
326	WNT1 inducible signaling pathway protein 2 (WISP2), mRNA	NM_003881	0	0.1413	0.7575	0.585	1.6245	-0.1806	0.1793	0.8365	-0.2906	-0.6886	-0.0671	-0.3596	0.2371	0.2163
327	zeta-chain (TCR) associated protein kina	NM_001079	-0.6824	-0.6654	0.2477	0.9467	1.6081	-0.357	-0.339	0.7176	0.09	-0.9285	-0.516	-0.7827	0.2707	-0.2266
328	aldehyde dehydrogenase 5 family, member A1 (succinate-semialdehyde dehydrogenase) (ALDH5A1), mRNA ^a	NM_001080	0.2103	-0.0874	0.221	1.6124	1.4391	0.2818	0.1731	0.6015	-0.4778	-1.2657	-0.0942	-0.6724	0.6015	-0.5226
329	cDNA FLJ33482 fis, clone BRAMY2002862, weakly similar to NICOTINATE-NUCLEOTIDE PYROPHOSPHORYLASE(EC 2.4.2.19)	AK090801	0.0536	-0.3594	0.5216	1.0654	1.8897	0.4275	0.076	0.3563	0.1613	-0.2835	0.0241	-0.0686	0.2574	-0.213
330	kallikrein 6 (neurosin, zyme) (KLK6), mRNA	NM_002774	0.0984	-0.3009	0.3509	1.7213	1.3141	-0.3433	-0.1615	0.5497	0.7247	-0.926	0.0458	-0.3009	0.7244	0.5793
331	ribosomal protein S4, Y-linked (RPS4Y), mRNA	NM_001008	-0.1492	-0.522	0.2068	1.4552	1.8007	-1	-0.1279	-0.173	-0.1122	-0.6761	-0.0984	-0.2375	-0.4551	-0.1563
332	transmembrane channel-like 4 (TMC4), mRN	NM_144686	0.0527	-0.4742	-0.0989	1.0246	1.9013	-0.6397	0.0278	-0.2366	-0.1508	-0.6802	0.3916	-0.8635	0.2049	0.9211
333	WAP four-disulfide core domain 2 (WFDC2), transcript variant 1, mRNA	NM_006103	0.189	-0.0514	0	1.4263	1.6029	0.9298	0.0143	0.3142	0.2936	-0.6073	-0.8524	0.4905	-0.508	0.2203
334	neuromedin U (NMU), mRNA	NM_006681	0.6679	0.0914	-0.3131	1.865	2.0255	0.3565	-0.041	0.2767	-0.0573	-0.6521	-1.012	-0.4936	-0.834	-0.0976
335	Down syndrome critical region gene 8 (DSCR8), mRNA	NM_032589	-0.1673	-0.1909	0.6039	0.6978	1.0612	0.2372	-0.2245	0.1141	-0.0785	-0.9669	-1.6486	-0.4109	-0.068	-0.0901
336	mRNA for FLJ00400 protein.	AK090478	0.3219	0.7153	0.8067	1.7564	1.4488	0.5719	0.8673	0.5006	0.2203	-0.848	-0.1883	1.0666	-0.2147	0.1999
337	T-box 21 (TBX21), mRNA	NM_013351	0.5054	0.5979	0.5456	1.8129	1.6044	0.584	1.0142	0.5615	-0.6398	-0.3936	0.1759	1.0525	-0.7083	0.0737
338	cDNA FLJ34274 fis, clone FEBRA2003327	AK091593	0.6554	0.3848	0.5533	1.7749	1.8233	1.2052	0.7249	0.4161	-0.2626	-0.2696	-0.2929	1.1922	-0.0583	0.3962
339	protein phosphatase 1, regulatory (inhibitor) subunit 1A (PPP1R1A), mRNA	NM_006741	0.4667	0.4268	0.0183	1.7678	1.1691	0.1836	0.798	-0.0281	-0.2055	0.0043	-0.3335	0.5631	-0.1876	0.3968
340	lysozyme (renal amyloidosis) (LYZ), mRNA	NM_000239	0.6167	1.6477	0.585	2.5025	1.415	1	1.4507	0.6724	-0.3464	-0.7478	-0.659	0.848	-0.1926	1.1375
341	chromosome 20 open reading frame 103 (C20orf103), mRNA	NM_012261	0.6977	0.957	0.1235	2.0395	0.889	0.7125	0.6444	0.8946	-0.1886	0.0215	-1.3797	0.8467	-0.9852	0.6826
342	perforin 1 (preforming protein) (PRF1), mRNA	NM_005041	-0.5185	0.4305	0.847	1.6392	1.3086	0.1652	0.1194	0.8401	0.0644	0.2757	-0.5197	0.1926	0.2883	0.3686
343	aldo-keto reductase family 1, member B10	NM_020299	0.322	0.3537	0.956	1.5474	1.6571	0.2895	0.078	1.4751	0.8283	0.2922	-0.0418	0.078	0.189	0.474
344	glycoprotein hormones, alpha polypeptide (CGA), mRNA	NM_000735	-0.4306	-0.5619	1.3356	1.5145	1.5849	0.6004	-0.0962	1.0671	0.3371	-0.341	-1.152	-0.4948	0.8172	0.5694
345	selenoprotein P, plasma, 1 (SEPP1), mRNA	NM_005410	0.2086	1.0317	1.7005	1.4493	1.5474	0.9511	0	1.3837	1	-0.2344	-1.6262	0.341	0.1699	-0.0325
346	FXYP domain-containing ion transport regulator 3 (FXYP3), transcript variant 1, mRNA	NM_005971	0.7467	0.9182	1.3721	1.8408	1.9367	0.8038	-0.0372	1.1169	-0.263	0.2121	-0.8921	0.5519	-0.1969	0.2258
347	solute carrier family 38, member 3 (SLC38A3), mRNA	NM_006841	0.5139	0.3198	0.4164	1.2101	1.6815	0.2962	0.4187	0.8019	0.4761	-0.759	-1.8121	0.7752	-0.238	0.1817
348	protein kinase C, beta 1 (PRKCB1), mRNA	NM_002738	0.3744	1.3675	0.913	2.1951	1.6829	0.415	0.7581	0.7055	0.6946	-0.756	-2.1093	0.6488	-0.772	-0.2106
349	chitinase 3-like 1 (cartilage glycoprotein-39) (CHI3L1), mRNA	NM_001276	0.4603	0.0178	0.9732	1.5749	1.534	0.4307	0.6803	0.8212	0.5356	0.3866	-2.6414	0.0528	-0.5673	-0.3479
350	spleen tyrosine kinase (SYK), mRNA	NM_003177	-0.3053	0.2517	0.6635	0.6793	0.7979	0.1507	0.7246	0.3696	1.6886	-0.1351	-1.6905	0.0302	-0.412	-0.0883
351	lymphocyte cytosolic protein 1 (L-plastin) (LCP1), mRNA	NM_002298	0.5973	0.8845	0.6424	0.7105	0.9669	0.8644	0.759	-0.5502	1.2411	0.6281	-2.7549	0.1069	-0.834	0.5726
352	cDNA FLJ11890 fis, clone HEMBA1007256	AK021952	0.3056	0.6022	-0.0429	1.9222	2.304	0.5168	0.7101	0.1106	-0.7258	-0.7655	-1.347	-0.045	0.0347	2.3927
353	cholinergic receptor, nicotinic, alpha polypeptide 1 (muscle) (CHRNA1), mRNA	NM_000079	-0.4151	0.6452	0.8868	1.9622	1.585	-0.1317	0.3811	0.4884	0.0254	-1.585	-0.7017	-0.2266	-1.0736	1.8568
354	cDNA FLJ43459 fis, clone OCBBF2035564	AK125448	-0.3268	-0.0597	0.7308	0.3487	-0.2793	-0.4021	-0.2132	1.691	0.4574	0.0092	0.0736	-0.385	0.9333	-0.0631
355	hypothetical protein FLJ30046 (FLJ30046	NM_144595	-0.1624	-0.1624	0.7393	0.1786	0.7031	0.41	0.6202	1.6141	0.0916	-0.3757	-0.1818	-0.2711	0.8182	0.3692
356	mRNA for KIAA0449 protein, partial cds.	AB007918	0.4193	-0.2298	1.5815	-0.0576	0.1556	0	0.3017	1.0053	0.9916	-0.4969	-0.6794	1.4436	1.1688	0.1786
357	nemo-like kinase (LOC51701), mRNA	NM_016231	0.1161	0.2882	1.7117	0.2044	0.2089	-0.0299	-0.4265	0.6986	-0.59	-0.7553	-0.8044	0.0725	0.419	0.1918
358	SEC7 homolog (TIC), mRNA	NM_012455	-0.4525	-0.5711	1.9922	0.7117	0.9843	-0.1407	-0.0662	1.0789	-0.3163	-1.0181	-0.6951	-0.656	0.6859	-0.1205
359	secreted phosphoprotein 1 (osteopontin, bone sialoprotein I, early T-lymphocyte activation 1) (SPP1), mRNA ^a	NM_000582	-0.6738	-0.4222	1.0381	1	1	-0.8182	-0.2847	2.0691	-0.2838	-0.5406	-1.1178	-0.7442	1.0255	-0.2847
360	transferrin (TF), mRNA	NM_001063	0.4052	-0.509	0.9786	0.9069	1.0444	0.0384	0.2824	1.9349	-1.2106	-0.8163	-0.4526	-0.6245	0.6404	-0.509
361	protein tyrosine phosphatase, receptor type, C (PTPRC), transcript variant 1, mRNA	NM_002838	-0.2031	-0.7225	1	1.7005	0	-0.4199	-0.4396	1.5224	-0.7567	-1.4649	0.1587	-1.17	0.5224	-0.0748
362	interleukin 2 receptor, gamma (severe combined immunodeficiency) (IL2RG), mRNA	NM_000206	-0.5555	-0.3711	1.4552	1.599	1.7952	-0.4914	-0.845	1.4209	-0.9038	-1.1575	-0.95	0.128	1.5536	0.3659
363	cDNA FLJ39155 fis, clone OCBBF2001983	AK096474	0.8542	1.0086	0.446	1.172	0.1984	0.8005	1.0615	2.5179	-1.0644	-1.8262	-0.558	0.7678	0.196	1.0698
364	thioredoxin interacting protein (TXNIP), mRNA	NM_006472	2.4528	1.165	0.0806	0.4991	1.0191	2.553	0.5204	0.9043	-1.2627	-1.3346	-1.3618	0.4791	-0.3804	2.0036
365	cDNA FLJ38631 fis, clone HHDPC2000104	AK095950	-0.0587	-0.1529	0.1373	0.2274	0.0899	1.6918	1.0258	0.3945	0.1453	-0.0128	-0.123	0.6112	0.5616	0.6896
366	fibrillin3 (KIAA1776), mRNA	XM_041569	-0.1565	-0.2756	-0.1566	0.0488	0.1025	1.6207	1.2365	0.5258	0.2427	0.2902	0.04	0.4241	0.5808	0.2516
367	hypothetical protein FLJ14464 (FLJ14464), mRNA	NM_032789	-0.033	-0.1696	-0.1559	-0.1908	-0.0223	1.8236	1.6065	0.3001	0.4298	0.3695	0.0711	0.7955	0.4406	0.9657
368	mRNA for FLJ00195 protein.	AK074123	-0.4558	-0.1899	-0.2435	0.3152	0.1636	1.9978	1.4725	0.5267	0.4515	0.5764	0.2357	0.373	0.6268	0.6592
369	hypothetical protein MGC16202, mRNA (cdN	BC007377	-0.2504	-0.0422	-0.121	-0.2161	-0.2071	1.7791	0.766	0.6372	-0.1674	-0.2005	-0.3129	0.5342	0.8727	1.2553
370	golgi phosphoprotein 2 (GOLPH2), mRNA	NM_016548	-0.1866	-0.1104	0.2196	-0.254	-0.1	1.9957	1.2361	1.2235	0.2479	0.185	0.0635	0.6137	1.291	0.864
371	nuclear phosphoprotein mRNA, complete cc	L22343	-0.0626	0.3245	0.0984	-0.5365	-0.5834	2.1739	1.6696	0.5389	0.3396	0.2302	-0.0328	0.6605	0.6019	1.0218
372	hypothetical protein FLJ11000 (FLJ11000), mRNA	NM_018295	0.0039	-0.0367	0.0414	-0.5064	-0.8792	2.2982	1.2315	0.4292	-0.1133	0.1938	-0.1144	1.2152	0.4324	0.3015
373	cDNA FLJ11524 fis, clone HEMBA1002547, f	AK021586	-0.3794	-0.5108	-0.2134	0.1488	0.375	1.7258	1.4413	0.838	0.6972	0.4724	0.3148	1.1466	1.3337	1.3459
374	opioid growth factor receptor (OGFR), mRNA	NM_007346	-0.354	-0.6429	-0.0122	0.0447	0.2474	1.9646	1.183	0.7731	0.694	0.3812	-0.0051	0.8983	1.3051	0.8584
375	hypothetical protein FLJ11286 (FLJ11286), mRNA	NM_018381	-0.129	-0.2107	-0.2475	-0.0581	0.005	1.9528	1.6626	0.5463	0.8743	0.584	0.5749	1.0024	1.1469	1.2653
376	chromosome 20 open reading frame 18 (C20orf18), transcript variant 3, mRNA	NM_031228	0.0013	-0.1326	-0.0643	0.5575	0.186	1.6279	1.156	0.5782	0.6249	0.6535	0.377	0.9076	0.8352	1.0438
377	hypothetical protein FLJ22693 (FLJ22693), mRNA	NM_022750	-0.561	-0.5377	-0.4553	0.2153	-0.1239	1.672	1.1034	0.9633	0.3	0.2345	-0.1737	1.2539	1.1284	1.2352
378	cDNA: FLJ21201 fis, clone COL00275, highly similar to HSU61084 phorbol-1-related protein mRNA ^a	AK024854	0.1505	0.0356	-0.1491	0.5694	0.3533	1.7115	0.8359	0.874	-0.0681	0.0965	0.0965	1.1077	1.2231	1.5582
379	2',3'-cyclic nucleotide 3' phosphodiesterase (CNP), mRNA	NM_033133	0.1289	-0.248	-0.0394	0.7757	0.0968	2.1215	1.3229	0.8296	0.1736	0.1117	0.1989	0.9765	1.0815	1.3764
380	solute carrier family 38, member 5 (SLC38A5), mRNA	NM_033518	0.1071	-0.1852	-0.023	0.456	0.317	2.108	0.9541	0.2385	0.0251	0.0416	0.1291	1.2499	1.0359	1.8177
381	hypothetical protein FLJ20037 (FLJ20037), mRNA	NM_017633	0.0978	-0.0668	0.1185	0.1435	0.3829	2.0963	1.397	0.6636	0.4339	-0.1038	-0.146	0.9212	0.5763	1.6236
382	GTP binding protein 1 (GTPBP1), mRNA	NM_004286	0.3163	0.1658	0.293											

No	Description of gene function	GenBank accession number	commercial OSM_2	<i>in vitro</i> synthesized FLAG-OSM	commercial OSM_1	<i>in vitro</i> synthesized His-FLAG-IL-1 β	<i>in vitro</i> synthesized GST-FLAG-IL-1 β	commercial IFN- β _2	<i>in vitro</i> synthesized FLAG-IFN- β	commercial IFN- β _1	commercial IL-1 β _1	<i>in vitro</i> synthesized mature IL-1 β	commercial IL-1 β _2	<i>in vitro</i> synthesized FLAG-TNF- α	commercial TNF- α _1	commercial TNF- α _2
403	butyrophilin, subfamily 3, member A3 (BTN3A3), mRNA	NM_006994	-0.0957	-0.079	0.3764	0.2326	-0.2076	1.9043	1.0506	1.561	1.3322	1.1038	1.1662	1.6421	2.0931	2.0836
404	retinoic acid- and interferon-inducible protein (58kD) (RI58), mRNA	NM_012420	-0.2279	0.2916	0.0943	0.3692	0.0327	1.1269	1.2929	1.8049	1.0647	1.3446	1.1962	1.8321	2.0969	1.7984
405	cDNA FLJ30106 fis, clone BNGH41000190, weakly similar to Rattus norvegicus schlafen-4 (SLFN-4) mRNA	AK054668	0.0576	0.5842	0.272	0.3358	-0.0459	1.5311	1.3568	1.4396	1.4199	1.2401	0.7653	2.5738	2.1866	1.9519
406	protein kinase, interferon-inducible double stranded RNA dependent (PRKR), mRNA ^a	NM_002759	-0.48	-0.1688	-0.1677	0.6421	0.0704	1.9815	1.7575	1.8036	1.4692	1.0484	0.705	1.8849	2.0082	1.7775
407	N-myc (and STAT) interactor (NMI), mRNA.	NM_004688	0.3358	0.6369	0.483	0.6262	-0.2086	1.8119	1.8423	1.9936	0.7519	0.591	0.7419	2.1999	1.8828	2.2943
408	phospholipid scramblase 2 (PLSCR2), mRNA.	NM_020359	0.9355	0.6213	0.3808	0.3313	-0.2799	1.6905	1.4234	1.7616	0.9269	0.8882	1.1492	1.6488	1.9097	2.0111
409	FLN29 gene product (FLN29), mRNA.	NM_006700	0.0817	0.0496	0.0806	0.3849	0.1818	1.5831	0.6868	0.7287	0.5975	0.6288	0.2695	1.5831	1.7535	2.0903
410	hypothetical protein FLJ10830 (FLJ10830), mRNA	NM_018235	0.0594	0.106	0.2266	0.0721	0.0075	1.4123	0.3889	0.2992	0.8571	0.6892	0.0703	1.8593	1.5898	1.9997
411	CD47 antigen (Rh-related antigen, integrin-associated signal transducer) (CD47), mRNA	NM_001777	0.1655	0.1212	0.2444	0.1009	0.4869	1.2949	0.5705	0.3402	1.2188	1.0122	0.0561	2.1041	1.8917	1.9767
412	promyelocytic leukemia (PML), transcript variant 6, mRNA	NM_002675	0.0439	0.0981	-0.0092	-0.2386	0.1702	1.5252	1.3148	0.3366	0.9637	0.983	0.4633	1.6717	1.5953	1.5739
413	promyelocytic leukemia (PML), transcript variant 1, mRNA	NM_033238	0.054	0.0205	0.1713	-0.3994	-0.0809	1.5446	0.9901	0.4014	0.2891	0.6424	0.5957	1.4331	1.6755	2
414	cDNA FLJ10602 fis, clone NT2RP2005001, f	AK001464	0.2227	-0.0485	0.1196	0.434	0.036	1.6915	1.0601	0.9587	0.185	0.2041	0.7491	1.6105	1.986	1.8805
415	zinc finger protein 313 (ZNF313), mRNA.	NM_018683	-0.3735	-0.2906	-0.0077	0.2091	0.0622	1.6586	0.8489	1.082	0.4305	0.5464	0.4512	1.5093	2.1009	1.7716
416	IBR domain containing 3 (IBRDC3), mRNA.	NM_153341	-0.1756	-0.28	-0.0664	0.3349	-0.2366	0.9307	0.7255	0.7837	0.2468	0.3377	0.5812	2.1379	1.9885	2.2367
417	proteasome (prosome, macropain) subunit, beta type, 10 (PSMB10), mRNA	NM_002801	-0.6125	-0.4398	0.3746	-0.0251	0.4208	1.5946	1.015	0.7178	0.8706	0.8425	0.7119	1.5286	1.9111	1.5437
418	optineurin (OPTN), mRNA.	NM_021980	-0.6034	-0.3435	-0.1479	0.2529	0.4861	1.3211	1.0733	0.2234	1.1402	1.143	0.5718	1.6969	1.3295	1.4469
419	F-box only protein 6 (FBXO6), mRNA.	NM_018438	-0.1768	-0.1514	0.0266	0.0704	0.1538	1.2676	0.939	0.4278	-0.0732	-0.4891	0.0881	1.5595	1.5946	1.585
420	NEDD8 ultimate buster-1 (LOC51667), mRNA.	NM_016118	0.4567	0.4591	-0.4384	0.4613	0.2405	1.6261	1.1183	0.3136	0.3946	-0.2565	0.1462	1.894	1.5147	2.2967
421	guanosine monophosphate reductase (GMPR), mRNA	NM_006877	-0.1067	0.2953	0.0143	-0.3644	-0.0392	3.0458	2.3947	1.0337	-0.4365	0.0951	-0.42	1.457	1.6959	1.3653
422	cDNA FLJ43620 fis, clone SPLEN2021701, f	AK125608	-0.0167	-0.267	0.1777	-0.0193	0.4193	1.8007	1.3994	0.9962	1.4796	0.7958	1.43	1.7032	1.5778	1.9804
423	TAP binding protein (tapasin) (TAPBP), mRNA.	NM_003190	-0.316	-0.3446	-0.1348	0.1861	0.3436	1.557	0.8711	0.7275	1.3999	1.3244	1.67	1.7157	1.8562	2.178
424	proteasome (prosome, macropain) activator subunit 2 (PA28 beta) (PSME2), mRNA.	NM_002818	-0.2115	-0.0878	-0.1401	1.0392	0.5386	1.2074	1.2083	0.873	1.4364	1.5063	1.3359	2.2493	2.1688	2.0942
425	apolipoprotein L_3 (APOI3), mRNA.	NM_014349	-0.0429	-0.3233	-0.5751	-0.3915	-0.3608	1.8415	1.3584	0.472	0.9705	1.4206	1.9656	1.6621	2.1483	2.3049
426	aminopeptidase (LOC64167), mRNA.	NM_022350	0.0849	0.0339	-0.3739	-0.2072	-0.3024	1.3914	1.2496	0.3617	1.376	1.3048	1.7297	1.6997	1.4713	1.2795
427	purinergic receptor P2X, ligand-gated ion channel, 4 (P2RX4), mRNA	NM_002560	-0.4373	-0.1654	0.0111	0.0666	-0.079	0.7951	0.0343	0.5559	1.9253	1.9159	1.5602	1.3846	1.5998	1.1987
428	sulfide dehydrogenase like (yeast) (SQRD1), mRNA	NM_021199	-0.4419	0.012	0.3293	-0.1114	-0.196	0.9695	0.6573	0.2765	1.6976	1.5564	1.0586	1.944	1.7873	1.485
429	spermidine/spermine N1-acetyltransferase (SAT), mRNA.	NM_002970	-0.8763	0.0349	-0.3223	0.1124	0.1226	1.0332	1.1164	1.3973	1.362	1.3523	1.1204	1.6428	2.1676	1.3003
430	tripartite motif-containing 22 (TRIM22), mRNA.	NM_006074	-0.3735	-0.1235	-0.0763	-0.3288	-0.8493	1.1336	1.2995	0.9721	1.6841	1.2964	0.9276	1.6229	1.8306	0.6626
431	endothelial cell growth factor 1 (platelet-derived) (ECGF1), mRNA	NM_001953	0.2713	-0.0861	-0.0917	0.5647	0.7262	2.1927	1.8542	0.3812	1.9341	1.7985	1.1959	2.6565	1.6488	2.347
432	cDNA FLJ37720 fis, clone BRHIP2019149, moderately similar to Interferon, alpha-inducible protein 27	AK095039	-0.8592	-0.9292	-0.4108	-0.1047	-1.165	1.6436	1.6016	0.9887	0.2115	1.4134	0.9336	1.442	1.666	1.3706
433	cDNA FLJ13288 fis, clone OVARC1001167.	AK023350	0.64	1.2136	-0.2026	0.1827	-0.4494	1.0922	1.1412	0.6581	0.4981	0.5812	0.4346	1.1472	0.5822	1.6343
434	striatin, calmodulin binding protein (STRN), mRNA	NM_003162	0.7867	1.5084	0.4854	0.4922	0.2201	1.8157	1.2998	0.5671	0.4451	0.2464	0.2241	1.235	0.5966	1.4663
435	nuclear receptor interacting protein 1 (NRIP1), mRNA	NM_003489	0.7791	1.2414	0.4703	0.4712	-0.0526	1.0975	1.0302	0.8173	0.8702	1.2586	1.1756	1.9502	1.3938	2.1521
436	RAB33A, member RAS oncogene family (RAB33A), mRNA.	NM_004794	1.6274	1.2274	0.1877	0.2569	0.1001	1.3749	1.0519	0.3953	0.0956	-0.7175	0.2662	1.6685	-0.0498	1.6236
437	KIAA0766 gene product (KIAA0766), mRNA.	NM_014805	1.8642	1.3111	0.6241	0.7337	0.5777	1.9195	1.2992	0.4098	-0.2847	-0.2711	0.7159	1.501	0.035	2.6132
438	exonuclease 1 (EXO1), transcript variant 3, mRNA.	NM_003686	1.3463	0.7763	0.2602	0.0402	0.8316	1.3342	1.5382	0.8452	1.2135	0.1225	-0.4151	2.0304	-0.2867	1.5061
439	guanylate binding protein 2, interferon-inducible (GBP2), mRNA	NM_004120	1.3522	1.2194	1.0633	1.0532	0.4551	2.3295	1.4749	1.0785	1.1791	0.9947	1.3587	1.1261	1.0511	0.6506
440	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 1 (B4GALT1), mRNA	NM_001497	0.2382	0.4891	0.1275	0.7534	-0.1062	-0.3237	-0.2344	0.5447	1.176	1.2743	0.9576	1.4418	1.5455	1.656
441	ATPase, H+ transporting, lysosomal (vacuolar proton pump), beta polypeptide, 56/58kD, isoform 2 (ATP6B2), mRNA	NM_001693	0.0419	0.3069	0.0533	0.8836	0.2598	-0.1446	-0.1402	0.8955	1.1419	1.2076	1.0666	1.184	1.8	1.4559
442	v-ets erythroblastosis virus E26 oncogene homolog 1 (avian) (ETS1), mRNA	NM_005238	0.8345	0.6313	0.5313	0.2877	-0.1576	-0.1797	-0.0358	0.9099	1.215	1.4547	0.9217	1.725	2.1432	1.6698
443	myosin, light polypeptide kinase (MYLK), transcript variant 6, mRNA	NM_005965	-0.0595	1.0618	0.0538	0.5993	-0.2657	-0.0195	0.348	0.4067	1.4222	1.5175	0.9274	2.1531	1.6877	2.0121
444	type 1 tumor necrosis factor receptor shedding aminopeptidase regulator (ARTS-1), mRNA	NM_016442	0.0386	0.192	-0.4217	0.4734	-0.226	0.0831	0.1942	1.0287	1.7731	1.6137	1.3047	1.8548	1.8949	1.7691
445	cDNA FLJ90460 fis, clone NT2RP3001858.	AK074941	-0.1042	-0.1016	-0.0111	-0.0652	-0.2853	1.1478	-0.0388	0.2933	1.2548	1.2808	1.1412	1.2045	1.564	1.7503
446	interferon gamma receptor 2 (interferon gamma transducer 1) (IFNGR2), mRNA.	XM_048563	0.0915	0.2035	-0.0849	0.3063	-0.066	0.3334	0.022	0.1054	0.7892	1.1713	0.6636	1.3581	1.7805	2.0179
447	paired immunoglobulin-like receptor alpha (PILR(ALPHA)), mRNA	NM_013439	0.1076	-0.2664	0.1715	-0.184	0.1719	0.076	0.1592	-0.1035	0.4757	0.9063	0.7855	1.6483	1.4218	1.7623
448	selenoprotein SeM (SELM), mRNA.	NM_080430	0.2969	0.1269	0.3006	-0.1645	0.1752	0.0944	0.2273	0.0163	1.771	1.6394	0.9914	1.4242	1.827	1.4917
449	podocalyxin-like (PODXL), mRNA.	NM_005397	-0.2502	-0.3425	-0.4073	0.6526	-0.1657	0.5474	0.2329	0.7852	1.0512	1.7812	0.2164	1.6497	2.051	1.6842
450	serologically defined colon cancer antigen 28 (SDCCAG28), mRNA	NM_006645	-0.5366	-0.3601	0.1113	0.601	0.2829	-0.2096	0.2847	-0.0991	1.313	1.2719	1.3397	2.4284	1.8156	1.7571
451	DNA segment on chromosome 6 (unique) 49 expressed sequence, NK cell triggering receptor, p30 (D6S49E), mRNA	NM_007161	-0.1275	-0.2519	-0.0555	0.488	0.4734	1.1903	-0.1774	0.3511	1.1353	0.8046	0.8898	2.2369	1.5005	1.5598
452	solute carrier family 2 (facilitated glucose transporter), member 6 (SLC2A6), mRNA.	NM_017585	-0.9029	-0.7767	-0.2772	0.5766	0.4462	-0.223	-0.0843	-0.3407	1.4437	1.6287	1.2637	1.6116	1.2734	0.9142
453	sequestosome 1 (SQSTM1), mRNA.	NM_003900	-0.946	-0.69	-0.4264	0.3355	0.2286	0	0.2643	0.4191	1.0877	1.0694	0.7572	1.4553	1.7064	1.5453
454	CD44 antigen (homing function and Indian blood group system) (CD44), mRNA	NM_000610	-0.379	-0.0023	-0.3408	0.6353	0.0976	-1	-0.7608	0.0788	1.3133	1.3146	1.0992	1.7158	2.0917	1.7081
455	proline-serine-threonine phosphatase interacting protein 2 (PSTPIP2), mRNA	NM_024430	-0.0055	0.671	0.1122	0.0489	-0.4181	-0.6954	-0.5064	0.5254	1.189	1.5508	1.7999	2.2425	2.2329	2.3858
456	Wilms' tumour 1-associated protein (KIAA0105), mRNA.	NM_004906	0.2197	0.2883	0.3842	0.1508	-0.1818	-0.6764	-0.6808	0.6092	2.4325	2.0598	1.6676	1.9136	1.9275	1.5528
457	nuclear factor of kappa light polypeptide gene enhancer in B-cells 2 (p49/p100) (NFKB2), mRNA	NM_002502	-0.4161	-0.5427	0.3114	1.0639	0.7797	0.068	0.0619	0.3937	2.2638	2.386	1.7109	2.3268	2.2549	2.1047
458	Nef-associated factor 1 (NAF1), mRNA.	NM_006058	-0.3324	-0.1838	0.048	0.8632	0.419	-0.172	-0.0365	-0.0719	2.4098	2.3962	2.2599	2.4063	1.9628	2.2009
459	lymphotoxin beta (TNF superfamily, member 3) (LTB), transcript variant 1, mRNA	NM_002341	0.1244	-0.1277	-0.0026	1.007	0.7472	0.2587	0.2909	-0.0572	1.5336	1.5416	1.2714	1.7439	1.6972	1.7006
460	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha (NFKBIA), mRNA	NM_020529	0.1718	0.0835	0.1438	0.8318	0.4768	0.3457	0.4118	-0.0037	1.9798	2.0287	1.7399	2.4968	1.763	2.0274
461	interleukin-1 receptor-associated kinase 2 (IRAK2), mRNA	NM_001570	-0.8668	-0.4677	-0.6663	0.4514	0.1932	0.2206	0.4935	0.1596	1.3985	1.9996	2.0417	2.4566	2.0598	2.1733
462	receptor-interacting serine-threonine kinase 2 (RIPK2), mRNA	NM_003821	-0.2643	0.298	0.3695	0.6057	-0.1137	0								

No	Description of gene function	GenBank accession number	commercial OSM_2	<i>in vitro</i> synthesized FLAG-OSM	commercial OSM_1	<i>in vitro</i> synthesized His-FLAG-IL-1 β	<i>in vitro</i> synthesized GST-FLAG-IL-1 β	commercial IFN- β _2	<i>in vitro</i> synthesized FLAG-IFN- β	commercial IFN- β _1	commercial IL-1 β _1	<i>in vitro</i> synthesized mature IL-1 β	commercial IL-1 β _2	<i>in vitro</i> synthesized FLAG-TNF- α	commercial TNF- α _1	commercial TNF- α _2
484	fatty-acid-Coenzyme A ligase, long-chain 3 (FACL3), mRNA	NM_004457	0.8231	0.8209	0.4395	0.1923	0.2527	-0.3734	-0.491	0.2029	0.7344	0.8887	0.995	1.6671	1.5782	1.7788
485	interleukin 4 receptor (IL4R), mRNA	NM_000418	0.6968	0.4445	0.2828	0.4981	-0.0301	0.2347	0.2341	-0.1108	0.6068	0.6665	0.5379	2.0291	1.2884	1.7166
486	membrane associated guanylate kinase in	NM_173515	0.4857	0.7269	0.4605	0.4599	-0.3286	0.0683	-0.5028	0.1907	0.3931	0.1028	0.5875	1.9309	1.5864	1.7502
487	cytochrome b-5 (CYB5), nuclear gene encoding mitochondrial protein, mRNA	NM_001914	0.2526	0.3463	0.0608	0.1347	0.1328	-0.2485	-0.1987	0.4417	-0.0799	0.1671	0.4686	1.8248	1.7823	1.7604
488	prolylcarboxypeptidase (angiotensinase C) (PRCP), mRNA	NM_005040	0.1113	0.3245	-0.1081	0.0601	-0.0553	-0.2796	-0.255	0.7884	0.5714	0.52	0.1612	1.3674	1.5138	1.6494
489	Nijmegen breakage syndrome 1 (nibrin) (NBS1), mRNA	NM_002485	-0.0201	0.272	0.4249	0.2433	0.1185	0.4723	-0.3355	0.6885	0.6479	0.9296	0.2679	1.4856	1.8684	1.7026
490	transcription factor BMAL2 (ARNTL2), mRNA	NM_020183	0.9951	0.9019	0.1871	0.8788	0.4239	-0.1699	-0.0845	0.5542	-0.0333	0.6629	0.98	2.3613	1.6176	1.7299
491	cDNA FLJ16480 fis, clone BRTHA2016318, f	AK131393	0.3203	0.0817	-0.0726	0.6136	0.1257	-0.7844	-0.1227	0.086	0.7686	0.7677	1.1176	1.657	0.9835	1.2023
492	dihydropyrimidinase-like 3 (DPYSL3), mRNA	NM_001387	0.6813	0.637	-0.1308	0.8459	0.1883	-0.8221	-0.1102	-0.0948	0.6742	0.8786	0.3895	1.7284	1.1019	1.7516
493	solute carrier family 21 (organic anion transporter), member 12 (SLC21A12), mRNA	NM_016354	-0.0595	-0.607	-0.287	0.605	0.7091	-0.3165	-0.0748	-0.1339	0.8333	0.3173	0.6325	1.9136	0.7863	1.152
494	chromosome 14 open reading frame 31 (C14	NM_152330	0.0729	0.888	-0.5982	1.2971	-0.1136	-0.0955	-0.3947	1.233	0.2764	0.5498	0.7266	1.6346	1.9375	2.0363
495	dual specificity phosphatase 5 (DUSP5), mRNA	NM_004419	0.4382	0.2048	0.6082	0.2976	-0.1218	-0.0516	0.3413	0.4965	0.4174	0.2976	0.0854	2.446	2.6398	2.3711
496	niban protein (NIBAN), mRNA	NM_022083	-0.063	0	0.7326	0.2122	-0.2119	-0.0186	0.4695	0.4204	0.208	-0.2539	-0.1369	1.8558	2.2929	2.0633
497	high-mobility group (nonhistone chromosomal) protein isoform I-C (HMGIC), mRNA	NM_003483	-0.7059	0.0493	-0.9215	0.8293	0.0178	-0.2605	-0.2308	-0.1166	0.4605	0.5012	0.4888	1.5187	1.1265	1.7225
498	pleckstrin 2 (mouse) homolog (PLEK2), mRNA	NM_016445	-0.1263	-0.1335	-0.3213	0.6166	-0.1453	0.3454	0.0085	-0.0153	-0.0495	0.7855	0.2581	1.8153	1.2415	1.839
499	hypothetical protein FLJ20234 (FLJ20234), mRNA	NM_017720	-0.7771	-0.6812	0.3323	-0.0062	-0.274	0.5383	-0.4999	0.0654	0.1886	0.5197	0.3479	2.056	1.4844	1.5725
500	folliculin-like 3 (secreted glycoprotein) (FSTL3), mRNA	NM_005860	-1.1304	-1.132	-0.3346	-0.0447	0.1235	-0.275	0.0273	-0.4349	0.2218	0.0038	0.0827	1.1754	0.9315	1.5938
501	endothelial differentiation, sphingolipid G-protein-coupled receptor, 3 (EDG3), mRNA	NM_005226	0.134	0.6643	-0.4832	0.5419	-0.5187	0.6139	0.6189	-0.371	0.9137	1.2141	0.4994	2.3183	0.6878	1.6893
502	pannexin 1 (PANX1), mRNA	NM_015368	0.2242	1.0195	-0.3783	0.2928	0.0191	0.7004	0.3324	0.1882	0.2151	1.0432	0.465	2.0236	1.3432	2.0974
503	fibroblast growth factor 5 (FGF5), transcript variant 1, mRNA	NM_004464	-0.3444	0.0019	-1.3252	-0.4166	-0.3006	0.6297	-0.1606	-0.52	1.0422	1.2718	0.4347	2.3254	0.5266	1.8804
504	plasminogen activator, tissue (PLAT), transcript variant 1, mRNA	NM_000930	-0.0988	0.1496	-0.645	-0.0433	-0.0252	1.1571	0.5165	0.1404	0.0864	-0.024	-0.1617	1.6141	0.639	1.2803
505	hypothetical protein LOC57333 (LOC57333), mRNA	NM_020650	0.2628	-0.0408	-0.2298	-0.6615	-0.1647	0.4484	0.5644	-0.2281	0.5542	0.4723	-0.0404	1.4894	1.0162	1.5955
506	hedghog interacting protein (HHIP), mRNA	NM_022475	-0.2292	0.2676	-0.428	-0.2554	0.2109	0.9473	0.5341	0.3545	-0.4344	0.8385	0.519	1.8182	0.245	0.8184
507	transferrin (prealbumin, amyloidosis type I) (TTR), mRNA	NM_000371	0.3815	-0.1604	0.1285	0.2176	0.4066	0.8074	-0.6933	0.4572	-0.0931	-0.1296	-0.0786	1.8289	0.3557	0.5203
508	DNA cross-link repair 1B (PSO2 homolog, S. cerevisiae) (DCLRE1B), mRNA	NM_022836	1.4813	0.2093	0.4798	-0.2761	-0.188	0.4843	0.4358	0.4101	0.2083	-0.418	0.3065	1.6998	0.7706	1.5312
509	cDNA FLJ35283 fis, clone PROST2007528	AK092602	0.962	1.1101	0.2705	-0.146	-0.12	0.1448	0.1792	-0.1792	-0.481	0.4512	-0.1405	1.7211	0.0053	0.5531
510	programmed death ligand 2 (PDL2), mRNA	NM_025239	0.1245	0.6121	0.3768	-0.5011	-1.0368	0.6876	0.0766	0.8819	0.9232	1.0848	-0.3582	1.9157	1.1031	0.9195
511	FXVD domain-containing ion transport regulator 2 (FXVD2), transcript variant a, mRNA	NM_001680	0.3155	0.6619	0.0478	0.8267	1.0403	1.0128	0.5349	-0.0728	0.7349	0.3408	0.3493	1.2415	0.7496	1.9577
512	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, epsilon (NFKBIE), mRNA	NM_004556	0.2408	-0.0654	-0.3606	1.2976	1.2432	0.2877	0.2095	-0.0812	0.6081	1.2461	0.2879	2.0122	0.9462	1.5748
513	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 6 (SERPINA6), mRNA	NM_001756	0.3334	-0.2192	0.4155	1.8005	2.028	-0.2357	0.0011	-0.0304	0.1404	0.6031	0.0258	1.1695	0.8759	1.3308
514	fem-1 homolog b (C. elegans) (FEM1B), mRNA	NM_015322	0.6685	1.3907	0.6912	1.2348	0.5641	0.3007	-0.2146	0.8924	0.1045	0.2233	0.0443	1.6005	0.4412	1.0434
515	monocyte to macrophage differentiation-associated (MMD), mRNA	NM_012329	1.3824	1.5806	0.4633	1.5212	0.3929	-0.5595	0.6602	0.518	0.904	0.4587	-0.3285	1.8073	0.4509	1.2801
516	LOC157570 (LOC157570), mRNA	XM_088331	1.0729	1.1383	-0.068	1.3057	1.04	-0.4507	1.3394	0.1558	0.149	-0.1511	0.3015	1.2008	0.6368	1.9255
517	6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase 3 (PFKFB3), mRNA	NM_004566	-0.385	0.0221	0.07	0.3421	-0.1989	-0.3777	-0.5108	0.2089	0.2811	0.9177	0.8861	1.1316	1.7288	1
518	hypothetical protein FLJ13710 (FLJ13710), mRNA	NM_024817	-0.7284	-0.5522	-0.7829	0.4259	-0.2652	-0.0626	0.1945	0.4681	0.6138	0.5354	1.7653	0.8177	1.7038	1.1334
519	nuclear factor (erythroid-derived 2)-like 3 (NFE2L3), mRNA	NM_004289	-0.7529	0.0811	-0.4384	0.7171	-0.3522	-0.8054	-0.4562	1.7155	0.2622	0.8157	0.7736	0.7609	1.6388	1.1006
520	cDNA FLJ10500 fis, clone NT2RP2000369	AK001362	-1.6268	-0.9358	-1.037	0.2915	-0.3872	-1.2167	-0.8378	0.8162	0.5597	0.5822	0.3382	0.8299	1.1201	1.2005
521	BCL2-related protein A1 (BCL2A1), mRNA	NM_004049	-0.0502	-1	-1.0133	0.6292	1.2164	0.3299	0.699	-0.1188	1.8173	1.1255	0.8441	0.8628	1.2692	1.3801
522	folliculin (FST), transcript variant FST317, mRNA	NM_006350	-1.5154	-1.7728	-1.4012	0.4965	-0.1931	0.489	0.3347	-0.3428	0.7099	0.7996	0.3523	2.3648	1.4383	1.843
523	5'-nucleotidase, ecto (CD73) (NT5E), mRNA	NM_002526	-0.8173	0.2184	-0.8892	-0.174	-1.4942	0.6508	0.3849	2.2744	1.0053	2.1275	1.0336	0.6231	1.5249	0.9214
524	interleukin 15 receptor, alpha (IL15RA), mRNA	NM_002189	0.7164	0.4138	0.6569	0.4579	-0.3911	2.2394	1.3794	0.8269	0.8195	0.9787	1.7744	3.0613	2.8358	3.2807
525	interferon regulatory factor 1 (IRF1), mRNA	NM_002198	0.6023	0.4007	0.4889	0.7791	0.3387	2.1998	1.3248	0.5372	1.5886	1.6932	1.8509	3.5258	2.677	3.7096
526	laminin, beta 3 (necin (125kD), kalinin (140kD), BM600 (125kD)) (LAMB3), mRNA	NM_000228	0.5685	0.0362	0.0743	1.3494	0.9423	0.8038	0.3934	0.2939	0.7222	1.306	0.8779	4.125	2.4107	3.3771
527	hypothetical protein DKFZp434J037 (DKFZP434J037), mRNA	NM_030952	-0.0129	-0.0601	0.7899	1.0433	0.2424	0.8828	0.6597	1.0439	0.8417	0.9951	1.5004	3.149	2.8916	2.7793
528	CCR4 carbon catabolite repression 4-like (S. cerevisiae) (CCR4L), mRNA	NM_012118	0.6454	0.1257	-0.0484	0.6292	0.6867	1.4812	1.0942	-0.0151	0.6467	0.9106	1.5082	2.9781	1.7248	2.8683
529	IKK-related kinase epsilon; inducible I kappa B kinase (IKKE), mRNA	NM_014002	0.54	0.6365	0.1746	0.6561	0.3206	0.659	1.0874	-0.3579	1.0701	1.6385	2.9028	2.5584	1.6069	2.8758
530	natural killer cell transcript 4 (NK4), mRNA	NM_004221	-1.6597	-1.3697	-1.0563	1.36	1.2661	0.3886	0.3921	0.0555	2.4077	2.357	1.9326	3.0576	2.4124	2.9848
531	v-rel reticuloendotheliosis viral oncogene homolog B, nuclear factor of kappa light polypeptide gene enhancer in B-cells 3 (avian) (RELB), mRNA	NM_006509	-0.5288	-0.2162	0.0427	2.1969	1.4083	0.2499	0.5356	0.2801	0.9631	1.6003	1.8526	2.6938	1.848	2.3742
532	ribosomal protein S5 (RPS5), mRNA	NM_001009	0.2639	-0.018	0.1821	0.6926	0.4078	-1.0285	-0.3458	-0.2398	-0.1148	0.0308	-0.0705	0.0966	-0.1742	4.3195
533	cDNA FLJ10616 fis, clone NT2RP2005453	AK001478	2.1716	1.8681	0.9693	0.4367	0.0656	0.7229	1.7623	0.5281	-0.4699	-0.2863	-0.1829	0.5952	-0.2123	1.1819
534	hypothetical protein FLJ22690 (FLJ22690), mRNA	NM_024711	1.9234	1.9534	0.8001	-0.3447	-0.7209	1.5696	1.3136	0.4188	-1.007	-0.3625	-0.4424	0.3444	-0.4283	0.1931
535	early growth response 1 (EGR1), mRNA	NM_001964	1.9859	1.1709	1.246	1.0356	0.237	0.6961	0.2027	0.8063	0.3169	-0.317	-0.2834	-0.3545	-0.0618	1.0121
536	solute carrier family 16 (monocarboxylic acid transporters), member 6 (SLC16A6), mRNA	NM_004694	0.7557	1.78	1.0773	-0.2985	-0.1121	1.1136	0.0234	1.1566	-0.0295	-0.3938	-0.0735	0.5849	0.2091	0.7697
537	glycoprotein A repetitions predominant (GARP), mRNA	NM_005512	1.7183	1.6517	0.8372	-1.3952	-0.4469	1.4978	0.642	-0.8307	-0.1191	0.5641	-0.7243	0.3205	-0.2985	0.1697
538	hypothetical protein FLJ10698 (LOC57863), mRNA	NM_021189	1.713	1.7072	0.7254	-0.4903	-1.0902	1.427	1.4612	-1.141	-0.1139	-0.2214	-0.4707	-0.039	-1.5159	-0.1846
539	Duffy blood group (FY), mRNA	NM_002036	2.3739	2.0304	2.2448	-1.2027	-0.2202	1.2796	0.7798	-1.2543	0.5026	0.0629	0.4843	1.2987	1.2841	1.5915
540	STAT induced STAT inhibitor 3 (SSI-3), mRNA	NM_003955	3.3959	2.6774	3.1864	0.0103	0.0896	0.2863	0.3317	0.0972	-0.0051	0.5047	0.6968	-0.7066	-0.2293	-0.5361
541	cadherin 5, type 2, VE-cadherin (vascular epithelium) (CDH5), mRNA	NM_001795	0.1695	-0.9238	-1.7003	-1.566	-1.7611	-0.3677	-0.1674	-0.3189	-0.5064	0.3475	2.2049	-0.2201	1.0407	-0.2584
542	phospholipase A2, group IVC (cytosolic, calcium-independent) (PLA2G4C), mRNA	NM_003706	-2.1283	-1.8728	-1.744	-1.137	-0.9894	0.2118	-0.2221	-0.5245	0.9794	1.3776	3.0345	1.1063	1.8912	0.4898
543	MHC class I antigen precursor (HLA-A) mR	AF305699	-0.1325	-0.3802	0.0196	0.4482	0.6123	2.4034	1.8194	1.86						

No	Description of gene function	GenBank accession number	commercial OSM_2	<i>in vitro</i> synthesized FLAG-OSM	commercial OSM_1	<i>in vitro</i> synthesized His-FLAG-IL-1 β	<i>in vitro</i> synthesized GST-FLAG-IL-1 β	commercial IFN- β _2	<i>in vitro</i> synthesized FLAG-IFN- β	commercial IFN- β _1	commercial IL-1 β _1	<i>in vitro</i> synthesized mature IL-1 β	commercial IL-1 β _2	<i>in vitro</i> synthesized FLAG-TNF- α	commercial TNF- α _1	commercial TNF- α _2
565	bone marrow stromal cell antigen 2 (BST2), mRNA.	NM_004335	-0.738	-0.7021	-0.0725	0.0512	0.2049	2.8789	2.6569	2.5042	1.902	1.6861	1.3675	1.6442	2.4777	2.0756
566	lectin, galactoside-binding, soluble, 3 binding protein (LGALS3BP), mRNA	NM_005567	-0.614	-1.0587	0.1462	0.6726	0.4831	3.2018	2.7053	3.078	1.8861	1.6845	1.6339	1.6385	3.0128	2.0333
567	XIAP associated factor-1 (HSXIAPAF1), mRNA.	NM_017523	-0.766	-0.4898	-0.1079	-0.0105	-0.38	2.4349	2.3817	2.3338	2.3681	1.8221	1.5575	2.7554	2.831	2.0657
568	interferon, alpha-inducible protein 27 (IFI27), mRNA	NM_005532	-1.1185	-1.0217	-0.5457	0.4842	0.4101	1.9803	1.9894	2.4546	1.4985	1.2446	1.4445	0.9334	2.2525	1.3764
569	cDNA FLJ12480 fis, clone NT2RM1001066	AK022542	-0.3948	0.3341	-0.2007	0.3707	-0.5959	2.2206	2.3994	2.7807	2.1791	2.0917	1.969	3.386	3.4673	3.3622
570	similar to hypothetical protein FLJ14464 (LOC201696), mRNA	XM_032269	-0.3236	0.2947	0.087	0.8377	-0.1136	2.9472	2.4359	3.1724	1.8999	2.4468	1.5291	3.2797	3.7244	3.2899
571	hypothetical protein FLJ20637 (FLJ20637), mRNA	NM_017912	-0.3174	-0.0652	0.2399	0.49	-0.0647	2.7127	2.4867	3.4684	2.8343	1.7989	2.0842	3.3192	4.1089	3.6601
572	proteasome (prosome, macropain) subunit, beta type, 9 (large multifunctional protease 2) (PSMB9), mRNA	NM_002800	-0.0853	-0.0279	0.3829	0.8132	0.7063	3.8162	2.8869	2.8394	2.4092	2.1904	2.5548	3.0834	3.7511	3.4347
573	epithelial stromal interaction 1 (breast) (EPSTI1), mRNA.	NM_033255	-0.2029	0.1602	0.297	0.4109	0.1766	3.471	3.0358	2.7275	1.8773	1.5624	1.7741	3.432	3.6954	3.5957
574	SAM domain and HD domain, 1 (SAMHD1), mRNA	NM_015474	-0.2265	0.4421	-0.0461	1.023	-0.2607	3.5251	3.5966	3.709	1.2264	1.0028	1.7257	3.6793	3.9006	4.2798
575	ubiquitin specific protease 18 (USP18), mRNA.	NM_017414	-0.6735	0.0264	-0.6517	0.3053	-0.0519	2.9184	2.8491	2.5202	1.448	1.2013	0.3763	3.2713	3.4768	3.0866
576	interferon induced transmembrane protein	BC000897	0.4244	0.3001	1.0295	0.7615	0.9575	4.4204	4.0043	4.1611	2.1789	1.6746	1.4799	2.3997	4.0819	3.2574
577	phospholipid scramblase 1 (PLSCR1), mRNA.	NM_021105	1.416	1.1097	1.0272	0.8996	0.1982	3.0886	2.8464	3.1246	2.0347	1.8017	1.9872	2.937	3.3961	2.8823
578	transcription factor ets (TEL2), mRNA.	NM_016135	0.0064	0.0127	0.141	0.5551	-0.2199	2.8591	1.7969	0.5246	-0.2361	-0.504	0.2919	3.2622	2.9233	2.556
579	cyclin-E binding protein 1 (LOC51191), mRNA	NM_016323	-0.4216	0.4671	1.0025	1.1497	0.3691	3.8821	3.0564	1.5599	0.3268	-1.7127	-0.6415	2.6964	2.146	2.3827
580	tumor-associated calcium signal transducer 1 (TACSTD1), mRNA.	NM_002354	0.6354	0.9429	-0.0527	1.7154	1.1277	2.4683	2.1653	1.5734	0.8928	-0.0482	0.3075	2.8947	1.5082	2.385
581	CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-associated) (CD74), mRNA	NM_004355	0.2295	-0.7287	0.9048	0.2631	0.2017	1.3515	-0.4317	1.3996	0.4561	0.1069	0.4151	2.8969	4.4538	3.5662
582	interferon, alpha-inducible protein (clone IFI-6-16) (G1P3), transcript variant 1, mRNA	NM_002038	-1.8148	-1.7177	-0.4652	0.592	0.5681	4.3281	3.9055	5.3824	3.294	2.769	2.3484	2.0041	4.9722	2.6109
583	myxovirus (influenza virus) resistance 1, interferon-inducible protein p78 (mouse) (MX1), mRNA ^a	NM_002462	-1.7196	-1.5934	-0.1295	0.5484	0.5606	4.8398	4.278	4.8745	3.0248	2.6398	2.2491	3.0932	4.8228	3.5715
584	interferon stimulated gene (20kD) (ISG20), mRNA.	NM_002201	-0.2279	0.262	0.171	0.6151	0.1761	5.5544	4.3298	3.1441	3.0669	2.5628	2.8299	4.5203	4.846	5.0789
585	2'-5'-oligoadenylate synthetase 3 (100 kD) (OAS3), mRNA	NM_006187	-0.512	-0.5588	0.0173	1.4661	0.4489	5.027	4.353	3.8827	2.4102	2.5353	2.0004	4.4014	4.65	5.0854
586	interferon-induced protein with tetratr	NM_001001887	-0.6932	-0.5198	0.0307	1.4588	0.4803	4.8935	4.0701	2.8526	2.5913	2.3124	2.0176	3.7232	3.2821	3.9884
587	peptide transporter 3 (PHT2), mRNA.	NM_016582	-0.2852	-0.737	0.0525	0.1606	0.736	4.2914	3.9586	2.7233	2.3598	2.3314	2.595	3.0219	3.6452	3.513
588	interferon-induced protein with tetratricopeptide repeats 4 (IFIT4), mRNA	NM_001549	-0.5973	-0.9014	0.631	0.9028	0.2175	4.3306	3.369	4.0562	2.5769	1.8845	2.1013	3.3481	4.4523	4.0041
589	2'-5'-oligoadenylate synthetase 2, 69/71	NM_002535	-0.9946	-0.503	-0.4134	0.6323	-0.2215	4.2936	3.7421	3.883	3.1832	2.8388	2.7582	3.9766	4.2802	4.4744
590	interferon-stimulated protein, 15 kDa (ISG15), mRNA.	NM_005101	-1.1146	-0.8792	-0.3333	1.034	0.4354	5.3212	4.7349	4.2188	2.4244	2.1369	1.8502	3.1737	4.063	3.8824
591	myxovirus (influenza virus) resistance 2 (mouse) (MX2), mRNA	NM_002463	-0.3872	-0.5451	0.6442	0.7795	1.1712	5.7287	5.0459	4.5432	1.5052	0.9674	1.4636	4.4563	5.2326	5.0078
592	interferon, gamma-inducible protein 30 (IFI30), mRNA	NM_006332	0.5626	0.2255	0.7213	1.2479	1.5078	4.8807	3.2112	2.8017	1.6061	1.3661	1.964	4.2642	4.4107	5.3001
593	colony stimulating factor 2 receptor, beta, low-affinity (granulocyte-macrophage) (CSF2RB), mRNA	NM_000395	1.3834	1.2548	1.0949	-0.3036	-0.3806	-0.1188	0.0131	0.3324	1.5329	2.0512	1.203	2.3223	2.159	1.7974
594	sialyltransferase 1 (beta-galactoside alpha-2,6-sialyltransferase) (SIAT1), mRNA	NM_003032	1.5699	1.5699	0.7852	0.3705	-0.1596	-0.3422	-0.3733	0.0524	2.1981	2.1846	1.7794	1.9486	1.4974	2.1308
595	UDP-glucose ceramide glucosyltransferase (UGCG), mRNA.	NM_003358	1.0855	1.5227	0.6619	0.8094	-0.2621	0.6533	0.2369	1.3868	2.1441	2.2498	1.8539	1.5782	1.5038	1.8522
596	pre-B-cell colony-enhancing factor (PBEF), mRNA	NM_005746	1.8444	2.0289	1.1267	0.7566	-0.4414	-0.3487	-0.1071	0.5042	1.978	1.9478	1.8189	0.9867	1.2679	0.6993
597	lipase, endothelial (LIPG), mRNA.	NM_006033	1.5669	2.0327	1.6253	-0.6884	-1.0472	-0.98	-0.9945	-0.0366	1.5307	2.6828	2.7679	1.7073	1.741	0.4422
598	cDNA: FLJ21551 fis, clone COL06266.	AK025204	0.2924	0.7445	-1.1329	-0.1934	-1.3447	-0.0059	0.61	0.8642	1.1295	1.3754	2.3507	2.8955	1.5631	1.5891
599	nuclear receptor coactivator 7 (NCOA7).	NM_181782	0.2786	1.1119	0.2187	0.2275	-1.0543	0.1202	0.0237	1.5618	1.5842	1.9292	1.6061	2.2119	3.2517	2.9308
600	colony stimulating factor 1 (macrophage) (CSF1), mRNA.	NM_000757	0.2929	0.2559	0.5976	0.858	0.0447	0.7708	0.5217	0.3147	4.0957	3.7661	3.3329	2.2953	2.648	2.5529
601	chemokine orphan receptor 1 (CMKOR1), mR	NM_020311	0.0893	0.2273	0.409	1.5073	0.109	-0.2501	-0.0712	0.15	3.5962	3.6488	3.316	3.6267	3.0061	3.1411
602	small inducible cytokine subfamily A (Cys-Cys), member 11 (eotaxin) (SCYA11), mRNA	NM_002986	0.5078	0.5955	0.6118	0.2978	0.0881	-0.1257	-0.0261	0.5389	2.5906	2.5487	2.6601	2.8825	3.1252	2.6529
603	similar to RIKEN cDNA 1110014B07 gene (LOC115908), mRNA	XM_057014	0.3245	0.1767	0.2441	-0.3298	-0.3183	-1.7302	-1.1429	-0.2475	3.2036	2.7057	2.4895	2.7179	3.002	2.6279
604	coagulation factor II (thrombin) receptor-like 1 (F2RL1), mRNA.	NM_005242	-0.8913	-0.3015	-0.5677	0.7691	0.1614	-0.6054	-0.4726	0.085	2.2837	2.7241	3.0078	2.4481	2.4327	2.6051
605	claudin 14 (CLDN14), mRNA.	NM_012130	0.0063	-0.1644	0.0522	-0.8583	-1.0255	0.4524	0.4741	-0.3606	2.1913	2.731	3.5024	2.6368	1.7164	2.4911
606	complement component 3 (C3), mRNA.	NM_000064	0.1845	1.4714	1.2109	0.9069	0.9386	1.3735	-0.0671	1.415	4.0262	4.1838	4.6818	1.8625	1.663	2.9157
607	CCAAT/enhancer binding protein (C/EBP), delta (CEBPD), mRNA	NM_005195	2.6473	2.2762	2.2723	0.9052	0.4184	1.2559	0.7215	0.5316	3.6637	3.6065	3.1643	1.7322	1.9025	2.0897
608	intercellular adhesion molecule 1 (CD54), human rhinovirus receptor (ICAM1), mRNA	NM_000201	0.389	0.7917	0.259	2.219	0.8541	0.7912	0.9909	0.3916	3.5336	3.6736	3.9967	5.1968	4.2413	5.2825
609	small inducible cytokine A2 (monocyte chemotactic protein 1) (SCYA2), mRNA	NM_002982	0.7051	1.0231	0.9515	2.8964	1.7583	-0.0595	-0.1655	0.3862	3.8626	3.896	3.8986	4.4952	3.9561	4.3696
610	inducible T-cell co-stimulator ligand (	NM_015259	-0.0746	-0.1942	-0.4559	1.4429	0.5647	-0.0294	0.6822	-0.4741	4.7173	4.1839	4.039	4.6839	3.4628	4.5722
611	tumor necrosis factor, alpha-induced protein 2 (TNFAIP2), mRNA	NM_006291	0.4871	0.33	0.0668	1.2765	1.0016	0.8538	1.1195	0.2611	2.6581	2.8266	3.3279	3.4191	2.7364	3.7315
612	tissue factor pathway inhibitor 2 (TFPI2), mRNA	NM_006528	0.026	0.241	0.4991	0.613	0.0169	0.891	1.1494	0.6891	3.2589	2.3176	2.8464	4.9643	3.5197	4.2101
613	TNF receptor-associated factor 1 (TRAF1), mRNA.	NM_005658	0.1949	-0.095	0.0405	0.5359	0.3091	0.5953	-0.0575	0.4173	2.1292	2.5083	2.665	4.966	5.3299	5.1695
614	tumor necrosis factor, alpha-induced protein 3 (TNFAIP3), mRNA	NM_006290	-0.6416	-0.6065	-0.161	2.33	0.8321	0.194	0.0337	0.5362	2.8043	3.1566	2.9949	5.0415	4.566	5.2046
615	G protein coupled receptor interacting protein, complement-c1q tumor necrosis factor-related (ZSIG37), mRNA	NM_030968	1.8281	1.1981	1.3316	-1.1372	-1.1991	0.6357	0.4497	0.863	2.5866	2.6192	2.953	4.8289	5.1443	5.1224
616	serine (or cysteine) proteinase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 3 (SERPINA3), mRNA ^a	NM_001085	3.9991	2.8779	2.6696	0.9344	2.0238	1.2456	0.7039	1.5145	0.8783	0.6203	1.0854	2.307	1.5329	3.5998
617	GRO2 oncogene (GRO2), mRNA.	NM_002089	0.7013	0.8192	0.9134	3.8747	1.7814	-0.0287	-0.0789	-0.4481	5.5919	6.0691	6.2023	3.2052	3.8171	3.4869
618	small inducible cytokine subfamily B (Cys-X-Cys), member 5 (epithelial-derived neutrophil-activating peptide 78) (SCYB5), mRNA ^a	NM_002994	-0.3734	-0.2135	-0.0213	2.381	0.8422	-0.5789	-0.3076	0.0321	6.2825	6.8253	6.3791	3.8969	3.722	3.9389
619	colony stimulating factor 3 (granulocyte) (CSF3), mRNA	NM_000759	-0.16	-0.1679	0.2299	1.6813	-0.0456	0.4004	0.3159	-0.193	7.0975	7.6662	6.9065	2.8555	2.8358	1.9268
620	superoxide dismutase 2, mitochondrial (SOD2), mRNA	NM_000636	0.9818	1.2894	1.1316	2.5967	0.585	0.2644	0.178	0.197	5.961	5.7591	5.9834	5.5902	5.2476	5.8194
621	interleukin 8 (IL8), mRNA.	NM_000584	-1.7569	-0.8752	-1.0877	3.648	1.2797	-1.2686	-0.6757	0.2738	4.9505	4.715	5.0623	5.0192	5.1654	5.1541
622	small inducible cytokine A5 (RANTES) (SCYA5), mRNA.	NM_002985	-0.2631	-0.4557	0.7521	0.9069	0.7814	1.8413	0.8744	1.7596	2.7478	2.4811	3.292	6.7524	7.4672	8.215

Supplementary Table 7. List of Gateway entry clones (processed type).

FLJ ID	Selected ORF region	Encoded protein	ORF size (number of aa residues)	MW (kDa)	Gateway entry clone ID	Accession number	Protein name	References
FLJ80001	BC028148.1 (386..856)	NP_000585.2 (77..233)	157	17.4	FLJ80001DABN	AB451492	Mature TNF- α	9
FLJ08204	NM_002176.2 (139..636)	NP_002167.1 (22..187)	166	20.0	FLJ08204DABN	AB451491	Mature IFN- β	10
FLJ80003	BC011589.1 (117..743)	NP_065391.1 (26..234)	209	23.7	FLJ80003DABN	AB451493	Mature OSM	11
FLJ80228	BC008678.1 (436..894)	NP_000567.1 (117..269)	153	17.4	FLJ80228DABN	AB451494	Mature IL-1 β	12

All clones are N-types. Amino acid sequences of these entry clones are the same as those of public data.

Supplementary Table 9. Antibodies and conditions of western blotting analysis.

Target (tag)		His	V5	FLAG	GST	IL-1 β	Src-pTyr416	pTyr
Wash	Buffer	-	-	-	-	-	TBS	TBS
	Time	-	-	-	-	-	5 min	5 min
	Temp	-	-	-	-	-	R.T.	R.T.
Blocking	Buffer	1.0% milk in PBST	1.0% milk in PBST	5.0% milk in PBST	5.0% Milk in PBST	5.0% milk in PBST	5.0% milk in TBST	5.0% milk in TBST
	Time	1 hour	1 hour	30 min	1 hour	1 hour	1 hour	1 hour
	Temp	R.T.	R.T.	R.T.	R.T.	R.T.	R.T.	R.T.
Wash	Buffer	-	-	-	-	-	TBST	TBST
	Time	-	-	-	-	-	5 min (3 times)	5 min (3 times)
	Temp	-	-	-	-	-	R.T.	R.T.
1st Ab	Ab	Anti-His rabbit poly Ab (Santa Cruz :Code No.sc-804, Lot No. K201T)	Anti-V5 HRP-Linked mouse mono Ab (Invitrogen : Cat.R961-25)	Anti-Flag M2 mouse mono Ab (SIGMA : Cat. No. F-3165)	Anti-GST HRP-Linked mouse mono Ab (nacalai : Cat. No. 04559-74)	Anti-human IL-1 β rabbit poly Ab (Upstate : Cat. No. #06-220)	Anti-phospho Src Family (P-Tyr-416) rabbit poly Ab (Cell Signaling : Cat. No. #2101)	Anti-pTyr mouse mono Ab (P-Tyr-100) (Cell Signaling : Cat. No. #9411S)
	Dilution	1/20,000	1/20,000	1/16,000	1/5,000	1/4,000	1/200	1/20,000
	Buffer	1.0% milk in PBST	1.0% milk in PBST	5.0% milk in PBST	5.0% Milk in PBST	5.0% Milk in PBST	5.0% BSA in TBST	5.0% BSA in TBST
	Time	1 hour	1 hour	30 min	1 hour	1 hour or O/N	1 hour or O/N	1 hour or O/N
	Temp	R.T.	R.T.	R.T.	R.T.	R.T.	4°C	4°C
Wash	Buffer	PBST	PBST	PBST	PBST	PBST	TBST	TBST
	Time	10 min (2 times)	10 min (2 times)	10 min (2 times)	10 min (2 times)	10 min (2 times)	5 min (3 times)	5 min (3 times)
	Temp	R.T.	R.T.	R.T.	R.T.	R.T.	R.T.	R.T.
2nd Ab	Ab	Anti-Rabbit IgG HRP-Linked Donkey poly Whole Ab (GE healthcare : Cat. No. NA934)	-	Anti-Mouse IgG HRP-Linked Sheep poly Whole Ab (GE healthcare : Cat. No. NA931)	-	Anti-Rabbit IgG HRP-Linked Donkey poly Whole Ab (GE healthcare : Cat. No. NA934)	Anti-Rabbit IgG HRP-Linked Donkey poly Whole Ab (GE healthcare : Cat. No. NA934)	-
	Dilution	1/2,000	-	1/4,000	-	1/2,000	1/2,000	-
	Buffer	1.0% Milk in PBST	-	5.0% milk in PBST	-	5.0% milk in PBST	5.0% milk in PBST	-
	Time	1 hour	-	30 min	-	1 hour	1 hour	-
	Temp	R.T.	-	R.T.	-	R.T.	R.T.	-
Wash	Buffer	PBST	-	PBST	-	PBST	PBST	TBST
	Time	10 min (2 times)	-	10 min (2 times)	-	10 min (2 times)	5 min (3 times)	5 min (3 times)
	Temp	R.T.	-	R.T.	-	R.T.	R.T.	R.T.

Supplementary Methods

1. Construction of Gateway entry clones

1.1 Overview

Gateway entry clones were constructed by cloning PCR-amplified open reading frame (ORF) fragments from resource cDNAs. The utilization of mixed primers makes it possible for ORF fragments, which can be used as templates for both N-type and F-type clones, to be amplified (**Supplementary Fig. 1**). In addition, we designed primers to place both Shine-Dalgarno (SD) sequence (GAAGGAGATA) and Kozak (Kz) sequence (ACC) upstream of the translational initiation codon (ATG) of the ORF. Clone-specific regions in the primers were determined by evaluating the T_m within 15–20 bp in size, either starting from the ATG site for the forward primers or starting from the stop codons for the reverse primers. In order to obtain *attB1* and *attB2* sequences for recombination with the *attP1* and *attP2* sequences of the Gateway donor vector pDONR201 (Invitrogen), *attB* universal primers retaining a 13–16 bp overlap with the gene-specific primers mentioned above were utilized, which enabled us to avoid the synthesis of long primers (**Supplementary Fig. 1**). To construct a set of Gateway entry clones starting from various vectors, three different methods, each with its own set of advantages, were used: the two-step non-selective method, the two-step selective method and the one-step selective method (**Supplementary Table 1**). The two-step non-selective method (**Supplementary Fig. 1a**) is a simple method of eliciting reactions for both N-type and F-type clones in the same well. In the two-step selective method (**Supplementary Fig. 1b**), all the reactions after second PCR must proceed in separate tubes. Therefore, the two-step selective method is somewhat more laborious compared to the two-step non-selective method; however, the efficiency of the two-step selective method in creating N-type and F-type clones is higher than that of the two-step non-selective method. In the one-step selective method (**Supplementary Fig. 1c**), which is a simplified version of the two-step selective method, all the four primers are added at the beginning of the reaction, thereby making it unnecessary to add primers at intermediate stages. If FLJ clones are used as templates, the one-step selective method gives results similar to those of the two-step selective method. On the other hand, for *attB*-harboring clones, the one-step selective method is not adequate and the two-step selective method should be used.

1.2 The two-step non-selective method (Protocol A)

The sequences of the primers used in the first PCR step were as follows: gene-specific forward (Fw) primer, 5'-GGAGATAGAACCATGNNN...NNN (NNN...NNN; gene-specific sequence, 15–20 bases)-3'; gene-specific reverse (Rv) primer, 5'-AGAAAGCTGGGTCWTANNN...NNN (W; A/T: NNN...NNN; gene-specific sequence, 15–20 bases)-3'. The PCR reaction mixture for the

first step (25 μ l) contained 50–100 ng of template DNA, 0.5 unit of Platinum Pfx (Invitrogen), 1x PCR reaction buffer (Invitrogen), 10% (v/v) enhancer solution (Invitrogen), 0.05 mM four dNTPs (Invitrogen), 1.5 mM magnesium sulfate (Invitrogen), 300 nM gene-specific Fw primer and 300 nM gene-specific Rv primer. In the second PCR step, the universal *attB1* and *attB2* primer were used for the addition of the *attB1* and *attB2* sequence, respectively. The sequences of the primers were as follows: universal *attB1* primer, 5'–GGGGACAAGTTTGTACAAAAAAGCAGGCTTCGAAGGA GATAGAACCATG–3'; universal *attB2* primer 1, 5'–GGGGACCACTTTGTAAAGAAAGCTGGG TC–3'. The PCR reaction mixture for the second step (25 μ l) contained 5 μ l of the reaction mixture used in the first step for the template, universal *attB1* primer (1.2 μ M), and universal *attB2* primer 1 (1.2 μ M). The concentrations of the enzyme, buffer and other components were the same as those in the first reaction. The reaction conditions of the PCR for all the construction methods (protocols) are described in **Supplementary Table 1**.

1.3 The two-step selective method (Protocols B and C)

The primers used for the first PCR in this method were the same as those used in Protocol A (**Supplementary Fig. 1**). The Fw primer of the second PCR was the universal *attB1* primer that was used in Protocol A. As the Rv primer for the N-type clones, we used universal *attB2* primer 2 (5'–GGGGACCACTTTGTACAAGAAAGCTGGGTCTTA–3'), and for the F-type clones, universal *attB2* primer 3 (5'–GGGGACCACTTTGTACAAGAAAGCTGGGTCATA–3'). The first-step PCR reaction mixture in Protocol B (25 μ l) contained 50–100 ng of template DNA, 0.5 unit of Platinum Taq High-Fidelity (Invitrogen), PCR reaction buffer (Invitrogen), 10% (v/v) enhancer solution (Invitrogen), 0.2 mM four dNTPs (Invitrogen), 2 mM magnesium sulfate (Invitrogen), 200 nM gene-specific Fw primer and 200 nM gene-specific Rv primer. The second-step PCR reaction mixture (25 μ l) for Protocol B contained 5 μ l of the first-step reaction mixture for the template, universal *attB2* primer 2 (0.8 μ M) for the N-type clones, and universal *attB2* primer 3 (0.8 μ M) for the F-type clones. The concentrations of enzyme, buffer and other components were the same as those in the first reaction in Protocol B. The temperature and cycling conditions were the same as those in Protocol A (**Supplementary Table 1**). The first PCR reaction mixture in Protocol C (25 μ l) contained 50–100 ng of template DNA, 0.5 unit of KOD-Plus- (Toyobo), PCR reaction buffer (Toyobo), 10% (v/v) enhancer solution, 0.2 mM four dNTPs (Toyobo), 1 mM magnesium sulfate (Toyobo), 200 nM gene-specific Fw primer and 200 nM gene-specific Rv primer. The second PCR reaction mixture in Protocol C (25 μ l) contained 5 μ l of the first-step reaction mixture for the template. The types and concentrations of the universal *attB* primers were the same as in Protocol B. The concentrations of enzyme and buffer were the same as those in the first reaction mixture in Protocol C. Temperature condition was the same as for the first step, and the number of cycles was five (**Supplementary Table 1**).

1.4 The one-step selective method (Protocols D, E and F)

The PCR reaction mixture (25 μ l) contained gene-specific Fw or Rv primer (80 nM for D, 52 nM for E and F), universal *attB1* primer (800 nM), universal *attB2* primer 2 (or *attB2* primer 3) (800 nM), 50–100 ng of template DNA, 0.5 unit of enzyme (D, Taq High-Fidelity; E, Pfx; F, KOD-Plus-), PCR reaction buffer (supplied by the manufacturers), 10% (v/v) enhancer solution, 0.2 mM four dNTPs and magnesium sulfate (D, 2 mM; E, 1.5 mM; F, 1 mM). The PCR conditions are described in **Supplementary Table 1**.

1.5 BP reaction

The BP reaction mixture (10 μ l) contained PCR fragments with *attB1* and *attB2* sequences attached to both termini (5 μ l), 150 ng of pDONR201, 2 μ l of BP Clonase (Invitrogen) and BP reaction buffer (Invitrogen). The mixture was incubated at 25°C for 24 h and then digested with proteinase K (1 μ l/1 reaction mix) (Invitrogen) at 37°C for 10 min. *E. coli* (DH5 α) were transformed with 5 μ l of the BP reaction mix, then plated on kanamycin (50 μ g/ml) plates. Four colonies for each reaction were picked up and subjected to sequencing analysis.

1.6 Sequencing

Firstly, both termini of the ORF regions, including a portion of *attL1* and *attL2*, were determined. The clones with no mutation were selected, and the sequencing of the entire ORF region was carried out by the primer walking method¹³. The sequencing reaction was carried out using a BigDye Terminator Cycle Sequencing Kit (Applied Biosystems), and an Applied Biosystems/Hitachi 3700, 3730xl, or 3100 DNA Analyzer was used for the analysis. The sequencing primers were automatically designed with Primer3¹⁴ at an interval of 300–350 nucleotides.

1.7 The N- and C-terminal cloning method

When a single source cDNA is not available, entry clones were made by combination of multiple templates such as DNA fragment(s) produced by RT-PCR or chemical-synthesis, and plasmid DNA(s). Multiple fragments were recombined *in vivo* by the “N- and C-terminal cloning method”¹⁵. The *attB1* added N-terminal fragment that overlaps with 20 bp of C-terminal one and the *attB2* added C-terminal fragment that overlaps with 20 bp of N-terminal one were separately PCR-amplified. After BP reaction DH5 α was transfected and entry clones that harbor entire sequences were obtained.

The success rate of Gateway entry clones that exceed 5 kb in size decreases for conventional methods. The N- and C-terminal cloning method also works well for construction of entry clones that harbor longer ORF (Goshima, N. *et al.* unpublished data).

2. Protein expression in the wheat germ cell-free system

2.1 LR reaction and template preparation for transcription

Gateway destination vectors were linearized with their appropriate restriction endonucleases for background reduction (i.e., pEW-5SG and pEW-5G were linearized with both *Xba*I (Toyobo) and *Pst*I (Nippon Gene), and pEW-N and pEW-5H were linearized with both *Bgl*II (Toyobo) and *Pst*I, in accordance with the manufacturer's instructions. The LR reaction mixture (5 μ l) was incubated at 25°C for 17 h with 2 ng of each Gateway entry clone, 10 ng of linearized destination vector, 1 μ l of LR Clonase enzyme mix (Invitrogen) and LR reaction buffer (Invitrogen). The PCR reaction mixture (50 μ l) contained 0.2 μ M primers, 0.2 mM dNTPs, 2 μ l of LR reaction mixture for supplying the template DNA, 0.63 unit of KOD Dash polymerase (Toyobo) and 10% (v/v) dimethyl sulfoxide. The PCR parameters were as follows: 30 cycles consisting of 20 sec at 94°C for denaturing, 5 sec at 55°C for annealing, and 4 min at 74°C for the extension. All of the reactions were preceded by a primary denaturation step at 95°C for 1 min. The PCR primers were designed to amplify the region from upstream of the SP6 promoter to 17 kb downstream of the *attR2* site. The forward and reverse primers were 5'-ACATACGATTTAGGTGACACT-3', and 5'-GTCAGACCCCGTAGAAAAGA-3', respectively.

2.2 Preparation of mRNAs for protein synthesis

The PCR products were transcribed *in vitro* (50 μ l) at 37°C for 17 h with 80 mM HEPES/KOH (pH 7.8), 16 mM magnesium acetate, 2 mM spermidine, 10 mM DTT, 2.5 mM of each nucleotide triphosphate (ATP, UTP, GTP, CTP), 40 units of ribonuclease inhibitor (Toyobo), and 150 units of SP6 RNA polymerase (Takara). mRNA fractions were used for translation without purification.

2.3 Wheat germ cell-free protein synthesis

A flow diagram of the wheat germ cell-free expression method is illustrated in **Figure 2**. Protein synthesis was conducted by the bilayer method¹⁶. Wheat germ extract was purchased from Toyobo, Cell Free Sciences and ZoeGene. Standard (reducing) buffers contained 24 mM HEPES/KOH (pH 7.8), 1.2 mM ATP, 0.25 mM GTP, 16 mM creatine phosphate, 2 mM dithiothreitol, 0.4 mM spermidine, 0.3 mM each of the 20 amino acids, 2.7 mM magnesium acetate, 100 mM potassium acetate. The upper layer (136.4 μ l) contained the standard buffer. We adjusted the volume of each lower layer for optimal yield. The lower layer (13.6 μ l) contained 7.5 μ l of mRNA from the *in vitro* transcription, 8.6 μ g of creatine kinase, 26 units of ribonuclease inhibitor and 5 μ l of wheat germ extract. The reaction mixture was incubated at 26°C for 17 h. For samples of protein microarrays, the reaction volume was reduced to one-fifth (upper layer, 27.3 μ l; lower layer, 2.7 μ l).

2.4 Comprehensive protein expression and its analysis

For the expression of 13,364 human proteins, pEW-3VH or pEW-3H was used as the destination vector. The levels of expression and solubility were analyzed by western-blotting with anti-V5 or anti-His antibody. For some clones, ^{14}C -Leu (GE Healthcare) or ^{35}S -Met (GE Healthcare) was used, and analysis was carried out on a BAS2000 (Fuji)¹⁶. The specific activities of radio-isotopes (RI) were adjusted to give the same intensity of images as that by staining with CBB. For fluorescence detection, pEW-5SG3Ven was used as the destination vector. The fluorescence was detected using a Typhoon 9200 (GE Healthcare) with SYAG laser (532 nm) excitation and a 526-short pass filter for emission.

2.5 Cell-free translation under the non-reducing condition

Translation buffer (24 mM HEPES/KOH (pH 7.8), 1.2 mM ATP, 0.25 mM GTP, 16 mM creatinine phosphate, 0.45 mg/ml creatine kinase, 0.4 mM spermidine, 0.3 mM of each of the 20 amino acids, 2.5 mM magnesium acetate, 100 mM potassium acetate, 1 mM reduced glutathione, 0.1 mM oxidized glutathione, 0.05% Nonidet P-40 and 0.005% NaN_3) was prepared prior to translation. The upper layer (125 μl) as described above and the lower layer (25 μl) containing 7.5 μl of the mRNA from the *in vitro* transcription, 8.5 μg of creatine kinase, 26 units of ribonuclease inhibitor, 5 μl of wheat germ extract and 3.0 μM protein disulfide isomerase (Takara) were prepared and incubated at 26°C for 24 h.

2.6 Western blotting analysis

The soluble fractions of the synthesized proteins were obtained by centrifugation (19,000 $\times g$, 20 min, 4°C). Three microliter of the total or soluble fraction were mixed with NuPAGE LDS sample buffer (Invitrogen) and 2-mercapt ethanol (2-ME), and were denatured at 70°C for 10 min. The denatured samples were loaded on NuPAGE 4–12% Bis-Tris gels (Invitrogen), and SDS-PAGE was carried out using MOPS buffer (Invitrogen). After electrophoresis, the proteins were electrophoretically transferred to PVDF membranes (Bio-Rad Laboratories) using the NuPAGE Blotting Module (Invitrogen). For the detection of V5-tagged and GST-tagged proteins, the PVDF membrane was incubated with 1.0% and 5% (w/v) skim milk, respectively, in PBST [140 mM NaCl, 20 mM Na_2HPO_4 , 2.7 mM KCl, 1.5 mM KH_2PO_4 , 0.1% (v/v) Tween 20] at 26°C for 1 h. The conditions of the antibody reactions are summarized in **Supplementary Table 9**. The signal was detected using the ECL Plus Western blotting detection system (GE Healthcare) in accordance with the manufacturer's instructions, and measured using Fluor-S MultiImager Max (Bio-Rad Laboratories).

3. Evaluation of cytokine activity

3.1 Preparation of mRNAs for protein synthesis

For *in vitro* cytokine synthesis, linearized pEW-N, pEW-5H and pEW-5G were used as Gateway destination vectors. All the procedures for the LR reaction, PCR and *in vitro* transcription are described in sections 2.1–2.3.

3.2 Preparation of mature IL-1 β

The total fraction of His-FLAG-IL-1 β was mixed with Ni-NTA agarose gel beads (Qiagen GmbH) at 4°C for 17 h, and then the beads were washed in accordance with the manufacturer's instructions. Mature IL-1 β was produced from His-FLAG-IL-1 β by proteolytic cleavage using Recombinant Enterokinase Kits (Merck). After the cleavage reaction, the enterokinase was eliminated using the Ekapture agarose from the Recombinant Enterokinase Kits (Merck) in accordance with the manufacturer's instructions.

3.3 Analysis of S-S bond formation

Three microliter samples from the soluble fractions separated by centrifugation at 19,000 $\times g$ for 20 min were used for the analysis of S-S bond formation. The samples were subjected to SDS-PAGE with denaturing-nonreductive SDS sample buffer (without 2-ME). After electrophoresis, the proteins were electrophoretically transferred to PVDF membranes (Bio-Rad Laboratories). The membranes were consecutively incubated with 5% milk-PBST, and then the proteins were detected by Western-blotting using anti-FLAG antibody. Since the presence of S-S bonds tightens the conformation of the protein molecule, the difference in electrophoretic mobility designates the formation of intra/inter-molecular S-S bonds.

3.4 Effects of the cytokines on endothelial cells

HCAECs were purchased from Cambrex Corp. and cultured in accordance with the previously published method¹⁷. Briefly, HCAECs were maintained at a near-confluent density for 24 h before the exposure experiments; the medium was then replaced with fresh medium, and the cells were incubated for another 24 h. At the fully confluent density, the HCAECs were exposed to the following cytokines and incubated for another 24 h: FLAG-TNF- α (10 nM), FLAG-IFN- β (1.3 nM), FLAG-OSM (2.7 nM), TNF- α (R&D Systems) (0.3 nM or 10 nM), IFN- β (PeproTech, Inc.) (0.03 nM or 1.3 nM), OSM (R&D Systems) (1.1 nM or 2.7 nM), mature IL-1 β (1.5 nM), His-FLAG-IL-1 β (0.28 nM), GST-FLAG-IL-1 β (0.27 nM) and IL-1 β (R&D Systems) (1.1 nM). The cells were exposed to two different concentrations, one slightly above the median effective dose (ED₅₀) specified by the manufacturers and the other excessively above the ED₅₀.

3.5 The DNA microarray

The cells were harvested 24 h after exposure to the cytokines using TRIzol Reagent (Invitrogen).

The cell lysates were subjected to total RNA extraction in accordance with the manufacturer's instructions. Subsequently, the total RNA was subjected to polyA(+) RNA isolation using a MicroPoly(A) Purist Kit (Ambion, Inc.) in accordance with the manufacturer's instructions. Eventually, the polyA(+) RNA was divided into aliquots of 2 µg, precipitated with ethanol, and stored at −20°C.

A set of synthetic polynucleotides (80-mers) representing 22,512 species of human transcript sequences that mostly originated from the RefSeq database in NCBI was purchased (MicroDiagnostic) and printed on a glass slide (coated glass slide for the microarray, type I; Matsunami Glass Ind., Ltd.) using a custom-made arrayer (designated as the 22K array)^{18,19}. Two micrograms of poly(A)+ RNA were labeled with SuperScript II (Invitrogen) and cyanine 5-deoxyuridine triphosphate (dUTP) (Perkin-Elmer) for each HCAEC sample or cyanine 3-dUTP (Perkin-Elmer) for a human common reference RNA that was prepared by mixing equal amounts of poly(A)+ RNA extracted from 22 cell lines (A431, A549, AKI, HBL-100, HeLa, HepG2, HL60, IMR-32, Jurkat, K562, KP4, MKN7, NK-92, Raji, RD, Saos-2, SK-N-MC, SW-13, T24, U251, U937 and Y79). Hybridization and subsequent washes of the arrays were performed with a Labeling and Hybridization Kit (MicroDiagnostic). The hybridization signals were measured with a GenePix 4000A scanner (Axon Instruments) and then processed into primary expression ratios (ratios of the cyanine 5 intensity of each sample to the cyanine 3 intensity of the human common reference RNA) by means of the GenePix Pro 3.0 software (Axon Instruments). Normalization was performed for each ratio by multiplying the normalization factors calculated by GenePix Pro 3.0. The primary expression ratios were converted into log₂ values (designated as log ratios).

Data processing and subsequent hierarchical clustering analysis were conducted using an MDI gene expression analysis software package (MicroDiagnostic). To compare the cytokine-treated samples against the mock-treated samples (negative controls) for each cytokine, the log ratios obtained for the mock-treated samples were subtracted from the log ratios obtained for each cytokine-treated sample (designated as relative log ratios). Next, the genes whose relative log ratios in the two independent samples for each cytokine were greater than 1 or smaller than −1 were extracted. In order to obtain data on these extracted genes, they were processed into a matrix (rows: genes; columns: samples) and subjected to two-dimensional hierarchical clustering analysis.

Supplementary Note

Comparison of phosphatase activity of human CDC25B expressed in wheat germ cell-free and *E. coli* systems.

Honda, R. *et al.* published that CDC25B (20 µg/ml) expressed in *E. coli* has the activity of about 1 A₄₁₀ unit/ml when incubated at 37°C for 30 min in the reaction buffer containing p-nitro-phenyl-phosphate (pNPP) as a substrate²⁰. CDC25B (7.94 µg/ml) expressed in a wheat germ cell-free system by us gave the activity of about 0.143 A₄₁₀ unit/ml at the same condition, indicating 36% of the activity obtained by Honda, R. *et al.*²⁰

Possible protein tyrosine kinase activity detected in STK16.

Berson, A.E. *et al.* reported that they purified GST-fused STK16 from GST-STK16 baculovirus infected Sf9 cells²¹. And they showed a faint phosphotyrosine spot derived from the purified STK16 protein. Their data in conjunction with our data might indicate that STK16 could be a Tyr/Ser/Thr kinase, albeit further fine analysis is needed to reach definite conclusion.

References

1. Sawasaki, T., Ogasawara, T., Morishita, R. & Endo, Y. A cell-free protein synthesis system for high-throughput proteomics. *Proc. Natl Acad. Sci. USA* **99**, 14652-14657 (2002).
2. Nagai, T. *et al.* A variant of yellow fluorescent protein with fast and efficient maturation for cell-biological applications. *Nat. Biotechnol.* **20**, 87-90 (2002).
3. Cui, L., Yu, W.P., DeAizpurua, H.J., Schmidli, R.S. & Pallen, C.J. Cloning and characterization of islet cell antigen-related protein-tyrosine phosphatase (PTP), a novel receptor-like PTP and autoantigen in insulin-dependent diabetes. *J. Biol. Chem.* **271**, 24817-24823 (1996).
4. Wishart, M.J., Denu, J.M., Williams, J.A. & Dixon, J.E. A single mutation converts a novel phosphotyrosine binding domain into a dual-specificity phosphatase. *J. Biol. Chem.* **270**, 26782-26785 (1995).
5. Taylor, G.S., Maehama, T. & Dixon, J.E. Inaugural article: myotubularin, a protein tyrosine phosphatase mutated in myotubular myopathy, dephosphorylates the lipid second messenger, phosphatidylinositol 3-phosphate. *Proc. Natl Acad. Sci. USA* **97**, 8910-8915 (2000).
6. Hafizi, S., Ibraimi, F. & Dahlback, B. C1-TEN is a negative regulator of the Akt/PKB signal transduction pathway and inhibits cell survival, proliferation, and migration. *Faseb. J.* **19**, 971-973 (2005).
7. Wishart, M.J. & Dixon, J.E. PTEN and myotubularin phosphatases: from 3-phosphoinositide dephosphorylation to disease. *Trends Cell Biol.* **12**, 579-585 (2002).
8. Tosch, V. *et al.* A novel PtdIns3P and PtdIns(3,5)P₂ phosphatase with an inactivating variant in centronuclear myopathy. *Hum. Mol. Genet.* **15**, 3098-3106 (2006).
9. Pennica, D. *et al.* Human tumour necrosis factor: precursor structure, expression and homology to lymphotoxin. *Nature* **312**, 724-729 (1984).
10. Gray, P.W. & Goeddel, D.V. Structure of the human immune interferon gene. *Nature* **298**, 859-863 (1982).
11. Linsley, P.S., Kallestad, J., Ochs, V. & Neubauer, M. Cleavage of a hydrophilic C-terminal domain increases growth-inhibitory activity of oncostatin M. *Mol. Cell Biol.* **10**, 1882-1890 (1990).
12. March, C.J. *et al.* Cloning, sequence and expression of two distinct human interleukin-1 complementary DNAs. *Nature* **315**, 641-647 (1985).
13. Otsuki, T. *et al.* Signal sequence and keyword trap *in silico* for selection of full-length human cDNAs encoding secretion or membrane proteins from oligo-capped cDNA libraries. *DNA Res.* **12**, 117-126 (2005).
14. Rozen, S. & Skaletsky, H. Primer3 on the WWW for general users and for biologist programmers. *Methods Mol. Biol.* **132**, 365-386 (2000).

15. Suzuki, Y. *et al.* A novel high-throughput (HTP) cloning strategy for site-directed designed chimeragenesis and mutation using the Gateway cloning system. *Nucleic Acids Res.* **33**, e109 (2005).
16. Sawasaki, T. *et al.* A bilayer cell-free protein synthesis system for high-throughput screening of gene products. *FEBS Lett.* **514**, 102-105 (2002).
17. Miura, A. *et al.* Differential responses of normal human coronary artery endothelial cells against multiple cytokines comparatively assessed by gene expression profiles. *FEBS Lett.* **580**, 6871-6879 (2006).
18. Ito, E. *et al.* A tetraspanin-family protein, T-cell acute lymphoblastic leukemia-associated antigen 1, is induced by the Ewing's sarcoma-Wilms' tumor 1 fusion protein of desmoplastic small round-cell tumor. *Am. J. Pathol.* **163**, 2165-2172 (2003).
19. Sakamoto, A. *et al.* Influence of inhalation anesthesia assessed by comprehensive gene expression profiling. *Gene* **356**, 39-48 (2005).
20. Honda, R., Ohba, Y., Nagata, A., Okayama, H. & Yasuda, H. Dephosphorylation of human p34^{cdc2} kinase on both Thr-14 and Tyr-15 by human cdc25B phosphatase. *FEBS Lett.* **318**, 331-334 (1993).
21. Berson, A.E. *et al.* Identification and characterization of a myristylated and palmitylated serine/threonine protein kinase. *Biochem. Biophys. Res. Comm.* **259**, 533-538 (1999).